Full wwPDB X-ray Structure Validation Report ⓘ

Nov 22, 2023 – 11:05 AM JST

PDB ID	:	7EI3
Title	:	Crystal structure of MasL, a thiolase from Massilia sp. YMA4
Authors	:	Lin, C.C.; Huang, K.F.; Yang, Y.L.
Deposited on	:	2021-03-30
Resolution	:	1.78 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

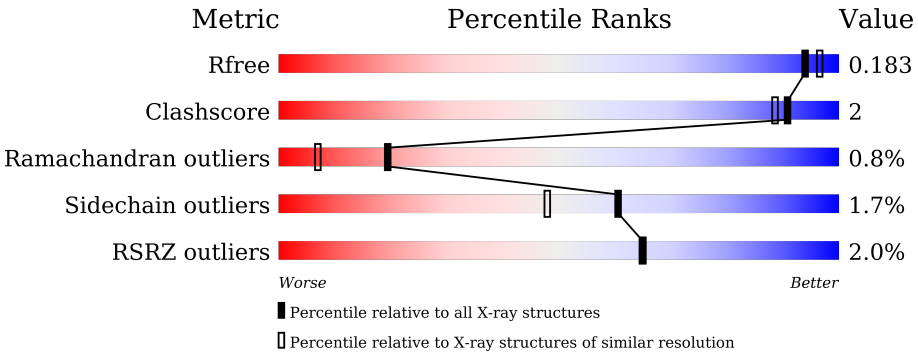
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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}	130704	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	407	92%
1	B	407	94%
1	C	407	91% 5%
1	D	407	92%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 13180 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 Acetyl-CoA C-acyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	0	0
			2872	1793	531	540	8			
1	B	393	Total	C	N	O	S	0	0	0
			2880	1799	532	541	8			
1	C	393	Total	C	N	O	S	0	0	0
			2880	1799	532	541	8			
1	D	394	Total	C	N	O	S	0	0	0
			2889	1805	534	542	8			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A5C7BKK5
A	2	VAL	-	expression tag	UNP A0A5C7BKK5
A	183	THR	VAL	engineered mutation	UNP A0A5C7BKK5
A	395	LYS	-	expression tag	UNP A0A5C7BKK5
A	396	LEU	-	expression tag	UNP A0A5C7BKK5
A	397	ALA	-	expression tag	UNP A0A5C7BKK5
A	398	ALA	-	expression tag	UNP A0A5C7BKK5
A	399	ALA	-	expression tag	UNP A0A5C7BKK5
A	400	LEU	-	expression tag	UNP A0A5C7BKK5
A	401	GLU	-	expression tag	UNP A0A5C7BKK5
A	402	HIS	-	expression tag	UNP A0A5C7BKK5
A	403	HIS	-	expression tag	UNP A0A5C7BKK5
A	404	HIS	-	expression tag	UNP A0A5C7BKK5
A	405	HIS	-	expression tag	UNP A0A5C7BKK5
A	406	HIS	-	expression tag	UNP A0A5C7BKK5
A	407	HIS	-	expression tag	UNP A0A5C7BKK5
B	1	MET	-	initiating methionine	UNP A0A5C7BKK5
B	2	VAL	-	expression tag	UNP A0A5C7BKK5
B	183	THR	VAL	engineered mutation	UNP A0A5C7BKK5
B	395	LYS	-	expression tag	UNP A0A5C7BKK5
B	396	LEU	-	expression tag	UNP A0A5C7BKK5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	397	ALA	-	expression tag	UNP A0A5C7BKK5
B	398	ALA	-	expression tag	UNP A0A5C7BKK5
B	399	ALA	-	expression tag	UNP A0A5C7BKK5
B	400	LEU	-	expression tag	UNP A0A5C7BKK5
B	401	GLU	-	expression tag	UNP A0A5C7BKK5
B	402	HIS	-	expression tag	UNP A0A5C7BKK5
B	403	HIS	-	expression tag	UNP A0A5C7BKK5
B	404	HIS	-	expression tag	UNP A0A5C7BKK5
B	405	HIS	-	expression tag	UNP A0A5C7BKK5
B	406	HIS	-	expression tag	UNP A0A5C7BKK5
B	407	HIS	-	expression tag	UNP A0A5C7BKK5
C	1	MET	-	initiating methionine	UNP A0A5C7BKK5
C	2	VAL	-	expression tag	UNP A0A5C7BKK5
C	183	THR	VAL	engineered mutation	UNP A0A5C7BKK5
C	395	LYS	-	expression tag	UNP A0A5C7BKK5
C	396	LEU	-	expression tag	UNP A0A5C7BKK5
C	397	ALA	-	expression tag	UNP A0A5C7BKK5
C	398	ALA	-	expression tag	UNP A0A5C7BKK5
C	399	ALA	-	expression tag	UNP A0A5C7BKK5
C	400	LEU	-	expression tag	UNP A0A5C7BKK5
C	401	GLU	-	expression tag	UNP A0A5C7BKK5
C	402	HIS	-	expression tag	UNP A0A5C7BKK5
C	403	HIS	-	expression tag	UNP A0A5C7BKK5
C	404	HIS	-	expression tag	UNP A0A5C7BKK5
C	405	HIS	-	expression tag	UNP A0A5C7BKK5
C	406	HIS	-	expression tag	UNP A0A5C7BKK5
C	407	HIS	-	expression tag	UNP A0A5C7BKK5
D	1	MET	-	initiating methionine	UNP A0A5C7BKK5
D	2	VAL	-	expression tag	UNP A0A5C7BKK5
D	183	THR	VAL	engineered mutation	UNP A0A5C7BKK5
D	395	LYS	-	expression tag	UNP A0A5C7BKK5
D	396	LEU	-	expression tag	UNP A0A5C7BKK5
D	397	ALA	-	expression tag	UNP A0A5C7BKK5
D	398	ALA	-	expression tag	UNP A0A5C7BKK5
D	399	ALA	-	expression tag	UNP A0A5C7BKK5
D	400	LEU	-	expression tag	UNP A0A5C7BKK5
D	401	GLU	-	expression tag	UNP A0A5C7BKK5
D	402	HIS	-	expression tag	UNP A0A5C7BKK5
D	403	HIS	-	expression tag	UNP A0A5C7BKK5
D	404	HIS	-	expression tag	UNP A0A5C7BKK5
D	405	HIS	-	expression tag	UNP A0A5C7BKK5
D	406	HIS	-	expression tag	UNP A0A5C7BKK5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	407	HIS	-	expression tag	UNP A0A5C7BKK5

