



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 03:15 PM BST

PDB ID : 3RCY
Title : CRYSTAL STRUCTURE OF Mandelate racemase/muconate lactonizing enzyme-like protein from Roseovarius sp. TM1035
Authors : Malashkevich, V.N.; Toro, R.; Seidel, R.; Garrett, S.; Foti, R.; Almo, S.C.; New York Structural Genomics Research Consortium (NYSGRG)
Deposited on : 2011-03-31
Resolution : 1.99 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

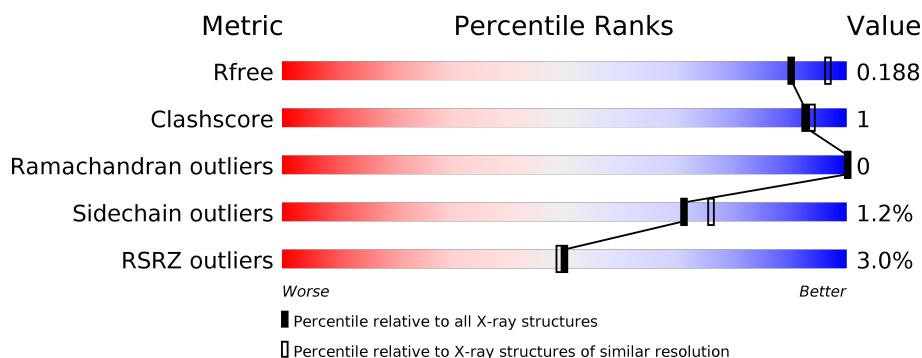
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	433	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>9%</div> </div> </div>
1	B	433	<div> <div>3%</div> <div> <div></div> <div>87%</div> <div>9%</div> </div> </div>
1	C	433	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>9%</div> </div> </div>
1	D	433	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>9%</div> </div> </div>
1	E	433	<div> <div>3%</div> <div> <div></div> <div>87%</div> <div>5%</div> <div>9%</div> </div> </div>
1	F	433	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>5%</div> <div>8%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	433	
1	H	433	

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
3	GOL	G	501	-	-	X	-
4	RIB	A	433	X	-	-	-
4	RIB	A	505	X	-	-	-
4	RIB	B	505	X	-	-	-
4	RIB	D	505	X	-	-	-
4	RIB	E	505	X	-	-	-
4	RIB	G	505	X	-	-	-
4	RIB	H	433	X	-	-	-
4	RIB	H	505	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 26806 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 Mandelate racemase/muconate lactonizing enzyme-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	4	0
			3042	1945	526	552	19			
1	B	395	Total	C	N	O	S	0	3	0
			3024	1934	522	549	19			
1	C	396	Total	C	N	O	S	0	6	0
			3044	1947	520	558	19			
1	D	396	Total	C	N	O	S	0	5	0
			3046	1948	523	556	19			
1	E	395	Total	C	N	O	S	0	3	0
			3027	1936	522	550	19			
1	F	397	Total	C	N	O	S	0	3	0
			3041	1944	524	554	19			
1	G	396	Total	C	N	O	S	0	7	0
			3062	1958	529	556	19			
1	H	395	Total	C	N	O	S	0	2	0
			3021	1932	522	548	19			

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP A6DZ31
A	1	VAL	-	expression tag	UNP A6DZ31
A	411	ALA	-	expression tag	UNP A6DZ31
A	412	GLU	-	expression tag	UNP A6DZ31
A	413	ASN	-	expression tag	UNP A6DZ31
A	414	LEU	-	expression tag	UNP A6DZ31
A	415	TYR	-	expression tag	UNP A6DZ31
A	416	PHE	-	expression tag	UNP A6DZ31
A	417	GLN	-	expression tag	UNP A6DZ31
A	418	SER	-	expression tag	UNP A6DZ31
A	419	HIS	-	expression tag	UNP A6DZ31
A	420	HIS	-	expression tag	UNP A6DZ31
A	421	HIS	-	expression tag	UNP A6DZ31

