



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 9, 2024 – 10:38 AM EST

PDB ID : 5VE2  
Title : Crystal structure of enoyl-CoA hydratase/isomerase from *Pseudoalteromonas atlantica* T6c at 2.3 Å resolution.  
Authors : Siuda, M.K.; Shabalin, I.G.; Cooper, D.R.; Chapman, H.C.; Tkaczuk, K.L.; Bonanno, J.; Almo, S.C.; Minor, W.; New York Structural Genomics Research Consortium (NYSGRG)  
Deposited on : 2017-04-03  
Resolution : 2.30 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](mailto: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>.

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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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39



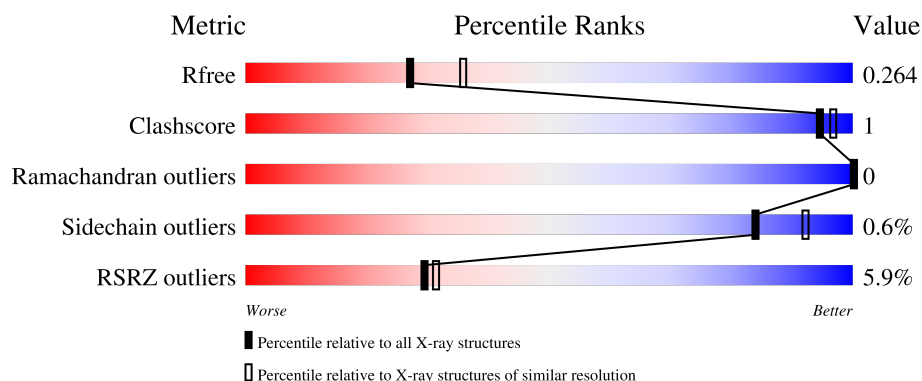
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	275	
1	B	275	
1	C	275	
1	D	275	

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Mol	Chain	Length	Quality of chain
1	E	275	
1	F	275	
1	G	275	
1	H	275	
1	I	275	
1	J	275	
1	K	275	
1	L	275	



## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 24561 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 Enoyl-CoA hydratase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	Se	0	0	0
			1863	1179	326	352	2	4			
1	B	251	Total	C	N	O	S	Se	0	0	0
			1864	1177	327	354	2	4			
1	C	251	Total	C	N	O	S	Se	0	0	0
			1883	1190	330	357	2	4			
1	D	251	Total	C	N	O	S	Se	0	0	0
			1880	1187	330	357	2	4			
1	E	251	Total	C	N	O	S	Se	0	0	0
			1869	1182	326	355	2	4			
1	F	251	Total	C	N	O	S	Se	0	0	0
			1872	1180	329	357	2	4			
1	G	251	Total	C	N	O	S	Se	0	0	0
			1890	1194	331	359	2	4			
1	H	251	Total	C	N	O	S	Se	0	0	0
			1884	1189	330	359	2	4			
1	I	248	Total	C	N	O	S	Se	0	0	0
			1859	1173	325	355	2	4			
1	J	251	Total	C	N	O	S	Se	0	0	0
			1881	1190	328	357	2	4			
1	K	251	Total	C	N	O	S	Se	0	0	0
			1866	1171	330	359	2	4			
1	L	251	Total	C	N	O	S	Se	0	0	0
			1885	1189	331	359	2	4			

There are 264 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MSE	-	initiating methionine	UNP Q15VV3
A	-20	HIS	-	expression tag	UNP Q15VV3
A	-19	HIS	-	expression tag	UNP Q15VV3
A	-18	HIS	-	expression tag	UNP Q15VV3
A	-17	HIS	-	expression tag	UNP Q15VV3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	HIS	-	expression tag	UNP Q15VV3
A	-15	HIS	-	expression tag	UNP Q15VV3
A	-14	SER	-	expression tag	UNP Q15VV3
A	-13	SER	-	expression tag	UNP Q15VV3
A	-12	GLY	-	expression tag	UNP Q15VV3
A	-11	VAL	-	expression tag	UNP Q15VV3
A	-10	ASP	-	expression tag	UNP Q15VV3
A	-9	LEU	-	expression tag	UNP Q15VV3
A	-8	GLY	-	expression tag	UNP Q15VV3
A	-7	THR	-	expression tag	UNP Q15VV3
A	-6	GLU	-	expression tag	UNP Q15VV3
A	-5	ASN	-	expression tag	UNP Q15VV3
A	-4	LEU	-	expression tag	UNP Q15VV3
A	-3	TYR	-	expression tag	UNP Q15VV3
A	-2	PHE	-	expression tag	UNP Q15VV3
A	-1	GLN	-	expression tag	UNP Q15VV3
A	0	SER	-	expression tag	UNP Q15VV3
B	-21	MSE	-	initiating methionine	UNP Q15VV3
B	-20	HIS	-	expression tag	UNP Q15VV3
B	-19	HIS	-	expression tag	UNP Q15VV3
B	-18	HIS	-	expression tag	UNP Q15VV3
B	-17	HIS	-	expression tag	UNP Q15VV3
B	-16	HIS	-	expression tag	UNP Q15VV3
B	-15	HIS	-	expression tag	UNP Q15VV3
B	-14	SER	-	expression tag	UNP Q15VV3
B	-13	SER	-	expression tag	UNP Q15VV3
B	-12	GLY	-	expression tag	UNP Q15VV3
B	-11	VAL	-	expression tag	UNP Q15VV3
B	-10	ASP	-	expression tag	UNP Q15VV3
B	-9	LEU	-	expression tag	UNP Q15VV3
B	-8	GLY	-	expression tag	UNP Q15VV3
B	-7	THR	-	expression tag	UNP Q15VV3
B	-6	GLU	-	expression tag	UNP Q15VV3
B	-5	ASN	-	expression tag	UNP Q15VV3
B	-4	LEU	-	expression tag	UNP Q15VV3
B	-3	TYR	-	expression tag	UNP Q15VV3
B	-2	PHE	-	expression tag	UNP Q15VV3
B	-1	GLN	-	expression tag	UNP Q15VV3
B	0	SER	-	expression tag	UNP Q15VV3
C	-21	MSE	-	initiating methionine	UNP Q15VV3
C	-20	HIS	-	expression tag	UNP Q15VV3
C	-19	HIS	-	expression tag	UNP Q15VV3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	HIS	-	expression tag	UNP Q15VV3
C	-17	HIS	-	expression tag	UNP Q15VV3
C	-16	HIS	-	expression tag	UNP Q15VV3
C	-15	HIS	-	expression tag	UNP Q15VV3
C	-14	SER	-	expression tag	UNP Q15VV3
C	-13	SER	-	expression tag	UNP Q15VV3
C	-12	GLY	-	expression tag	UNP Q15VV3
C	-11	VAL	-	expression tag	UNP Q15VV3
C	-10	ASP	-	expression tag	UNP Q15VV3
C	-9	LEU	-	expression tag	UNP Q15VV3
C	-8	GLY	-	expression tag	UNP Q15VV3
C	-7	THR	-	expression tag	UNP Q15VV3
C	-6	GLU	-	expression tag	UNP Q15VV3
C	-5	ASN	-	expression tag	UNP Q15VV3
C	-4	LEU	-	expression tag	UNP Q15VV3
C	-3	TYR	-	expression tag	UNP Q15VV3
C	-2	PHE	-	expression tag	UNP Q15VV3
C	-1	GLN	-	expression tag	UNP Q15VV3
C	0	SER	-	expression tag	UNP Q15VV3
D	-21	MSE	-	initiating methionine	UNP Q15VV3
D	-20	HIS	-	expression tag	UNP Q15VV3
D	-19	HIS	-	expression tag	UNP Q15VV3
D	-18	HIS	-	expression tag	UNP Q15VV3
D	-17	HIS	-	expression tag	UNP Q15VV3
D	-16	HIS	-	expression tag	UNP Q15VV3
D	-15	HIS	-	expression tag	UNP Q15VV3
D	-14	SER	-	expression tag	UNP Q15VV3
D	-13	SER	-	expression tag	UNP Q15VV3
D	-12	GLY	-	expression tag	UNP Q15VV3
D	-11	VAL	-	expression tag	UNP Q15VV3
D	-10	ASP	-	expression tag	UNP Q15VV3
D	-9	LEU	-	expression tag	UNP Q15VV3
D	-8	GLY	-	expression tag	UNP Q15VV3
D	-7	THR	-	expression tag	UNP Q15VV3
D	-6	GLU	-	expression tag	UNP Q15VV3
D	-5	ASN	-	expression tag	UNP Q15VV3
D	-4	LEU	-	expression tag	UNP Q15VV3
D	-3	TYR	-	expression tag	UNP Q15VV3
D	-2	PHE	-	expression tag	UNP Q15VV3
D	-1	GLN	-	expression tag	UNP Q15VV3
D	0	SER	-	expression tag	UNP Q15VV3
E	-21	MSE	-	initiating methionine	UNP Q15VV3

