



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 08:48 am GMT

PDB ID : 3MQT
Title : Crystal structure of a mandelate racemase/muconate lactonizing enzyme from *Shewanella pealeana*
Authors : Agarwal, R.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2010-04-28
Resolution : 2.10 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

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

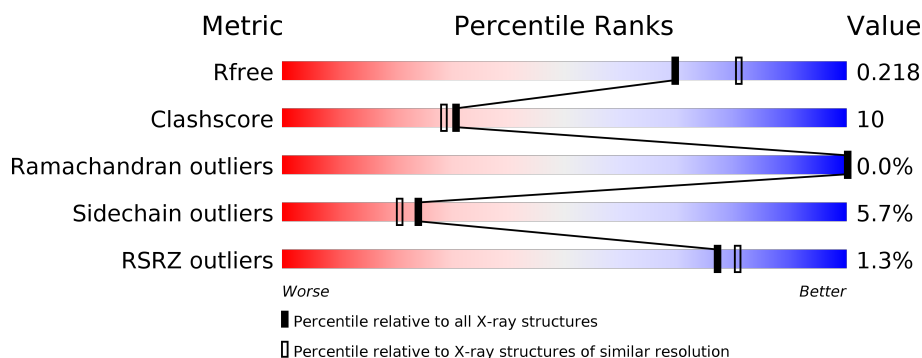
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.



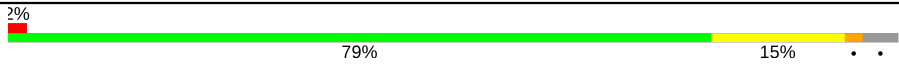

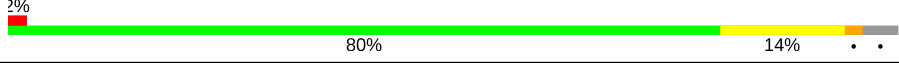
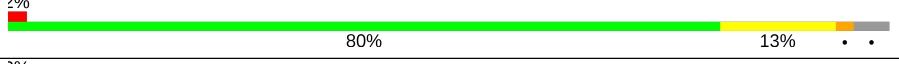

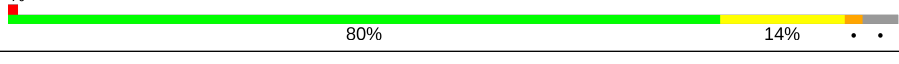
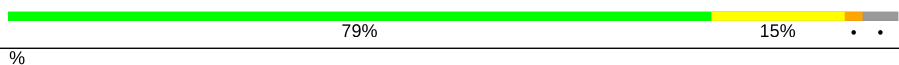

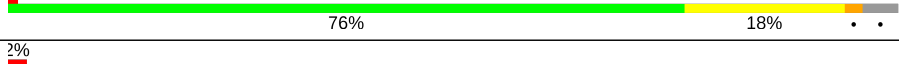






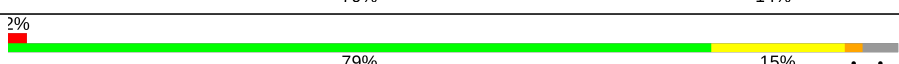
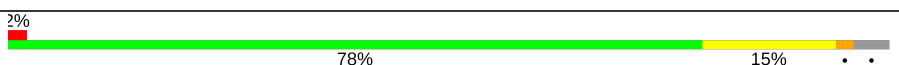

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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. 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	394	<div> <div>78%</div> <div>15%</div> <div>• •</div> </div>
1	B	394	<div> <div>%</div> <div>76%</div> <div>18%</div> <div>• •</div> </div>
1	C	394	<div> <div>%</div> <div>78%</div> <div>16%</div> <div>• •</div> </div>
1	D	394	<div> <div>%</div> <div>74%</div> <div>19%</div> <div>• •</div> </div>
1	E	394	<div> <div>%</div> <div>80%</div> <div>14%</div> <div>• •</div> </div>
1	F	394	<div> <div>2%</div> <div>76%</div> <div>17%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	394	
1	H	394	
1	I	394	
1	J	394	
1	K	394	
1	L	394	
1	M	394	
1	N	394	
1	O	394	
1	P	394	
1	Q	394	
1	R	394	
1	S	394	
1	T	394	
1	U	394	
1	V	394	
1	W	394	
1	X	394	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MG	E	395	-	-	-	X
2	MG	F	1460	-	-	-	X
2	MG	G	395	-	-	-	X
2	MG	K	683	-	-	-	X
2	MG	U	974	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 72942 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 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	0	0
			2978	1902	501	556	19			
1	B	377	Total	C	N	O	S	0	0	0
			2978	1902	501	556	19			
1	C	377	Total	C	N	O	S	0	0	0
			2978	1902	501	556	19			
1	D	377	Total	C	N	O	S	0	0	0
			2978	1902	501	556	19			
1	E	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	F	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	G	377	Total	C	N	O	S	0	0	0
			2978	1902	501	556	19			
1	H	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	I	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	J	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	K	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	L	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	M	377	Total	C	N	O	S	0	0	0
			2978	1902	501	556	19			
1	N	377	Total	C	N	O	S	0	0	0
			2978	1902	501	556	19			
1	O	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	P	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	R	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	S	377	Total	C	N	O	S	0	0	0
			2978	1902	501	556	19			
1	T	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	U	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	V	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	W	378	Total	C	N	O	S	0	0	0
			2983	1905	502	557	19			
1	X	377	Total	C	N	O	S	0	0	0
			2978	1902	501	556	19			

