



wwPDB X-ray Structure Validation Summary Report

Feb 15, 2017 – 02:43 am GMT

PDB ID : 2C9M
Title : STRUCTURE OF (SR) CALCIUM-ATPASE IN THE CA2E1 STATE SOLVED IN A P1 CRYSTAL FORM.
Authors : Lund Jensen, A.-M.; Sorensen, T.L.-M.; Olesen, C.; Moller, J.V.; Nissen, P.
Deposited on : 2005-12-13
Resolution : 3.00 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) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

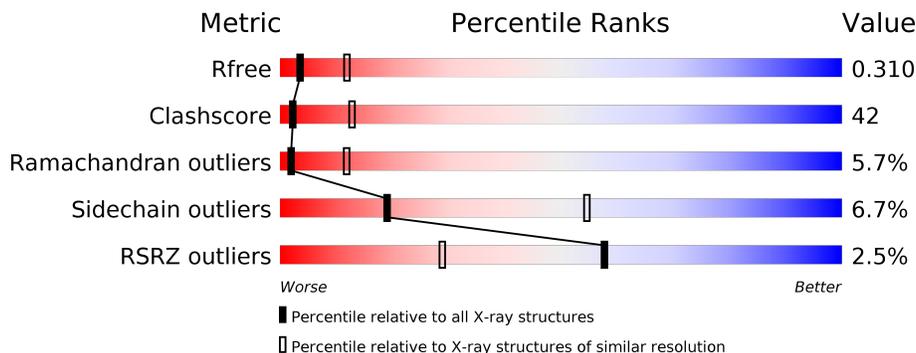
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	100719	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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 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	994	 2% 41% 51% 7%
1	B	994	 3% 39% 53% 7%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CA	B	996	-	-	-	X
3	K	B	997	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15351 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 SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	994	7670	4876	1287	1450	57	0	0	0
1	B	994	7670	4876	1287	1450	57	0	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total 3	Ca 3	0	0
2	A	4	Total 4	Ca 4	0	0

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

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

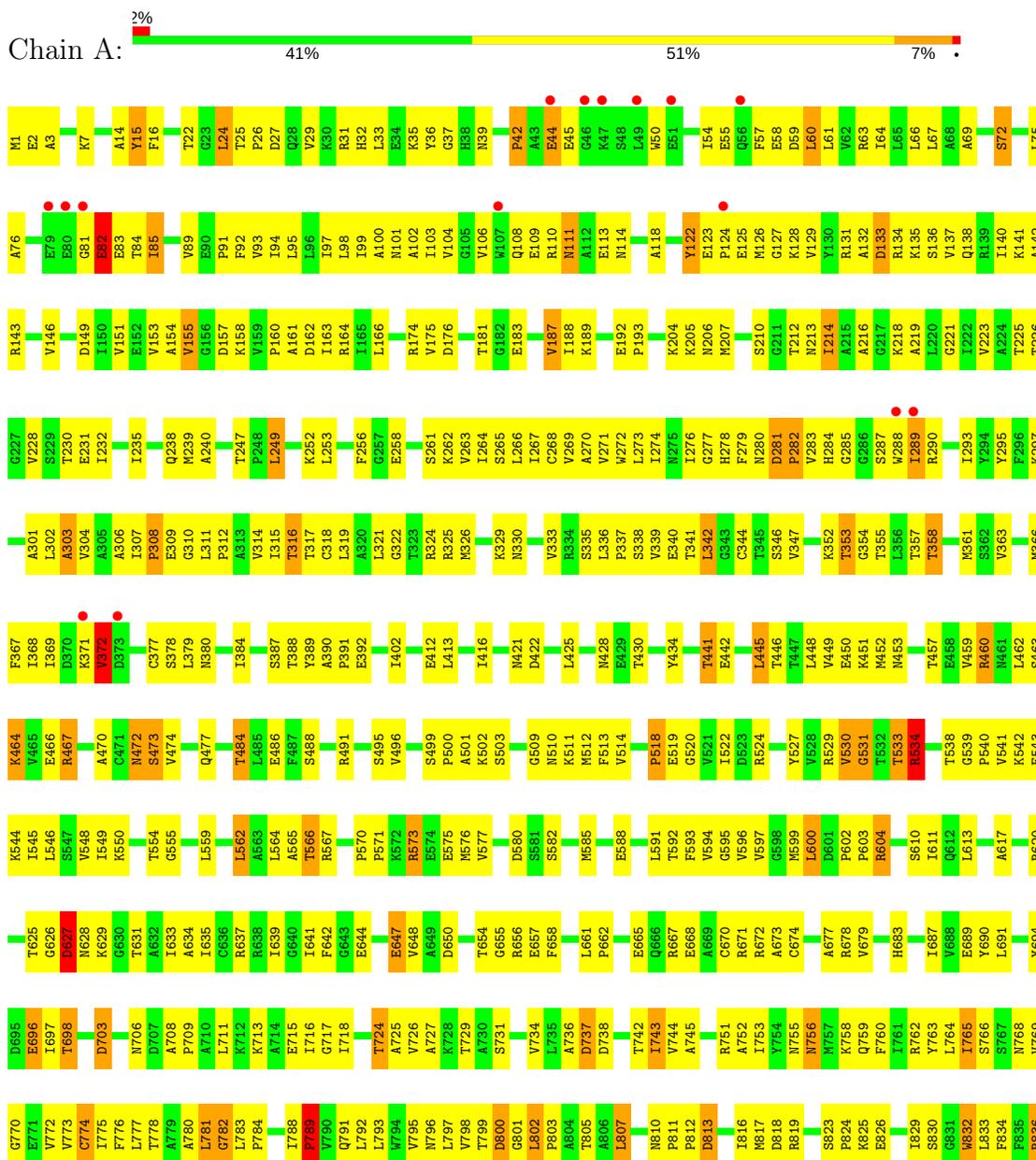
- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

