



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 29, 2014 – 10:34 AM EDT

PDB ID : 4C2K  
Title : Crystal structure of human mitochondrial 3-ketoacyl-CoA thiolase  
Authors : Kiema, T.-R.; Harijan, R.K.; Wierenga, R.K.  
Deposited on : 2013-08-19  
Resolution : 2.00 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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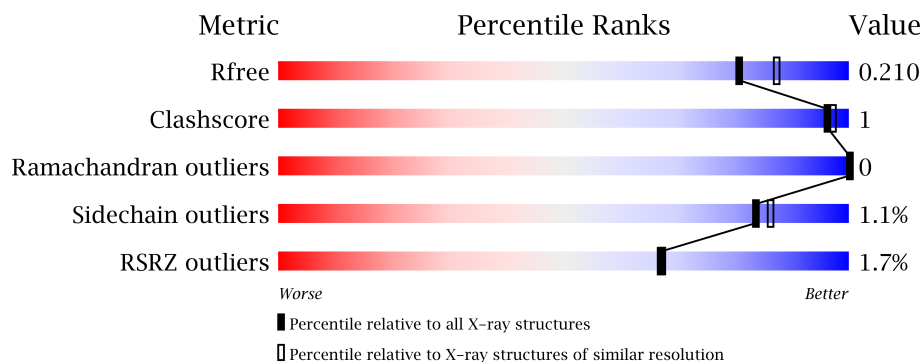
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable23489  
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) : stable23489

# 1 Overall quality at a glance

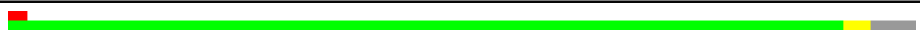



The reported resolution of this entry is 2.00 Å.

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))
$R_{free}$	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

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  $\geq 3$ , 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	417	
1	B	417	
1	C	417	
1	D	417	

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	EDO	A	1397	-	X
2	EDO	B	1401	-	X
2	EDO	C	1400	-	X
2	EDO	C	1402	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
2	EDO	C	1404	-	X
2	EDO	D	1400	-	X
2	EDO	D	1401	-	X
2	EDO	D	1402	-	X
3	DTT	A	1400	-	X
4	MES	D	1403	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12340 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 3-KETOACYL-COA THIOLASE, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			2925	1835	516	558	16			
1	B	395	Total	C	N	O	S	0	0	0
			2921	1831	514	559	17			
1	C	394	Total	C	N	O	S	0	0	0
			2913	1826	513	558	16			
1	D	399	Total	C	N	O	S	0	0	0
			2953	1851	522	563	17			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP P42765
A	-18	GLY	-	EXPRESSION TAG	UNP P42765
A	-17	SER	-	EXPRESSION TAG	UNP P42765
A	-16	SER	-	EXPRESSION TAG	UNP P42765
A	-15	HIS	-	EXPRESSION TAG	UNP P42765
A	-14	HIS	-	EXPRESSION TAG	UNP P42765
A	-13	HIS	-	EXPRESSION TAG	UNP P42765
A	-12	HIS	-	EXPRESSION TAG	UNP P42765
A	-11	HIS	-	EXPRESSION TAG	UNP P42765
A	-10	HIS	-	EXPRESSION TAG	UNP P42765
A	-9	SER	-	EXPRESSION TAG	UNP P42765
A	-8	SER	-	EXPRESSION TAG	UNP P42765
A	-7	GLY	-	EXPRESSION TAG	UNP P42765
A	-6	LEU	-	EXPRESSION TAG	UNP P42765
A	-5	VAL	-	EXPRESSION TAG	UNP P42765
A	-4	PRO	-	EXPRESSION TAG	UNP P42765
A	-3	ARG	-	EXPRESSION TAG	UNP P42765
A	-2	GLY	-	EXPRESSION TAG	UNP P42765
A	-1	SER	-	EXPRESSION TAG	UNP P42765
A	0	HIS	-	EXPRESSION TAG	UNP P42765
B	-19	MET	-	EXPRESSION TAG	UNP P42765