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Chain	Residue	Modelled	Actual	Comment	Reference
A	422	HIS	-	expression tag	UNP A6DZ31
A	423	HIS	-	expression tag	UNP A6DZ31
A	424	HIS	-	expression tag	UNP A6DZ31
A	425	TRP	-	expression tag	UNP A6DZ31
A	426	SER	-	expression tag	UNP A6DZ31
A	427	HIS	-	expression tag	UNP A6DZ31
A	428	PRO	-	expression tag	UNP A6DZ31
A	429	GLN	-	expression tag	UNP A6DZ31
A	430	PHE	-	expression tag	UNP A6DZ31
A	431	GLU	-	expression tag	UNP A6DZ31
A	432	LYS	-	expression tag	UNP A6DZ31
B	0	MET	-	expression tag	UNP A6DZ31
B	1	VAL	-	expression tag	UNP A6DZ31
B	411	ALA	-	expression tag	UNP A6DZ31
B	412	GLU	-	expression tag	UNP A6DZ31
B	413	ASN	-	expression tag	UNP A6DZ31
B	414	LEU	-	expression tag	UNP A6DZ31
B	415	TYR	-	expression tag	UNP A6DZ31
B	416	PHE	-	expression tag	UNP A6DZ31
B	417	GLN	-	expression tag	UNP A6DZ31
B	418	SER	-	expression tag	UNP A6DZ31
B	419	HIS	-	expression tag	UNP A6DZ31
B	420	HIS	-	expression tag	UNP A6DZ31
B	421	HIS	-	expression tag	UNP A6DZ31
B	422	HIS	-	expression tag	UNP A6DZ31
B	423	HIS	-	expression tag	UNP A6DZ31
B	424	HIS	-	expression tag	UNP A6DZ31
B	425	TRP	-	expression tag	UNP A6DZ31
B	426	SER	-	expression tag	UNP A6DZ31
B	427	HIS	-	expression tag	UNP A6DZ31
B	428	PRO	-	expression tag	UNP A6DZ31
B	429	GLN	-	expression tag	UNP A6DZ31
B	430	PHE	-	expression tag	UNP A6DZ31
B	431	GLU	-	expression tag	UNP A6DZ31
B	432	LYS	-	expression tag	UNP A6DZ31
C	0	MET	-	expression tag	UNP A6DZ31
C	1	VAL	-	expression tag	UNP A6DZ31
C	411	ALA	-	expression tag	UNP A6DZ31
C	412	GLU	-	expression tag	UNP A6DZ31
C	413	ASN	-	expression tag	UNP A6DZ31
C	414	LEU	-	expression tag	UNP A6DZ31
C	415	TYR	-	expression tag	UNP A6DZ31

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Chain	Residue	Modelled	Actual	Comment	Reference
C	416	PHE	-	expression tag	UNP A6DZ31
C	417	GLN	-	expression tag	UNP A6DZ31
C	418	SER	-	expression tag	UNP A6DZ31
C	419	HIS	-	expression tag	UNP A6DZ31
C	420	HIS	-	expression tag	UNP A6DZ31
C	421	HIS	-	expression tag	UNP A6DZ31
C	422	HIS	-	expression tag	UNP A6DZ31
C	423	HIS	-	expression tag	UNP A6DZ31
C	424	HIS	-	expression tag	UNP A6DZ31
C	425	TRP	-	expression tag	UNP A6DZ31
C	426	SER	-	expression tag	UNP A6DZ31
C	427	HIS	-	expression tag	UNP A6DZ31
C	428	PRO	-	expression tag	UNP A6DZ31
C	429	GLN	-	expression tag	UNP A6DZ31
C	430	PHE	-	expression tag	UNP A6DZ31
C	431	GLU	-	expression tag	UNP A6DZ31
C	432	LYS	-	expression tag	UNP A6DZ31
D	0	MET	-	expression tag	UNP A6DZ31
D	1	VAL	-	expression tag	UNP A6DZ31
D	411	ALA	-	expression tag	UNP A6DZ31
D	412	GLU	-	expression tag	UNP A6DZ31
D	413	ASN	-	expression tag	UNP A6DZ31
D	414	LEU	-	expression tag	UNP A6DZ31
D	415	TYR	-	expression tag	UNP A6DZ31
D	416	PHE	-	expression tag	UNP A6DZ31
D	417	GLN	-	expression tag	UNP A6DZ31
D	418	SER	-	expression tag	UNP A6DZ31
D	419	HIS	-	expression tag	UNP A6DZ31
D	420	HIS	-	expression tag	UNP A6DZ31
D	421	HIS	-	expression tag	UNP A6DZ31
D	422	HIS	-	expression tag	UNP A6DZ31
D	423	HIS	-	expression tag	UNP A6DZ31
D	424	HIS	-	expression tag	UNP A6DZ31
D	425	TRP	-	expression tag	UNP A6DZ31
D	426	SER	-	expression tag	UNP A6DZ31
D	427	HIS	-	expression tag	UNP A6DZ31
D	428	PRO	-	expression tag	UNP A6DZ31
D	429	GLN	-	expression tag	UNP A6DZ31
D	430	PHE	-	expression tag	UNP A6DZ31
D	431	GLU	-	expression tag	UNP A6DZ31
D	432	LYS	-	expression tag	UNP A6DZ31
E	0	MET	-	expression tag	UNP A6DZ31

