



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 08:14 PM UTC

PDB ID : 4RCN / pdb_00004rcn
Title : Structure and function of a single-chain, multi-domain long-chain acyl-coa carboxylase
Authors : Tran, T.H.; Tong, L.
Deposited on : 2014-09-16
Resolution : 3.01 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
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

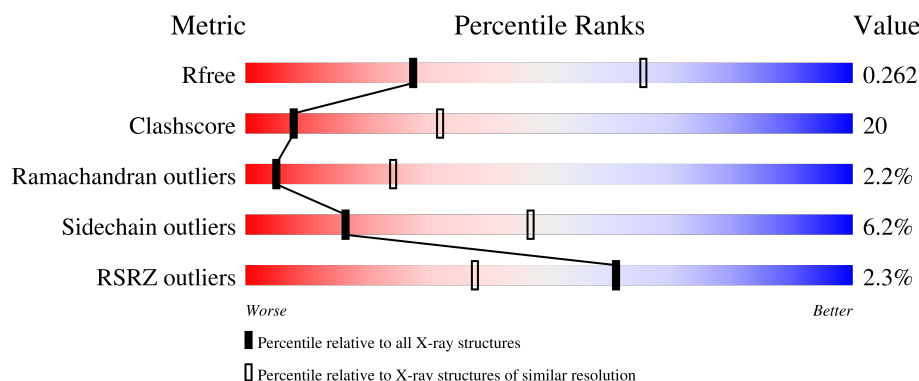
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.01 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	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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	1093	2% 54% 31% • 11%
1	B	1093	3% 56% 32% • 9%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14630 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 long-chain acyl-CoA carboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	972	Total	C	N	O	S	0	0	0
			7211	4528	1319	1340	24			
1	B	1000	Total	C	N	O	S	0	0	0
			7419	4661	1354	1377	27			

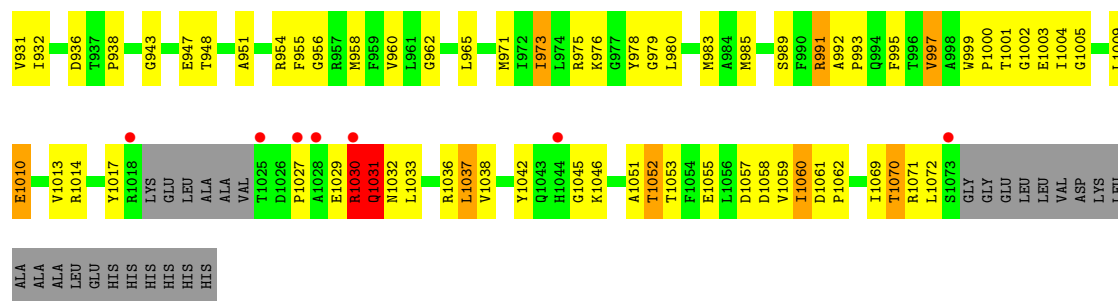
There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1076	GLU	-	expression tag	UNP Q73VY8
A	1077	LEU	-	expression tag	UNP Q73VY8
A	1078	LEU	-	expression tag	UNP Q73VY8
A	1079	VAL	-	expression tag	UNP Q73VY8
A	1080	ASP	-	expression tag	UNP Q73VY8
A	1081	LYS	-	expression tag	UNP Q73VY8
A	1082	LEU	-	expression tag	UNP Q73VY8
A	1083	ALA	-	expression tag	UNP Q73VY8
A	1084	ALA	-	expression tag	UNP Q73VY8
A	1085	ALA	-	expression tag	UNP Q73VY8
A	1086	LEU	-	expression tag	UNP Q73VY8
A	1087	GLU	-	expression tag	UNP Q73VY8
A	1088	HIS	-	expression tag	UNP Q73VY8
A	1089	HIS	-	expression tag	UNP Q73VY8
A	1090	HIS	-	expression tag	UNP Q73VY8
A	1091	HIS	-	expression tag	UNP Q73VY8
A	1092	HIS	-	expression tag	UNP Q73VY8
A	1093	HIS	-	expression tag	UNP Q73VY8
B	1076	GLU	-	expression tag	UNP Q73VY8
B	1077	LEU	-	expression tag	UNP Q73VY8
B	1078	LEU	-	expression tag	UNP Q73VY8
B	1079	VAL	-	expression tag	UNP Q73VY8
B	1080	ASP	-	expression tag	UNP Q73VY8
B	1081	LYS	-	expression tag	UNP Q73VY8
B	1082	LEU	-	expression tag	UNP Q73VY8

