



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2017 – 01:58 pm GMT

PDB ID : 4FSH
Title : Crystal Structure of Shikimate Dehydrogenase (aroE) Clinical Variant v2356 from *Helicobacter pylori* in Complex with Shikimate
Authors : Cheng, W.C.; Chen, T.J.; Wang, W.C.
Deposited on : 2012-06-27
Resolution : 2.85 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
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

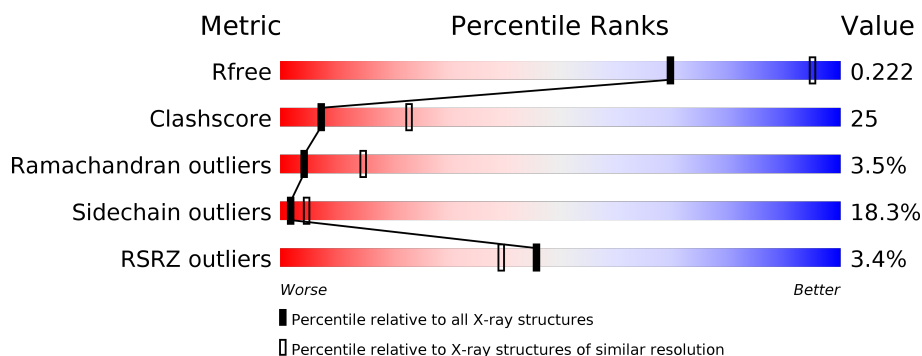
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	2469 (2.90-2.82)
Clashscore	112137	2749 (2.90-2.82)
Ramachandran outliers	110173	2687 (2.90-2.82)
Sidechain outliers	110143	2690 (2.90-2.82)
RSRZ outliers	101464	2487 (2.90-2.82)

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	271	<div> <div>6%</div> <div>45%</div> <div>37%</div> <div>12%</div> <div>• •</div> </div>
1	B	271	<div> <div>64%</div> <div>28%</div> <div>• •</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4150 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 Shikimate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	0	0
			2036	1330	337	359	10			
1	B	263	Total	C	N	O	S	0	0	0
			2061	1345	341	365	10			

There are 52 discrepancies between the modelled and reference sequences:

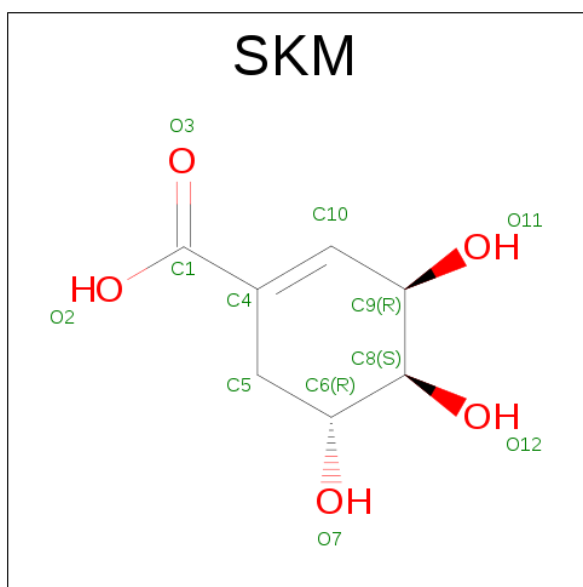
Chain	Residue	Modelled	Actual	Comment	Reference
A	32	LYS	GLU	CONFLICT	UNP P56119
A	34	GLY	ARG	CONFLICT	UNP P56119
A	40	ARG	HIS	CONFLICT	UNP P56119
A	52	ASN	SER	CONFLICT	UNP P56119
A	87	ALA	GLY	CONFLICT	UNP P56119
A	88	SER	ALA	CONFLICT	UNP P56119
A	89	ILE	VAL	CONFLICT	UNP P56119
A	115	HIS	GLN	CONFLICT	UNP P56119
A	116	GLN	LYS	CONFLICT	UNP P56119
A	126	SER	ALA	CONFLICT	UNP P56119
A	136	GLY	GLU	CONFLICT	UNP P56119
A	143	LYS	GLN	CONFLICT	UNP P56119
A	151	PRO	SER	CONFLICT	UNP P56119
A	185	ASN	HIS	CONFLICT	UNP P56119
A	202	ALA	GLY	CONFLICT	UNP P56119
A	218	ALA	SER	CONFLICT	UNP P56119
A	225	ILE	THR	CONFLICT	UNP P56119
A	239	SER	ALA	CONFLICT	UNP P56119
A	264	LEU	-	EXPRESSION TAG	UNP P56119
A	265	GLU	-	EXPRESSION TAG	UNP P56119
A	266	HIS	-	EXPRESSION TAG	UNP P56119
A	267	HIS	-	EXPRESSION TAG	UNP P56119
A	268	HIS	-	EXPRESSION TAG	UNP P56119
A	269	HIS	-	EXPRESSION TAG	UNP P56119
A	270	HIS	-	EXPRESSION TAG	UNP P56119

