



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 04:04 PM UTC

PDB ID : 3FB7 / pdb\_00003fb7  
Title : Open KcsA potassium channel in the presence of Rb<sup>+</sup> ion  
Authors : Cuello, L.G.; Jogini, V.; Cortes, D.M.; Pan, A.C.; Gagnon, D.H.; Cordero-Morales, J.F.; Chakrapani, S.; Roux, B.; Perozo, E.  
Deposited on : 2008-11-18  
Resolution : 3.30 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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

MolProbity : 4-5-2 with Phenix2.0  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

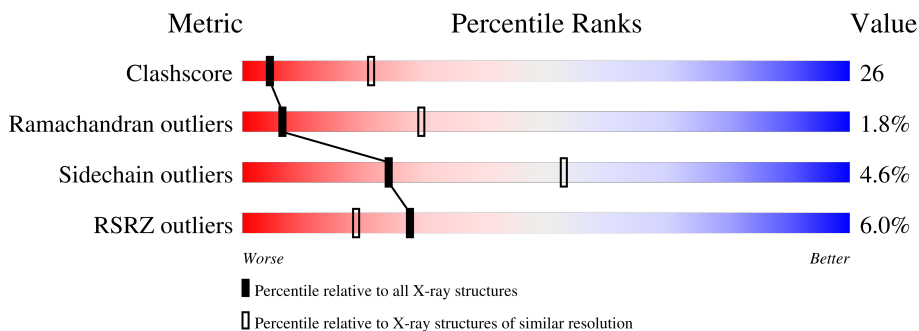
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	219	
2	B	212	
3	C	104	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3926 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 antibody fab fragment heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	219	1648	1042	275	325	6	0	0	0

- Molecule 2 is a protein called antibody fab fragment light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	212	1649	1023	283	338	5	0	0	0

- Molecule 3 is a protein called Voltage-gated potassium channel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	89	625	410	102	111	2	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	25	GLN	HIS	engineered mutation	UNP P0A334
C	90	CYS	LEU	engineered mutation	UNP P0A334
C	117	GLN	ARG	engineered mutation	UNP P0A334
C	120	GLN	GLU	engineered mutation	UNP P0A334
C	121	GLN	ARG	engineered mutation	UNP P0A334
C	122	GLN	ARG	engineered mutation	UNP P0A334
C	124	GLN	HIS	engineered mutation	UNP P0A334

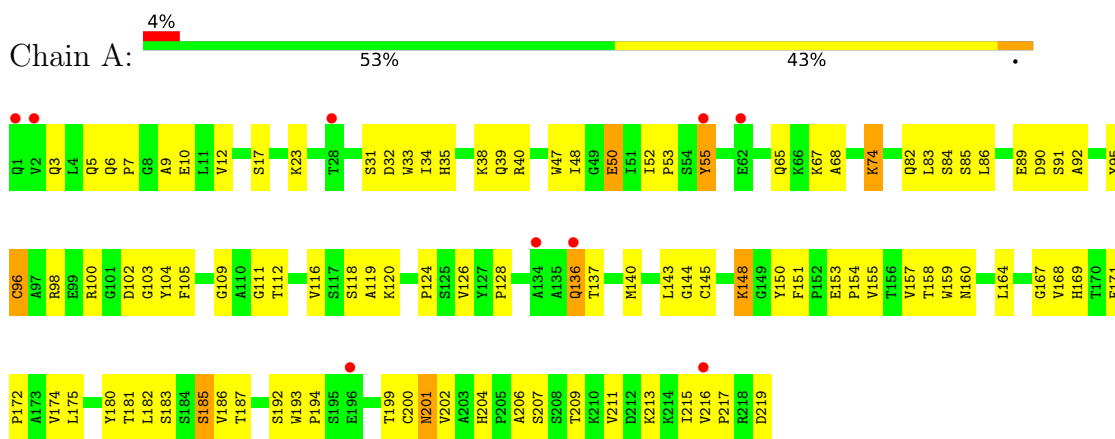
- Molecule 4 is RUBIDIUM ION (CCD ID: RB) (formula: Rb).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	4	Total	Rb	0	0
			4	4		

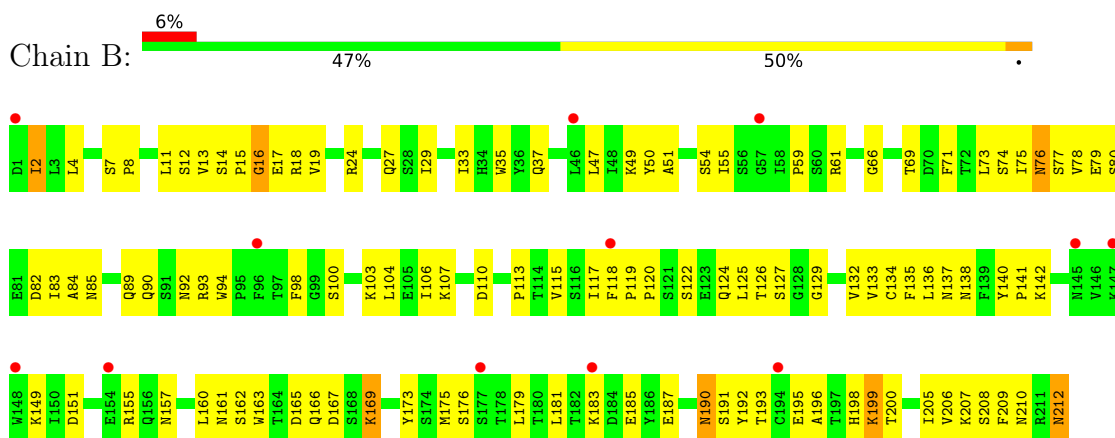
### 3 Residue-property plots [i](#)

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.