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-20	HIS	-	expression tag	UNP Q15VV3
E	-19	HIS	-	expression tag	UNP Q15VV3
E	-18	HIS	-	expression tag	UNP Q15VV3
E	-17	HIS	-	expression tag	UNP Q15VV3
E	-16	HIS	-	expression tag	UNP Q15VV3
E	-15	HIS	-	expression tag	UNP Q15VV3
E	-14	SER	-	expression tag	UNP Q15VV3
E	-13	SER	-	expression tag	UNP Q15VV3
E	-12	GLY	-	expression tag	UNP Q15VV3
E	-11	VAL	-	expression tag	UNP Q15VV3
E	-10	ASP	-	expression tag	UNP Q15VV3
E	-9	LEU	-	expression tag	UNP Q15VV3
E	-8	GLY	-	expression tag	UNP Q15VV3
E	-7	THR	-	expression tag	UNP Q15VV3
E	-6	GLU	-	expression tag	UNP Q15VV3
E	-5	ASN	-	expression tag	UNP Q15VV3
E	-4	LEU	-	expression tag	UNP Q15VV3
E	-3	TYR	-	expression tag	UNP Q15VV3
E	-2	PHE	-	expression tag	UNP Q15VV3
E	-1	GLN	-	expression tag	UNP Q15VV3
E	0	SER	-	expression tag	UNP Q15VV3
F	-21	MSE	-	initiating methionine	UNP Q15VV3
F	-20	HIS	-	expression tag	UNP Q15VV3
F	-19	HIS	-	expression tag	UNP Q15VV3
F	-18	HIS	-	expression tag	UNP Q15VV3
F	-17	HIS	-	expression tag	UNP Q15VV3
F	-16	HIS	-	expression tag	UNP Q15VV3
F	-15	HIS	-	expression tag	UNP Q15VV3
F	-14	SER	-	expression tag	UNP Q15VV3
F	-13	SER	-	expression tag	UNP Q15VV3
F	-12	GLY	-	expression tag	UNP Q15VV3
F	-11	VAL	-	expression tag	UNP Q15VV3
F	-10	ASP	-	expression tag	UNP Q15VV3
F	-9	LEU	-	expression tag	UNP Q15VV3
F	-8	GLY	-	expression tag	UNP Q15VV3
F	-7	THR	-	expression tag	UNP Q15VV3
F	-6	GLU	-	expression tag	UNP Q15VV3
F	-5	ASN	-	expression tag	UNP Q15VV3
F	-4	LEU	-	expression tag	UNP Q15VV3
F	-3	TYR	-	expression tag	UNP Q15VV3
F	-2	PHE	-	expression tag	UNP Q15VV3
F	-1	GLN	-	expression tag	UNP Q15VV3

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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	SER	-	expression tag	UNP Q15VV3
G	-21	MSE	-	initiating methionine	UNP Q15VV3
G	-20	HIS	-	expression tag	UNP Q15VV3
G	-19	HIS	-	expression tag	UNP Q15VV3
G	-18	HIS	-	expression tag	UNP Q15VV3
G	-17	HIS	-	expression tag	UNP Q15VV3
G	-16	HIS	-	expression tag	UNP Q15VV3
G	-15	HIS	-	expression tag	UNP Q15VV3
G	-14	SER	-	expression tag	UNP Q15VV3
G	-13	SER	-	expression tag	UNP Q15VV3
G	-12	GLY	-	expression tag	UNP Q15VV3
G	-11	VAL	-	expression tag	UNP Q15VV3
G	-10	ASP	-	expression tag	UNP Q15VV3
G	-9	LEU	-	expression tag	UNP Q15VV3
G	-8	GLY	-	expression tag	UNP Q15VV3
G	-7	THR	-	expression tag	UNP Q15VV3
G	-6	GLU	-	expression tag	UNP Q15VV3
G	-5	ASN	-	expression tag	UNP Q15VV3
G	-4	LEU	-	expression tag	UNP Q15VV3
G	-3	TYR	-	expression tag	UNP Q15VV3
G	-2	PHE	-	expression tag	UNP Q15VV3
G	-1	GLN	-	expression tag	UNP Q15VV3
G	0	SER	-	expression tag	UNP Q15VV3
H	-21	MSE	-	initiating methionine	UNP Q15VV3
H	-20	HIS	-	expression tag	UNP Q15VV3
H	-19	HIS	-	expression tag	UNP Q15VV3
H	-18	HIS	-	expression tag	UNP Q15VV3
H	-17	HIS	-	expression tag	UNP Q15VV3
H	-16	HIS	-	expression tag	UNP Q15VV3
H	-15	HIS	-	expression tag	UNP Q15VV3
H	-14	SER	-	expression tag	UNP Q15VV3
H	-13	SER	-	expression tag	UNP Q15VV3
H	-12	GLY	-	expression tag	UNP Q15VV3
H	-11	VAL	-	expression tag	UNP Q15VV3
H	-10	ASP	-	expression tag	UNP Q15VV3
H	-9	LEU	-	expression tag	UNP Q15VV3
H	-8	GLY	-	expression tag	UNP Q15VV3
H	-7	THR	-	expression tag	UNP Q15VV3
H	-6	GLU	-	expression tag	UNP Q15VV3
H	-5	ASN	-	expression tag	UNP Q15VV3
H	-4	LEU	-	expression tag	UNP Q15VV3
H	-3	TYR	-	expression tag	UNP Q15VV3

