



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 02:36 am 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 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

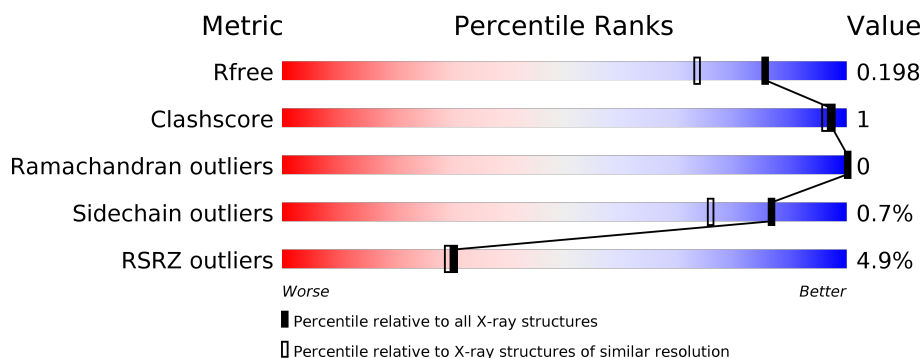
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.65 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))
$R_{free}$	100719	1368 (1.66-1.66)
Clashscore	112137	1468 (1.66-1.66)
Ramachandran outliers	110173	1438 (1.66-1.66)
Sidechain outliers	110143	1438 (1.66-1.66)
RSRZ outliers	101464	1371 (1.66-1.66)

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. 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	495	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>9%</div> </div> </div>
1	B	495	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>9%</div> </div> </div>
1	C	495	<div> <div>6%</div> <div> <div></div> <div>89%</div> <div>8%</div> </div> </div>
1	D	495	<div> <div>7%</div> <div> <div></div> <div>87%</div> <div>9%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15056 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 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

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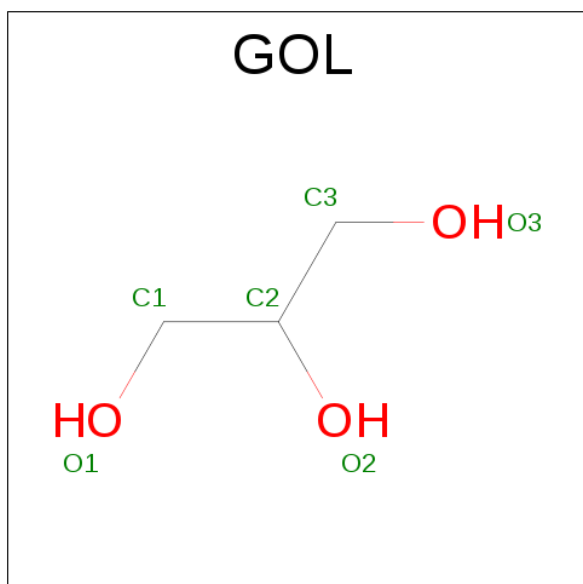
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP O53446
B	-21	MET	-	EXPRESSION TAG	UNP O53446
B	-20	SER	-	EXPRESSION TAG	UNP O53446
B	-19	TYR	-	EXPRESSION TAG	UNP O53446
B	-18	TYR	-	EXPRESSION TAG	UNP O53446
B	-17	HIS	-	EXPRESSION TAG	UNP O53446
B	-16	HIS	-	EXPRESSION TAG	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

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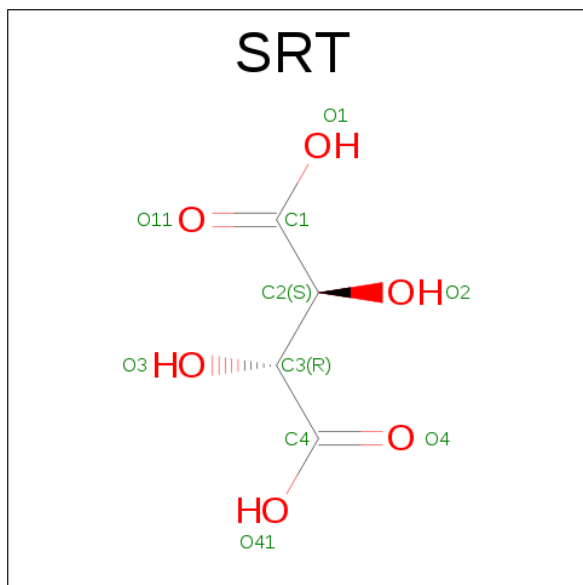
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	ALA	-	EXPRESSION TAG	UNP O53446
C	-1	GLY	-	EXPRESSION TAG	UNP O53446
C	0	SER	-	EXPRESSION TAG	UNP O53446
D	-21	MET	-	EXPRESSION TAG	UNP O53446
D	-20	SER	-	EXPRESSION TAG	UNP O53446
D	-19	TYR	-	EXPRESSION TAG	UNP O53446
D	-18	TYR	-	EXPRESSION TAG	UNP 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:  $C_3H_8O_3$ ).