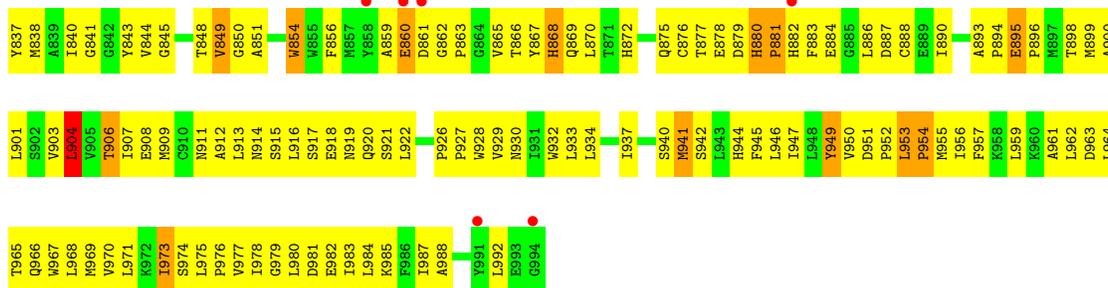
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Cl 1	0	0
4	A	1	Total 1	Cl 1	0	0

3 Residue-property plots

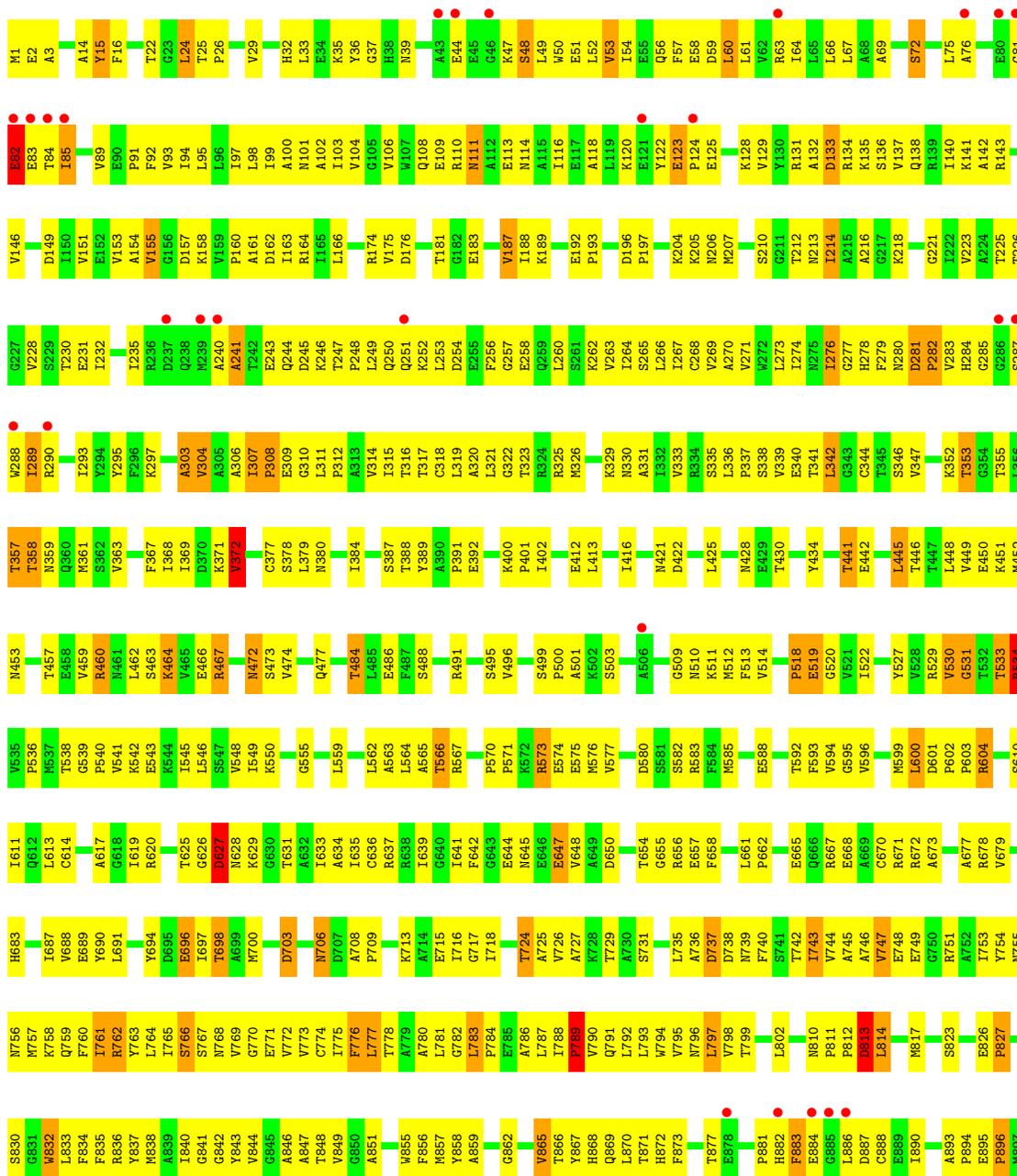
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

- Molecule 1: SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE 1





● Molecule 1: SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE 1



T898	A961	I937	Y949
M899	L962	G988	V950
A900	D963	L939	D951
L901	L964	S940	P952
S902	T965	M941	L953
L903	Q966	S942	P954
L904	M967	L943	M955
V905	L968	F945	I956
T906	P969	L946	F957
L907	V970	I947	K958
E908	L971	L948	L959
M909	K972	Y949	K960
G910	I973	V950	
M911	S974	D951	
A912	L975	P952	
L913	P976	L953	
M914	V977	M955	
S915	I978	I956	
L916	G979	F957	
S917	L980	K958	
E918	D981	L959	
M919	E982	K960	
Q920	I983		
S921	L984		
L922	K985		
	F986		
P926	I987		
P927	A988		
M928	V991		
V929	L992		
M930	E993		
L931	G994		
M932			
L933			
L934			