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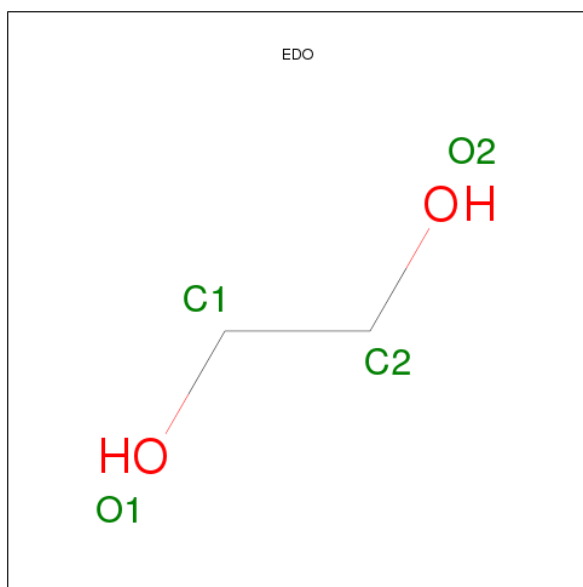
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP P42765
B	-17	SER	-	EXPRESSION TAG	UNP P42765
B	-16	SER	-	EXPRESSION TAG	UNP P42765
B	-15	HIS	-	EXPRESSION TAG	UNP P42765
B	-14	HIS	-	EXPRESSION TAG	UNP P42765
B	-13	HIS	-	EXPRESSION TAG	UNP P42765
B	-12	HIS	-	EXPRESSION TAG	UNP P42765
B	-11	HIS	-	EXPRESSION TAG	UNP P42765
B	-10	HIS	-	EXPRESSION TAG	UNP P42765
B	-9	SER	-	EXPRESSION TAG	UNP P42765
B	-8	SER	-	EXPRESSION TAG	UNP P42765
B	-7	GLY	-	EXPRESSION TAG	UNP P42765
B	-6	LEU	-	EXPRESSION TAG	UNP P42765
B	-5	VAL	-	EXPRESSION TAG	UNP P42765
B	-4	PRO	-	EXPRESSION TAG	UNP P42765
B	-3	ARG	-	EXPRESSION TAG	UNP P42765
B	-2	GLY	-	EXPRESSION TAG	UNP P42765
B	-1	SER	-	EXPRESSION TAG	UNP P42765
B	0	HIS	-	EXPRESSION TAG	UNP P42765
C	-19	MET	-	EXPRESSION TAG	UNP P42765
C	-18	GLY	-	EXPRESSION TAG	UNP P42765
C	-17	SER	-	EXPRESSION TAG	UNP P42765
C	-16	SER	-	EXPRESSION TAG	UNP P42765
C	-15	HIS	-	EXPRESSION TAG	UNP P42765
C	-14	HIS	-	EXPRESSION TAG	UNP P42765
C	-13	HIS	-	EXPRESSION TAG	UNP P42765
C	-12	HIS	-	EXPRESSION TAG	UNP P42765
C	-11	HIS	-	EXPRESSION TAG	UNP P42765
C	-10	HIS	-	EXPRESSION TAG	UNP P42765
C	-9	SER	-	EXPRESSION TAG	UNP P42765
C	-8	SER	-	EXPRESSION TAG	UNP P42765
C	-7	GLY	-	EXPRESSION TAG	UNP P42765
C	-6	LEU	-	EXPRESSION TAG	UNP P42765
C	-5	VAL	-	EXPRESSION TAG	UNP P42765
C	-4	PRO	-	EXPRESSION TAG	UNP P42765
C	-3	ARG	-	EXPRESSION TAG	UNP P42765
C	-2	GLY	-	EXPRESSION TAG	UNP P42765
C	-1	SER	-	EXPRESSION TAG	UNP P42765
C	0	HIS	-	EXPRESSION TAG	UNP P42765
D	-19	MET	-	EXPRESSION TAG	UNP P42765
D	-18	GLY	-	EXPRESSION TAG	UNP P42765
D	-17	SER	-	EXPRESSION TAG	UNP P42765

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	EXPRESSION TAG	UNP P42765
D	-15	HIS	-	EXPRESSION TAG	UNP P42765
D	-14	HIS	-	EXPRESSION TAG	UNP P42765
D	-13	HIS	-	EXPRESSION TAG	UNP P42765
D	-12	HIS	-	EXPRESSION TAG	UNP P42765
D	-11	HIS	-	EXPRESSION TAG	UNP P42765
D	-10	HIS	-	EXPRESSION TAG	UNP P42765
D	-9	SER	-	EXPRESSION TAG	UNP P42765
D	-8	SER	-	EXPRESSION TAG	UNP P42765
D	-7	GLY	-	EXPRESSION TAG	UNP P42765
D	-6	LEU	-	EXPRESSION TAG	UNP P42765
D	-5	VAL	-	EXPRESSION TAG	UNP P42765
D	-4	PRO	-	EXPRESSION TAG	UNP P42765
D	-3	ARG	-	EXPRESSION TAG	UNP P42765
D	-2	GLY	-	EXPRESSION TAG	UNP P42765
D	-1	SER	-	EXPRESSION TAG	UNP P42765
D	0	HIS	-	EXPRESSION TAG	UNP P42765

