



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 28, 2024 – 02:16 PM EDT

PDB ID : 3E6Q  
Title : Putative 5-carboxymethyl-2-hydroxymuconate isomerase from *Pseudomonas aeruginosa*.  
Authors : Osipiuk, J.; Xu, X.; Cui, H.; Savchenko, A.; Edwards, A.M.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2008-08-15  
Resolution : 1.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

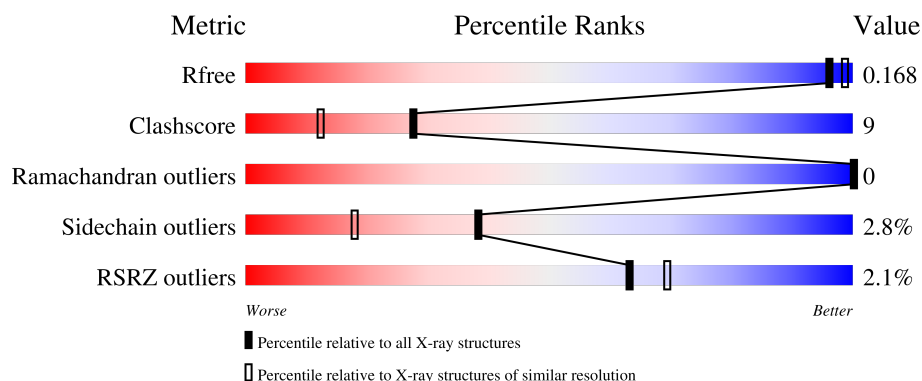
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 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	2888 (1.76-1.76)
Clashscore	180529	3097 (1.76-1.76)
Ramachandran outliers	177936	3072 (1.76-1.76)
Sidechain outliers	177891	3072 (1.76-1.76)
RSRZ outliers	164620	2887 (1.76-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	146	<div> <div>74%</div> <div>11%</div> <div>14%</div> </div>
1	B	146	<div> <div>76%</div> <div>9%</div> <div>14%</div> </div>
1	C	146	<div> <div>75%</div> <div>10%</div> <div>14%</div> </div>
1	D	146	<div> <div>5%</div> <div>78%</div> <div>9%</div> <div>12%</div> </div>
1	E	146	<div> <div>76%</div> <div>10%</div> <div>13%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	146	
1	G	146	
1	H	146	
1	I	146	
1	J	146	
1	K	146	
1	L	146	

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	EDO	K	323	-	-	X	-
2	EDO	K	324	-	-	X	-
3	FMT	A	335	-	-	X	-
3	FMT	B	345	-	-	X	-
3	FMT	L	336	-	-	X	-
3	FMT	L	340	-	-	X	-
4	ACT	A	337	-	-	X	-
6	GOL	E	301[A]	-	-	X	-
6	GOL	E	301[B]	-	-	X	-
6	GOL	H	305[A]	-	-	X	-
6	GOL	H	305[B]	-	-	X	-
6	GOL	J	307[B]	-	-	X	-

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14344 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 putative 5-carboxymethyl-2-hydroxymuconate isomerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	126	Total	C	N	O	S	Se	0	12	0
			1013	637	174	198	2	2			
1	B	126	Total	C	N	O	S	Se	0	14	0
			1025	642	178	201	2	2			
1	C	126	Total	C	N	O	S	Se	0	16	0
			1032	648	177	203	2	2			
1	D	128	Total	C	N	O	S	Se	0	14	0
			1033	643	183	203	2	2			
1	E	127	Total	C	N	O	S	Se	0	17	0
			1039	645	185	205	2	2			
1	F	128	Total	C	N	O	S	Se	0	14	0
			1031	642	179	206	2	2			
1	G	126	Total	C	N	O	S	Se	0	9	0
			994	623	170	197	2	2			
1	H	126	Total	C	N	O	S	Se	0	8	0
			992	617	175	196	2	2			
1	I	126	Total	C	N	O	S	Se	0	16	0
			1030	645	177	204	2	2			
1	J	127	Total	C	N	O	S	Se	0	16	0
			1046	652	189	201	2	2			
1	K	127	Total	C	N	O	S	Se	0	15	0
			1021	636	179	202	2	2			
1	L	127	Total	C	N	O	S	Se	0	13	0
			1015	633	175	203	2	2			