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	64.95Å 81.28Å 131.01Å 97.64° 99.94° 95.22°	Depositor
Resolution (Å)	15.00 – 3.00 23.79 – 3.00	Depositor EDS
% Data completeness (in resolution range)	80.4 (15.00-3.00) 79.9 (23.79-3.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.99Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.266 , 0.317 0.262 , 0.310	Depositor DCC
R_{free} test set	1057 reflections (2.55%)	DCC
Wilson B-factor (Å ²)	75.2	Xtrriage
Anisotropy	0.441	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	15351	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.63% 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, CA, CL

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	0.49	1/7811 (0.0%)	0.72	2/10592 (0.0%)
1	B	0.48	0/7811	0.71	1/10592 (0.0%)
All	All	0.48	1/15622 (0.0%)	0.72	3/21184 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	674	CYS	CB-SG	-6.05	1.72	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	GLU	CA-CB-CG	5.91	126.40	113.40
1	A	800	ASP	N-CA-C	-5.73	95.52	111.00
1	B	82	GLU	CA-CB-CG	5.44	125.36	113.40

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	7670	0	7764	632	0
1	B	7670	0	7766	677	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	4	0	0	0	0
2	B	3	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	1	0
4	B	1	0	0	0	0
All	All	15351	0	15530	1309	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 42.

The worst 5 of 1309 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:830:SER:HB3	1:B:833:LEU:HB2	1.40	1.03
1:A:372:VAL:HG13	1:A:377:CYS:HB3	1.44	0.99
1:A:263:VAL:HG12	1:A:267:ILE:HD11	1.44	0.97
1:B:372:VAL:HG13	1:B:377:CYS:HB3	1.46	0.97
1:B:559:LEU:HD23	1:B:600:LEU:HB3	1.47	0.95

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	992/994 (100%)	785 (79%)	152 (15%)	55 (6%)	2	12
1	B	992/994 (100%)	774 (78%)	160 (16%)	58 (6%)	2	11
All	All	1984/1988 (100%)	1559 (79%)	312 (16%)	113 (6%)	2	12

5 of 113 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	ILE
1	A	205	LYS
1	A	283	VAL
1	A	518	PRO
1	A	519	GLU

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	840/840 (100%)	782 (93%)	58 (7%)	18	53
1	B	840/840 (100%)	786 (94%)	54 (6%)	20	57
All	All	1680/1680 (100%)	1568 (93%)	112 (7%)	19	54

5 of 112 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	895	GLU
1	B	111	ASN
1	B	832	TRP
1	A	906	THR
1	A	971	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	919	ASN
1	B	138	GLN
1	B	911	ASN
1	B	111	ASN
1	A	360	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 11 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, 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	994/994 (100%)	-0.32	21 (2%) 64 34	24, 73, 138, 174	0
1	B	994/994 (100%)	-0.21	29 (2%) 52 24	24, 77, 138, 175	0
All	All	1988/1988 (100%)	-0.26	50 (2%) 58 29	24, 75, 138, 175	0

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	80	GLU	7.8
1	B	287	SER	6.8
1	B	85	ILE	5.1
1	A	49	LEU	4.7
1	B	83	GLU	4.7

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 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(\AA^2)	Q<0.9
3	K	B	997	1/1	0.94	0.29	5.52	69,69,69,69	0
2	CA	B	996	1/1	0.96	0.31	2.11	52,52,52,52	0
3	K	A	997	1/1	0.87	0.20	1.16	91,91,91,91	0
2	CA	A	995	1/1	0.97	0.28	0.99	49,49,49,49	0
2	CA	B	995	1/1	0.93	0.26	0.84	70,70,70,70	0
2	CA	A	996	1/1	0.98	0.26	0.84	39,39,39,39	0
2	CA	B	998	1/1	0.96	0.23	0.54	84,84,84,84	0
2	CA	A	998	1/1	0.89	0.14	-0.65	64,64,64,64	0
4	CL	A	1000	1/1	0.97	0.14	-0.72	56,56,56,56	0
4	CL	B	999	1/1	0.95	0.11	-2.10	40,40,40,40	0
2	CA	A	999	1/1	0.87	0.11	-	83,83,83,83	0

6.5 Other polymers [i](#)

There are no such residues in this entry.