wwPDB X-ray Structure Validation Summary Report (i)

Nov 14, 2026 – 02:53 PM EST

PDB ID	:	7ULH / pdb_00007ulh
Title	:	Crystal Structure of a Short chain dehydrogenase from Mycobacterium avium 104
Authors	:	Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on	:	2022-04-04
Resolution	:	2.60 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

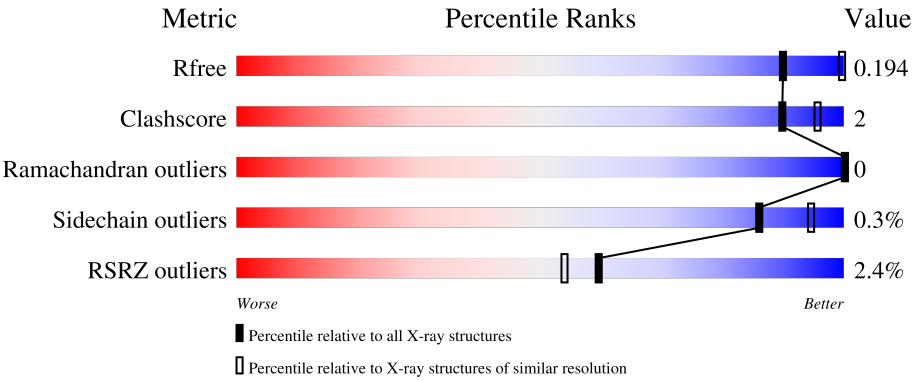
MolProbity	:	4-5-2 with Phenix2.2
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.



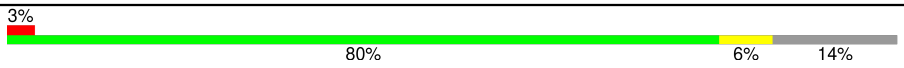
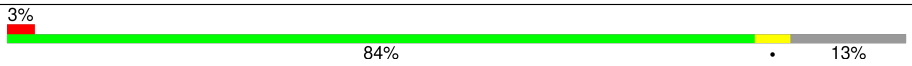
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 of 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 <=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	328	83% 5% 12%
1	B	328	83% 5% 12%
1	C	328	2% 84% • 13%
1	D	328	2% 82% • 14%
1	E	328	3% 79% • 17%

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Mol	Chain	Length	Quality of chain
1	F	328	
1	G	328	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 15788 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 Short chain dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	1	0
			2122	1318	389	412	3			
1	B	289	Total	C	N	O	S	0	0	0
			2121	1319	388	411	3			
1	C	284	Total	C	N	O	S	0	1	0
			2091	1303	383	402	3			
1	D	282	Total	C	N	O	S	0	0	0
			2051	1280	379	389	3			
1	E	272	Total	C	N	O	S	0	0	0
			1958	1223	355	377	3			
1	F	282	Total	C	N	O	S	0	2	0
			2056	1283	374	396	3			
1	G	286	Total	C	N	O	S	0	3	0
			2112	1315	389	405	3			

