



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2017 – 04:24 pm GMT

PDB ID : 4CHV
Title : The electron crystallography structure of the cAMP-bound potassium channel MloK1
Authors : Kowal, J.; Chami, M.; Baumgartner, P.; Arheit, M.; Chiu, P.L.; Rangl, M.; Scheuring, S.; Schroeder, G.F.; Nimigean, C.M.; Stahlberg, H.
Deposited on : 2013-12-04
Resolution : 7.00 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29102

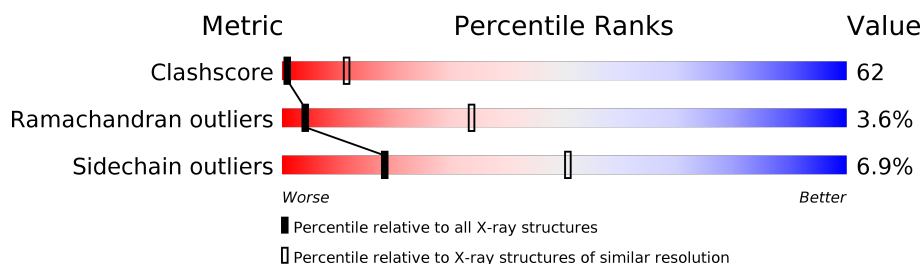
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON CRYSTALLOGRAPHY

The reported resolution of this entry is 7.00 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))
Clashscore	112137	1035 (10.00-3.80)
Ramachandran outliers	110173	1003 (10.00-3.76)
Sidechain outliers	110143	1098 (10.00-3.70)

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 ≥ 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	361	
1	B	361	
1	C	361	
1	D	361	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10342 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 CYCLIC NUCLEOTIDE-GATED POTASSIUM CHANNEL MLL3241.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	0	1
			2585	1684	444	447	10			
1	B	344	Total	C	N	O	S	0	0	1
			2585	1684	444	447	10			
1	C	344	Total	C	N	O	S	0	0	1
			2585	1684	444	447	10			
1	D	344	Total	C	N	O	S	0	0	1
			2585	1684	444	447	10			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	HIS	-	EXPRESSION TAG	UNP Q98GN8
A	357	HIS	-	EXPRESSION TAG	UNP Q98GN8
A	358	HIS	-	EXPRESSION TAG	UNP Q98GN8
A	359	HIS	-	EXPRESSION TAG	UNP Q98GN8
A	360	HIS	-	EXPRESSION TAG	UNP Q98GN8
A	361	HIS	-	EXPRESSION TAG	UNP Q98GN8
B	356	HIS	-	EXPRESSION TAG	UNP Q98GN8
B	357	HIS	-	EXPRESSION TAG	UNP Q98GN8
B	358	HIS	-	EXPRESSION TAG	UNP Q98GN8
B	359	HIS	-	EXPRESSION TAG	UNP Q98GN8
B	360	HIS	-	EXPRESSION TAG	UNP Q98GN8
B	361	HIS	-	EXPRESSION TAG	UNP Q98GN8
C	356	HIS	-	EXPRESSION TAG	UNP Q98GN8
C	357	HIS	-	EXPRESSION TAG	UNP Q98GN8
C	358	HIS	-	EXPRESSION TAG	UNP Q98GN8
C	359	HIS	-	EXPRESSION TAG	UNP Q98GN8
C	360	HIS	-	EXPRESSION TAG	UNP Q98GN8
C	361	HIS	-	EXPRESSION TAG	UNP Q98GN8
D	356	HIS	-	EXPRESSION TAG	UNP Q98GN8
D	357	HIS	-	EXPRESSION TAG	UNP Q98GN8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	358	HIS	-	EXPRESSION TAG	UNP Q98GN8
D	359	HIS	-	EXPRESSION TAG	UNP Q98GN8
D	360	HIS	-	EXPRESSION TAG	UNP Q98GN8
D	361	HIS	-	EXPRESSION TAG	UNP Q98GN8

