



Full wwPDB X-ray Structure Validation Report i

Feb 28, 2014 – 03:19 AM GMT

PDB ID : 2IB9
Title : Crystallographic and kinetic studies of human mitochondrial acetoacetyl-CoA thiolase (T2): the importance of potassium and chloride for its structure and function
Authors : Haapalainen, A.M.; Wierenga, R.K.
Deposited on : 2006-09-11
Resolution : 2.05 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

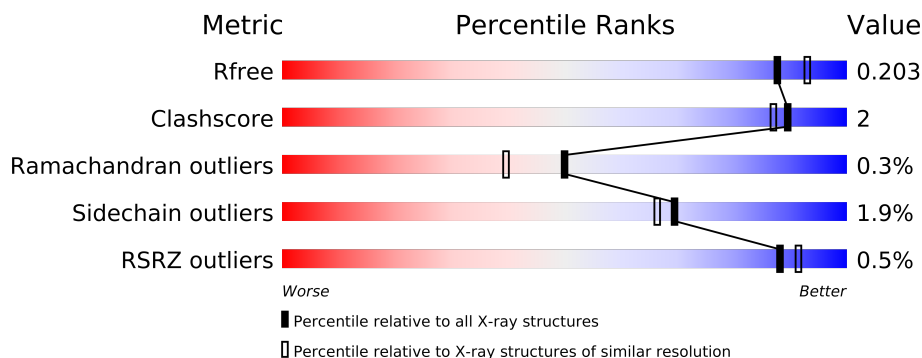
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.05 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}	66092	1380 (2.06-2.02)
Clashscore	79885	1577 (2.06-2.02)
Ramachandran outliers	78287	1565 (2.06-2.02)
Sidechain outliers	78261	1565 (2.06-2.02)
RSRZ outliers	66119	1381 (2.06-2.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	395	
1	B	395	
1	C	395	
1	D	395	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	CL	A	2002	-	X
4	MES	A	5001	-	X
4	MES	B	5002	-	X
4	MES	C	5003	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	MES	D	5004	-	X
5	GOL	A	4001	-	X
5	GOL	A	4003	-	X
5	GOL	A	4004	-	X
5	GOL	B	4002	-	X
5	GOL	C	4005	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12658 atoms, of which 0 are hydrogen and 0 are deuterium.

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 acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	S	0	11	0
			2910	1839	492	556	23			
1	B	391	Total	C	N	O	S	0	12	0
			2910	1840	492	555	23			
1	C	392	Total	C	N	O	S	0	10	0
			2915	1841	494	557	23			
1	D	393	Total	C	N	O	S	0	4	0
			2899	1829	493	554	23			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	MET	-	INITIATING METHIONINE	UNP P24752
A	34	ALA	VAL	ENGINEERED	UNP P24752
B	33	MET	-	INITIATING METHIONINE	UNP P24752
B	34	ALA	VAL	ENGINEERED	UNP P24752
C	33	MET	-	INITIATING METHIONINE	UNP P24752
C	34	ALA	VAL	ENGINEERED	UNP P24752
D	33	MET	-	INITIATING METHIONINE	UNP P24752
D	34	ALA	VAL	ENGINEERED	UNP P24752

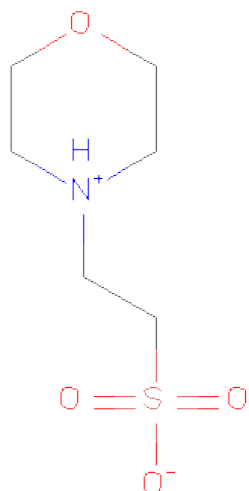
- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		
2	A	1	Total	Cl	0	0
			1	1		
2	D	1	Total	Cl	0	0
			1	1		
2	C	1	Total	Cl	0	0
			1	1		

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

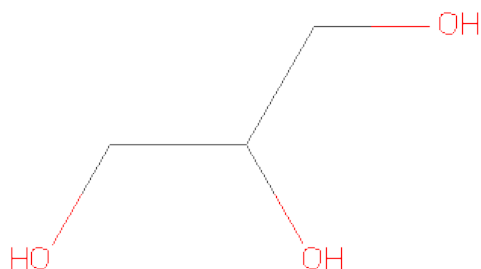
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	K	0	0
			1	1		
3	A	1	Total	K	0	0
			1	1		
3	D	1	Total	K	0	0
			1	1		
3	C	1	Total	K	0	0
			1	1		

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONICACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	327	Total	O	0	0
			327	327		
6	B	279	Total	O	0	0
			279	279		
6	C	179	Total	O	0	0
			179	179		
6	D	153	Total	O	0	0
			153	153		

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.