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-2	PHE	-	expression tag	UNP Q15VV3
H	-1	GLN	-	expression tag	UNP Q15VV3
H	0	SER	-	expression tag	UNP Q15VV3
I	-21	MSE	-	initiating methionine	UNP Q15VV3
I	-20	HIS	-	expression tag	UNP Q15VV3
I	-19	HIS	-	expression tag	UNP Q15VV3
I	-18	HIS	-	expression tag	UNP Q15VV3
I	-17	HIS	-	expression tag	UNP Q15VV3
I	-16	HIS	-	expression tag	UNP Q15VV3
I	-15	HIS	-	expression tag	UNP Q15VV3
I	-14	SER	-	expression tag	UNP Q15VV3
I	-13	SER	-	expression tag	UNP Q15VV3
I	-12	GLY	-	expression tag	UNP Q15VV3
I	-11	VAL	-	expression tag	UNP Q15VV3
I	-10	ASP	-	expression tag	UNP Q15VV3
I	-9	LEU	-	expression tag	UNP Q15VV3
I	-8	GLY	-	expression tag	UNP Q15VV3
I	-7	THR	-	expression tag	UNP Q15VV3
I	-6	GLU	-	expression tag	UNP Q15VV3
I	-5	ASN	-	expression tag	UNP Q15VV3
I	-4	LEU	-	expression tag	UNP Q15VV3
I	-3	TYR	-	expression tag	UNP Q15VV3
I	-2	PHE	-	expression tag	UNP Q15VV3
I	-1	GLN	-	expression tag	UNP Q15VV3
I	0	SER	-	expression tag	UNP Q15VV3
J	-21	MSE	-	initiating methionine	UNP Q15VV3
J	-20	HIS	-	expression tag	UNP Q15VV3
J	-19	HIS	-	expression tag	UNP Q15VV3
J	-18	HIS	-	expression tag	UNP Q15VV3
J	-17	HIS	-	expression tag	UNP Q15VV3
J	-16	HIS	-	expression tag	UNP Q15VV3
J	-15	HIS	-	expression tag	UNP Q15VV3
J	-14	SER	-	expression tag	UNP Q15VV3
J	-13	SER	-	expression tag	UNP Q15VV3
J	-12	GLY	-	expression tag	UNP Q15VV3
J	-11	VAL	-	expression tag	UNP Q15VV3
J	-10	ASP	-	expression tag	UNP Q15VV3
J	-9	LEU	-	expression tag	UNP Q15VV3
J	-8	GLY	-	expression tag	UNP Q15VV3
J	-7	THR	-	expression tag	UNP Q15VV3
J	-6	GLU	-	expression tag	UNP Q15VV3
J	-5	ASN	-	expression tag	UNP Q15VV3

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-4	LEU	-	expression tag	UNP Q15VV3
J	-3	TYR	-	expression tag	UNP Q15VV3
J	-2	PHE	-	expression tag	UNP Q15VV3
J	-1	GLN	-	expression tag	UNP Q15VV3
J	0	SER	-	expression tag	UNP Q15VV3
K	-21	MSE	-	initiating methionine	UNP Q15VV3
K	-20	HIS	-	expression tag	UNP Q15VV3
K	-19	HIS	-	expression tag	UNP Q15VV3
K	-18	HIS	-	expression tag	UNP Q15VV3
K	-17	HIS	-	expression tag	UNP Q15VV3
K	-16	HIS	-	expression tag	UNP Q15VV3
K	-15	HIS	-	expression tag	UNP Q15VV3
K	-14	SER	-	expression tag	UNP Q15VV3
K	-13	SER	-	expression tag	UNP Q15VV3
K	-12	GLY	-	expression tag	UNP Q15VV3
K	-11	VAL	-	expression tag	UNP Q15VV3
K	-10	ASP	-	expression tag	UNP Q15VV3
K	-9	LEU	-	expression tag	UNP Q15VV3
K	-8	GLY	-	expression tag	UNP Q15VV3
K	-7	THR	-	expression tag	UNP Q15VV3
K	-6	GLU	-	expression tag	UNP Q15VV3
K	-5	ASN	-	expression tag	UNP Q15VV3
K	-4	LEU	-	expression tag	UNP Q15VV3
K	-3	TYR	-	expression tag	UNP Q15VV3
K	-2	PHE	-	expression tag	UNP Q15VV3
K	-1	GLN	-	expression tag	UNP Q15VV3
K	0	SER	-	expression tag	UNP Q15VV3
L	-21	MSE	-	initiating methionine	UNP Q15VV3
L	-20	HIS	-	expression tag	UNP Q15VV3
L	-19	HIS	-	expression tag	UNP Q15VV3
L	-18	HIS	-	expression tag	UNP Q15VV3
L	-17	HIS	-	expression tag	UNP Q15VV3
L	-16	HIS	-	expression tag	UNP Q15VV3
L	-15	HIS	-	expression tag	UNP Q15VV3
L	-14	SER	-	expression tag	UNP Q15VV3
L	-13	SER	-	expression tag	UNP Q15VV3
L	-12	GLY	-	expression tag	UNP Q15VV3
L	-11	VAL	-	expression tag	UNP Q15VV3
L	-10	ASP	-	expression tag	UNP Q15VV3
L	-9	LEU	-	expression tag	UNP Q15VV3
L	-8	GLY	-	expression tag	UNP Q15VV3
L	-7	THR	-	expression tag	UNP Q15VV3

