



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:37 PM GMT

PDB ID : 3U6N
Title : Open Structure of the BK channel Gating Ring
Authors : Yuan, P.; MacKinnon, R.
Deposited on : 2011-10-12
Resolution : 3.61 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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

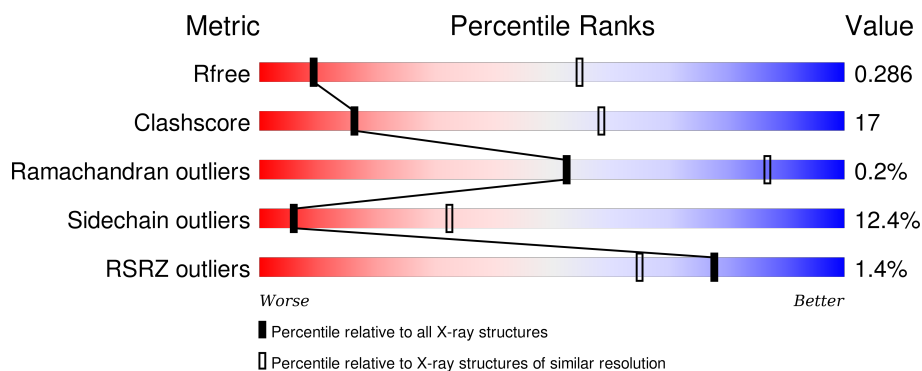
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.61 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}	91344	1093 (3.80-3.44)
Clashscore	102246	1043 (3.78-3.46)
Ramachandran outliers	100387	1003 (3.78-3.46)
Sidechain outliers	100360	1003 (3.78-3.46)
RSRZ outliers	91569	1100 (3.80-3.44)

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.

