



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 02:01 am BST

PDB ID : 2YZ7
Title : X-ray analyses of 3-hydroxybutyrate dehydrogenase from *Alcaligenes faecalis*
Authors : Hoque, M.M.; Juan, E.C.M.; Shimizu, S.; Hossain, M.T.; Takenaka, A.
Deposited on : 2007-05-04
Resolution : 2.19 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

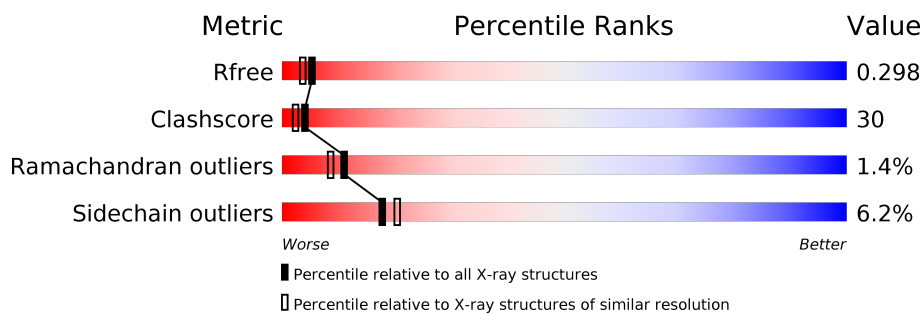
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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	260	
1	B	260	
1	C	260	
1	D	260	
1	E	260	
1	F	260	
1	G	260	

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Mol	Chain	Length	Quality of chain
1	H	260	 A horizontal bar chart showing the quality of chain H. The bar is divided into three segments: green (52%), yellow (44%), and red (4%). The red segment is at the end of the bar, followed by two dots. The percentages 52% and 44% are written below the green and yellow segments respectively.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15660 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 D-3-hydroxybutyrate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	0	0
			1906	1203	331	366	6			
1	B	260	Total	C	N	O	S	0	0	0
			1906	1203	331	366	6			
1	C	260	Total	C	N	O	S	0	0	0
			1906	1203	331	366	6			
1	D	260	Total	C	N	O	S	0	0	0
			1906	1203	331	366	6			
1	E	260	Total	C	N	O	S	0	0	0
			1906	1203	331	366	6			
1	F	260	Total	C	N	O	S	0	0	0
			1906	1203	331	366	6			
1	G	260	Total	C	N	O	S	0	0	0
			1906	1203	331	366	6			
1	H	260	Total	C	N	O	S	0	0	0
			1906	1203	331	366	6			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	A	1	Total	Ca	0	0
			1	1		
2	F	1	Total	Ca	0	0
			1	1		
2	E	1	Total	Ca	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

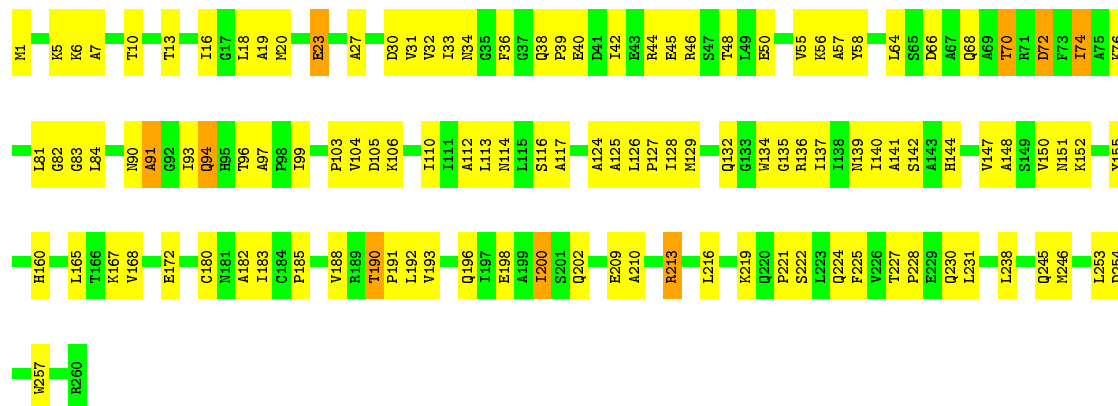
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Cl 1 1	0	0
3	D	1	Total Cl 1 1	0	0
3	E	1	Total Cl 1 1	0	0
3	H	1	Total Cl 1 1	0	0
3	B	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0
3	A	1	Total Cl 1 1	0	0
3	F	1	Total Cl 1 1	0	0

- Molecule 4 is water.

