



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Aug 16, 2018 – 12:53 PM EDT

PDB ID : 6EBM
EMDB ID: : EMD-9026
Title : The voltage-activated Kv1.2-2.1 paddle chimera channel in lipid nanodiscs, transmembrane domain of subunit alpha
Authors : Matthies, D.; Bae, C.; Fox, T.; Bartesaghi, A.; Subramaniam, S.; Swartz, K.J.
Deposited on : 2018-08-06
Resolution : 4.00 Å(reported)
Based on PDB ID : 2R9R

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

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ 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-20031172

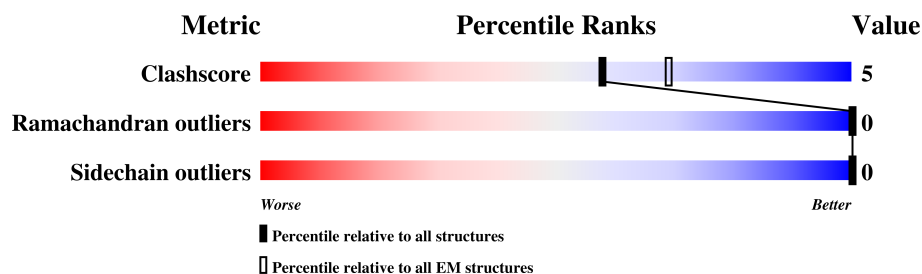
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY





The reported resolution of this entry is 4.00 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain		
1	B	513		52%	6% 42%
1	D	513		49%	9% 42%
1	F	513		50%	8% 42%
1	H	513		52%	6% 42%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8532 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 Potassium voltage-gated channel subfamily A member 2, Potassium voltage-gated channel subfamily B member 2 chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	298	Total	C	N	O	S	0	0
			2133	1409	348	367	9		
1	D	298	Total	C	N	O	S	0	0
			2133	1409	348	367	9		
1	F	298	Total	C	N	O	S	0	0
			2133	1409	348	367	9		
1	H	298	Total	C	N	O	S	0	0
			2133	1409	348	367	9		

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	MET	-	expression tag	UNP P63142
B	-16	ALA	-	expression tag	UNP P63142
B	-15	HIS	-	expression tag	UNP P63142
B	-14	HIS	-	expression tag	UNP P63142
B	-13	HIS	-	expression tag	UNP P63142
B	-12	HIS	-	expression tag	UNP P63142
B	-11	HIS	-	expression tag	UNP P63142
B	-10	HIS	-	expression tag	UNP P63142
B	-9	HIS	-	expression tag	UNP P63142
B	-8	HIS	-	expression tag	UNP P63142
B	-7	GLU	-	expression tag	UNP P63142
B	-6	ASN	-	expression tag	UNP P63142
B	-5	LEU	-	expression tag	UNP P63142
B	-4	TYR	-	expression tag	UNP P63142
B	-3	PHE	-	expression tag	UNP P63142
B	-2	GLN	-	expression tag	UNP P63142
B	-1	GLY	-	expression tag	UNP P63142
B	0	SER	-	expression tag	UNP P63142
B	15	HIS	LEU	conflict	UNP P63142
B	207	GLN	ASN	conflict	UNP P63142
D	-17	MET	-	expression tag	UNP P63142