There are 264 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP A8H7M5
A	2	SER	-	expression tag	UNP A8H7M5
A	3	LEU	-	expression tag	UNP A8H7M5
A	387	GLU	-	expression tag	UNP A8H7M5
A	388	GLY	-	expression tag	UNP A8H7M5
A	389	HIS	-	expression tag	UNP A8H7M5
A	390	HIS	-	expression tag	UNP A8H7M5
A	391	HIS	-	expression tag	UNP A8H7M5
A	392	HIS	-	expression tag	UNP A8H7M5
A	393	HIS	-	expression tag	UNP A8H7M5
A	394	HIS	-	expression tag	UNP A8H7M5
B	1	MET	-	expression tag	UNP A8H7M5
B	2	SER	-	expression tag	UNP A8H7M5
B	3	LEU	-	expression tag	UNP A8H7M5
B	387	GLU	-	expression tag	UNP A8H7M5
B	388	GLY	-	expression tag	UNP A8H7M5
B	389	HIS	-	expression tag	UNP A8H7M5
B	390	HIS	-	expression tag	UNP A8H7M5
B	391	HIS	-	expression tag	UNP A8H7M5
B	392	HIS	-	expression tag	UNP A8H7M5
B	393	HIS	-	expression tag	UNP A8H7M5
B	394	HIS	-	expression tag	UNP A8H7M5
C	1	MET	-	expression tag	UNP A8H7M5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	2	SER	-	expression tag	UNP A8H7M5
C	3	LEU	-	expression tag	UNP A8H7M5
C	387	GLU	-	expression tag	UNP A8H7M5
C	388	GLY	-	expression tag	UNP A8H7M5
C	389	HIS	-	expression tag	UNP A8H7M5
C	390	HIS	-	expression tag	UNP A8H7M5
C	391	HIS	-	expression tag	UNP A8H7M5
C	392	HIS	-	expression tag	UNP A8H7M5
C	393	HIS	-	expression tag	UNP A8H7M5
C	394	HIS	-	expression tag	UNP A8H7M5
D	1	MET	-	expression tag	UNP A8H7M5
D	2	SER	-	expression tag	UNP A8H7M5
D	3	LEU	-	expression tag	UNP A8H7M5
D	387	GLU	-	expression tag	UNP A8H7M5
D	388	GLY	-	expression tag	UNP A8H7M5
D	389	HIS	-	expression tag	UNP A8H7M5
D	390	HIS	-	expression tag	UNP A8H7M5
D	391	HIS	-	expression tag	UNP A8H7M5
D	392	HIS	-	expression tag	UNP A8H7M5
D	393	HIS	-	expression tag	UNP A8H7M5
D	394	HIS	-	expression tag	UNP A8H7M5
E	1	MET	-	expression tag	UNP A8H7M5
E	2	SER	-	expression tag	UNP A8H7M5
E	3	LEU	-	expression tag	UNP A8H7M5
E	387	GLU	-	expression tag	UNP A8H7M5
E	388	GLY	-	expression tag	UNP A8H7M5
E	389	HIS	-	expression tag	UNP A8H7M5
E	390	HIS	-	expression tag	UNP A8H7M5
E	391	HIS	-	expression tag	UNP A8H7M5
E	392	HIS	-	expression tag	UNP A8H7M5
E	393	HIS	-	expression tag	UNP A8H7M5
E	394	HIS	-	expression tag	UNP A8H7M5
F	1	MET	-	expression tag	UNP A8H7M5
F	2	SER	-	expression tag	UNP A8H7M5
F	3	LEU	-	expression tag	UNP A8H7M5
F	387	GLU	-	expression tag	UNP A8H7M5
F	388	GLY	-	expression tag	UNP A8H7M5
F	389	HIS	-	expression tag	UNP A8H7M5
F	390	HIS	-	expression tag	UNP A8H7M5
F	391	HIS	-	expression tag	UNP A8H7M5
F	392	HIS	-	expression tag	UNP A8H7M5
F	393	HIS	-	expression tag	UNP A8H7M5

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Chain	Residue	Modelled	Actual	Comment	Reference
F	394	HIS	-	expression tag	UNP A8H7M5
G	1	MET	-	expression tag	UNP A8H7M5
G	2	SER	-	expression tag	UNP A8H7M5
G	3	LEU	-	expression tag	UNP A8H7M5
G	387	GLU	-	expression tag	UNP A8H7M5
G	388	GLY	-	expression tag	UNP A8H7M5
G	389	HIS	-	expression tag	UNP A8H7M5
G	390	HIS	-	expression tag	UNP A8H7M5
G	391	HIS	-	expression tag	UNP A8H7M5
G	392	HIS	-	expression tag	UNP A8H7M5
G	393	HIS	-	expression tag	UNP A8H7M5
G	394	HIS	-	expression tag	UNP A8H7M5
H	1	MET	-	expression tag	UNP A8H7M5
H	2	SER	-	expression tag	UNP A8H7M5
H	3	LEU	-	expression tag	UNP A8H7M5
H	387	GLU	-	expression tag	UNP A8H7M5
H	388	GLY	-	expression tag	UNP A8H7M5
H	389	HIS	-	expression tag	UNP A8H7M5
H	390	HIS	-	expression tag	UNP A8H7M5
H	391	HIS	-	expression tag	UNP A8H7M5
H	392	HIS	-	expression tag	UNP A8H7M5
H	393	HIS	-	expression tag	UNP A8H7M5
H	394	HIS	-	expression tag	UNP A8H7M5
I	1	MET	-	expression tag	UNP A8H7M5
I	2	SER	-	expression tag	UNP A8H7M5
I	3	LEU	-	expression tag	UNP A8H7M5
I	387	GLU	-	expression tag	UNP A8H7M5
I	388	GLY	-	expression tag	UNP A8H7M5
I	389	HIS	-	expression tag	UNP A8H7M5
I	390	HIS	-	expression tag	UNP A8H7M5
I	391	HIS	-	expression tag	UNP A8H7M5
I	392	HIS	-	expression tag	UNP A8H7M5
I	393	HIS	-	expression tag	UNP A8H7M5
I	394	HIS	-	expression tag	UNP A8H7M5
J	1	MET	-	expression tag	UNP A8H7M5
J	2	SER	-	expression tag	UNP A8H7M5
J	3	LEU	-	expression tag	UNP A8H7M5
J	387	GLU	-	expression tag	UNP A8H7M5
J	388	GLY	-	expression tag	UNP A8H7M5
J	389	HIS	-	expression tag	UNP A8H7M5
J	390	HIS	-	expression tag	UNP A8H7M5
J	391	HIS	-	expression tag	UNP A8H7M5

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Chain	Residue	Modelled	Actual	Comment	Reference
J	392	HIS	-	expression tag	UNP A8H7M5
J	393	HIS	-	expression tag	UNP A8H7M5
J	394	HIS	-	expression tag	UNP A8H7M5
K	1	MET	-	expression tag	UNP A8H7M5
K	2	SER	-	expression tag	UNP A8H7M5
K	3	LEU	-	expression tag	UNP A8H7M5
K	387	GLU	-	expression tag	UNP A8H7M5
K	388	GLY	-	expression tag	UNP A8H7M5
K	389	HIS	-	expression tag	UNP A8H7M5
K	390	HIS	-	expression tag	UNP A8H7M5
K	391	HIS	-	expression tag	UNP A8H7M5
K	392	HIS	-	expression tag	UNP A8H7M5
K	393	HIS	-	expression tag	UNP A8H7M5
K	394	HIS	-	expression tag	UNP A8H7M5
L	1	MET	-	expression tag	UNP A8H7M5
L	2	SER	-	expression tag	UNP A8H7M5
L	3	LEU	-	expression tag	UNP A8H7M5
L	387	GLU	-	expression tag	UNP A8H7M5
L	388	GLY	-	expression tag	UNP A8H7M5
L	389	HIS	-	expression tag	UNP A8H7M5
L	390	HIS	-	expression tag	UNP A8H7M5
L	391	HIS	-	expression tag	UNP A8H7M5
L	392	HIS	-	expression tag	UNP A8H7M5
L	393	HIS	-	expression tag	UNP A8H7M5
L	394	HIS	-	expression tag	UNP A8H7M5
M	1	MET	-	expression tag	UNP A8H7M5
M	2	SER	-	expression tag	UNP A8H7M5
M	3	LEU	-	expression tag	UNP A8H7M5
M	387	GLU	-	expression tag	UNP A8H7M5
M	388	GLY	-	expression tag	UNP A8H7M5
M	389	HIS	-	expression tag	UNP A8H7M5
M	390	HIS	-	expression tag	UNP A8H7M5
M	391	HIS	-	expression tag	UNP A8H7M5
M	392	HIS	-	expression tag	UNP A8H7M5
M	393	HIS	-	expression tag	UNP A8H7M5
M	394	HIS	-	expression tag	UNP A8H7M5
N	1	MET	-	expression tag	UNP A8H7M5
N	2	SER	-	expression tag	UNP A8H7M5
N	3	LEU	-	expression tag	UNP A8H7M5
N	387	GLU	-	expression tag	UNP A8H7M5
N	388	GLY	-	expression tag	UNP A8H7M5
N	389	HIS	-	expression tag	UNP A8H7M5

