



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 10:37 PM UTC

PDB ID : 3RCY / pdb_00003rcy
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 Full wwPDB X-ray Structure Validation 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

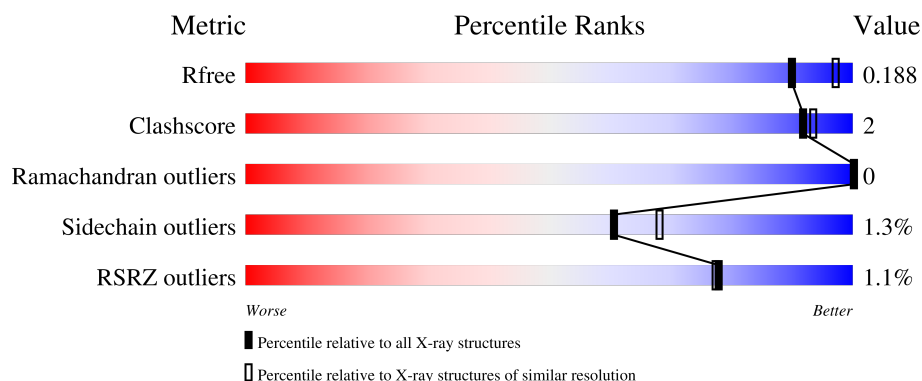
1 Overall quality at a glance

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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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 of 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	88% 9%
1	B	433	86% 5% 9%
1	C	433	87% 9%
1	D	433	88% 9%
1	E	433	86% 5% 9%

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Mol	Chain	Length	Quality of chain
1	F	433	 87% 5% 8%
1	G	433	 88% 9%
1	H	433	 90% 9%

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 (CCD ID: MG) (formula: Mg).

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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



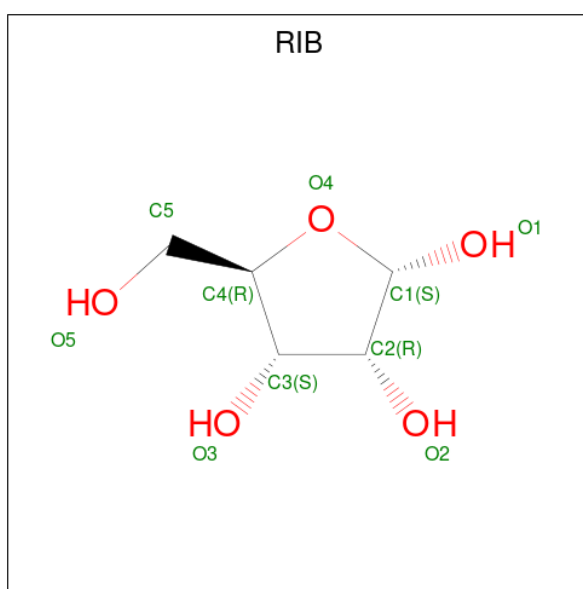
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	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 (CCD ID: 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		

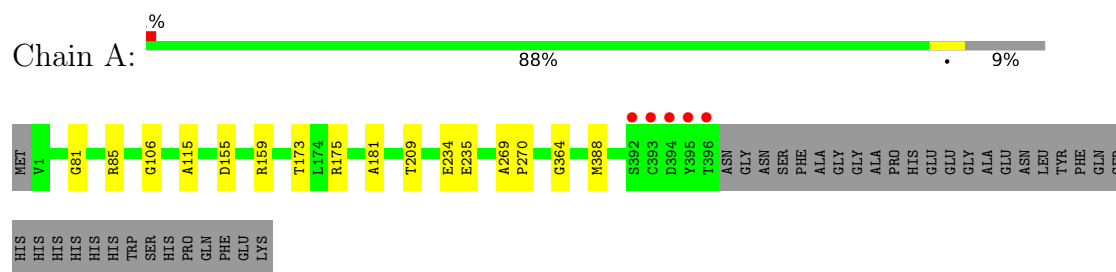
- Molecule 5 is water.