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

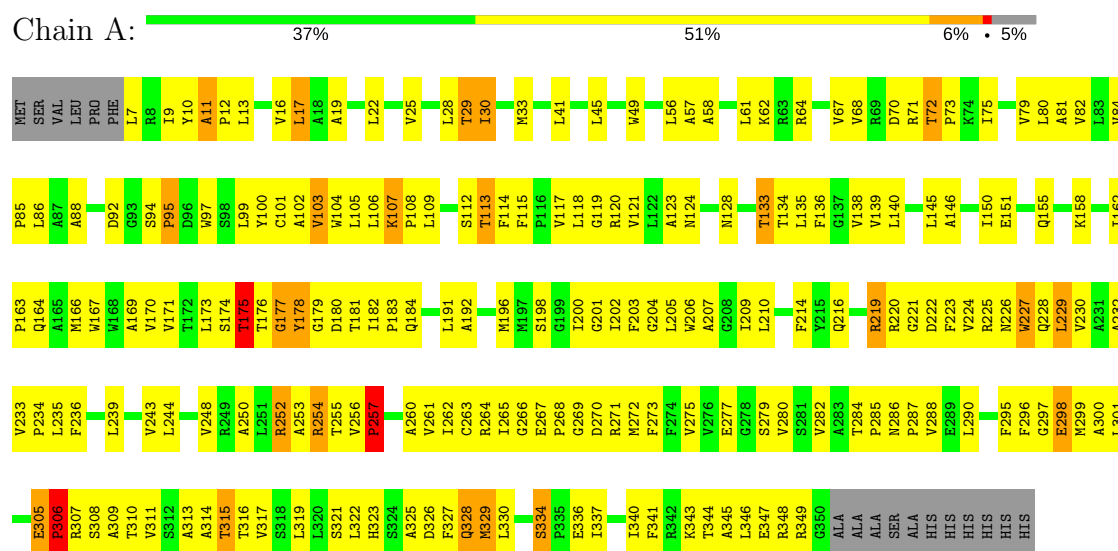
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total K 1 1	0	0
2	A	1	Total K 1 1	0	0

3 Residue-property plots

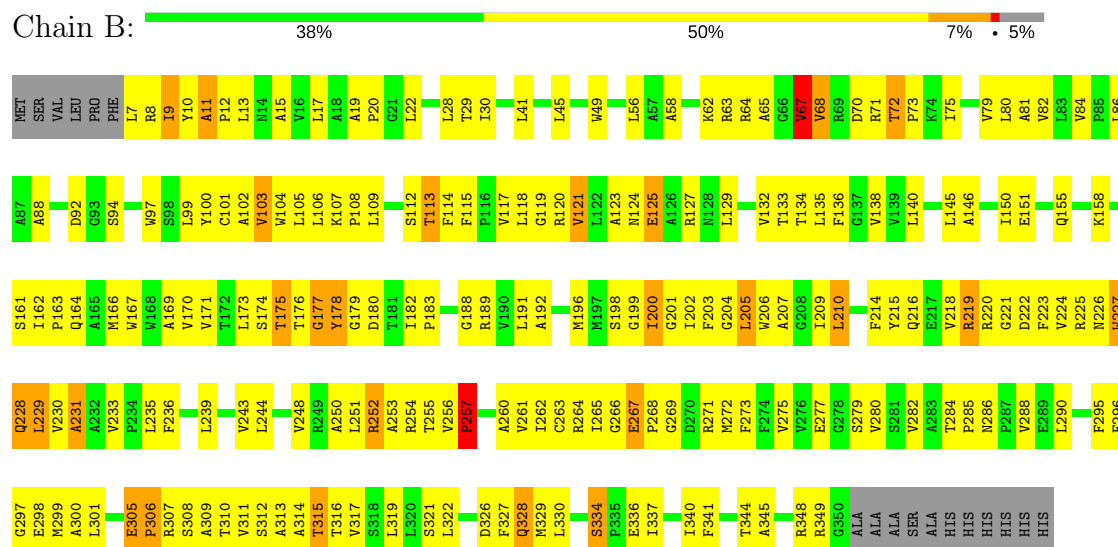
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