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



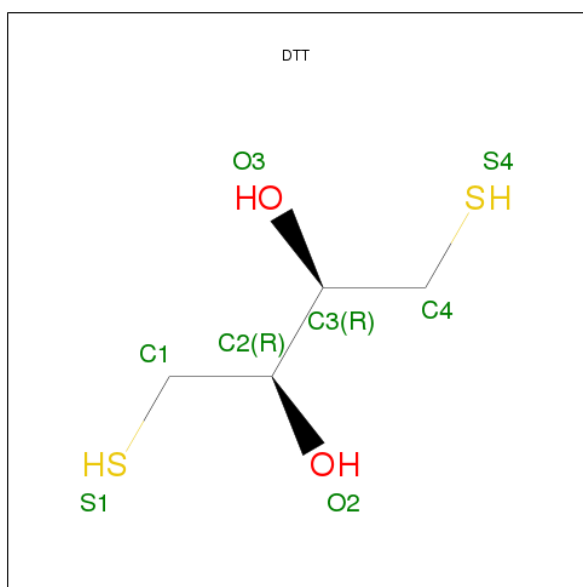
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0

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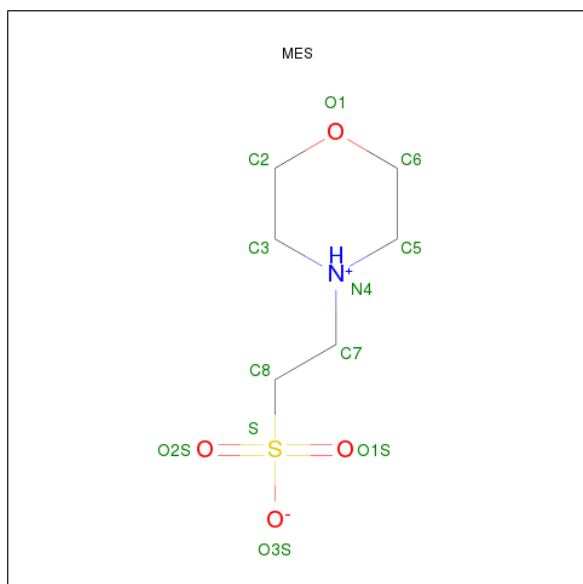
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (three-letter code: DTT) (formula:  $C_4H_{10}O_2S_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			8	4	2	2		

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONICACID (three-letter code: MES) (formula:  $C_6H_{13}NO_4S$ ).



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		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	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 water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	141	Total	O	0	0
			141	141		
5	B	108	Total	O	0	0
			108	108		
5	C	138	Total	O	0	0
			138	138		
5	D	101	Total	O	0	0
			101	101		

### 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.

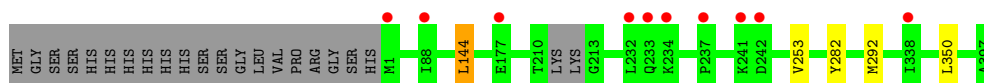
- Molecule 1: 3-KETOACYL-COA THIOLASE, MITOCHONDRIAL

Chain A: 



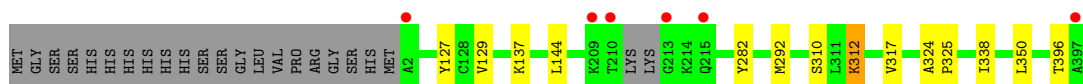
- Molecule 1: 3-KETOACYL-COA THIOLASE, MITOCHONDRIAL

Chain B: 



- Molecule 1: 3-KETOACYL-COA THIOLASE, MITOCHONDRIAL

Chain C: 



- Molecule 1: 3-KETOACYL-COA THIOLASE, MITOCHONDRIAL

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.73Å 196.77Å 79.65Å 90.00° 103.78° 90.00°	Depositor
Resolution (Å)	48.17 – 2.00 48.17 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.17-2.00) 99.7 (48.17-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.84 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.195 , 0.229 0.181 , 0.210	Depositor DCC
$R_{free}$ test set	5461 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.8	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 39.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 109510 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	12340	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities 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: EDO, MES, DTT