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	ALA	-	expression tag	UNP P63142
D	-15	HIS	-	expression tag	UNP P63142
D	-14	HIS	-	expression tag	UNP P63142
D	-13	HIS	-	expression tag	UNP P63142
D	-12	HIS	-	expression tag	UNP P63142
D	-11	HIS	-	expression tag	UNP P63142
D	-10	HIS	-	expression tag	UNP P63142
D	-9	HIS	-	expression tag	UNP P63142
D	-8	HIS	-	expression tag	UNP P63142
D	-7	GLU	-	expression tag	UNP P63142
D	-6	ASN	-	expression tag	UNP P63142
D	-5	LEU	-	expression tag	UNP P63142
D	-4	TYR	-	expression tag	UNP P63142
D	-3	PHE	-	expression tag	UNP P63142
D	-2	GLN	-	expression tag	UNP P63142
D	-1	GLY	-	expression tag	UNP P63142
D	0	SER	-	expression tag	UNP P63142
D	15	HIS	LEU	conflict	UNP P63142
D	207	GLN	ASN	conflict	UNP P63142
F	-17	MET	-	expression tag	UNP P63142
F	-16	ALA	-	expression tag	UNP P63142
F	-15	HIS	-	expression tag	UNP P63142
F	-14	HIS	-	expression tag	UNP P63142
F	-13	HIS	-	expression tag	UNP P63142
F	-12	HIS	-	expression tag	UNP P63142
F	-11	HIS	-	expression tag	UNP P63142
F	-10	HIS	-	expression tag	UNP P63142
F	-9	HIS	-	expression tag	UNP P63142
F	-8	HIS	-	expression tag	UNP P63142
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F	-3	PHE	-	expression tag	UNP P63142
F	-2	GLN	-	expression tag	UNP P63142
F	-1	GLY	-	expression tag	UNP P63142
F	0	SER	-	expression tag	UNP P63142
F	15	HIS	LEU	conflict	UNP P63142
F	207	GLN	ASN	conflict	UNP P63142
H	-17	MET	-	expression tag	UNP P63142
H	-16	ALA	-	expression tag	UNP P63142
H	-15	HIS	-	expression tag	UNP P63142

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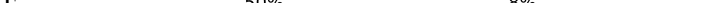
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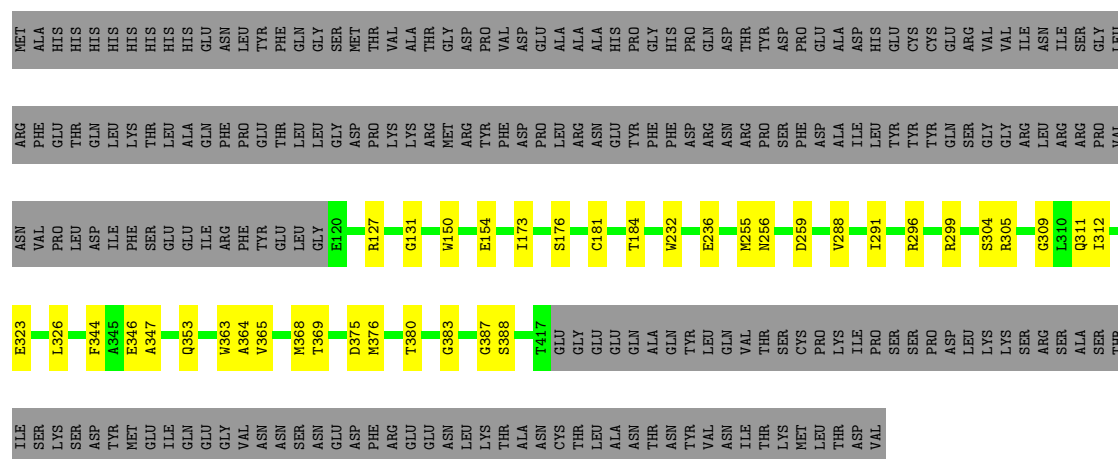
Chain	Residue	Modelled	Actual	Comment	Reference
H	-14	HIS	-	expression tag	UNP P63142
H	-13	HIS	-	expression tag	UNP P63142
H	-12	HIS	-	expression tag	UNP P63142
H	-11	HIS	-	expression tag	UNP P63142
H	-10	HIS	-	expression tag	UNP P63142
H	-9	HIS	-	expression tag	UNP P63142
H	-8	HIS	-	expression tag	UNP P63142
H	-7	GLU	-	expression tag	UNP P63142
H	-6	ASN	-	expression tag	UNP P63142
H	-5	LEU	-	expression tag	UNP P63142
H	-4	TYR	-	expression tag	UNP P63142
H	-3	PHE	-	expression tag	UNP P63142
H	-2	GLN	-	expression tag	UNP P63142
H	-1	GLY	-	expression tag	UNP P63142
H	0	SER	-	expression tag	UNP P63142
H	15	HIS	LEU	conflict	UNP P63142
H	207	GLN	ASN	conflict	UNP P63142

