



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 11:26 PM GMT

PDB ID : 4ADM  
Title : Crystal structure of Rv1098c in complex with meso-tartrate  
Authors : Mechaly, A.E.; Haouz, A.; Miras, I.; Weber, P.; Shepard, W.; Cole, S.; Alzari, P.M.; Bellinzoni, M.  
Deposited on : 2011-12-27  
Resolution : 1.65 Å(reported)

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

---

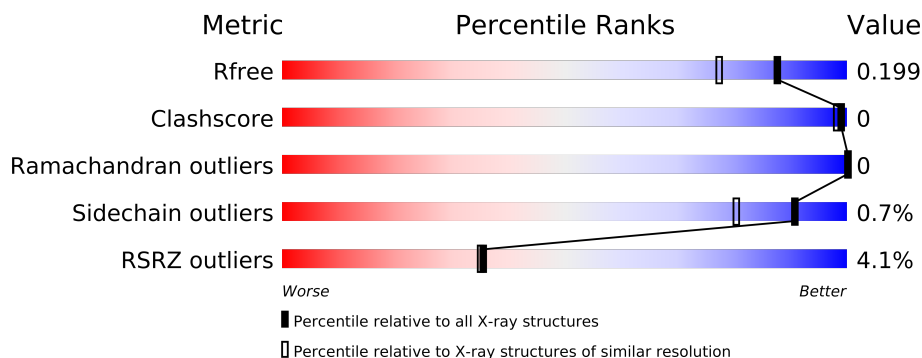
The following versions of software and data (see [references](#)) were used in the production of this report:

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

# 1 Overall quality at a glance

The reported resolution of this entry is 1.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1404 (1.68-1.64)
Clashscore	79885	1001 (1.66-1.66)
Ramachandran outliers	78287	1581 (1.68-1.64)
Sidechain outliers	78261	1580 (1.68-1.64)
RSRZ outliers	66119	1404 (1.68-1.64)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	495	
1	B	495	
1	C	495	
1	D	495	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15056 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called FUMARATE HYDRATASE CLASS II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	2	0
			3348	2088	607	642	11			
1	B	449	Total	C	N	O	S	0	0	0
			3339	2080	607	641	11			
1	C	456	Total	C	N	O	S	0	1	0
			3334	2077	605	640	12			
1	D	451	Total	C	N	O	S	0	1	0
			3314	2071	599	632	12			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	EXPRESSION TAG	UNP O53446
A	-20	SER	-	EXPRESSION TAG	UNP O53446
A	-19	TYR	-	EXPRESSION TAG	UNP O53446
A	-18	TYR	-	EXPRESSION TAG	UNP O53446
A	-17	HIS	-	EXPRESSION TAG	UNP O53446
A	-16	HIS	-	EXPRESSION TAG	UNP O53446
A	-15	HIS	-	EXPRESSION TAG	UNP O53446
A	-14	HIS	-	EXPRESSION TAG	UNP O53446
A	-13	HIS	-	EXPRESSION TAG	UNP O53446
A	-12	HIS	-	EXPRESSION TAG	UNP O53446
A	-11	LEU	-	EXPRESSION TAG	UNP O53446
A	-10	GLU	-	EXPRESSION TAG	UNP O53446
A	-9	SER	-	EXPRESSION TAG	UNP O53446
A	-8	THR	-	EXPRESSION TAG	UNP O53446
A	-7	SER	-	EXPRESSION TAG	UNP O53446
A	-6	LEU	-	EXPRESSION TAG	UNP O53446
A	-5	TYR	-	EXPRESSION TAG	UNP O53446
A	-4	LYS	-	EXPRESSION TAG	UNP O53446
A	-3	LYS	-	EXPRESSION TAG	UNP O53446
A	-2	ALA	-	EXPRESSION TAG	UNP O53446
A	-1	GLY	-	EXPRESSION TAG	UNP O53446