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Chain	Residue	Modelled	Actual	Comment	Reference
A	271	HIS	-	EXPRESSION TAG	UNP P56119
B	32	LYS	GLU	CONFLICT	UNP P56119
B	34	GLY	ARG	CONFLICT	UNP P56119
B	40	ARG	HIS	CONFLICT	UNP P56119
B	52	ASN	SER	CONFLICT	UNP P56119
B	87	ALA	GLY	CONFLICT	UNP P56119
B	88	SER	ALA	CONFLICT	UNP P56119
B	89	ILE	VAL	CONFLICT	UNP P56119
B	115	HIS	GLN	CONFLICT	UNP P56119
B	116	GLN	LYS	CONFLICT	UNP P56119
B	126	SER	ALA	CONFLICT	UNP P56119
B	136	GLY	GLU	CONFLICT	UNP P56119
B	143	LYS	GLN	CONFLICT	UNP P56119
B	151	PRO	SER	CONFLICT	UNP P56119
B	185	ASN	HIS	CONFLICT	UNP P56119
B	202	ALA	GLY	CONFLICT	UNP P56119
B	218	ALA	SER	CONFLICT	UNP P56119
B	225	ILE	THR	CONFLICT	UNP P56119
B	239	SER	ALA	CONFLICT	UNP P56119
B	264	LEU	-	EXPRESSION TAG	UNP P56119
B	265	GLU	-	EXPRESSION TAG	UNP P56119
B	266	HIS	-	EXPRESSION TAG	UNP P56119
B	267	HIS	-	EXPRESSION TAG	UNP P56119
B	268	HIS	-	EXPRESSION TAG	UNP P56119
B	269	HIS	-	EXPRESSION TAG	UNP P56119
B	270	HIS	-	EXPRESSION TAG	UNP P56119
B	271	HIS	-	EXPRESSION TAG	UNP P56119

- Molecule 2 is (3R,4S,5R)-3,4,5-TRIHIDROXYCYCLOHEX-1-ENE-1-CARBOXYLIC ACID (three-letter code: SKM) (formula: C₇H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	7	5		

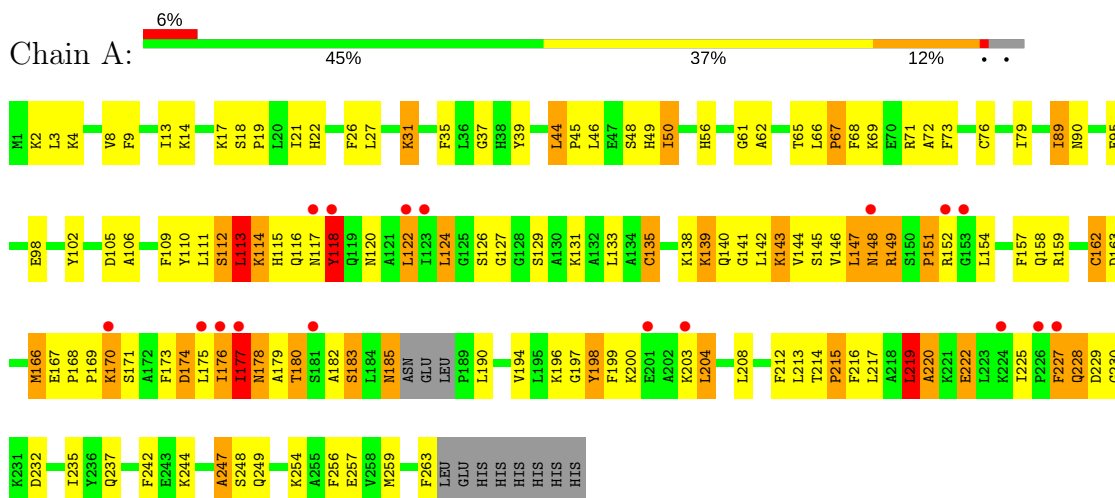
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	19	Total	O	0	0
			19	19		
3	B	22	Total	O	0	0
			22	22		

