



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 07:40 pm GMT

PDB ID : 3VBL
Title : Crystal Structure of the S84C mutant of AntD, an N-acyltransferase from *Bacillus cereus* in complex with dTDP-4-amino-4,6-dideoxyglucose and Coenzyme A
Authors : Kubiak, R.L.; Holden, H.M.
Deposited on : 2012-01-02
Resolution : 1.90 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

<https://www.wwpdb.org/validation/2017/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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

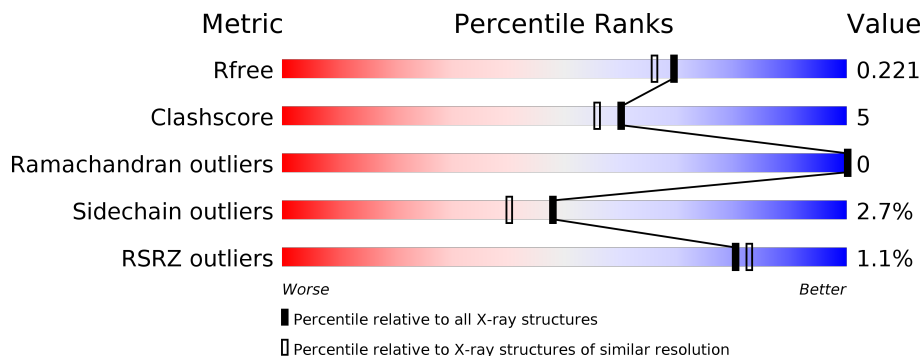
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	111664	5502 (1.90-1.90)
Clashscore	122126	6115 (1.90-1.90)
Ramachandran outliers	120053	6048 (1.90-1.90)
Sidechain outliers	120020	6048 (1.90-1.90)
RSRZ outliers	108989	5379 (1.90-1.90)

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	205	
1	C	205	
1	E	205	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4992 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 Galactoside O-acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	187	Total	C	N	O	S	0	5	0
			1472	954	245	265	8			
1	C	189	Total	C	N	O	S	0	1	0
			1465	945	244	268	8			
1	E	188	Total	C	N	O	S	0	2	0
			1460	944	242	266	8			

There are 54 discrepancies between the modelled and reference sequences:

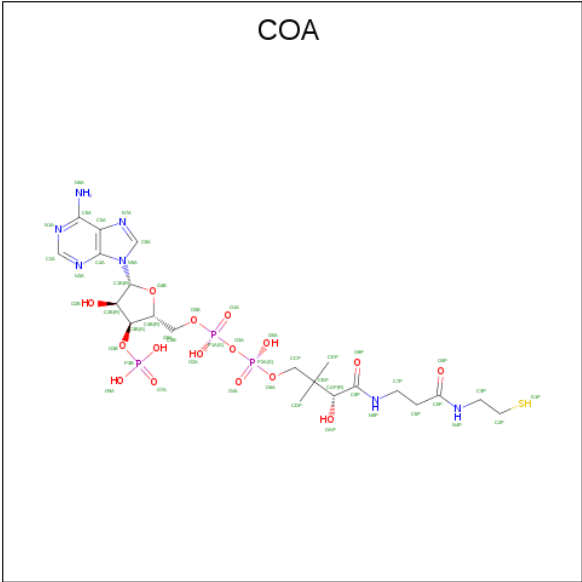
Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	MET	-	EXPRESSION TAG	UNP D7WGJ0
A	-15	GLY	-	EXPRESSION TAG	UNP D7WGJ0
A	-14	SER	-	EXPRESSION TAG	UNP D7WGJ0
A	-13	HIS	-	EXPRESSION TAG	UNP D7WGJ0
A	-12	HIS	-	EXPRESSION TAG	UNP D7WGJ0
A	-11	HIS	-	EXPRESSION TAG	UNP D7WGJ0
A	-10	HIS	-	EXPRESSION TAG	UNP D7WGJ0
A	-9	HIS	-	EXPRESSION TAG	UNP D7WGJ0
A	-8	HIS	-	EXPRESSION TAG	UNP D7WGJ0
A	-7	GLU	-	EXPRESSION TAG	UNP D7WGJ0
A	-6	ASN	-	EXPRESSION TAG	UNP D7WGJ0
A	-5	LEU	-	EXPRESSION TAG	UNP D7WGJ0
A	-4	TYR	-	EXPRESSION TAG	UNP D7WGJ0
A	-3	PHE	-	EXPRESSION TAG	UNP D7WGJ0
A	-2	GLN	-	EXPRESSION TAG	UNP D7WGJ0
A	-1	GLY	-	EXPRESSION TAG	UNP D7WGJ0
A	0	HIS	-	EXPRESSION TAG	UNP D7WGJ0
A	84	CYS	SER	ENGINEERED MUTATION	UNP D7WGJ0
C	-16	MET	-	EXPRESSION TAG	UNP D7WGJ0
C	-15	GLY	-	EXPRESSION TAG	UNP D7WGJ0
C	-14	SER	-	EXPRESSION TAG	UNP D7WGJ0
C	-13	HIS	-	EXPRESSION TAG	UNP D7WGJ0
C	-12	HIS	-	EXPRESSION TAG	UNP D7WGJ0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-11	HIS	-	EXPRESSION TAG	UNP D7WGJ0
C	-10	HIS	-	EXPRESSION TAG	UNP D7WGJ0
C	-9	HIS	-	EXPRESSION TAG	UNP D7WGJ0
C	-8	HIS	-	EXPRESSION TAG	UNP D7WGJ0
C	-7	GLU	-	EXPRESSION TAG	UNP D7WGJ0
C	-6	ASN	-	EXPRESSION TAG	UNP D7WGJ0
C	-5	LEU	-	EXPRESSION TAG	UNP D7WGJ0
C	-4	TYR	-	EXPRESSION TAG	UNP D7WGJ0
C	-3	PHE	-	EXPRESSION TAG	UNP D7WGJ0
C	-2	GLN	-	EXPRESSION TAG	UNP D7WGJ0
C	-1	GLY	-	EXPRESSION TAG	UNP D7WGJ0
C	0	HIS	-	EXPRESSION TAG	UNP D7WGJ0
C	84	CYS	SER	ENGINEERED MUTATION	UNP D7WGJ0
E	-16	MET	-	EXPRESSION TAG	UNP D7WGJ0
E	-15	GLY	-	EXPRESSION TAG	UNP D7WGJ0
E	-14	SER	-	EXPRESSION TAG	UNP D7WGJ0
E	-13	HIS	-	EXPRESSION TAG	UNP D7WGJ0
E	-12	HIS	-	EXPRESSION TAG	UNP D7WGJ0
E	-11	HIS	-	EXPRESSION TAG	UNP D7WGJ0
E	-10	HIS	-	EXPRESSION TAG	UNP D7WGJ0
E	-9	HIS	-	EXPRESSION TAG	UNP D7WGJ0
E	-8	HIS	-	EXPRESSION TAG	UNP D7WGJ0
E	-7	GLU	-	EXPRESSION TAG	UNP D7WGJ0
E	-6	ASN	-	EXPRESSION TAG	UNP D7WGJ0
E	-5	LEU	-	EXPRESSION TAG	UNP D7WGJ0
E	-4	TYR	-	EXPRESSION TAG	UNP D7WGJ0
E	-3	PHE	-	EXPRESSION TAG	UNP D7WGJ0
E	-2	GLN	-	EXPRESSION TAG	UNP D7WGJ0
E	-1	GLY	-	EXPRESSION TAG	UNP D7WGJ0
E	0	HIS	-	EXPRESSION TAG	UNP D7WGJ0
E	84	CYS	SER	ENGINEERED MUTATION	UNP D7WGJ0

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).