*Continued on next page...*

*Continued from previous page...*

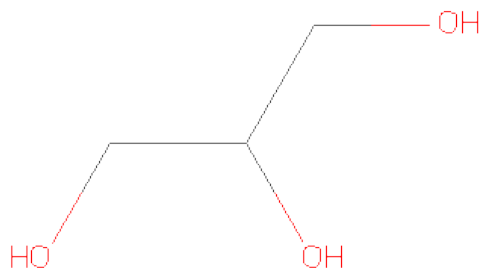
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP O53446
B	-21	MET	-	EXPRESSION TAG	UNP O53446
B	-20	SER	-	EXPRESSION TAG	UNP O53446
B	-19	TYR	-	EXPRESSION TAG	UNP O53446
B	-18	TYR	-	EXPRESSION TAG	UNP O53446
B	-17	HIS	-	EXPRESSION TAG	UNP O53446
B	-16	HIS	-	EXPRESSION TAG	UNP O53446
B	-15	HIS	-	EXPRESSION TAG	UNP O53446
B	-14	HIS	-	EXPRESSION TAG	UNP O53446
B	-13	HIS	-	EXPRESSION TAG	UNP O53446
B	-12	HIS	-	EXPRESSION TAG	UNP O53446
B	-11	LEU	-	EXPRESSION TAG	UNP O53446
B	-10	GLU	-	EXPRESSION TAG	UNP O53446
B	-9	SER	-	EXPRESSION TAG	UNP O53446
B	-8	THR	-	EXPRESSION TAG	UNP O53446
B	-7	SER	-	EXPRESSION TAG	UNP O53446
B	-6	LEU	-	EXPRESSION TAG	UNP O53446
B	-5	TYR	-	EXPRESSION TAG	UNP O53446
B	-4	LYS	-	EXPRESSION TAG	UNP O53446
B	-3	LYS	-	EXPRESSION TAG	UNP O53446
B	-2	ALA	-	EXPRESSION TAG	UNP O53446
B	-1	GLY	-	EXPRESSION TAG	UNP O53446
B	0	SER	-	EXPRESSION TAG	UNP O53446
C	-21	MET	-	EXPRESSION TAG	UNP O53446
C	-20	SER	-	EXPRESSION TAG	UNP O53446
C	-19	TYR	-	EXPRESSION TAG	UNP O53446
C	-18	TYR	-	EXPRESSION TAG	UNP O53446
C	-17	HIS	-	EXPRESSION TAG	UNP O53446
C	-16	HIS	-	EXPRESSION TAG	UNP O53446
C	-15	HIS	-	EXPRESSION TAG	UNP O53446
C	-14	HIS	-	EXPRESSION TAG	UNP O53446
C	-13	HIS	-	EXPRESSION TAG	UNP O53446
C	-12	HIS	-	EXPRESSION TAG	UNP O53446
C	-11	LEU	-	EXPRESSION TAG	UNP O53446
C	-10	GLU	-	EXPRESSION TAG	UNP O53446
C	-9	SER	-	EXPRESSION TAG	UNP O53446
C	-8	THR	-	EXPRESSION TAG	UNP O53446
C	-7	SER	-	EXPRESSION TAG	UNP O53446
C	-6	LEU	-	EXPRESSION TAG	UNP O53446
C	-5	TYR	-	EXPRESSION TAG	UNP O53446
C	-4	LYS	-	EXPRESSION TAG	UNP O53446
C	-3	LYS	-	EXPRESSION TAG	UNP O53446