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		

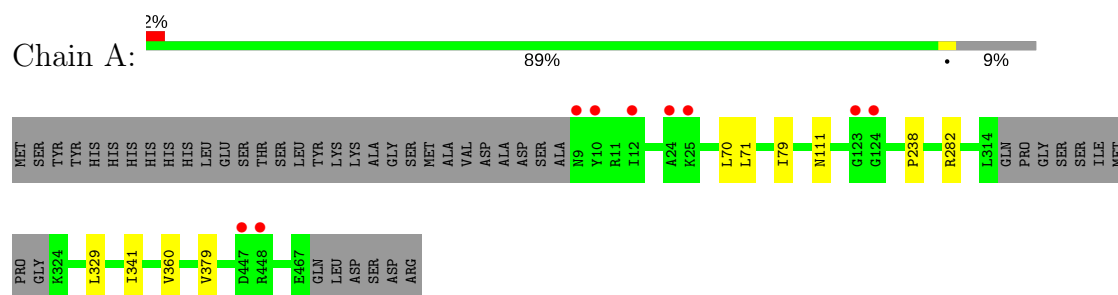
- Molecule 4 is water.

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		

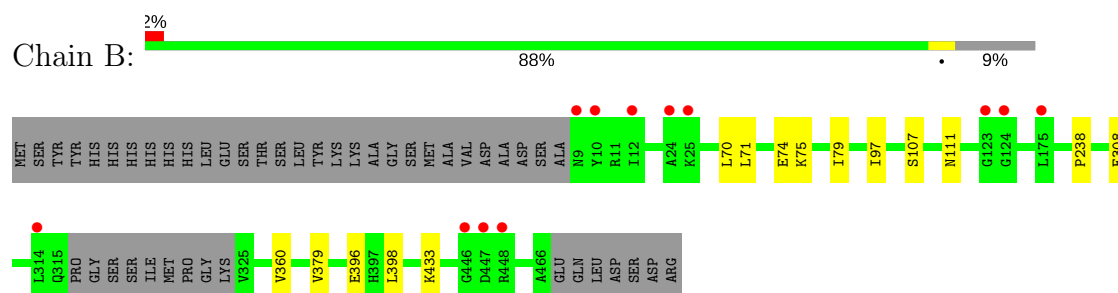
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

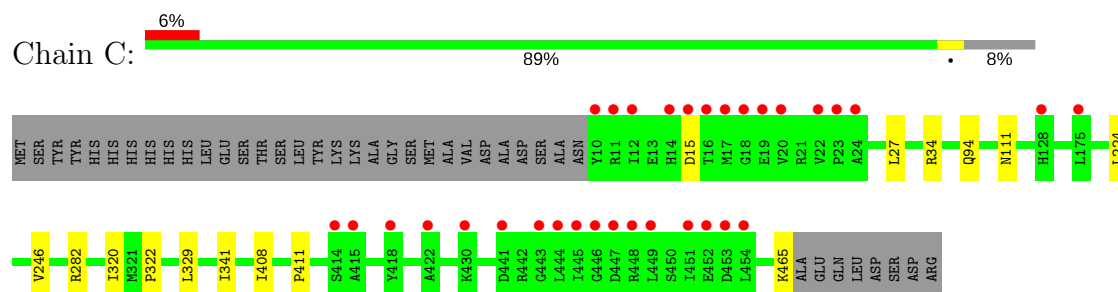
#### • Molecule 1: FUMARATE HYDRATASE CLASS II



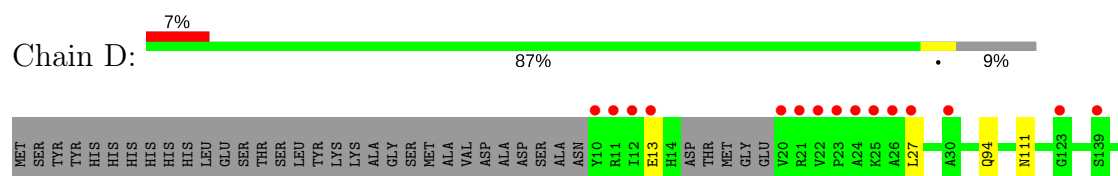
#### • Molecule 1: FUMARATE HYDRATASE CLASS II