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1	VAL	-	expression tag	UNP A6DZ31
E	411	ALA	-	expression tag	UNP A6DZ31
E	412	GLU	-	expression tag	UNP A6DZ31
E	413	ASN	-	expression tag	UNP A6DZ31
E	414	LEU	-	expression tag	UNP A6DZ31
E	415	TYR	-	expression tag	UNP A6DZ31
E	416	PHE	-	expression tag	UNP A6DZ31
E	417	GLN	-	expression tag	UNP A6DZ31
E	418	SER	-	expression tag	UNP A6DZ31
E	419	HIS	-	expression tag	UNP A6DZ31
E	420	HIS	-	expression tag	UNP A6DZ31
E	421	HIS	-	expression tag	UNP A6DZ31
E	422	HIS	-	expression tag	UNP A6DZ31
E	423	HIS	-	expression tag	UNP A6DZ31
E	424	HIS	-	expression tag	UNP A6DZ31
E	425	TRP	-	expression tag	UNP A6DZ31
E	426	SER	-	expression tag	UNP A6DZ31
E	427	HIS	-	expression tag	UNP A6DZ31
E	428	PRO	-	expression tag	UNP A6DZ31
E	429	GLN	-	expression tag	UNP A6DZ31
E	430	PHE	-	expression tag	UNP A6DZ31
E	431	GLU	-	expression tag	UNP A6DZ31
E	432	LYS	-	expression tag	UNP A6DZ31
F	0	MET	-	expression tag	UNP A6DZ31
F	1	VAL	-	expression tag	UNP A6DZ31
F	411	ALA	-	expression tag	UNP A6DZ31
F	412	GLU	-	expression tag	UNP A6DZ31
F	413	ASN	-	expression tag	UNP A6DZ31
F	414	LEU	-	expression tag	UNP A6DZ31
F	415	TYR	-	expression tag	UNP A6DZ31
F	416	PHE	-	expression tag	UNP A6DZ31
F	417	GLN	-	expression tag	UNP A6DZ31
F	418	SER	-	expression tag	UNP A6DZ31
F	419	HIS	-	expression tag	UNP A6DZ31
F	420	HIS	-	expression tag	UNP A6DZ31
F	421	HIS	-	expression tag	UNP A6DZ31
F	422	HIS	-	expression tag	UNP A6DZ31
F	423	HIS	-	expression tag	UNP A6DZ31
F	424	HIS	-	expression tag	UNP A6DZ31
F	425	TRP	-	expression tag	UNP A6DZ31
F	426	SER	-	expression tag	UNP A6DZ31
F	427	HIS	-	expression tag	UNP A6DZ31

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Chain	Residue	Modelled	Actual	Comment	Reference
F	428	PRO	-	expression tag	UNP A6DZ31
F	429	GLN	-	expression tag	UNP A6DZ31
F	430	PHE	-	expression tag	UNP A6DZ31
F	431	GLU	-	expression tag	UNP A6DZ31
F	432	LYS	-	expression tag	UNP A6DZ31
G	0	MET	-	expression tag	UNP A6DZ31
G	1	VAL	-	expression tag	UNP A6DZ31
G	411	ALA	-	expression tag	UNP A6DZ31
G	412	GLU	-	expression tag	UNP A6DZ31
G	413	ASN	-	expression tag	UNP A6DZ31
G	414	LEU	-	expression tag	UNP A6DZ31
G	415	TYR	-	expression tag	UNP A6DZ31
G	416	PHE	-	expression tag	UNP A6DZ31
G	417	GLN	-	expression tag	UNP A6DZ31
G	418	SER	-	expression tag	UNP A6DZ31
G	419	HIS	-	expression tag	UNP A6DZ31
G	420	HIS	-	expression tag	UNP A6DZ31
G	421	HIS	-	expression tag	UNP A6DZ31
G	422	HIS	-	expression tag	UNP A6DZ31
G	423	HIS	-	expression tag	UNP A6DZ31
G	424	HIS	-	expression tag	UNP A6DZ31
G	425	TRP	-	expression tag	UNP A6DZ31
G	426	SER	-	expression tag	UNP A6DZ31
G	427	HIS	-	expression tag	UNP A6DZ31
G	428	PRO	-	expression tag	UNP A6DZ31
G	429	GLN	-	expression tag	UNP A6DZ31
G	430	PHE	-	expression tag	UNP A6DZ31
G	431	GLU	-	expression tag	UNP A6DZ31
G	432	LYS	-	expression tag	UNP A6DZ31
H	0	MET	-	expression tag	UNP A6DZ31
H	1	VAL	-	expression tag	UNP A6DZ31
H	411	ALA	-	expression tag	UNP A6DZ31
H	412	GLU	-	expression tag	UNP A6DZ31
H	413	ASN	-	expression tag	UNP A6DZ31
H	414	LEU	-	expression tag	UNP A6DZ31
H	415	TYR	-	expression tag	UNP A6DZ31
H	416	PHE	-	expression tag	UNP A6DZ31
H	417	GLN	-	expression tag	UNP A6DZ31
H	418	SER	-	expression tag	UNP A6DZ31
H	419	HIS	-	expression tag	UNP A6DZ31
H	420	HIS	-	expression tag	UNP A6DZ31
H	421	HIS	-	expression tag	UNP A6DZ31