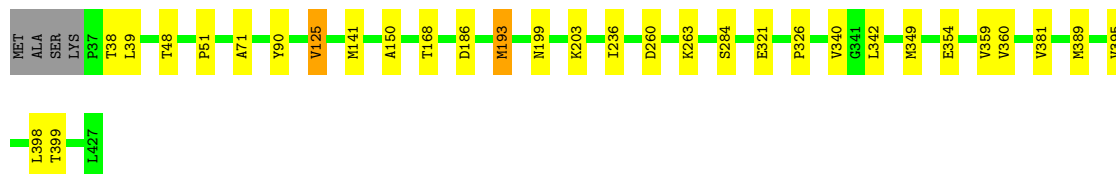
- Molecule 1: Acetyl-CoA acetyltransferase

Chain A: 



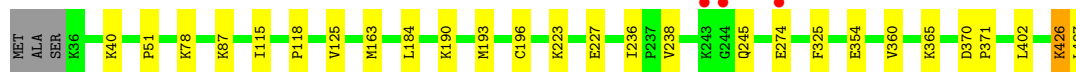
- Molecule 1: Acetyl-CoA acetyltransferase

Chain B: 



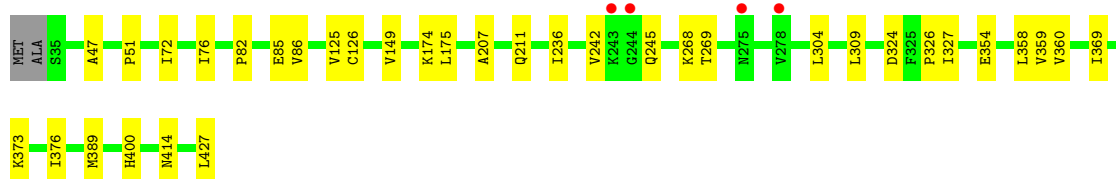
- Molecule 1: Acetyl-CoA acetyltransferase

Chain C: 



- Molecule 1: Acetyl-CoA acetyltransferase

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.75Å 107.44Å 102.33Å 90.00° 103.06° 90.00°	Depositor
Resolution (Å)	73.72 – 2.05 73.79 – 2.05	Depositor EDS
% Data completeness (in resolution range)	100.0 (73.72-2.05) 100.0 (73.79-2.05)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.156 , 0.199 0.160 , 0.203	Depositor DCC
R_{free} test set	4998 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 99953 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12658	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, K, MES, 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	0.64	0/2998	0.62	0/4057
1	B	0.60	0/3005	0.62	0/4068
1	C	0.50	0/2999	0.60	0/4059
1	D	0.50	0/2957	0.58	0/4001
All	All	0.57	0/11959	0.61	0/16185