There are 276 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MSE	-	expression tag	UNP Q9I2D8
A	-19	GLY	-	expression tag	UNP Q9I2D8
A	-18	SER	-	expression tag	UNP Q9I2D8
A	-17	SER	-	expression tag	UNP Q9I2D8
A	-16	HIS	-	expression tag	UNP Q9I2D8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	HIS	-	expression tag	UNP Q9I2D8
A	-14	HIS	-	expression tag	UNP Q9I2D8
A	-13	HIS	-	expression tag	UNP Q9I2D8
A	-12	HIS	-	expression tag	UNP Q9I2D8
A	-11	HIS	-	expression tag	UNP Q9I2D8
A	-10	SER	-	expression tag	UNP Q9I2D8
A	-9	SER	-	expression tag	UNP Q9I2D8
A	-8	GLY	-	expression tag	UNP Q9I2D8
A	-7	ARG	-	expression tag	UNP Q9I2D8
A	-6	GLU	-	expression tag	UNP Q9I2D8
A	-5	ASN	-	expression tag	UNP Q9I2D8
A	-4	LEU	-	expression tag	UNP Q9I2D8
A	-3	TYR	-	expression tag	UNP Q9I2D8
A	-2	PHE	-	expression tag	UNP Q9I2D8
A	-1	GLN	-	expression tag	UNP Q9I2D8
A	0	GLY	-	expression tag	UNP Q9I2D8
A	124	GLY	-	expression tag	UNP Q9I2D8
A	125	SER	-	expression tag	UNP Q9I2D8
B	-20	MSE	-	expression tag	UNP Q9I2D8
B	-19	GLY	-	expression tag	UNP Q9I2D8
B	-18	SER	-	expression tag	UNP Q9I2D8
B	-17	SER	-	expression tag	UNP Q9I2D8
B	-16	HIS	-	expression tag	UNP Q9I2D8
B	-15	HIS	-	expression tag	UNP Q9I2D8
B	-14	HIS	-	expression tag	UNP Q9I2D8
B	-13	HIS	-	expression tag	UNP Q9I2D8
B	-12	HIS	-	expression tag	UNP Q9I2D8
B	-11	HIS	-	expression tag	UNP Q9I2D8
B	-10	SER	-	expression tag	UNP Q9I2D8
B	-9	SER	-	expression tag	UNP Q9I2D8
B	-8	GLY	-	expression tag	UNP Q9I2D8
B	-7	ARG	-	expression tag	UNP Q9I2D8
B	-6	GLU	-	expression tag	UNP Q9I2D8
B	-5	ASN	-	expression tag	UNP Q9I2D8
B	-4	LEU	-	expression tag	UNP Q9I2D8
B	-3	TYR	-	expression tag	UNP Q9I2D8
B	-2	PHE	-	expression tag	UNP Q9I2D8
B	-1	GLN	-	expression tag	UNP Q9I2D8
B	0	GLY	-	expression tag	UNP Q9I2D8
B	124	GLY	-	expression tag	UNP Q9I2D8
B	125	SER	-	expression tag	UNP Q9I2D8
C	-20	MSE	-	expression tag	UNP Q9I2D8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-19	GLY	-	expression tag	UNP Q9I2D8
C	-18	SER	-	expression tag	UNP Q9I2D8
C	-17	SER	-	expression tag	UNP Q9I2D8
C	-16	HIS	-	expression tag	UNP Q9I2D8
C	-15	HIS	-	expression tag	UNP Q9I2D8
C	-14	HIS	-	expression tag	UNP Q9I2D8
C	-13	HIS	-	expression tag	UNP Q9I2D8
C	-12	HIS	-	expression tag	UNP Q9I2D8
C	-11	HIS	-	expression tag	UNP Q9I2D8
C	-10	SER	-	expression tag	UNP Q9I2D8
C	-9	SER	-	expression tag	UNP Q9I2D8
C	-8	GLY	-	expression tag	UNP Q9I2D8
C	-7	ARG	-	expression tag	UNP Q9I2D8
C	-6	GLU	-	expression tag	UNP Q9I2D8
C	-5	ASN	-	expression tag	UNP Q9I2D8
C	-4	LEU	-	expression tag	UNP Q9I2D8
C	-3	TYR	-	expression tag	UNP Q9I2D8
C	-2	PHE	-	expression tag	UNP Q9I2D8
C	-1	GLN	-	expression tag	UNP Q9I2D8
C	0	GLY	-	expression tag	UNP Q9I2D8
C	124	GLY	-	expression tag	UNP Q9I2D8
C	125	SER	-	expression tag	UNP Q9I2D8
D	-20	MSE	-	expression tag	UNP Q9I2D8
D	-19	GLY	-	expression tag	UNP Q9I2D8
D	-18	SER	-	expression tag	UNP Q9I2D8
D	-17	SER	-	expression tag	UNP Q9I2D8
D	-16	HIS	-	expression tag	UNP Q9I2D8
D	-15	HIS	-	expression tag	UNP Q9I2D8
D	-14	HIS	-	expression tag	UNP Q9I2D8
D	-13	HIS	-	expression tag	UNP Q9I2D8
D	-12	HIS	-	expression tag	UNP Q9I2D8
D	-11	HIS	-	expression tag	UNP Q9I2D8
D	-10	SER	-	expression tag	UNP Q9I2D8
D	-9	SER	-	expression tag	UNP Q9I2D8
D	-8	GLY	-	expression tag	UNP Q9I2D8
D	-7	ARG	-	expression tag	UNP Q9I2D8
D	-6	GLU	-	expression tag	UNP Q9I2D8
D	-5	ASN	-	expression tag	UNP Q9I2D8
D	-4	LEU	-	expression tag	UNP Q9I2D8
D	-3	TYR	-	expression tag	UNP Q9I2D8
D	-2	PHE	-	expression tag	UNP Q9I2D8
D	-1	GLN	-	expression tag	UNP Q9I2D8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	0	GLY	-	expression tag	UNP Q9I2D8
D	124	GLY	-	expression tag	UNP Q9I2D8
D	125	SER	-	expression tag	UNP Q9I2D8
E	-20	MSE	-	expression tag	UNP Q9I2D8
E	-19	GLY	-	expression tag	UNP Q9I2D8
E	-18	SER	-	expression tag	UNP Q9I2D8
E	-17	SER	-	expression tag	UNP Q9I2D8
E	-16	HIS	-	expression tag	UNP Q9I2D8
E	-15	HIS	-	expression tag	UNP Q9I2D8
E	-14	HIS	-	expression tag	UNP Q9I2D8
E	-13	HIS	-	expression tag	UNP Q9I2D8
E	-12	HIS	-	expression tag	UNP Q9I2D8
E	-11	HIS	-	expression tag	UNP Q9I2D8
E	-10	SER	-	expression tag	UNP Q9I2D8
E	-9	SER	-	expression tag	UNP Q9I2D8
E	-8	GLY	-	expression tag	UNP Q9I2D8
E	-7	ARG	-	expression tag	UNP Q9I2D8
E	-6	GLU	-	expression tag	UNP Q9I2D8
E	-5	ASN	-	expression tag	UNP Q9I2D8
E	-4	LEU	-	expression tag	UNP Q9I2D8
E	-3	TYR	-	expression tag	UNP Q9I2D8
E	-2	PHE	-	expression tag	UNP Q9I2D8
E	-1	GLN	-	expression tag	UNP Q9I2D8
E	0	GLY	-	expression tag	UNP Q9I2D8
E	124	GLY	-	expression tag	UNP Q9I2D8
E	125	SER	-	expression tag	UNP Q9I2D8
F	-20	MSE	-	expression tag	UNP Q9I2D8
F	-19	GLY	-	expression tag	UNP Q9I2D8
F	-18	SER	-	expression tag	UNP Q9I2D8
F	-17	SER	-	expression tag	UNP Q9I2D8
F	-16	HIS	-	expression tag	UNP Q9I2D8
F	-15	HIS	-	expression tag	UNP Q9I2D8
F	-14	HIS	-	expression tag	UNP Q9I2D8
F	-13	HIS	-	expression tag	UNP Q9I2D8
F	-12	HIS	-	expression tag	UNP Q9I2D8
F	-11	HIS	-	expression tag	UNP Q9I2D8
F	-10	SER	-	expression tag	UNP Q9I2D8
F	-9	SER	-	expression tag	UNP Q9I2D8
F	-8	GLY	-	expression tag	UNP Q9I2D8
F	-7	ARG	-	expression tag	UNP Q9I2D8
F	-6	GLU	-	expression tag	UNP Q9I2D8
F	-5	ASN	-	expression tag	UNP Q9I2D8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-4	LEU	-	expression tag	UNP Q9I2D8
F	-3	TYR	-	expression tag	UNP Q9I2D8
F	-2	PHE	-	expression tag	UNP Q9I2D8
F	-1	GLN	-	expression tag	UNP Q9I2D8
F	0	GLY	-	expression tag	UNP Q9I2D8
F	124	GLY	-	expression tag	UNP Q9I2D8
F	125	SER	-	expression tag	UNP Q9I2D8
G	-20	MSE	-	expression tag	UNP Q9I2D8
G	-19	GLY	-	expression tag	UNP Q9I2D8
G	-18	SER	-	expression tag	UNP Q9I2D8
G	-17	SER	-	expression tag	UNP Q9I2D8
G	-16	HIS	-	expression tag	UNP Q9I2D8
G	-15	HIS	-	expression tag	UNP Q9I2D8
G	-14	HIS	-	expression tag	UNP Q9I2D8
G	-13	HIS	-	expression tag	UNP Q9I2D8
G	-12	HIS	-	expression tag	UNP Q9I2D8
G	-11	HIS	-	expression tag	UNP Q9I2D8
G	-10	SER	-	expression tag	UNP Q9I2D8
G	-9	SER	-	expression tag	UNP Q9I2D8
G	-8	GLY	-	expression tag	UNP Q9I2D8
G	-7	ARG	-	expression tag	UNP Q9I2D8
G	-6	GLU	-	expression tag	UNP Q9I2D8
G	-5	ASN	-	expression tag	UNP Q9I2D8
G	-4	LEU	-	expression tag	UNP Q9I2D8
G	-3	TYR	-	expression tag	UNP Q9I2D8
G	-2	PHE	-	expression tag	UNP Q9I2D8
G	-1	GLN	-	expression tag	UNP Q9I2D8
G	0	GLY	-	expression tag	UNP Q9I2D8
G	124	GLY	-	expression tag	UNP Q9I2D8
G	125	SER	-	expression tag	UNP Q9I2D8
H	-20	MSE	-	expression tag	UNP Q9I2D8
H	-19	GLY	-	expression tag	UNP Q9I2D8
H	-18	SER	-	expression tag	UNP Q9I2D8
H	-17	SER	-	expression tag	UNP Q9I2D8
H	-16	HIS	-	expression tag	UNP Q9I2D8
H	-15	HIS	-	expression tag	UNP Q9I2D8
H	-14	HIS	-	expression tag	UNP Q9I2D8
H	-13	HIS	-	expression tag	UNP Q9I2D8
H	-12	HIS	-	expression tag	UNP Q9I2D8
H	-11	HIS	-	expression tag	UNP Q9I2D8
H	-10	SER	-	expression tag	UNP Q9I2D8
H	-9	SER	-	expression tag	UNP Q9I2D8

