



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 5, 2017 – 03:37 PM EST

PDB ID : 4KU2
Title : Crystal Structure C143A from Xanthomonas campestris Bound with Myristoyl-CoA
Authors : Goblirsch, B.R.
Deposited on : 2013-05-21
Resolution : 1.97 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

<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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
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) : rb-20028442

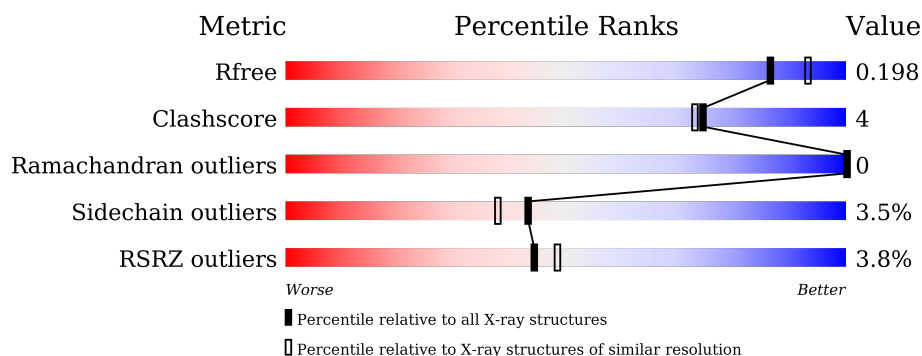
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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	8664 (2.00-1.96)
Clashscore	102246	9905 (2.00-1.96)
Ramachandran outliers	100387	9792 (2.00-1.96)
Sidechain outliers	100360	9791 (2.00-1.96)
RSRZ outliers	91569	8679 (2.00-1.96)

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	358	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 87%, yellow 8%, green 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 87% 8% 5% </div> </div>
1	B	358	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 6%, orange 81%, yellow 13%, green 6%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 6% 81% 13% • 6% </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5772 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 3-oxoacyl-[ACP] synthase III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	10	0
			2652	1665	468	505	14			
1	B	338	Total	C	N	O	S	0	7	0
			2610	1645	454	496	15			

There are 42 discrepancies between the modelled and reference sequences:

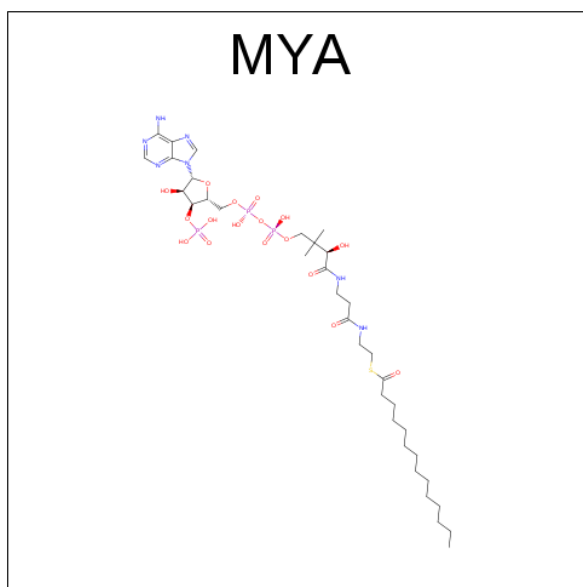
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP Q8PDX2
A	2	GLY	-	EXPRESSION TAG	UNP Q8PDX2
A	3	SER	-	EXPRESSION TAG	UNP Q8PDX2
A	4	SER	-	EXPRESSION TAG	UNP Q8PDX2
A	5	HIS	-	EXPRESSION TAG	UNP Q8PDX2
A	6	HIS	-	EXPRESSION TAG	UNP Q8PDX2
A	7	HIS	-	EXPRESSION TAG	UNP Q8PDX2
A	8	HIS	-	EXPRESSION TAG	UNP Q8PDX2
A	9	HIS	-	EXPRESSION TAG	UNP Q8PDX2
A	10	HIS	-	EXPRESSION TAG	UNP Q8PDX2
A	11	SER	-	EXPRESSION TAG	UNP Q8PDX2
A	12	SER	-	EXPRESSION TAG	UNP Q8PDX2
A	13	GLY	-	EXPRESSION TAG	UNP Q8PDX2
A	14	LEU	-	EXPRESSION TAG	UNP Q8PDX2
A	15	VAL	-	EXPRESSION TAG	UNP Q8PDX2
A	16	PRO	-	EXPRESSION TAG	UNP Q8PDX2
A	17	ARG	-	EXPRESSION TAG	UNP Q8PDX2
A	18	GLY	-	EXPRESSION TAG	UNP Q8PDX2
A	19	SER	-	EXPRESSION TAG	UNP Q8PDX2
A	20	HIS	-	EXPRESSION TAG	UNP Q8PDX2
A	143	ALA	CYS	ENGINEERED MUTATION	UNP Q8PDX2
B	1	MET	-	INITIATING METHIONINE	UNP Q8PDX2
B	2	GLY	-	EXPRESSION TAG	UNP Q8PDX2
B	3	SER	-	EXPRESSION TAG	UNP Q8PDX2
B	4	SER	-	EXPRESSION TAG	UNP Q8PDX2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5	HIS	-	EXPRESSION TAG	UNP Q8PDX2
B	6	HIS	-	EXPRESSION TAG	UNP Q8PDX2
B	7	HIS	-	EXPRESSION TAG	UNP Q8PDX2
B	8	HIS	-	EXPRESSION TAG	UNP Q8PDX2
B	9	HIS	-	EXPRESSION TAG	UNP Q8PDX2
B	10	HIS	-	EXPRESSION TAG	UNP Q8PDX2
B	11	SER	-	EXPRESSION TAG	UNP Q8PDX2
B	12	SER	-	EXPRESSION TAG	UNP Q8PDX2
B	13	GLY	-	EXPRESSION TAG	UNP Q8PDX2
B	14	LEU	-	EXPRESSION TAG	UNP Q8PDX2
B	15	VAL	-	EXPRESSION TAG	UNP Q8PDX2
B	16	PRO	-	EXPRESSION TAG	UNP Q8PDX2
B	17	ARG	-	EXPRESSION TAG	UNP Q8PDX2
B	18	GLY	-	EXPRESSION TAG	UNP Q8PDX2
B	19	SER	-	EXPRESSION TAG	UNP Q8PDX2
B	20	HIS	-	EXPRESSION TAG	UNP Q8PDX2
B	143	ALA	CYS	ENGINEERED MUTATION	UNP Q8PDX2