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2910	0	3004	6	0
1	B	2910	0	3003	20	0
1	C	2915	0	3006	13	0
1	D	2899	0	2989	16	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	12	0	12	0	0
4	B	12	0	12	0	0
4	C	12	0	12	0	0
4	D	12	0	12	0	0
5	A	18	0	24	0	0
5	B	6	0	8	1	0
5	C	6	0	8	0	0
6	A	327	0	0	1	0
6	B	279	0	0	0	0
6	C	179	0	0	1	0
6	D	153	0	0	0	0
All	All	12658	0	12090	52	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (52) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:47:ALA:O	1:D:400:HIS:HE1	1.75	0.68
1:A:48[A]:THR:HG22	6:A:5105:HOH:O	1.95	0.66
1:B:395:VAL:O	1:B:399[B]:THR:HG23	1.97	0.65
1:B:186:ASP:HB2	1:B:193[B]:MET:CE	2.33	0.58
1:B:186:ASP:HB2	1:B:193[B]:MET:HE1	1.85	0.58
1:D:86:VAL:HG11	1:D:149:VAL:HG23	1.86	0.57
1:B:51:PRO:HD3	1:B:236:ILE:O	2.08	0.53
1:D:72:ILE:O	1:D:76:ILE:HG12	2.09	0.53
1:D:51:PRO:HD3	1:D:236:ILE:O	2.10	0.52
1:C:354:GLU:HG2	1:C:360:VAL:HG21	1.91	0.51
1:D:373:LYS:C	1:D:376:ILE:HD11	2.31	0.51
1:B:260:ASP:OD2	1:B:263:LYS:HE2	2.12	0.50
1:B:284:SER:O	5:B:4002:GOL:H12	2.13	0.49
1:D:324:ASP:O	1:D:327:ILE:HG12	2.13	0.48
1:B:199:ASN:ND2	1:B:203:LYS:HE2	2.30	0.46
1:D:126[A]:CYS:HB2	1:D:414:ASN:HA	1.97	0.46
1:C:402:LEU:O	1:C:426:LYS:HE3	2.16	0.45
1:C:184:LEU:O	1:C:193[A]:MET:HG2	2.16	0.45
1:C:402:LEU:HB2	1:C:426:LYS:HG3	1.99	0.45
1:B:349:MET:HG3	1:B:398:LEU:CD2	2.46	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:39:LEU:HD13	1:B:141:MET:CE	2.47	0.45
1:B:168[B]:THR:HG21	1:C:163:MET:CE	2.48	0.44
1:D:47:ALA:O	1:D:400:HIS:CE1	2.64	0.44
1:A:76:ILE:CD1	1:A:113:LEU:HD11	2.48	0.44
1:B:340[A]:VAL:HG13	1:B:342:LEU:HG	1.99	0.44
1:B:326:PRO:HB3	1:B:359:VAL:HG22	1.98	0.44
1:A:354:GLU:HB3	1:A:381:VAL:HG23	2.00	0.44
1:A:354:GLU:HG2	1:A:360:VAL:HG21	2.00	0.43
1:A:115:ILE:HD13	1:B:321:GLU:HG2	2.00	0.43
1:D:268:LYS:HG2	1:D:269:THR:N	2.34	0.43
1:B:168[B]:THR:HG21	1:C:163:MET:HE3	2.00	0.43
1:B:354:GLU:HB3	1:B:381:VAL:HG23	2.01	0.43
1:C:223:LYS:HE2	1:C:227:GLU:OE2	2.18	0.43
1:D:326:PRO:HB3	1:D:359:VAL:HG22	2.00	0.43
1:C:87:LYS:O	1:C:118:PRO:HD2	2.19	0.42
1:D:242:VAL:HB	1:D:245:GLN:HB2	2.00	0.42
1:B:39:LEU:HD13	1:B:141:MET:HE2	2.02	0.42
1:C:370:ASP:HA	1:C:371:PRO:HD2	1.90	0.42
1:D:354:GLU:HG2	1:D:360:VAL:HG21	2.01	0.42
1:C:40:LYS:HA	1:C:40:LYS:HD2	1.83	0.42
1:B:354:GLU:HG2	1:B:360:VAL:HG21	2.02	0.42
1:D:86:VAL:CG1	1:D:149:VAL:HG23	2.49	0.41
1:B:90:TYR:O	1:B:150:ALA:HA	2.20	0.41
1:D:207:ALA:O	1:D:211:GLN:HG3	2.21	0.41
1:C:51:PRO:HD3	1:C:236:ILE:O	2.21	0.41
1:B:48[B]:THR:CG2	1:B:71:ALA:O	2.69	0.41
1:C:196:CYS:HB2	1:C:325:PHE:HE2	1.85	0.40
1:D:82:PRO:HG2	1:D:85:GLU:HG2	2.01	0.40
1:A:395:VAL:O	1:A:399[B]:THR:HG23	2.20	0.40
1:D:358:LEU:C	1:D:358:LEU:HD13	2.41	0.40
1:C:190:LYS:HD3	6:C:5178:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	400/395 (101%)	395 (99%)	4 (1%)	1 (0%)	50	39
1	B	401/395 (102%)	394 (98%)	6 (2%)	1 (0%)	56	47
1	C	400/395 (101%)	392 (98%)	7 (2%)	1 (0%)	50	39
1	D	395/395 (100%)	384 (97%)	10 (2%)	1 (0%)	50	39
All	All	1596/1580 (101%)	1565 (98%)	27 (2%)	4 (0%)	50	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	125	VAL
1	B	125	VAL
1	C	125	VAL
1	D	125	VAL