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-8	GLY	-	expression tag	UNP Q9I2D8
H	-7	ARG	-	expression tag	UNP Q9I2D8
H	-6	GLU	-	expression tag	UNP Q9I2D8
H	-5	ASN	-	expression tag	UNP Q9I2D8
H	-4	LEU	-	expression tag	UNP Q9I2D8
H	-3	TYR	-	expression tag	UNP Q9I2D8
H	-2	PHE	-	expression tag	UNP Q9I2D8
H	-1	GLN	-	expression tag	UNP Q9I2D8
H	0	GLY	-	expression tag	UNP Q9I2D8
H	124	GLY	-	expression tag	UNP Q9I2D8
H	125	SER	-	expression tag	UNP Q9I2D8
I	-20	MSE	-	expression tag	UNP Q9I2D8
I	-19	GLY	-	expression tag	UNP Q9I2D8
I	-18	SER	-	expression tag	UNP Q9I2D8
I	-17	SER	-	expression tag	UNP Q9I2D8
I	-16	HIS	-	expression tag	UNP Q9I2D8
I	-15	HIS	-	expression tag	UNP Q9I2D8
I	-14	HIS	-	expression tag	UNP Q9I2D8
I	-13	HIS	-	expression tag	UNP Q9I2D8
I	-12	HIS	-	expression tag	UNP Q9I2D8
I	-11	HIS	-	expression tag	UNP Q9I2D8
I	-10	SER	-	expression tag	UNP Q9I2D8
I	-9	SER	-	expression tag	UNP Q9I2D8
I	-8	GLY	-	expression tag	UNP Q9I2D8
I	-7	ARG	-	expression tag	UNP Q9I2D8
I	-6	GLU	-	expression tag	UNP Q9I2D8
I	-5	ASN	-	expression tag	UNP Q9I2D8
I	-4	LEU	-	expression tag	UNP Q9I2D8
I	-3	TYR	-	expression tag	UNP Q9I2D8
I	-2	PHE	-	expression tag	UNP Q9I2D8
I	-1	GLN	-	expression tag	UNP Q9I2D8
I	0	GLY	-	expression tag	UNP Q9I2D8
I	124	GLY	-	expression tag	UNP Q9I2D8
I	125	SER	-	expression tag	UNP Q9I2D8
J	-20	MSE	-	expression tag	UNP Q9I2D8
J	-19	GLY	-	expression tag	UNP Q9I2D8
J	-18	SER	-	expression tag	UNP Q9I2D8
J	-17	SER	-	expression tag	UNP Q9I2D8
J	-16	HIS	-	expression tag	UNP Q9I2D8
J	-15	HIS	-	expression tag	UNP Q9I2D8
J	-14	HIS	-	expression tag	UNP Q9I2D8
J	-13	HIS	-	expression tag	UNP Q9I2D8