There are 147 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP A0A0H2ZRP4
A	-19	ALA	-	expression tag	UNP A0A0H2ZRP4
A	-18	HIS	-	expression tag	UNP A0A0H2ZRP4
A	-17	HIS	-	expression tag	UNP A0A0H2ZRP4
A	-16	HIS	-	expression tag	UNP A0A0H2ZRP4
A	-15	HIS	-	expression tag	UNP A0A0H2ZRP4
A	-14	HIS	-	expression tag	UNP A0A0H2ZRP4
A	-13	HIS	-	expression tag	UNP A0A0H2ZRP4
A	-12	MET	-	expression tag	UNP A0A0H2ZRP4
A	-11	GLY	-	expression tag	UNP A0A0H2ZRP4
A	-10	THR	-	expression tag	UNP A0A0H2ZRP4
A	-9	LEU	-	expression tag	UNP A0A0H2ZRP4
A	-8	GLU	-	expression tag	UNP A0A0H2ZRP4
A	-7	ALA	-	expression tag	UNP A0A0H2ZRP4
A	-6	GLN	-	expression tag	UNP A0A0H2ZRP4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	THR	-	expression tag	UNP A0A0H2ZRP4
A	-4	GLN	-	expression tag	UNP A0A0H2ZRP4
A	-3	GLY	-	expression tag	UNP A0A0H2ZRP4
A	-2	PRO	-	expression tag	UNP A0A0H2ZRP4
A	-1	GLY	-	expression tag	UNP A0A0H2ZRP4
A	0	SER	-	expression tag	UNP A0A0H2ZRP4
B	-20	MET	-	initiating methionine	UNP A0A0H2ZRP4
B	-19	ALA	-	expression tag	UNP A0A0H2ZRP4
B	-18	HIS	-	expression tag	UNP A0A0H2ZRP4
B	-17	HIS	-	expression tag	UNP A0A0H2ZRP4
B	-16	HIS	-	expression tag	UNP A0A0H2ZRP4
B	-15	HIS	-	expression tag	UNP A0A0H2ZRP4
B	-14	HIS	-	expression tag	UNP A0A0H2ZRP4
B	-13	HIS	-	expression tag	UNP A0A0H2ZRP4
B	-12	MET	-	expression tag	UNP A0A0H2ZRP4
B	-11	GLY	-	expression tag	UNP A0A0H2ZRP4
B	-10	THR	-	expression tag	UNP A0A0H2ZRP4
B	-9	LEU	-	expression tag	UNP A0A0H2ZRP4
B	-8	GLU	-	expression tag	UNP A0A0H2ZRP4
B	-7	ALA	-	expression tag	UNP A0A0H2ZRP4
B	-6	GLN	-	expression tag	UNP A0A0H2ZRP4
B	-5	THR	-	expression tag	UNP A0A0H2ZRP4
B	-4	GLN	-	expression tag	UNP A0A0H2ZRP4
B	-3	GLY	-	expression tag	UNP A0A0H2ZRP4
B	-2	PRO	-	expression tag	UNP A0A0H2ZRP4
B	-1	GLY	-	expression tag	UNP A0A0H2ZRP4
B	0	SER	-	expression tag	UNP A0A0H2ZRP4
C	-20	MET	-	initiating methionine	UNP A0A0H2ZRP4
C	-19	ALA	-	expression tag	UNP A0A0H2ZRP4
C	-18	HIS	-	expression tag	UNP A0A0H2ZRP4
C	-17	HIS	-	expression tag	UNP A0A0H2ZRP4
C	-16	HIS	-	expression tag	UNP A0A0H2ZRP4
C	-15	HIS	-	expression tag	UNP A0A0H2ZRP4
C	-14	HIS	-	expression tag	UNP A0A0H2ZRP4
C	-13	HIS	-	expression tag	UNP A0A0H2ZRP4
C	-12	MET	-	expression tag	UNP A0A0H2ZRP4
C	-11	GLY	-	expression tag	UNP A0A0H2ZRP4
C	-10	THR	-	expression tag	UNP A0A0H2ZRP4
C	-9	LEU	-	expression tag	UNP A0A0H2ZRP4
C	-8	GLU	-	expression tag	UNP A0A0H2ZRP4
C	-7	ALA	-	expression tag	UNP A0A0H2ZRP4
C	-6	GLN	-	expression tag	UNP A0A0H2ZRP4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	THR	-	expression tag	UNP A0A0H2ZRP4
C	-4	GLN	-	expression tag	UNP A0A0H2ZRP4
C	-3	GLY	-	expression tag	UNP A0A0H2ZRP4
C	-2	PRO	-	expression tag	UNP A0A0H2ZRP4
C	-1	GLY	-	expression tag	UNP A0A0H2ZRP4
C	0	SER	-	expression tag	UNP A0A0H2ZRP4
D	-20	MET	-	initiating methionine	UNP A0A0H2ZRP4
D	-19	ALA	-	expression tag	UNP A0A0H2ZRP4
D	-18	HIS	-	expression tag	UNP A0A0H2ZRP4
D	-17	HIS	-	expression tag	UNP A0A0H2ZRP4
D	-16	HIS	-	expression tag	UNP A0A0H2ZRP4
D	-15	HIS	-	expression tag	UNP A0A0H2ZRP4
D	-14	HIS	-	expression tag	UNP A0A0H2ZRP4
D	-13	HIS	-	expression tag	UNP A0A0H2ZRP4
D	-12	MET	-	expression tag	UNP A0A0H2ZRP4
D	-11	GLY	-	expression tag	UNP A0A0H2ZRP4