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Chain	Residue	Modelled	Actual	Comment	Reference
H	422	HIS	-	expression tag	UNP A6DZ31
H	423	HIS	-	expression tag	UNP A6DZ31
H	424	HIS	-	expression tag	UNP A6DZ31
H	425	TRP	-	expression tag	UNP A6DZ31
H	426	SER	-	expression tag	UNP A6DZ31
H	427	HIS	-	expression tag	UNP A6DZ31
H	428	PRO	-	expression tag	UNP A6DZ31
H	429	GLN	-	expression tag	UNP A6DZ31
H	430	PHE	-	expression tag	UNP A6DZ31
H	431	GLU	-	expression tag	UNP A6DZ31
H	432	LYS	-	expression tag	UNP A6DZ31

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0
2	H	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	A	1	Total Mg 1 1	0	0
2	F	1	Total Mg 1 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



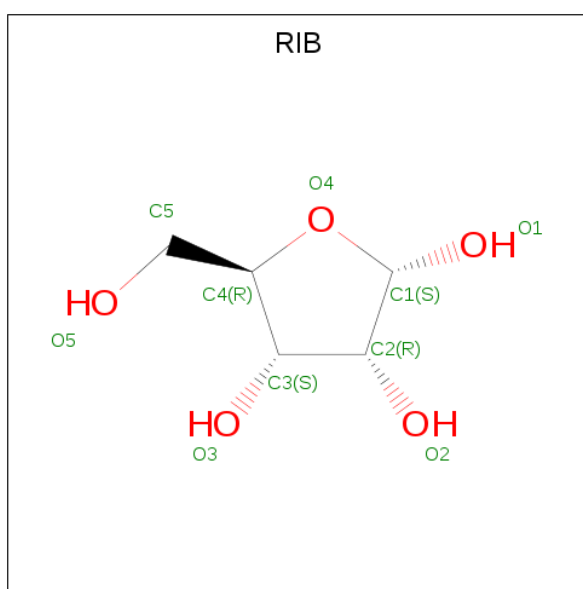
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	G	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	C	O	0	0
			6	3	3		
3	G	1	Total	C	O	0	0
			6	3	3		
3	G	1	Total	C	O	0	0
			6	3	3		
3	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is alpha-D-ribofuranose (three-letter code: RIB) (formula: C₅H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	5	5		
4	A	1	Total	C	O	0	0
			10	5	5		
4	B	1	Total	C	O	0	0
			10	5	5		
4	D	1	Total	C	O	0	0
			10	5	5		
4	E	1	Total	C	O	0	0
			10	5	5		
4	G	1	Total	C	O	0	0
			10	5	5		
4	H	1	Total	C	O	0	0
			10	5	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			10	5	5		

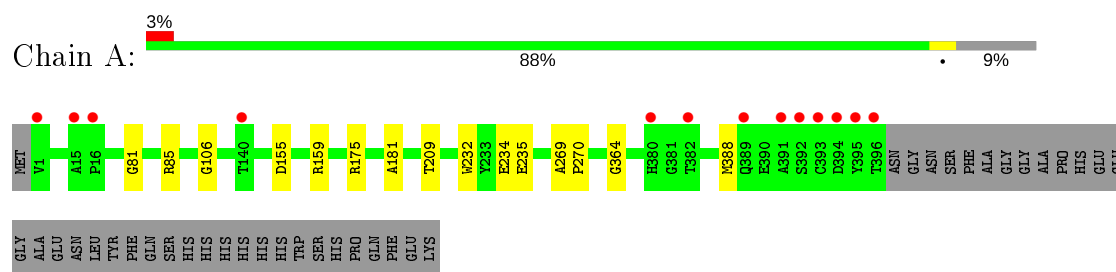
- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	305	Total	O		0	0
			305	305			
5	B	284	Total	O		0	0
			284	284			
5	C	307	Total	O		0	0
			307	307			
5	D	333	Total	O		0	0
			333	333			
5	E	290	Total	O		0	0
			290	290			
5	F	269	Total	O		0	0
			269	269			
5	G	281	Total	O		0	0
			281	281			
5	H	234	Total	O		0	0
			234	234			