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Chain	Residue	Modelled	Actual	Comment	Reference
N	390	HIS	-	expression tag	UNP A8H7M5
N	391	HIS	-	expression tag	UNP A8H7M5
N	392	HIS	-	expression tag	UNP A8H7M5
N	393	HIS	-	expression tag	UNP A8H7M5
N	394	HIS	-	expression tag	UNP A8H7M5
O	1	MET	-	expression tag	UNP A8H7M5
O	2	SER	-	expression tag	UNP A8H7M5
O	3	LEU	-	expression tag	UNP A8H7M5
O	387	GLU	-	expression tag	UNP A8H7M5
O	388	GLY	-	expression tag	UNP A8H7M5
O	389	HIS	-	expression tag	UNP A8H7M5
O	390	HIS	-	expression tag	UNP A8H7M5
O	391	HIS	-	expression tag	UNP A8H7M5
O	392	HIS	-	expression tag	UNP A8H7M5
O	393	HIS	-	expression tag	UNP A8H7M5
O	394	HIS	-	expression tag	UNP A8H7M5
P	1	MET	-	expression tag	UNP A8H7M5
P	2	SER	-	expression tag	UNP A8H7M5
P	3	LEU	-	expression tag	UNP A8H7M5
P	387	GLU	-	expression tag	UNP A8H7M5
P	388	GLY	-	expression tag	UNP A8H7M5
P	389	HIS	-	expression tag	UNP A8H7M5
P	390	HIS	-	expression tag	UNP A8H7M5
P	391	HIS	-	expression tag	UNP A8H7M5
P	392	HIS	-	expression tag	UNP A8H7M5
P	393	HIS	-	expression tag	UNP A8H7M5
P	394	HIS	-	expression tag	UNP A8H7M5
Q	1	MET	-	expression tag	UNP A8H7M5
Q	2	SER	-	expression tag	UNP A8H7M5
Q	3	LEU	-	expression tag	UNP A8H7M5
Q	387	GLU	-	expression tag	UNP A8H7M5
Q	388	GLY	-	expression tag	UNP A8H7M5
Q	389	HIS	-	expression tag	UNP A8H7M5
Q	390	HIS	-	expression tag	UNP A8H7M5
Q	391	HIS	-	expression tag	UNP A8H7M5
Q	392	HIS	-	expression tag	UNP A8H7M5
Q	393	HIS	-	expression tag	UNP A8H7M5
Q	394	HIS	-	expression tag	UNP A8H7M5
R	1	MET	-	expression tag	UNP A8H7M5
R	2	SER	-	expression tag	UNP A8H7M5
R	3	LEU	-	expression tag	UNP A8H7M5
R	387	GLU	-	expression tag	UNP A8H7M5

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Chain	Residue	Modelled	Actual	Comment	Reference
R	388	GLY	-	expression tag	UNP A8H7M5
R	389	HIS	-	expression tag	UNP A8H7M5
R	390	HIS	-	expression tag	UNP A8H7M5
R	391	HIS	-	expression tag	UNP A8H7M5
R	392	HIS	-	expression tag	UNP A8H7M5
R	393	HIS	-	expression tag	UNP A8H7M5
R	394	HIS	-	expression tag	UNP A8H7M5
S	1	MET	-	expression tag	UNP A8H7M5
S	2	SER	-	expression tag	UNP A8H7M5
S	3	LEU	-	expression tag	UNP A8H7M5
S	387	GLU	-	expression tag	UNP A8H7M5
S	388	GLY	-	expression tag	UNP A8H7M5
S	389	HIS	-	expression tag	UNP A8H7M5
S	390	HIS	-	expression tag	UNP A8H7M5
S	391	HIS	-	expression tag	UNP A8H7M5
S	392	HIS	-	expression tag	UNP A8H7M5
S	393	HIS	-	expression tag	UNP A8H7M5
S	394	HIS	-	expression tag	UNP A8H7M5
T	1	MET	-	expression tag	UNP A8H7M5
T	2	SER	-	expression tag	UNP A8H7M5
T	3	LEU	-	expression tag	UNP A8H7M5
T	387	GLU	-	expression tag	UNP A8H7M5
T	388	GLY	-	expression tag	UNP A8H7M5
T	389	HIS	-	expression tag	UNP A8H7M5
T	390	HIS	-	expression tag	UNP A8H7M5
T	391	HIS	-	expression tag	UNP A8H7M5
T	392	HIS	-	expression tag	UNP A8H7M5
T	393	HIS	-	expression tag	UNP A8H7M5
T	394	HIS	-	expression tag	UNP A8H7M5
U	1	MET	-	expression tag	UNP A8H7M5
U	2	SER	-	expression tag	UNP A8H7M5
U	3	LEU	-	expression tag	UNP A8H7M5
U	387	GLU	-	expression tag	UNP A8H7M5
U	388	GLY	-	expression tag	UNP A8H7M5
U	389	HIS	-	expression tag	UNP A8H7M5
U	390	HIS	-	expression tag	UNP A8H7M5
U	391	HIS	-	expression tag	UNP A8H7M5
U	392	HIS	-	expression tag	UNP A8H7M5
U	393	HIS	-	expression tag	UNP A8H7M5
U	394	HIS	-	expression tag	UNP A8H7M5
V	1	MET	-	expression tag	UNP A8H7M5
V	2	SER	-	expression tag	UNP A8H7M5

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Chain	Residue	Modelled	Actual	Comment	Reference
V	3	LEU	-	expression tag	UNP A8H7M5
V	387	GLU	-	expression tag	UNP A8H7M5
V	388	GLY	-	expression tag	UNP A8H7M5
V	389	HIS	-	expression tag	UNP A8H7M5
V	390	HIS	-	expression tag	UNP A8H7M5
V	391	HIS	-	expression tag	UNP A8H7M5
V	392	HIS	-	expression tag	UNP A8H7M5
V	393	HIS	-	expression tag	UNP A8H7M5
V	394	HIS	-	expression tag	UNP A8H7M5
W	1	MET	-	expression tag	UNP A8H7M5
W	2	SER	-	expression tag	UNP A8H7M5
W	3	LEU	-	expression tag	UNP A8H7M5
W	387	GLU	-	expression tag	UNP A8H7M5
W	388	GLY	-	expression tag	UNP A8H7M5
W	389	HIS	-	expression tag	UNP A8H7M5
W	390	HIS	-	expression tag	UNP A8H7M5
W	391	HIS	-	expression tag	UNP A8H7M5
W	392	HIS	-	expression tag	UNP A8H7M5
W	393	HIS	-	expression tag	UNP A8H7M5
W	394	HIS	-	expression tag	UNP A8H7M5
X	1	MET	-	expression tag	UNP A8H7M5
X	2	SER	-	expression tag	UNP A8H7M5
X	3	LEU	-	expression tag	UNP A8H7M5
X	387	GLU	-	expression tag	UNP A8H7M5
X	388	GLY	-	expression tag	UNP A8H7M5
X	389	HIS	-	expression tag	UNP A8H7M5
X	390	HIS	-	expression tag	UNP A8H7M5
X	391	HIS	-	expression tag	UNP A8H7M5
X	392	HIS	-	expression tag	UNP A8H7M5
X	393	HIS	-	expression tag	UNP A8H7M5
X	394	HIS	-	expression tag	UNP A8H7M5