*Continued on next page...*

*Continued from previous page...*

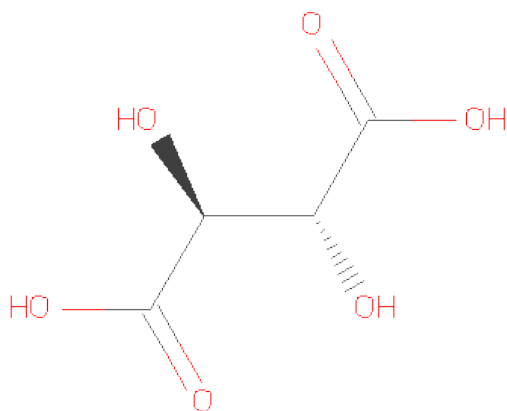
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	ALA	-	EXPRESSION TAG	UNP O53446
C	-1	GLY	-	EXPRESSION TAG	UNP O53446
C	0	SER	-	EXPRESSION TAG	UNP O53446
D	-21	MET	-	EXPRESSION TAG	UNP O53446
D	-20	SER	-	EXPRESSION TAG	UNP O53446
D	-19	TYR	-	EXPRESSION TAG	UNP O53446
D	-18	TYR	-	EXPRESSION TAG	UNP O53446
D	-17	HIS	-	EXPRESSION TAG	UNP O53446
D	-16	HIS	-	EXPRESSION TAG	UNP O53446
D	-15	HIS	-	EXPRESSION TAG	UNP O53446
D	-14	HIS	-	EXPRESSION TAG	UNP O53446
D	-13	HIS	-	EXPRESSION TAG	UNP O53446
D	-12	HIS	-	EXPRESSION TAG	UNP O53446
D	-11	LEU	-	EXPRESSION TAG	UNP O53446
D	-10	GLU	-	EXPRESSION TAG	UNP O53446
D	-9	SER	-	EXPRESSION TAG	UNP O53446
D	-8	THR	-	EXPRESSION TAG	UNP O53446
D	-7	SER	-	EXPRESSION TAG	UNP O53446
D	-6	LEU	-	EXPRESSION TAG	UNP O53446
D	-5	TYR	-	EXPRESSION TAG	UNP O53446
D	-4	LYS	-	EXPRESSION TAG	UNP O53446
D	-3	LYS	-	EXPRESSION TAG	UNP O53446
D	-2	ALA	-	EXPRESSION TAG	UNP O53446
D	-1	GLY	-	EXPRESSION TAG	UNP O53446
D	0	SER	-	EXPRESSION TAG	UNP O53446

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

- Molecule 3 is S,R MESO-TARTARIC ACID (three-letter code: SRT) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			10	4	6		
3	D	1	Total	C	O	0	0
			10	4	6		

- Molecule 4 is water.

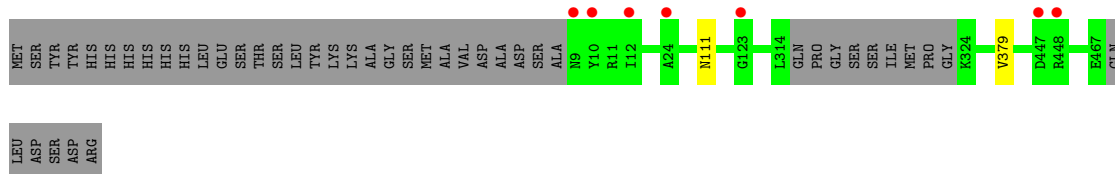
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	517	Total	O	0	0
			517	517		
4	B	411	Total	O	0	0
			411	411		
4	C	392	Total	O	0	0
			392	392		
4	D	369	Total	O	0	0
			369	369		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

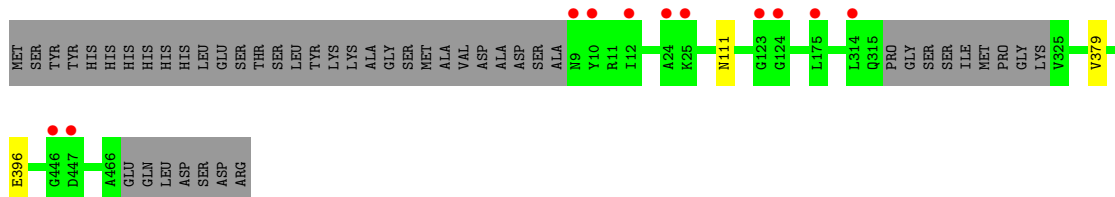
#### • Molecule 1: FUMARATE HYDRATASE CLASS II

Chain A: 



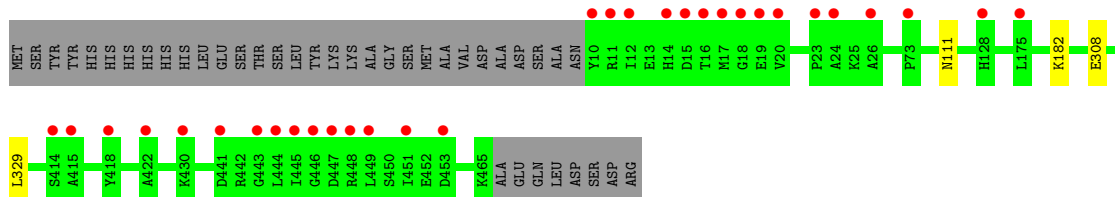
#### • Molecule 1: FUMARATE HYDRATASE CLASS II