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		

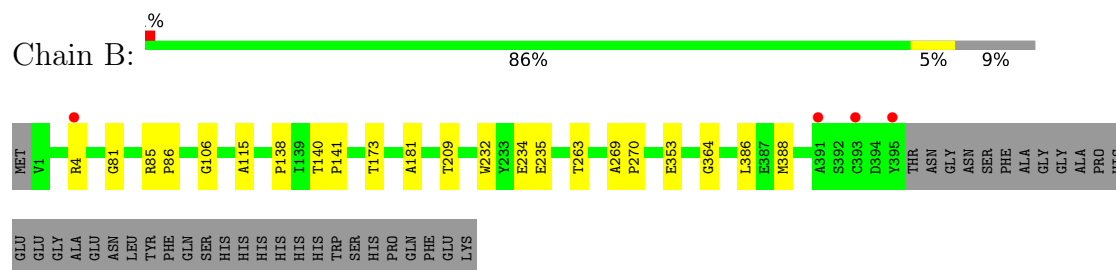
3 Residue-property plots [i](#)

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.

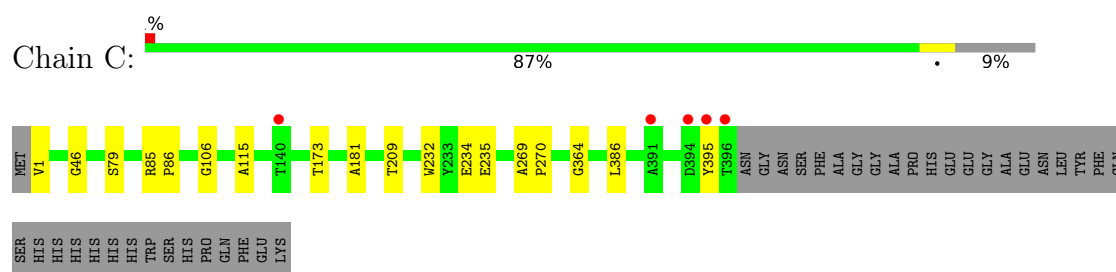
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



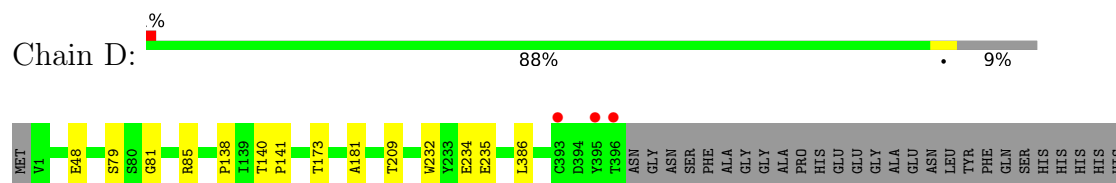
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



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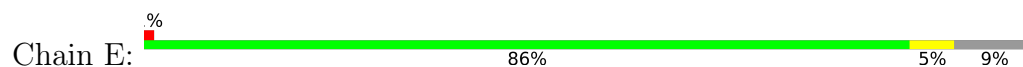


- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



HIS
TRP
SER
HIS
PRO
GLN
PHE
GLU
LYS

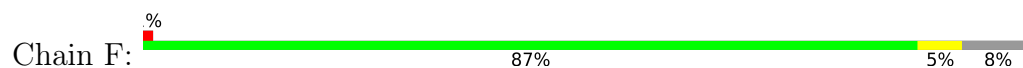
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



MET VI P13 P14 E48 R51 S79 S80 G81 R85 L105 G106 N122 T140 P141 T173 A181 T209 E234 E235 A269 P270 G364 H380 L386 A391 S392 C393 D394 Y395 THR ASN GLY ASN SER PHE ALA GLY GLY ALA PRO HIS GLU

