



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2018 – 04:37 pm GMT

PDB ID : 2A79  
Title : Mammalian Shaker Kv1.2 potassium channel- beta subunit complex  
Authors : Long, S.B.; Campbell, E.B.; MacKinnon, R.  
Deposited on : 2005-07-05  
Resolution : 2.90 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](mailto: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 ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

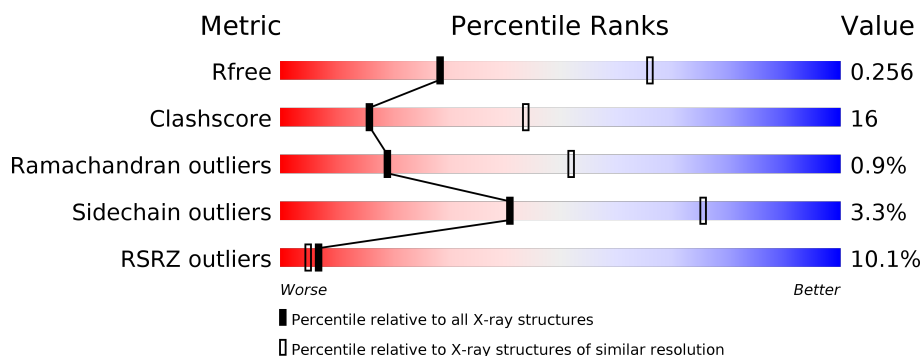
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	111664	1716 (2.90-2.90)
Clashscore	122126	1924 (2.90-2.90)
Ramachandran outliers	120053	1884 (2.90-2.90)
Sidechain outliers	120020	1886 (2.90-2.90)
RSRZ outliers	108989	1669 (2.90-2.90)

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 on the lower 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  $\leq 5\%$ . 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	333	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>%</span> <span>67%</span> <span>30%</span> <span>..</span> </div> </div>
2	B	499	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 11%, orange 1%, yellow 16%, green 72%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>11%</span> <span>35%</span> <span>16%</span> <span>48%</span> <span>.</span> </div> </div>
3	C	52	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 96%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>96%</span> <span>.</span> </div> </div>
4	D	21	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 90%, yellow 10%);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> <span>90%</span> <span>10%</span> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	K	B	505	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4997 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 Voltage-gated potassium channel beta-2 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	0	0
			2556	1627	443	470	16			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	35	MET	-	CLONING ARTIFACT	UNP P62483

- Molecule 2 is a protein called Potassium voltage-gated channel subfamily A member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	259	Total	C	N	O	S	0	0	0
			1972	1298	322	345	7			

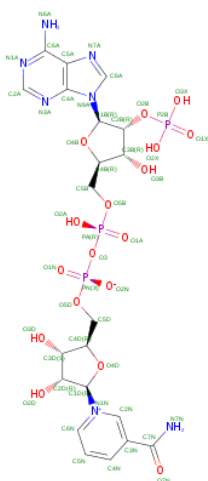
- Molecule 3 is a protein called poly-unknown chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	52	Total	C	N	O	0	0	0
			227	123	52	52			

- Molecule 4 is a protein called poly-unknown chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	21	Total	C	N	O	0	0	0
			105	63	21	21			

- Molecule 5 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 48	C 21	N 7	O 17	P 3	0	0


- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	6	Total K 6 6	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	67	Total O 67 67	0	0
7	B	16	Total O 16 16	0	0

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 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.

- Chain A: 

Legend: ARG, SER, %

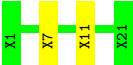
- Chain B:
- 
- 11%
- 35%
- 16%
- 48%
- MET THR VAL ALA THR GLY ASP PRO VAL THR ASP GLU ALA ALA LEU PRO GLY HIS PRO GLN ASP THR TYR ASP PRO PRO GLU ALA ASP HIS GLU CYS C32 V36 E45 F54 P55 E56 T57 L58 D70 R82 P83 D86 L98 R99 R100 P101 V102 N103 V104 P105 L106 F109 I113 L118 G119 E120 E121 M123 E124 R127 E130 G131 T132 I133 L134 L135 L136 L137 T138 A139 N140 I141 M142 S143 A144 T145 I146 I147 I148 I149 I150 I151 I152 I153 I154 I155 I156 I157 I158 I159 I160 I161 I162 I163 I164 I165 I166 I167 I168 I169 I170 I171 I172 I173 I174 I175 I176 I177 I178 I179 I180 I181 I182 I183 I184 I185 I186 I187 I188 I189 I190 I191 I192 I193 I194 I195 I196 I197 I198 I199 I200 I201 I202 I203 I204 I205 I206 I207 I208 I209 I210 I211 I212 I213 I214 I215 I216 I217 I218 I219 I220 I221 I222 I223 I224 I225 I226 I227 I228 I229 I230 I231 I232 I233 I234 I235 I236 I237 I238 I239 I240 I241 I242 I243 I244 I245 I246 I247 I248 I249 I250 I251 I252 I253 I254 I255 I256 I257 I258 I259 I260 I261 I262 I263 I264 I265 I266 I267 I268 I269 I270 I271 I272 I273 I274 I275 I276 I277 I278 I279 I280 I281 I282 I283 I284 I285 I286 I287 I288 I289 I290 I291 I292 I293 I294 I295 I296 I297 I298 I299 I300 I301 I302 I303 I304 I305 I306 I307 I308 I309 I310 I311 I312 I313 I314 I315 I316 I317 I318 I319 I320 I321 I322 I323 I324 I325 I326 I327 I328 I329 I330 I331 I332 I333 I334 I335 I336 I337 I338 I339 I340 I341 I342 I343 I344 I345 I346 I347 I348 I349 I350 I351 I352 I353 I354 I355 I356 I357 I358 I359 I

