



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:55 PM GMT

PDB ID : 4ZDC
Title : Yeast enoyl-CoA isomerase complexed with octanoyl-CoA
Authors : Onwukwe, G.U.; Koski, M.K.; Wierenga, R.K.
Deposited on : 2015-04-17
Resolution : 2.13 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-20026982
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-20026982

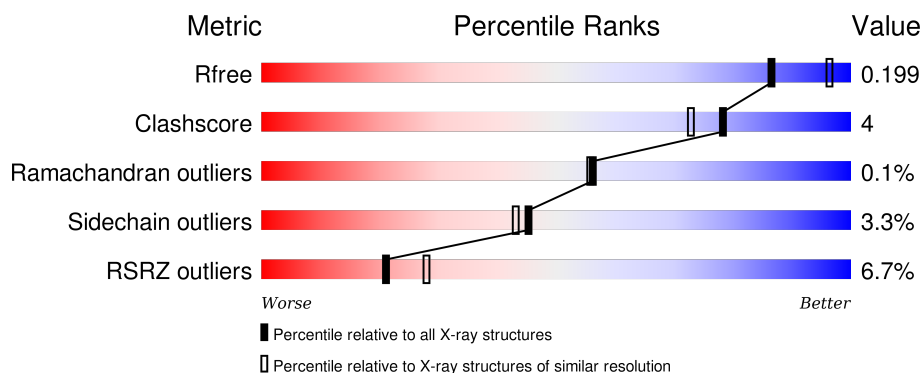
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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	1693 (2.16-2.12)
Clashscore	102246	1824 (2.16-2.12)
Ramachandran outliers	100387	1798 (2.16-2.12)
Sidechain outliers	100360	1798 (2.16-2.12)
RSRZ outliers	91569	1699 (2.16-2.12)

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	300	<div> <div>6%</div> <div> <div></div> <div>81%</div> <div>7%</div> <div>•</div> <div>11%</div> </div> </div>
1	B	300	<div> <div>6%</div> <div> <div></div> <div>81%</div> <div>6%</div> <div>13%</div> </div> </div>
1	C	300	<div> <div>5%</div> <div> <div></div> <div>81%</div> <div>6%</div> <div>•</div> <div>13%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	301	-	-	-	X
2	SO4	A	302	-	-	-	X
2	SO4	B	303	-	-	-	X
2	SO4	C	301	-	-	-	X
2	SO4	C	303	-	-	-	X
3	CO8	A	304	-	-	-	X
3	CO8	B	304	-	-	-	X
3	CO8	C	305	-	-	-	X
4	GOL	A	305	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6946 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 3,2-trans-enoyl-CoA isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	2	0
			2146	1380	356	399	11			
1	B	262	Total	C	N	O	S	0	0	0
			2092	1351	343	387	11			
1	C	262	Total	C	N	O	S	0	1	0
			2103	1357	347	388	11			

There are 63 discrepancies between the modelled and reference sequences:

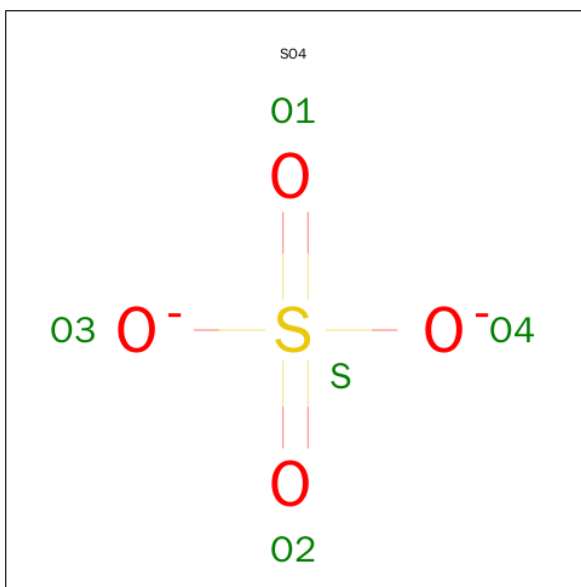
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q05871
A	-18	GLY	-	expression tag	UNP Q05871
A	-17	SER	-	expression tag	UNP Q05871
A	-16	SER	-	expression tag	UNP Q05871
A	-15	HIS	-	expression tag	UNP Q05871
A	-14	HIS	-	expression tag	UNP Q05871
A	-13	HIS	-	expression tag	UNP Q05871
A	-12	HIS	-	expression tag	UNP Q05871
A	-11	HIS	-	expression tag	UNP Q05871
A	-10	HIS	-	expression tag	UNP Q05871
A	-9	SER	-	expression tag	UNP Q05871
A	-8	SER	-	expression tag	UNP Q05871
A	-7	GLY	-	expression tag	UNP Q05871
A	-6	LEU	-	expression tag	UNP Q05871
A	-5	VAL	-	expression tag	UNP Q05871
A	-4	PRO	-	expression tag	UNP Q05871
A	-3	ARG	-	expression tag	UNP Q05871
A	-2	GLY	-	expression tag	UNP Q05871
A	-1	SER	-	expression tag	UNP Q05871
A	0	HIS	-	expression tag	UNP Q05871
A	25	ILE	MET	conflict	UNP Q05871
B	-19	MET	-	initiating methionine	UNP Q05871
B	-18	GLY	-	expression tag	UNP Q05871

