



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 02:07 AM EDT

PDB ID : 8QZ2 / pdb_00008qz2
Title : Crystal structure of human two pore domain potassium ion channel TREK-2 (K2P10.1) in complex with an inhibitory nanobody (Nb61)
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Deposited on : 2023-10-26
Resolution : 3.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ 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

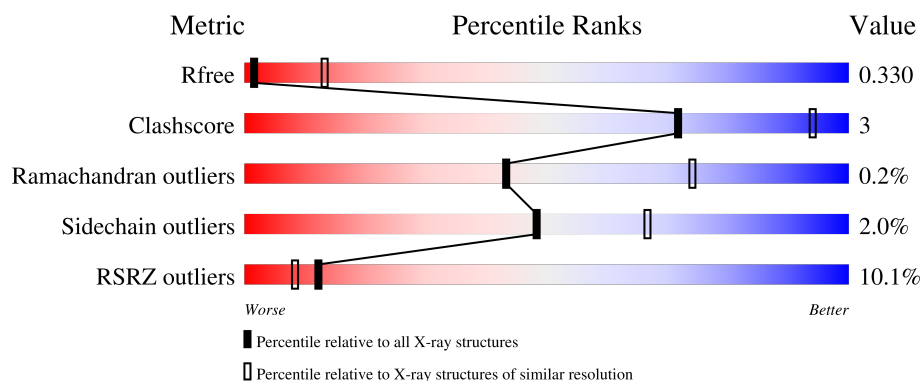
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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 $\leq 5\%$. 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	274	9% 78% 9% 13%
1	B	274	8% 82% 8% 10%
2	C	134	11% 78% 11% 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4511 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 Potassium channel subfamily K member 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	239	Total	C	N	O	S	0	0	0
			1749	1168	265	313	3			
1	B	246	Total	C	N	O	S	0	0	0
			1832	1224	280	324	4			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	74	MET	-	initiating methionine	UNP P57789
A	149	GLN	ASN	engineered mutation	UNP P57789
A	152	GLN	ASN	engineered mutation	UNP P57789
A	153	GLN	ASN	engineered mutation	UNP P57789
A	341	ALA	-	expression tag	UNP P57789
A	342	GLU	-	expression tag	UNP P57789
A	343	ASN	-	expression tag	UNP P57789
A	344	LEU	-	expression tag	UNP P57789
A	345	TYR	-	expression tag	UNP P57789
A	346	PHE	-	expression tag	UNP P57789
A	347	GLN	-	expression tag	UNP P57789
B	74	MET	-	initiating methionine	UNP P57789
B	149	GLN	ASN	engineered mutation	UNP P57789
B	152	GLN	ASN	engineered mutation	UNP P57789
B	153	GLN	ASN	engineered mutation	UNP P57789
B	341	ALA	-	expression tag	UNP P57789
B	342	GLU	-	expression tag	UNP P57789
B	343	ASN	-	expression tag	UNP P57789
B	344	LEU	-	expression tag	UNP P57789
B	345	TYR	-	expression tag	UNP P57789
B	346	PHE	-	expression tag	UNP P57789
B	347	GLN	-	expression tag	UNP P57789

- Molecule 2 is a protein called Nanobody 61.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	121	Total	C	N	O	S	0	0	0
			926	580	161	179	6			

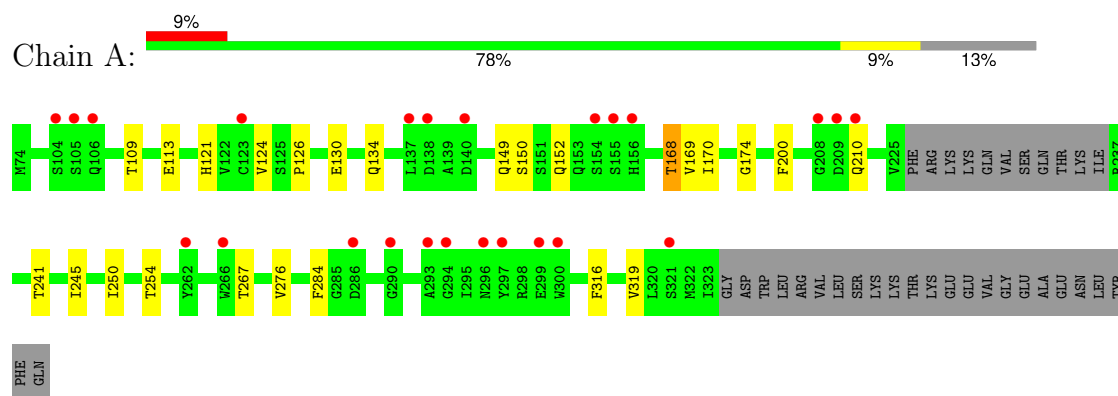
- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	4	Total	K	0	0
			4	4		