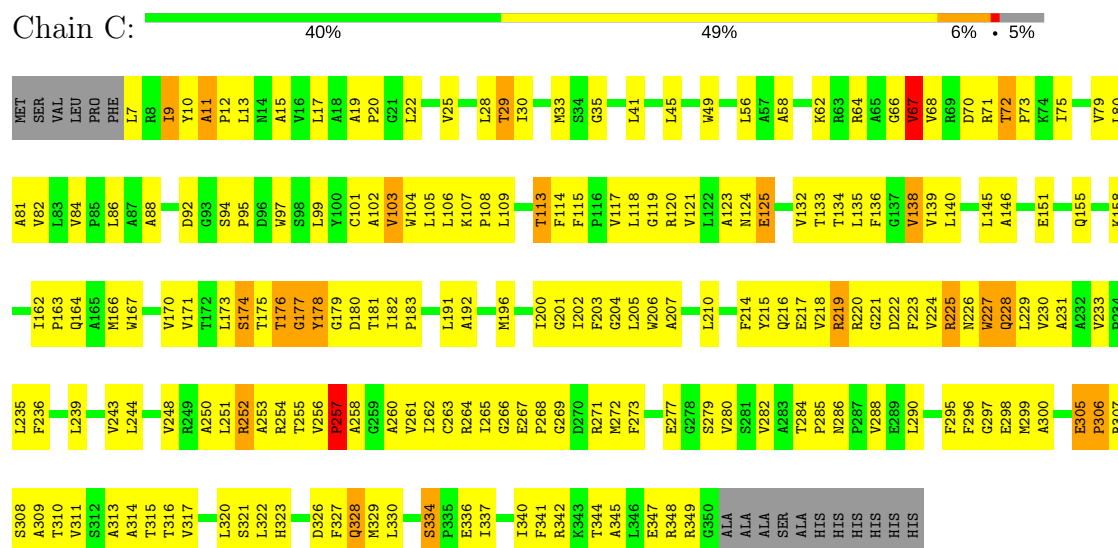
• Molecule 1: CYCLIC NUCLEOTIDE-GATED POTASSIUM CHANNEL MLL3241



• Molecule 1: CYCLIC NUCLEOTIDE-GATED POTASSIUM CHANNEL MLL3241



• Molecule 1: CYCLIC NUCLEOTIDE-GATED POTASSIUM CHANNEL MLL3241



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	104.33Å 104.33Å 104.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 7.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-7.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10342	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

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	0.69	2/2642 (0.1%)	0.88	4/3607 (0.1%)
1	B	0.70	3/2642 (0.1%)	0.92	4/3607 (0.1%)
1	C	0.70	3/2642 (0.1%)	0.89	2/3607 (0.1%)
1	D	0.70	3/2642 (0.1%)	0.92	6/3607 (0.2%)
All	All	0.70	11/10568 (0.1%)	0.90	16/14428 (0.1%)

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	178	TYR	C-O	7.60	1.37	1.23
1	D	178	TYR	C-O	7.52	1.37	1.23
1	B	178	TYR	C-O	7.50	1.37	1.23
1	A	178	TYR	C-O	7.45	1.37	1.23
1	B	253	ALA	C-O	6.74	1.36	1.23

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	252	ARG	N-CA-CB	-7.80	96.56	110.60
1	D	252	ARG	N-CA-CB	-7.25	97.56	110.60
1	A	252	ARG	N-CA-CB	-7.01	97.99	110.60
1	B	257	PRO	N-CA-CB	-6.88	95.03	102.60
1	D	257	PRO	N-CA-CB	-6.62	95.32	102.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	2585	0	2694	362	0
1	B	2585	0	2694	352	0
1	C	2585	0	2694	422	0
1	D	2585	0	2694	409	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
All	All	10342	0	10776	1303	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 62.

The worst 5 of 1303 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:D:226:ASN:CB	1:D:248:VAL:HG22	1.43	1.49
1:B:230:VAL:HG13	1:B:236:PHE:CD2	1.49	1.46
1:D:226:ASN:CG	1:D:248:VAL:HG13	1.09	1.40
1:C:229:LEU:CD1	1:C:251:LEU:HD13	1.53	1.36
1:D:226:ASN:ND2	1:D:248:VAL:CB	1.84	1.36

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	342/361 (95%)	320 (94%)	11 (3%)	11 (3%)	5 35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	342/361 (95%)	320 (94%)	8 (2%)	14 (4%)	3	30
1	C	342/361 (95%)	323 (94%)	6 (2%)	13 (4%)	4	32
1	D	342/361 (95%)	322 (94%)	9 (3%)	11 (3%)	5	35
All	All	1368/1444 (95%)	1285 (94%)	34 (2%)	49 (4%)	4	33

5 of 49 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	29	THR
1	A	72	THR
1	A	95	PRO
1	A	175	THR
1	A	254	ARG

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	266/279 (95%)	248 (93%)	18 (7%)	18	51
1	B	266/279 (95%)	246 (92%)	20 (8%)	16	48
1	C	266/279 (95%)	251 (94%)	15 (6%)	25	57
1	D	266/279 (95%)	246 (92%)	20 (8%)	16	48
All	All	1064/1116 (95%)	991 (93%)	73 (7%)	18	50

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	305	GLU
1	C	125	GLU
1	D	267	GLU
1	B	334	SER
1	C	174	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	323	HIS
1	C	124	ASN
1	D	124	ASN
1	B	216	GLN
1	D	226	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.