



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 04:43 pm BST

PDB ID : 3CKY
Title : Structural and Kinetic Properties of a beta-hydroxyacid dehydrogenase involved in nicotinate fermentation
Authors : Reitz, S.; Alhapel, A.; Pierik, A.J.; Essen, L.-O.
Deposited on : 2008-03-18
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

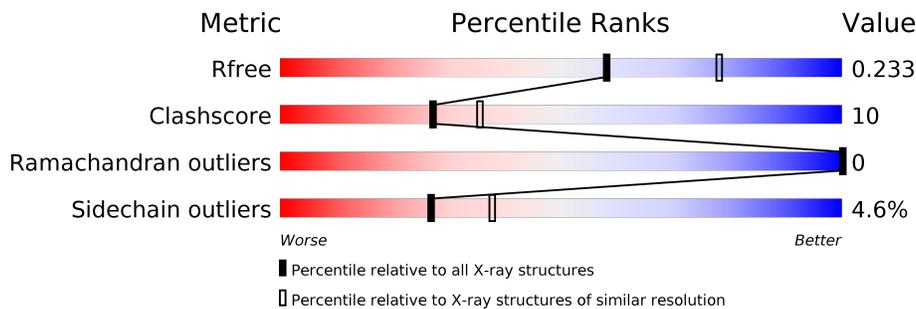
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	301	82% (green), 14% (yellow), 2% (orange), 2% (red), 0% (grey)
1	B	301	85% (green), 12% (yellow), 2% (orange), 2% (red), 0% (grey)
1	C	301	82% (green), 15% (yellow), 2% (orange), 2% (red), 0% (grey)
1	D	301	67% (green), 11% (yellow), 1% (orange), 20% (grey)

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8515 atoms, of which 0 are hydrogens and 0 are deuteriums.

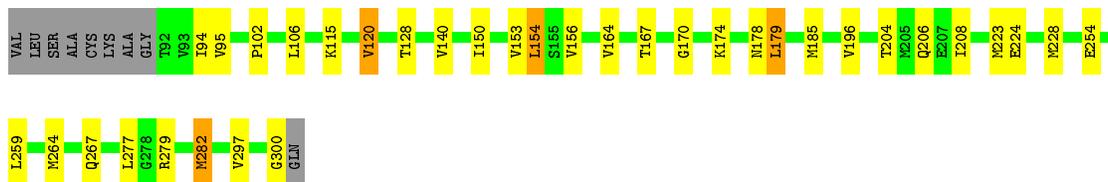
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 2-hydroxymethyl glutarate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	297	2117	1333	349	412	23	3	1	0
1	B	296	2113	1331	348	411	23	6	1	0
1	C	296	2111	1330	348	410	23	14	1	0
1	D	240	1727	1089	282	338	18	0	2	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	123	Total 123	O 123	0	0
2	B	158	Total 158	O 158	0	0
2	C	96	Total 96	O 96	0	0
2	D	70	Total 70	O 70	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.98Å 175.78Å 83.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.47 – 2.30 24.47 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.1 (24.47-2.30) 95.2 (24.47-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 2.31Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.194 , 0.222 0.203 , 0.233	Depositor DCC
R_{free} test set	2674 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtrriage
Anisotropy	0.136	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 59.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.019 for l,-k,h	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8515	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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

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	0.45	0/2144	0.53	1/2888 (0.0%)
1	B	0.51	0/2140	0.57	1/2883 (0.0%)
1	C	0.45	0/2138	0.54	1/2880 (0.0%)
1	D	0.45	0/1751	0.54	1/2354 (0.0%)
All	All	0.47	0/8173	0.54	4/11005 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	179	LEU	CA-CB-CG	5.99	129.08	115.30
1	A	179	LEU	CA-CB-CG	5.76	128.56	115.30
1	D	179	LEU	CA-CB-CG	5.67	128.35	115.30
1	C	179	LEU	CA-CB-CG	5.33	127.56	115.30

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	2117	0	2174	60	0
1	B	2113	0	2171	46	0
1	C	2111	0	2169	55	0
1	D	1727	0	1772	43	0
2	A	123	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	158	0	0	3	0
2	C	96	0	0	0	0
2	D	70	0	0	2	0
All	All	8515	0	8286	165	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 165 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:264[A]:MET:CE	1:B:264[A]:MET:HE3	1.45	1.46
1:C:264[B]:MET:HE1	1:D:264[B]:MET:SD	1.83	1.16
1:C:264[B]:MET:CE	1:D:264[B]:MET:HE1	1.76	1.14
1:A:264[A]:MET:SD	1:B:264[A]:MET:HE3	1.89	1.13
1:C:264[B]:MET:HE2	1:D:264[B]:MET:CE	1.81	1.10

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	296/301 (98%)	294 (99%)	2 (1%)	0	100	100
1	B	295/301 (98%)	293 (99%)	2 (1%)	0	100	100
1	C	295/301 (98%)	290 (98%)	5 (2%)	0	100	100
1	D	236/301 (78%)	230 (98%)	6 (2%)	0	100	100
All	All	1122/1204 (93%)	1107 (99%)	15 (1%)	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	221/224 (99%)	212 (96%)	9 (4%)	30	43
1	B	221/224 (99%)	212 (96%)	9 (4%)	30	43
1	C	220/224 (98%)	206 (94%)	14 (6%)	17	23
1	D	183/224 (82%)	176 (96%)	7 (4%)	33	47
All	All	845/896 (94%)	806 (95%)	39 (5%)	27	38

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	282	MET
1	C	56	LYS
1	D	277	LEU
1	C	5	ILE
1	C	6	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	163	HIS
1	B	267	GLN
1	D	256	ASN
1	B	242	HIS
1	B	256	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.