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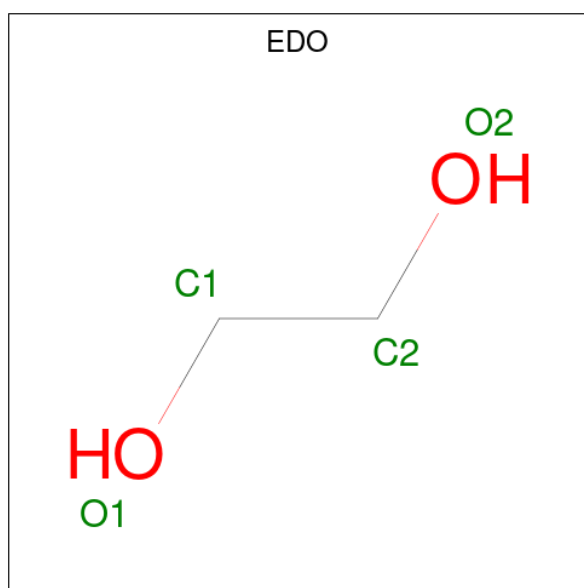
Chain	Residue	Modelled	Actual	Comment	Reference
J	-12	HIS	-	expression tag	UNP Q9I2D8
J	-11	HIS	-	expression tag	UNP Q9I2D8
J	-10	SER	-	expression tag	UNP Q9I2D8
J	-9	SER	-	expression tag	UNP Q9I2D8
J	-8	GLY	-	expression tag	UNP Q9I2D8
J	-7	ARG	-	expression tag	UNP Q9I2D8
J	-6	GLU	-	expression tag	UNP Q9I2D8
J	-5	ASN	-	expression tag	UNP Q9I2D8
J	-4	LEU	-	expression tag	UNP Q9I2D8
J	-3	TYR	-	expression tag	UNP Q9I2D8
J	-2	PHE	-	expression tag	UNP Q9I2D8
J	-1	GLN	-	expression tag	UNP Q9I2D8
J	0	GLY	-	expression tag	UNP Q9I2D8
J	124	GLY	-	expression tag	UNP Q9I2D8
J	125	SER	-	expression tag	UNP Q9I2D8
K	-20	MSE	-	expression tag	UNP Q9I2D8
K	-19	GLY	-	expression tag	UNP Q9I2D8
K	-18	SER	-	expression tag	UNP Q9I2D8
K	-17	SER	-	expression tag	UNP Q9I2D8
K	-16	HIS	-	expression tag	UNP Q9I2D8
K	-15	HIS	-	expression tag	UNP Q9I2D8
K	-14	HIS	-	expression tag	UNP Q9I2D8
K	-13	HIS	-	expression tag	UNP Q9I2D8
K	-12	HIS	-	expression tag	UNP Q9I2D8
K	-11	HIS	-	expression tag	UNP Q9I2D8
K	-10	SER	-	expression tag	UNP Q9I2D8
K	-9	SER	-	expression tag	UNP Q9I2D8
K	-8	GLY	-	expression tag	UNP Q9I2D8
K	-7	ARG	-	expression tag	UNP Q9I2D8
K	-6	GLU	-	expression tag	UNP Q9I2D8
K	-5	ASN	-	expression tag	UNP Q9I2D8
K	-4	LEU	-	expression tag	UNP Q9I2D8
K	-3	TYR	-	expression tag	UNP Q9I2D8
K	-2	PHE	-	expression tag	UNP Q9I2D8
K	-1	GLN	-	expression tag	UNP Q9I2D8
K	0	GLY	-	expression tag	UNP Q9I2D8
K	124	GLY	-	expression tag	UNP Q9I2D8
K	125	SER	-	expression tag	UNP Q9I2D8
L	-20	MSE	-	expression tag	UNP Q9I2D8
L	-19	GLY	-	expression tag	UNP Q9I2D8
L	-18	SER	-	expression tag	UNP Q9I2D8
L	-17	SER	-	expression tag	UNP Q9I2D8

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-16	HIS	-	expression tag	UNP Q9I2D8
L	-15	HIS	-	expression tag	UNP Q9I2D8
L	-14	HIS	-	expression tag	UNP Q9I2D8
L	-13	HIS	-	expression tag	UNP Q9I2D8
L	-12	HIS	-	expression tag	UNP Q9I2D8
L	-11	HIS	-	expression tag	UNP Q9I2D8
L	-10	SER	-	expression tag	UNP Q9I2D8
L	-9	SER	-	expression tag	UNP Q9I2D8
L	-8	GLY	-	expression tag	UNP Q9I2D8
L	-7	ARG	-	expression tag	UNP Q9I2D8
L	-6	GLU	-	expression tag	UNP Q9I2D8
L	-5	ASN	-	expression tag	UNP Q9I2D8
L	-4	LEU	-	expression tag	UNP Q9I2D8
L	-3	TYR	-	expression tag	UNP Q9I2D8
L	-2	PHE	-	expression tag	UNP Q9I2D8
L	-1	GLN	-	expression tag	UNP Q9I2D8
L	0	GLY	-	expression tag	UNP Q9I2D8
L	124	GLY	-	expression tag	UNP Q9I2D8
L	125	SER	-	expression tag	UNP Q9I2D8

- 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	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total 4	C 2	O 2	0	0
2	D	1	Total 4	C 2	O 2	0	0
2	E	1	Total 4	C 2	O 2	0	0
2	F	1	Total 4	C 2	O 2	0	0
2	G	1	Total 4	C 2	O 2	0	0
2	H	1	Total 4	C 2	O 2	0	0
2	H	1	Total 4	C 2	O 2	0	0
2	I	1	Total 4	C 2	O 2	0	0
2	I	1	Total 4	C 2	O 2	0	0
2	I	1	Total 4	C 2	O 2	0	0
2	J	1	Total 4	C 2	O 2	0	0
2	K	1	Total 4	C 2	O 2	0	0
2	K	1	Total 4	C 2	O 2	0	0
2	K	1	Total 4	C 2	O 2	0	0
2	L	1	Total 4	C 2	O 2	0	0

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			3	1	2		
3	A	1	Total	C	O	0	0
			3	1	2		
3	A	1	Total	C	O	0	0
			3	1	2		
3	B	1	Total	C	O	0	0
			3	1	2		
3	B	1	Total	C	O	0	0
			3	1	2		
3	F	1	Total	C	O	0	0
			3	1	2		
3	F	1	Total	C	O	0	0
			3	1	2		
3	H	1	Total	C	O	0	0
			3	1	2		
3	H	1	Total	C	O	0	0
			3	1	2		
3	H	1	Total	C	O	0	0
			3	1	2		
3	I	1	Total	C	O	0	0
			3	1	2		
3	I	1	Total	C	O	0	0
			3	1	2		
3	L	1	Total	C	O	0	0
			3	1	2		
3	L	1	Total	C	O	0	0
			3	1	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	L	1	Total	C	O	0	0
			3	1	2		