- Molecule 2 is water.

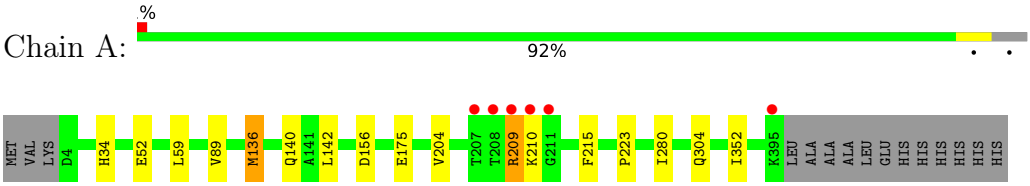
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	434	Total O 434 434	0	0
2	B	406	Total O 406 406	0	0
2	C	428	Total O 428 428	0	0
2	D	391	Total O 391 391	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

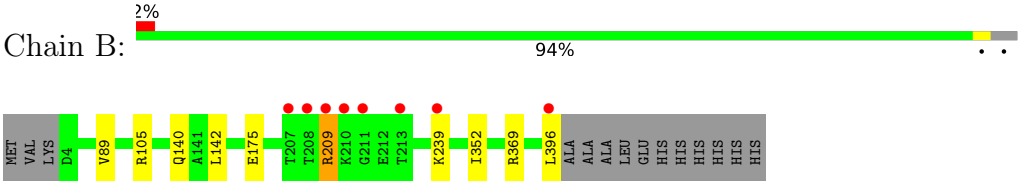
• Molecule 1: Acetyl-CoA C-acyltransferase

Chain A:



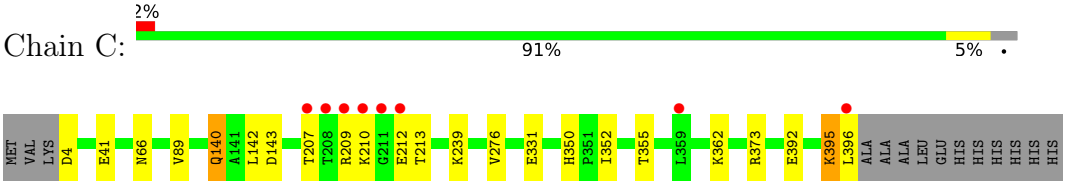
• Molecule 1: Acetyl-CoA C-acyltransferase

Chain B:



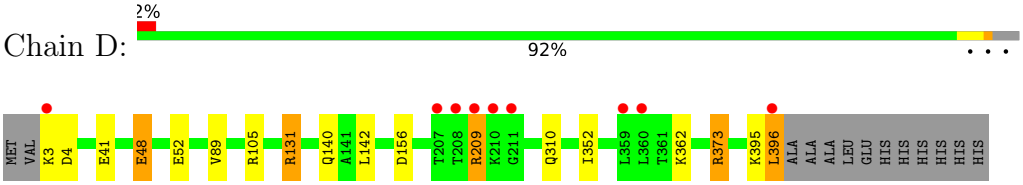
• Molecule 1: Acetyl-CoA C-acyltransferase

Chain C:



• Molecule 1: Acetyl-CoA C-acyltransferase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	71.79Å 77.00Å 98.08Å 79.77° 79.00° 62.98°	Depositor
Resolution (Å)	29.90 – 1.78 29.88 – 1.78	Depositor EDS
% Data completeness (in resolution range)	92.0 (29.90-1.78) 92.0 (29.88-1.78)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.23 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.128 , 0.180 0.130 , 0.183	Depositor DCC
R_{free} test set	7924 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	17.6	Xtriage
Anisotropy	0.291	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 42.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	13180	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.72% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	0.65	0/2919	0.76	0/3968
1	B	0.66	0/2927	0.79	4/3979 (0.1%)
1	C	0.68	1/2927 (0.0%)	0.77	0/3979
1	D	0.66	0/2936	0.84	3/3990 (0.1%)
All	All	0.66	1/11709 (0.0%)	0.79	7/15916 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	331	GLU	CD-OE2	5.97	1.32	1.25

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	131	ARG	NE-CZ-NH1	-14.33	113.13	120.30
1	D	131	ARG	NE-CZ-NH2	10.58	125.59	120.30
1	D	131	ARG	CG-CD-NE	-10.14	90.51	111.80
1	B	369	ARG	NE-CZ-NH2	-10.04	115.28	120.30
1	B	369	ARG	NE-CZ-NH1	8.42	124.51	120.30
1	B	369	ARG	CG-CD-NE	-6.83	97.45	111.80
1	B	105	ARG	CG-CD-NE	-5.16	100.97	111.80

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	2872	0	2891	10	0
1	B	2880	0	2902	4	0
1	C	2880	0	2902	14	0
1	D	2889	0	2915	13	0
2	A	434	0	0	4	0
2	B	406	0	0	3	0
2	C	428	0	0	8	0
2	D	391	0	0	7	0
All	All	13180	0	11610	39	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 2.

All (39) 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:4:ASP:HB2	2:D:760:HOH:O	1.40	1.16
1:D:156:ASP:HB2	2:D:768:HOH:O	1.62	0.96
1:B:175:GLU:HG2	2:B:843:HOH:O	1.66	0.96
1:C:207:THR:HG22	1:C:212:GLU:HG2	1.55	0.88
1:A:156:ASP:HB3	2:A:764:HOH:O	1.80	0.82
1:C:207:THR:HG22	1:C:212:GLU:CG	2.21	0.70
1:C:4:ASP:N	2:C:501:HOH:O	2.31	0.62
1:B:175:GLU:CB	2:B:843:HOH:O	2.53	0.56
1:A:175:GLU:HG3	2:A:730:HOH:O	2.05	0.56
1:D:310:GLN:HG2	2:D:675:HOH:O	2.08	0.52
1:B:140:GLN:HG2	1:B:142:LEU:HD23	1.91	0.52
1:C:350:HIS:HD2	1:C:355:THR:OG1	1.93	0.51
1:A:280:ILE:H	1:A:304:GLN:NE2	2.08	0.51
1:D:140:GLN:HG2	1:D:142:LEU:HD23	1.93	0.50
1:C:350:HIS:HE1	2:C:819:HOH:O	1.92	0.50
1:D:362:LYS:HE3	2:D:600:HOH:O	2.10	0.50
1:C:140:GLN:HG2	1:C:142:LEU:HD23	1.94	0.49
1:C:143:ASP:OD2	1:D:131:ARG:NH1	2.40	0.49
1:D:373:ARG:NH1	2:D:503:HOH:O	2.46	0.49
1:A:136:MET:HE1	2:C:623:HOH:O	2.13	0.48
2:C:675:HOH:O	1:D:105:ARG:HD2	2.13	0.48
1:C:362:LYS:HD3	2:C:534:HOH:O	2.14	0.48
1:D:48:GLU:HG3	2:D:732:HOH:O	2.14	0.48
1:A:223:PRO:HG3	2:A:566:HOH:O	2.13	0.47
1:C:143:ASP:CG	1:D:131:ARG:HH12	2.18	0.47
1:C:276:VAL:CG1	1:C:392:GLU:HB3	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:GLN:HG2	1:A:142:LEU:HD23	1.98	0.46
1:C:362:LYS:CD	2:C:534:HOH:O	2.65	0.44
1:A:136:MET:CE	2:C:623:HOH:O	2.65	0.44
1:C:41:GLU:HG3	2:C:696:HOH:O	2.19	0.43
1:B:175:GLU:HB3	2:B:843:HOH:O	2.17	0.42
1:D:41:GLU:HG3	2:D:522:HOH:O	2.20	0.42
1:D:395:LYS:O	1:D:396:LEU:HB3	2.19	0.42
1:A:34:HIS:CD2	1:A:204:VAL:HG12	2.55	0.42
1:C:395:LYS:HB3	1:C:395:LYS:HE3	1.77	0.41
1:D:3:LYS:HD2	1:D:105:ARG:NH2	2.34	0.41
1:A:156:ASP:CB	2:A:764:HOH:O	2.54	0.41
1:A:204:VAL:HG22	1:A:215:PHE:HB3	2.02	0.41
1:C:276:VAL:HG13	1:C:392:GLU:HB3	2.04	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	390/407 (96%)	380 (97%)	7 (2%)	3 (1%)	19 7
1	B	391/407 (96%)	381 (97%)	7 (2%)	3 (1%)	19 7
1	C	391/407 (96%)	380 (97%)	7 (2%)	4 (1%)	15 4
1	D	392/407 (96%)	382 (97%)	7 (2%)	3 (1%)	19 7
All	All	1564/1628 (96%)	1523 (97%)	28 (2%)	13 (1%)	19 7