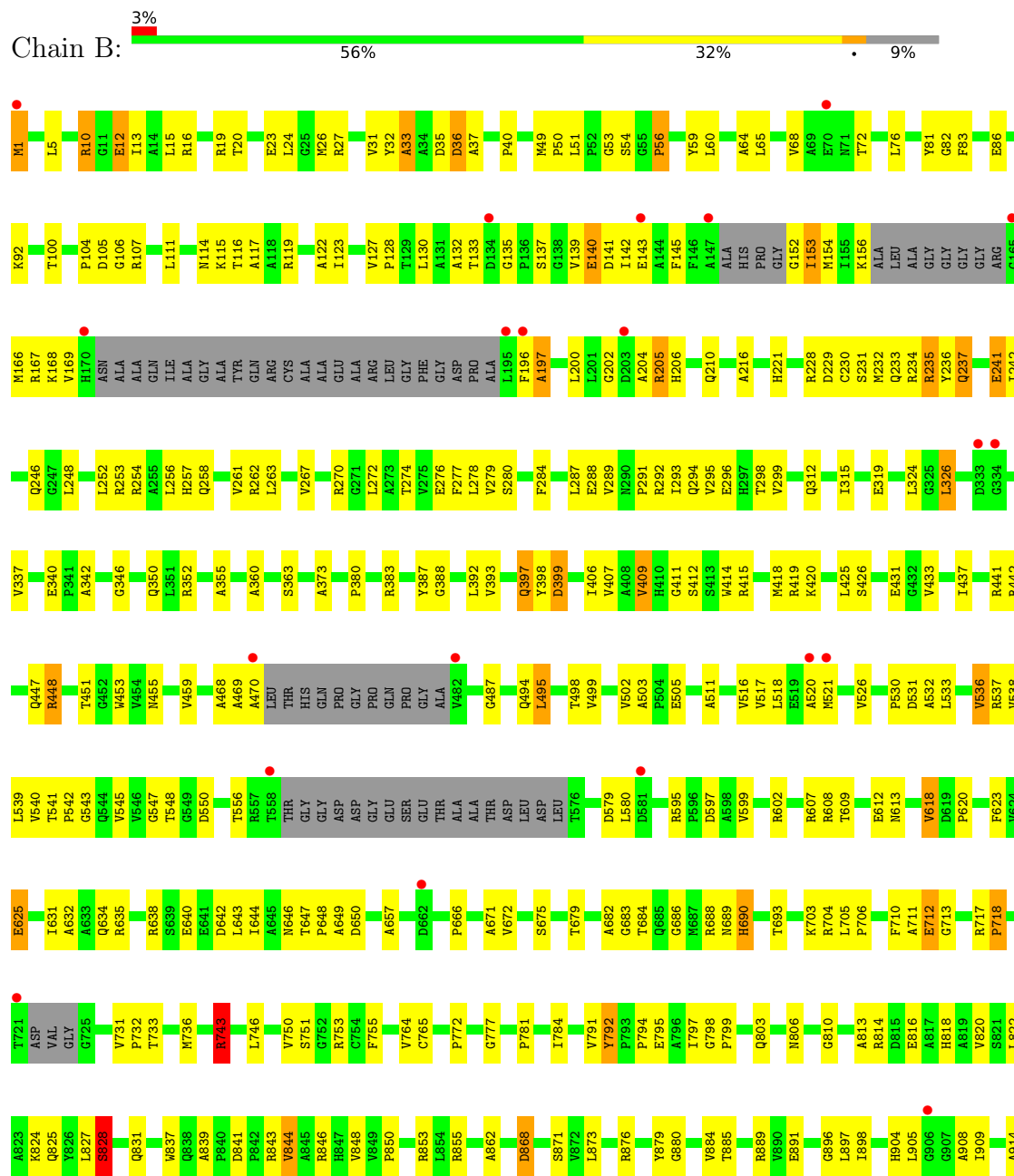
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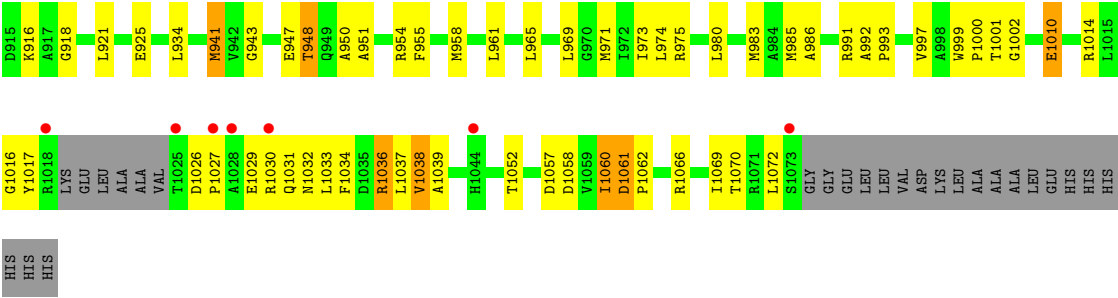
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Chain	Residue	Modelled	Actual	Comment	Reference
B	1083	ALA	-	expression tag	UNP Q73VY8
B	1084	ALA	-	expression tag	UNP Q73VY8
B	1085	ALA	-	expression tag	UNP Q73VY8
B	1086	LEU	-	expression tag	UNP Q73VY8
B	1087	GLU	-	expression tag	UNP Q73VY8
B	1088	HIS	-	expression tag	UNP Q73VY8
B	1089	HIS	-	expression tag	UNP Q73VY8
B	1090	HIS	-	expression tag	UNP Q73VY8
B	1091	HIS	-	expression tag	UNP Q73VY8
B	1092	HIS	-	expression tag	UNP Q73VY8
B	1093	HIS	-	expression tag	UNP Q73VY8