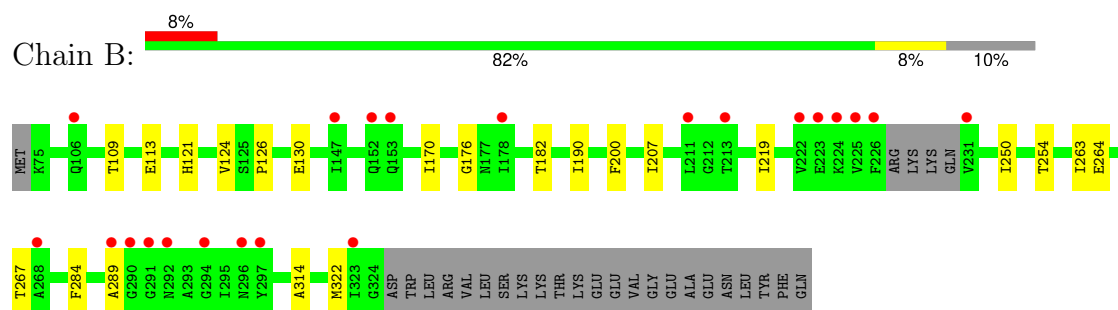
3 Residue-property plots [i](#)

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.

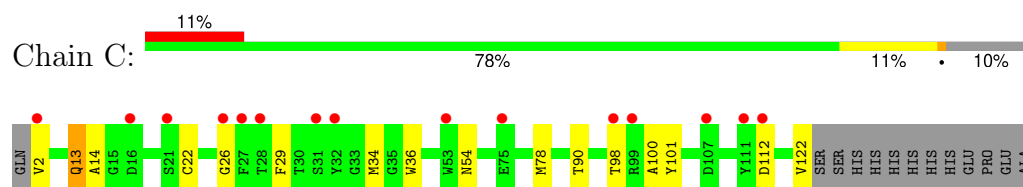
- Molecule 1: Potassium channel subfamily K member 10



- Molecule 1: Potassium channel subfamily K member 10



- Molecule 2: Nanobody 61



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	56.54Å 111.70Å 289.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.10 – 3.50 52.10 – 3.50	Depositor EDS
% Data completeness (in resolution range)	95.0 (52.10-3.50) 95.0 (52.10-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 3.48Å)	Xtriage
Refinement program	BUSTER 2.10.4	Depositor
R, R_{free}	0.280 , 0.308 0.265 , 0.330	Depositor DCC
R_{free} test set	2013 reflections (17.55%)	wwPDB-VP
Wilson B-factor (Å ²)	66.4	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 50.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	4511	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.76% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	0/1793	1.01	2/2458 (0.1%)
1	B	0.56	0/1879	0.98	0/2569
2	C	0.61	1/948 (0.1%)	0.89	0/1285
All	All	0.57	1/4620 (0.0%)	0.98	2/6312 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	54	ASN	CA-C	7.55	1.56	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	210	GLN	CA-C-N	5.19	127.67	120.29
1	A	210	GLN	C-N-CA	5.19	127.67	120.29

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	1749	0	1687	13	0
1	B	1832	0	1798	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	926	0	859	9	0
3	B	4	0	0	0	0
All	All	4511	0	4344	29	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 3.

All (29) 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:C:36:TRP:NE1	2:C:78:MET:HE3	1.87	0.89
2:C:90:THR:HB	2:C:122:VAL:H	1.53	0.71
2:C:98:THR:HG22	2:C:100:ALA:H	1.62	0.66
2:C:36:TRP:CE2	2:C:78:MET:HE3	2.32	0.64
1:A:245:ILE:HD12	1:A:319:VAL:HG22	1.87	0.56
1:A:121:HIS:CD2	1:B:124:VAL:HG22	2.41	0.55
1:A:168:THR:HG23	1:A:174:GLY:HA2	1.89	0.55
1:B:264:GLU:OE2	1:B:289:ALA:O	2.27	0.53
1:A:276:VAL:HG21	1:B:190:ILE:HG23	1.93	0.50
2:C:13:GLN:HG3	2:C:14:ALA:N	2.26	0.49
1:A:109:THR:O	1:A:113:GLU:HG3	2.12	0.48
1:A:250:ILE:HA	1:A:254:THR:HB	1.96	0.47
1:B:250:ILE:HA	1:B:254:THR:HB	1.97	0.47
1:A:124:VAL:HG22	1:B:121:HIS:CD2	2.50	0.46
1:A:284:PHE:O	1:B:176:GLY:HA3	2.16	0.46
1:A:170:ILE:HD12	1:A:200:PHE:HB2	1.98	0.45
1:A:169:VAL:HG22	1:B:284:PHE:HZ	1.83	0.44
1:A:241:THR:O	1:A:245:ILE:HG12	2.18	0.44
2:C:22:CYS:HB3	2:C:78:MET:HE2	1.98	0.44
1:B:109:THR:O	1:B:113:GLU:HG3	2.17	0.43
2:C:2:VAL:HG12	2:C:26:GLY:HA3	2.00	0.43
1:B:263:ILE:O	2:C:101:TYR:OH	2.33	0.43
1:B:170:ILE:HD12	1:B:200:PHE:HB2	2.00	0.43
1:B:126:PRO:O	1:B:130:GLU:HG2	2.19	0.42
1:B:207:ILE:HG21	1:B:314:ALA:HB1	2.02	0.42
1:A:130:GLU:O	1:A:134:GLN:HG3	2.20	0.41
1:A:126:PRO:O	1:A:130:GLU:HG2	2.20	0.41
2:C:29:PHE:CE1	2:C:34:MET:SD	3.13	0.41
1:B:219:ILE:HG13	1:B:322:MET:HE1	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	235/274 (86%)	228 (97%)	6 (3%)	1 (0%)	30	62
1	B	242/274 (88%)	237 (98%)	5 (2%)	0	100	100
2	C	119/134 (89%)	115 (97%)	4 (3%)	0	100	100
All	All	596/682 (87%)	580 (97%)	15 (2%)	1 (0%)	43	74