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



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

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

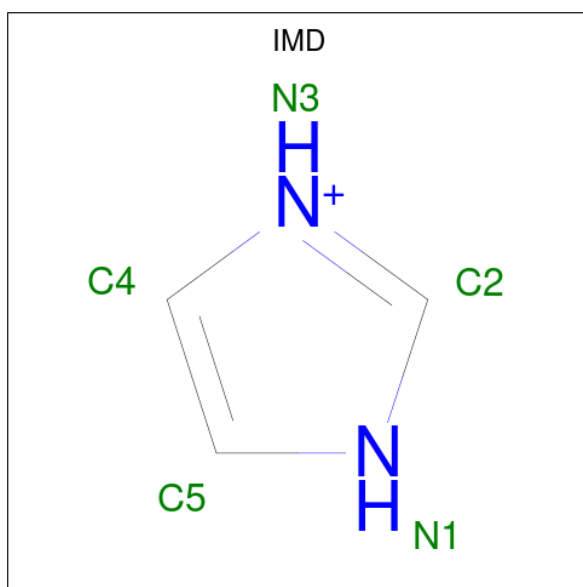
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Na	0	0
			1	1		
5	B	1	Total	Na	0	0
			1	1		
5	F	1	Total	Na	0	0
			1	1		
5	G	1	Total	Na	0	0
			1	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	C	1	Total	C	O	0	1
			12	6	6		
6	E	1	Total	C	O	0	1
			12	6	6		
6	E	1	Total	C	O	0	0
			6	3	3		
6	H	1	Total	C	O	0	0
			6	3	3		
6	H	1	Total	C	O	0	1
			12	6	6		
6	J	1	Total	C	O	0	1
			12	6	6		

- Molecule 7 is IMIDAZOLE (three-letter code: IMD) (formula: C<sub>3</sub>H<sub>5</sub>N<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	J	1	Total	C	N	0	0
			5	3	2		
7	L	1	Total	C	N	0	1
			10	6	4		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	160	Total	O	0	0
			160	160		
8	B	193	Total	O	0	0
			193	193		
8	C	151	Total	O	0	1
			152	152		
8	D	132	Total	O	0	0
			132	132		
8	E	145	Total	O	0	2
			147	147		
8	F	146	Total	O	0	0
			146	146		
8	G	146	Total	O	0	0
			146	146		
8	H	156	Total	O	0	0
			156	156		
8	I	181	Total	O	0	0
			181	181		
8	J	152	Total	O	0	0
			152	152		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	K	143	Total 144	O 144	0	1
8	L	158	Total 158	O 158	0	0

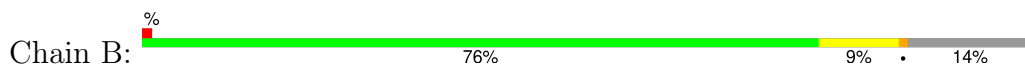
### 3 Residue-property plots [i](#)

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.

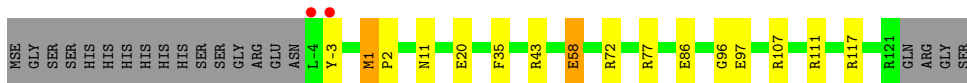
- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase



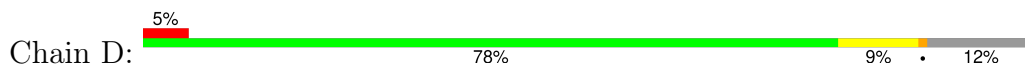
- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase



- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase



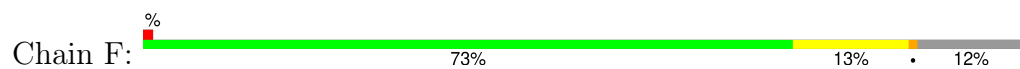
- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase



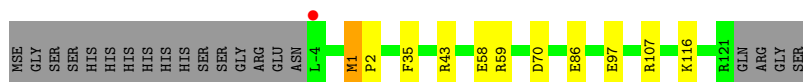
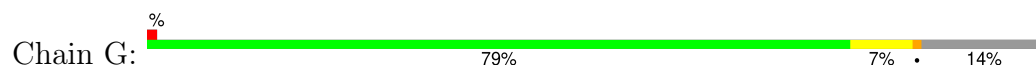
- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase



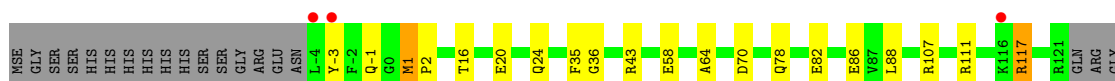
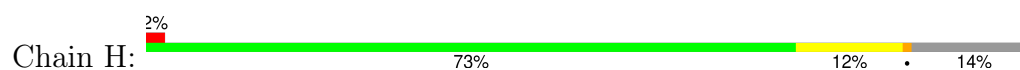
- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase



- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase

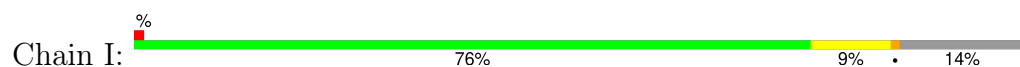


- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase

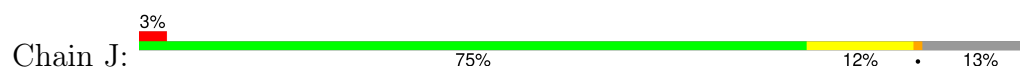


SER

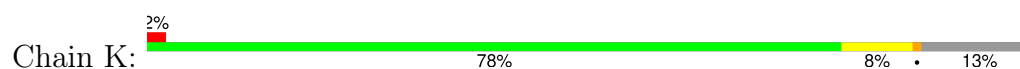
- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase



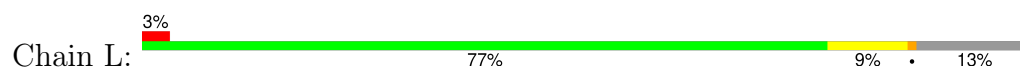
- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase



- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase



- Molecule 1: putative 5-carboxymethyl-2-hydroxymuconate isomerase





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	172.80Å 145.24Å 122.25Å 90.00° 134.91° 90.00°	Depositor
Resolution (Å)	45.00 – 1.75 45.00 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.4 (45.00-1.75) 99.5 (45.00-1.75)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.29 (at 1.75Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.136 , 0.164 0.143 , 0.168	Depositor DCC
$R_{free}$ test set	10707 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.2	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 38.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.010 for h+2*k,-h-l 0.011 for h,-k,-h-l 0.016 for -h-2*k,-k,l	Xtriage
$F_o$ , $F_c$ correlation	0.96	EDS
Total number of atoms	14344	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% of the height of the origin peak. No significant pseudotranslation is detected.*

