



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 03:58 AM UTC

PDB ID : 6V5A / pdb_00006v5a
Title : Crystal structure of the human BK channel gating ring L390P mutant
Authors : Deng, Z.; Yuan, P.
Deposited on : 2019-12-03
Resolution : 2.00 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
Mogul : 2022.3.0, CSD as543be (2022)
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

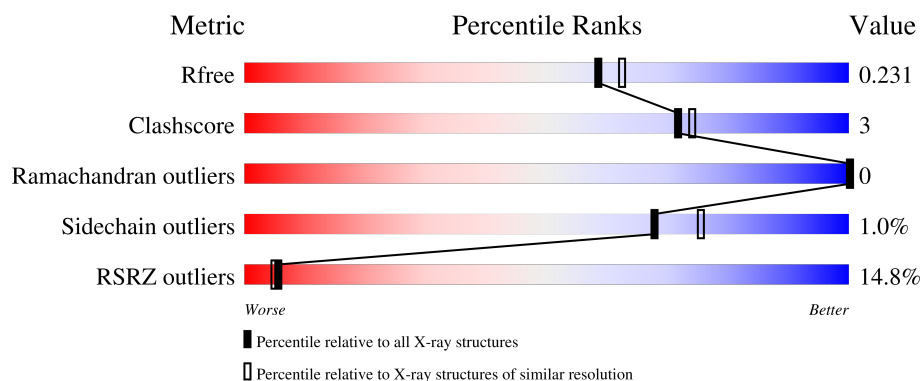
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	726	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4915 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 Calcium-activated potassium channel subunit alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	594	Total	C	N	O	S	0	0	0
			4683	2999	777	873	34			

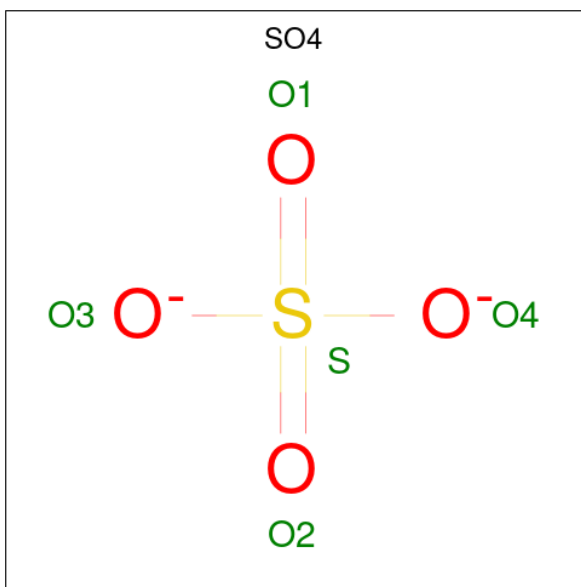
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	340	MET	-	initiating methionine	UNP Q12791
A	390	PRO	LEU	engineered mutation	UNP Q12791
A	1057	SER	-	expression tag	UNP Q12791
A	1058	ASN	-	expression tag	UNP Q12791
A	1059	SER	-	expression tag	UNP Q12791
A	1060	LEU	-	expression tag	UNP Q12791
A	1061	GLU	-	expression tag	UNP Q12791
A	1062	VAL	-	expression tag	UNP Q12791
A	1063	LEU	-	expression tag	UNP Q12791
A	1064	PHE	-	expression tag	UNP Q12791
A	1065	GLN	-	expression tag	UNP Q12791

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	226	Total	O	0	0
			226	226		

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: Calcium-activated potassium channel subunit alpha-1



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	145.52Å 145.52Å 242.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.00 30.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.00-2.00) 99.9 (30.00-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.203 , 0.226 (Not available) , 0.231	Depositor DCC
R_{free} test set	3340 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	36.5	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4915	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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: CA, SO4

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	0.59	1/4777 (0.0%)	0.81	5/6470 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	386	GLU	CA-C	-5.75	1.47	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	384	ASN	N-CA-C	-9.84	94.65	110.20
1	A	386	GLU	N-CA-C	-8.01	96.65	109.39
1	A	388	GLU	N-CA-C	-6.53	104.17	111.28
1	A	387	LEU	N-CA-C	-6.18	105.33	112.86
1	A	385	LEU	N-CA-C	-5.05	100.04	110.80