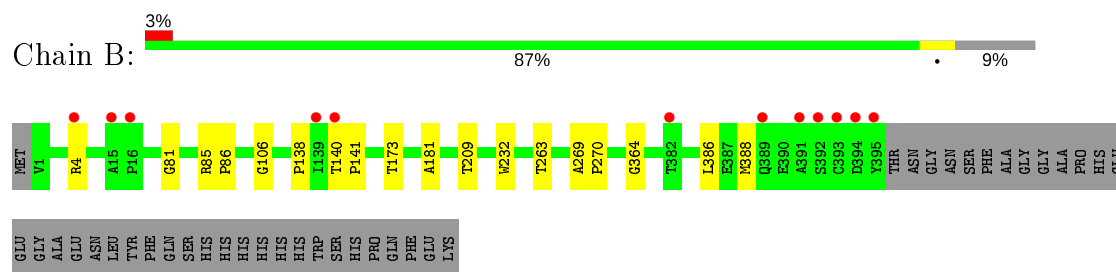
3 Residue-property plots [i](#)

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.

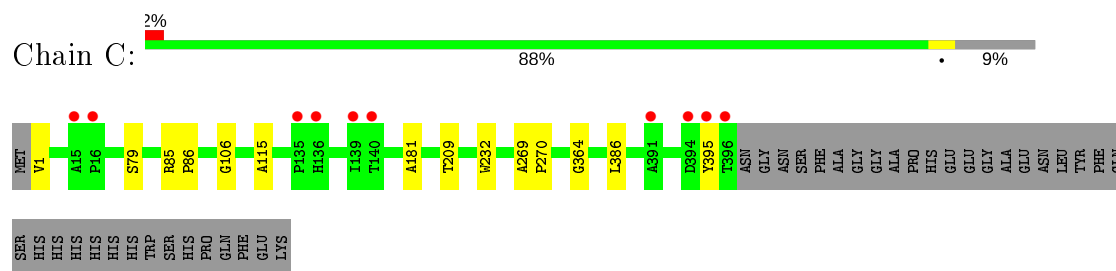
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



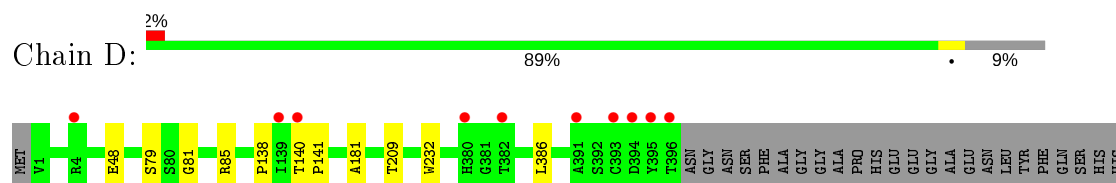
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein

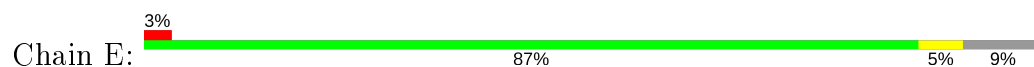


- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



HIS
HIS
HIS
HIS
TRP
SER
HIS
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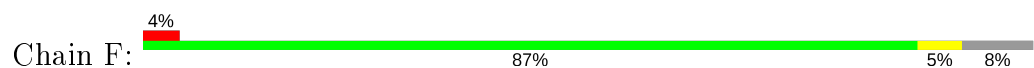
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



MET VI P13 P14 A15 P16 E48 R51 S79 S80 G81 R85 L105 G106 N122 T140 P141 T173 A181 T209 W232 A269 P270 G364 H380 G381 T382 L386 Q389 E390 A391 S392 C393 D394 Y395 THR ASN GLY ASN SER PHE ALA GLY

GLY ALA PRO HIS GLU GLY ALA ASN TVR PHE GLN SER HIS HIS HIS HIS TRP SER HIS PRO GLN PHE GLU LYS

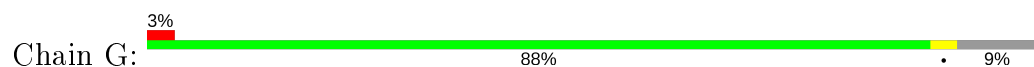
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



MET VI R4 P13 P14 A15 D31 G38 P47 R51 G64 P67 E68 R85 G96 R124 I139 T140 P141 H178 T209 W232 Y233 E234 E235 Y303 E368 H380 G381 T382 L386 Q389 E390 A391 S392 C393 D394 Y395 N397