- 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	K	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	1	Total 1	Mg 1	0	0
2	V	1	Total 1	Mg 1	0	0
2	W	1	Total 1	Mg 1	0	0
2	A	1	Total 1	Mg 1	0	0
2	U	1	Total 1	Mg 1	0	0
2	X	1	Total 1	Mg 1	0	0
2	L	1	Total 1	Mg 1	0	0
2	F	1	Total 1	Mg 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	64	Total 64	O 64	0	0
3	B	58	Total 58	O 58	0	0
3	C	73	Total 73	O 73	0	0
3	D	67	Total 67	O 67	0	0
3	E	62	Total 62	O 62	0	0
3	F	59	Total 59	O 59	0	0
3	G	58	Total 58	O 58	0	0
3	H	70	Total 70	O 70	0	0
3	I	54	Total 54	O 54	0	0
3	J	52	Total 52	O 52	0	0
3	K	53	Total 53	O 53	0	0

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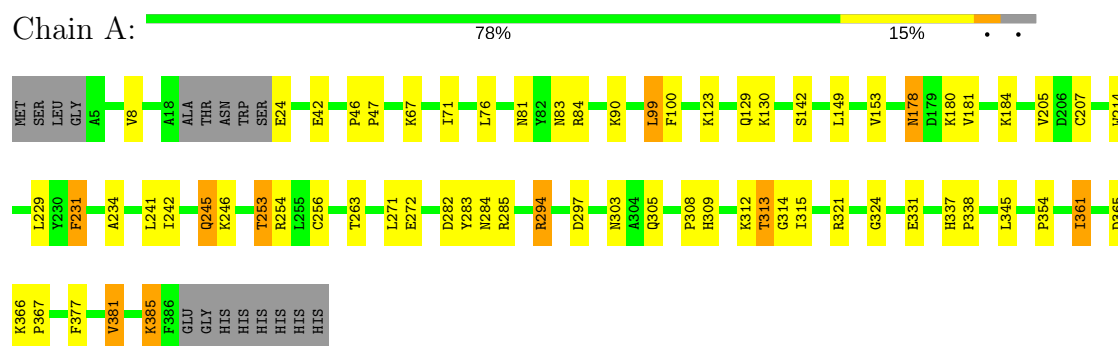
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	58	Total 58	O 58	0	0
3	M	55	Total 55	O 55	0	0
3	N	51	Total 51	O 51	0	0
3	O	52	Total 52	O 52	0	0
3	P	53	Total 53	O 53	0	0
3	Q	55	Total 55	O 55	0	0
3	R	56	Total 56	O 56	0	0
3	S	54	Total 54	O 54	0	0
3	T	58	Total 58	O 58	0	0
3	U	54	Total 54	O 54	0	0
3	V	59	Total 59	O 59	0	0
3	W	55	Total 55	O 55	0	0
3	X	53	Total 53	O 53	0	0

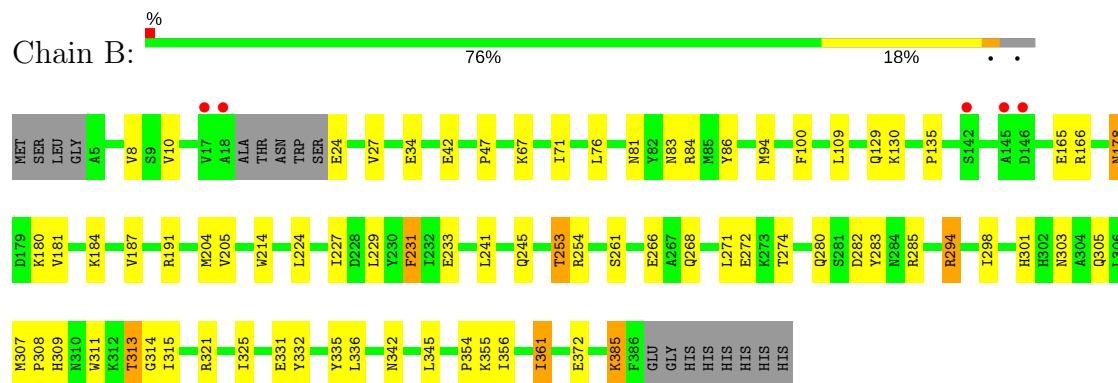
3 Residue-property plots [i](#)

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.

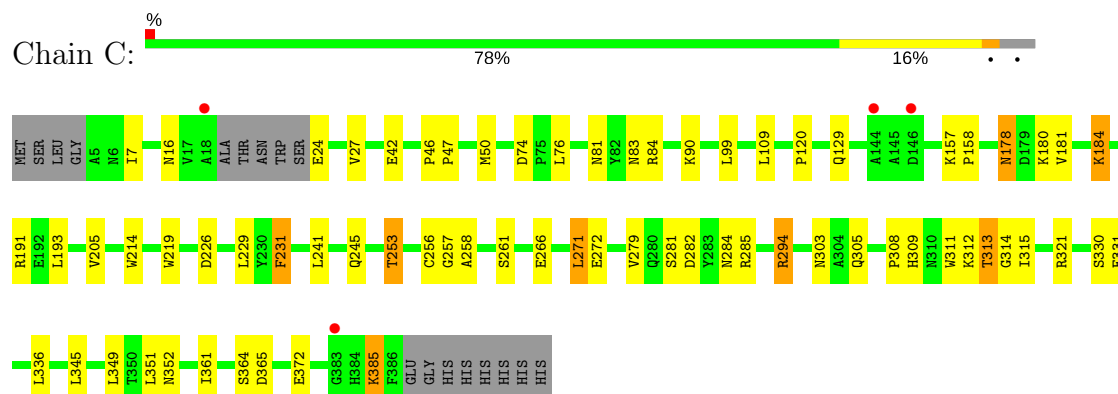
- Molecule 1: Mandelate racemase/muconate lactonizing protein



- Molecule 1: Mandelate racemase/muconate lactonizing protein



- Molecule 1: Mandelate racemase/muconate lactonizing protein

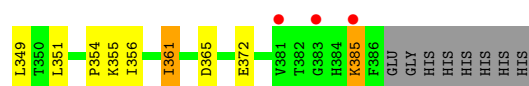


- Chain D: 

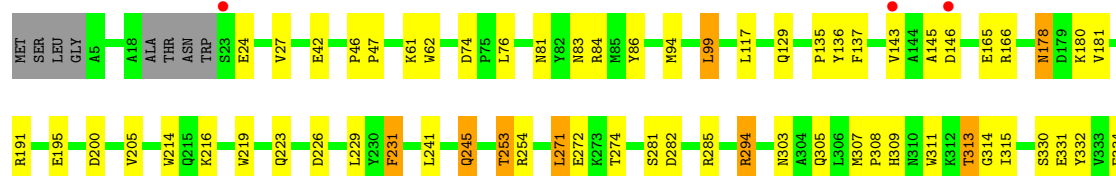
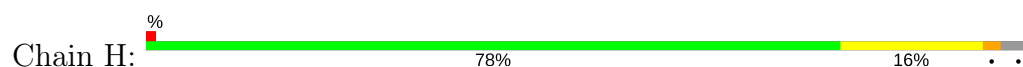
- Chain E:

- [illegible]