Mol	Chain	Length	Quality of chain
1	A	696	<div> <div>56%</div> <div>25%</div> <div>•</div> <div>16%</div> </div>
1	B	696	<div> <div>56%</div> <div>25%</div> <div>•</div> <div>16%</div> </div>
1	C	696	<div> <div>55%</div> <div>26%</div> <div>•</div> <div>16%</div> </div>
1	D	696	<div> <div>56%</div> <div>24%</div> <div>•</div> <div>16%</div> </div>
1	E	696	<div> <div>56%</div> <div>25%</div> <div>•</div> <div>16%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	696	<div><div><div></div><div></div><div></div><div></div></div><div>%</div><div><div></div><div></div><div></div><div></div></div><div>57%</div><div>24%</div><div>•</div><div>16%</div></div>
1	G	696	<div><div><div></div><div></div><div></div><div></div></div><div>2%</div><div><div></div><div></div><div></div><div></div></div><div>56%</div><div>25%</div><div>•</div><div>16%</div></div>
1	H	696	<div><div><div></div><div></div><div></div><div></div></div><div>2%</div><div><div></div><div></div><div></div><div></div></div><div>56%</div><div>24%</div><div>•</div><div>16%</div></div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 34504 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 High-Conductance Ca²⁺-Activated K⁺ Channel protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	585	Total	C	N	O	S	0	0	0
			4312	2756	722	800	34			
1	B	585	Total	C	N	O	S	0	0	0
			4312	2756	722	800	34			
1	C	585	Total	C	N	O	S	0	0	0
			4312	2756	722	800	34			
1	D	585	Total	C	N	O	S	0	0	0
			4312	2756	722	800	34			
1	E	585	Total	C	N	O	S	0	0	0
			4312	2756	722	800	34			
1	F	585	Total	C	N	O	S	0	0	0
			4312	2756	722	800	34			
1	G	585	Total	C	N	O	S	0	0	0
			4312	2756	722	800	34			
1	H	585	Total	C	N	O	S	0	0	0
			4312	2756	722	800	34			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	340	MET	-	INITIATING METHIONINE	UNP F1QHV6
A	578	ARG	-	SEE REMARK 999	UNP F1QHV6
A	580	ARG	-	SEE REMARK 999	UNP F1QHV6
A	581	LYS	-	SEE REMARK 999	UNP F1QHV6
A	582	ARG	-	SEE REMARK 999	UNP F1QHV6
A	1061	SER	-	EXPRESSION TAG	UNP F1QHV6
A	1062	ASN	-	EXPRESSION TAG	UNP F1QHV6
A	1063	SER	-	EXPRESSION TAG	UNP F1QHV6
A	1064	LEU	-	EXPRESSION TAG	UNP F1QHV6
A	1065	GLU	-	EXPRESSION TAG	UNP F1QHV6
A	1066	VAL	-	EXPRESSION TAG	UNP F1QHV6
A	1067	LEU	-	EXPRESSION TAG	UNP F1QHV6
A	1068	PHE	-	EXPRESSION TAG	UNP F1QHV6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1069	GLN	-	EXPRESSION TAG	UNP F1QHV6
B	340	MET	-	INITIATING METHIONINE	UNP F1QHV6
B	578	ARG	-	SEE REMARK 999	UNP F1QHV6
B	580	ARG	-	SEE REMARK 999	UNP F1QHV6
B	581	LYS	-	SEE REMARK 999	UNP F1QHV6
B	582	ARG	-	SEE REMARK 999	UNP F1QHV6
B	1061	SER	-	EXPRESSION TAG	UNP F1QHV6
B	1062	ASN	-	EXPRESSION TAG	UNP F1QHV6
B	1063	SER	-	EXPRESSION TAG	UNP F1QHV6
B	1064	LEU	-	EXPRESSION TAG	UNP F1QHV6
B	1065	GLU	-	EXPRESSION TAG	UNP F1QHV6
B	1066	VAL	-	EXPRESSION TAG	UNP F1QHV6
B	1067	LEU	-	EXPRESSION TAG	UNP F1QHV6
