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

Jan 10, 2017 – 11:19 AM EST

PDB ID	:	5TJ6
EMDB ID:	:	EMD-8410
Title	:	Ca2+ bound aplysia Slo1
Authors	:	MacKinnon, R.; Tao, X.; Hite, R.K.
Deposited on	:	2016-10-03
Resolution	:	3.40 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
http://wwpdb.org/validation/2016/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

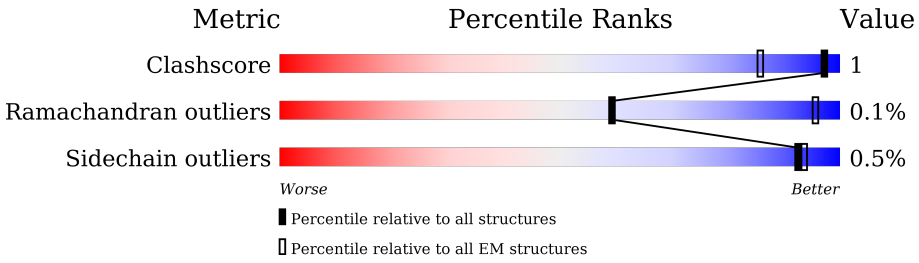
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

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 3.40 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
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

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	1070	81% · 17%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7212 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 High conductance calcium-activated potassium channel.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	890	7041	4567	1157	1275	42	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	THR	conflict	UNP Q5QJC5

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
			Total	K	
2	A	5	5	5	0

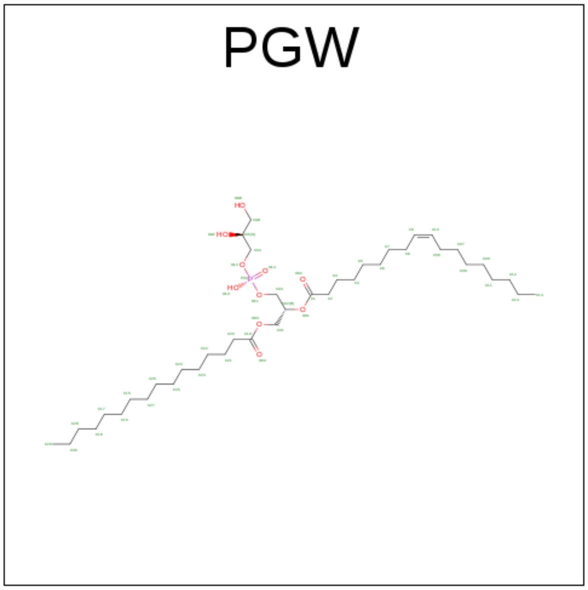
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
3	A	1	1	1	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
			Total	Ca	
4	A	2	2	2	0

- Molecule 5 is (1R)-2-{[(S)-{[(2S)-2,3-dihydroxypropyl]oxy}(hydroxy)phosphoryl]oxy}-1-[(hexadecanoyloxy)methyl]ethyl (9Z)-octadec-9-enoate (three-letter code: PGW) (formula: $C_{40}H_{77}O_{10}P$).



Mol	Chain	Residues	Atoms	AltConf
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0
5	A	1	Total C O P 163 142 18 3	0

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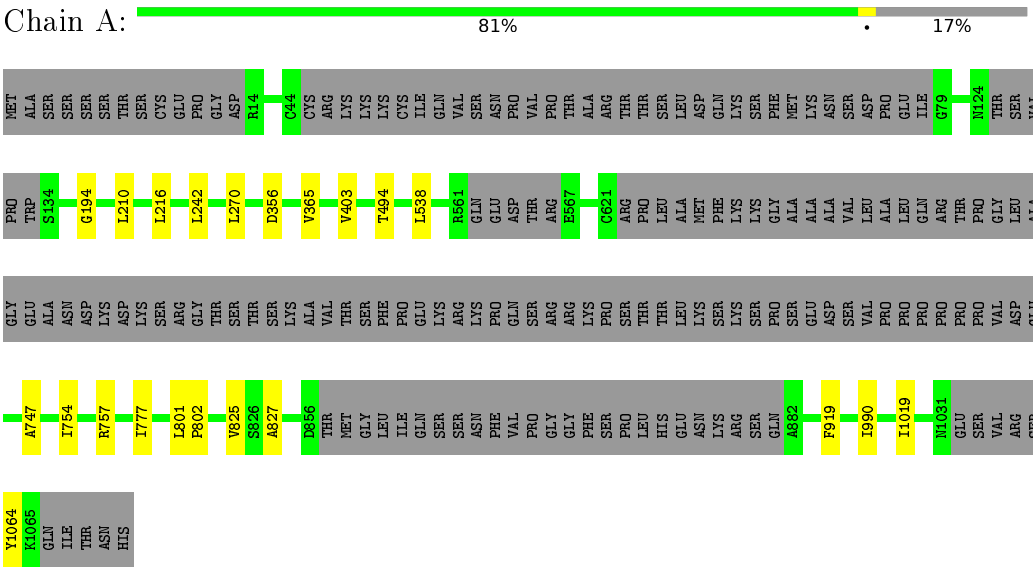
Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	O	P	0
			163	142	18	3	

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: High conductance calcium-activated potassium channel

Chain A:



4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C	Depositor
Number of particles used	115000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	Not provided	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	Not provided	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PGW, MG, CA, K

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	0.36	0/7208	0.51	0/9789

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	7041	0	6949	13	0
2	A	5	0	0	0	0
3	A	1	0	0	0	0
4	A	2	0	0	0	0
5	A	163	0	215	0	0
All	All	7212	0	7164	13	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 1.