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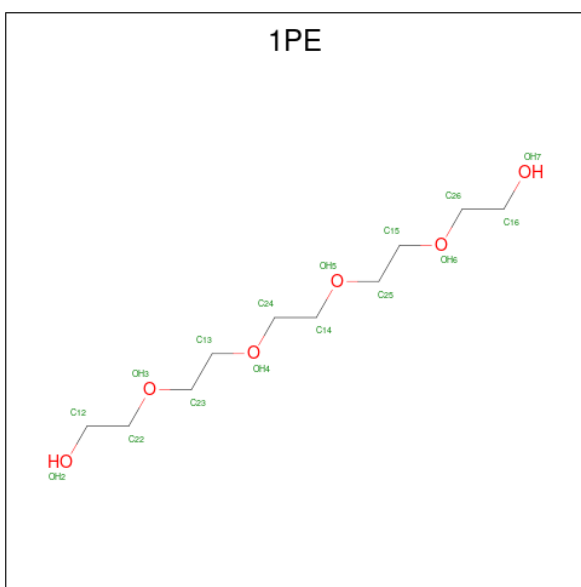
Chain	Residue	Modelled	Actual	Comment	Reference
L	-6	GLU	-	expression tag	UNP Q15VV3
L	-5	ASN	-	expression tag	UNP Q15VV3
L	-4	LEU	-	expression tag	UNP Q15VV3
L	-3	TYR	-	expression tag	UNP Q15VV3
L	-2	PHE	-	expression tag	UNP Q15VV3
L	-1	GLN	-	expression tag	UNP Q15VV3
L	0	SER	-	expression tag	UNP Q15VV3

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0
2	B	1	Total Na 1 1	0	0
2	C	1	Total Na 1 1	0	0
2	D	1	Total Na 1 1	0	0
2	E	1	Total Na 1 1	0	0
2	F	1	Total Na 1 1	0	0
2	G	1	Total Na 1 1	0	0
2	H	1	Total Na 1 1	0	0
2	I	1	Total Na 1 1	0	0
2	J	1	Total Na 1 1	0	0
2	K	1	Total Na 1 1	0	0
2	L	1	Total Na 1 1	0	0

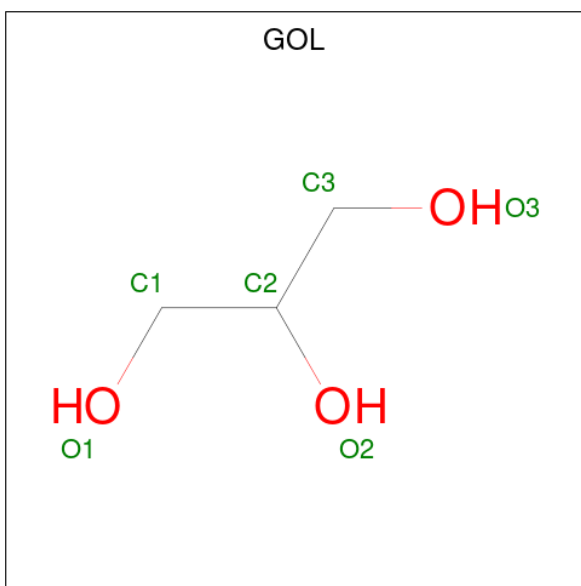
- Molecule 3 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C<sub>10</sub>H<sub>22</sub>O<sub>6</sub>).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			16	10	6		
3	D	1	Total	C	O	0	0
			13	8	5		

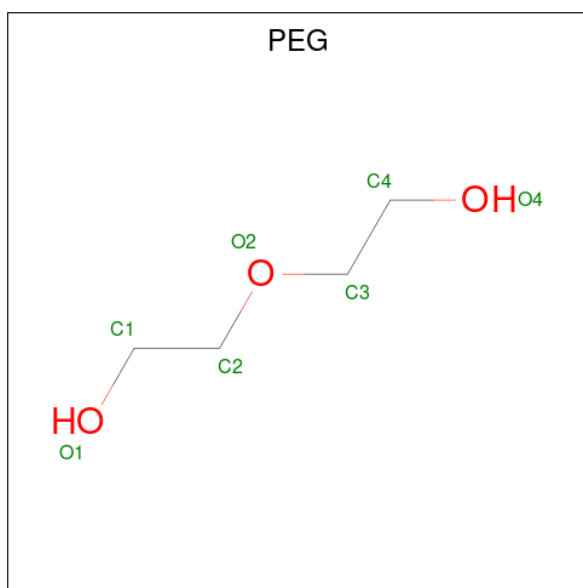
- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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



- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	G	1	Total	C	O	0	0
			7	4	3		
5	H	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	176	Total	O	0	0
			176	176		
6	B	156	Total	O	0	0
			156	156		
6	C	209	Total	O	0	0
			209	209		
6	D	182	Total	O	0	0
			182	182		
6	E	155	Total	O	0	0
			155	155		
6	F	169	Total	O	0	0
			169	169		
6	G	165	Total	O	0	0
			165	165		
6	H	167	Total	O	0	0
			167	167		
6	I	146	Total	O	0	0
			146	146		

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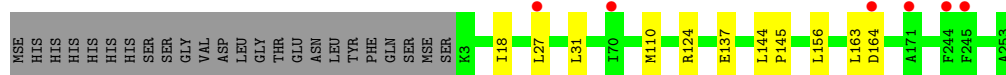
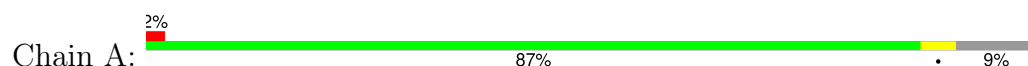
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	J	167	Total 167	O 167	0	0
6	K	150	Total 150	O 150	0	0
6	L	156	Total 156	O 156	0	0



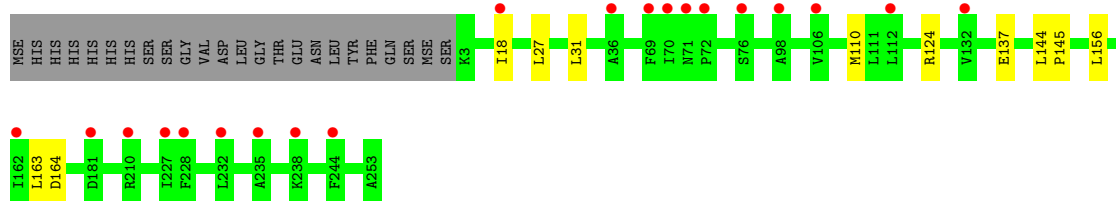
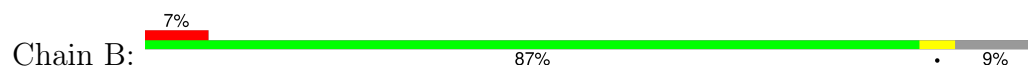
### 3 Residue-property plots [i](#)

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.