B	1068	PHE	-	EXPRESSION TAG	UNP F1QHV6
B	1069	GLN	-	EXPRESSION TAG	UNP F1QHV6
C	340	MET	-	INITIATING METHIONINE	UNP F1QHV6
C	578	ARG	-	SEE REMARK 999	UNP F1QHV6
C	580	ARG	-	SEE REMARK 999	UNP F1QHV6
C	581	LYS	-	SEE REMARK 999	UNP F1QHV6
C	582	ARG	-	SEE REMARK 999	UNP F1QHV6
C	1061	SER	-	EXPRESSION TAG	UNP F1QHV6
C	1062	ASN	-	EXPRESSION TAG	UNP F1QHV6
C	1063	SER	-	EXPRESSION TAG	UNP F1QHV6
C	1064	LEU	-	EXPRESSION TAG	UNP F1QHV6
C	1065	GLU	-	EXPRESSION TAG	UNP F1QHV6
C	1066	VAL	-	EXPRESSION TAG	UNP F1QHV6
C	1067	LEU	-	EXPRESSION TAG	UNP F1QHV6
C	1068	PHE	-	EXPRESSION TAG	UNP F1QHV6
C	1069	GLN	-	EXPRESSION TAG	UNP F1QHV6
D	340	MET	-	INITIATING METHIONINE	UNP F1QHV6
D	578	ARG	-	SEE REMARK 999	UNP F1QHV6
D	580	ARG	-	SEE REMARK 999	UNP F1QHV6
D	581	LYS	-	SEE REMARK 999	UNP F1QHV6
D	582	ARG	-	SEE REMARK 999	UNP F1QHV6
D	1061	SER	-	EXPRESSION TAG	UNP F1QHV6
D	1062	ASN	-	EXPRESSION TAG	UNP F1QHV6
D	1063	SER	-	EXPRESSION TAG	UNP F1QHV6
D	1064	LEU	-	EXPRESSION TAG	UNP F1QHV6
D	1065	GLU	-	EXPRESSION TAG	UNP F1QHV6
D	1066	VAL	-	EXPRESSION TAG	UNP F1QHV6
D	1067	LEU	-	EXPRESSION TAG	UNP F1QHV6
D	1068	PHE	-	EXPRESSION TAG	UNP F1QHV6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1069	GLN	-	EXPRESSION TAG	UNP F1QHV6
E	340	MET	-	INITIATING METHIONINE	UNP F1QHV6
E	578	ARG	-	SEE REMARK 999	UNP F1QHV6
E	580	ARG	-	SEE REMARK 999	UNP F1QHV6
E	581	LYS	-	SEE REMARK 999	UNP F1QHV6
E	582	ARG	-	SEE REMARK 999	UNP F1QHV6
E	1061	SER	-	EXPRESSION TAG	UNP F1QHV6
E	1062	ASN	-	EXPRESSION TAG	UNP F1QHV6
E	1063	SER	-	EXPRESSION TAG	UNP F1QHV6
E	1064	LEU	-	EXPRESSION TAG	UNP F1QHV6
E	1065	GLU	-	EXPRESSION TAG	UNP F1QHV6
E	1066	VAL	-	EXPRESSION TAG	UNP F1QHV6
E	1067	LEU	-	EXPRESSION TAG	UNP F1QHV6
E	1068	PHE	-	EXPRESSION TAG	UNP F1QHV6
E	1069	GLN	-	EXPRESSION TAG	UNP F1QHV6
F	340	MET	-	INITIATING METHIONINE	UNP F1QHV6
F	578	ARG	-	SEE REMARK 999	UNP F1QHV6
F	580	ARG	-	SEE REMARK 999	UNP F1QHV6
F	581	LYS	-	SEE REMARK 999	UNP F1QHV6
F	582	ARG	-	SEE REMARK 999	UNP F1QHV6
F	1061	SER	-	EXPRESSION TAG	UNP F1QHV6
F	1062	ASN	-	EXPRESSION TAG	UNP F1QHV6
F	1063	SER	-	EXPRESSION TAG	UNP F1QHV6
F	1064	LEU	-	EXPRESSION TAG	UNP F1QHV6
F	1065	GLU	-	EXPRESSION TAG	UNP F1QHV6
F	1066	VAL	-	EXPRESSION TAG	UNP F1QHV6
F	1067	LEU	-	EXPRESSION TAG	UNP F1QHV6
F	1068	PHE	-	EXPRESSION TAG	UNP F1QHV6
F	1069	GLN	-	EXPRESSION TAG	UNP F1QHV6
G	340	MET	-	INITIATING METHIONINE	UNP F1QHV6
G	578	ARG	-	SEE REMARK 999	UNP F1QHV6
G	580	ARG	-	SEE REMARK 999	UNP F1QHV6
G	581	LYS	-	SEE REMARK 999	UNP F1QHV6
G	582	ARG	-	SEE REMARK 999	UNP F1QHV6
G	1061	SER	-	EXPRESSION TAG	UNP F1QHV6
G	1062	ASN	-	EXPRESSION TAG	UNP F1QHV6
G	1063	SER	-	EXPRESSION TAG	UNP F1QHV6
G	1064	LEU	-	EXPRESSION TAG	UNP F1QHV6
G	1065	GLU	-	EXPRESSION TAG	UNP F1QHV6
G	1066	VAL	-	EXPRESSION TAG	UNP F1QHV6
G	1067	LEU	-	EXPRESSION TAG	UNP F1QHV6
G	1068	PHE	-	EXPRESSION TAG	UNP F1QHV6