Chain B: 



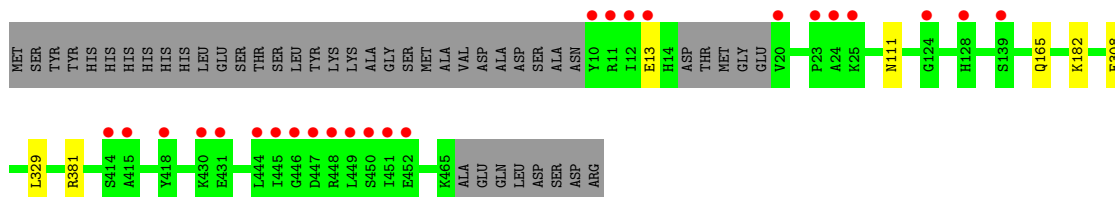
#### • Molecule 1: FUMARATE HYDRATASE CLASS II

Chain C: 



#### • Molecule 1: FUMARATE HYDRATASE CLASS II

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	188.94Å 96.49Å 139.65Å 90.00° 112.44° 90.00°	Depositor
Resolution (Å)	24.16 – 1.65 39.59 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.5 (24.16-1.65) 99.5 (39.59-1.65)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 1.65Å)	Xtriage
Refinement program	BUSTER 2.11.1	Depositor
R, $R_{free}$	0.163 , 0.185 0.178 , 0.199	Depositor DCC
$R_{free}$ test set	14032 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	18.7	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 44.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 277922 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	15056	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.87% of the height of the origin peak. No significant pseudotranslation is detected.*

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



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SRT

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	0.49	0/3400	0.57	0/4623
1	B	0.48	0/3385	0.57	0/4601
1	C	0.50	0/3384	0.56	0/4607
1	D	0.50	0/3364	0.57	0/4577
All	All	0.49	0/13533	0.57	0/18408

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3348	0	0	0	0
1	B	3339	0	0	0	0
1	C	3334	0	0	1	0
1	D	3314	0	0	2	0
2	A	6	0	8	0	0
2	B	6	0	8	0	0
3	C	10	0	4	0	0
3	D	10	0	4	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	517	0	0	0	1
4	B	411	0	0	0	0
4	C	392	0	0	0	0
4	D	369	0	0	0	0
All	All	15056	0	24	3	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 0.

All (3) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:165:GLN:OE1	1:D:381:ARG:NH1	2.19	0.76
1:D:182:LYS:NZ	1:D:308:GLU:OE1	2.53	0.42
1:C:182:LYS:NZ	1:C:308:GLU:OE1	2.54	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:2333:HOH:O	4:A:2333:HOH:O[2_656]	1.88	0.32

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	448/495 (90%)	435 (97%)	13 (3%)	0	100	100
1	B	445/495 (90%)	432 (97%)	13 (3%)	0	100	100
1	C	455/495 (92%)	446 (98%)	9 (2%)	0	100	100
1	D	448/495 (90%)	439 (98%)	9 (2%)	0	100	100
All	All	1796/1980 (91%)	1752 (98%)	44 (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	344/383 (90%)	342 (99%)	2 (1%)	92	83
1	B	343/383 (90%)	340 (99%)	3 (1%)	87	74
1	C	339/383 (88%)	337 (99%)	2 (1%)	92	83
1	D	338/383 (88%)	335 (99%)	3 (1%)	87	74
All	All	1364/1532 (89%)	1354 (99%)	10 (1%)	91	80

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	111	ASN
1	A	379	VAL
1	B	111	ASN
1	B	379	VAL
1	B	396	GLU
1	C	111	ASN
1	C	329	LEU
1	D	13	GLU
1	D	111	ASN
1	D	329	LEU

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

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

4 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	GOL	A	1468	-	5,5,5	0.35	0	5,5,5	0.74	0
2	GOL	B	1467	-	5,5,5	0.41	0	5,5,5	1.50	1 (20%)
3	SRT	C	1466	-	9,9,9	1.48	1 (11%)	12,12,12	1.36	1 (8%)
3	SRT	D	1466	-	9,9,9	1.40	1 (11%)	12,12,12	0.96	1 (8%)

