



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:00 PM UTC

PDB ID : 3SVK / pdb_00003svk
Title : Crystal structure of Acetyl-CoA acetyltransferase from Mycobacterium avium
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2011-07-12
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

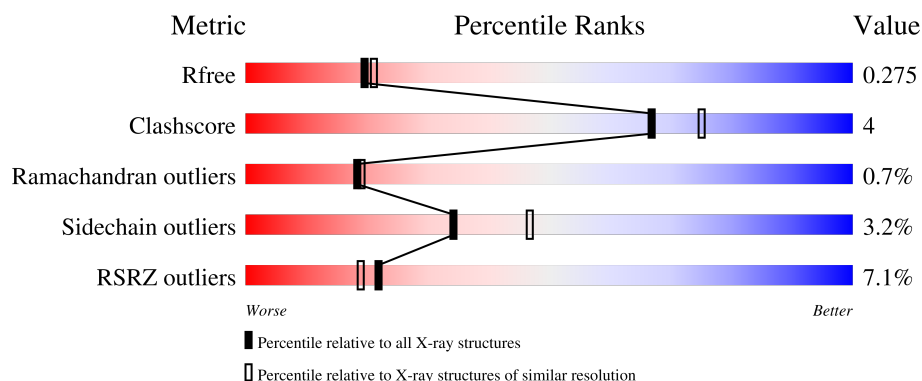
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

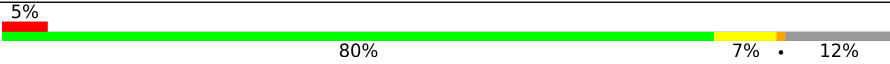
The reported resolution of this entry is 2.20 Å.

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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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 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 $\leq 5\%$. 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	407	
1	B	407	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5333 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 Acetyl-CoA acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	360	Total	C	N	O	S	0	0	0
			2576	1609	455	503	9			
1	B	359	Total	C	N	O	S	0	0	0
			2591	1622	457	503	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP A0QBF2
A	-2	PRO	-	expression tag	UNP A0QBF2
A	-1	GLY	-	expression tag	UNP A0QBF2
A	0	SER	-	expression tag	UNP A0QBF2
B	-3	GLY	-	expression tag	UNP A0QBF2
B	-2	PRO	-	expression tag	UNP A0QBF2
B	-1	GLY	-	expression tag	UNP A0QBF2
B	0	SER	-	expression tag	UNP A0QBF2

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		

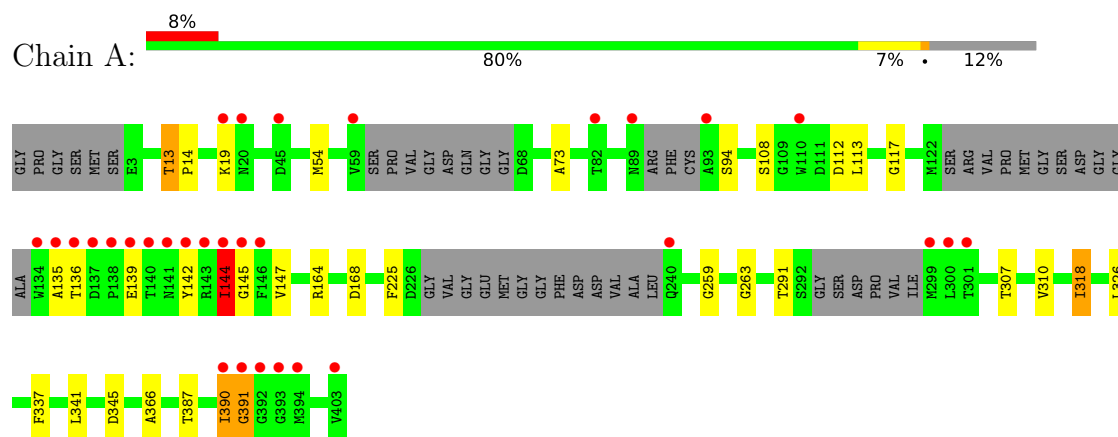
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	87	Total	O	0	0
			87	87		
3	B	78	Total	O	0	0
			78	78		