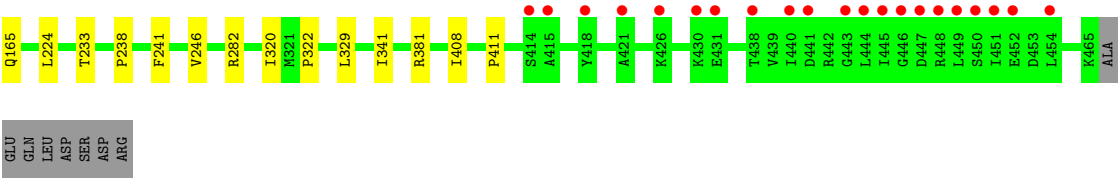


#### • Molecule 1: FUMARATE HYDRATASE CLASS II



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







## 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 0.177 , 0.198	Depositor DCC
$R_{free}$ test set	13997 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 , 53.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	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.

<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 [i](#)

### 5.1 Standard geometry [i](#)

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 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3348	0	3385	5	0
1	B	3339	0	3373	7	0
1	C	3334	0	3347	7	0
1	D	3314	0	3344	8	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
4	A	517	0	0	1	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	411	0	0	2	0
4	C	392	0	0	0	0
4	D	369	0	0	0	0
All	All	15056	0	13473	26	1

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 (26) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:ARG:HG2	1:A:341:ILE:HD13	1.55	0.86
1:D:165:GLN:OE1	1:D:381:ARG:NH1	2.19	0.76
1:B:360:VAL:HG22	4:B:2318:HOH:O	1.87	0.75
1:A:360:VAL:HG22	4:A:2411:HOH:O	1.89	0.73
1:C:15:ASP:HB3	1:C:34:ARG:HH21	1.67	0.59
1:C:282:ARG:HG2	1:C:341:ILE:HD12	1.89	0.55
1:C:320:ILE:O	1:C:322:PRO:HD3	2.08	0.54
1:D:320:ILE:O	1:D:322:PRO:HD3	2.09	0.53
1:D:282:ARG:HG2	1:D:341:ILE:HD12	1.93	0.51
1:B:74:GLU:HG3	1:B:75:LYS:N	2.29	0.48
1:C:408:ILE:O	1:C:411:PRO:HD2	2.14	0.47
1:D:408:ILE:O	1:D:411:PRO:HD2	2.15	0.46
1:B:433:LYS:HD2	4:B:2372:HOH:O	2.17	0.45
1:C:465:LYS:HD3	1:D:233:THR:O	2.17	0.44
1:A:71:LEU:HD21	1:A:79:ILE:HD12	2.01	0.43
1:A:70:LEU:HD11	1:A:238:PRO:HG3	2.02	0.42
1:B:71:LEU:HD21	1:B:79:ILE:HD12	2.02	0.42
1:C:224:LEU:HD12	1:C:246:VAL:HG22	2.02	0.42
1:C:27:LEU:HD12	1:C:94:GLN:HG3	2.02	0.42
1:D:27:LEU:HD12	1:D:94:GLN:HG3	2.01	0.41
1:A:329:LEU:HA	1:A:329:LEU:HD23	1.91	0.41
1:B:70:LEU:HD11	1:B:238:PRO:HG3	2.02	0.41
1:B:308:GLU:HB3	1:B:398:LEU:HD21	2.03	0.41
1:D:238:PRO:HD2	1:D:241:PHE:HB2	2.03	0.41
1:B:97:ILE:HD13	1:B:107:SER:HB3	2.02	0.40
1:D:224:LEU:HD12	1:D:246:VAL:HG22	2.03	0.40

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	Interatomic distance (Å)	Clash overlap (Å)
4:A:2333:HOH:O	4:A:2333:HOH:O[2_656]	1.88	0.32

## 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	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 [i](#)

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%)	89	79
1	B	343/383 (90%)	340 (99%)	3 (1%)	82	69
1	C	339/383 (88%)	337 (99%)	2 (1%)	89	79
1	D	338/383 (88%)	335 (99%)	3 (1%)	82	69
All	All	1364/1532 (89%)	1354 (99%)	10 (1%)	87	76

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. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	158	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	0.40	0	5,5,5	0.67	0
2	GOL	B	1467	-	5,5,5	0.43	0	5,5,5	1.40	1 (20%)
3	SRT	C	1466	-	3,9,9	0.85	0	6,12,12	1.08	0
3	SRT	D	1466	-	3,9,9	0.99	0	6,12,12	0.83	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	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	-	-	0/4/12/12	0/0/0/0
3	SRT	D	1466	-	-	0/4/12/12	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1467	GOL	O2-C2-C3	2.53	120.78	108.84

There are no chirality outliers.