- Molecule 2 is TETRADECANOYL-COA (three-letter code: MYA) (formula: $C_{35}H_{62}N_7O_{17}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	S	0	0
			63	35	7	17	3	1		

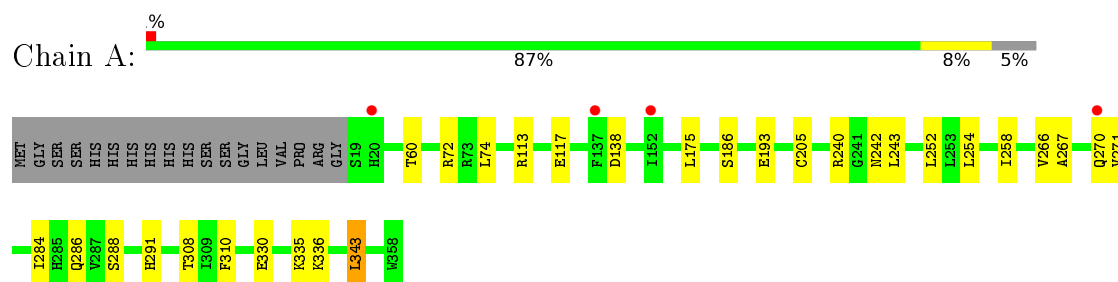
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	242	Total 242	O 242	0	4
3	B	205	Total 205	O 205	0	0

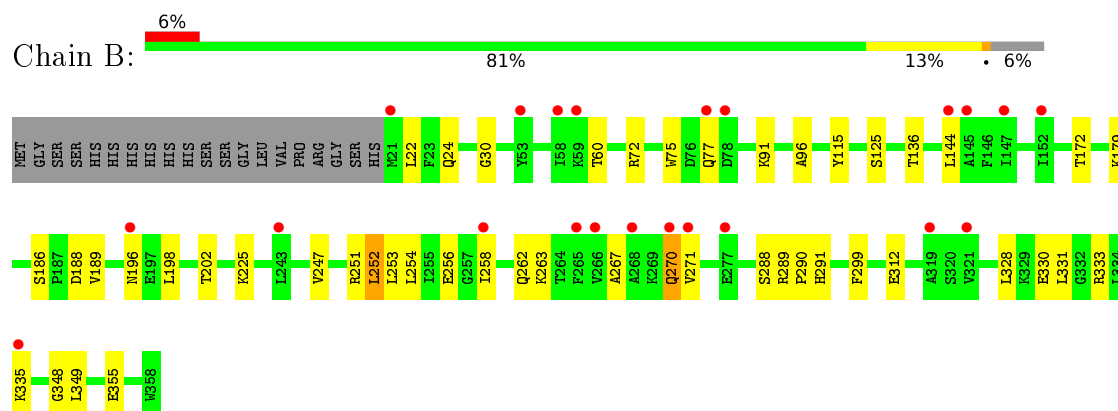
3 Residue-property plots

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 ($RSRZ > 2$). 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: 3-oxoacyl-[ACP] synthase III