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1069	GLN	-	EXPRESSION TAG	UNP F1QHV6
H	340	MET	-	INITIATING METHIONINE	UNP F1QHV6
H	578	ARG	-	SEE REMARK 999	UNP F1QHV6
H	580	ARG	-	SEE REMARK 999	UNP F1QHV6
H	581	LYS	-	SEE REMARK 999	UNP F1QHV6
H	582	ARG	-	SEE REMARK 999	UNP F1QHV6
H	1061	SER	-	EXPRESSION TAG	UNP F1QHV6
H	1062	ASN	-	EXPRESSION TAG	UNP F1QHV6
H	1063	SER	-	EXPRESSION TAG	UNP F1QHV6
H	1064	LEU	-	EXPRESSION TAG	UNP F1QHV6
H	1065	GLU	-	EXPRESSION TAG	UNP F1QHV6
H	1066	VAL	-	EXPRESSION TAG	UNP F1QHV6
H	1067	LEU	-	EXPRESSION TAG	UNP F1QHV6
H	1068	PHE	-	EXPRESSION TAG	UNP F1QHV6
H	1069	GLN	-	EXPRESSION TAG	UNP F1QHV6

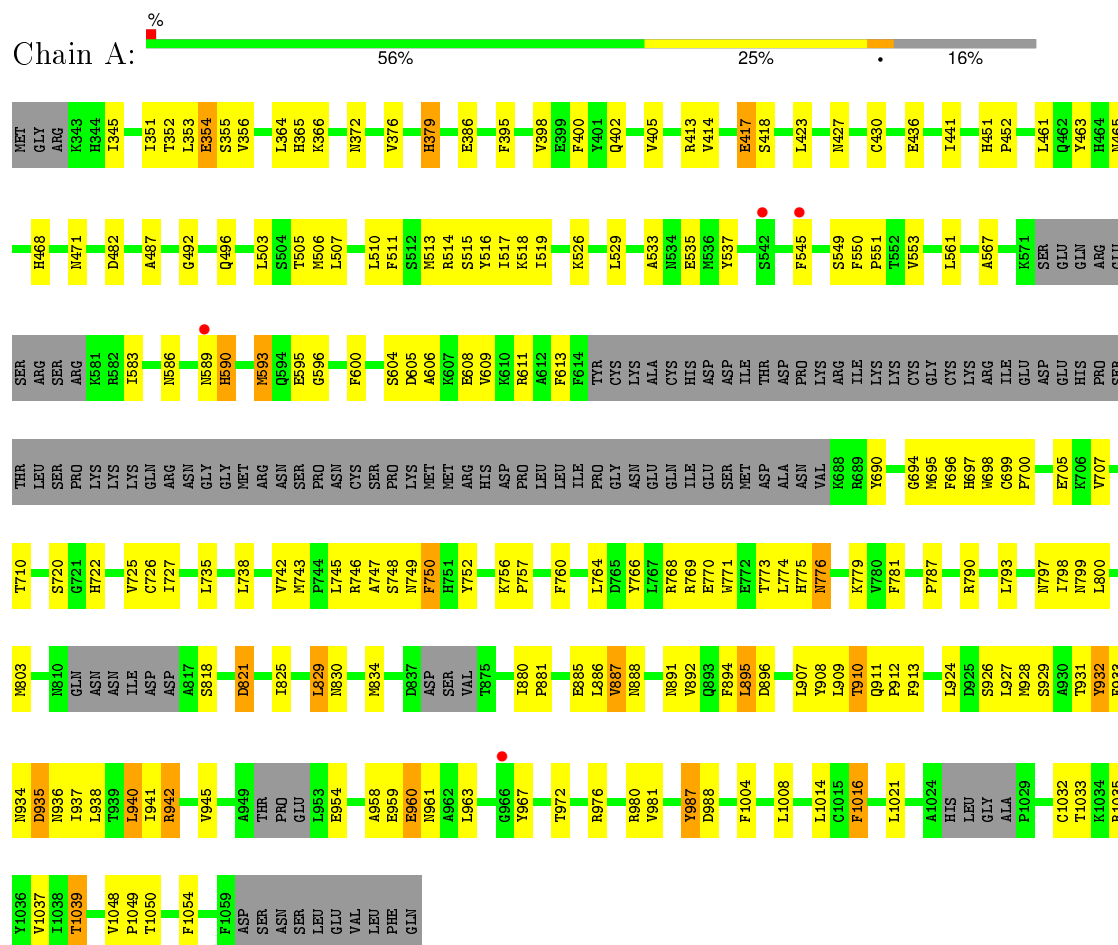
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	E	1	Total Ca 1 1	0	0
2	H	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0
2	F	1	Total Ca 1 1	0	0