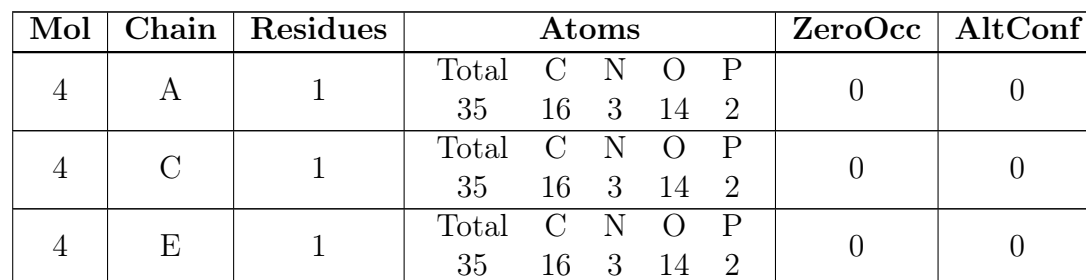


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	E	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is dTDP-4-amino-4,6-dideoxyglucose (three-letter code: 0FX) (formula: C₁₆H₂₇N₃O₁₄P₂).



- BCT
-
- The diagram shows the chemical structure of Bicarbonate (BCT). A central carbon atom (labeled 'C' in green) is bonded to three oxygen atoms and one hydrogen atom. One oxygen atom (labeled 'O1' in green) is double-bonded to the carbon. Another oxygen atom (labeled 'O2' in green) is single-bonded to the carbon and carries a negative charge (O⁻). The third oxygen atom (labeled 'O3' in green) is single-bonded to the carbon and is part of a hydroxyl group (OH). The hydrogen atom is also labeled 'O3' in green. The bonds are shown in grey, with red lines indicating the double bond and the single bonds to the negatively charged oxygen and the hydroxyl group.

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



Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			4	1	3		
5	E	1	Total	C	O	0	0
			4	1	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	143	Total	O	0	0
			143	143		
6	C	99	Total	O	0	0
			99	99		
6	E	91	Total	O	0	0
			91	91		

- Molecule 1: Galactoside O-acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	70.75Å 70.75Å 138.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.95 – 1.90 33.95 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.3 (33.95-1.90) 97.3 (33.95-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.170 , 0.220 0.170 , 0.221	Depositor DCC
R_{free} test set	2630 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	14.6	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.047 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4992	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% 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: COA, BCT, CL, OFX

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	0/1514	1.10	3/2040 (0.1%)
1	C	0.50	0/1495	1.14	7/2014 (0.3%)
1	E	0.49	0/1493	1.08	4/2012 (0.2%)
All	All	0.49	0/4502	1.11	14/6066 (0.2%)

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	166	ARG	NE-CZ-NH2	-7.67	116.46	120.30
1	E	148[A]	SER	CB-CA-C	6.97	123.34	110.10
1	E	148[B]	SER	CB-CA-C	6.97	123.34	110.10
1	A	95	ASP	CB-CG-OD2	6.37	124.03	118.30
1	C	1	MET	CG-SD-CE	6.28	110.24	100.20

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	1472	0	1538	15	0
1	C	1465	0	1512	21	0
1	E	1460	0	1510	15	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	48	0	31	0	0
2	C	48	0	31	0	0
2	E	48	0	31	1	0
3	A	1	0	0	0	0
4	A	35	0	26	1	0
4	C	35	0	26	0	0
4	E	35	0	26	0	0
5	A	4	0	0	0	0
5	C	4	0	0	0	0
5	E	4	0	0	0	0
6	A	143	0	0	2	0
6	C	99	0	0	3	0
6	E	91	0	0	1	0
All	All	4992	0	4731	47	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 5.

The worst 5 of 47 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:E:144:VAL:HG13	1:E:148[B]:SER:OG	1.85	0.77
1:C:1:MET:H	1:C:1:MET:HE2	1.57	0.69
1:C:76:GLU:OE2	1:C:117:LYS:NZ	2.26	0.69
1:C:1:MET:HG2	1:C:2:ASN:N	2.07	0.68
1:C:7:GLN:O	1:C:7:GLN:NE2	2.25	0.68

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	190/205 (93%)	182 (96%)	8 (4%)	0	100	100
1	C	188/205 (92%)	181 (96%)	7 (4%)	0	100	100
1	E	188/205 (92%)	182 (97%)	6 (3%)	0	100	100
All	All	566/615 (92%)	545 (96%)	21 (4%)	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	163/174 (94%)	158 (97%)	5 (3%)	43	34
1	C	161/174 (92%)	156 (97%)	5 (3%)	43	34
1	E	160/174 (92%)	157 (98%)	3 (2%)	60	55
All	All	484/522 (93%)	471 (97%)	13 (3%)	48	40