<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, FMT, IMD, NA, ACT, EDO

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	0.89	0/1059	0.83	3/1425 (0.2%)
1	B	0.87	0/1076	0.88	4/1447 (0.3%)
1	C	0.83	0/1087	0.80	0/1464
1	D	0.77	0/1087	0.77	0/1462
1	E	0.80	0/1099	0.85	2/1478 (0.1%)
1	F	0.85	0/1084	0.87	1/1457 (0.1%)
1	G	0.77	0/1031	0.80	1/1388 (0.1%)
1	H	0.82	0/1021	0.80	1/1371 (0.1%)
1	I	0.84	0/1090	0.82	1/1467 (0.1%)
1	J	0.84	0/1102	0.90	2/1478 (0.1%)
1	K	0.84	0/1079	0.84	0/1454
1	L	0.86	0/1066	0.83	0/1435
All	All	0.83	0/12881	0.83	15/17326 (0.1%)

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	70	ASP	CB-CG-OD1	6.85	124.47	118.30
1	J	73[A]	ASP	CB-CG-OD1	6.72	124.35	118.30
1	J	73[B]	ASP	CB-CG-OD1	6.72	124.35	118.30
1	B	117	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	I	117	ARG	NE-CZ-NH2	-6.42	117.09	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	1013	0	1029	16	0
1	B	1025	0	1034	14	0
1	C	1032	0	1035	18	0
1	D	1033	0	1036	19	0
1	E	1039	0	1028	23	0
1	F	1031	0	1027	19	0
1	G	994	0	997	10	0
1	H	992	0	993	23	0
1	I	1030	0	1039	9	0
1	J	1046	0	1069	21	0
1	K	1021	0	1011	22	0
1	L	1015	0	1010	16	0
2	A	4	0	6	2	0
2	B	4	0	6	0	0
2	C	4	0	6	0	0
2	D	4	0	6	1	0
2	E	4	0	6	0	0
2	F	4	0	6	0	0
2	G	4	0	6	0	0
2	H	8	0	12	1	0
2	I	12	0	18	0	0
2	J	4	0	6	0	0
2	K	12	0	15	21	0
2	L	4	0	6	0	0
3	A	9	0	3	6	0
3	B	6	0	2	9	0
3	F	6	0	2	0	0
3	H	9	0	3	0	0
3	I	6	0	2	1	0
3	L	9	0	3	6	0
4	A	4	0	3	3	0
4	E	4	0	3	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
6	B	6	0	8	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	12	0	16	5	0
6	E	18	0	24	11	0
6	H	18	0	24	10	0
6	J	12	0	16	10	0
7	J	5	0	5	0	0
7	L	10	0	10	2	0
8	A	160	0	0	4	0
8	B	193	0	0	7	0
8	C	152	0	0	2	0
8	D	132	0	0	4	0
8	E	147	0	0	6	0
8	F	146	0	0	2	0
8	G	146	0	0	2	0
8	H	156	0	0	9	0
8	I	181	0	0	4	0
8	J	152	0	0	3	0
8	K	144	0	0	8	0
8	L	158	0	0	4	0
All	All	14344	0	12531	223	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 9.

The worst 5 of 223 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)
2:K:323:EDO:O2	2:K:324:EDO:O2	1.53	1.24
2:K:323:EDO:C1	2:K:324:EDO:O2	1.85	1.23
2:K:323:EDO:H22	8:K:454:HOH:O	1.38	1.17
2:K:323:EDO:C2	2:K:324:EDO:O2	1.94	1.15
3:A:335:FMT:O2	3:B:345:FMT:C	1.95	1.15

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	136/146 (93%)	136 (100%)	0	0	100	100
1	B	138/146 (94%)	138 (100%)	0	0	100	100
1	C	139/146 (95%)	139 (100%)	0	0	100	100
1	D	140/146 (96%)	138 (99%)	2 (1%)	0	100	100
1	E	141/146 (97%)	136 (96%)	5 (4%)	0	100	100
1	F	139/146 (95%)	138 (99%)	1 (1%)	0	100	100
1	G	133/146 (91%)	133 (100%)	0	0	100	100
1	H	131/146 (90%)	130 (99%)	1 (1%)	0	100	100
1	I	141/146 (97%)	141 (100%)	0	0	100	100
1	J	140/146 (96%)	137 (98%)	3 (2%)	0	100	100
1	K	140/146 (96%)	138 (99%)	2 (1%)	0	100	100
1	L	138/146 (94%)	138 (100%)	0	0	100	100
All	All	1656/1752 (94%)	1642 (99%)	14 (1%)	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	105/107 (98%)	102 (97%)	3 (3%)	37	17
1	B	106/107 (99%)	104 (98%)	2 (2%)	52	34
1	C	108/107 (101%)	104 (96%)	4 (4%)	29	10
1	D	108/107 (101%)	104 (96%)	4 (4%)	29	10
1	E	110/107 (103%)	108 (98%)	2 (2%)	54	37
1	F	108/107 (101%)	102 (94%)	6 (6%)	17	4
1	G	102/107 (95%)	100 (98%)	2 (2%)	50	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	101/107 (94%)	99 (98%)	2 (2%)	50	31
1	I	108/107 (101%)	105 (97%)	3 (3%)	38	18
1	J	109/107 (102%)	107 (98%)	2 (2%)	54	37
1	K	108/107 (101%)	106 (98%)	2 (2%)	52	34
1	L	106/107 (99%)	104 (98%)	2 (2%)	52	34
All	All	1279/1284 (100%)	1245 (97%)	34 (3%)	38	19

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	1	MSE
1	J	43	ARG
1	L	1	MSE
1	D	57[B]	VAL
1	D	57[A]	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	24	GLN
1	G	24	GLN
1	H	-1	GLN
1	L	24	GLN