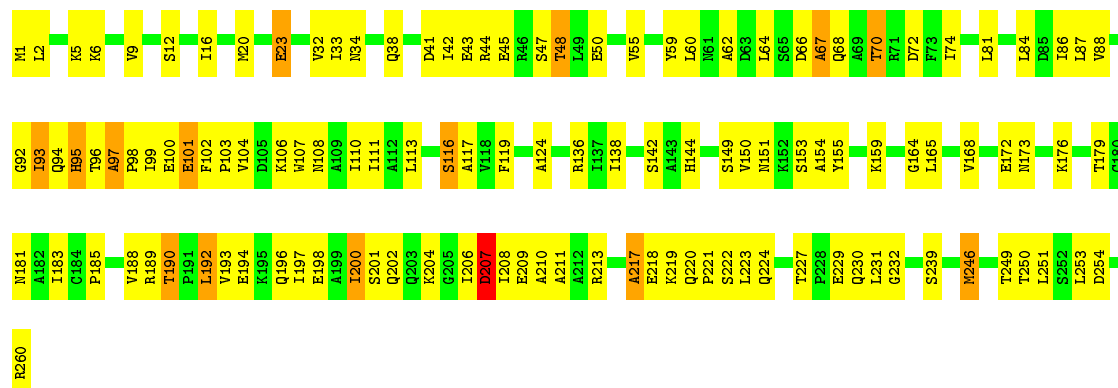
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	43	Total O 43 43	0	0
4	B	40	Total O 40 40	0	0
4	C	76	Total O 76 76	0	0
4	D	72	Total O 72 72	0	0
4	E	42	Total O 42 42	0	0
4	F	59	Total O 59 59	0	0
4	G	39	Total O 39 39	0	0
4	H	29	Total O 29 29	0	0



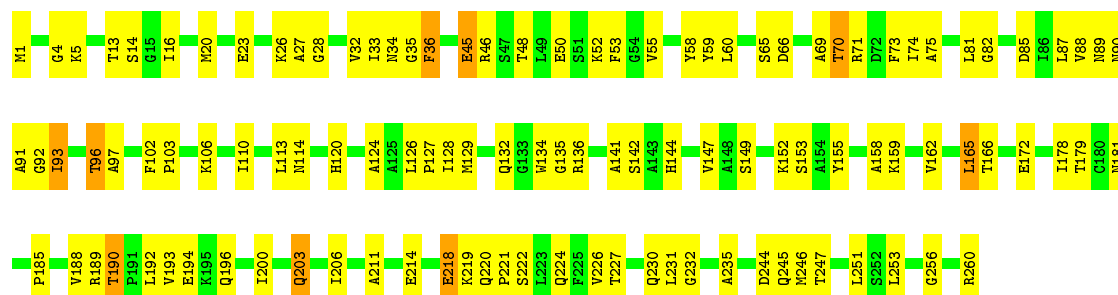
- Molecule 1: D-3-hydroxybutyrate dehydrogenase



- Molecule 1: D-3-hydroxybutyrate dehydrogenase

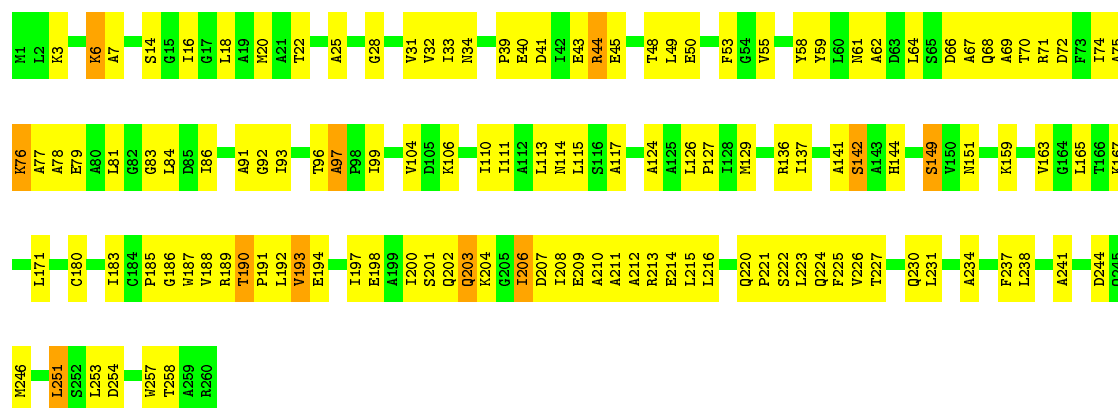


- Molecule 1: D-3-hydroxybutyrate dehydrogenase



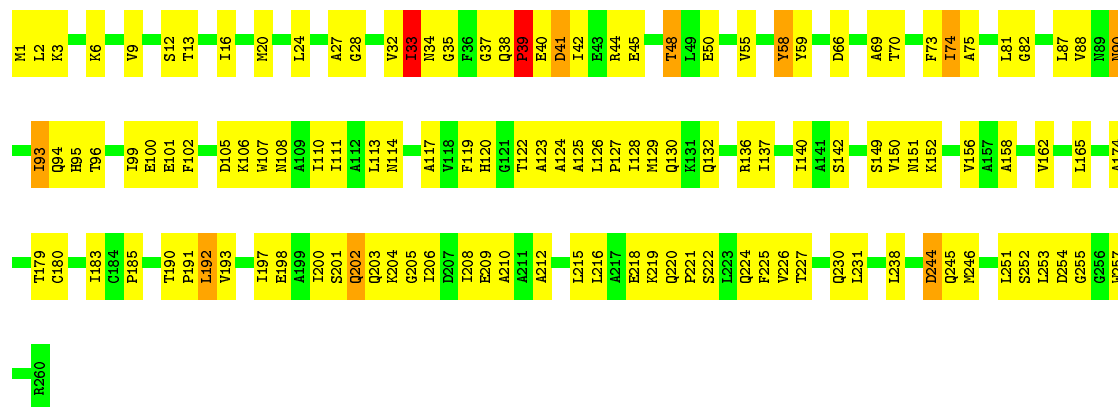
- Molecule 1: D-3-hydroxybutyrate dehydrogenase