All (13) 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:754:ILE:HD11	1:A:827:ALA:HB2	1.74	0.69
1:A:1019:ILE:HG23	1:A:1061:VAL:HG13	1.80	0.63
1:A:990:ILE:HD12	1:A:1061:VAL:HG21	1.87	0.56
1:A:494:THR:HG21	1:A:919:PHE:O	2.07	0.54
1:A:365:VAL:HG11	1:A:403:VAL:HG13	1.92	0.51
1:A:737:LEU:HD13	1:A:777:ILE:HD11	1.91	0.51
1:A:801:LEU:HD12	1:A:802:PRO:HD2	1.97	0.45
1:A:210:LEU:HB3	1:A:216:LEU:HD13	1.99	0.44
1:A:737:LEU:HD13	1:A:777:ILE:CD1	2.49	0.42
1:A:754:ILE:HD13	1:A:825:VAL:HG11	2.02	0.41
1:A:494:THR:HG22	1:A:919:PHE:CZ	2.55	0.41
1:A:242:LEU:HD11	1:A:270:LEU:HD21	2.03	0.41
1:A:747:ALA:HB2	1:A:827:ALA:HB3	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	876/1070 (82%)	832 (95%)	43 (5%)	1 (0%)	56 89

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	194	GLY

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	759/936 (81%)	755 (100%)	4 (0%)	92 96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	356	ASP
1	A	538	LEU
1	A	757	ARG
1	A	1064	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	585	GLN
1	A	781	ASN
1	A	942	ASN

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)

Of 23 ligands modelled in this entry, 8 are monoatomic - leaving 15 for Mogul analysis.

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	$\#\|Z\| > 2$
5	PGW	A	1109	-	8,8,50	0.23	0	7,7,56	0.51	0
5	PGW	A	1110	-	8,8,50	0.23	0	7,7,56	0.53	0
5	PGW	A	1111	-	8,8,50	0.24	0	7,7,56	0.51	0
5	PGW	A	1112	-	8,8,50	0.23	0	7,7,56	0.53	0
5	PGW	A	1113	-	8,8,50	0.24	0	7,7,56	0.50	0
5	PGW	A	1114	-	18,18,50	1.39	2 (11%)	20,21,56	1.24	2 (10%)
5	PGW	A	1115	-	6,6,50	0.27	0	5,5,56	0.43	0
5	PGW	A	1116	-	11,11,50	0.28	0	10,10,56	0.54	0
5	PGW	A	1117	-	18,18,50	1.20	1 (5%)	20,21,56	1.19	2 (10%)
5	PGW	A	1118	-	6,6,50	0.26	0	5,5,56	0.45	0
5	PGW	A	1119	-	11,11,50	0.27	0	10,10,56	0.56	0
5	PGW	A	1120	-	18,18,50	1.20	1 (5%)	20,21,56	1.15	2 (10%)
5	PGW	A	1121	-	6,6,50	0.27	0	5,5,56	0.44	0
5	PGW	A	1122	-	8,8,50	0.28	0	7,7,56	0.45	0
5	PGW	A	1123	-	6,6,50	0.26	0	5,5,56	0.45	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
5	PGW	A	1109	-	-	0/6/6/55	0/0/0/0
5	PGW	A	1110	-	-	0/6/6/55	0/0/0/0
5	PGW	A	1111	-	-	0/6/6/55	0/0/0/0
5	PGW	A	1112	-	-	0/6/6/55	0/0/0/0
5	PGW	A	1113	-	-	0/6/6/55	0/0/0/0
5	PGW	A	1114	-	-	0/17/17/55	0/0/0/0
5	PGW	A	1115	-	-	0/4/4/55	0/0/0/0
5	PGW	A	1116	-	-	0/9/9/55	0/0/0/0
5	PGW	A	1117	-	-	0/17/17/55	0/0/0/0
5	PGW	A	1118	-	-	0/4/4/55	0/0/0/0
5	PGW	A	1119	-	-	0/9/9/55	0/0/0/0
5	PGW	A	1120	-	-	0/17/17/55	0/0/0/0
5	PGW	A	1121	-	-	0/4/4/55	0/0/0/0
5	PGW	A	1122	-	-	0/6/6/55	0/0/0/0
5	PGW	A	1123	-	-	0/4/4/55	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1114	PGW	P-O14	3.38	1.61	1.50
5	A	1117	PGW	O01-C1	4.27	1.46	1.33
5	A	1120	PGW	O01-C1	4.28	1.46	1.33
5	A	1114	PGW	O01-C1	4.33	1.46	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	1114	PGW	O01-C1-C2	2.63	119.93	111.85
5	A	1120	PGW	O01-C1-C2	2.64	119.98	111.85
5	A	1117	PGW	O13-P-O14	2.67	119.33	110.63
5	A	1120	PGW	O13-P-O14	2.78	119.70	110.63
5	A	1117	PGW	O01-C1-C2	2.96	120.95	111.85
5	A	1114	PGW	O12-P-O13	3.39	119.90	107.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.