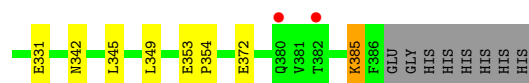
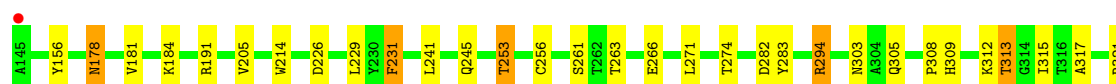
- Chain G:
-
- 2% 79% 15% • •
- MET SER LEU GLY A5 A18 ALA THR ASN TRP SER E24 E42 K67 I71 L76 N81 N83 R84 M85 Y86 M94 L99 P120 A121 Y122 K123 L124 M125 Q129 A144 A145 E165 K169 P177 N178 V181 V205 L208 W214
- L229 Y230 F231 L236 L241 H244 Q245 T263 C266 S261 E266 A267 L271 E272 K273 T274 V279 D282 Y283 T284 R285 R294 N303 A304 Q305 P308 H309 N310 W311 K312 T313 G314 I315 R321 V326 S330 E331 L336 N342 L345



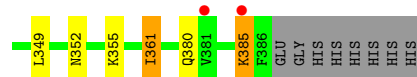
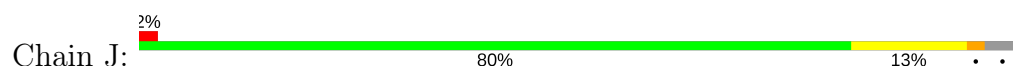
- Molecule 1: Mandelate racemase/muconate lactonizing protein



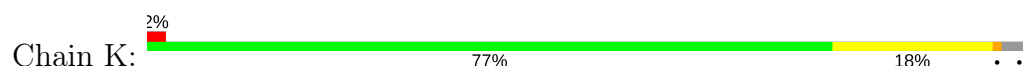
- Molecule 1: Mandelate racemase/muconate lactonizing protein

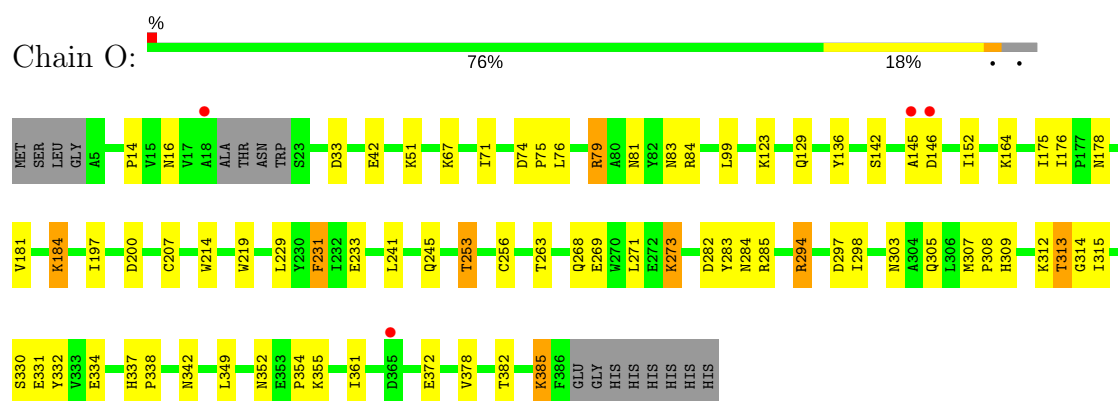


- Molecule 1: Mandelate racemase/muconate lactonizing protein

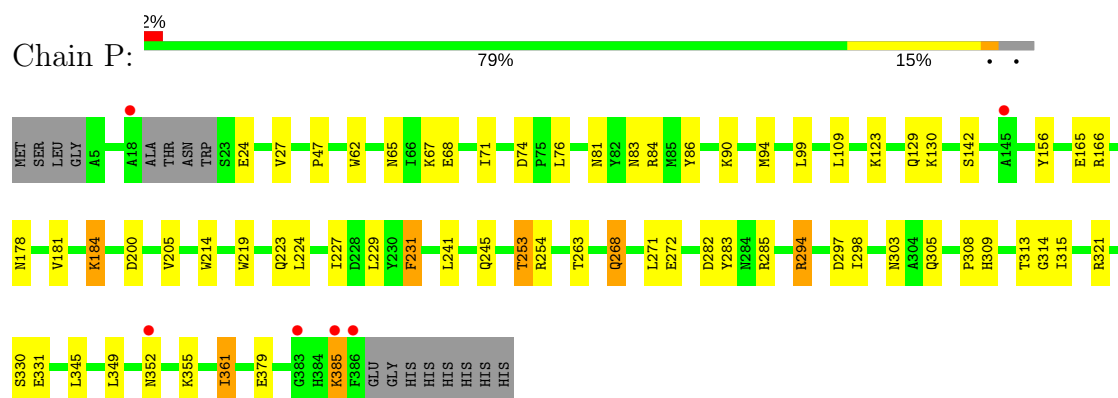


- Molecule 1: Mandelate racemase/muconate lactonizing protein

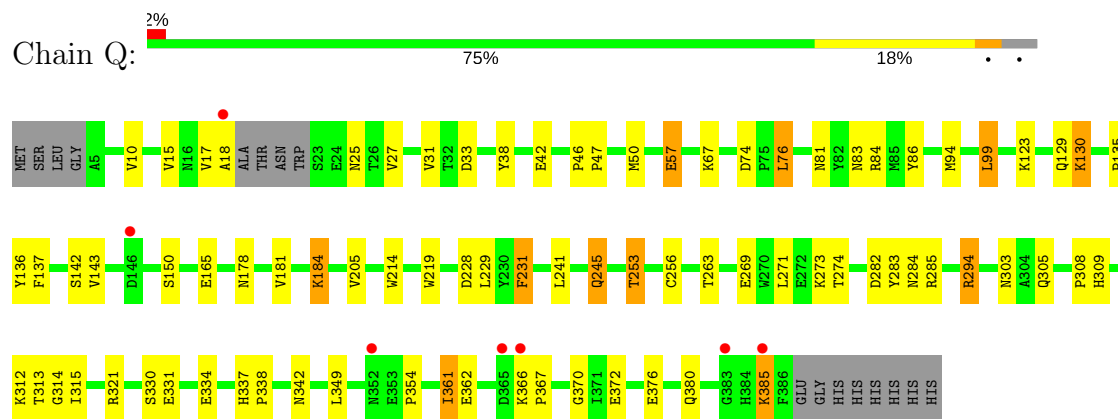




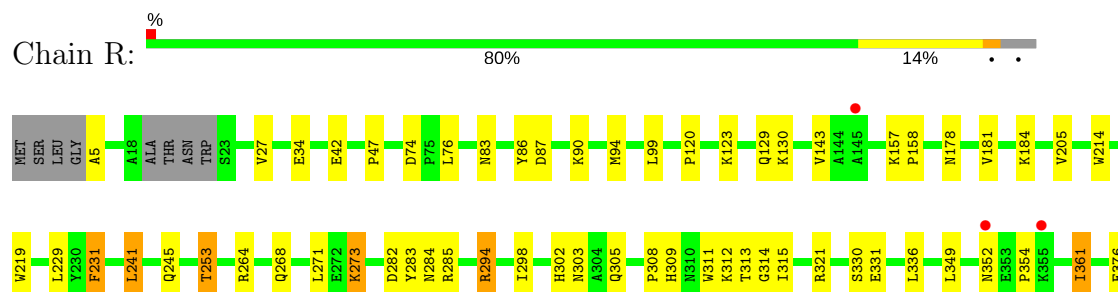
- Molecule 1: Mandelate racemase/muconate lactonizing protein