GLY ASN SER PHE ALA GLY ALA PRO GLU GLU GLY ALA ASN TVR PHE GLN SER HIS HIS HIS HIS TRP SER HIS PRO GLN PHE GLU LYS

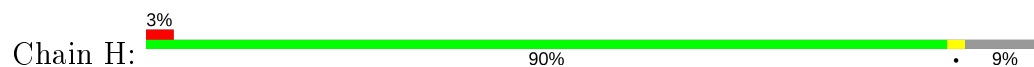
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



MET VI R21 G81 R85 I139 T140 H178 T209 W232 Y233 E234 E235 A269 P270 Y303 H380 G381 T382 G383 L384 H385 L386 E387 M388 A391 S392 C393 D394 Y395 T396 ASN GLY ASN SER PHE ALA GLY GLY ALA PRO HIS GLU GLU GLY ALA GLU ASN THR

TYR PHE GLN SER HIS HIS HIS HIS TRP SER HIS PRO GLN PHE GLU LYS

- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



MET VI A15 P16 R51 G81 R85 P135 I139 T140 T173 H178 T209 W232 H380 G381 T382 A391 S392 C393 D394 Y395 THR ASN GLY ASN SER PHE ALA GLY GLY ALA PRO HIS GLU GLU GLY ALA GLU ASN THR LEU TYR PHE GLN SER HIS HIS HIS

HIS HIS HIS TRP SER HIS HIS PRO GLN PHE GLU LYS

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	144.98Å 162.14Å 141.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.99 20.00 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-1.99) 99.7 (20.00-1.99)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 1.99Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.147 , 0.181 0.154 , 0.188	Depositor DCC
R_{free} test set	11321 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	26806	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 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, MG, RIB

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	0.46	0/3139	0.55	0/4280
1	B	0.44	0/3118	0.54	0/4252
1	C	0.44	1/3147 (0.0%)	0.54	0/4292
1	D	0.44	0/3146	0.53	0/4290
1	E	0.42	0/3121	0.54	0/4256
1	F	0.41	0/3134	0.53	0/4272
1	G	0.41	0/3168	0.52	0/4318
1	H	0.40	0/3112	0.51	0/4244
All	All	0.43	1/25085 (0.0%)	0.53	0/34204

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1	VAL	C-N	-5.03	1.22	1.34

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	3042	0	3005	10	0
1	B	3024	0	2984	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3044	0	3001	9	0
1	D	3046	0	3004	7	0
1	E	3027	0	2985	15	0
1	F	3041	0	2996	15	0
1	G	3062	0	3030	11	0
1	H	3021	0	2979	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
3	A	12	0	16	2	0
3	B	18	0	24	2	0
3	C	12	0	16	5	0
3	D	18	0	24	2	0
3	E	12	0	16	2	0
3	F	6	0	8	0	0
3	G	24	0	32	8	0
3	H	6	0	8	0	0
4	A	20	0	0	1	0
4	B	10	0	0	0	0
4	D	10	0	0	0	0
4	E	10	0	0	0	0
4	G	10	0	0	0	0
4	H	20	0	0	0	0
5	A	305	0	0	1	0
5	B	284	0	0	0	0
5	C	307	0	0	0	0
5	D	333	0	0	0	0
5	E	290	0	0	0	0
5	F	269	0	0	3	0
5	G	281	0	0	2	0
5	H	234	0	0	4	0
All	All	26806	0	24128	72	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.

The worst 5 of 72 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:G:303:TYR:HE1	3:G:501:GOL:H2	1.33	0.90
1:C:181:ALA:HB1	3:C:502:GOL:H31	1.69	0.74
4:A:433:RIB:O3	1:C:86:PRO:HD2	1.88	0.73
1:G:303:TYR:CE1	3:G:501:GOL:H2	2.23	0.72
1:B:181:ALA:HB1	3:B:502:GOL:H12	1.72	0.72

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	398/433 (92%)	384 (96%)	14 (4%)	0	100	100
1	B	396/433 (92%)	383 (97%)	13 (3%)	0	100	100
1	C	400/433 (92%)	386 (96%)	14 (4%)	0	100	100
1	D	399/433 (92%)	382 (96%)	17 (4%)	0	100	100
1	E	396/433 (92%)	382 (96%)	14 (4%)	0	100	100
1	F	396/433 (92%)	382 (96%)	14 (4%)	0	100	100
1	G	401/433 (93%)	389 (97%)	12 (3%)	0	100	100
1	H	395/433 (91%)	383 (97%)	12 (3%)	0	100	100
All	All	3181/3464 (92%)	3071 (96%)	110 (4%)	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	306/332 (92%)	303 (99%)	3 (1%)	76	81
1	B	304/332 (92%)	299 (98%)	5 (2%)	62	67
1	C	308/332 (93%)	305 (99%)	3 (1%)	76	81
1	D	307/332 (92%)	304 (99%)	3 (1%)	76	81
1	E	304/332 (92%)	300 (99%)	4 (1%)	69	74
1	F	305/332 (92%)	300 (98%)	5 (2%)	62	67
1	G	309/332 (93%)	306 (99%)	3 (1%)	76	81
1	H	303/332 (91%)	299 (99%)	4 (1%)	69	74
All	All	2446/2656 (92%)	2416 (99%)	30 (1%)	71	76

