



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 5CS4 / pdb_00005cs4
Title : Crystal structure of domains AC3-AC5 of yeast acetyl-CoA carboxylase
Authors : Wei, J.; Tong, L.
Deposited on : 2015-07-23
Resolution : 3.19 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 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) : 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

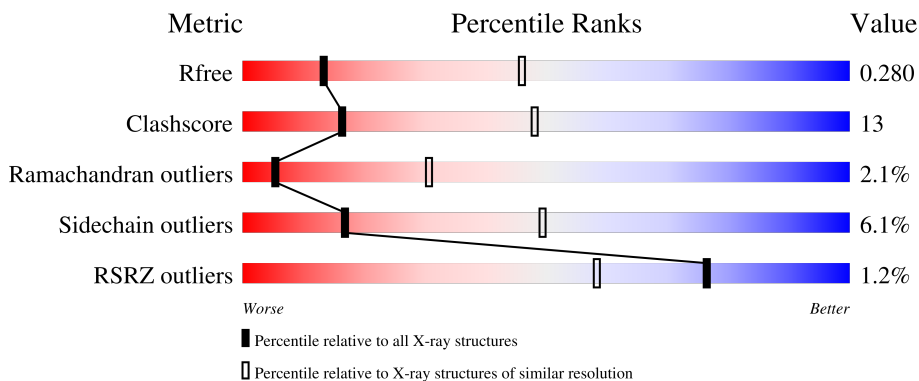
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	474	 53% 28% 15%
1	B	474	 59% 20% 19%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6353 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 carboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	402	3235	2066	555	608	1	5	0	0	0
1	B	385	3118	1997	536	579	1	5	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1504	HIS	-	expression tag	UNP Q00955
A	1505	HIS	-	expression tag	UNP Q00955
A	1506	HIS	-	expression tag	UNP Q00955
A	1507	HIS	-	expression tag	UNP Q00955
A	1508	HIS	-	expression tag	UNP Q00955
A	1509	HIS	-	expression tag	UNP Q00955
B	1504	HIS	-	expression tag	UNP Q00955
B	1505	HIS	-	expression tag	UNP Q00955
B	1506	HIS	-	expression tag	UNP Q00955
B	1507	HIS	-	expression tag	UNP Q00955
B	1508	HIS	-	expression tag	UNP Q00955
B	1509	HIS	-	expression tag	UNP Q00955

Y1356	GLY
L1367	GLU
T1358	V1467
S1359	F1469
N1362	K1470
R1363	S1471
L1364	L1472
M1365	G1473
S1366	M1479
D1367	R1481
I1368	P1495
E1373	LYS
S1378	ARG
N1379	TYR
S1380	LYS
N1383	ALA
F1393	HIS
D1394	LEU
I1395	MSE
S1396	HIS
D1399	HIS
V1400	HIS
L1415	HIS
S1422	HIS
I1427	
I1428	
I1429	
P1432	
GLN	
THR	
GLY	
A1436	
N1445	
N1446	
V1447	
SER	
GLY	
Y1450	
E1455	
M1456	
Y1457	
T1458	
E1459	
V1460	
K1461	
M1462	
ALA	
LYS	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.85Å 93.28Å 111.14Å 90.00° 100.62° 90.00°	Depositor
Resolution (Å)	42.90 – 3.19 42.90 – 3.19	Depositor EDS
% Data completeness (in resolution range)	99.8 (42.90-3.19) 99.8 (42.90-3.19)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.00 (at 3.19Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.234 , 0.287 0.233 , 0.280	Depositor DCC
R_{free} test set	980 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	74.6	Xtrriage
Anisotropy	0.206	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 43.5	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	0.92	EDS
Total number of atoms	6353	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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](#)

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	0.75	0/3294	1.00	5/4456 (0.1%)
1	B	0.69	2/3172 (0.1%)	0.96	4/4287 (0.1%)
All	All	0.72	2/6466 (0.0%)	0.98	9/8743 (0.1%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1264	MSE	CA-C	-6.10	1.46	1.52
1	B	1478	MSE	CA-C	-5.53	1.46	1.53

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	1478	MSE	CB-CA-C	-7.15	101.95	111.82
1	B	1445	ASN	N-CA-C	6.00	119.26	109.24
1	A	1478	MSE	CA-CB-CG	-5.71	102.68	114.10
1	A	1405	GLY	N-CA-C	-5.50	103.33	111.03
1	A	1448	SER	N-CA-C	-5.29	104.72	110.91

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1279	ASN	Peptide

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	3235	0	3242	99	0
1	B	3118	0	3134	68	0
All	All	6353	0	6376	165	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 13.

The worst 5 of 165 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:1272:TYR:O	1:A:1318:ARG:NH1	1.93	1.01
1:B:1087:LEU:HD11	1:B:1264:MSE:HE2	1.54	0.89
1:B:1272:TYR:O	1:B:1318:ARG:NH2	2.08	0.86
1:A:1036:SER:O	1:A:1037:VAL:C	2.40	0.64
1:A:1124:VAL:HG23	1:A:1192:GLN:HG2	1.79	0.64

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	396/474 (84%)	330 (83%)	57 (14%)	9 (2%)	5 29
1	B	371/474 (78%)	314 (85%)	50 (14%)	7 (2%)	6 33
All	All	767/948 (81%)	644 (84%)	107 (14%)	16 (2%)	5 31

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1190	LEU
1	A	1449	GLY
1	B	1086	LEU
1	B	1190	LEU
1	A	1230	GLU

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	360/414 (87%)	337 (94%)	23 (6%)	16	48
1	B	348/414 (84%)	328 (94%)	20 (6%)	18	51
All	All	708/828 (86%)	665 (94%)	43 (6%)	17	49

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1173	ARG
1	B	1373	GLU
1	B	1178	MSE
1	B	1292	ILE
1	B	1422	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1299	GLN
1	B	1346	HIS
1	A	1291	HIS
1	A	1309	ASN
1	B	1046	HIS

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 [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	397/474 (83%)	-0.07	3 (0%) 82 67	28, 72, 112, 136	0
1	B	380/474 (80%)	0.08	6 (1%) 70 51	47, 85, 121, 148	0
All	All	777/948 (81%)	0.00	9 (1%) 76 58	28, 78, 117, 148	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1447	VAL	4.2
1	A	1124	VAL	3.1
1	B	1087	LEU	2.9
1	A	1092	HIS	2.6
1	A	1197	ILE	2.4

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.