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	0.75	0/2971	0.73	0/4017
1	B	0.72	0/2966	0.74	0/4009
1	C	0.76	0/2958	0.75	0/3999
1	D	0.68	0/3000	0.72	0/4055
All	All	0.73	0/11895	0.74	0/16080

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	396	THR	Peptide

### 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	2925	0	2974	10	0
1	B	2921	0	2964	3	0
1	C	2913	0	2952	10	0
1	D	2953	0	3001	7	0
2	A	12	0	18	1	0
2	B	20	0	30	1	0
2	C	28	0	42	5	0
2	D	24	0	36	0	0
3	A	8	0	10	3	0
4	A	12	0	13	0	0
4	B	24	0	26	1	0
4	D	12	0	13	0	0
5	A	141	0	0	0	0
5	B	108	0	0	0	0
5	C	138	0	0	0	0
5	D	101	0	0	0	0
All	All	12340	0	12079	27	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 1.

All (27) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:371:ARG:HH12	3:A:1400:DTT:H42	1.17	1.06
1:A:371:ARG:NH1	3:A:1400:DTT:H42	1.85	0.90
1:A:371:ARG:HH12	3:A:1400:DTT:C4	1.96	0.78
1:C:338:ILE:HG12	2:C:1403:EDO:H12	1.68	0.73
1:C:338:ILE:HG12	2:C:1403:EDO:C1	2.22	0.69
1:C:310:SER:OG	1:C:312:LYS:HE2	1.92	0.68
1:D:-1:SER:CB	1:D:305:LYS:HE2	2.32	0.60
1:D:-1:SER:HB3	1:D:305:LYS:HE2	1.87	0.55
1:B:144:LEU:CD1	1:C:144:LEU:HD13	2.39	0.52
1:C:127:TYR:HB3	1:C:144:LEU:HG	1.93	0.51
1:A:149:TRP:CE2	2:A:1397:EDO:H12	2.47	0.50
1:A:127:TYR:HB3	1:A:144:LEU:HG	1.93	0.49
1:C:317:VAL:HG21	2:C:1400:EDO:H21	1.98	0.46
2:C:1402:EDO:H11	1:D:124:GLN:HG2	1.98	0.45
1:B:253:VAL:HB	4:B:1403:MES:H21	1.99	0.45
1:C:282:TYR:OH	1:D:110:GLU:OE2	2.27	0.45
1:C:317:VAL:HG21	2:C:1400:EDO:C2	2.48	0.43
1:A:129:VAL:CG2	1:A:144:LEU:HD12	2.49	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:324:ALA:N	1:C:325:PRO:HD2	2.34	0.43
1:A:324:ALA:N	1:A:325:PRO:HD2	2.34	0.42
1:C:129:VAL:CG2	1:C:144:LEU:HD12	2.50	0.41
1:D:324:ALA:N	1:D:325:PRO:HD2	2.35	0.41
1:A:69:LEU:HD23	1:A:69:LEU:C	2.41	0.41
1:A:129:VAL:HG22	1:A:144:LEU:HD12	2.03	0.41
1:A:139:GLY:HA2	1:D:149:TRP:CG	2.56	0.41
1:B:282:TYR:CZ	2:B:1400:EDO:H21	2.56	0.40
1:D:-1:SER:HB2	1:D:305:LYS:HE2	2.04	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	393/417 (94%)	387 (98%)	6 (2%)	0	100	100
1	B	391/417 (94%)	385 (98%)	6 (2%)	0	100	100
1	C	390/417 (94%)	383 (98%)	7 (2%)	0	100	100
1	D	397/417 (95%)	391 (98%)	6 (2%)	0	100	100
All	All	1571/1668 (94%)	1546 (98%)	25 (2%)	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	310/328 (94%)	307 (99%)	3 (1%)	85	88
1	B	309/328 (94%)	306 (99%)	3 (1%)	85	88
1	C	308/328 (94%)	304 (99%)	4 (1%)	80	82
1	D	313/328 (95%)	309 (99%)	4 (1%)	80	82
All	All	1240/1312 (94%)	1226 (99%)	14 (1%)	84	86

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	137	LYS
1	A	292	MET
1	A	350	LEU
1	B	144	LEU
1	B	292	MET
1	B	350	LEU
1	C	137	LYS
1	C	292	MET
1	C	312	LYS
1	C	350	LEU
1	D	137	LYS
1	D	144	LEU
1	D	292	MET
1	D	350	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

