



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:53 PM GMT

PDB ID : 4N45
Title : Crystal structure of reduced form of thiolase from Clostridium acetobutylicum
Authors : Kim, S.; Ha, S.C.; Ahn, J.W.; Kim, E.J.; Lim, J.H.; Kim, K.J.
Deposited on : 2013-10-08
Resolution : 1.60 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

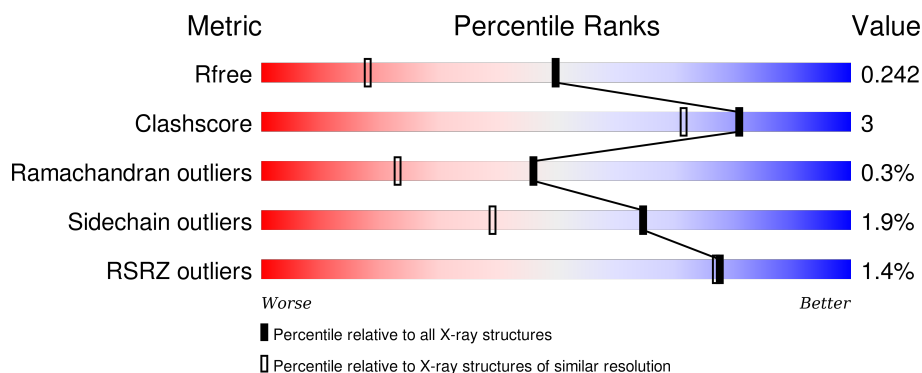
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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}	91344	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	400	<div> <div></div> <div>91% 7% •</div> </div>
1	B	400	<div> <div>2%</div> <div>90% 8% ••</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6337 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	392	Total	C	N	O	S	0	0	0
			2892	1824	501	553	14			
1	B	392	Total	C	N	O	S	0	0	0
			2892	1824	501	553	14			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	378	SER	CYS	ENGINEERED MUTATION	UNP F0K5D8
A	393	LEU	-	EXPRESSION TAG	UNP F0K5D8
A	394	GLU	-	EXPRESSION TAG	UNP F0K5D8
A	395	HIS	-	EXPRESSION TAG	UNP F0K5D8
A	396	HIS	-	EXPRESSION TAG	UNP F0K5D8
A	397	HIS	-	EXPRESSION TAG	UNP F0K5D8
A	398	HIS	-	EXPRESSION TAG	UNP F0K5D8
A	399	HIS	-	EXPRESSION TAG	UNP F0K5D8
A	400	HIS	-	EXPRESSION TAG	UNP F0K5D8
B	378	SER	CYS	ENGINEERED MUTATION	UNP F0K5D8
B	393	LEU	-	EXPRESSION TAG	UNP F0K5D8
B	394	GLU	-	EXPRESSION TAG	UNP F0K5D8
B	395	HIS	-	EXPRESSION TAG	UNP F0K5D8
B	396	HIS	-	EXPRESSION TAG	UNP F0K5D8
B	397	HIS	-	EXPRESSION TAG	UNP F0K5D8
B	398	HIS	-	EXPRESSION TAG	UNP F0K5D8
B	399	HIS	-	EXPRESSION TAG	UNP F0K5D8
B	400	HIS	-	EXPRESSION TAG	UNP F0K5D8

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	304	Total	O	0	0
			304	304		

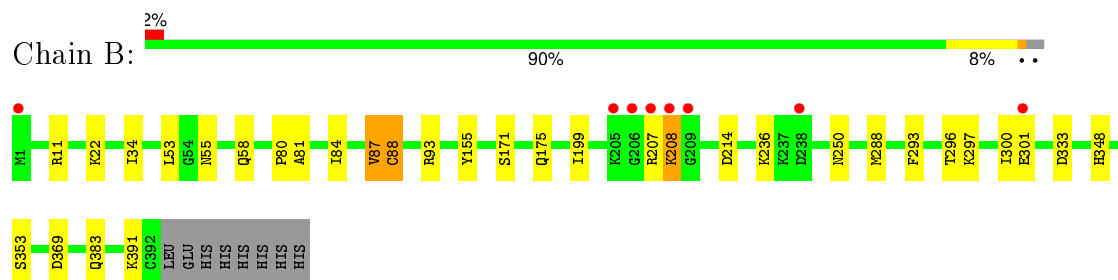
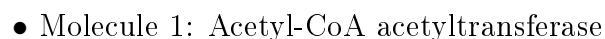
Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	249	Total	O	0	0
			249	249		

i

- Molecule 1: Acetyl-CoA acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	203.68 Å 54.14 Å 73.20 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.60 32.55 – 1.59	Depositor EDS
% Data completeness (in resolution range)	91.5 (50.00-1.60) 91.5 (32.55-1.59)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 1.59 Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.195 , 0.234 0.203 , 0.242	Depositor DCC
R_{free} test set	4905 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	16.8	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 46.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Outliers	0 of 99451 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6337	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.91	2/2933 (0.1%)	0.92	3/3958 (0.1%)
1	B	0.90	1/2933 (0.0%)	0.92	4/3958 (0.1%)
All	All	0.91	3/5866 (0.1%)	0.92	7/7916 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	378	SER	CB-OG	7.38	1.51	1.42
1	A	88	CYS	CB-SG	-7.13	1.70	1.82
1	B	88	CYS	CB-SG	-6.95	1.70	1.82

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	88	CYS	CA-CB-SG	-7.71	100.13	114.00
1	B	333	ASP	CB-CG-OD1	6.60	124.24	118.30
1	A	333	ASP	CB-CG-OD1	6.57	124.21	118.30
1	A	88	CYS	CA-CB-SG	-6.50	102.30	114.00
1	B	214	ASP	CB-CG-OD1	6.24	123.92	118.30
1	A	377	LEU	CA-CB-CG	5.05	126.92	115.30
1	B	93	ARG	NE-CZ-NH1	-5.01	117.80	120.30

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	2892	0	2963	24	0
1	B	2892	0	2963	22	0
2	A	304	0	0	3	0
2	B	249	0	0	2	0
All	All	6337	0	5926	39	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 3.