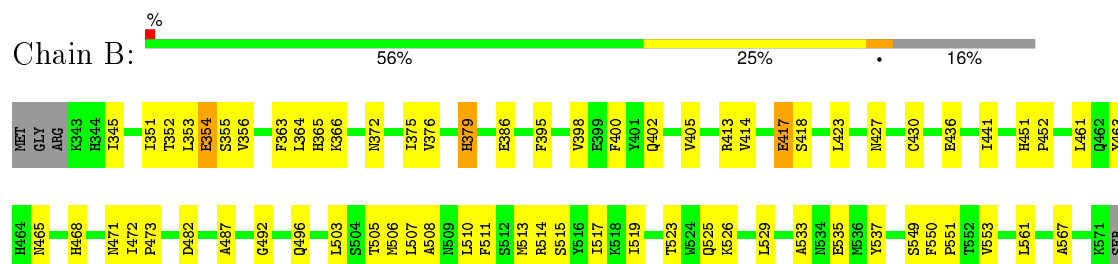
3 Residue-property plots

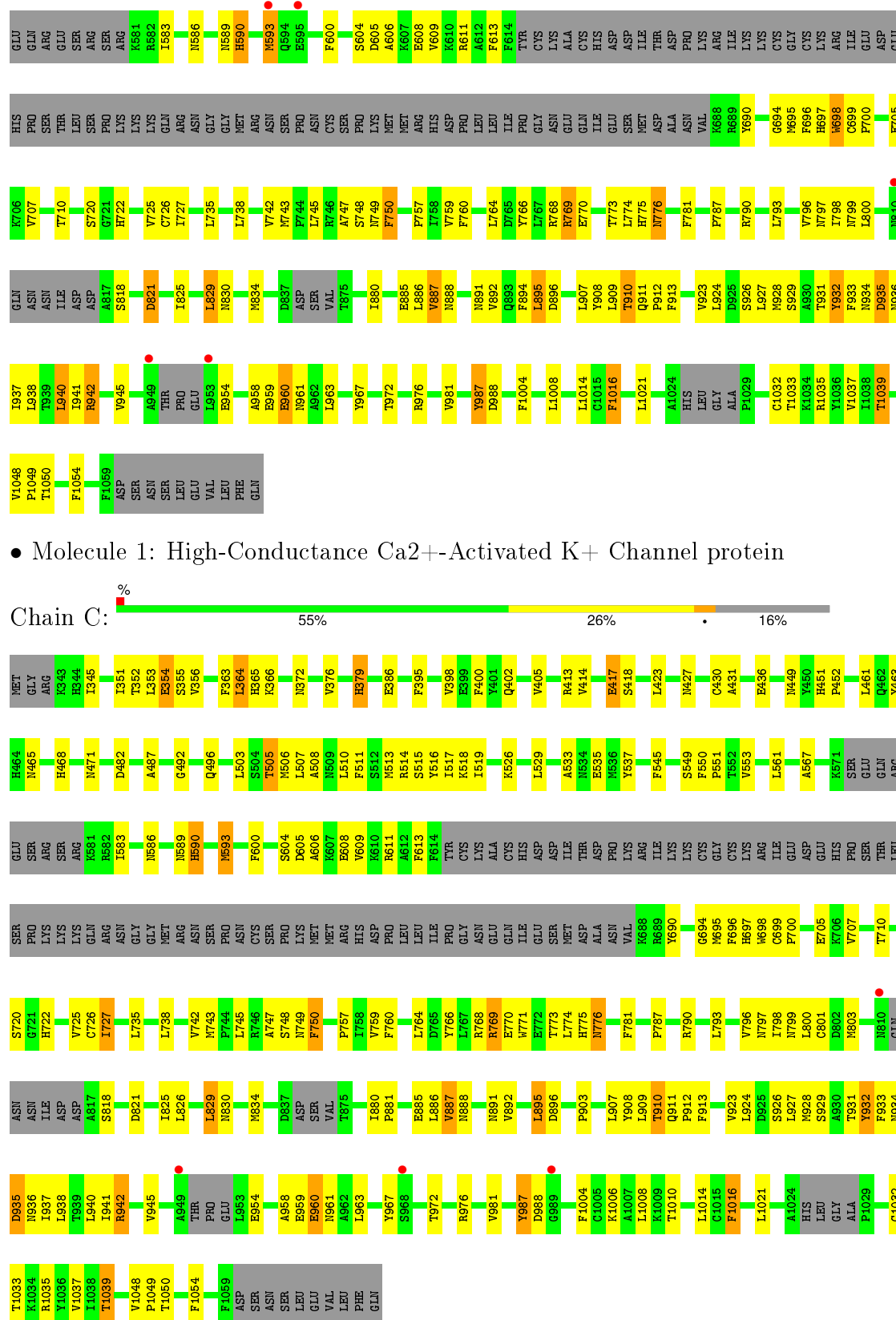
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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: High-Conductance Ca^{2+} -Activated K^{+} Channel protein