There are no torsion outliers.

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	450/495 (90%)	-0.15	9 (2%) 65 70	12, 22, 43, 72	0
1	B	449/495 (90%)	-0.03	12 (2%) 55 57	12, 24, 47, 77	0
1	C	456/495 (92%)	0.13	32 (7%) 17 16	12, 23, 59, 92	0
1	D	451/495 (91%)	0.21	36 (7%) 13 12	13, 24, 59, 97	0
All	All	1806/1980 (91%)	0.04	89 (4%) 30 29	12, 23, 52, 97	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	10	TYR	10.7
1	C	446	GLY	8.3
1	D	447	ASP	6.3
1	C	447	ASP	6.0
1	C	19	GLU	5.7
1	C	14	HIS	5.7
1	B	10	TYR	5.6
1	C	10	TYR	5.6
1	D	446	GLY	5.5
1	A	10	TYR	5.0
1	D	25	LYS	4.8
1	D	418	TYR	4.8
1	D	13	GLU	4.7
1	C	448	ARG	4.7
1	B	314	LEU	4.7
1	D	445	ILE	4.5
1	C	445	ILE	4.4
1	D	451	ILE	4.4
1	C	18	GLY	4.4
1	B	9	ASN	4.3
1	C	451	ILE	4.2

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Mol	Chain	Res	Type	RSRZ
1	C	415	ALA	4.2
1	C	449	LEU	4.1
1	C	16	THR	4.1
1	D	24	ALA	4.0
1	C	453	ASP	4.0
1	C	12	ILE	3.9
1	C	15	ASP	3.8
1	A	448	ARG	3.8
1	D	448	ARG	3.6
1	D	12	ILE	3.5
1	A	447	ASP	3.5
1	C	443	GLY	3.5
1	D	452	GLU	3.5
1	C	17	MET	3.5
1	D	23	PRO	3.2
1	A	123	GLY	3.2
1	D	444	LEU	3.2
1	D	430	LYS	3.2
1	D	449	LEU	3.1
1	D	431	GLU	3.1
1	A	24	ALA	3.0
1	C	23	PRO	3.0
1	D	443	GLY	3.0
1	D	11	ARG	3.0
1	B	175	LEU	3.0
1	B	12	ILE	2.9
1	D	440	ILE	2.9
1	C	418	TYR	2.9
1	D	450	SER	2.8
1	B	25	LYS	2.7
1	D	22	VAL	2.7
1	C	441	ASP	2.6
1	D	441	ASP	2.6
1	D	21	ARG	2.6
1	C	414	SER	2.6
1	B	24	ALA	2.5
1	C	444	LEU	2.5
1	C	20	VAL	2.5
1	C	422	ALA	2.4
1	C	430	LYS	2.4
1	D	26	ALA	2.4
1	B	124	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	452	GLU	2.4
1	A	9	ASN	2.3
1	C	22	VAL	2.3
1	D	20	VAL	2.3
1	B	123	GLY	2.3
1	A	25	LYS	2.3
1	C	24	ALA	2.2
1	C	175	LEU	2.2
1	D	415	ALA	2.2
1	D	454	LEU	2.2
1	A	12	ILE	2.2
1	B	447	ASP	2.2
1	B	448	ARG	2.2
1	B	446	GLY	2.2
1	D	421	ALA	2.2
1	D	414	SER	2.2
1	D	27	LEU	2.2
1	C	128	HIS	2.1
1	C	454	LEU	2.1
1	D	438	THR	2.1
1	D	139	SER	2.1
1	D	30	ALA	2.1
1	A	124	GLY	2.0
1	D	123	GLY	2.0
1	C	11	ARG	2.0
1	D	426	LYS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

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

of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GOL	A	1468	6/6	0.80	0.13	1.00	36,38,38,38	0
2	GOL	B	1467	6/6	0.91	0.10	0.46	30,31,32,33	0
3	SRT	C	1466	10/10	0.96	0.09	-0.28	20,22,26,34	0
3	SRT	D	1466	10/10	0.95	0.10	-0.55	23,25,30,39	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.