All (39) 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:362:VAL:HG12	1:A:389:LEU:CD1	2.20	0.71
1:A:84:ILE:CD1	1:B:84:ILE:HD12	2.25	0.67
1:A:79:ILE:HD11	2:A:718:HOH:O	1.93	0.67
1:A:362:VAL:HG12	1:A:389:LEU:HD13	1.75	0.66
1:B:22:LYS:HE2	2:B:713:HOH:O	1.98	0.63
1:A:84:ILE:HD12	1:B:84:ILE:HD12	1.84	0.59
1:A:250:ASN:HD22	1:A:348:HIS:H	1.51	0.59
1:A:383:GLN:HE22	1:B:81:ALA:H	1.52	0.58
1:A:362:VAL:CG1	1:A:389:LEU:CD1	2.82	0.57
1:A:133:ARG:HD2	2:A:727:HOH:O	2.07	0.55
1:A:133:ARG:HH11	1:A:133:ARG:HG2	1.72	0.54
1:B:293:PHE:CZ	1:B:297:LYS:HD2	2.43	0.53
1:A:81:ALA:H	1:B:383:GLN:HE22	1.56	0.53
1:B:250:ASN:HD22	1:B:348:HIS:H	1.56	0.52
1:A:250:ASN:ND2	1:A:348:HIS:H	2.07	0.52
1:A:85:ASN:HD22	1:B:58:GLN:NE2	2.08	0.52
1:B:55:ASN:HD22	1:B:58:GLN:HG2	1.74	0.52
1:A:88:CYS:HG	1:A:348:HIS:CE1	2.29	0.51
1:B:171:SER:O	1:B:175:GLN:HG3	2.11	0.51
1:B:296:THR:HG22	1:B:300:ILE:HD12	1.93	0.50
1:B:34:ILE:HD11	1:B:53:LEU:HD11	1.94	0.49
1:A:55:ASN:HD22	1:A:58:GLN:HG2	1.78	0.48
1:A:55:ASN:ND2	1:A:58:GLN:HG2	2.29	0.47
1:B:293:PHE:O	1:B:297:LYS:HG3	2.14	0.47
1:B:301:GLU:HG3	2:B:676:HOH:O	2.14	0.47
1:B:207:ARG:HB2	1:B:208:LYS:HD2	1.96	0.47
1:B:55:ASN:ND2	1:B:58:GLN:HG2	2.30	0.46
1:A:40:LYS:NZ	2:A:765:HOH:O	2.48	0.46
1:B:250:ASN:ND2	1:B:348:HIS:H	2.14	0.45
1:B:11:ARG:O	1:B:199:ILE:HA	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:CYS:HG	1:B:348:HIS:CE1	2.35	0.44
1:A:379:ILE:HB	1:A:383:GLN:HB2	2.00	0.43
1:B:369:ASP:HA	1:B:391:LYS:HE2	1.99	0.43
1:A:319:PHE:H	1:A:322:GLN:HE21	1.65	0.43
1:A:55:ASN:HD21	1:A:61:LEU:HD12	1.81	0.43
1:A:362:VAL:CG1	1:A:389:LEU:HD13	2.45	0.42
1:A:383:GLN:NE2	1:B:80:PRO:HA	2.36	0.40
1:A:317:GLU:CD	1:A:342:GLY:HA3	2.41	0.40
1:A:85:ASN:HD22	1:B:58:GLN:HE22	1.68	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	390/400 (98%)	375 (96%)	14 (4%)	1 (0%)	46	23
1	B	390/400 (98%)	378 (97%)	11 (3%)	1 (0%)	46	23
All	All	780/800 (98%)	753 (96%)	25 (3%)	2 (0%)	46	23

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	87	VAL
1	B	87	VAL

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	294/302 (97%)	289 (98%)	5 (2%)	68	44
1	B	294/302 (97%)	288 (98%)	6 (2%)	63	36
All	All	588/604 (97%)	577 (98%)	11 (2%)	65	39

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	155	TYR
1	A	207	ARG
1	A	288	MET
1	A	297	LYS
1	A	353	SER
1	B	87	VAL
1	B	155	TYR
1	B	208	LYS
1	B	236	LYS
1	B	288	MET
1	B	353	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	58	GLN
1	A	250	ASN
1	A	322	GLN
1	A	366	GLN
1	A	383	GLN
1	B	55	ASN
1	B	58	GLN
1	B	250	ASN
1	B	316	ASN
1	B	322	GLN
1	B	383	GLN

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 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 [i](#)

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

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	392/400 (98%)	-0.22	3 (0%) 87 87	11, 17, 30, 60	0
1	B	392/400 (98%)	-0.06	8 (2%) 68 67	11, 19, 35, 73	0
All	All	784/800 (98%)	-0.14	11 (1%) 78 77	11, 18, 33, 73	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	207	ARG	7.1
1	B	209	GLY	6.9
1	B	206	GLY	5.7
1	B	208	LYS	5.1
1	B	205	LYS	3.8
1	A	207	ARG	3.8
1	B	301	GLU	3.4
1	A	209	GLY	2.7
1	B	238	ASP	2.5
1	A	208	LYS	2.3
1	B	1	MET	2.3

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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.