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	317/309 (103%)	313 (99%)	4 (1%)	80	79
1	B	318/309 (103%)	313 (98%)	5 (2%)	75	73
1	C	317/309 (103%)	309 (98%)	8 (2%)	60	55
1	D	312/309 (101%)	305 (98%)	7 (2%)	64	60
All	All	1264/1236 (102%)	1240 (98%)	24 (2%)	69	66

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	VAL
1	A	175	LEU
1	A	243	LYS
1	A	389	MET
1	B	38	THR
1	B	125	VAL
1	B	193[A]	MET
1	B	193[B]	MET

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Mol	Chain	Res	Type
1	B	389	MET
1	C	78	LYS
1	C	115	ILE
1	C	238	VAL
1	C	245	GLN
1	C	274	GLU
1	C	365	LYS
1	C	426	LYS
1	C	427	LEU
1	D	174	LYS
1	D	175	LEU
1	D	304	LEU
1	D	309	LEU
1	D	369	ILE
1	D	389	MET
1	D	427	LEU

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

Mol	Chain	Res	Type
1	A	93	ASN
1	B	93	ASN
1	B	199	ASN
1	B	209	ASN
1	C	93	ASN
1	C	272	GLN
1	D	93	ASN
1	D	138	GLN
1	D	164	ASN
1	D	400	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 17 ligands modelled in this entry, 8 are 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$
5	GOL	A	4001	-	5,5,5	0.36	0	5,5,5	0.35	0
5	GOL	A	4003	-	5,5,5	0.33	0	5,5,5	0.22	0
5	GOL	A	4004	-	5,5,5	0.32	0	5,5,5	0.34	0
4	MES	A	5001	-	12,12,12	2.15	1 (8%)	16,16,16	2.42	6 (37%)
5	GOL	B	4002	-	5,5,5	0.36	0	5,5,5	0.59	0
4	MES	B	5002	-	12,12,12	2.11	1 (8%)	16,16,16	2.34	5 (31%)
5	GOL	C	4005	-	5,5,5	0.33	0	5,5,5	0.33	0
4	MES	C	5003	-	12,12,12	2.15	1 (8%)	16,16,16	2.39	5 (31%)
4	MES	D	5004	-	12,12,12	2.07	1 (8%)	16,16,16	2.33	6 (37%)

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
5	GOL	A	4001	-	-	0/4/4/4	0/0/0/0
5	GOL	A	4003	-	-	0/4/4/4	0/0/0/0
5	GOL	A	4004	-	-	0/4/4/4	0/0/0/0
4	MES	A	5001	-	-	0/6/14/14	1/1/1/1
5	GOL	B	4002	-	-	0/4/4/4	0/0/0/0
4	MES	B	5002	-	-	0/6/14/14	1/1/1/1
5	GOL	C	4005	-	-	0/4/4/4	0/0/0/0
4	MES	C	5003	-	-	0/6/14/14	1/1/1/1
4	MES	D	5004	-	-	0/6/14/14	1/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	5003	MES	C8-S	-6.51	1.66	1.78
4	B	5002	MES	C8-S	-6.40	1.66	1.78
4	A	5001	MES	C8-S	-6.38	1.66	1.78
4	D	5004	MES	C8-S	-6.19	1.67	1.78