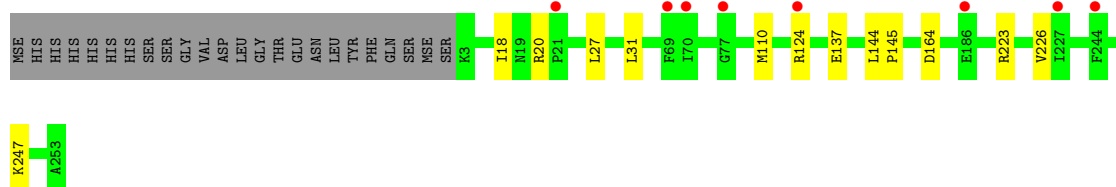
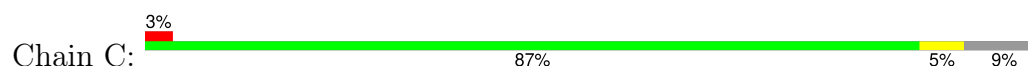
- Molecule 1: Enoyl-CoA hydratase



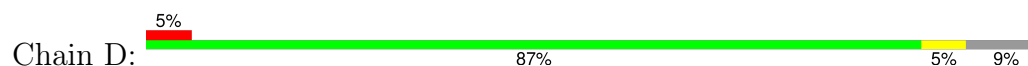
- Molecule 1: Enoyl-CoA hydratase



- Molecule 1: Enoyl-CoA hydratase



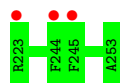
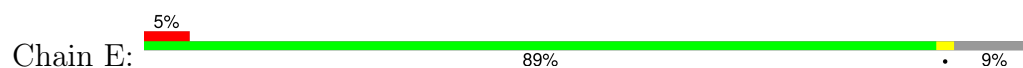
- Molecule 1: Enoyl-CoA hydratase



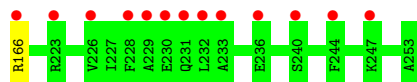
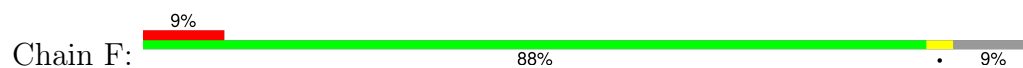




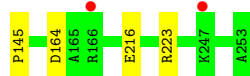
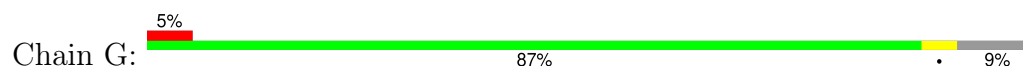
- Molecule 1: Enoyl-CoA hydratase



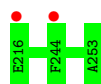
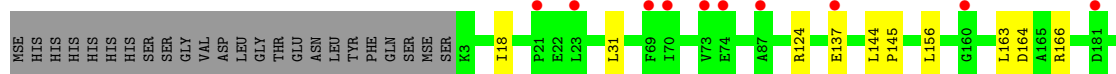
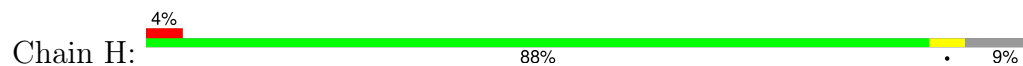
- Molecule 1: Enoyl-CoA hydratase



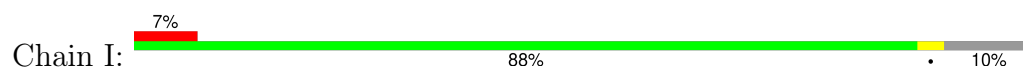
- Molecule 1: Enoyl-CoA hydratase



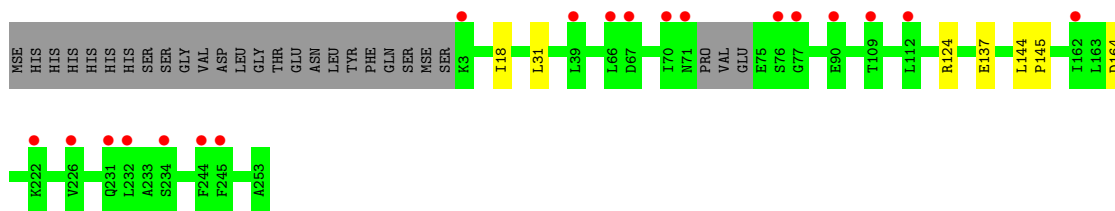
- Molecule 1: Enoyl-CoA hydratase



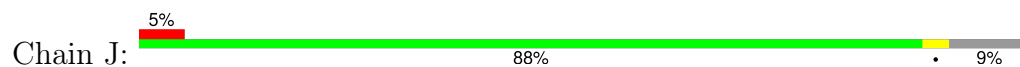
- Molecule 1: Enoyl-CoA hydratase



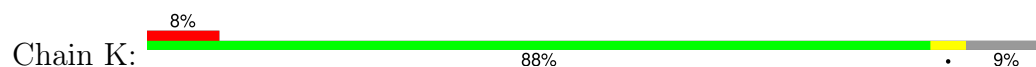




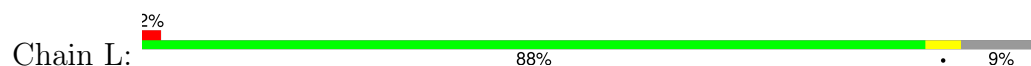
• Molecule 1: Enoyl-CoA hydratase



• Molecule 1: Enoyl-CoA hydratase



• Molecule 1: Enoyl-CoA hydratase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.66Å 160.14Å 136.27Å 90.00° 90.12° 90.00°	Depositor
Resolution (Å)	38.00 – 2.30 38.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.1 (38.00-2.30) 95.1 (38.00-2.30)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.80 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.205 , 0.258 0.218 , 0.264	Depositor DCC
$R_{free}$ test set	7526 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.0	Xtriage
Anisotropy	0.421	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 54.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.138 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	24561	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 58.70 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.9664e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PEG, NA, 1PE