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	232	TRP
1	E	209	THR
1	H	173	THR
1	E	173	THR
1	E	232	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	178	HIS
1	F	377	ASN
1	G	385	HIS
1	E	385	HIS
1	G	178	HIS

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 [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 8 are monoatomic - leaving 26 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	GOL	B	502	-	5,5,5	0.47	0	5,5,5	0.46	0
4	RIB	A	505	-	10,10,10	0.62	0	13,14,14	1.35	2 (15%)
3	GOL	F	501	-	5,5,5	0.31	0	5,5,5	0.51	0
3	GOL	C	502	-	5,5,5	0.53	0	5,5,5	0.44	0
3	GOL	G	501	-	5,5,5	0.33	0	5,5,5	0.27	0
3	GOL	B	433	-	5,5,5	0.33	0	5,5,5	0.56	0
3	GOL	G	503	-	5,5,5	0.45	0	5,5,5	0.31	0
4	RIB	G	505	-	10,10,10	0.58	0	13,14,14	1.30	2 (15%)
4	RIB	D	505	-	10,10,10	0.62	0	13,14,14	1.16	1 (7%)
3	GOL	G	502	-	5,5,5	0.42	0	5,5,5	0.30	0
4	RIB	H	433	-	10,10,10	0.58	0	13,14,14	1.37	2 (15%)
4	RIB	A	433	-	10,10,10	0.67	0	13,14,14	1.20	2 (15%)
3	GOL	A	503	-	5,5,5	0.39	0	5,5,5	0.36	0
3	GOL	G	504	-	5,5,5	0.28	0	5,5,5	0.28	0
3	GOL	D	502	-	5,5,5	0.46	0	5,5,5	0.32	0
4	RIB	B	505	-	10,10,10	0.60	0	13,14,14	1.12	1 (7%)
3	GOL	H	501	-	5,5,5	0.32	0	5,5,5	0.26	0
3	GOL	E	502	-	5,5,5	0.46	0	5,5,5	0.44	0
3	GOL	B	503	-	5,5,5	0.43	0	5,5,5	0.27	0
3	GOL	D	433	-	5,5,5	0.35	0	5,5,5	0.28	0
4	RIB	H	505	-	10,10,10	0.59	0	13,14,14	1.23	1 (7%)
3	GOL	D	501	-	5,5,5	0.32	0	5,5,5	0.19	0
3	GOL	C	501	-	5,5,5	0.36	0	5,5,5	0.47	0
4	RIB	E	505	-	10,10,10	0.60	0	13,14,14	1.31	1 (7%)
3	GOL	E	501	-	5,5,5	0.30	0	5,5,5	0.12	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	502	-	5,5,5	0.48	0	5,5,5	0.47	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	GOL	B	502	-	-	4/4/4/4	-
4	RIB	A	505	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	F	501	-	-	2/4/4/4	-
3	GOL	C	502	-	-	4/4/4/4	-
3	GOL	G	501	-	-	4/4/4/4	-
3	GOL	B	433	-	-	2/4/4/4	-
3	GOL	G	503	-	-	2/4/4/4	-
4	RIB	G	505	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	C	501	-	-	2/4/4/4	-
3	GOL	G	502	-	-	2/4/4/4	-
4	RIB	H	433	-	1/1/4/4	2/2/18/18	0/1/1/1
4	RIB	A	433	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	A	503	-	-	2/4/4/4	-
3	GOL	G	504	-	-	1/4/4/4	-
3	GOL	D	502	-	-	1/4/4/4	-
4	RIB	B	505	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	H	501	-	-	0/4/4/4	-
3	GOL	E	502	-	-	4/4/4/4	-
3	GOL	B	503	-	-	4/4/4/4	-
3	GOL	D	433	-	-	3/4/4/4	-
4	RIB	H	505	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	D	501	-	-	0/4/4/4	-
4	RIB	D	505	-	1/1/4/4	2/2/18/18	0/1/1/1
4	RIB	E	505	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	E	501	-	-	0/4/4/4	-
3	GOL	A	502	-	-	4/4/4/4	-

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	505	RIB	C1-C2-C3	3.09	106.17	102.30
4	A	505	RIB	C1-C2-C3	3.01	106.06	102.30
4	H	433	RIB	C1-C2-C3	2.98	106.03	102.30
4	D	505	RIB	C1-C2-C3	2.85	105.86	102.30
4	H	505	RIB	C1-C2-C3	2.71	105.69	102.30

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	505	RIB	C1
4	G	505	RIB	C1
4	D	505	RIB	C1
4	H	433	RIB	C1
4	A	433	RIB	C1

5 of 57 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	505	RIB	O4-C4-C5-O5
4	A	505	RIB	C3-C4-C5-O5
3	A	503	GOL	C1-C2-C3-O3
3	A	503	GOL	O2-C2-C3-O3
3	F	501	GOL	O1-C1-C2-C3

There are no ring outliers.