26 ligands are 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	EDO	A	1397	-	3,3,3	0.59	0	2,2,2	0.40	0
2	EDO	A	1398	-	3,3,3	0.31	0	2,2,2	0.39	0
2	EDO	A	1399	-	3,3,3	0.29	0	2,2,2	0.61	0
3	DTT	A	1400	-	7,7,7	0.70	0	8,8,8	2.05	2 (25%)
4	MES	A	1401	-	12,12,12	1.97	1 (8%)	16,16,16	2.27	5 (31%)
2	EDO	B	1398	-	3,3,3	0.62	0	2,2,2	0.25	0
2	EDO	B	1399	-	3,3,3	0.44	0	2,2,2	0.31	0
2	EDO	B	1400	-	3,3,3	0.61	0	2,2,2	0.78	0
2	EDO	B	1401	-	3,3,3	0.69	0	2,2,2	0.26	0
2	EDO	B	1402	-	3,3,3	0.49	0	2,2,2	0.34	0
4	MES	B	1403	-	12,12,12	1.59	1 (8%)	16,16,16	1.99	5 (31%)
4	MES	B	1404	-	12,12,12	1.79	1 (8%)	16,16,16	1.27	3 (18%)
2	EDO	C	1398	-	3,3,3	0.48	0	2,2,2	0.36	0
2	EDO	C	1399	-	3,3,3	0.47	0	2,2,2	0.43	0
2	EDO	C	1400	-	3,3,3	0.35	0	2,2,2	0.38	0
2	EDO	C	1401	-	3,3,3	0.79	0	2,2,2	0.30	0
2	EDO	C	1402	-	3,3,3	0.52	0	2,2,2	0.53	0
2	EDO	C	1403	-	3,3,3	0.56	0	2,2,2	0.58	0
2	EDO	C	1404	-	3,3,3	0.42	0	2,2,2	0.40	0
2	EDO	D	1397	-	3,3,3	0.71	0	2,2,2	0.13	0
2	EDO	D	1398	-	3,3,3	0.40	0	2,2,2	0.51	0
2	EDO	D	1399	-	3,3,3	0.48	0	2,2,2	0.19	0
2	EDO	D	1400	-	3,3,3	0.27	0	2,2,2	0.25	0
2	EDO	D	1401	-	3,3,3	0.46	0	2,2,2	0.31	0
2	EDO	D	1402	-	3,3,3	0.48	0	2,2,2	0.68	0
4	MES	D	1403	-	12,12,12	1.64	1 (8%)	16,16,16	1.40	2 (12%)

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	EDO	A	1397	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1398	-	-	0/1/1/1	0/0/0/0
2	EDO	A	1399	-	-	0/1/1/1	0/0/0/0
3	DTT	A	1400	-	-	0/8/8/8	0/0/0/0
4	MES	A	1401	-	-	0/6/14/14	0/1/1/1
2	EDO	B	1398	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1399	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1400	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1401	-	-	0/1/1/1	0/0/0/0
2	EDO	B	1402	-	-	0/1/1/1	0/0/0/0
4	MES	B	1403	-	-	0/6/14/14	1/1/1/1
4	MES	B	1404	-	-	0/6/14/14	0/1/1/1
2	EDO	C	1398	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1399	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1400	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1401	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1402	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1403	-	-	0/1/1/1	0/0/0/0
2	EDO	C	1404	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1397	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1398	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1399	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1400	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1401	-	-	0/1/1/1	0/0/0/0
2	EDO	D	1402	-	-	0/1/1/1	0/0/0/0
4	MES	D	1403	-	-	0/6/14/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1401	MES	C8-S	-6.04	1.67	1.78
4	B	1404	MES	C8-S	-5.71	1.68	1.78
4	D	1403	MES	C8-S	-5.02	1.69	1.78
4	B	1403	MES	C8-S	-4.59	1.70	1.78