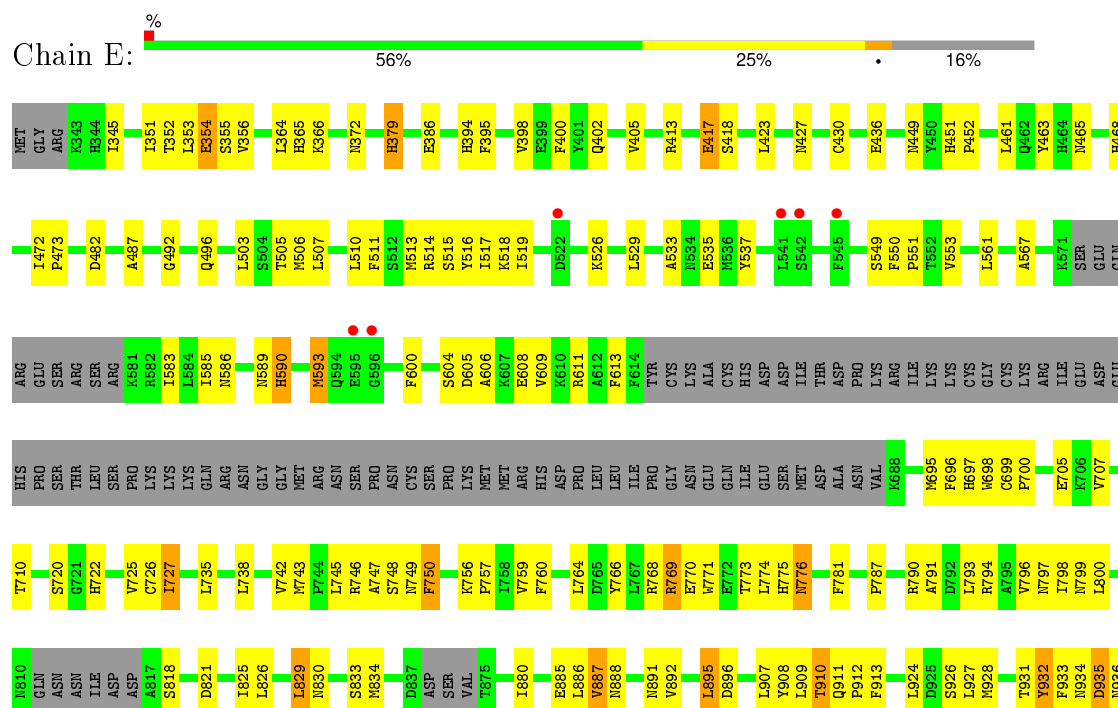
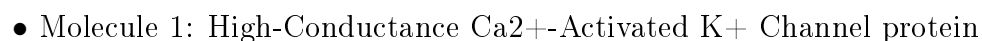