D	-10	THR	-	expression tag	UNP A0A0H2ZRP4
D	-9	LEU	-	expression tag	UNP A0A0H2ZRP4
D	-8	GLU	-	expression tag	UNP A0A0H2ZRP4
D	-7	ALA	-	expression tag	UNP A0A0H2ZRP4
D	-6	GLN	-	expression tag	UNP A0A0H2ZRP4
D	-5	THR	-	expression tag	UNP A0A0H2ZRP4
D	-4	GLN	-	expression tag	UNP A0A0H2ZRP4
D	-3	GLY	-	expression tag	UNP A0A0H2ZRP4
D	-2	PRO	-	expression tag	UNP A0A0H2ZRP4
D	-1	GLY	-	expression tag	UNP A0A0H2ZRP4
D	0	SER	-	expression tag	UNP A0A0H2ZRP4
E	-20	MET	-	initiating methionine	UNP A0A0H2ZRP4
E	-19	ALA	-	expression tag	UNP A0A0H2ZRP4
E	-18	HIS	-	expression tag	UNP A0A0H2ZRP4
E	-17	HIS	-	expression tag	UNP A0A0H2ZRP4
E	-16	HIS	-	expression tag	UNP A0A0H2ZRP4
E	-15	HIS	-	expression tag	UNP A0A0H2ZRP4
E	-14	HIS	-	expression tag	UNP A0A0H2ZRP4
E	-13	HIS	-	expression tag	UNP A0A0H2ZRP4
E	-12	MET	-	expression tag	UNP A0A0H2ZRP4
E	-11	GLY	-	expression tag	UNP A0A0H2ZRP4
E	-10	THR	-	expression tag	UNP A0A0H2ZRP4
E	-9	LEU	-	expression tag	UNP A0A0H2ZRP4
E	-8	GLU	-	expression tag	UNP A0A0H2ZRP4
E	-7	ALA	-	expression tag	UNP A0A0H2ZRP4
E	-6	GLN	-	expression tag	UNP A0A0H2ZRP4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-5	THR	-	expression tag	UNP A0A0H2ZRP4
E	-4	GLN	-	expression tag	UNP A0A0H2ZRP4
E	-3	GLY	-	expression tag	UNP A0A0H2ZRP4
E	-2	PRO	-	expression tag	UNP A0A0H2ZRP4
E	-1	GLY	-	expression tag	UNP A0A0H2ZRP4
E	0	SER	-	expression tag	UNP A0A0H2ZRP4
F	-20	MET	-	initiating methionine	UNP A0A0H2ZRP4
F	-19	ALA	-	expression tag	UNP A0A0H2ZRP4
F	-18	HIS	-	expression tag	UNP A0A0H2ZRP4
F	-17	HIS	-	expression tag	UNP A0A0H2ZRP4
F	-16	HIS	-	expression tag	UNP A0A0H2ZRP4
F	-15	HIS	-	expression tag	UNP A0A0H2ZRP4
F	-14	HIS	-	expression tag	UNP A0A0H2ZRP4
F	-13	HIS	-	expression tag	UNP A0A0H2ZRP4
F	-12	MET	-	expression tag	UNP A0A0H2ZRP4
F	-11	GLY	-	expression tag	UNP A0A0H2ZRP4
F	-10	THR	-	expression tag	UNP A0A0H2ZRP4
F	-9	LEU	-	expression tag	UNP A0A0H2ZRP4
F	-8	GLU	-	expression tag	UNP A0A0H2ZRP4
F	-7	ALA	-	expression tag	UNP A0A0H2ZRP4
F	-6	GLN	-	expression tag	UNP A0A0H2ZRP4
F	-5	THR	-	expression tag	UNP A0A0H2ZRP4
F	-4	GLN	-	expression tag	UNP A0A0H2ZRP4
F	-3	GLY	-	expression tag	UNP A0A0H2ZRP4
F	-2	PRO	-	expression tag	UNP A0A0H2ZRP4
F	-1	GLY	-	expression tag	UNP A0A0H2ZRP4
F	0	SER	-	expression tag	UNP A0A0H2ZRP4
G	-20	MET	-	initiating methionine	UNP A0A0H2ZRP4
G	-19	ALA	-	expression tag	UNP A0A0H2ZRP4
G	-18	HIS	-	expression tag	UNP A0A0H2ZRP4
G	-17	HIS	-	expression tag	UNP A0A0H2ZRP4
G	-16	HIS	-	expression tag	UNP A0A0H2ZRP4
G	-15	HIS	-	expression tag	UNP A0A0H2ZRP4
G	-14	HIS	-	expression tag	UNP A0A0H2ZRP4
G	-13	HIS	-	expression tag	UNP A0A0H2ZRP4
G	-12	MET	-	expression tag	UNP A0A0H2ZRP4
G	-11	GLY	-	expression tag	UNP A0A0H2ZRP4
G	-10	THR	-	expression tag	UNP A0A0H2ZRP4
G	-9	LEU	-	expression tag	UNP A0A0H2ZRP4
G	-8	GLU	-	expression tag	UNP A0A0H2ZRP4
G	-7	ALA	-	expression tag	UNP A0A0H2ZRP4
G	-6	GLN	-	expression tag	UNP A0A0H2ZRP4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-5	THR	-	expression tag	UNP A0A0H2ZRP4
G	-4	GLN	-	expression tag	UNP A0A0H2ZRP4
G	-3	GLY	-	expression tag	UNP A0A0H2ZRP4
G	-2	PRO	-	expression tag	UNP A0A0H2ZRP4
G	-1	GLY	-	expression tag	UNP A0A0H2ZRP4
G	0	SER	-	expression tag	UNP A0A0H2ZRP4