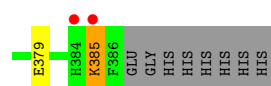


- Molecule 1: Mandelate racemase/muconate lactonizing protein

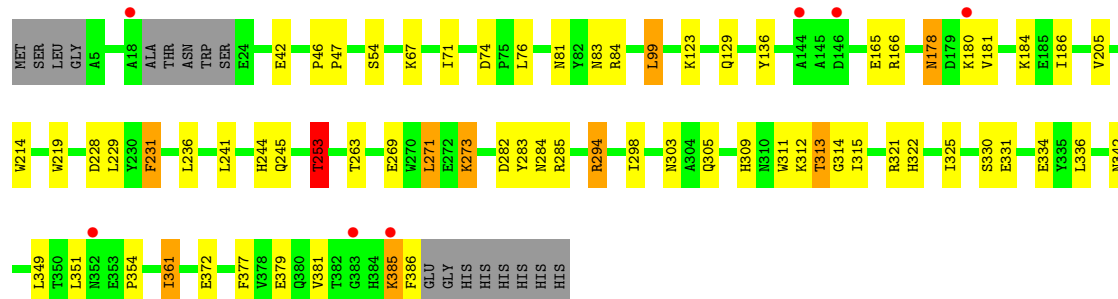
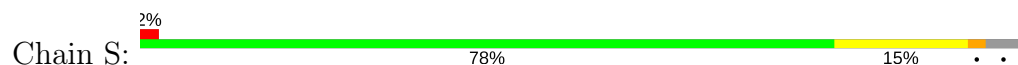


- Molecule 1: Mandelate racemase/muconate lactonizing protein

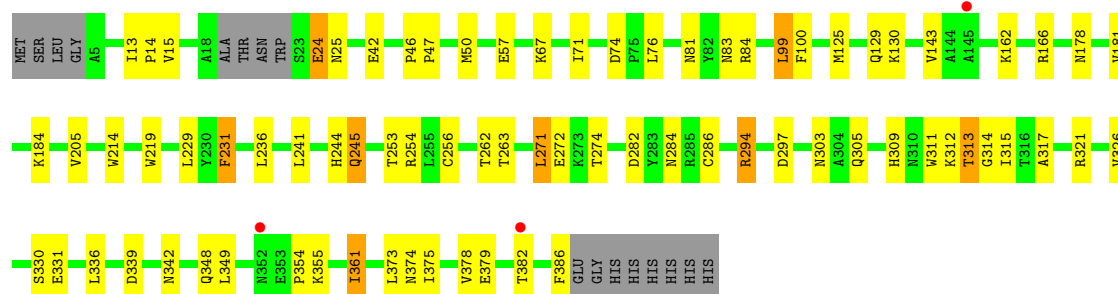
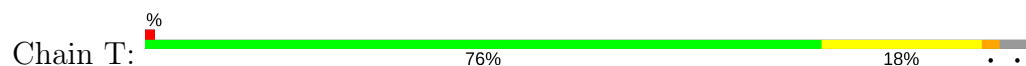




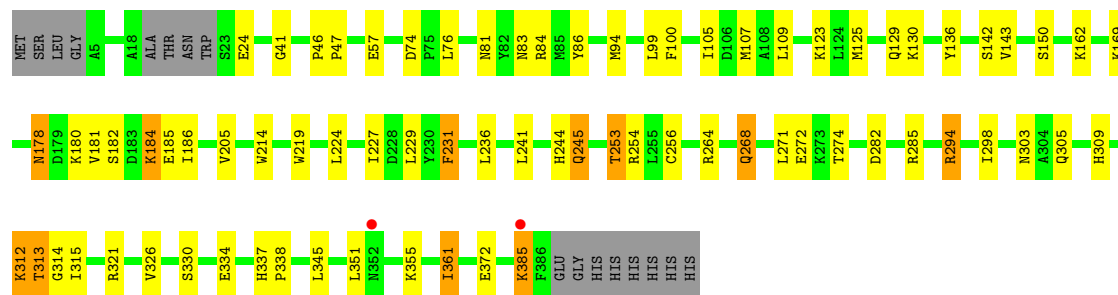
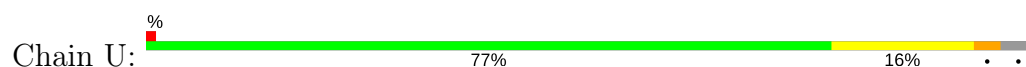
- Molecule 1: Mandelate racemase/muconate lactonizing protein



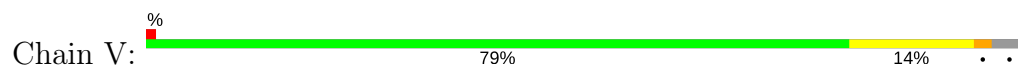
- Molecule 1: Mandelate racemase/muconate lactonizing protein

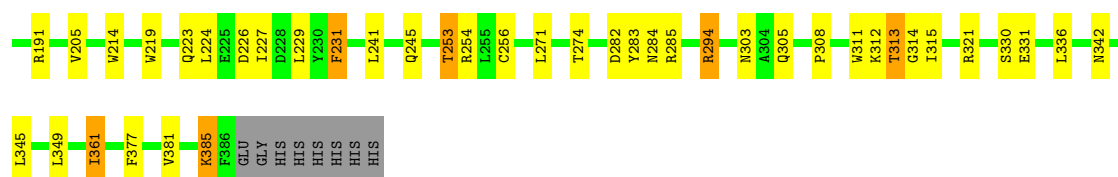


- Molecule 1: Mandelate racemase/muconate lactonizing protein

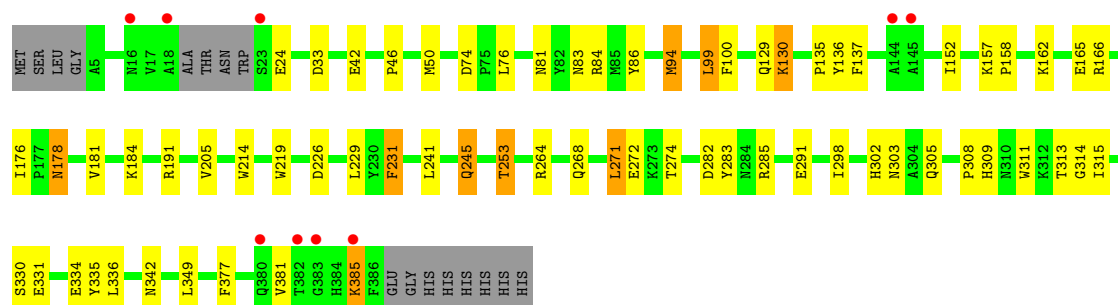
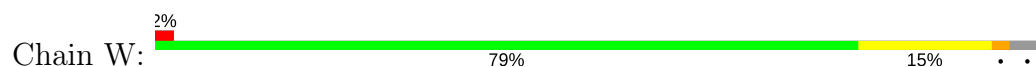