- Molecule 1: High-Conductance Ca^{2+} -Activated K^{+} Channel protein

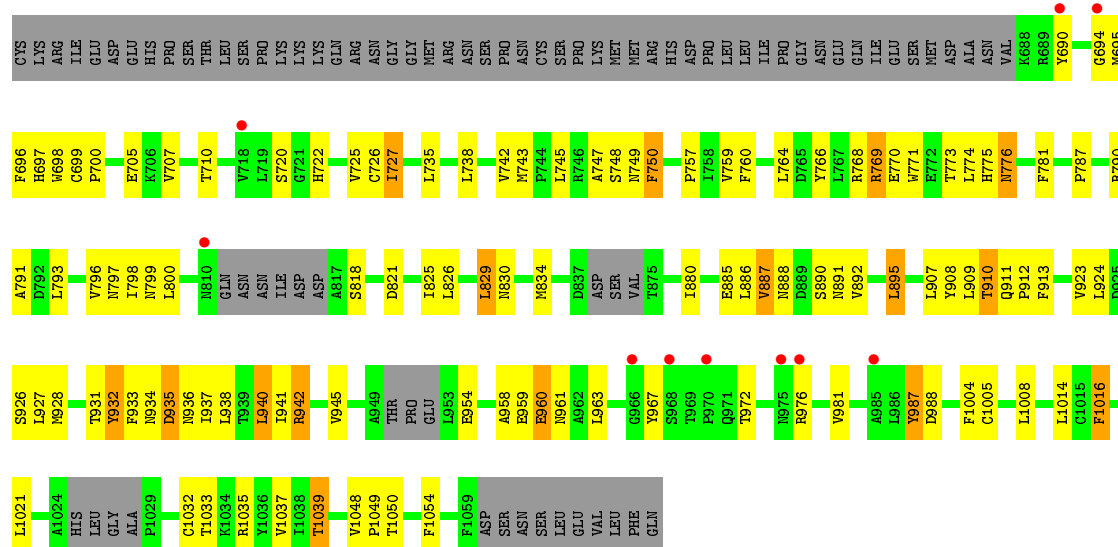




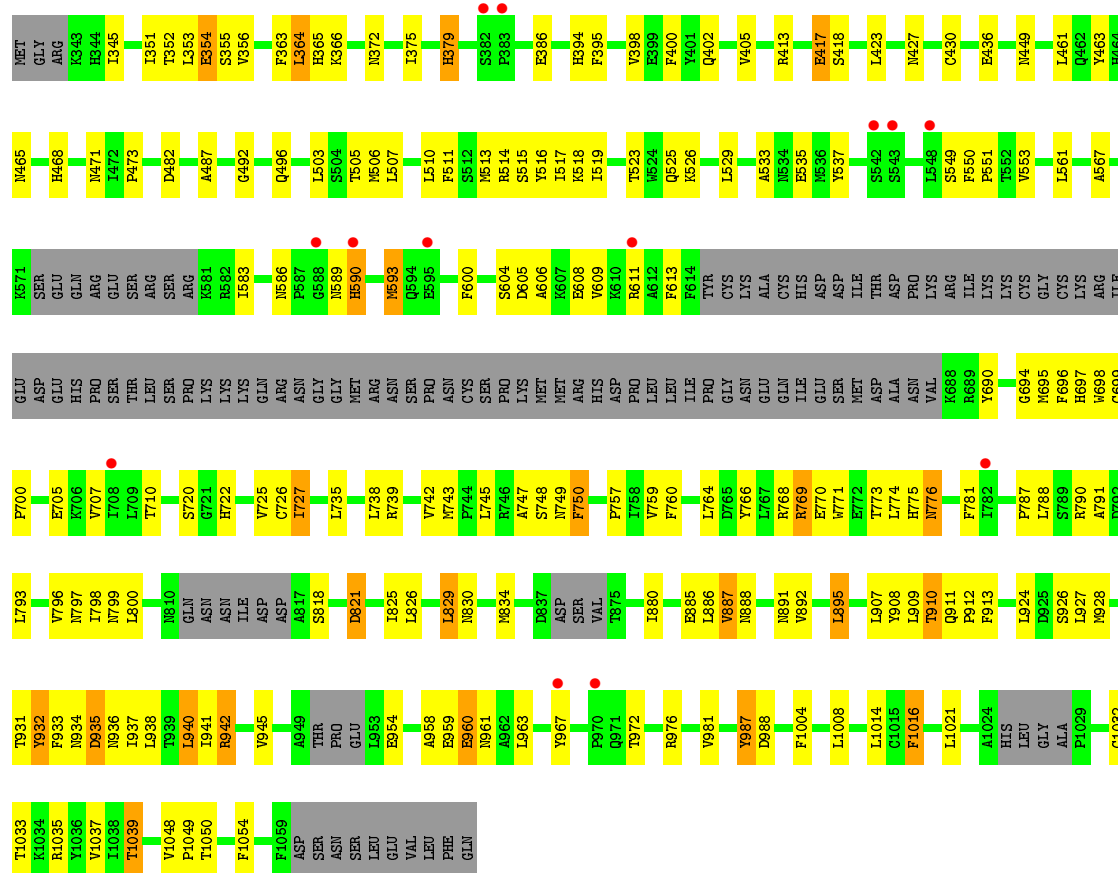
• Molecule 1: High-Conductance Ca²⁺-Activated K⁺ Channel protein







• Molecule 1: High-Conductance Ca²⁺-Activated K⁺ Channel protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	137.65Å 210.82Å 238.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.22 – 3.61 48.21 – 3.61	Depositor EDS
% Data completeness (in resolution range)	89.0 (48.22-3.61) 89.1 (48.21-3.61)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.37 (at 3.57Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.260 , 0.289 0.258 , 0.286	Depositor DCC
R_{free} test set	3620 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	91.1	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 49.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 71878 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	34504	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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

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	0.42	0/4398	0.56	0/6001
1	B	0.42	1/4398 (0.0%)	0.56	0/6001
1	C	0.43	0/4398	0.56	0/6001
1	D	0.42	1/4398 (0.0%)	0.56	0/6001
1	E	0.43	0/4398	0.57	0/6001
1	F	0.43	0/4398	0.57	0/6001
1	G	0.42	0/4398	0.56	0/6001
1	H	0.41	0/4398	0.56	0/6001
All	All	0.42	2/35184 (0.0%)	0.56	0/48008

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	698	TRP	CD2-CE2	5.27	1.47	1.41
1	D	698	TRP	CD2-CE2	5.12	1.47	1.41

There are no bond angle outliers.

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	4312	0	4016	143	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	4312	0	4016	144	0
1	C	4312	0	4017	145	0
1	D	4312	0	4016	148	1
1	E	4312	0	4017	147	1
1	F	4312	0	4017	147	1
1	G	4312	0	4017	155	1
1	H	4312	0	4017	145	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
All	All	34504	0	32133	1117	2

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 17.