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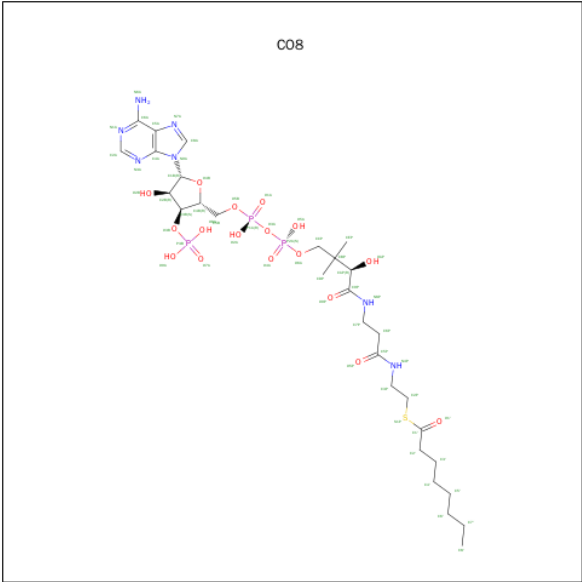
Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	SER	-	expression tag	UNP Q05871
B	-16	SER	-	expression tag	UNP Q05871
B	-15	HIS	-	expression tag	UNP Q05871
B	-14	HIS	-	expression tag	UNP Q05871
B	-13	HIS	-	expression tag	UNP Q05871
B	-12	HIS	-	expression tag	UNP Q05871
B	-11	HIS	-	expression tag	UNP Q05871
B	-10	HIS	-	expression tag	UNP Q05871
B	-9	SER	-	expression tag	UNP Q05871
B	-8	SER	-	expression tag	UNP Q05871
B	-7	GLY	-	expression tag	UNP Q05871
B	-6	LEU	-	expression tag	UNP Q05871
B	-5	VAL	-	expression tag	UNP Q05871
B	-4	PRO	-	expression tag	UNP Q05871
B	-3	ARG	-	expression tag	UNP Q05871
B	-2	GLY	-	expression tag	UNP Q05871
B	-1	SER	-	expression tag	UNP Q05871
B	0	HIS	-	expression tag	UNP Q05871
B	25	ILE	MET	conflict	UNP Q05871
C	-19	MET	-	initiating methionine	UNP Q05871
C	-18	GLY	-	expression tag	UNP Q05871
C	-17	SER	-	expression tag	UNP Q05871
C	-16	SER	-	expression tag	UNP Q05871
C	-15	HIS	-	expression tag	UNP Q05871
C	-14	HIS	-	expression tag	UNP Q05871
C	-13	HIS	-	expression tag	UNP Q05871
C	-12	HIS	-	expression tag	UNP Q05871
C	-11	HIS	-	expression tag	UNP Q05871
C	-10	HIS	-	expression tag	UNP Q05871
C	-9	SER	-	expression tag	UNP Q05871
C	-8	SER	-	expression tag	UNP Q05871
C	-7	GLY	-	expression tag	UNP Q05871
C	-6	LEU	-	expression tag	UNP Q05871
C	-5	VAL	-	expression tag	UNP Q05871
C	-4	PRO	-	expression tag	UNP Q05871
C	-3	ARG	-	expression tag	UNP Q05871
C	-2	GLY	-	expression tag	UNP Q05871
C	-1	SER	-	expression tag	UNP Q05871
C	0	HIS	-	expression tag	UNP Q05871
C	25	ILE	MET	conflict	UNP Q05871

