



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 10:02 AM UTC

PDB ID : 1F8M / pdb_00001f8m
Title : CRYSTAL STRUCTURE OF 3-BROMOPYRUVATE MODIFIED ISOCITRATE LYASE (ICL) FROM MYCOBACTERIUM TUBERCULOSIS
Authors : Sharma, V.; Sharma, S.; Hoener zu Bentrup, K.; McKinney, J.D.; Russell, D.G.; Jacobs Jr., W.R.; Sacchettini, J.C.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 2000-06-30
Resolution : 1.80 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

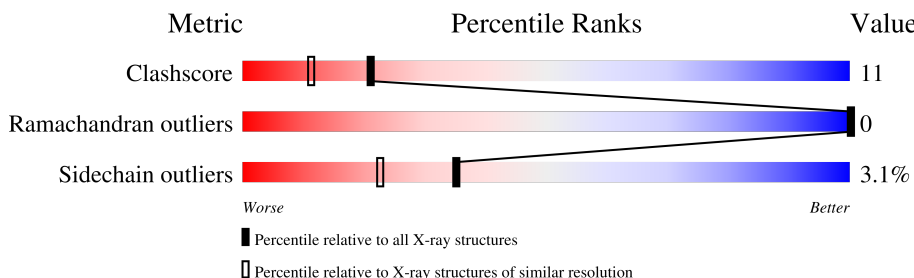
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	429	
1	B	429	
1	C	429	
1	D	429	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14276 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 ISOCITRATE LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	0	0
			3308	2078	575	646	9			
1	B	427	Total	C	N	O	S	0	0	0
			3308	2078	575	646	9			
1	C	427	Total	C	N	O	S	0	0	0
			3308	2078	575	646	9			
1	D	427	Total	C	N	O	S	0	0	0
			3308	2078	575	646	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	insertion	UNP P0A5H3
B	1	ALA	-	insertion	UNP P0A5H3
C	1	ALA	-	insertion	UNP P0A5H3
D	1	ALA	-	insertion	UNP P0A5H3

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		
2	D	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PYRUVIC ACID (CCD ID: PYR) (formula: C₃H₄O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

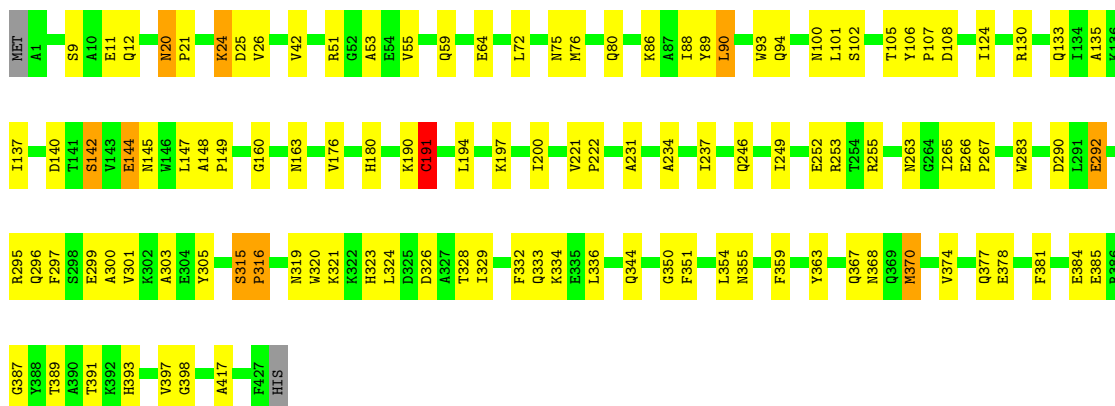
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	238	Total	O	0	0
			238	238		
4	B	282	Total	O	0	0
			282	282		
4	C	272	Total	O	0	0
			272	272		
4	D	224	Total	O	0	0
			224	224		



• Molecule 1: ISOCITRATE LYASE

Chain D: 73% 24%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.31Å 129.04Å 166.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.86 – 1.80	Depositor
% Data completeness (in resolution range)	87.2 (19.86-1.80)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.203 , 0.247	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14276	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

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: PYR, MG

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	0.79	0/3379	1.08	14/4595 (0.3%)
1	B	0.78	0/3379	1.11	14/4595 (0.3%)
1	C	0.76	0/3379	1.07	18/4595 (0.4%)
1	D	0.75	0/3379	1.13	26/4595 (0.6%)
All	All	0.77	0/13516	1.10	72/18380 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 72 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	315	SER	N-CA-C	11.19	123.74	109.65
1	A	315	SER	N-CA-C	10.70	123.19	109.93
1	D	315	SER	N-CA-C	9.69	122.13	109.83
1	D	417	ALA	N-CA-C	9.60	125.12	113.12
1	A	417	ALA	N-CA-C	9.20	124.63	113.41

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	373	TYR	Sidechain
1	C	373	TYR	Sidechain

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	3308	0	3192	64	0
1	B	3308	0	3192	77	0
1	C	3308	0	3192	86	0
1	D	3308	0	3192	94	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
3	C	6	0	0	0	0
3	D	6	0	0	0	0
4	A	238	0	0	5	0
4	B	282	0	0	13	0
4	C	272	0	0	10	0
4	D	224	0	0	6	0
All	All	14276	0	12768	287	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 11.

The worst 5 of 287 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:D:51:ARG:HH12	1:D:145:ASN:HD21	1.07	0.99
1:B:9:SER:OG	1:B:12:GLN:HG3	1.68	0.94
1:C:130:ARG:HH11	1:C:133:GLN:HE22	1.21	0.86
1:D:51:ARG:HH12	1:D:145:ASN:ND2	1.74	0.85
1:B:77:ALA:HB1	1:B:88:ILE:HD13	1.60	0.83

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	425/429 (99%)	415 (98%)	10 (2%)	0	100	100
1	B	425/429 (99%)	415 (98%)	10 (2%)	0	100	100
1	C	425/429 (99%)	417 (98%)	8 (2%)	0	100	100
1	D	425/429 (99%)	413 (97%)	12 (3%)	0	100	100
All	All	1700/1716 (99%)	1660 (98%)	40 (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	337/339 (99%)	327 (97%)	10 (3%)	36	24
1	B	337/339 (99%)	328 (97%)	9 (3%)	39	27
1	C	337/339 (99%)	326 (97%)	11 (3%)	33	21
1	D	337/339 (99%)	325 (96%)	12 (4%)	31	18
All	All	1348/1356 (99%)	1306 (97%)	42 (3%)	35	23

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	371	SER
1	D	144	GLU
1	C	391	THR
1	D	90	LEU
1	D	191	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	377	GLN
1	C	133	GLN
1	D	377	GLN
1	D	145	ASN
1	C	12	GLN

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](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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
3	PYR	C	500	1	5,5,5	1.44	1 (20%)	3,6,6	1.08	0
3	PYR	B	500	1	5,5,5	1.34	0	3,6,6	1.25	0
3	PYR	A	500	1	5,5,5	1.24	0	3,6,6	2.11	1 (33%)
3	PYR	D	500	1	5,5,5	1.33	1 (20%)	3,6,6	1.34	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
3	PYR	C	500	1	-	0/4/4/4	-
3	PYR	B	500	1	-	0/4/4/4	-
3	PYR	A	500	1	-	0/4/4/4	-
3	PYR	D	500	1	-	0/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	500	PYR	CA-C	-2.17	1.47	1.54
3	D	500	PYR	CA-C	-2.13	1.47	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	500	PYR	OXT-C-CA	3.22	122.53	113.59

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.