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	209	ARG
1	C	209	ARG

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Mol	Chain	Res	Type
1	A	352	ILE
1	B	352	ILE
1	C	352	ILE
1	D	352	ILE
1	A	89	VAL
1	B	89	VAL
1	B	209	ARG
1	C	89	VAL
1	D	89	VAL
1	D	209	ARG
1	C	66	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	286/298 (96%)	281 (98%)	5 (2%)	60 48
1	B	287/298 (96%)	284 (99%)	3 (1%)	76 68
1	C	287/298 (96%)	280 (98%)	7 (2%)	49 33
1	D	288/298 (97%)	283 (98%)	5 (2%)	60 48
All	All	1148/1192 (96%)	1128 (98%)	20 (2%)	60 48

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

Mol	Chain	Res	Type
1	A	52	GLU
1	A	59	LEU
1	A	136	MET
1	A	209	ARG
1	A	210	LYS
1	B	209	ARG
1	B	239	LYS
1	B	396	LEU
1	C	140	GLN
1	C	210	LYS

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Mol	Chain	Res	Type
1	C	213	THR
1	C	239	LYS
1	C	373	ARG
1	C	395	LYS
1	C	396	LEU
1	D	48	GLU
1	D	52	GLU
1	D	209	ARG
1	D	373	ARG
1	D	396	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	304	GLN
1	B	306	GLN
1	B	318	ASN
1	C	103	GLN
1	C	110	ASN
1	C	318	ASN
1	C	350	HIS
1	D	110	ASN
1	D	306	GLN
1	D	318	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 monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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, 95^{th} 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	392/407 (96%)	-0.39	6 (1%)	73	73	13, 19, 37, 105	0
1	B	393/407 (96%)	-0.37	8 (2%)	65	65	13, 20, 38, 108	0
1	C	393/407 (96%)	-0.36	8 (2%)	65	65	13, 18, 34, 106	0
1	D	394/407 (96%)	-0.38	9 (2%)	60	60	13, 19, 36, 96	0
All	All	1572/1628 (96%)	-0.37	31 (1%)	65	65	13, 19, 37, 108	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	209	ARG	8.1
1	C	209	ARG	7.5
1	A	210	LYS	7.4
1	C	210	LYS	6.9
1	C	211	GLY	6.1
1	D	210	LYS	5.8
1	D	209	ARG	5.1
1	C	208	THR	5.0
1	B	210	LYS	5.0
1	A	209	ARG	4.8
1	A	208	THR	4.8
1	C	396	LEU	4.4
1	D	3	LYS	4.3
1	D	211	GLY	4.2
1	B	211	GLY	4.1
1	A	211	GLY	3.7
1	D	208	THR	3.3
1	D	359	LEU	3.1
1	B	208	THR	2.9
1	A	207	THR	2.6
1	B	239	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	360	LEU	2.5
1	D	396	LEU	2.5
1	C	212	GLU	2.4
1	C	207	THR	2.4
1	A	395	LYS	2.2
1	B	207	THR	2.2
1	B	396	LEU	2.1
1	B	213	THR	2.0
1	C	359	LEU	2.0
1	D	207	THR	2.0

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 monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.