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



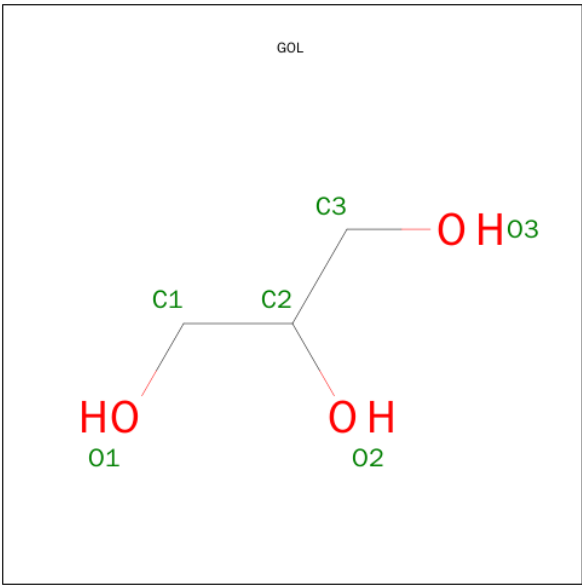
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is OCTANOYL-COENZYME A (three-letter code: CO8) (formula: C₂₉H₅₀N₇O₁₇P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			57	29	7	17	3	1		
3	B	1	Total	C	N	O	P		0	0
			40	16	6	15	3			
3	C	1	Total	C	N	O	P	S	0	0
			57	29	7	17	3	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

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

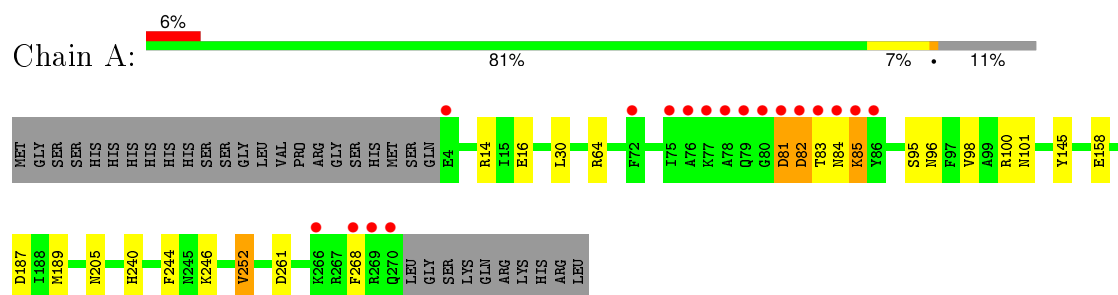
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	131	Total 131	O 131	0	0
5	B	97	Total 97	O 97	0	0
5	C	125	Total 125	O 125	0	0

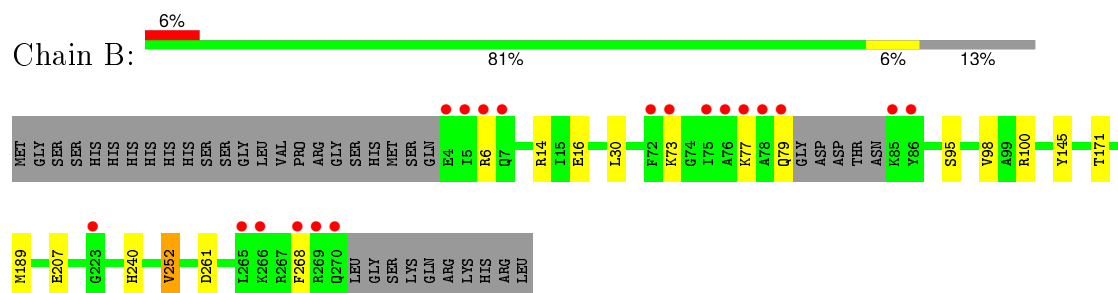
3 Residue-property plots [i](#)

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.