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	0.58	0/1887	0.71	0/2558
1	B	0.58	0/1887	0.71	0/2557
1	C	0.59	0/1907	0.72	1/2583 (0.0%)
1	D	0.60	0/1904	0.72	0/2579
1	E	0.59	0/1893	0.70	0/2567
1	F	0.59	0/1895	0.71	0/2568
1	G	0.61	0/1914	0.73	2/2591 (0.1%)
1	H	0.58	0/1908	0.72	1/2584 (0.0%)
1	I	0.61	0/1880	0.73	0/2544
1	J	0.59	0/1905	0.72	0/2580
1	K	0.60	0/1887	0.72	1/2557 (0.0%)
1	L	0.58	0/1909	0.73	0/2585
All	All	0.59	0/22776	0.72	5/30853 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	216	GLU	OE1-CD-OE2	-5.64	116.53	123.30
1	H	166	ARG	NE-CZ-NH2	5.51	123.05	120.30
1	K	216	GLU	OE1-CD-OE2	-5.27	116.97	123.30
1	C	20	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	G	223	ARG	NE-CZ-NH1	-5.08	117.76	120.30

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	1863	0	1849	5	0
1	B	1864	0	1855	5	0
1	C	1883	0	1881	6	0
1	D	1880	0	1872	6	0
1	E	1869	0	1855	3	0
1	F	1872	0	1858	3	0
1	G	1890	0	1894	6	0
1	H	1884	0	1876	4	0
1	I	1859	0	1855	3	0
1	J	1881	0	1881	4	0
1	K	1866	0	1855	4	0
1	L	1885	0	1881	4	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
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	C	16	0	22	0	0
3	D	13	0	17	0	0
4	E	12	0	16	0	0
5	G	7	0	10	0	0
5	H	7	0	10	0	0
6	A	176	0	0	0	0
6	B	156	0	0	0	0
6	C	209	0	0	1	0
6	D	182	0	0	0	0
6	E	155	0	0	0	0
6	F	169	0	0	0	0
6	G	165	0	0	0	0
6	H	167	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	I	146	0	0	0	0
6	J	167	0	0	0	0
6	K	150	0	0	0	0
6	L	156	0	0	0	0
All	All	24561	0	22487	53	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 1.

All (53) 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:223:ARG:O	1:D:226:VAL:HG12	2.12	0.49
1:C:223:ARG:O	1:C:226:VAL:HG12	2.13	0.48
1:F:18:ILE:HG23	1:F:31:LEU:HD21	1.97	0.47
1:G:27:LEU:HD21	1:G:110:MSE:HE1	1.96	0.46
1:E:18:ILE:HG23	1:E:31:LEU:HD21	1.98	0.46
1:J:18:ILE:HG23	1:J:31:LEU:HD21	1.98	0.46
1:D:18:ILE:HG23	1:D:31:LEU:HD21	1.98	0.45
1:I:18:ILE:HG23	1:I:31:LEU:HD21	1.98	0.45
1:K:18:ILE:HG23	1:K:31:LEU:HD21	1.98	0.45
1:B:18:ILE:HG23	1:B:31:LEU:HD21	1.98	0.45
1:C:247:LYS:NZ	6:C:406:HOH:O	2.49	0.45
1:E:124:ARG:HD3	1:E:164:ASP:HA	1.99	0.45
1:F:124:ARG:HD3	1:F:164:ASP:HA	1.99	0.45
1:I:124:ARG:HD3	1:I:164:ASP:HA	1.99	0.45
1:J:124:ARG:HD3	1:J:164:ASP:HA	1.99	0.45
1:D:124:ARG:HD3	1:D:164:ASP:HA	1.99	0.44
1:L:18:ILE:HG23	1:L:31:LEU:HD21	1.98	0.44
1:G:18:ILE:HG23	1:G:31:LEU:HD21	1.97	0.44
1:A:18:ILE:HG23	1:A:31:LEU:HD21	1.98	0.44
1:C:124:ARG:HD3	1:C:164:ASP:HA	1.99	0.44
1:B:124:ARG:HD3	1:B:164:ASP:HA	1.99	0.44
1:K:124:ARG:HD3	1:K:164:ASP:HA	1.99	0.44
1:G:124:ARG:HD3	1:G:164:ASP:HA	1.99	0.44
1:H:18:ILE:HG23	1:H:31:LEU:HD21	1.99	0.44
1:C:18:ILE:HG23	1:C:31:LEU:HD21	1.99	0.43
1:H:124:ARG:HD3	1:H:164:ASP:HA	1.99	0.43
1:A:27:LEU:HD11	1:A:110:MSE:HE1	2.01	0.43
1:L:124:ARG:HD3	1:L:164:ASP:HA	2.00	0.43
1:A:124:ARG:HD3	1:A:164:ASP:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:27:LEU:HD11	1:C:110:MSE:HE1	2.01	0.42
1:G:27:LEU:CD1	1:G:61:THR:OG1	2.67	0.42
1:E:27:LEU:HD11	1:E:110:MSE:HE1	2.01	0.42
1:G:27:LEU:HD11	1:G:61:THR:OG1	2.20	0.42
1:F:27:LEU:HD11	1:F:110:MSE:HE1	2.02	0.42
1:J:144:LEU:HB3	1:J:145:PRO:HD3	2.02	0.42
1:L:156:LEU:HD21	1:L:163:LEU:HD13	2.02	0.41
1:I:144:LEU:HB3	1:I:145:PRO:HD3	2.03	0.41
1:A:144:LEU:HB3	1:A:145:PRO:HD3	2.03	0.41
1:B:144:LEU:HB3	1:B:145:PRO:HD3	2.03	0.41
1:J:27:LEU:HD11	1:J:110:MSE:HE1	2.01	0.41
1:B:27:LEU:HD11	1:B:110:MSE:HE1	2.02	0.41
1:D:27:LEU:HD11	1:D:110:MSE:HE1	2.03	0.41
1:K:156:LEU:HD21	1:K:163:LEU:HD13	2.03	0.41
1:D:144:LEU:HB3	1:D:145:PRO:HD3	2.03	0.41
1:K:144:LEU:HB3	1:K:145:PRO:HD3	2.03	0.41
1:L:144:LEU:HB3	1:L:145:PRO:HD3	2.03	0.41
1:G:144:LEU:HB3	1:G:145:PRO:HD3	2.03	0.40
1:C:144:LEU:HB3	1:C:145:PRO:HD3	2.03	0.40
1:H:156:LEU:HD21	1:H:163:LEU:HD13	2.04	0.40
1:H:144:LEU:HB3	1:H:145:PRO:HD3	2.03	0.40
1:A:156:LEU:HD21	1:A:163:LEU:HD13	2.04	0.40
1:B:156:LEU:HD21	1:B:163:LEU:HD13	2.04	0.40
1:D:11:ASN:ND2	1:D:192:GLU:OE1	2.50	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	249/275 (90%)	244 (98%)	5 (2%)	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
1	C	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
1	D	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
1	E	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
1	F	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
1	G	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
1	H	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
1	I	244/275 (89%)	240 (98%)	4 (2%)	0	100	100
1	J	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
1	K	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
1	L	249/275 (90%)	244 (98%)	5 (2%)	0	100	100
All	All	2983/3300 (90%)	2924 (98%)	59 (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	189/221 (86%)	188 (100%)	1 (0%)	86	93
1	B	190/221 (86%)	189 (100%)	1 (0%)	86	93
1	C	194/221 (88%)	193 (100%)	1 (0%)	86	93
1	D	193/221 (87%)	192 (100%)	1 (0%)	86	93
1	E	191/221 (86%)	191 (100%)	0	100	100
1	F	191/221 (86%)	189 (99%)	2 (1%)	73	85
1	G	196/221 (89%)	195 (100%)	1 (0%)	86	93
1	H	194/221 (88%)	193 (100%)	1 (0%)	86	93
1	I	191/221 (86%)	190 (100%)	1 (0%)	86	93
1	J	194/221 (88%)	193 (100%)	1 (0%)	86	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	191/221 (86%)	190 (100%)	1 (0%)	86	93
1	L	195/221 (88%)	193 (99%)	2 (1%)	73	85
All	All	2309/2652 (87%)	2296 (99%)	13 (1%)	84	92