The worst 5 of 1117 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:B:511:PHE:CZ	1:B:941:ILE:CG2	2.27	1.17
1:G:511:PHE:CZ	1:G:941:ILE:CG2	2.28	1.17
1:H:511:PHE:CZ	1:H:941:ILE:CG2	2.28	1.16
1:C:511:PHE:CZ	1:C:941:ILE:CG2	2.29	1.15
1:E:511:PHE:CZ	1:E:941:ILE:CG2	2.29	1.15

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:716:MET:CE	1:G:1005:CYS:CB[3_454]	2.06	0.14
1:E:987:TYR:OH	1:F:702:LYS:C[4_555]	2.17	0.03

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	571/696 (82%)	540 (95%)	30 (5%)	1 (0%)	52	87
1	B	571/696 (82%)	539 (94%)	31 (5%)	1 (0%)	52	87
1	C	571/696 (82%)	538 (94%)	32 (6%)	1 (0%)	52	87
1	D	571/696 (82%)	540 (95%)	30 (5%)	1 (0%)	52	87
1	E	571/696 (82%)	538 (94%)	32 (6%)	1 (0%)	52	87
1	F	571/696 (82%)	539 (94%)	31 (5%)	1 (0%)	52	87
1	G	571/696 (82%)	539 (94%)	31 (5%)	1 (0%)	52	87
1	H	571/696 (82%)	537 (94%)	33 (6%)	1 (0%)	52	87
All	All	4568/5568 (82%)	4310 (94%)	250 (6%)	8 (0%)	52	87

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	799	ASN
1	D	799	ASN
1	F	799	ASN
1	G	799	ASN
1	H	799	ASN

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	432/616 (70%)	378 (88%)	54 (12%)	6	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	432/616 (70%)	379 (88%)	53 (12%)	6	33
1	C	432/616 (70%)	378 (88%)	54 (12%)	6	32
1	D	432/616 (70%)	378 (88%)	54 (12%)	6	32
1	E	432/616 (70%)	379 (88%)	53 (12%)	6	33
1	F	432/616 (70%)	379 (88%)	53 (12%)	6	33
1	G	432/616 (70%)	378 (88%)	54 (12%)	6	32
1	H	432/616 (70%)	379 (88%)	53 (12%)	6	33
All	All	3456/4928 (70%)	3028 (88%)	428 (12%)	6	32

5 of 428 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	885	GLU
1	E	768	ARG
1	H	745	LEU
1	D	935	ASP
1	E	365	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	468	HIS
1	E	468	HIS
1	H	465	ASN
1	D	697	HIS
1	D	891	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 8 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	585/696 (84%)	-0.20	4 (0%) 89 81	58, 105, 158, 185	0
1	B	585/696 (84%)	-0.19	5 (0%) 85 75	67, 105, 151, 179	0
1	C	585/696 (84%)	-0.28	4 (0%) 89 81	55, 95, 141, 181	0
1	D	585/696 (84%)	-0.19	6 (1%) 84 73	57, 102, 155, 217	0
1	E	585/696 (84%)	-0.25	8 (1%) 78 65	50, 86, 134, 180	0
1	F	585/696 (84%)	-0.19	9 (1%) 76 63	59, 96, 149, 200	0
1	G	585/696 (84%)	-0.06	15 (2%) 59 45	68, 108, 160, 198	0
1	H	585/696 (84%)	-0.05	13 (2%) 65 50	75, 112, 161, 203	0
All	All	4680/5568 (84%)	-0.18	64 (1%) 78 65	50, 101, 154, 217	0

The worst 5 of 64 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	875	THR	4.5
1	F	595	GLU	4.4
1	D	718	VAL	4.1
1	A	966	GLY	3.7
1	G	970	PRO	3.7

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 ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	CA	H	2001	1/1	0.91	0.14	-1.02	82,82,82,82	0
2	CA	B	2001	1/1	0.98	0.12	-1.29	73,73,73,73	0
2	CA	F	2001	1/1	0.91	0.15	-1.35	72,72,72,72	0
2	CA	D	2001	1/1	0.97	0.10	-1.93	50,50,50,50	0
2	CA	E	2001	1/1	0.97	0.09	-1.95	57,57,57,57	0
2	CA	G	2001	1/1	0.98	0.11	-1.99	57,57,57,57	0
2	CA	A	2001	1/1	0.97	0.08	-2.26	68,68,68,68	0
2	CA	C	2001	1/1	0.96	0.08	-3.44	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.