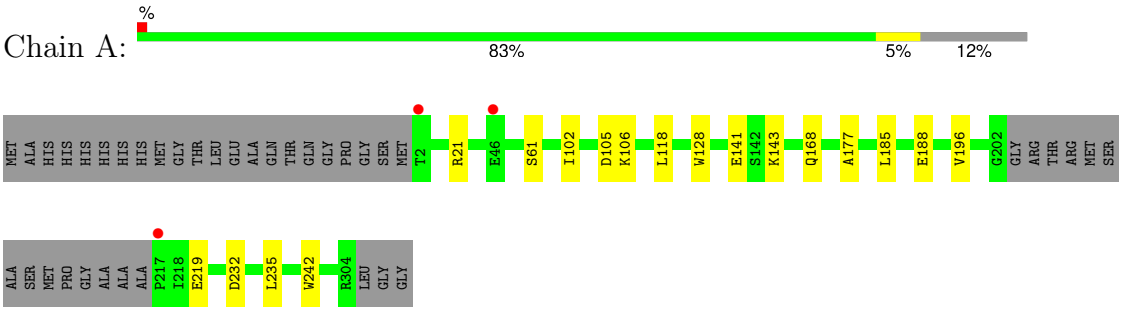
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	195	Total O 195 195	0	0
2	B	219	Total O 219 219	0	0
2	C	211	Total O 211 211	0	0
2	D	169	Total O 171 171	0	2
2	E	82	Total O 82 82	0	0
2	F	121	Total O 121 121	0	0
2	G	277	Total O 278 278	0	1