- Molecule 1: Potassium voltage-gated channel subfamily A member 2, Potassium voltage-gated channel subfamily B member 2 chimera

- Molecule 1: Potassium voltage-gated channel subfamily A member 2, Potassium voltage-gated channel subfamily B member 2 chimera

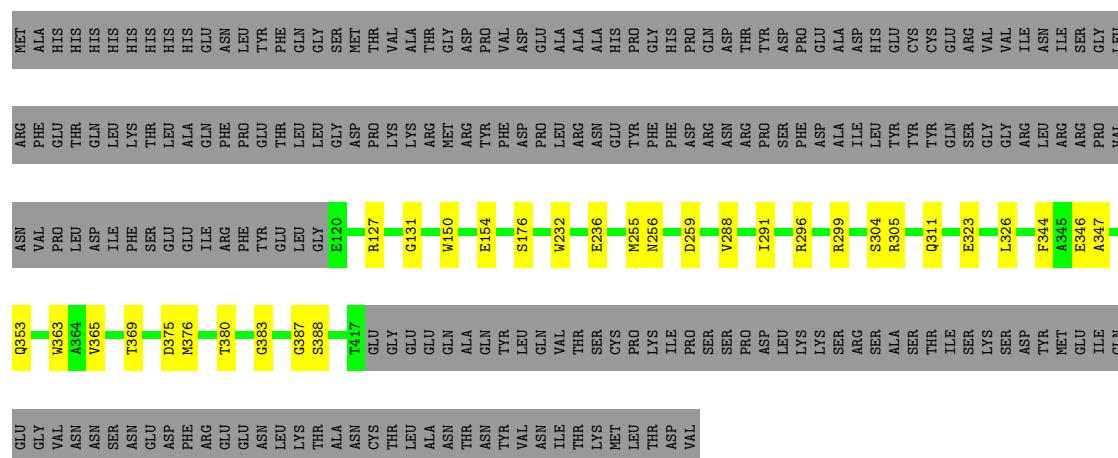
- Molecule 1: Potassium voltage-gated channel subfamily A member 2, Potassium voltage-gated channel subfamily B member 2 chimera

Chain F:  50% 8% 42%



- Molecule 1: Potassium voltage-gated channel subfamily A member 2, Potassium voltage-gated channel subfamily B member 2 chimera

Chain H: 52% 6% 42%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	65745	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	29000	Depositor
Image detector	GATAN K2 SUMMIT (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	B	0.56	0/2185	0.59	0/2982
1	D	0.55	0/2185	0.59	0/2982
1	F	0.55	0/2185	0.59	0/2982
1	H	0.55	0/2185	0.59	0/2982
All	All	0.55	0/8740	0.59	0/11928

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	B	2133	0	1960	19	0
1	D	2133	0	1960	28	0
1	F	2133	0	1960	24	0
1	H	2133	0	1960	20	0
All	All	8532	0	7840	88	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 5.

The worst 5 of 88 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:D:375:ASP:OD1	1:D:376:MET:N	2.05	0.89
1:B:375:ASP:OD1	1:B:376:MET:N	2.05	0.89
1:F:375:ASP:OD1	1:F:376:MET:N	2.05	0.88
1:H:375:ASP:OD1	1:H:376:MET:N	2.05	0.88
1:D:296:ARG:HB3	1:D:299:ARG:HH21	1.57	0.69

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	B	296/513 (58%)	281 (95%)	15 (5%)	0	100	100
1	D	296/513 (58%)	281 (95%)	15 (5%)	0	100	100
1	F	296/513 (58%)	279 (94%)	17 (6%)	0	100	100
1	H	296/513 (58%)	279 (94%)	17 (6%)	0	100	100
All	All	1184/2052 (58%)	1120 (95%)	64 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	B	193/459 (42%)	193 (100%)	0	100	100
1	D	193/459 (42%)	193 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	193/459 (42%)	193 (100%)	0	100	100
1	H	193/459 (42%)	193 (100%)	0	100	100
All	All	772/1836 (42%)	772 (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. There are no such sidechains identified.

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.