- Molecule 1: Mandelate racemase/muconate lactonizing protein

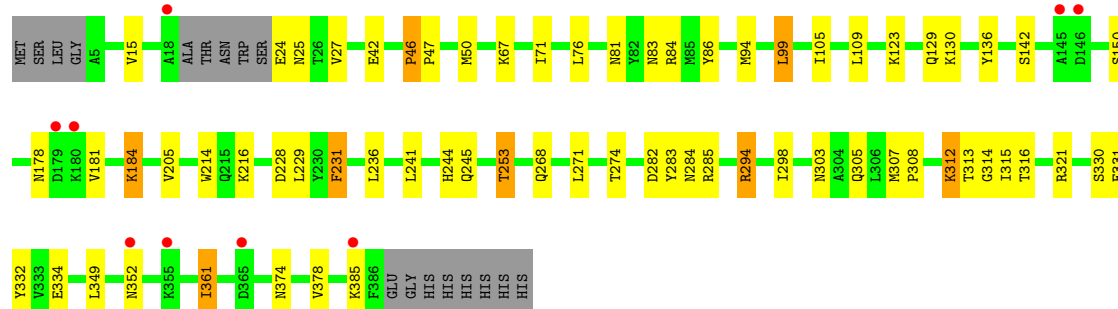
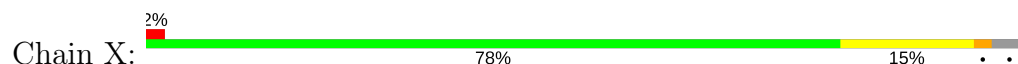




- Molecule 1: Mandelate racemase/muconate lactonizing protein



- Molecule 1: Mandelate racemase/muconate lactonizing protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	111.16Å 146.14Å 158.71Å 98.47° 96.80° 105.04°	Depositor
Resolution (Å)	49.33 – 2.10 49.32 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.33-2.10) 85.1 (49.32-2.10)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.185 , 0.213 0.189 , 0.218	Depositor DCC
R_{free} test set	4843 reflections (1.01%)	DCC
Wilson B-factor (Å ²)	18.6	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	72942	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.45% 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: MG

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	0/3042	0.59	0/4125
1	B	0.49	0/3042	0.61	0/4125
1	C	0.50	0/3042	0.60	0/4125
1	D	0.50	0/3042	0.60	0/4125
1	E	0.50	0/3047	0.58	0/4132
1	F	0.49	0/3047	0.59	1/4132 (0.0%)
1	G	0.49	0/3042	0.60	1/4125 (0.0%)
1	H	0.50	0/3047	0.60	2/4132 (0.0%)
1	I	0.47	0/3047	0.59	1/4132 (0.0%)
1	J	0.48	0/3047	0.59	1/4132 (0.0%)
1	K	0.48	0/3047	0.59	0/4132
1	L	0.51	0/3047	0.61	2/4132 (0.0%)
1	M	0.47	0/3042	0.58	1/4125 (0.0%)
1	N	0.48	0/3042	0.58	0/4125
1	O	0.47	0/3047	0.59	0/4132
1	P	0.48	0/3047	0.58	0/4132
1	Q	0.48	0/3047	0.59	1/4132 (0.0%)
1	R	0.48	0/3047	0.58	0/4132
1	S	0.47	0/3042	0.58	2/4125 (0.0%)
1	T	0.49	0/3047	0.61	2/4132 (0.0%)
1	U	0.48	0/3047	0.59	1/4132 (0.0%)
1	V	0.49	0/3047	0.58	1/4132 (0.0%)
1	W	0.47	0/3047	0.59	1/4132 (0.0%)
1	X	0.48	0/3042	0.59	1/4125 (0.0%)
All	All	0.49	0/73083	0.59	18/99105 (0.0%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	99	LEU	CA-CB-CG	-7.26	98.61	115.30
1	M	99	LEU	CA-CB-CG	-6.36	100.67	115.30
1	U	99	LEU	CA-CB-CG	-6.36	100.67	115.30
1	S	99	LEU	CA-CB-CG	-6.25	100.92	115.30
1	I	99	LEU	CA-CB-CG	-6.13	101.20	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2978	0	2938	65	0
1	B	2978	0	2938	65	0
1	C	2978	0	2938	74	0
1	D	2978	0	2938	78	0
1	E	2983	0	2940	71	0
1	F	2983	0	2940	76	0
1	G	2978	0	2938	68	0
1	H	2983	0	2940	70	0
1	I	2983	0	2940	60	0
1	J	2983	0	2940	70	0
1	K	2983	0	2940	67	0
1	L	2983	0	2940	66	0
1	M	2978	0	2938	66	0
1	N	2978	0	2938	65	0
1	O	2983	0	2940	73	0
1	P	2983	0	2940	64	0
1	Q	2983	0	2940	85	0
1	R	2983	0	2940	62	0
1	S	2978	0	2938	67	0
1	T	2983	0	2940	82	0
1	U	2983	0	2940	67	0
1	V	2983	0	2940	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	W	2983	0	2940	56	0
1	X	2978	0	2938	66	0
2	A	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
2	K	1	0	0	0	0
2	L	1	0	0	0	0
2	U	1	0	0	0	0
2	V	1	0	0	0	0
2	W	1	0	0	0	0
2	X	1	0	0	0	0
3	A	64	0	0	1	0
3	B	58	0	0	1	0
3	C	73	0	0	1	0
3	D	67	0	0	2	0
3	E	62	0	0	2	0
3	F	59	0	0	1	0
3	G	58	0	0	2	0
3	H	70	0	0	1	0
3	I	54	0	0	4	0
3	J	52	0	0	3	0
3	K	53	0	0	1	0
3	L	58	0	0	5	0
3	M	55	0	0	4	0
3	N	51	0	0	0	0
3	O	52	0	0	1	0
3	P	53	0	0	1	0
3	Q	55	0	0	1	0
3	R	56	0	0	0	0
3	S	54	0	0	0	0
3	T	58	0	0	1	0
3	U	54	0	0	2	0
3	V	59	0	0	6	0
3	W	55	0	0	3	0
3	X	53	0	0	1	0
All	All	72942	0	70542	1476	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 10.

The worst 5 of 1476 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:294:ARG:HH11	1:A:294:ARG:HG2	1.03	1.19
1:A:321:ARG:HD3	1:A:361:ILE:HD11	1.21	1.16
1:S:313:THR:HG22	1:S:315:ILE:H	1.08	1.15
1:C:313:THR:HG22	1:C:315:ILE:H	1.13	1.14
1:J:321:ARG:CD	1:J:361:ILE:HD11	1.76	1.14