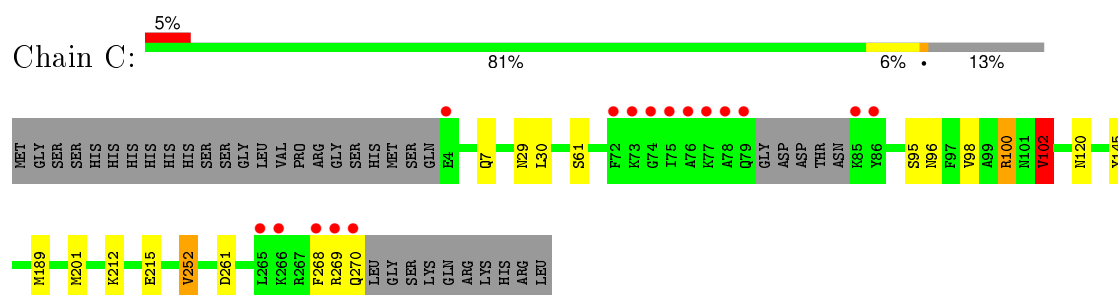
- Molecule 1: 3,2-trans-enoyl-CoA isomerase



- Molecule 1: 3,2-trans-enoyl-CoA isomerase



- Molecule 1: 3,2-trans-enoyl-CoA isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	117.26Å 117.26Å 219.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.31 – 2.13 45.75 – 2.13	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.31-2.13) 99.9 (45.75-2.13)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.168 , 0.190 0.178 , 0.199	Depositor DCC
R_{free} test set	4307 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	41.3	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 51.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 85995 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6946	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, CME, SO4, CO8

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	0.66	0/2184	0.73	0/2948
1	B	0.62	0/2126	0.71	0/2869
1	C	0.65	0/2137	0.72	1/2883 (0.0%)
All	All	0.64	0/6447	0.72	1/8700 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	102	VAL	CB-CA-C	-5.91	100.18	111.40

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	2146	0	2139	18	0
1	B	2092	0	2092	8	0
1	C	2103	0	2101	12	0
2	A	15	0	0	0	0
2	B	15	0	0	1	0
2	C	20	0	0	0	0
3	A	57	0	38	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	40	0	21	1	0
3	C	57	0	36	3	0
4	A	12	0	11	8	0
4	B	18	0	24	0	0
4	C	18	0	17	0	0
5	A	131	0	0	7	0
5	B	97	0	0	2	0
5	C	125	0	0	1	0
All	All	6946	0	6479	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 4.