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1	MET
1	C	7	GLN
1	E	32	ASN
1	A	185	SER
1	C	109	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	7	GLN
1	C	21	ASN
1	C	108	ASN
1	A	108	ASN
1	C	41	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 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	$\# Z > 2$
4	0FX	A	1500	-	29,37,37	0.59	0	41,57,57	1.94	11 (26%)
2	COA	A	189	1	41,50,50	0.72	1 (2%)	51,75,75	1.82	7 (13%)
5	BCT	A	453	-	0,3,3	0.00	-	0,3,3	0.00	-
4	0FX	C	1500	-	29,37,37	0.60	0	41,57,57	2.34	11 (26%)
2	COA	C	189	1	41,50,50	0.81	1 (2%)	51,75,75	1.86	7 (13%)
5	BCT	C	453	-	0,3,3	0.00	-	0,3,3	0.00	-
4	0FX	E	1500	-	29,37,37	0.60	0	41,57,57	1.94	11 (26%)
2	COA	E	189	1	41,50,50	0.87	2 (4%)	51,75,75	2.10	7 (13%)
5	BCT	E	453	-	0,3,3	0.00	-	0,3,3	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	0FX	A	1500	-	-	0/17/53/53	0/3/3/3
2	COA	A	189	1	-	0/44/64/64	0/3/3/3
5	BCT	A	453	-	-	0/0/0/0	0/0/0/0
4	0FX	C	1500	-	-	0/17/53/53	0/3/3/3
2	COA	C	189	1	-	0/44/64/64	0/3/3/3
5	BCT	C	453	-	-	0/0/0/0	0/0/0/0
4	0FX	E	1500	-	-	0/17/53/53	0/3/3/3
2	COA	E	189	1	-	0/44/64/64	0/3/3/3
5	BCT	E	453	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	189	COA	C8A-N9A	-2.72	1.33	1.36
2	A	189	COA	P3B-O3B	2.20	1.63	1.59
2	C	189	COA	O4B-C1B	2.35	1.44	1.41
2	E	189	COA	P3B-O3B	2.40	1.63	1.59

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	189	COA	N3A-C2A-N1A	-11.47	119.05	128.86
2	C	189	COA	N3A-C2A-N1A	-10.09	120.22	128.86
2	A	189	COA	N3A-C2A-N1A	-8.79	121.34	128.86
4	C	1500	0FX	C1G-C2G-C3G	-5.82	97.80	109.98
4	E	1500	0FX	C1G-C2G-C3G	-3.97	101.67	109.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1500	0FX	1	0
2	E	189	COA	1	0

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 [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	187/205 (91%)	-0.22	1 (0%) 90 92	6, 14, 32, 55	0
1	C	189/205 (92%)	-0.16	2 (1%) 80 83	8, 16, 36, 68	0
1	E	188/205 (91%)	-0.13	3 (1%) 72 75	7, 16, 38, 51	0
All	All	564/615 (91%)	-0.17	6 (1%) 80 83	6, 15, 36, 68	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	188	SER	5.0
1	C	187	ASN	3.9
1	E	-1	GLY	3.9
1	E	73	VAL	2.8
1	A	184	LYS	2.6

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. 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(\AA^2)	Q<0.9
4	0FX	C	1500	35/35	0.95	0.11	18,26,56,60	0
5	BCT	A	453	4/4	0.96	0.08	21,25,27,27	0
4	0FX	A	1500	35/35	0.97	0.09	12,23,50,53	0
5	BCT	C	453	4/4	0.97	0.07	15,19,20,21	0
2	COA	C	189	48/48	0.97	0.08	6,14,31,36	0
2	COA	A	189	48/48	0.97	0.07	5,13,34,36	0
4	0FX	E	1500	35/35	0.97	0.09	9,19,47,49	0
2	COA	E	189	48/48	0.97	0.07	4,13,26,32	0
5	BCT	E	453	4/4	0.97	0.08	19,21,23,25	0
3	CL	A	190	1/1	0.99	0.06	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.