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	137	GLU
1	B	137	GLU
1	C	137	GLU
1	D	137	GLU
1	F	137	GLU
1	F	166	ARG
1	G	137	GLU
1	H	137	GLU
1	I	137	GLU
1	J	137	GLU
1	K	137	GLU
1	L	137	GLU
1	L	166	ARG

Sometimes 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 molecules 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 oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 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	$\# Z  > 2$
3	1PE	D	302	-	12,12,15	0.53	0	11,11,14	0.32	0
5	PEG	H	302	-	6,6,6	0.60	0	5,5,5	0.51	0
4	GOL	E	302	-	5,5,5	0.59	0	5,5,5	0.42	0
4	GOL	E	301	-	5,5,5	0.51	0	5,5,5	0.56	0
5	PEG	G	302	-	6,6,6	0.59	0	5,5,5	0.29	0
3	1PE	C	302	-	15,15,15	0.50	0	14,14,14	0.41	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
3	1PE	D	302	-	-	7/10/10/13	-
5	PEG	H	302	-	-	2/4/4/4	-
4	GOL	E	302	-	-	2/4/4/4	-
4	GOL	E	301	-	-	3/4/4/4	-
5	PEG	G	302	-	-	2/4/4/4	-
3	1PE	C	302	-	-	5/13/13/13	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	302	GOL	C1-C2-C3-O3
4	E	302	GOL	O2-C2-C3-O3
3	C	302	1PE	OH4-C13-C23-OH3
3	C	302	1PE	OH6-C15-C25-OH5
4	E	301	GOL	O1-C1-C2-C3
3	D	302	1PE	OH7-C16-C26-OH6

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Mol	Chain	Res	Type	Atoms
5	H	302	PEG	O1-C1-C2-O2
3	D	302	1PE	OH4-C13-C23-OH3
4	E	301	GOL	O2-C2-C3-O3
5	H	302	PEG	O2-C3-C4-O4
4	E	301	GOL	C1-C2-C3-O3
3	C	302	1PE	C25-C15-OH6-C26
3	C	302	1PE	C13-C23-OH3-C22
5	G	302	PEG	O1-C1-C2-O2
3	D	302	1PE	OH6-C15-C25-OH5
3	D	302	1PE	C14-C24-OH4-C13
3	D	302	1PE	C15-C25-OH5-C14
3	D	302	1PE	OH5-C14-C24-OH4
3	D	302	1PE	C23-C13-OH4-C24
5	G	302	PEG	C4-C3-O2-C2
3	C	302	1PE	OH5-C14-C24-OH4

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	247/275 (89%)	0.41	6 (2%) 59 61	27, 40, 79, 143	0
1	B	247/275 (89%)	0.70	20 (8%) 19 21	27, 42, 96, 177	0
1	C	247/275 (89%)	0.42	8 (3%) 50 52	25, 38, 76, 113	0
1	D	247/275 (89%)	0.50	14 (5%) 30 32	25, 39, 75, 115	0
1	E	247/275 (89%)	0.52	15 (6%) 28 30	24, 40, 88, 141	0
1	F	247/275 (89%)	0.67	26 (10%) 13 14	23, 41, 101, 166	0
1	G	247/275 (89%)	0.54	13 (5%) 33 34	26, 40, 78, 119	0
1	H	247/275 (89%)	0.48	12 (4%) 36 37	23, 40, 79, 117	0
1	I	244/275 (88%)	0.72	19 (7%) 20 22	26, 43, 94, 139	0
1	J	247/275 (89%)	0.49	14 (5%) 30 32	25, 41, 86, 155	0
1	K	247/275 (89%)	0.67	21 (8%) 18 20	28, 41, 97, 195	0
1	L	247/275 (89%)	0.44	6 (2%) 59 61	27, 41, 86, 165	0
All	All	2961/3300 (89%)	0.55	174 (5%) 29 31	23, 41, 87, 195	0