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

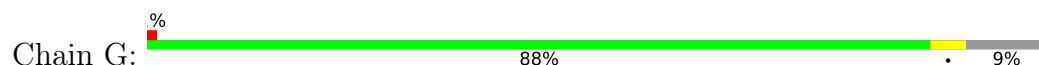
- Molecule 1: Mandelate racemase/muconate lactonizing enzyme-like protein



MET VI R4 P13 P14 G38 P47 R51 G64 P67 E68 R85 G96 T140 P141 H178 T209 W232 Y233 E234 E235 Y303 G314 L386 A391 S392 C393 D394 Y395 T396 N397 GLY ASN SER PHE ALA GLY GLY ALA PRO HIS GLU

GLY ALA ASN LEU TVR PHE GLN SER HIS 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 H178 T209 F213 W232 Y233 E234 E235 A269 P270 Y303 L384 H385 L386 E387 M388 A391 Y395 T396 ASN GLY ASN PHE SER PHE ALA GLY ALA GLY ALA PRO HIS HIS GLU GLY GLY ALA

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

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



MET VI R51 G81 R85 T173 H178 T209 H380 C393 D394 Y395 THR ASN GLY ASN SER PHE ALA GLY ALA PRO HIS HIS GLU GLY ALA ASN LEU TYR PHE GLN 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) 99.5 (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)	0.39 , 41.9	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	0.97	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

5.1 Standard geometry

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

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	0.57	0/3139	0.76	0/4280
1	B	0.55	0/3118	0.78	0/4252
1	C	0.57	1/3147 (0.0%)	0.78	2/4292 (0.0%)
1	D	0.56	0/3146	0.77	0/4290
1	E	0.53	0/3121	0.77	0/4256
1	F	0.53	0/3134	0.78	2/4272 (0.0%)
1	G	0.53	0/3168	0.77	1/4318 (0.0%)
1	H	0.53	1/3112 (0.0%)	0.77	0/4244
All	All	0.55	2/25085 (0.0%)	0.77	5/34204 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1	VAL	C-N	-7.33	1.22	1.33
1	H	1	VAL	C-N	-5.14	1.25	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	314	GLY	CA-C-N	5.76	125.38	119.56
1	F	314	GLY	C-N-CA	5.76	125.38	119.56
1	G	213	PHE	N-CA-C	5.22	118.26	109.95
1	C	46	GLY	CA-C-N	5.12	125.16	119.32
1	C	46	GLY	C-N-CA	5.12	125.16	119.32

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	3042	0	3005	11	0
1	B	3024	0	2984	11	0
1	C	3044	0	3001	10	0
1	D	3046	0	3004	8	0
1	E	3027	0	2985	16	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	3	0
3	B	18	0	24	3	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	H	234	0	0	4	0
All	All	26806	0	24128	78	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 2.