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1401	MES	O1-C2-C3	6.15	118.54	111.35
4	B	1403	MES	C6-C5-N4	4.29	115.42	109.97
3	A	1400	DTT	C2-C1-S1	-3.92	106.71	114.21
4	D	1403	MES	O3S-S-C8	3.70	115.35	105.98
4	B	1403	MES	O1-C2-C3	3.36	115.27	111.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1403	MES	O2S-S-O1S	-3.33	104.61	112.39
4	D	1403	MES	O1-C2-C3	-3.17	107.64	111.35
3	A	1400	DTT	C4-C3-C2	-3.09	106.02	113.07
4	B	1404	MES	O3S-S-C8	3.04	113.67	105.98
4	A	1401	MES	O1-C6-C5	2.89	114.72	111.35
4	A	1401	MES	C6-O1-C2	2.87	119.66	109.90
4	A	1401	MES	O2S-S-O1S	-2.86	105.72	112.39
4	B	1404	MES	O1-C6-C5	-2.50	108.42	111.35
4	B	1404	MES	O3S-S-O1S	-2.42	106.18	112.50
4	B	1403	MES	C2-C3-N4	2.28	112.86	109.97
4	A	1401	MES	C5-N4-C3	-2.17	105.09	109.77
4	B	1403	MES	O1-C6-C5	-2.05	108.95	111.35

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1403	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	395/417 (94%)	-0.10	7 (1%) 65 66	12, 20, 37, 64	0
1	B	395/417 (94%)	0.06	10 (2%) 54 54	13, 22, 39, 56	0
1	C	394/417 (94%)	-0.19	6 (1%) 70 70	12, 20, 37, 58	0
1	D	399/417 (95%)	-0.09	4 (1%) 79 80	14, 23, 40, 66	0
All	All	1583/1668 (94%)	-0.08	27 (1%) 67 67	12, 21, 38, 66	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	210	THR	5.1
1	C	397	ALA	4.1
1	D	211	LYS	3.5
1	A	211	LYS	3.3
1	B	242	ASP	3.2
1	B	1	MET	3.0
1	A	88	ILE	2.9
1	B	338	ILE	2.8
1	A	230	GLU	2.6
1	C	215	GLN	2.5
1	B	233	GLN	2.5
1	A	236	PRO	2.4
1	A	2	ALA	2.4
1	C	209	LYS	2.3
1	B	237	PRO	2.3
1	B	234	LYS	2.3
1	D	210	THR	2.2
1	D	243	GLY	2.1
1	B	88	ILE	2.1
1	C	2	ALA	2.1
1	A	3	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	241	LYS	2.1
1	B	177	GLU	2.1
1	D	209	LYS	2.0
1	A	226	GLN	2.0
1	C	213	GLY	2.0
1	B	232	LEU	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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	DTT	A	1400	8/8	0.41	6.52	46,53,61,66	0
2	EDO	A	1397	4/4	0.15	6.39	21,22,23,23	0
2	EDO	D	1401	4/4	0.15	5.76	35,41,41,42	0
2	EDO	C	1404	4/4	0.28	4.56	33,39,40,45	0
4	MES	D	1403	12/12	0.21	4.25	33,43,51,51	0
2	EDO	D	1402	4/4	0.20	3.09	43,44,47,49	0
2	EDO	B	1401	4/4	0.20	2.55	37,38,39,46	0
2	EDO	C	1402	4/4	0.23	2.26	41,44,47,47	0
2	EDO	D	1400	4/4	0.16	2.20	30,33,34,34	0
2	EDO	C	1400	4/4	0.23	2.11	27,29,29,30	0
2	EDO	C	1399	4/4	0.13	1.91	34,37,42,47	0
2	EDO	C	1403	4/4	0.14	1.87	37,37,38,44	0
2	EDO	D	1398	4/4	0.21	1.83	29,33,34,34	0
2	EDO	B	1402	4/4	0.17	1.74	40,41,42,45	0
4	MES	A	1401	12/12	0.20	0.99	33,37,42,44	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MES	B	1403	12/12	0.15	0.95	36,40,46,54	0
2	EDO	D	1399	4/4	0.15	0.93	25,31,34,39	0
2	EDO	A	1399	4/4	0.13	0.90	28,30,30,32	0
2	EDO	B	1400	4/4	0.21	0.77	28,32,34,35	0
4	MES	B	1404	12/12	0.14	0.58	32,41,47,55	0
2	EDO	C	1401	4/4	0.20	0.58	24,28,32,35	0
2	EDO	B	1399	4/4	0.14	-0.26	30,32,33,34	0
2	EDO	D	1397	4/4	0.10	-0.54	25,25,27,28	0
2	EDO	C	1398	4/4	0.10	-1.02	24,25,26,29	0
2	EDO	A	1398	4/4	0.07	-1.06	28,28,30,30	0
2	EDO	B	1398	4/4	0.08	-1.46	27,31,32,34	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.