

wwPDB X-ray Structure Validation Summary Report (i)

Jan 6, 2022 – 04:28 pm GMT

PDB ID : 7ADI

Title: KirBac3.1 W46R: role of a highly conserved tryptophan at the membrane-

water interface of Kir channel

Authors: Venien-Bryan, C.; Fagnen, C.; De Zorzi, R.; Bannwarth, L.; Oubella, I.; Haouz,

A.

Deposited on : 2020-09-15

Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity: 4.02b-467 Xtriage (Phenix): 1.13

EDS: 2.24

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0267

CCP4 : 7.1.010 (Gargrove)
oteins) : Engh & Huber (2007)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

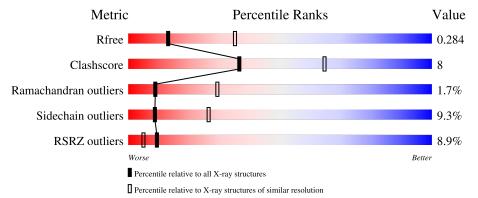
Validation Pipeline (wwPDB-VP) : 2.24

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	Similar resolution $(\# \text{Entries, resolution range}(\text{\AA}))$
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain				
1	A	301	71%	19%	• 8%		
1	В	301	64%	22%	•• 12%		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	K	A	1001	-	-	-	X



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4303 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Inward rectifier potassium channel Kirbac3.1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	276	Total 2194	C 1403	N 390	O 391	S 10	0	3	0
1	В	265	Total 2082	C 1337	N 368	O 367	S 10	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	ARG	TRP	engineered mutation	UNP D9N164
A	296	HIS	-	expression tag	UNP D9N164
A	297	HIS	-	expression tag	UNP D9N164
A	298	HIS	-	expression tag	UNP D9N164
A	299	HIS	-	expression tag	UNP D9N164
A	300	HIS	-	expression tag	UNP D9N164
A	301	HIS	-	expression tag	UNP D9N164
В	46	ARG	TRP	engineered mutation	UNP D9N164
В	296	HIS	-	expression tag	UNP D9N164
В	297	HIS	-	expression tag	UNP D9N164
В	298	HIS	-	expression tag	UNP D9N164
В	299	HIS	-	expression tag	UNP D9N164
В	300	HIS	-	expression tag	UNP D9N164
В	301	HIS	-	expression tag	UNP D9N164

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total K 3 3	0	0

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



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

• Molecule 4 is water.

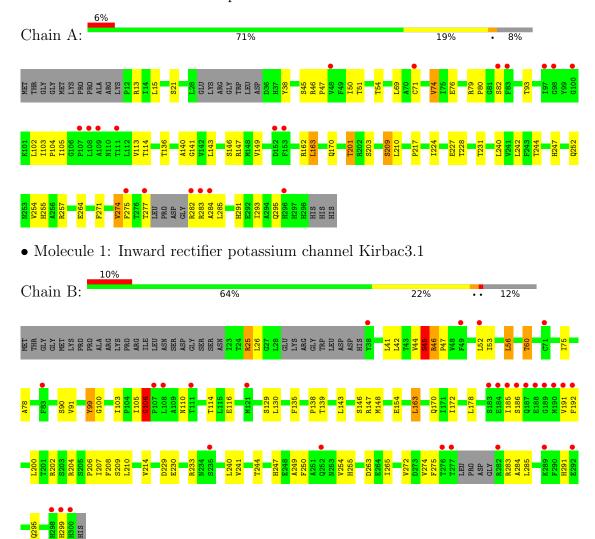
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	8	Total O 8 8	0	0
4	В	15	Total O 15 15	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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: Inward rectifier potassium channel Kirbac3.1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	106.77Å 113.98Å 89.18Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.02 - 2.80	Depositor
resolution (A)	48.02 - 2.80	EDS
% Data completeness	99.7 (48.02-2.80)	Depositor
(in resolution range)	99.7 (48.02-2.80)	EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) > 1$	1.56 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0266, BUSTER	Depositor
P. P.	0.222 , 0.287	Depositor
R, R_{free}	0.225 , 0.284	DCC
R_{free} test set	1372 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	89.3	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	4303	wwPDB-VP
Average B, all atoms (Å ²)	105.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.22% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: MG, 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		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.69	0/2249	0.89	0/3054	
1	В	0.71	0/2134	0.89	0/2897	
All	All	0.70	0/4383	0.89	0/5951	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	В	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	141	GLY	Peptide
1	В	106	GLY	Peptide

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	2194	0	2148	41	0
1	В	2082	0	2044	36	0
2	A	3	0	0	0	0
3	A	1	0	0	0	0
4	A	8	0	0	0	0
4	В	15	0	0	0	0
All	All	4303	0	4192	67	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 8.

The worst 5 of 67 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$	
1:A:114:THR:HG22	1:B:91:VAL:HG11	1.58	0.84	
1:B:244:THR:HG22	1:B:255:HIS:CD2	2.18	0.78	
1:A:257:ARG:NH2	1:B:170:GLN:OE1	2.18	0.77	
1:B:56:LEU:O	1:B:60:THR:OG1	2.03	0.76	
1:A:170:GLN:HE21	1:A:209:SER:HB3	1.55	0.71	

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 X-ray entries followed by that with respect to entries of similar resolution.

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	273/301 (91%)	246 (90%)	25 (9%)	2 (1%)	22 53
1	В	259/301~(86%)	228 (88%)	24 (9%)	7 (3%)	5 17
All	All	532/602 (88%)	474 (89%)	49 (9%)	9 (2%)	9 29

5 of 9 Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	38	TYR
1	В	45	SER
1	В	106	GLY
1	A	283	ARG
1	В	99	TYR

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 X-ray entries followed by that with respect to entries of similar resolution.

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	$236/256 \ (92\%)$	222 (94%)	14 (6%)	19 49		
1	В	221/256~(86%)	193 (87%)	28 (13%)	4 14		
All	All	457/512 (89%)	415 (91%)	42 (9%)	9 27		

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	186	SER
1	В	240	LEU
1	В	192	PHE
1	В	209	SER
1	В	263	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	61	ASN
1	В	255	HIS
1	В	296	HIS
1	В	291	HIS
1	A	221	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ>2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ $>$	# RSRZ > 2		$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	276/301 (91%)	0.32	19 (6%) 16	10	56, 100, 159, 193	0
1	В	265/301~(88%)	0.53	29 (10%) 5	3	58, 107, 167, 181	0
All	All	541/602 (89%)	0.42	48 (8%) 9	5	56, 103, 164, 193	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	186	SER	7.9
1	В	108	LEU	5.8
1	В	183	SER	5.5
1	В	188	GLU	5.3
1	В	187	GLN	5.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
2	K	A	1001	1/1	0.58	0.63	110,110,110,110	1
3	MG	A	1004	1/1	0.78	0.11	37,37,37,37	1
2	K	A	1003	1/1	0.86	0.40	106,106,106,106	1
2	K	A	1002	1/1	0.94	0.29	78,78,78,78	1

6.5 Other polymers (i)

There are no such residues in this entry.

