



wwPDB X-ray Structure Validation Summary Report

Jun 10, 2014 – 11:37 AM EDT

PDB ID : 1WUE
Title : Crystal structure of protein GI:29375081, unknown member of enolase super-family from enterococcus faecalis V583
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Deposited on : 2004-12-05
Resolution : 2.10 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

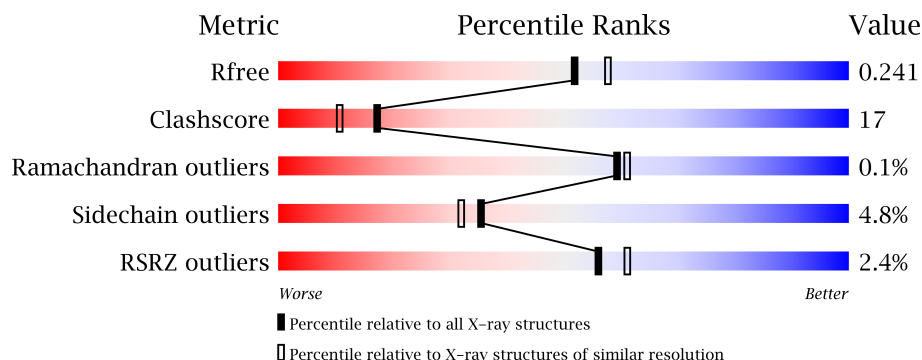
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : **FAILED**
Xtriage (Phenix) : dev-1439
EDS : stable23161
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23161

1 Overall quality at a glance

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}	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	386	
1	B	386	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6319 atoms, of which 0 are hydrogen and 0 are deuterium.

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

- Molecule 1 is a protein called mandelate racemase/muconate lactonizing enzyme family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	370	Total	C	N	O	S	0	0	0
			2959	1900	497	551	11			
1	B	369	Total	C	N	O	S	0	0	0
			2955	1898	496	550	11			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	998	GLY	-	EXPRESSION TAG	UNP Q838J7
A	999	SER	-	EXPRESSION TAG	UNP Q838J7
A	1000	HIS	-	EXPRESSION TAG	UNP Q838J7
B	1999	SER	-	EXPRESSION TAG	UNP Q838J7
B	2000	HIS	-	EXPRESSION TAG	UNP Q838J7

- Molecule 2 is water.

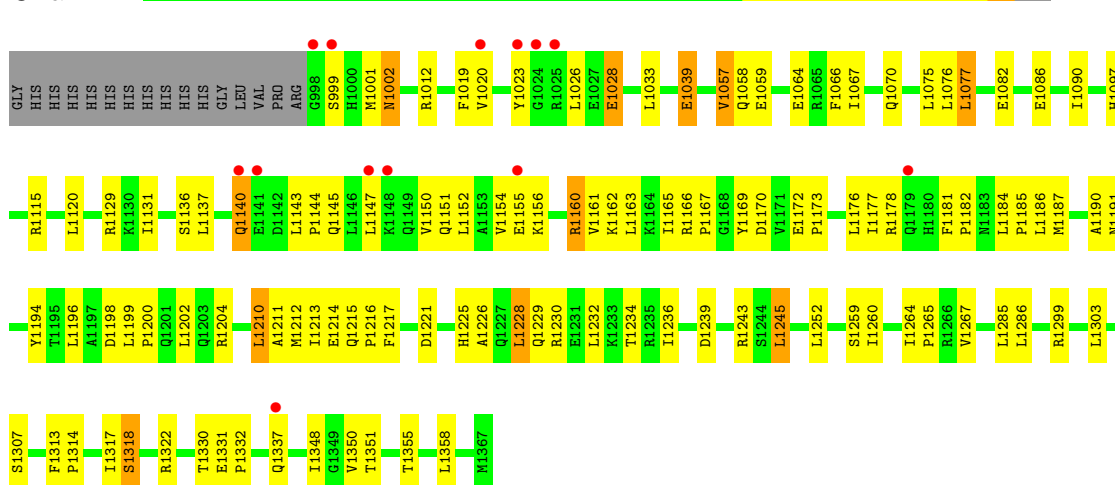
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	220	Total	O	0	0
			220	220		
2	B	185	Total	O	0	0
			185	185		