All (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:A:14[A]:ARG:NH1	1:A:16:GLU:OE2	1.92	1.03
1:B:14:ARG:NH1	1:B:16:GLU:OE2	1.96	0.97
1:A:84:ASN:HB3	1:A:85:LYS:HA	1.68	0.75
1:A:84:ASN:CB	1:A:85:LYS:HA	2.23	0.69
1:C:215:GLU:OE2	5:C:401:HOH:O	2.13	0.66
3:A:304:CO8:O1'	4:A:305:GOL:O3	0.64	0.64
1:B:98:VAL:HG13	1:B:252:VAL:HG13	1.80	0.63
1:A:30:LEU:HD12	3:A:304:CO8:H8A	1.80	0.63
1:C:98:VAL:HG13	1:C:252:VAL:HG13	1.81	0.62
1:A:98:VAL:HG13	1:A:252:VAL:HG13	1.80	0.61
1:A:81:ASP:HA	1:A:82:ASP:HB2	1.83	0.61
1:A:187:ASP:HB2	5:A:503:HOH:O	2.03	0.59
1:A:100[A]:ARG:HG3	1:A:101:ASN:N	2.18	0.58
3:A:304:CO8:C2P	4:A:305:GOL:O3	2.52	0.56
3:A:304:CO8:S1P	4:A:305:GOL:O3	1.91	0.56
1:B:30:LEU:HD12	3:B:304:CO8:H8A	1.88	0.56
1:C:145:TYR:HA	1:C:189:MET:HE1	1.87	0.56
1:A:81:ASP:HA	1:A:82:ASP:CB	2.37	0.55
1:C:30:LEU:HD12	3:C:305:CO8:H8A	1.88	0.55
1:B:240:HIS:HD2	5:B:485:HOH:O	1.90	0.54
1:A:84:ASN:HB3	1:A:85:LYS:CA	2.37	0.53
1:B:73:LYS:O	1:B:77:LYS:HG2	2.09	0.52
1:A:96:ASN:O	1:A:100[B]:ARG:HD3	2.10	0.51
3:A:304:CO8:H122	3:A:304:CO8:O9P	2.11	0.51
1:B:240:HIS:HE1	5:B:489:HOH:O	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:306:GOL:H31	5:A:459:HOH:O	2.11	0.50
1:C:98:VAL:O	1:C:102:VAL:HG22	2.11	0.50
4:A:306:GOL:C3	5:A:459:HOH:O	2.59	0.50
1:A:145:TYR:HA	1:A:189:MET:HE1	1.92	0.50
1:C:102:VAL:HG13	1:C:252:VAL:HG11	1.94	0.49
1:B:207:GLU:HB2	2:B:301:SO4:O3	2.13	0.48
1:C:201:MET:CE	1:C:212:LYS:HG2	2.44	0.48
1:C:29:ASN:OD1	3:C:305:CO8:H1B	2.13	0.47
3:C:305:CO8:CCP	3:C:305:CO8:O9P	2.61	0.47
1:A:240:HIS:HD2	5:A:517:HOH:O	1.97	0.47
1:B:145:TYR:HA	1:B:189:MET:HE1	1.97	0.46
1:A:240:HIS:HE1	5:A:519:HOH:O	1.98	0.45
1:C:269:ARG:O	1:C:270:GLN:C	2.54	0.45
1:C:201:MET:HE3	1:C:212:LYS:HG2	2.00	0.44
1:C:96:ASN:O	1:C:100[B]:ARG:HD3	2.17	0.44
1:A:244:PHE:CE2	4:A:306:GOL:H2	2.53	0.43
1:A:205:ASN:HB3	5:A:411:HOH:O	2.19	0.43
1:A:158:GLU:OE1	4:A:305:GOL:O2	2.38	0.42
3:A:304:CO8:OAP	3:A:304:CO8:C6P	2.68	0.41
3:A:304:CO8:H22	4:A:305:GOL:O3	2.21	0.40
1:C:61:SER:HB3	1:C:120:ASN:OD1	2.21	0.40
1:A:64:ARG:NH1	5:A:408:HOH:O	2.54	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	266/300 (89%)	253 (95%)	12 (4%)	1 (0%)	39	33
1	B	257/300 (86%)	248 (96%)	9 (4%)	0	100	100
1	C	258/300 (86%)	250 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	781/900 (87%)	751 (96%)	29 (4%)	1 (0%)	56	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	83	THR

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	234/261 (90%)	226 (97%)	8 (3%)	44	41
1	B	228/261 (87%)	220 (96%)	8 (4%)	43	40
1	C	229/261 (88%)	221 (96%)	8 (4%)	43	40
All	All	691/783 (88%)	667 (96%)	24 (4%)	45	40

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

Mol	Chain	Res	Type
1	A	81	ASP
1	A	82	ASP
1	A	85	LYS
1	A	95	SER
1	A	246	LYS
1	A	252	VAL
1	A	261	ASP
1	A	268	PHE
1	B	6	ARG
1	B	79	GLN
1	B	95	SER
1	B	100	ARG
1	B	171	THR
1	B	252	VAL
1	B	261	ASP

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Mol	Chain	Res	Type
1	B	268	PHE
1	C	7	GLN
1	C	95	SER
1	C	100[A]	ARG
1	C	100[B]	ARG
1	C	102	VAL
1	C	252	VAL
1	C	261	ASP
1	C	268	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
1	B	240	HIS
1	C	79	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CME	A	190	1	7,9,10	0.93	0	6,9,11	1.89	2 (33%)
1	CME	B	190	1	7,9,10	0.75	0	6,9,11	1.83	2 (33%)
1	CME	C	190	1	7,9,10	0.79	0	6,9,11	2.04	3 (50%)