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	373/394 (95%)	362 (97%)	11 (3%)	0	100	100
1	B	373/394 (95%)	363 (97%)	10 (3%)	0	100	100
1	C	373/394 (95%)	360 (96%)	13 (4%)	0	100	100
1	D	373/394 (95%)	358 (96%)	15 (4%)	0	100	100
1	E	374/394 (95%)	363 (97%)	11 (3%)	0	100	100
1	F	374/394 (95%)	362 (97%)	12 (3%)	0	100	100
1	G	373/394 (95%)	362 (97%)	11 (3%)	0	100	100
1	H	374/394 (95%)	358 (96%)	16 (4%)	0	100	100
1	I	374/394 (95%)	360 (96%)	14 (4%)	0	100	100
1	J	374/394 (95%)	364 (97%)	10 (3%)	0	100	100
1	K	374/394 (95%)	364 (97%)	10 (3%)	0	100	100
1	L	374/394 (95%)	364 (97%)	10 (3%)	0	100	100
1	M	373/394 (95%)	360 (96%)	12 (3%)	1 (0%)	44	44
1	N	373/394 (95%)	361 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	374/394 (95%)	360 (96%)	14 (4%)	0	100	100
1	P	374/394 (95%)	361 (96%)	13 (4%)	0	100	100
1	Q	374/394 (95%)	358 (96%)	16 (4%)	0	100	100
1	R	374/394 (95%)	361 (96%)	13 (4%)	0	100	100
1	S	373/394 (95%)	360 (96%)	13 (4%)	0	100	100
1	T	374/394 (95%)	361 (96%)	13 (4%)	0	100	100
1	U	374/394 (95%)	359 (96%)	15 (4%)	0	100	100
1	V	374/394 (95%)	361 (96%)	13 (4%)	0	100	100
1	W	374/394 (95%)	358 (96%)	16 (4%)	0	100	100
1	X	373/394 (95%)	360 (96%)	13 (4%)	0	100	100
All	All	8967/9456 (95%)	8660 (97%)	306 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	94	MET

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	314/330 (95%)	295 (94%)	19 (6%)	22	18
1	B	314/330 (95%)	299 (95%)	15 (5%)	30	27
1	C	314/330 (95%)	297 (95%)	17 (5%)	26	23
1	D	314/330 (95%)	294 (94%)	20 (6%)	20	17
1	E	314/330 (95%)	297 (95%)	17 (5%)	26	23
1	F	314/330 (95%)	294 (94%)	20 (6%)	20	17
1	G	314/330 (95%)	300 (96%)	14 (4%)	32	30
1	H	314/330 (95%)	296 (94%)	18 (6%)	24	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	314/330 (95%)	298 (95%)	16 (5%)	28	25
1	J	314/330 (95%)	297 (95%)	17 (5%)	26	23
1	K	314/330 (95%)	299 (95%)	15 (5%)	30	27
1	L	314/330 (95%)	297 (95%)	17 (5%)	26	23
1	M	314/330 (95%)	292 (93%)	22 (7%)	18	14
1	N	314/330 (95%)	296 (94%)	18 (6%)	24	21
1	O	314/330 (95%)	294 (94%)	20 (6%)	20	17
1	P	314/330 (95%)	296 (94%)	18 (6%)	24	21
1	Q	314/330 (95%)	292 (93%)	22 (7%)	18	14
1	R	314/330 (95%)	297 (95%)	17 (5%)	26	23
1	S	314/330 (95%)	298 (95%)	16 (5%)	28	25
1	T	314/330 (95%)	296 (94%)	18 (6%)	24	21
1	U	314/330 (95%)	293 (93%)	21 (7%)	19	15
1	V	314/330 (95%)	296 (94%)	18 (6%)	24	21
1	W	314/330 (95%)	299 (95%)	15 (5%)	30	27
1	X	314/330 (95%)	294 (94%)	20 (6%)	20	17
All	All	7536/7920 (95%)	7106 (94%)	430 (6%)	24	21

5 of 430 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	184	LYS
1	N	313	THR
1	W	94	MET
1	L	272	GLU
1	M	271	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 217 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	132	GLN
1	N	237	GLN
1	W	178	ASN
1	L	301	HIS
1	M	301	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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 ⓘ

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	377/394 (95%)	-0.47	0 100 100	8, 16, 33, 51	0
1	B	377/394 (95%)	-0.36	5 (1%) 77 81	8, 15, 32, 47	0
1	C	377/394 (95%)	-0.30	4 (1%) 80 84	7, 15, 32, 49	0
1	D	377/394 (95%)	-0.33	3 (0%) 86 88	7, 16, 33, 55	0
1	E	378/394 (95%)	-0.44	5 (1%) 77 81	7, 15, 32, 46	0
1	F	378/394 (95%)	-0.29	8 (2%) 64 68	6, 16, 34, 51	0
1	G	377/394 (95%)	-0.35	6 (1%) 72 76	8, 16, 34, 49	0
1	H	378/394 (95%)	-0.40	4 (1%) 80 84	7, 15, 33, 57	0
1	I	378/394 (95%)	-0.38	6 (1%) 72 76	7, 17, 34, 49	0
1	J	378/394 (95%)	-0.25	7 (1%) 67 71	9, 17, 38, 59	0
1	K	378/394 (95%)	-0.28	8 (2%) 64 68	8, 18, 37, 58	0
1	L	378/394 (95%)	-0.39	5 (1%) 77 81	9, 16, 32, 51	0
1	M	377/394 (95%)	-0.37	0 100 100	9, 17, 33, 48	0
1	N	377/394 (95%)	-0.29	3 (0%) 86 88	9, 18, 38, 57	0
1	O	378/394 (95%)	-0.31	4 (1%) 80 84	9, 18, 37, 51	0
1	P	378/394 (95%)	-0.31	6 (1%) 72 76	7, 18, 41, 62	0
1	Q	378/394 (95%)	-0.25	7 (1%) 67 71	10, 18, 38, 60	0
1	R	378/394 (95%)	-0.38	5 (1%) 77 81	8, 17, 35, 60	0
1	S	377/394 (95%)	-0.25	7 (1%) 67 71	11, 19, 39, 64	0
1	T	378/394 (95%)	-0.36	3 (0%) 86 88	7, 16, 36, 52	0
1	U	378/394 (95%)	-0.35	2 (0%) 90 92	8, 18, 37, 60	0
1	V	378/394 (95%)	-0.30	5 (1%) 77 81	9, 18, 37, 54	0
1	W	378/394 (95%)	-0.30	9 (2%) 59 64	9, 18, 36, 56	0
1	X	377/394 (95%)	-0.26	9 (2%) 59 64	8, 17, 35, 62	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	9063/9456 (95%)	-0.33	121 (1%) 77 81	6, 17, 36, 64	0

The worst 5 of 121 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	18	ALA	6.4
1	W	23	SER	5.5
1	K	18	ALA	5.2
1	G	18	ALA	4.9
1	S	18	ALA	4.8

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å ²)	Q<0.9
2	MG	E	395	1/1	0.86	0.17	18.18	28,28,28,28	0
2	MG	K	683	1/1	0.85	0.19	16.89	3,3,3,3	1
2	MG	G	395	1/1	0.93	0.29	13.61	10,10,10,10	1
2	MG	U	974	1/1	0.80	0.18	7.20	4,4,4,4	1
2	MG	F	1460	1/1	0.83	0.18	7.08	8,8,8,8	1
2	MG	L	395	1/1	0.89	0.11	1.98	26,26,26,26	0
2	MG	V	395	1/1	0.76	0.10	0.37	30,30,30,30	0
2	MG	W	395	1/1	0.83	0.07	-1.54	38,38,38,38	0
2	MG	D	395	1/1	0.98	0.06	-2.56	24,24,24,24	0
2	MG	H	626	1/1	0.98	0.04	-6.55	22,22,22,22	0
2	MG	A	1243	1/1	0.97	0.05	-	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	MG	X	1479	1/1	0.69	0.31	-	17,17,17,17	1

6.5 Other polymers [i](#)

There are no such residues in this entry.