All (78) 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:F:67:PRO:C	1:F:68:GLU:CA	2.62	0.72
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
1:E:181:ALA:HB1	3:E:502:GOL:H12	1.73	0.70
1:A:159[A]:ARG:NH1	5:A:2793:HOH:O	2.24	0.69
1:A:175[B]:ARG:NH2	1:E:122:ASN:OD1	2.30	0.65
1:G:303:TYR:OH	3:G:501:GOL:H11	1.98	0.62
1:A:181:ALA:HB1	3:A:502:GOL:H12	1.81	0.62
1:D:181:ALA:HB1	3:D:502:GOL:H12	1.81	0.62
1:D:48[A]:GLU:OE2	1:D:48[A]:GLU:HA	2.02	0.59
1:C:395:TYR:O	3:C:502:GOL:O2	2.21	0.58
1:F:303:TYR:OH	3:G:501:GOL:H12	2.02	0.58
1:E:48[A]:GLU:OE1	1:E:51[A]:ARG:HD2	2.04	0.56
1:H:178:HIS:HD2	5:H:448:HOH:O	1.85	0.56
1:G:178:HIS:HD2	5:G:2625:HOH:O	1.89	0.54
1:F:47:PRO:O	1:F:51:ARG:HG3	2.08	0.54
1:F:140:THR:HB	1:F:141:PRO:HD3	1.90	0.53
1:A:269:ALA:HB3	1:A:270:PRO:HD3	1.90	0.52
1:F:386:LEU:O	1:H:81:GLY:HA2	2.10	0.51
1:G:178:HIS:HE1	5:G:1891:HOH:O	1.94	0.51
1:B:106:GLY:HA3	1:B:364:GLY:HA2	1.92	0.50
1:B:269:ALA:HB3	1:B:270:PRO:HD3	1.94	0.50
1:F:178:HIS:HD2	5:F:744:HOH:O	1.95	0.50
1:E:48[A]:GLU:CD	1:E:51[A]:ARG:HE	2.19	0.50
1:B:140:THR:HB	1:B:141:PRO:HD3	1.94	0.49
1:E:48[A]:GLU:OE1	1:E:51[A]:ARG:NE	2.46	0.49
1:A:155:ASP:OD2	1:A:159[A]:ARG:NH2	2.45	0.48
3:D:433:GOL:H31	5:H:457:HOH:O	2.13	0.48
1:C:181:ALA:HB1	3:C:502:GOL:C3	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:303:TYR:HE1	3:G:501:GOL:H31	1.80	0.47
1:H:178:HIS:HE1	5:H:466:HOH:O	1.97	0.47
1:A:234:GLU:O	1:A:235:GLU:C	2.57	0.47
1:B:81:GLY:HA2	1:D:386:LEU:O	2.15	0.47
1:A:388:MET:SD	1:C:79:SER:HB3	2.55	0.46
1:F:303:TYR:CE1	3:G:501:GOL:H31	2.50	0.46
1:E:269:ALA:HB3	1:E:270:PRO:HD3	1.98	0.46
1:F:234:GLU:O	1:F:235:GLU:C	2.59	0.46
1:G:234:GLU:O	1:G:235:GLU:C	2.59	0.46
3:B:503:GOL:H12	5:F:3010:HOH:O	2.15	0.45
1:A:81:GLY:HA2	1:C:386:LEU:O	2.16	0.45
1:E:48[A]:GLU:OE1	1:E:51[A]:ARG:CD	2.64	0.45
1:F:178:HIS:HE1	5:F:1179:HOH:O	2.00	0.45
1:B:138:PRO:HB2	1:B:141:PRO:HD2	1.99	0.45
1:E:81:GLY:HA2	1:G:386:LEU:O	2.17	0.45
1:E:140:THR:HB	1:E:141:PRO:HD3	1.99	0.45
1:E:106:GLY:HA3	1:E:364:GLY:HA2	1.99	0.45
1:E:181:ALA:HB1	3:E:502:GOL:C1	2.45	0.44
1:E:386:LEU:O	1:G:81:GLY:HA2	2.17	0.44
1:C:106:GLY:HA3	1:C:364:GLY:HA2	1.98	0.44
1:C:115:ALA:O	3:C:501:GOL:O2	2.34	0.44
1:F:38:GLY:HA3	1:F:96:GLY:O	2.17	0.44
1:G:269:ALA:HB3	1:G:270:PRO:HD3	1.99	0.44
1:E:234:GLU:O	1:E:235:GLU:C	2.60	0.43
3:C:501:GOL:H2	1:E:105:LEU:HD13	1.99	0.43
1:D:140:THR:HB	1:D:141:PRO:HD3	2.00	0.43
1:C:269:ALA:HB3	1:C:270:PRO:HD3	2.00	0.43
1:D:234:GLU:O	1:D:235:GLU:C	2.61	0.43
1:A:181:ALA:HB1	3:A:502:GOL:C1	2.47	0.43
1:A:106:GLY:HA3	1:A:364:GLY:HA2	2.00	0.43
1:F:303:TYR:CZ	3:G:501:GOL:H12	2.54	0.43
1:B:386:LEU:O	1:D:81:GLY:HA2	2.19	0.42
1:E:79:SER:HB3	1:G:388:MET:SD	2.59	0.42
1:B:115:ALA:O	3:B:433:GOL:O2	2.36	0.42
1:B:388:MET:SD	1:D:79:SER:HB3	2.59	0.42
1:F:4:ARG:NH2	1:F:64:GLY:HA2	2.34	0.42
1:F:303:TYR:CE1	3:G:501:GOL:H12	2.54	0.42
1:H:51:ARG:NH2	5:H:1313:HOH:O	2.53	0.42
1:G:21:ARG:HD2	1:G:384:LEU:O	2.20	0.42
1:A:115:ALA:O	3:A:503:GOL:O2	2.38	0.41
1:D:138:PRO:HB2	1:D:141:PRO:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:GLU:O	1:C:235:GLU:C	2.63	0.41
1:B:86:PRO:HB3	1:B:263:THR:HG23	2.03	0.41
1:E:13:PRO:HA	1:E:14:PRO:HD3	1.99	0.40
1:B:234:GLU:O	1:B:235:GLU:C	2.64	0.40
1:F:13:PRO:HA	1:F:14:PRO:HD3	1.97	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	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%)	68	75
1	B	304/332 (92%)	298 (98%)	6 (2%)	48	54
1	C	308/332 (93%)	304 (99%)	4 (1%)	61	68
1	D	307/332 (92%)	303 (99%)	4 (1%)	61	68
1	E	304/332 (92%)	301 (99%)	3 (1%)	68	75
1	F	305/332 (92%)	301 (99%)	4 (1%)	61	68
1	G	309/332 (93%)	305 (99%)	4 (1%)	61	68
1	H	303/332 (91%)	300 (99%)	3 (1%)	68	75
All	All	2446/2656 (92%)	2415 (99%)	31 (1%)	61	68