ASP	LEU	LYS	SER	ARG	SER	ALA	SER	THR	ILE	SER	LYS	SER	ASP	TYR	MET	GLU	ILE	GLN	GLU	GLY	VAL	ASN	ASN	SER	ASN	GLU	ASP	PHE	ARG	GLU	GLU	ASN	LEU	LYS	THR	ALA	ASN	CYS	THR	LEU	ALA	ASN	THR	ASN	TYR	VAL	ASN	ILE	THR	LYS	MET	LEU	THR	ASP	VAL
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- Molecule 3: poly-unknown chain



- Molecule 4: poly-unknown chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.61Å 113.61Å 260.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.48 – 2.90 30.63 – 2.80	Depositor EDS
% Data completeness (in resolution range)	91.6 (29.48-2.90) 89.9 (30.63-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 2.81Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.222 , 0.252 0.224 , 0.256	Depositor DCC
$R_{free}$ test set	1952 reflections (5.37%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.5	Xtriage
Anisotropy	0.711	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 74.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4997	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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



## 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: K, NAP

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	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.75	0/2608	0.75	1/3524 (0.0%)
2	B	0.51	0/2021	0.58	0/2748
All	All	0.66	0/4629	0.68	1/6272 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	157	ALA	N-CA-C	-5.36	96.52	111.00

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	2556	0	2582	74	0
2	B	1972	0	1846	71	0
3	C	227	0	23	7	0
4	D	105	0	23	1	0
5	A	48	0	25	4	0
6	B	6	0	0	0	0
7	A	67	0	0	7	0
7	B	16	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4997	0	4499	147	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 16.

The worst 5 of 147 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)
2:B:404:LEU:HB2	2:B:405:PRO:HD3	1.49	0.95
2:B:131:GLY:C	3:C:1:UNK:N	2.22	0.93
2:B:113:ILE:HG23	2:B:118:LEU:HD12	1.60	0.82
1:A:286:GLN:HA	1:A:289:LEU:HD12	1.62	0.82
2:B:32:CYS:HB3	7:B:561:HOH:O	1.80	0.81

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	324/333 (97%)	307 (95%)	15 (5%)	2 (1%)	27	61
2	B	253/499 (51%)	232 (92%)	18 (7%)	3 (1%)	14	43
All	All	577/832 (69%)	539 (93%)	33 (6%)	5 (1%)	19	52

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	120	PHE
2	B	359	PRO
2	B	121	GLU
2	B	404	LEU

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Mol	Chain	Res	Type
1	A	58	VAL

### 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	273/280 (98%)	265 (97%)	8 (3%)	45	79
2	B	188/441 (43%)	181 (96%)	7 (4%)	37	72
All	All	461/721 (64%)	446 (97%)	15 (3%)	41	75

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	283	ARG
1	A	354	ILE
2	B	123	MET
1	A	268	LYS
2	B	103	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	326	ASN
1	A	333	ASN
2	B	53	GLN
1	A	234	HIS
2	B	47	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](#)

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 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	NAP	A	1001	-	44,52,52	1.55	9 (20%)	53,80,80	1.30	7 (13%)

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	NAP	A	1001	-	-	0/27/67/67	0/5/5/5

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1001	NAP	O4D-C1D	-3.40	1.36	1.41
5	A	1001	NAP	C7N-N7N	2.24	1.37	1.33
5	A	1001	NAP	P2B-O2B	2.35	1.63	1.59
5	A	1001	NAP	O4B-C4B	2.40	1.50	1.45
5	A	1001	NAP	C6N-N1N	2.74	1.42	1.35

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1001	NAP	N3A-C2A-N1A	-2.82	126.45	128.86
5	A	1001	NAP	C3N-C7N-N7N	-2.07	115.35	117.76
5	A	1001	NAP	C2A-N1A-C6A	2.05	122.23	118.75
5	A	1001	NAP	C2B-C3B-C4B	2.40	107.29	102.02
5	A	1001	NAP	PN-O3-PA	2.53	141.13	132.63

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1001	NAP	4	0

## 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<sup>th</sup> 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	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	326/333 (97%)	-0.23	3 (0%) 84 83	31, 50, 79, 91	0
2	B	259/499 (51%)	0.94	56 (21%) 0 0	47, 157, 164, 165	0
3	C	0/52	-	-	-	-
4	D	0/21	-	-	-	-
All	All	585/905 (64%)	0.29	59 (10%) 7 5	31, 68, 163, 165	0

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	386	GLY	8.1
2	B	382	PRO	7.6
2	B	356	SER	7.5
2	B	355	ASP	7.4
2	B	243	ALA	7.1

### 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 carbohydrates 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<sup>th</sup> 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	B-factors( $\text{\AA}^2$ )	Q<0.9
6	K	B	505	1/1	0.70	0.42	89,89,89,89	1
6	K	B	504	1/1	0.70	0.30	89,89,89,89	1
6	K	B	502	1/1	0.80	0.17	89,89,89,89	1
6	K	B	500	1/1	0.83	0.17	89,89,89,89	1
6	K	B	503	1/1	0.95	0.14	89,89,89,89	1
5	NAP	A	1001	48/48	0.95	0.23	46,51,59,60	0
6	K	B	501	1/1	0.97	0.19	89,89,89,89	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.