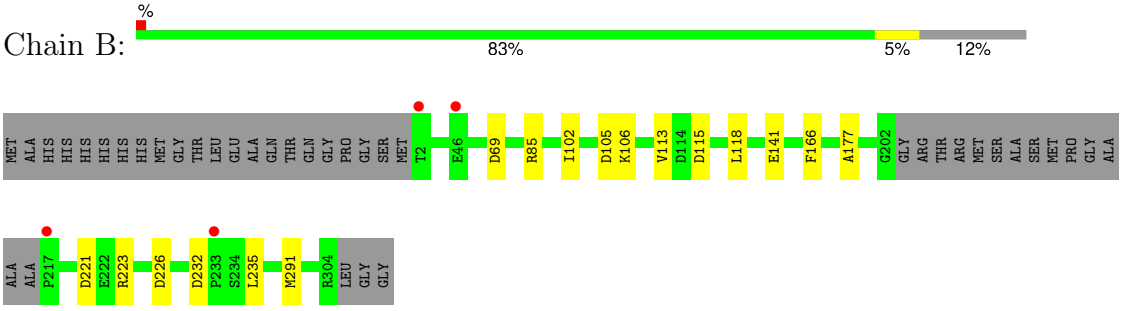
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

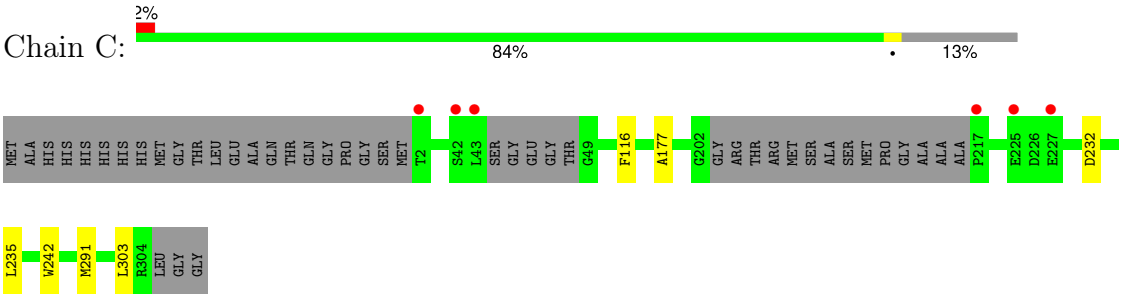
• Molecule 1: Short chain dehydrogenase



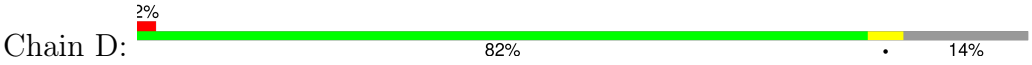
• Molecule 1: Short chain dehydrogenase

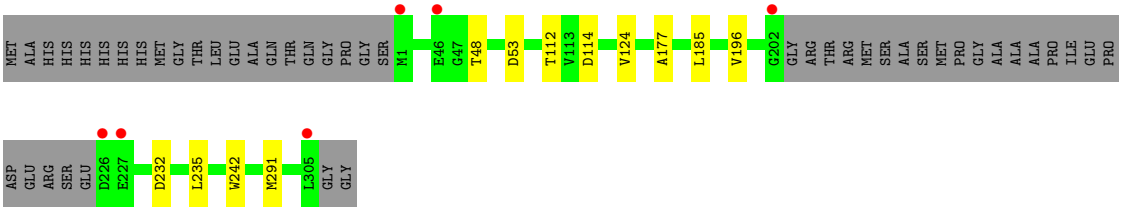


• Molecule 1: Short chain dehydrogenase

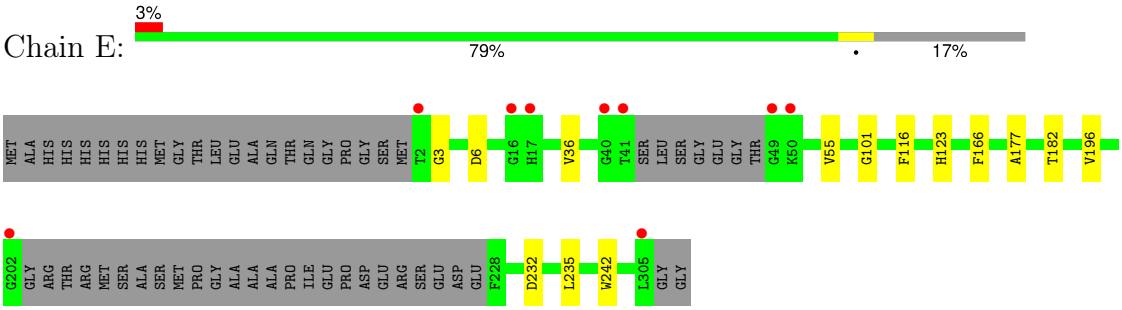


• Molecule 1: Short chain dehydrogenase

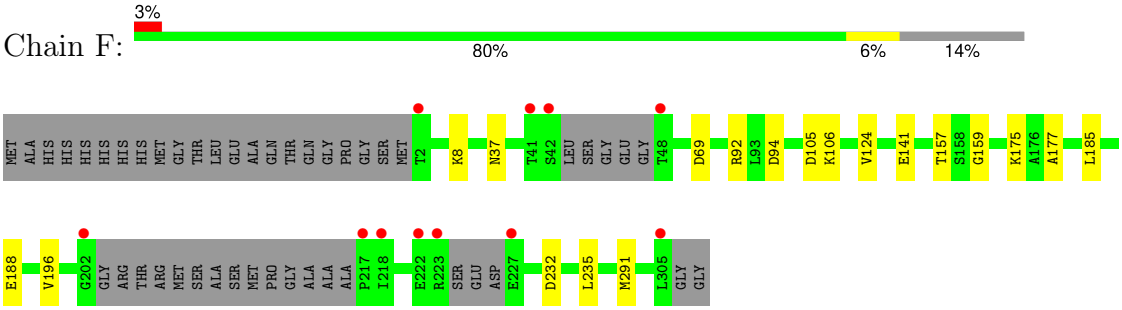




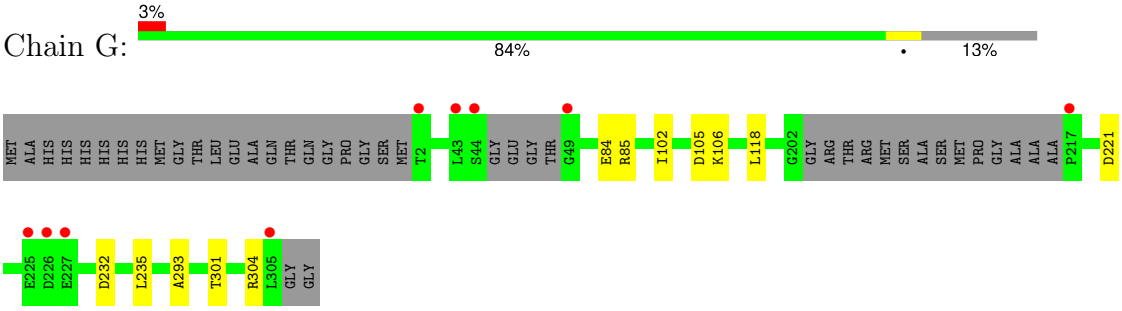
• Molecule 1: Short chain dehydrogenase



• Molecule 1: Short chain dehydrogenase



• Molecule 1: Short chain dehydrogenase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	241.81Å 241.81Å 241.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.37 – 2.60 48.37 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.37-2.60) 99.9 (48.37-2.60)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.01 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.20.1-4487	Depositor
R, R_{free}	0.158 , 0.193 0.159 , 0.194	Depositor DCC
R_{free} test set	1915 reflections (2.31%)	wwPDB-VP
Wilson B-factor (Å^2)	26.2	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 51.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	15788	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.19	0/2160	0.36	0/2930
1	B	0.20	0/2156	0.39	0/2926
1	C	0.20	0/2128	0.37	0/2887
1	D	0.18	0/2084	0.36	0/2828
1	E	0.15	0/1990	0.32	0/2708
1	F	0.17	0/2095	0.35	0/2845
1	G	0.22	0/2155	0.40	0/2922
All	All	0.19	0/14768	0.37	0/20046