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	ARG
1	A	173	THR
1	A	209	THR
1	B	4	ARG
1	B	85	ARG
1	B	173	THR
1	B	209	THR
1	B	232	TRP
1	B	353	GLU
1	C	85	ARG
1	C	173	THR
1	C	209	THR
1	C	232	TRP
1	D	85	ARG
1	D	173	THR
1	D	209	THR
1	D	232	TRP
1	E	85	ARG
1	E	173	THR
1	E	209	THR
1	F	4	ARG
1	F	85	ARG
1	F	209	THR
1	F	232	TRP

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Mol	Chain	Res	Type
1	G	85	ARG
1	G	139	ILE
1	G	209	THR
1	G	232	TRP
1	H	85	ARG
1	H	173	THR
1	H	209	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	306	GLN
1	A	385	HIS
1	B	306	GLN
1	B	385	HIS
1	C	306	GLN
1	C	385	HIS
1	D	306	GLN
1	D	385	HIS
1	E	306	GLN
1	E	385	HIS
1	E	389	GLN
1	F	178	HIS
1	F	385	HIS
1	G	178	HIS
1	G	306	GLN
1	G	385	HIS
1	H	178	HIS
1	H	385	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 oligosaccharides 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	C	502	-	5,5,5	0.54	0	5,5,5	0.47	0
3	GOL	G	501	-	5,5,5	0.33	0	5,5,5	0.28	0
3	GOL	C	501	-	5,5,5	0.36	0	5,5,5	0.49	0
3	GOL	D	502	-	5,5,5	0.47	0	5,5,5	0.35	0
4	RIB	B	505	-	10,10,10	0.61	0	13,14,14	1.11	1 (7%)
3	GOL	E	502	-	5,5,5	0.47	0	5,5,5	0.47	0
4	RIB	H	505	-	10,10,10	0.59	0	13,14,14	1.23	1 (7%)
3	GOL	G	503	-	5,5,5	0.45	0	5,5,5	0.31	0
4	RIB	E	505	-	10,10,10	0.61	0	13,14,14	1.30	1 (7%)
3	GOL	A	502	-	5,5,5	0.48	0	5,5,5	0.50	0
4	RIB	D	505	-	10,10,10	0.64	0	13,14,14	1.15	1 (7%)
3	GOL	E	501	-	5,5,5	0.30	0	5,5,5	0.15	0
3	GOL	G	502	-	5,5,5	0.43	0	5,5,5	0.31	0
3	GOL	B	502	-	5,5,5	0.48	0	5,5,5	0.49	0
4	RIB	A	433	-	10,10,10	0.68	0	13,14,14	1.17	1 (7%)
3	GOL	D	433	-	5,5,5	0.35	0	5,5,5	0.29	0
3	GOL	D	501	-	5,5,5	0.32	0	5,5,5	0.22	0
3	GOL	F	501	-	5,5,5	0.31	0	5,5,5	0.53	0
3	GOL	G	504	-	5,5,5	0.28	0	5,5,5	0.32	0
3	GOL	H	501	-	5,5,5	0.32	0	5,5,5	0.31	0
4	RIB	A	505	-	10,10,10	0.63	0	13,14,14	1.34	2 (15%)
3	GOL	B	433	-	5,5,5	0.33	0	5,5,5	0.58	0
4	RIB	H	433	-	10,10,10	0.59	0	13,14,14	1.35	2 (15%)
3	GOL	A	503	-	5,5,5	0.40	0	5,5,5	0.37	0
3	GOL	B	503	-	5,5,5	0.44	0	5,5,5	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	RIB	G	505	-	10,10,10	0.59	0	13,14,14	1.30	2 (15%)