- Molecule 1: 3-oxoacyl-[ACP] synthase III



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.20Å 85.38Å 102.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.78 – 1.97 31.78 – 1.97	Depositor EDS
% Data completeness (in resolution range)	98.4 (31.78-1.97) 96.4 (31.78-1.97)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.35 (at 1.98Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.157 , 0.199 0.155 , 0.198	Depositor DCC
R_{free} test set	2489 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	28.0	Xtriage
Anisotropy	0.617	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.028 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5772	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MYA

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	0.60	0/2708	0.64	0/3667
1	B	0.59	0/2660	0.63	0/3602
All	All	0.60	0/5368	0.64	0/7269

There are no bond length outliers.

There are no bond angle outliers.

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	2652	0	2685	17	0
1	B	2610	0	2661	27	0
2	B	63	0	58	3	0
3	A	242	0	0	2	0
3	B	205	0	0	7	0
All	All	5772	0	5404	43	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 4.

All (43) 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:91:LYS:NZ	3:B:704:HOH:O	2.18	0.75
1:B:312:GLU:OE1	3:B:681:HOH:O	2.10	0.70
1:A:288:SER:HG	1:A:291[B]:HIS:HD1	1.34	0.67
1:B:330[B]:GLU:OE2	3:B:626:HOH:O	2.13	0.66
1:A:240:ARG:HD3	3:A:521:HOH:O	1.96	0.65
1:B:270:GLN:HG3	1:B:271:VAL:HG12	1.79	0.64
1:A:254:LEU:O	1:A:258:ILE:HG12	2.05	0.56
1:A:240:ARG:HD2	1:B:115:TYR:CZ	2.42	0.55
1:A:113[A]:ARG:NH2	1:A:138:ASP:OD2	2.40	0.54
1:B:251:ARG:NH2	2:B:401:MYA:O1A	2.38	0.54
1:A:286:GLN:HE22	1:A:308[A]:THR:HB	1.71	0.54
1:B:330[B]:GLU:OE1	3:B:603:HOH:O	2.19	0.52
1:B:198:LEU:O	1:B:198:LEU:HG	2.10	0.51
1:B:289:ARG:HB3	1:B:290:PRO:HD3	1.92	0.51
1:B:254:LEU:HD12	1:B:291:HIS:CE1	2.46	0.51
1:A:266:VAL:O	1:A:270:GLN:HG3	2.11	0.49
1:A:113[B]:ARG:NH2	1:A:138:ASP:OD2	2.47	0.48
1:B:77:GLN:NE2	3:B:556:HOH:O	2.42	0.48
1:B:60:THR:OG1	2:B:401:MYA:O7A	2.30	0.46
1:B:202:THR:HG21	2:B:401:MYA:H7A	1.98	0.46
1:B:75:TRP:CD1	1:B:172[A]:THR:HG22	2.52	0.45
1:B:196:ASN:ND2	1:B:247:VAL:HG13	2.32	0.45
1:B:348:GLY:N	1:B:349:LEU:HA	2.32	0.45
1:A:242[B]:ASN:C	1:A:242[B]:ASN:HD22	2.20	0.44
1:A:252:LEU:HD23	1:A:252:LEU:HA	1.90	0.43
1:B:125:SER:OG	1:B:136:THR:HG21	2.18	0.43
1:B:186:SER:HB3	1:B:188:ASP:OD1	2.17	0.43
1:A:193[B]:GLU:HG3	3:A:576:HOH:O	2.17	0.43
1:B:328:LEU:HD22	1:B:333:ARG:HD2	2.01	0.43
1:A:288:SER:OG	1:A:291[B]:HIS:ND1	2.27	0.43
1:A:267:ALA:O	1:A:271:VAL:HG13	2.20	0.42
1:A:288:SER:HA	1:A:310:PHE:CZ	2.55	0.42
1:A:284:ILE:HG12	1:A:343:LEU:HD13	2.01	0.42
1:B:288:SER:OG	1:B:290:PRO:HD2	2.20	0.41
1:B:355:GLU:OE2	3:B:621:HOH:O	2.22	0.41
1:B:30:GLY:HA3	1:B:96:ALA:HB2	2.01	0.41
1:B:252:LEU:HD22	1:B:256:GLU:HG2	2.03	0.41
1:B:263:LYS:O	3:B:605:HOH:O	2.22	0.41
1:A:74:LEU:HA	1:A:205:CYS:SG	2.61	0.41
1:A:175:LEU:HD23	1:A:243:LEU:HD13	2.01	0.41
1:B:267:ALA:O	1:B:271:VAL:HG13	2.20	0.41
1:B:22:LEU:HD13	1:B:225:LYS:HE2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:262:GLN:HA	1:B:299:PHE:HZ	1.86	0.40