Chain G:  51% 45%



• Molecule 1: D-3-hydroxybutyrate dehydrogenase

Chain H:  52% 44%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.30Å 118.83Å 118.73Å 90.00° 93.90° 90.00°	Depositor
Resolution (Å)	50.00 – 2.19 45.50 – 2.19	Depositor EDS
% Data completeness (in resolution range)	54.8 (50.00-2.19) 93.4 (45.50-2.19)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.84 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.197 , 0.270 0.239 , 0.298	Depositor DCC
R_{free} test set	10253 reflections (10.04%)	wwPDB-VP
Wilson B-factor (Å ²)	38.7	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15660	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% 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: CA, CL

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	0.37	0/1935	0.63	0/2623
1	B	0.38	0/1935	0.63	0/2623
1	C	0.40	0/1935	0.66	0/2623
1	D	0.43	0/1935	0.65	0/2623
1	E	0.37	0/1935	0.62	0/2623
1	F	0.41	0/1935	0.66	0/2623
1	G	0.36	0/1935	0.63	0/2623
1	H	0.36	0/1935	0.62	0/2623
All	All	0.39	0/15480	0.64	0/20984

There are no bond length outliers.

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	1906	0	1941	121	0
1	B	1906	0	1941	131	0
1	C	1906	0	1941	90	0
1	D	1906	0	1941	112	0
1	E	1906	0	1941	129	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1906	0	1941	108	0
1	G	1906	0	1941	137	0
1	H	1906	0	1941	143	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	1	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	1	0
3	F	1	0	0	1	0
3	G	1	0	0	0	0
3	H	1	0	0	1	0
4	A	43	0	0	3	0
4	B	40	0	0	3	0
4	C	76	0	0	4	0
4	D	72	0	0	4	0
4	E	42	0	0	6	0
4	F	59	0	0	2	0
4	G	39	0	0	0	0
4	H	29	0	0	1	0
All	All	15660	0	15528	926	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 30.

The worst 5 of 926 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:F:92:GLY:HA2	1:F:114:ASN:HD21	1.13	1.07
1:E:190:THR:HG22	1:E:193:VAL:HG23	1.37	1.06
1:G:200:ILE:HG23	1:G:211:ALA:HB1	1.37	1.06
1:E:16:ILE:HD11	1:E:188:VAL:HG11	1.40	1.04
1:B:204:LYS:HB2	1:B:206:ILE:HD12	1.44	0.99

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	258/260 (99%)	232 (90%)	22 (8%)	4 (2%)	9	7
1	B	258/260 (99%)	236 (92%)	20 (8%)	2 (1%)	19	19
1	C	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	13	10
1	D	258/260 (99%)	229 (89%)	27 (10%)	2 (1%)	19	19
1	E	258/260 (99%)	226 (88%)	24 (9%)	8 (3%)	4	2
1	F	258/260 (99%)	241 (93%)	16 (6%)	1 (0%)	34	37
1	G	258/260 (99%)	229 (89%)	24 (9%)	5 (2%)	8	5
1	H	258/260 (99%)	227 (88%)	28 (11%)	3 (1%)	13	10
All	All	2064/2080 (99%)	1863 (90%)	173 (8%)	28 (1%)	11	8

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	91	ALA
1	B	208	ILE
1	E	67	ALA
1	E	95	HIS
1	E	97	ALA

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	192/192 (100%)	187 (97%)	5 (3%)	46	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	192/192 (100%)	177 (92%)	15 (8%)	12	13
1	C	192/192 (100%)	174 (91%)	18 (9%)	8	8
1	D	192/192 (100%)	181 (94%)	11 (6%)	20	24
1	E	192/192 (100%)	178 (93%)	14 (7%)	14	15
1	F	192/192 (100%)	183 (95%)	9 (5%)	26	33
1	G	192/192 (100%)	181 (94%)	11 (6%)	20	24
1	H	192/192 (100%)	179 (93%)	13 (7%)	16	17
All	All	1536/1536 (100%)	1440 (94%)	96 (6%)	18	20

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	94	GLN
1	E	70	THR
1	H	74	ILE
1	D	105	ASP
1	D	213	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	139	ASN
1	E	139	ASN
1	H	132	GLN
1	D	173	ASN
1	E	130	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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 [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.