### 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 52 ligands modelled in this entry, 4 are monoatomic - leaving 48 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	$\# Z  > 2$
2	EDO	D	313	-	3,3,3	0.27	0	2,2,2	0.44	0
2	EDO	H	321	-	3,3,3	0.38	0	2,2,2	0.33	0
6	GOL	J	307[B]	-	5,5,5	0.52	0	5,5,5	0.64	0
2	EDO	E	322	-	3,3,3	0.31	0	2,2,2	0.62	0
7	IMD	L	339[A]	-	3,5,5	0.44	0	4,5,5	0.49	0
2	EDO	C	318	-	3,3,3	0.27	0	2,2,2	0.61	0
2	EDO	I	317	-	3,3,3	0.35	0	2,2,2	0.39	0
2	EDO	K	323	-	3,3,3	1.09	0	2,2,2	0.13	0
2	EDO	H	311	-	3,3,3	0.50	0	2,2,2	0.77	0
3	FMT	A	325	-	2,2,2	1.02	0	1,1,1	0.05	0
2	EDO	B	309	-	3,3,3	0.53	0	2,2,2	0.31	0
2	EDO	K	324	-	3,3,3	0.92	0	2,2,2	0.69	0
2	EDO	F	312	-	3,3,3	0.31	0	2,2,2	0.46	0
3	FMT	F	326	-	2,2,2	0.85	0	1,1,1	0.30	0
4	ACT	A	337	-	3,3,3	0.83	0	3,3,3	1.87	2 (66%)
2	EDO	J	316	-	3,3,3	0.29	0	2,2,2	0.63	0
6	GOL	J	307[A]	-	5,5,5	0.33	0	5,5,5	0.94	1 (20%)
6	GOL	E	301[B]	-	5,5,5	0.34	0	5,5,5	0.70	0
2	EDO	G	319	-	3,3,3	0.33	0	2,2,2	0.43	0
2	EDO	A	310	-	3,3,3	0.65	0	2,2,2	0.20	0
3	FMT	L	331	-	2,2,2	0.74	0	1,1,1	0.30	0
3	FMT	A	335	-	2,2,2	0.44	0	1,1,1	0.73	0
6	GOL	H	305[B]	-	5,5,5	0.66	0	5,5,5	0.82	0
6	GOL	C	303[B]	-	5,5,5	0.46	0	5,5,5	1.40	1 (20%)
2	EDO	I	315	-	3,3,3	0.62	0	2,2,2	0.35	0
3	FMT	A	333	-	2,2,2	0.62	0	1,1,1	0.35	0
3	FMT	H	328	-	2,2,2	0.59	0	1,1,1	0.35	0
3	FMT	F	324	-	2,2,2	0.66	0	1,1,1	0.63	0
2	EDO	L	320	-	3,3,3	0.48	0	2,2,2	0.56	0
6	GOL	E	301[A]	-	5,5,5	0.27	0	5,5,5	1.31	0
3	FMT	B	345	-	2,2,2	0.76	0	1,1,1	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	FMT	I	329	-	2,2,2	0.60	0	1,1,1	0.35	0
6	GOL	E	306	-	5,5,5	0.49	0	5,5,5	0.65	0
6	GOL	H	305[A]	-	5,5,5	0.92	0	5,5,5	0.77	0
6	GOL	B	304	-	5,5,5	0.49	0	5,5,5	0.69	0
3	FMT	L	336	-	2,2,2	0.33	0	1,1,1	0.39	0
6	GOL	C	303[A]	-	5,5,5	0.37	0	5,5,5	0.61	0
4	ACT	E	338	-	3,3,3	0.79	0	3,3,3	1.50	0
7	IMD	L	339[B]	-	3,5,5	0.55	0	4,5,5	0.70	0
2	EDO	I	314	-	3,3,3	0.58	0	2,2,2	0.34	0
3	FMT	H	327	-	2,2,2	0.54	0	1,1,1	0.31	0
3	FMT	I	330	-	2,2,2	0.40	0	1,1,1	0.42	0
3	FMT	L	340	-	2,2,2	0.33	0	1,1,1	0.28	0
2	EDO	K	308	-	3,3,3	0.97	0	2,2,2	0.48	0
6	GOL	H	302	-	5,5,5	0.50	0	5,5,5	0.58	0
3	FMT	H	334	-	2,2,2	0.65	0	1,1,1	0.40	0
7	IMD	J	340	-	3,5,5	0.33	0	4,5,5	0.72	0
3	FMT	B	332	-	2,2,2	0.66	0	1,1,1	0.30	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	EDO	D	313	-	-	1/1/1/1	-
2	EDO	H	321	-	-	1/1/1/1	-
6	GOL	J	307[B]	-	-	0/4/4/4	-
2	EDO	E	322	-	-	1/1/1/1	-
7	IMD	L	339[A]	-	-	-	0/1/1/1
2	EDO	C	318	-	-	1/1/1/1	-
2	EDO	I	317	-	-	1/1/1/1	-
2	EDO	K	323	-	-	1/1/1/1	-
2	EDO	H	311	-	-	1/1/1/1	-
2	EDO	B	309	-	-	0/1/1/1	-
2	EDO	K	324	-	-	0/1/1/1	-
2	EDO	F	312	-	-	1/1/1/1	-
2	EDO	J	316	-	-	1/1/1/1	-
6	GOL	J	307[A]	-	-	2/4/4/4	-
6	GOL	E	301[B]	-	-	0/4/4/4	-
2	EDO	G	319	-	-	1/1/1/1	-
2	EDO	A	310	-	-	1/1/1/1	-
6	GOL	H	305[B]	-	-	4/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	C	303[B]	-	-	2/4/4/4	-
2	EDO	I	315	-	-	0/1/1/1	-
2	EDO	L	320	-	-	0/1/1/1	-
6	GOL	E	301[A]	-	-	2/4/4/4	-
6	GOL	E	306	-	-	2/4/4/4	-
6	GOL	H	305[A]	-	-	4/4/4/4	-
6	GOL	B	304	-	-	4/4/4/4	-
6	GOL	C	303[A]	-	-	4/4/4/4	-
7	IMD	L	339[B]	-	-	-	0/1/1/1
2	EDO	I	314	-	-	0/1/1/1	-
2	EDO	K	308	-	-	1/1/1/1	-
6	GOL	H	302	-	-	4/4/4/4	-
7	IMD	J	340	-	-	-	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	337	ACT	OXT-C-O	-2.45	112.92	122.03
6	C	303[B]	GOL	C3-C2-C1	-2.45	102.81	111.80
4	A	337	ACT	OXT-C-CH3	2.10	123.87	115.05
6	J	307[A]	GOL	C3-C2-C1	-2.03	104.35	111.80

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	304	GOL	O1-C1-C2-O2
6	B	304	GOL	O1-C1-C2-C3
6	C	303[A]	GOL	O1-C1-C2-C3
6	H	302	GOL	O1-C1-C2-C3
6	H	302	GOL	C1-C2-C3-O3

There are no ring outliers.