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

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	2122	0	2082	11	0
1	B	2121	0	2090	11	0
1	C	2091	0	2060	6	0
1	D	2051	0	2034	9	0
1	E	1958	0	1898	9	0
1	F	2056	0	2001	13	0
1	G	2112	0	2082	6	0
2	A	195	0	0	1	0
2	B	219	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	211	0	0	0	0
2	D	171	0	0	2	1
2	E	82	0	0	0	0
2	F	121	0	0	2	0
2	G	278	0	0	2	1
All	All	15788	0	14247	52	2

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 2.

The worst 5 of 52 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:E:232:ASP:HB3	1:E:235:LEU:HG	1.67	0.77
1:B:141:GLU:OE1	2:B:401:HOH:O	2.05	0.74
1:A:141:GLU:OE1	2:A:401:HOH:O	2.12	0.68
1:G:84:GLU:OE1	2:G:401:HOH:O	2.13	0.66
1:G:232:ASP:HB3	1:G:235:LEU:HG	1.80	0.64

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:401:HOH:O	2:D:401:HOH:O[4_555]	1.92	0.28
2:G:601:HOH:O	2:G:601:HOH:O[10_455]	2.13	0.07

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	286/328 (87%)	282 (99%)	4 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	285/328 (87%)	281 (99%)	4 (1%)	0	100	100
1	C	279/328 (85%)	274 (98%)	5 (2%)	0	100	100
1	D	278/328 (85%)	273 (98%)	5 (2%)	0	100	100
1	E	266/328 (81%)	262 (98%)	4 (2%)	0	100	100
1	F	276/328 (84%)	272 (99%)	4 (1%)	0	100	100
1	G	283/328 (86%)	279 (99%)	4 (1%)	0	100	100
All	All	1953/2296 (85%)	1923 (98%)	30 (2%)	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	215/247 (87%)	213 (99%)	2 (1%)	70	87
1	B	216/247 (87%)	215 (100%)	1 (0%)	81	92
1	C	212/247 (86%)	212 (100%)	0	100	100
1	D	205/247 (83%)	205 (100%)	0	100	100
1	E	193/247 (78%)	193 (100%)	0	100	100
1	F	205/247 (83%)	205 (100%)	0	100	100
1	G	214/247 (87%)	212 (99%)	2 (1%)	70	87
All	All	1460/1729 (84%)	1455 (100%)	5 (0%)	86	94

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	SER
1	A	143	LYS
1	B	221	ASP
1	G	221	ASP
1	G	304	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	285	ASN
1	D	285	ASN
1	F	285	ASN
1	E	285	ASN
1	F	98	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 oligosaccharides 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

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, 95^{th} 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	289/328 (88%)	-0.66	3 (1%)	79	76	16, 29, 58, 94	1 (0%)
1	B	289/328 (88%)	-0.70	4 (1%)	73	69	16, 26, 60, 94	0
1	C	284/328 (86%)	-0.79	6 (2%)	63	58	13, 22, 53, 95	1 (0%)
1	D	282/328 (85%)	-0.63	6 (2%)	63	58	17, 31, 65, 115	0
1	E	272/328 (82%)	-0.06	9 (3%)	49	43	23, 51, 75, 95	0
1	F	282/328 (85%)	-0.36	11 (3%)	43	38	24, 37, 68, 99	2 (0%)
1	G	286/328 (87%)	-0.82	9 (3%)	51	45	9, 17, 53, 102	3 (1%)
All	All	1984/2296 (86%)	-0.58	48 (2%)	59	54	9, 30, 69, 115	7 (0%)

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	48	THR	5.9
1	C	2	THR	5.4
1	C	217	PRO	5.3
1	D	226	ASP	4.7
1	F	2	THR	4.5

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 oligosaccharides 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.