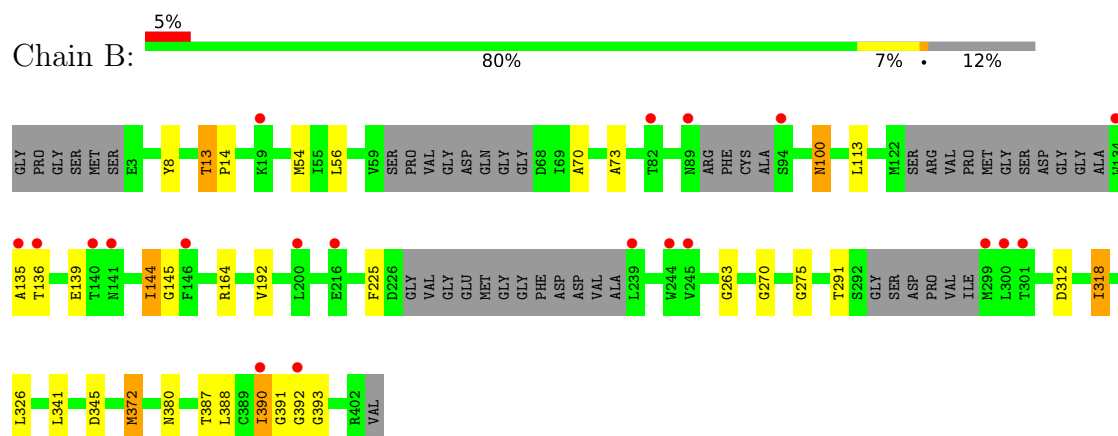
3 Residue-property plots [i](#)

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: Acetyl-CoA acetyltransferase



- Molecule 1: Acetyl-CoA acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.31Å 98.33Å 151.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.54 – 2.20 47.54 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.8 (47.54-2.20) 96.8 (47.54-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.99 (at 2.20Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.240 , 0.274 0.247 , 0.275	Depositor DCC
R_{free} test set	2051 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtrriage
Anisotropy	0.359	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5333	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.70 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.2281e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 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	0.83	0/2608	0.95	3/3545 (0.1%)
1	B	0.83	0/2626	0.91	4/3570 (0.1%)
All	All	0.83	0/5234	0.93	7/7115 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	144	ILE	N-CA-C	7.57	125.09	109.34
1	A	390	ILE	N-CA-C	7.17	117.78	110.82
1	A	144	ILE	N-CA-C	6.56	122.98	109.34
1	B	390	ILE	N-CA-C	6.21	117.76	111.00
1	B	192	VAL	N-CA-C	5.43	112.93	107.55
1	B	372	MET	N-CA-C	5.37	117.21	111.36
1	A	144	ILE	CB-CA-C	-5.07	102.97	111.29

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	2576	0	2473	18	0
1	B	2591	0	2485	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
3	A	87	0	0	1	0
3	B	78	0	0	2	0
All	All	5333	0	4958	37	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 4.

All (37) 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:13:THR:HG23	1:A:14:PRO:O	1.66	0.95
1:B:13:THR:HG23	1:B:14:PRO:O	1.68	0.94
1:A:13:THR:CG2	1:A:14:PRO:O	2.33	0.76
1:B:13:THR:CG2	1:B:14:PRO:O	2.36	0.72
1:A:13:THR:HG21	1:A:263:GLY:HA2	1.75	0.67
1:B:13:THR:HG21	1:B:263:GLY:HA2	1.78	0.64
1:A:135:ALA:HB1	1:A:225:PHE:HE1	1.67	0.58
1:B:164:ARG:NH2	3:B:480:HOH:O	2.37	0.58
1:B:391:GLY:O	1:B:393:GLY:N	2.32	0.56
1:A:144:ILE:HG22	1:A:259:GLY:HA2	1.88	0.55
1:B:326:LEU:HD13	1:B:387:THR:HG23	1.90	0.53
1:B:390:ILE:N	1:B:391:GLY:CA	2.72	0.53
1:A:326:LEU:HD13	1:A:387:THR:HG23	1.91	0.52
1:B:390:ILE:N	1:B:391:GLY:HA3	2.26	0.50
1:B:113:LEU:HD23	1:B:270:GLY:HA3	1.93	0.50
1:B:100:ASN:ND2	3:B:419:HOH:O	2.46	0.48
3:A:459:HOH:O	1:B:291:THR:HG21	2.14	0.48
1:A:112:ASP:O	1:A:113:LEU:HD23	2.16	0.46
1:B:318:ILE:HD11	1:B:341:LEU:HD22	1.98	0.45
1:B:388:LEU:HD23	1:B:388:LEU:N	2.32	0.45
1:A:318:ILE:HD13	1:A:341:LEU:O	2.17	0.45
1:A:136:THR:CB	1:A:142:TYR:O	2.65	0.45
1:A:326:LEU:HD22	1:A:337:PHE:CG	2.51	0.45
1:B:54:MET:HE3	1:B:73:ALA:HB3	2.00	0.44
1:A:54:MET:HE3	1:A:73:ALA:CB	2.48	0.44
1:B:144:ILE:N	1:B:145:GLY:HA2	2.33	0.44
1:A:117:GLY:HA2	1:A:366:ALA:HB2	2.00	0.43
1:A:135:ALA:HB2	1:A:147:VAL:HA	2.00	0.43
1:A:164:ARG:HD2	1:A:168:ASP:OD2	2.19	0.43
1:A:390:ILE:N	1:A:391:GLY:HA3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:ILE:HD11	1:A:341:LEU:HB3	2.01	0.42
1:B:372:MET:HE2	1:B:372:MET:HA	2.01	0.42
1:A:390:ILE:N	1:A:391:GLY:CA	2.82	0.41
1:B:56:LEU:HD12	1:B:70:ALA:HA	2.03	0.41
1:A:307:THR:O	1:A:310:VAL:HG12	2.21	0.40
1:B:135:ALA:HB1	1:B:225:PHE:HE1	1.86	0.40
1:B:8:TYR:CZ	1:B:275:GLY:HA3	2.56	0.40