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
1	CME	A	190	1	-	0/5/8/10	0/0/0/0
1	CME	B	190	1	-	0/5/8/10	0/0/0/0
1	CME	C	190	1	-	0/5/8/10	0/0/0/0

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	190	CME	O-C-CA	-2.08	120.15	125.72
1	A	190	CME	CE-SD-SG	2.21	114.01	103.75
1	C	190	CME	CE-SD-SG	2.25	114.21	103.75
1	B	190	CME	CE-SD-SG	2.27	114.27	103.75
1	B	190	CME	CB-SG-SD	2.99	109.76	103.95
1	A	190	CME	CB-SG-SD	3.18	110.13	103.95
1	C	190	CME	CB-SG-SD	3.53	110.81	103.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

21 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	SO4	A	301	-	4,4,4	0.71	0	6,6,6	1.24	1 (16%)
2	SO4	A	302	-	4,4,4	0.50	0	6,6,6	1.21	1 (16%)
2	SO4	A	303	-	4,4,4	0.48	0	6,6,6	0.29	0
3	CO8	A	304	1,4	50,59,59	1.20	3 (6%)	60,85,85	2.45	12 (20%)
4	GOL	A	305	3	5,5,5	0.21	0	5,5,5	0.37	0
4	GOL	A	306	-	5,5,5	0.89	0	5,5,5	1.06	0
2	SO4	B	301	-	4,4,4	0.63	0	6,6,6	0.67	0
2	SO4	B	302	-	4,4,4	0.50	0	6,6,6	0.60	0
2	SO4	B	303	-	4,4,4	0.57	0	6,6,6	0.53	0
3	CO8	B	304	-	33,42,59	0.94	2 (6%)	41,66,85	1.81	7 (17%)
4	GOL	B	305	-	5,5,5	0.54	0	5,5,5	0.84	0
4	GOL	B	306	-	5,5,5	0.67	0	5,5,5	0.92	0
4	GOL	B	307	-	5,5,5	0.47	0	5,5,5	0.31	0
2	SO4	C	301	-	4,4,4	0.55	0	6,6,6	0.52	0
2	SO4	C	302	-	4,4,4	0.58	0	6,6,6	0.36	0
2	SO4	C	303	-	4,4,4	0.58	0	6,6,6	0.75	0
2	SO4	C	304	-	4,4,4	0.37	0	6,6,6	0.45	0
3	CO8	C	305	1,4	50,59,59	1.25	3 (6%)	60,85,85	2.20	11 (18%)
4	GOL	C	306	-	5,5,5	0.52	0	5,5,5	0.63	0
4	GOL	C	307	3	5,5,5	0.26	0	5,5,5	0.42	0
4	GOL	C	308	-	5,5,5	0.68	0	5,5,5	0.66	0

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	SO4	A	301	-	-	0/0/0/0	0/0/0/0
2	SO4	A	302	-	-	0/0/0/0	0/0/0/0
2	SO4	A	303	-	-	0/0/0/0	0/0/0/0
3	CO8	A	304	1,4	-	1/54/74/74	0/3/3/3
4	GOL	A	305	3	-	0/4/4/4	0/0/0/0
4	GOL	A	306	-	-	0/4/4/4	0/0/0/0
2	SO4	B	301	-	-	0/0/0/0	0/0/0/0
2	SO4	B	302	-	-	0/0/0/0	0/0/0/0
2	SO4	B	303	-	-	0/0/0/0	0/0/0/0
3	CO8	B	304	-	-	0/33/54/74	0/3/3/3
4	GOL	B	305	-	-	0/4/4/4	0/0/0/0
4	GOL	B	306	-	-	0/4/4/4	0/0/0/0
4	GOL	B	307	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	C	301	-	-	0/0/0/0	0/0/0/0
2	SO4	C	302	-	-	0/0/0/0	0/0/0/0
2	SO4	C	303	-	-	0/0/0/0	0/0/0/0
2	SO4	C	304	-	-	0/0/0/0	0/0/0/0
3	CO8	C	305	1,4	-	1/54/74/74	0/3/3/3
4	GOL	C	306	-	-	0/4/4/4	0/0/0/0
4	GOL	C	307	3	-	0/4/4/4	0/0/0/0
4	GOL	C	308	-	-	0/4/4/4	0/0/0/0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	304	CO8	C1'-S1P	-5.85	1.68	1.76
3	C	305	CO8	C1'-S1P	-5.64	1.68	1.76
3	B	304	CO8	O4B-C1B	2.09	1.44	1.41
3	A	304	CO8	O4B-C1B	2.55	1.44	1.41
3	A	304	CO8	C5A-C4A	3.21	1.47	1.40
3	C	305	CO8	C2'-C1'	3.23	1.53	1.50
3	B	304	CO8	C5A-C4A	3.25	1.47	1.40
3	C	305	CO8	C5A-C4A	3.62	1.48	1.40