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	SER

5.3.2 Protein sidechains

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	171/226 (76%)	166 (97%)	5 (3%)	37	60
1	B	184/226 (81%)	182 (99%)	2 (1%)	65	74
2	C	94/110 (86%)	92 (98%)	2 (2%)	47	66
All	All	449/562 (80%)	440 (98%)	9 (2%)	48	67

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	149	GLN
1	A	152	GLN

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Mol	Chain	Res	Type
1	A	168	THR
1	A	267	THR
1	A	316	PHE
1	B	182	THR
1	B	267	THR
2	C	13	GLN
2	C	112	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	GLN
1	B	135	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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, 95th 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 ²)	Q<0.9
1	A	239/274 (87%)	0.92	24 (10%) 12 8	50, 67, 101, 111	0
1	B	246/274 (89%)	0.78	22 (8%) 15 10	42, 62, 94, 110	0
2	C	121/134 (90%)	0.86	15 (12%) 8 6	43, 53, 62, 66	0
All	All	606/682 (88%)	0.85	61 (10%) 12 8	42, 61, 98, 111	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	26	GLY	4.5
1	A	156	HIS	4.4
1	B	223	GLU	4.3
1	B	153	GLN	4.3
1	A	123	CYS	4.1
1	B	213	THR	3.9
1	B	225	VAL	3.7
2	C	16	ASP	3.7
1	A	106	GLN	3.5
1	A	140	ASP	3.4
2	C	111	TYR	3.4
2	C	107	ASP	3.4
1	A	294	GLY	3.3
1	A	293	ALA	3.3
1	B	294	GLY	3.3
2	C	112	ASP	3.3
1	B	297	TYR	3.2
1	A	155	SER	3.2
1	B	231	VAL	3.0
1	B	147	ILE	2.9
1	B	226	PHE	2.9
2	C	31	SER	2.8
1	B	152	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	291	GLY	2.8
1	A	286	ASP	2.8
1	A	266	TRP	2.8
1	B	178	ILE	2.8
1	A	138	ASP	2.8
1	A	290	GLY	2.7
1	B	289	ALA	2.7
1	B	323	ILE	2.6
1	A	296	ASN	2.6
1	B	296	ASN	2.5
1	A	299	GLU	2.5
1	B	222	VAL	2.5
1	A	300	TRP	2.5
1	A	209	ASP	2.5
1	A	210	GLN	2.5
2	C	98	THR	2.4
1	A	137	LEU	2.4
1	B	211	LEU	2.4
1	B	106	GLN	2.4
2	C	27	PHE	2.4
1	B	290	GLY	2.3
1	A	262	TYR	2.3
2	C	32	TYR	2.3
1	A	105	SER	2.3
2	C	21	SER	2.3
2	C	2	VAL	2.2
1	A	208	GLY	2.2
2	C	75	GLU	2.2
1	A	321	SER	2.2
2	C	28	THR	2.2
1	A	154	SER	2.1
1	B	224	LYS	2.1
1	A	297	TYR	2.1
2	C	53	TRP	2.1
2	C	99	ARG	2.1
1	B	292	ASN	2.0
1	A	104	SER	2.0
1	B	268	ALA	2.0

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

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, 95th 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
3	K	B	600	1/1	0.96	0.05	63,63,63,63	0
3	K	B	603	1/1	0.98	0.04	34,34,34,34	0
3	K	B	602	1/1	0.99	0.08	24,24,24,24	0
3	K	B	601	1/1	0.99	0.06	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.