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	GOL	A	1468	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1467	-	-	0/4/4/4	0/0/0/0
3	SRT	C	1466	-	-	0/12/12/12	0/0/0/0
3	SRT	D	1466	-	-	0/12/12/12	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1466	SRT	C2-C1	3.11	1.57	1.52
3	D	1466	SRT	C2-C1	2.47	1.56	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	C	1466	SRT	O2-C2-C3	-3.33	103.31	110.19
2	B	1467	GOL	O2-C2-C3	2.76	120.78	108.22
3	D	1466	SRT	C2-C3-C4	2.13	115.50	109.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	450/495 (90%)	-0.19	7 (1%) 68 71	12, 22, 43, 72	0
1	B	449/495 (90%)	-0.10	11 (2%) 56 56	12, 24, 47, 77	0
1	C	456/495 (92%)	0.09	31 (6%) 17 15	12, 23, 59, 92	0
1	D	451/495 (91%)	0.11	25 (5%) 24 22	13, 24, 59, 97	0
All	All	1806/1980 (91%)	-0.02	74 (4%) 35 35	12, 23, 52, 97	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	10	TYR	10.2
1	C	446	GLY	7.6
1	C	19	GLU	6.3
1	C	14	HIS	6.1
1	D	447	ASP	6.0
1	C	447	ASP	5.4
1	C	10	TYR	5.3
1	D	446	GLY	5.2
1	B	10	TYR	5.1
1	A	10	TYR	5.0
1	B	9	ASN	4.4
1	D	25	LYS	4.3
1	D	13	GLU	4.3
1	C	12	ILE	4.2
1	D	445	ILE	4.1
1	C	15	ASP	4.1
1	C	18	GLY	4.0
1	D	448	ARG	3.9
1	D	451	ILE	3.9
1	C	451	ILE	3.8
1	C	16	THR	3.8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	447	ASP	3.8
1	A	448	ARG	3.8
1	C	415	ALA	3.7
1	C	448	ARG	3.7
1	C	449	LEU	3.6
1	D	418	TYR	3.5
1	C	445	ILE	3.4
1	D	430	LYS	3.4
1	C	17	MET	3.3
1	B	314	LEU	3.3
1	D	24	ALA	3.2
1	C	453	ASP	3.1
1	D	452	GLU	3.1
1	D	431	GLU	3.1
1	C	20	VAL	3.0
1	A	12	ILE	2.9
1	B	175	LEU	2.9
1	C	24	ALA	2.8
1	C	430	LYS	2.7
1	D	444	LEU	2.7
1	C	418	TYR	2.7
1	A	123	GLY	2.6
1	C	23	PRO	2.6
1	C	443	GLY	2.6
1	D	23	PRO	2.6
1	B	25	LYS	2.5
1	B	24	ALA	2.5
1	D	449	LEU	2.5
1	B	12	ILE	2.4
1	A	24	ALA	2.4
1	D	450	SER	2.4
1	A	9	ASN	2.4
1	C	444	LEU	2.3
1	C	11	ARG	2.3
1	C	414	SER	2.2
1	B	446	GLY	2.2
1	D	12	ILE	2.2
1	C	128	HIS	2.2
1	D	20	VAL	2.2
1	C	422	ALA	2.2
1	D	414	SER	2.2
1	B	123	GLY	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	447	ASP	2.1
1	B	124	GLY	2.1
1	D	415	ALA	2.1
1	D	139	SER	2.1
1	D	11	ARG	2.1
1	C	175	LEU	2.1
1	D	128	HIS	2.1
1	C	26	ALA	2.0
1	C	73	PRO	2.0
1	D	124	GLY	2.0
1	C	441	ASP	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	GOL	A	1468	6/6	0.13	1.19	36,38,38,38	0
2	GOL	B	1467	6/6	0.12	1.07	30,31,32,33	0
3	SRT	D	1466	10/10	0.10	-0.88	23,25,30,39	0
3	SRT	C	1466	10/10	0.08	-1.18	20,22,26,34	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.