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	304	CO8	O1'-C1'-C2'	-9.81	117.19	123.94
3	B	304	CO8	N3A-C2A-N1A	-7.71	122.82	128.87
3	A	304	CO8	N3A-C2A-N1A	-7.58	122.92	128.87
3	C	305	CO8	N3A-C2A-N1A	-7.11	123.29	128.87
3	C	305	CO8	O1'-C1'-C2'	-6.40	119.53	123.94
3	C	305	CO8	O1'-C1'-S1P	-5.28	118.65	122.83
3	A	304	CO8	O9P-C9P-N8P	-2.91	117.25	123.04
3	A	304	CO8	O5P-C5P-C6P	-2.78	117.13	121.97
3	A	304	CO8	C2B-C1B-N9A	-2.58	106.55	113.47
3	C	305	CO8	C3P-C2P-S1P	-2.41	105.08	111.47
2	A	302	SO4	O2-S-O1	-2.28	101.97	109.59
3	A	304	CO8	O3B-P3B-O7A	-2.19	102.25	107.48
3	C	305	CO8	O3B-P3B-O7A	-2.19	102.26	107.48
3	C	305	CO8	C7P-N8P-C9P	2.02	126.68	122.62
3	B	304	CO8	O9A-P3B-O8A	2.06	115.02	107.44
2	A	301	SO4	O4-S-O3	2.11	117.58	109.09
3	B	304	CO8	N6A-C6A-N1A	2.16	122.14	118.52
3	C	305	CO8	C2A-N1A-C6A	2.29	122.86	118.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	305	CO8	O4B-C1B-N9A	2.30	112.45	108.11
3	A	304	CO8	C2A-N1A-C6A	2.35	122.97	118.77
3	C	305	CO8	C2P-S1P-C1'	2.36	110.49	102.09
3	A	304	CO8	N6A-C6A-N1A	2.44	122.60	118.52
3	B	304	CO8	C2A-N1A-C6A	2.47	123.17	118.77
3	B	304	CO8	O4B-C1B-N9A	2.69	113.19	108.11
3	B	304	CO8	CDP-CBP-CCP	2.97	112.36	108.50
3	C	305	CO8	CDP-CBP-CCP	3.04	112.44	108.50
3	A	304	CO8	O4B-C1B-N9A	3.44	114.61	108.11
3	A	304	CO8	C6P-C7P-N8P	3.56	119.93	111.94
3	B	304	CO8	O9P-C9P-CAP	3.77	121.66	118.95
3	A	304	CO8	CAP-C9P-N8P	3.80	125.27	116.31
3	A	304	CO8	C2'-C1'-S1P	8.60	121.09	113.36
3	C	305	CO8	C2'-C1'-S1P	9.30	121.72	113.36

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	304	CO8	CAP-C9P-N8P-C7P
3	C	305	CO8	CAP-C9P-N8P-C7P

There are no ring outliers.