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	5003	MES	C5-N4-C3	6.02	121.68	109.75
4	B	5002	MES	C5-N4-C3	5.75	121.16	109.75
4	A	5001	MES	C5-N4-C3	5.45	120.55	109.75
4	D	5004	MES	C5-N4-C3	5.40	120.45	109.75
4	A	5001	MES	C2-C3-N4	-3.82	105.07	109.96
4	C	5003	MES	C2-C3-N4	-3.35	105.66	109.96
4	D	5004	MES	C7-N4-C5	3.34	120.40	111.66
4	A	5001	MES	C8-C7-N4	-3.33	106.74	112.44
4	A	5001	MES	C7-N4-C5	3.16	119.91	111.66
4	B	5002	MES	C8-C7-N4	-3.11	107.12	112.44
4	D	5004	MES	C2-C3-N4	-3.08	106.01	109.96
4	C	5003	MES	C8-C7-N4	-3.05	107.21	112.44
4	D	5004	MES	C6-C5-N4	-3.01	106.09	109.96
4	A	5001	MES	C7-N4-C3	3.01	119.52	111.66
4	B	5002	MES	C7-N4-C3	2.97	119.42	111.66
4	B	5002	MES	C7-N4-C5	2.96	119.41	111.66
4	C	5003	MES	C7-N4-C5	2.93	119.32	111.66
4	B	5002	MES	C2-C3-N4	-2.89	106.25	109.96
4	D	5004	MES	C7-N4-C3	2.86	119.14	111.66
4	C	5003	MES	C7-N4-C3	2.80	118.98	111.66
4	D	5004	MES	C8-C7-N4	-2.50	108.16	112.44
4	A	5001	MES	C6-C5-N4	-2.38	106.91	109.96

There are no chirality outliers.

There are no torsion outliers.

All (4) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	5004	MES	C2-C3-C5-C6-N4-O1
4	A	5001	MES	C2-C3-C5-C6-N4-O1
4	C	5003	MES	C2-C3-C5-C6-N4-O1
4	B	5002	MES	C2-C3-C5-C6-N4-O1

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	391/395 (98%)	-0.70	0	100 100	14, 21, 35, 65	12 (3%)
1	B	391/395 (98%)	-0.65	0	100 100	17, 25, 41, 59	9 (2%)
1	C	392/395 (99%)	-0.49	3 (0%)	83 86	21, 32, 48, 70	8 (2%)
1	D	393/395 (99%)	-0.24	4 (1%)	79 81	23, 37, 54, 73	13 (3%)
All	All	1567/1580 (99%)	-0.52	7 (0%)	88 93	14, 29, 50, 73	42 (2%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	274	GLU	3.1
1	D	243	LYS	2.3
1	D	244	GLY	2.3
1	D	275	ASN	2.2
1	C	244	GLY	2.2
1	C	243	LYS	2.1
1	D	278	VAL	2.0

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 ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	MES	B	5002	12/12	0.36	63.44	97,97,98,98	5
4	MES	C	5003	12/12	0.42	34.68	86,87,88,88	5
4	MES	D	5004	12/12	0.36	29.06	88,89,90,90	5
4	MES	A	5001	12/12	0.23	21.87	55,57,58,58	5
5	GOL	B	4002	6/6	0.23	17.03	41,43,43,43	6
5	GOL	C	4005	6/6	0.23	10.94	62,63,63,63	0
5	GOL	A	4001	6/6	0.17	7.75	52,54,54,55	0
5	GOL	A	4004	6/6	0.16	4.13	69,70,70,70	0
5	GOL	A	4003	6/6	0.14	3.63	42,45,46,46	0
2	CL	A	2002	1/1	0.10	2.59	23,23,23,23	0
2	CL	D	2003	1/1	0.06	-0.96	29,29,29,29	0
3	K	B	3002	1/1	0.07	-1.23	21,21,21,21	0
2	CL	B	2001	1/1	0.06	-1.37	22,22,22,22	0
3	K	C	3003	1/1	0.05	-1.61	27,27,27,27	0
3	K	A	3001	1/1	0.05	-2.00	17,17,17,17	0
3	K	D	3004	1/1	0.04	-2.30	36,36,36,36	0
2	CL	C	2004	1/1	0.05	-2.33	34,34,34,34	0

6.5 Other polymers ⓘ

There are no such residues in this entry.