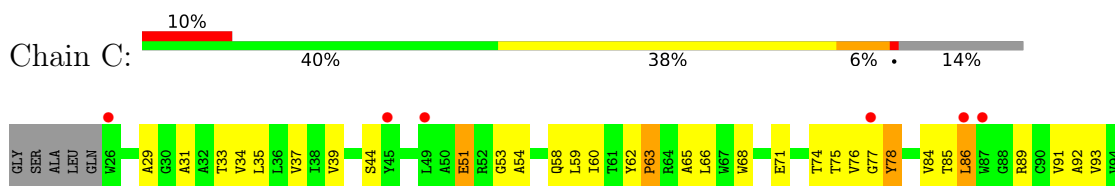
- Molecule 1: antibody fab fragment heavy chain



- Molecule 2: antibody fab fragment light chain



- Molecule 3: Voltage-gated potassium channel



V95	M96	V97	A98	G99	I100	T101	S102	F103	G104	L105	V106	T107	A108	A109	L110	A111	T112	W113	F114	VAL	GLY	GLN	GLN	GLU	GLN	GLN	GLN	GLN	GLY	GLN
-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 4 Data and refinement statistics i

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	157.80Å 157.80Å 73.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.30 50.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.30) 96.1 (50.00-3.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.11 (at 3.32Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.241 , 0.255 0.248 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	98.7	Xtrriage
Anisotropy	0.020	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 73.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.034 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	3926	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	112.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% 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: RB

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	0.57	1/1692 (0.1%)	1.00	3/2312 (0.1%)
2	B	0.46	0/1686	0.99	4/2287 (0.2%)
3	C	0.52	0/638	1.34	9/881 (1.0%)
All	All	0.52	1/4016 (0.0%)	1.06	16/5480 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	118	SER	C-N	12.67	1.51	1.33

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	60	ILE	N-CA-C	11.11	123.32	111.77
3	C	78	TYR	N-CA-C	-9.27	100.60	112.93
1	A	103	GLY	N-CA-C	8.23	124.49	114.69
2	B	137	ASN	N-CA-C	8.04	122.53	109.59
2	B	66	GLY	N-CA-C	7.67	119.24	111.95

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	1648	0	1616	83	0
2	B	1649	0	1576	97	0
3	C	625	0	626	41	0
4	C	4	0	0	0	0
All	All	3926	0	3818	204	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 26.

The worst 5 of 204 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:140:MET:HE3	1:A:187:THR:HG22	1.46	0.97
3:C:91:VAL:O	3:C:95:VAL:HG23	1.79	0.83
2:B:136:LEU:HD11	2:B:196:ALA:HB2	1.60	0.82
1:A:148:LYS:HB3	1:A:181:THR:HG23	1.63	0.79
2:B:92:ASN:HD21	3:C:58:GLN:NE2	1.82	0.78

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	217/219 (99%)	199 (92%)	15 (7%)	3 (1%)	9	33
2	B	210/212 (99%)	189 (90%)	17 (8%)	4 (2%)	6	28
3	C	87/104 (84%)	74 (85%)	11 (13%)	2 (2%)	5	25
All	All	514/535 (96%)	462 (90%)	43 (8%)	9 (2%)	6	29

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	199	LYS
1	A	55	TYR
1	A	192	SER
2	B	190	ASN
3	C	77	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 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	185/185 (100%)	174 (94%)	11 (6%)	18	46
2	B	190/190 (100%)	184 (97%)	6 (3%)	34	60
3	C	57/75 (76%)	54 (95%)	3 (5%)	20	49
All	All	432/450 (96%)	412 (95%)	20 (5%)	24	53

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	100	SER
3	C	84	VAL
3	C	105	LEU
3	C	86	LEU
1	A	148	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	212	ASN
2	B	190	ASN
2	B	38	GLN
2	B	138	ASN
2	B	27	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 oligosaccharides 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<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	219/219 (100%)	0.66	9 (4%) 41 27	81, 121, 148, 163	0
2	B	212/212 (100%)	0.63	12 (5%) 29 20	70, 115, 153, 170	0
3	C	89/104 (85%)	0.50	10 (11%) 10 9	65, 80, 142, 171	0
All	All	520/535 (97%)	0.62	31 (5%) 27 19	65, 116, 152, 171	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	145	ASN	4.5
3	C	108	ALA	3.8
1	A	196	GLU	3.7
1	A	55	TYR	3.7
1	A	28	THR	3.0

### 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 oligosaccharides 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
4	RB	C	4	1/1	0.89	0.35	23,23,23,23	1
4	RB	C	2	1/1	0.94	0.38	54,54,54,54	1
4	RB	C	3	1/1	0.97	0.07	54,54,54,54	1
4	RB	C	1	1/1	1.00	0.48	54,54,54,54	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.