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	4683	0	4646	31	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	5	0	0	0	0
4	A	226	0	0	2	0
All	All	4915	0	4646	31	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 (31) 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:387:LEU:C	1:A:390:PRO:HD2	2.06	0.81
1:A:384:ASN:O	1:A:386:GLU:N	2.21	0.73
1:A:387:LEU:HA	1:A:390:PRO:HD2	1.71	0.70
1:A:387:LEU:CA	1:A:390:PRO:HD2	2.21	0.70
1:A:387:LEU:HA	1:A:390:PRO:CD	2.23	0.69
1:A:387:LEU:O	1:A:390:PRO:HG2	1.97	0.64
1:A:367:ASP:OD2	1:A:373:VAL:HG11	2.04	0.57
1:A:447:ILE:HG22	1:A:454:ILE:HG21	1.86	0.57
1:A:387:LEU:CA	1:A:390:PRO:CD	2.86	0.53
1:A:388:GLU:OE2	1:A:392:LYS:NZ	2.39	0.52
1:A:387:LEU:CA	1:A:390:PRO:CG	2.88	0.51
1:A:387:LEU:CB	1:A:390:PRO:CG	2.89	0.50
1:A:477:TRP:HE3	4:A:2231:HOH:O	1.94	0.50
1:A:384:ASN:C	1:A:386:GLU:N	2.71	0.48
1:A:366:LYS:HG2	1:A:513:MET:HE2	1.96	0.48
1:A:387:LEU:CB	1:A:390:PRO:HG3	2.45	0.47
1:A:730:ALA:HB3	1:A:806:ASN:HB3	1.97	0.46
1:A:387:LEU:HA	1:A:390:PRO:CG	2.45	0.45
1:A:385:LEU:C	1:A:387:LEU:N	2.73	0.44
1:A:387:LEU:C	1:A:390:PRO:CD	2.84	0.44
1:A:374:GLU:HG2	1:A:397:GLN:NE2	2.32	0.44
1:A:451:HIS:O	1:A:454:ILE:HG22	2.18	0.44
1:A:904:TYR:HA	1:A:909:PHE:CD2	2.52	0.44
1:A:385:LEU:HA	1:A:388:GLU:HB2	2.00	0.44
1:A:477:TRP:CE3	4:A:2231:HOH:O	2.56	0.42
1:A:513:MET:HE1	1:A:926:ALA:N	2.35	0.42
1:A:519:ILE:HD11	1:A:526:LYS:N	2.36	0.41
1:A:385:LEU:O	1:A:387:LEU:N	2.53	0.41
1:A:916:ALA:O	1:A:919:VAL:HG22	2.20	0.40
1:A:373:VAL:O	1:A:373:VAL:CG1	2.69	0.40
1:A:390:PRO:O	1:A:391:PHE:C	2.64	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	580/726 (80%)	570 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	520/644 (81%)	515 (99%)	5 (1%)	68	75

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	388	GLU
1	A	423	LEU
1	A	477	TRP
1	A	521	GLU
1	A	1027	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	344	HIS
1	A	397	GLN
1	A	451	HIS
1	A	496	GLN
1	A	590	GLN
1	A	772	ASN
1	A	806	ASN
1	A	889	GLN
1	A	1027	GLN
1	A	1036	ASN

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 2 ligands modelled in this entry, 1 is 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	$\# Z > 2$
3	SO4	A	2002	-	4,4,4	0.46	0	6,6,6	0.10	0

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	594/726 (81%)	0.71	88 (14%) 5 5	24, 39, 89, 127	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	381	ILE	7.2
1	A	901	THR	6.6
1	A	1025	PRO	6.2
1	A	517	ILE	6.1
1	A	952	LEU	5.7
1	A	519	ILE	5.7
1	A	516	PHE	5.5
1	A	385	LEU	5.5
1	A	371	VAL	5.1
1	A	680	ASP	5.0
1	A	387	LEU	5.0
1	A	953	ILE	5.0
1	A	955	GLU	5.0
1	A	945	ALA	4.9
1	A	1060	LEU	4.9
1	A	397	GLN	4.6
1	A	515	SER	4.6
1	A	870	ILE	4.5
1	A	386	GLU	4.5
1	A	951	ALA	4.3
1	A	384	ASN	4.2
1	A	950	GLU	4.2
1	A	904	TYR	4.2
1	A	389	ALA	4.0
1	A	513	MET	3.9
1	A	477	TRP	3.9
1	A	905	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	954	ALA	3.8
1	A	430	CYS	3.7
1	A	396	THR	3.6
1	A	871	THR	3.6
1	A	369	ASP	3.5
1	A	372	ASN	3.4
1	A	1058	ASN	3.3
1	A	398	VAL	3.3
1	A	409	HIS	3.2
1	A	570	TYR	3.2
1	A	373	VAL	3.2
1	A	1020	ALA	3.2
1	A	806	ASN	3.1
1	A	357	SER	3.1
1	A	899	PRO	3.0
1	A	378	LEU	3.0
1	A	518	LYS	3.0
1	A	370	ASP	2.9
1	A	390	PRO	2.9
1	A	807	GLN	2.9
1	A	522	ASP	2.9
1	A	391	PHE	2.9
1	A	527	TYR	2.8
1	A	383	PRO	2.8
1	A	429	TYR	2.8
1	A	833	ASP	2.7
1	A	681	SER	2.7
1	A	683	VAL	2.7
1	A	393	ARG	2.6
1	A	395	PHE	2.6
1	A	379	HIS	2.6
1	A	613	LYS	2.6
1	A	682	ASN	2.5
1	A	577	SER	2.5
1	A	869	SER	2.5
1	A	400	PHE	2.5
1	A	612	CYS	2.5
1	A	896	ASP	2.5
1	A	388	GLU	2.5
1	A	959	LEU	2.5
1	A	900	ASP	2.4
1	A	958	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	960	ARG	2.4
1	A	479	GLU	2.4
1	A	611	TYR	2.4
1	A	394	HIS	2.4
1	A	1028	CYS	2.4
1	A	368	ARG	2.2
1	A	601	ASP	2.2
1	A	586	HIS	2.2
1	A	708	SER	2.2
1	A	382	SER	2.1
1	A	353	LEU	2.1
1	A	889	GLN	2.1
1	A	712	MET	2.1
1	A	401	TYR	2.1
1	A	523	THR	2.1
1	A	604	GLU	2.0
1	A	963	TYR	2.0
1	A	964	SER	2.0
1	A	884	ASN	2.0

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, 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
2	CA	A	2001	1/1	0.97	0.08	46,46,46,46	0
3	SO4	A	2002	5/5	1.00	0.02	27,27,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.