3 Residue-property plots

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

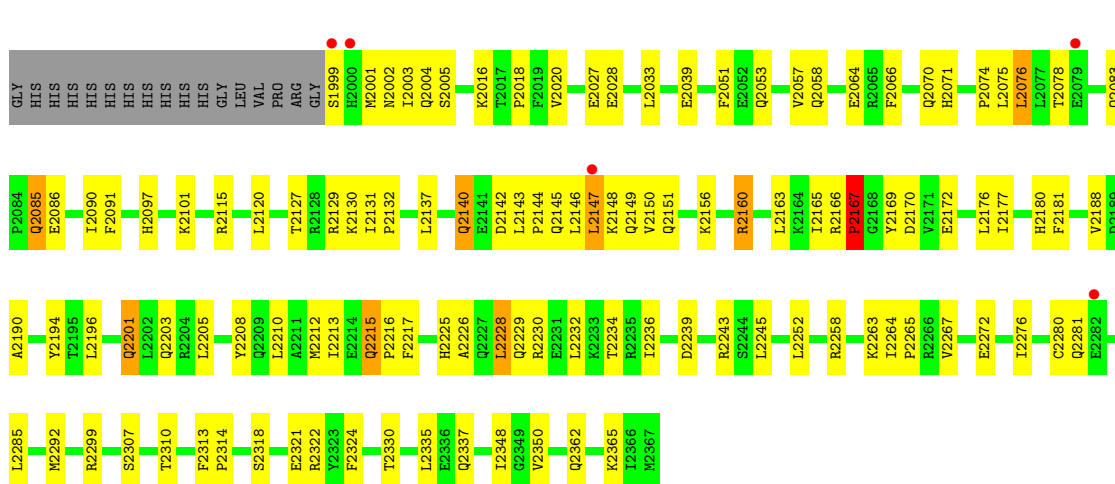
- Molecule 1: mandelate racemase/muconate lactonizing enzyme family protein

Chain A:



- Molecule 1: mandelate racemase/muconate lactonizing enzyme family protein

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	136.81Å 136.81Å 112.77Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 2.10 28.65 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-2.10) 98.6 (28.65-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.32 (at 2.10Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.207 , 0.242 0.206 , 0.241	Depositor DCC
R_{free} test set	2260 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	21.4	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.1	EDS
Estimated twinning fraction	0.024 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 45927 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6319	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.34	0/3021	0.72	3/4093 (0.1%)
1	B	0.32	0/3017	0.65	4/4088 (0.1%)
All	All	0.33	0/6038	0.68	7/8181 (0.1%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1196	LEU	CB-CG-CD2	-19.36	78.08	111.00
1	A	1351	THR	CA-CB-OG1	9.95	129.90	109.00
1	B	2172	GLU	CA-CB-CG	-9.88	91.67	113.40
1	B	2201	GLN	CA-CB-CG	6.83	128.43	113.40
1	A	1318	SER	CA-CB-OG	5.85	126.99	111.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2959	0	2973	103	0
1	B	2955	0	2970	109	0
2	A	220	0	0	7	0
2	B	185	0	0	2	0
All	All	6319	0	5943	207	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 17.

The worst 5 of 207 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:2163:LEU:HD11	1:B:2177:ILE:HD12	1.39	1.03
1:A:1165:ILE:HD12	1:A:1170:ASP:HA	1.52	0.89
1:B:2071:HIS:O	1:B:2075:LEU:HD13	1.74	0.87
1:A:1163:LEU:HD11	1:A:1177:ILE:HD12	1.56	0.87
1:B:2165:ILE:HD12	1:B:2170:ASP:HA	1.58	0.85

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	368/386 (95%)	355 (96%)	13 (4%)	0	100	100
1	B	367/386 (95%)	356 (97%)	10 (3%)	1 (0%)	50	49
All	All	735/772 (95%)	711 (97%)	23 (3%)	1 (0%)	59	61

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2167	PRO

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	322/336 (96%)	306 (95%)	16 (5%)	34	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	322/336 (96%)	307 (95%)	15 (5%)	36	33
All	All	644/672 (96%)	613 (95%)	31 (5%)	35	32

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1245	LEU
1	B	2028	GLU
1	B	2228	LEU
1	A	1322	ARG
1	B	2033	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1354	GLN
1	B	2010	GLN
1	B	2354	GLN
1	A	1362	GLN
1	A	1364	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

Mogul failed to run properly - this section will therefore be empty.

5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

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	370/386 (95%)	0.14	13 (3%) 42 46	9, 21, 45, 55	0
1	B	369/386 (95%)	0.02	5 (1%) 72 76	11, 24, 42, 51	0
All	All	739/772 (95%)	0.08	18 (2%) 56 61	9, 23, 43, 55	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	998	GLY	4.6
1	A	1155	GLU	4.0
1	A	1023	TYR	3.5
1	A	1024	GLY	3.2
1	B	2000	HIS	3.1

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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.