10 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502	GOL	1	0
3	C	502	GOL	3	0
3	G	501	GOL	8	0
4	A	433	RIB	1	0
3	D	502	GOL	1	0
3	E	502	GOL	2	0
3	B	503	GOL	1	0
3	D	433	GOL	1	0
3	C	501	GOL	2	0
3	A	502	GOL	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	396/433 (91%)	-0.30	13 (3%) 46 45	10, 15, 27, 57	0
1	B	395/433 (91%)	-0.28	12 (3%) 50 49	11, 17, 31, 49	0
1	C	396/433 (91%)	-0.33	10 (2%) 57 56	11, 16, 29, 55	0
1	D	396/433 (91%)	-0.38	10 (2%) 57 56	10, 16, 27, 56	0
1	E	395/433 (91%)	-0.26	11 (2%) 53 51	12, 18, 30, 52	0
1	F	397/433 (91%)	-0.13	17 (4%) 35 34	13, 20, 35, 61	0
1	G	396/433 (91%)	-0.22	11 (2%) 53 51	13, 20, 32, 54	0
1	H	395/433 (91%)	-0.12	12 (3%) 50 49	12, 21, 37, 53	0
All	All	3166/3464 (91%)	-0.25	96 (3%) 50 49	10, 18, 32, 61	0

The worst 5 of 96 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	396	THR	7.8
1	F	396	THR	6.4
1	F	397	ASN	5.9
1	E	394	ASP	5.8
1	D	396	THR	5.5

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 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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	RIB	H	505	10/10	0.68	0.32	53,54,54,54	0
4	RIB	A	505	10/10	0.72	0.30	50,50,51,51	0
4	RIB	E	505	10/10	0.72	0.29	51,51,52,52	0
4	RIB	H	433	10/10	0.73	0.31	56,57,57,57	0
4	RIB	B	505	10/10	0.73	0.31	53,53,54,54	0
3	GOL	G	501	6/6	0.74	0.26	37,38,45,45	0
4	RIB	D	505	10/10	0.78	0.33	55,55,55,55	0
4	RIB	A	433	10/10	0.80	0.27	51,51,51,51	0
4	RIB	G	505	10/10	0.82	0.27	53,53,54,54	0
3	GOL	D	433	6/6	0.84	0.16	45,45,48,48	0
3	GOL	E	502	6/6	0.90	0.20	24,26,44,44	0
3	GOL	D	502	6/6	0.90	0.20	26,27,41,42	0
3	GOL	A	502	6/6	0.90	0.20	19,21,39,39	0
3	GOL	G	502	6/6	0.91	0.21	22,24,42,42	0
3	GOL	F	501	6/6	0.91	0.15	27,29,31,31	0
3	GOL	B	502	6/6	0.92	0.19	19,21,39,40	0
3	GOL	G	504	6/6	0.93	0.13	27,30,31,31	0
3	GOL	E	501	6/6	0.93	0.12	26,27,29,29	0
3	GOL	B	503	6/6	0.93	0.17	20,21,42,43	0
3	GOL	C	501	6/6	0.94	0.12	29,30,35,36	0
3	GOL	C	502	6/6	0.94	0.18	24,25,39,39	0
3	GOL	B	433	6/6	0.94	0.12	23,25,30,30	0
3	GOL	D	501	6/6	0.94	0.13	24,26,27,27	0
3	GOL	H	501	6/6	0.95	0.11	26,26,29,29	0
3	GOL	G	503	6/6	0.96	0.14	20,21,36,36	0
3	GOL	A	503	6/6	0.96	0.10	26,26,28,28	0
2	MG	H	500	1/1	0.96	0.10	25,25,25,25	0
2	MG	B	500	1/1	0.97	0.07	19,19,19,19	0
2	MG	E	500	1/1	0.97	0.08	23,23,23,23	0
2	MG	C	500	1/1	0.98	0.07	18,18,18,18	0
2	MG	A	500	1/1	0.98	0.07	19,19,19,19	0
2	MG	F	500	1/1	0.99	0.07	21,21,21,21	0
2	MG	D	500	1/1	0.99	0.03	19,19,19,19	0
2	MG	G	500	1/1	0.99	0.05	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.