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	348/358 (97%)	340 (98%)	8 (2%)	0	100	100
1	B	343/358 (96%)	334 (97%)	9 (3%)	0	100	100
All	All	691/716 (96%)	674 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	284/289 (98%)	275 (97%)	9 (3%)	46	41
1	B	279/289 (96%)	268 (96%)	11 (4%)	39	32
All	All	563/578 (97%)	543 (96%)	20 (4%)	43	36

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	THR
1	A	72	ARG
1	A	117	GLU
1	A	186	SER
1	A	330[A]	GLU
1	A	330[B]	GLU
1	A	335	LYS
1	A	336	LYS
1	A	343	LEU
1	B	24	GLN
1	B	72	ARG
1	B	144	LEU
1	B	179	LYS
1	B	189	VAL
1	B	252	LEU
1	B	253	LEU
1	B	258	ILE
1	B	270	GLN
1	B	331	LEU
1	B	335	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	286	GLN
1	B	108	ASN
1	B	196	ASN
1	B	262	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

1 ligand is modelled in this entry.

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$
2	MYA	B	401	-	53,65,65	1.56	6 (11%)	64,91,91	2.72	11 (17%)

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
2	MYA	B	401	-	-	0/59/80/80	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	MYA	C2X-C3X	-2.60	1.47	1.53
2	B	401	MYA	O10-C10	-2.44	1.37	1.42
2	B	401	MYA	C14-C11	-2.15	1.49	1.53
2	B	401	MYA	C6A-N6A	2.41	1.44	1.34
2	B	401	MYA	C5-N4	5.20	1.46	1.33
2	B	401	MYA	C9-N8	6.92	1.48	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	MYA	N3A-C2A-N1A	-11.21	120.07	128.87
2	B	401	MYA	O8A-P3X-O9A	-8.26	83.67	110.63
2	B	401	MYA	C4X-O4X-C1X	-6.18	103.09	109.64
2	B	401	MYA	O7A-P3X-O8A	-5.63	86.78	107.44
2	B	401	MYA	C2X-C3X-C4X	-2.39	98.67	103.25
2	B	401	MYA	C5X-C4X-C3X	-2.12	106.50	114.30
2	B	401	MYA	O4X-C4X-C3X	2.37	110.36	104.89
2	B	401	MYA	O4X-C1X-N9A	2.38	112.61	108.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	MYA	C2-S1-C2M	5.40	107.96	100.70
2	B	401	MYA	O2M-C2M-C3M	6.29	120.65	109.26
2	B	401	MYA	O7A-P3X-O9A	9.21	140.69	110.63

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	MYA	3	0

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

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	340/358 (94%)	-0.15	4 (1%) 81 83	18, 30, 48, 70	0
1	B	338/358 (94%)	0.25	22 (6%) 22 25	18, 34, 66, 84	0
All	All	678/716 (94%)	0.05	26 (3%) 44 48	18, 32, 60, 84	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	59	LYS	3.4
1	B	78	ASP	3.3
1	B	321	VAL	3.3
1	B	277	GLU	3.2
1	B	144	LEU	3.1
1	B	271	VAL	3.0
1	B	243	LEU	3.0
1	B	147	ILE	2.9
1	B	58	ILE	2.9
1	A	20	HIS	2.7
1	A	152	ILE	2.6
1	A	270	GLN	2.6
1	B	77	GLN	2.6
1	B	319	ALA	2.5
1	B	270	GLN	2.4
1	B	53	TYR	2.4
1	B	145	ALA	2.3
1	B	258	ILE	2.3
1	B	268	ALA	2.3
1	A	137	PHE	2.2
1	B	196	ASN	2.2
1	B	152	ILE	2.2
1	B	21	MET	2.2
1	B	335	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	266	VAL	2.1
1	B	265	PHE	2.1

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
2	MYA	B	401	63/63	0.86	0.16	0.94	30,44,73,158	63

6.5 Other polymers [i](#)

There are no such residues in this entry.