All (174) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	71	ASN	5.1
1	F	76	SER	4.9
1	E	76	SER	4.9
1	I	76	SER	4.6
1	K	244	PHE	4.6
1	L	244	PHE	4.6
1	L	72	PRO	4.2
1	L	69	PHE	4.1
1	K	232	LEU	4.1
1	I	109	THR	4.1
1	B	244	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
1	K	72	PRO	3.8
1	F	69	PHE	3.6
1	I	245	PHE	3.6
1	E	21	PRO	3.6
1	D	70	ILE	3.4
1	G	87	ALA	3.4
1	G	166	ARG	3.3
1	F	232	LEU	3.3
1	A	164	ASP	3.2
1	B	235	ALA	3.2
1	B	71	ASN	3.2
1	L	247	LYS	3.2
1	B	70	ILE	3.1
1	H	160	GLY	3.1
1	H	244	PHE	3.1
1	I	66	LEU	3.1
1	H	73	VAL	3.1
1	B	112	LEU	3.0
1	A	244	PHE	3.0
1	C	244	PHE	3.0
1	K	162	ILE	3.0
1	F	74	GLU	3.0
1	K	76	SER	3.0
1	F	236	GLU	3.0
1	D	150	GLN	3.0
1	J	245	PHE	2.9
1	J	22	GLU	2.9
1	J	69	PHE	2.9
1	J	132	VAL	2.9
1	F	233	ALA	2.9
1	K	238	LYS	2.9
1	C	227	ILE	2.9
1	F	166	ARG	2.9
1	H	70	ILE	2.8
1	B	162	ILE	2.8
1	I	3	LYS	2.8
1	I	77	GLY	2.8
1	F	72	PRO	2.8
1	J	72	PRO	2.8
1	E	245	PHE	2.7
1	G	69	PHE	2.7
1	G	70	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	223	ARG	2.7
1	K	40	GLU	2.7
1	H	21	PRO	2.7
1	J	3	LYS	2.7
1	K	247	LYS	2.7
1	L	77	GLY	2.7
1	B	18	ILE	2.7
1	I	70	ILE	2.7
1	A	245	PHE	2.7
1	D	166	ARG	2.6
1	B	98	ALA	2.6
1	B	232	LEU	2.6
1	E	23	LEU	2.6
1	F	70	ILE	2.6
1	F	162	ILE	2.6
1	E	101	GLY	2.6
1	J	244	PHE	2.6
1	F	229	ALA	2.6
1	K	226	VAL	2.6
1	J	6	ASN	2.6
1	I	222	LYS	2.6
1	H	74	GLU	2.5
1	E	69	PHE	2.5
1	A	27	LEU	2.5
1	G	23	LEU	2.5
1	B	76	SER	2.5
1	F	230	GLU	2.5
1	G	106	VAL	2.5
1	I	244	PHE	2.5
1	K	73	VAL	2.5
1	H	216	GLU	2.5
1	B	69	PHE	2.5
1	D	69	PHE	2.5
1	F	228	PHE	2.5
1	H	23	LEU	2.5
1	F	150	GLN	2.5
1	E	165	ALA	2.4
1	B	228	PHE	2.4
1	K	112	LEU	2.4
1	J	43	ASN	2.4
1	H	181	ASP	2.4
1	C	77	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	36	ALA	2.4
1	B	106	VAL	2.4
1	K	150	GLN	2.4
1	I	112	LEU	2.4
1	D	106	VAL	2.4
1	G	73	VAL	2.4
1	G	247	LYS	2.4
1	I	67	ASP	2.4
1	C	69	PHE	2.3
1	E	244	PHE	2.3
1	B	72	PRO	2.3
1	B	210	ARG	2.3
1	C	186	GLU	2.3
1	J	137	GLU	2.3
1	K	44	HIS	2.3
1	E	171	ALA	2.3
1	G	76	SER	2.3
1	J	70	ILE	2.3
1	F	111	LEU	2.3
1	I	232	LEU	2.3
1	K	68	ASP	2.3
1	F	77	GLY	2.3
1	C	70	ILE	2.2
1	G	107	GLY	2.2
1	J	77	GLY	2.2
1	D	27	LEU	2.2
1	B	181	ASP	2.2
1	D	90	GLU	2.2
1	K	166	ARG	2.2
1	H	69	PHE	2.2
1	I	231	GLN	2.2
1	A	70	ILE	2.2
1	I	162	ILE	2.2
1	G	39	LEU	2.2
1	G	71	ASN	2.2
1	D	21	PRO	2.2
1	B	132	VAL	2.2
1	D	244	PHE	2.2
1	F	240	SER	2.1
1	H	137	GLU	2.1
1	F	223	ARG	2.1
1	J	193	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	K	231	GLN	2.1
1	B	227	ILE	2.1
1	C	124	ARG	2.1
1	E	131	HIS	2.1
1	F	71	ASN	2.1
1	F	112	LEU	2.1
1	J	23	LEU	2.1
1	C	21	PRO	2.1
1	D	145	PRO	2.1
1	B	238	LYS	2.1
1	K	241	VAL	2.1
1	K	69	PHE	2.1
1	F	247	LYS	2.1
1	A	171	ALA	2.1
1	F	132	VAL	2.1
1	F	226	VAL	2.1
1	I	90	GLU	2.1
1	I	226	VAL	2.1
1	K	106	VAL	2.1
1	F	244	PHE	2.1
1	D	77	GLY	2.1
1	D	107	GLY	2.1
1	I	234	SER	2.1
1	F	39	LEU	2.1
1	K	111	LEU	2.1
1	K	78	THR	2.1
1	E	216	GLU	2.0
1	F	231	GLN	2.0
1	D	35	LEU	2.0
1	E	72	PRO	2.0
1	I	39	LEU	2.0
1	H	87	ALA	2.0
1	L	13	VAL	2.0
1	E	77	GLY	2.0
1	G	141	SER	2.0
1	D	162	ILE	2.0
1	E	16	LEU	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 [i](#)

There are no monosaccharides 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. 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	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	1PE	D	302	13/16	0.78	0.18	32,55,73,77	0
4	GOL	E	302	6/6	0.80	0.14	44,56,66,67	0
3	1PE	C	302	16/16	0.84	0.14	44,60,79,79	0
5	PEG	H	302	7/7	0.86	0.16	40,58,68,85	0
4	GOL	E	301	6/6	0.87	0.12	58,71,90,98	0
5	PEG	G	302	7/7	0.89	0.14	43,62,76,90	0
2	NA	G	301	1/1	0.89	0.09	29,29,29,29	0
2	NA	E	303	1/1	0.91	0.06	36,36,36,36	0
2	NA	B	301	1/1	0.94	0.06	38,38,38,38	0
2	NA	H	301	1/1	0.94	0.07	38,38,38,38	0
2	NA	C	301	1/1	0.94	0.07	40,40,40,40	0
2	NA	A	301	1/1	0.94	0.04	39,39,39,39	0
2	NA	D	301	1/1	0.95	0.06	38,38,38,38	0
2	NA	F	301	1/1	0.96	0.07	33,33,33,33	0
2	NA	J	301	1/1	0.96	0.09	41,41,41,41	0
2	NA	I	301	1/1	0.97	0.07	41,41,41,41	0
2	NA	K	301	1/1	0.98	0.05	39,39,39,39	0
2	NA	L	301	1/1	0.98	0.03	39,39,39,39	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.