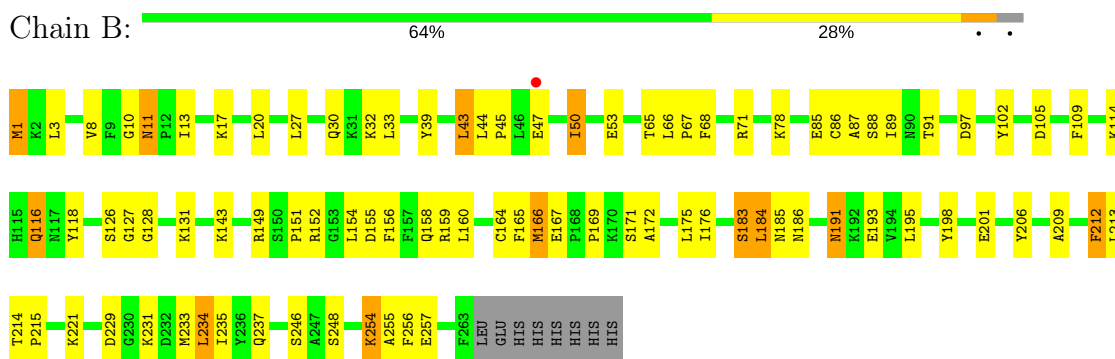
3 Residue-property plots

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



• Molecule 1: Shikimate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.12Å 71.87Å 176.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.85 25.49 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.5 (30.00-2.85) 99.6 (25.49-2.85)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.99 (at 2.85Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.214 , 0.260 0.211 , 0.222	Depositor DCC
R_{free} test set	988 reflections (5.39%)	DCC
Wilson B-factor (Å ²)	68.3	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 45.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4150	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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: SKM

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	0.86	5/2082 (0.2%)	0.63	0/2800
1	B	0.87	1/2108 (0.0%)	0.65	0/2838
All	All	0.86	6/4190 (0.1%)	0.64	0/5638

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	118	TYR	CG-CD2	14.42	1.57	1.39
1	A	118	TYR	CE1-CZ	10.29	1.51	1.38
1	A	118	TYR	CE2-CZ	9.38	1.50	1.38
1	A	135	CYS	CB-SG	-7.39	1.69	1.82
1	A	118	TYR	CG-CD1	6.93	1.48	1.39

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	2036	0	2091	148	0
1	B	2061	0	2114	61	0
2	A	12	0	9	0	0
3	A	19	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	22	0	0	2	0
All	All	4150	0	4214	207	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 25.

The worst 5 of 207 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:147:LEU:C	1:A:148:ASN:HD22	1.47	1.17
1:A:50:ILE:HD11	1:A:72:ALA:HA	1.25	1.14
1:A:113:LEU:HA	1:A:114:LYS:CB	1.74	1.13
1:A:113:LEU:CA	1:A:114:LYS:HB3	1.91	1.00
1:A:113:LEU:HA	1:A:114:LYS:HB3	0.99	0.98

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	256/271 (94%)	213 (83%)	27 (10%)	16 (6%)	1	4
1	B	261/271 (96%)	240 (92%)	19 (7%)	2 (1%)	22	52
All	All	517/542 (95%)	453 (88%)	46 (9%)	18 (4%)	4	15

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	ALA
1	A	112	SER
1	A	151	PRO

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Mol	Chain	Res	Type
1	A	216	PHE
1	A	220	ALA

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	220/231 (95%)	170 (77%)	50 (23%)	1	2
1	B	223/231 (96%)	192 (86%)	31 (14%)	4	10
All	All	443/462 (96%)	362 (82%)	81 (18%)	2	5

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	194	VAL
1	A	237	GLN
1	B	191	ASN
1	A	198	TYR
1	A	219	LEU

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	A	237	GLN
1	B	15	HIS
1	B	116	GLN
1	A	228	GLN
1	B	63	ASN

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 ⓘ

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SKM	A	500	-	10,12,12	1.42	2 (20%)	10,17,17	0.56	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SKM	A	500	-	-	0/0/20/20	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	SKM	C9-C10	2.50	1.53	1.50
2	A	500	SKM	C10-C4	3.08	1.39	1.34

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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	260/271 (95%)	0.24	17 (6%)	20 15	42, 76, 127, 141	0
1	B	263/271 (97%)	-0.35	1 (0%)	92 92	36, 52, 71, 86	0
All	All	523/542 (96%)	-0.06	18 (3%)	46 39	36, 60, 123, 141	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	117	ASN	5.4
1	A	118	TYR	3.8
1	A	177	ILE	3.6
1	A	227	PHE	3.2
1	A	181	SER	3.2

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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(\AA^2)	Q<0.9
2	SKM	A	500	12/12	0.93	0.22	0.56	67,71,74,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.