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	348/407 (86%)	338 (97%)	6 (2%)	4 (1%)	11	10
1	B	347/407 (85%)	338 (97%)	8 (2%)	1 (0%)	36	42
All	All	695/814 (85%)	676 (97%)	14 (2%)	5 (1%)	18	19

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	392	GLY
1	A	19	LYS
1	A	144	ILE
1	A	145	GLY
1	A	391	GLY

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	248/314 (79%)	240 (97%)	8 (3%)	34	47
1	B	250/314 (80%)	242 (97%)	8 (3%)	34	47
All	All	498/628 (79%)	482 (97%)	16 (3%)	34	47

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	THR
1	A	94	SER
1	A	108	SER
1	A	139	GLU
1	A	144	ILE
1	A	291	THR
1	A	318	ILE
1	A	345	ASP
1	B	13	THR
1	B	100	ASN
1	B	136	THR
1	B	139	GLU
1	B	312	ASP
1	B	318	ILE
1	B	345	ASP
1	B	380	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	243	HIS
1	A	327	ASN
1	A	359	HIS

5.3.3 RNA ⓘ

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 1 ligands modelled in this entry, 1 is 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

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	360/407 (88%)	0.35	31 (8%) 16 14	18, 36, 59, 77	0
1	B	359/407 (88%)	0.29	20 (5%) 30 27	17, 35, 60, 77	0
All	All	719/814 (88%)	0.32	51 (7%) 22 19	17, 36, 59, 77	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	THR	5.8
1	A	136	THR	5.7
1	A	144	ILE	5.2
1	A	134	TRP	5.1
1	A	141	ASN	4.9
1	A	145	GLY	4.6
1	A	138	PRO	4.6
1	B	146	PHE	4.1
1	A	390	ILE	4.0
1	A	300	LEU	3.9
1	A	392	GLY	3.8
1	A	393	GLY	3.8
1	A	137	ASP	3.7
1	A	142	TYR	3.6
1	A	135	ALA	3.5
1	B	89	ASN	3.5
1	B	134	TRP	3.4
1	B	300	LEU	3.4
1	B	141	ASN	3.3
1	A	391	GLY	3.3
1	B	239	LEU	3.3
1	A	143	ARG	3.2
1	A	240	GLN	3.2
1	B	136	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	140	THR	3.1
1	B	301	THR	3.1
1	A	20	ASN	2.9
1	A	93	ALA	2.8
1	B	390	ILE	2.8
1	A	299	MET	2.7
1	B	19	LYS	2.7
1	A	19	LYS	2.7
1	A	82	THR	2.7
1	A	394	MET	2.6
1	B	82	THR	2.6
1	B	299	MET	2.5
1	B	94	SER	2.4
1	B	245	VAL	2.4
1	A	110	TRP	2.4
1	A	139	GLU	2.3
1	A	301	THR	2.3
1	A	403	VAL	2.3
1	B	392	GLY	2.3
1	A	59	VAL	2.3
1	A	89	ASN	2.2
1	B	216	GLU	2.2
1	B	200	LEU	2.1
1	A	146	PHE	2.1
1	B	135	ALA	2.1
1	B	244	TRP	2.1
1	A	45	ASP	2.0

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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
2	CL	B	404	1/1	0.85	0.17	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.