6 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	304	CO8	7	0
4	A	305	GOL	5	0
4	A	306	GOL	3	0
2	B	301	SO4	1	0
3	B	304	CO8	1	0
3	C	305	CO8	3	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

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	266/300 (88%)	0.07	18 (6%) 20 27	27, 38, 96, 147	0
1	B	261/300 (87%)	0.14	19 (7%) 18 24	30, 46, 86, 116	0
1	C	261/300 (87%)	-0.01	16 (6%) 25 32	29, 39, 76, 121	0
All	All	788/900 (87%)	0.07	53 (6%) 21 28	27, 41, 94, 147	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	83	THR	11.4
1	A	81	ASP	10.0
1	A	82	ASP	8.6
1	A	78	ALA	8.2
1	B	76	ALA	7.4
1	B	72	PHE	7.1
1	A	84	ASN	7.0
1	C	78	ALA	7.0
1	A	80	GLY	6.8
1	C	79	GLN	6.5
1	B	78	ALA	6.4
1	C	72	PHE	6.2
1	A	269	ARG	5.8
1	B	79	GLN	5.7
1	C	269	ARG	5.2
1	B	268	PHE	5.1
1	C	268	PHE	5.0
1	C	77	LYS	4.8
1	A	75	ILE	4.7
1	C	76	ALA	4.7
1	A	268	PHE	4.6
1	A	79	GLN	4.4
1	B	75	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
1	C	75	ILE	4.3
1	A	77	LYS	4.3
1	A	72	PHE	4.1
1	B	269	ARG	3.9
1	B	77	LYS	3.8
1	B	5	ILE	3.4
1	B	4	GLU	3.4
1	B	7	GLN	3.3
1	A	270	GLN	3.2
1	A	76	ALA	3.2
1	C	265	LEU	3.1
1	C	85	LYS	2.9
1	A	4	GLU	2.8
1	B	266	LYS	2.8
1	B	265	LEU	2.6
1	B	270	GLN	2.5
1	C	4	GLU	2.4
1	C	266	LYS	2.4
1	B	86	TYR	2.4
1	A	266	LYS	2.3
1	A	85	LYS	2.3
1	A	86	TYR	2.2
1	B	223	GLY	2.2
1	C	86	TYR	2.2
1	C	270	GLN	2.1
1	B	85	LYS	2.1
1	B	6	ARG	2.1
1	C	73	LYS	2.1
1	B	73	LYS	2.1
1	C	74	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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(Å ²)	Q<0.9
1	CME	C	190	10/11	0.91	0.13	-	39,50,78,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	CME	A	190	10/11	0.90	0.12	-	39,48,74,79	0
1	CME	B	190	10/11	0.89	0.11	-	43,58,77,85	0

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	SO4	C	303	5/5	0.85	0.23	5.18	46,62,72,75	5
2	SO4	B	303	5/5	0.68	0.37	4.11	101,106,123,132	0
3	CO8	C	305	57/57	0.53	0.45	3.36	66,105,125,133	57
2	SO4	A	301	5/5	0.94	0.21	2.80	68,71,77,81	0
2	SO4	C	301	5/5	0.92	0.23	2.77	73,90,100,101	0
3	CO8	B	304	40/57	0.62	0.45	2.69	81,106,122,124	40
3	CO8	A	304	57/57	0.59	0.35	2.63	58,92,120,123	57
2	SO4	A	302	5/5	0.90	0.17	2.32	49,63,67,68	5
4	GOL	C	308	6/6	0.89	0.19	1.80	47,63,63,68	0
4	GOL	C	306	6/6	0.88	0.15	1.64	64,80,84,85	0
4	GOL	A	306	6/6	0.89	0.18	1.53	50,65,68,68	0
2	SO4	B	301	5/5	0.91	0.24	1.40	70,76,87,102	0
4	GOL	B	305	6/6	0.85	0.20	1.29	56,70,75,88	0
4	GOL	B	306	6/6	0.93	0.16	1.26	49,63,65,67	0
2	SO4	B	302	5/5	0.93	0.21	0.92	76,85,89,95	0
4	GOL	A	305	6/6	0.95	0.15	0.60	38,44,45,49	6
4	GOL	C	307	6/6	0.96	0.15	0.42	34,41,45,45	6
4	GOL	B	307	6/6	0.62	0.64	-	73,75,78,79	0
2	SO4	C	302	5/5	0.92	0.34	-	96,99,115,117	0
2	SO4	A	303	5/5	0.91	0.17	-	67,77,79,81	5
2	SO4	C	304	5/5	0.91	0.20	-	75,77,80,85	5

6.5 Other polymers

There are no such residues in this entry.