22 monomers are involved in 84 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	313	EDO	1	0
2	H	321	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	J	307[B]	GOL	9	0
7	L	339[A]	IMD	2	0
2	K	323	EDO	15	0
2	K	324	EDO	14	0
4	A	337	ACT	3	0
6	J	307[A]	GOL	1	0
6	E	301[B]	GOL	5	0
2	A	310	EDO	2	0
3	A	335	FMT	6	0
6	H	305[B]	GOL	6	0
6	C	303[B]	GOL	3	0
6	E	301[A]	GOL	5	0
3	B	345	FMT	9	0
6	E	306	GOL	1	0
6	H	305[A]	GOL	4	0
6	B	304	GOL	2	0
3	L	336	FMT	4	0
6	C	303[A]	GOL	2	0
3	I	330	FMT	1	0
3	L	340	FMT	5	0

## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	124/146 (84%)	-0.41	1 (0%) 82 86	10, 18, 24, 34	12 (9%)
1	B	124/146 (84%)	-0.28	2 (1%) 70 76	10, 18, 25, 33	14 (11%)
1	C	124/146 (84%)	-0.13	2 (1%) 70 76	11, 18, 26, 30	16 (12%)
1	D	126/146 (86%)	0.12	7 (5%) 31 35	10, 18, 26, 29	14 (11%)
1	E	125/146 (85%)	-0.18	0 100 100	8, 18, 25, 29	17 (13%)
1	F	126/146 (86%)	-0.10	2 (1%) 70 76	10, 18, 24, 31	14 (11%)
1	G	124/146 (84%)	-0.12	1 (0%) 82 86	11, 19, 26, 32	9 (7%)
1	H	124/146 (84%)	-0.22	3 (2%) 59 66	10, 18, 26, 34	8 (6%)
1	I	124/146 (84%)	-0.35	2 (1%) 70 76	10, 18, 25, 36	16 (12%)
1	J	125/146 (85%)	-0.15	4 (3%) 50 57	10, 18, 25, 33	16 (12%)
1	K	125/146 (85%)	-0.29	3 (2%) 59 66	10, 18, 25, 29	15 (12%)
1	L	125/146 (85%)	-0.23	4 (3%) 50 57	9, 18, 25, 29	13 (10%)
All	All	1496/1752 (85%)	-0.19	31 (2%) 63 69	8, 18, 26, 36	164 (10%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	-4[A]	LEU	5.7
1	L	118	VAL	5.0
1	D	118	VAL	4.3
1	D	117[A]	ARG	4.0
1	L	117	ARG	4.0

### 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 ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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(Å <sup>2</sup> )	Q<0.9
3	FMT	L	336	3/3	0.57	0.23	83,83,83,84	0
6	GOL	J	307[A]	6/6	0.68	0.22	32,34,38,40	6
6	GOL	J	307[B]	6/6	0.68	0.22	16,21,24,24	6
3	FMT	H	334	3/3	0.74	0.22	52,52,53,53	0
3	FMT	H	328	3/3	0.75	0.22	61,61,61,62	0
6	GOL	H	305[A]	6/6	0.77	0.18	24,31,32,33	6
6	GOL	H	305[B]	6/6	0.77	0.18	27,29,29,31	6
6	GOL	E	301[A]	6/6	0.77	0.19	24,28,29,32	6
6	GOL	E	301[B]	6/6	0.77	0.19	33,34,34,36	6
7	IMD	J	340	5/5	0.78	0.20	47,47,48,48	0
3	FMT	B	345	3/3	0.80	0.25	82,82,82,82	0
6	GOL	H	302	6/6	0.81	0.17	46,46,48,49	0
2	EDO	K	323	4/4	0.81	0.18	36,47,50,52	0
6	GOL	B	304	6/6	0.81	0.19	48,49,50,51	0
3	FMT	L	340	3/3	0.83	0.17	41,41,44,46	0
4	ACT	E	338	4/4	0.83	0.24	58,58,59,59	0
5	NA	B	344	1/1	0.83	0.19	50,50,50,50	0
3	FMT	A	333	3/3	0.83	0.22	45,45,46,47	0
3	FMT	H	327	3/3	0.84	0.16	36,36,36,37	0
4	ACT	A	337	4/4	0.85	0.22	37,40,40,40	0
2	EDO	A	310	4/4	0.85	0.15	45,46,46,47	0
6	GOL	C	303[A]	6/6	0.85	0.14	29,32,33,35	6
6	GOL	C	303[B]	6/6	0.85	0.14	18,19,21,22	6
3	FMT	A	325	3/3	0.86	0.16	31,31,31,33	0
3	FMT	F	324	3/3	0.86	0.16	51,51,51,52	0
3	FMT	A	335	3/3	0.86	0.26	30,30,36,41	0
2	EDO	K	324	4/4	0.87	0.16	42,50,50,50	0
3	FMT	B	332	3/3	0.88	0.16	48,48,48,48	0
3	FMT	I	329	3/3	0.88	0.16	46,46,47,48	0
7	IMD	L	339[A]	5/5	0.88	0.13	25,25,26,28	5
7	IMD	L	339[B]	5/5	0.88	0.13	30,30,31,32	5
2	EDO	L	320	4/4	0.91	0.15	28,35,36,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	EDO	C	318	4/4	0.91	0.18	21,28,33,38	0
2	EDO	D	313	4/4	0.91	0.16	24,32,37,38	0
6	GOL	E	306	6/6	0.91	0.12	20,35,39,45	0
3	FMT	F	326	3/3	0.92	0.11	36,36,38,39	0
2	EDO	K	308	4/4	0.92	0.13	19,26,27,35	0
5	NA	G	341	1/1	0.93	0.22	50,50,50,50	0
2	EDO	F	312	4/4	0.93	0.18	22,31,33,37	0
2	EDO	H	311	4/4	0.93	0.17	23,29,31,37	0
2	EDO	H	321	4/4	0.93	0.20	30,31,32,33	0
2	EDO	J	316	4/4	0.93	0.17	21,29,33,37	0
2	EDO	E	322	4/4	0.94	0.15	22,32,33,37	0
2	EDO	G	319	4/4	0.94	0.18	23,30,34,39	0
3	FMT	L	331	3/3	0.95	0.11	42,42,44,44	0
2	EDO	I	317	4/4	0.95	0.17	20,26,32,36	0
3	FMT	I	330	3/3	0.95	0.12	28,28,32,36	0
2	EDO	I	315	4/4	0.96	0.20	29,29,30,31	0
2	EDO	I	314	4/4	0.96	0.12	23,25,25,27	0
5	NA	F	342	1/1	0.98	0.14	30,30,30,30	0
5	NA	A	343	1/1	0.98	0.13	27,27,27,27	0
2	EDO	B	309	4/4	0.99	0.11	22,22,23,24	0

## 6.5 Other polymers

There are no such residues in this entry.