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	C	502	-	-	4/4/4/4	-
3	GOL	C	501	-	-	2/4/4/4	-
3	GOL	G	501	-	-	4/4/4/4	-
3	GOL	D	502	-	-	2/4/4/4	-
4	RIB	B	505	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	E	502	-	-	4/4/4/4	-
4	RIB	H	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	G	503	-	-	2/4/4/4	-
3	GOL	A	502	-	-	4/4/4/4	-
4	RIB	D	505	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	E	501	-	-	0/4/4/4	-
3	GOL	G	502	-	-	2/4/4/4	-
3	GOL	B	502	-	-	4/4/4/4	-
4	RIB	A	433	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	D	433	-	-	3/4/4/4	-
3	GOL	D	501	-	-	0/4/4/4	-
3	GOL	F	501	-	-	2/4/4/4	-
3	GOL	G	504	-	-	1/4/4/4	-
4	RIB	A	505	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	H	501	-	-	0/4/4/4	-
4	RIB	H	433	-	1/1/4/4	2/2/18/18	0/1/1/1
3	GOL	B	433	-	-	2/4/4/4	-
3	GOL	A	503	-	-	2/4/4/4	-
3	GOL	B	503	-	-	4/4/4/4	-
4	RIB	G	505	-	1/1/4/4	2/2/18/18	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	505	RIB	C1-C2-C3	3.15	106.17	102.29
4	A	505	RIB	C1-C2-C3	3.07	106.06	102.29
4	H	433	RIB	C1-C2-C3	3.04	106.03	102.29
4	D	505	RIB	C1-C2-C3	2.90	105.86	102.29
4	H	505	RIB	C1-C2-C3	2.76	105.69	102.29
4	G	505	RIB	C1-C2-C3	2.76	105.68	102.29
4	B	505	RIB	C1-C2-C3	2.68	105.58	102.29
4	A	433	RIB	C1-C2-C3	2.53	105.41	102.29
4	G	505	RIB	C5-C4-C3	-2.25	109.78	115.10
4	A	505	RIB	C5-C4-C3	-2.20	109.91	115.10
4	H	433	RIB	C5-C4-C3	-2.16	110.00	115.10

All (8) chirality outliers are listed below:

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

All (58) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	GOL	O1-C1-C2-O2
3	A	502	GOL	C1-C2-C3-O3
3	A	503	GOL	C1-C2-C3-O3
3	A	503	GOL	O2-C2-C3-O3
3	B	433	GOL	O1-C1-C2-C3
3	C	502	GOL	O1-C1-C2-C3
3	C	501	GOL	C1-C2-C3-O3
3	E	502	GOL	C1-C2-C3-O3
3	E	502	GOL	O2-C2-C3-O3
3	F	501	GOL	O1-C1-C2-C3
3	G	502	GOL	C1-C2-C3-O3
3	G	502	GOL	O2-C2-C3-O3
4	A	505	RIB	O4-C4-C5-O5
4	A	505	RIB	C3-C4-C5-O5
4	B	505	RIB	O4-C4-C5-O5
4	B	505	RIB	C3-C4-C5-O5

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Mol	Chain	Res	Type	Atoms
4	E	505	RIB	O4-C4-C5-O5
4	E	505	RIB	C3-C4-C5-O5
4	D	505	RIB	O4-C4-C5-O5
4	H	433	RIB	C3-C4-C5-O5
4	H	433	RIB	O4-C4-C5-O5
4	D	505	RIB	C3-C4-C5-O5
4	G	505	RIB	C3-C4-C5-O5
4	H	505	RIB	C3-C4-C5-O5
4	A	433	RIB	O4-C4-C5-O5
3	B	433	GOL	O1-C1-C2-O2
3	C	502	GOL	O2-C2-C3-O3
4	G	505	RIB	O4-C4-C5-O5
3	A	502	GOL	O1-C1-C2-C3
3	B	502	GOL	O1-C1-C2-C3
3	B	502	GOL	C1-C2-C3-O3
3	B	503	GOL	C1-C2-C3-O3
3	C	502	GOL	C1-C2-C3-O3
3	D	433	GOL	O1-C1-C2-C3
3	D	502	GOL	C1-C2-C3-O3
3	E	502	GOL	O1-C1-C2-C3
3	G	503	GOL	O1-C1-C2-C3
3	G	501	GOL	C1-C2-C3-O3
4	H	505	RIB	O4-C4-C5-O5
3	A	502	GOL	O2-C2-C3-O3
3	B	502	GOL	O2-C2-C3-O3
3	B	503	GOL	O2-C2-C3-O3
3	C	502	GOL	O1-C1-C2-O2
3	F	501	GOL	O1-C1-C2-O2
3	G	503	GOL	O1-C1-C2-O2
3	C	501	GOL	O2-C2-C3-O3
3	G	501	GOL	O2-C2-C3-O3
3	B	503	GOL	O1-C1-C2-C3
3	G	501	GOL	O1-C1-C2-O2
3	B	502	GOL	O1-C1-C2-O2
3	G	504	GOL	O2-C2-C3-O3
3	E	502	GOL	O1-C1-C2-O2
4	A	433	RIB	C3-C4-C5-O5
3	B	503	GOL	O1-C1-C2-O2
3	G	501	GOL	O1-C1-C2-C3
3	D	433	GOL	O2-C2-C3-O3
3	D	433	GOL	O1-C1-C2-O2
3	D	502	GOL	O2-C2-C3-O3

There are no ring outliers.

12 monomers are involved in 24 short contacts:

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

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%)	-0.58	5 (1%) 75 74	10, 15, 27, 57	4 (1%)
1	B	395/433 (91%)	-0.54	4 (1%) 79 79	10, 17, 31, 49	3 (0%)
1	C	396/433 (91%)	-0.59	5 (1%) 75 74	11, 16, 29, 55	6 (1%)
1	D	396/433 (91%)	-0.61	3 (0%) 82 82	10, 16, 27, 56	5 (1%)
1	E	395/433 (91%)	-0.52	6 (1%) 72 71	11, 18, 30, 52	3 (0%)
1	F	397/433 (91%)	-0.41	6 (1%) 72 71	12, 20, 35, 61	3 (0%)
1	G	396/433 (91%)	-0.48	3 (0%) 82 82	11, 20, 32, 54	7 (1%)
1	H	395/433 (91%)	-0.42	3 (0%) 82 82	12, 21, 37, 53	2 (0%)
All	All	3166/3464 (91%)	-0.52	35 (1%) 78 77	10, 18, 32, 61	33 (1%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	395	TYR	5.1
1	A	395	TYR	4.9
1	A	396	THR	4.5
1	E	395	TYR	3.9
1	D	396	THR	3.9
1	G	396	THR	3.8
1	A	393	CYS	3.6
1	C	396	THR	3.5
1	F	392	SER	3.4
1	H	395	TYR	3.3
1	F	396	THR	3.2
1	A	392	SER	3.2
1	E	394	ASP	3.1
1	H	393	CYS	3.1
1	E	393	CYS	3.0
1	E	392	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	395	TYR	2.9
1	E	391	ALA	2.9
1	F	391	ALA	2.8
1	A	394	ASP	2.8
1	C	391	ALA	2.7
1	D	395	TYR	2.6
1	E	380	HIS	2.6
1	G	391	ALA	2.5
1	F	393	CYS	2.4
1	B	4	ARG	2.4
1	G	395	TYR	2.4
1	C	394	ASP	2.4
1	H	380	HIS	2.3
1	F	395	TYR	2.2
1	C	140	THR	2.2
1	B	393	CYS	2.2
1	D	393	CYS	2.1
1	F	140	THR	2.1
1	B	391	ALA	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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($\text{\AA}^2$)	Q<0.9
4	RIB	H	433	10/10	0.64	0.23	56,57,57,57	0
4	RIB	E	505	10/10	0.65	0.21	51,51,52,52	0
4	RIB	H	505	10/10	0.66	0.23	53,54,54,54	0
4	RIB	D	505	10/10	0.70	0.24	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	RIB	B	505	10/10	0.71	0.25	53,53,54,54	0
4	RIB	G	505	10/10	0.72	0.21	53,53,54,54	0
4	RIB	A	505	10/10	0.74	0.22	50,50,51,51	0
4	RIB	A	433	10/10	0.77	0.23	51,51,51,51	0
3	GOL	G	501	6/6	0.78	0.19	37,38,45,45	0
3	GOL	D	433	6/6	0.82	0.13	45,45,48,48	0
3	GOL	F	501	6/6	0.88	0.11	27,29,31,31	0
3	GOL	A	502	6/6	0.90	0.13	19,21,39,39	0
3	GOL	E	502	6/6	0.90	0.13	24,26,44,44	0
3	GOL	E	501	6/6	0.91	0.09	26,27,29,29	0
3	GOL	C	501	6/6	0.91	0.09	29,30,35,36	0
3	GOL	D	502	6/6	0.91	0.14	26,27,41,42	0
3	GOL	G	502	6/6	0.92	0.11	22,24,42,42	0
3	GOL	G	504	6/6	0.92	0.09	27,30,31,31	0
3	GOL	C	502	6/6	0.92	0.12	24,25,39,39	0
3	GOL	B	433	6/6	0.92	0.09	23,25,30,30	0
3	GOL	D	501	6/6	0.92	0.09	24,26,27,27	0
3	GOL	B	502	6/6	0.93	0.13	19,21,39,40	0
3	GOL	B	503	6/6	0.93	0.12	20,21,42,43	0
3	GOL	H	501	6/6	0.94	0.09	26,26,29,29	0
3	GOL	G	503	6/6	0.94	0.09	20,21,36,36	0
3	GOL	A	503	6/6	0.94	0.06	26,26,28,28	0
2	MG	E	500	1/1	0.95	0.06	23,23,23,23	0
2	MG	C	500	1/1	0.96	0.04	18,18,18,18	0
2	MG	B	500	1/1	0.97	0.06	19,19,19,19	0
2	MG	H	500	1/1	0.97	0.06	25,25,25,25	0
2	MG	G	500	1/1	0.98	0.03	21,21,21,21	0
2	MG	A	500	1/1	0.99	0.05	19,19,19,19	0
2	MG	F	500	1/1	0.99	0.06	21,21,21,21	0
2	MG	D	500	1/1	0.99	0.02	19,19,19,19	0

6.5 Other polymers ⓘ

There are no such residues in this entry.