• Molecule 1: long-chain acyl-CoA carboxylase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	220.88Å 220.88Å 220.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.39 – 3.01 49.39 – 3.01	Depositor EDS
% Data completeness (in resolution range)	91.0 (49.39-3.01) 91.1 (49.39-3.01)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 3.01Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.209 , 0.262 0.209 , 0.262	Depositor DCC
R_{free} test set	3516 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	63.4	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14630	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.77% 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	0.48	0/7339	1.02	30/9980 (0.3%)
1	B	0.51	0/7550	1.00	21/10259 (0.2%)
All	All	0.50	0/14889	1.01	51/20239 (0.3%)

There are no bond length outliers.

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	764	VAL	N-CA-C	-9.28	103.99	112.90
1	B	1061	ASP	N-CA-C	-7.26	98.67	109.42
1	A	37	ALA	N-CA-C	7.03	118.95	111.28
1	A	1060	ILE	N-CA-C	6.99	119.93	109.17
1	A	387	TYR	N-CA-C	-6.79	106.19	114.75

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	7211	0	7244	285	0
1	B	7419	0	7452	300	0
All	All	14630	0	14696	577	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 20.

The worst 5 of 577 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:632:ALA:H	1:A:647:THR:HG21	1.27	1.00
1:A:504:PRO:HD2	1:A:509:TYR:OH	1.65	0.96
1:A:210:GLN:HE21	1:A:228:ARG:HH12	1.03	0.94
1:B:753:ARG:HG2	1:B:753:ARG:HH11	1.34	0.92
1:B:92:LYS:HE2	1:B:107:ARG:NH1	1.84	0.92

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	958/1093 (88%)	870 (91%)	64 (7%)	24 (2%)	4	21
1	B	984/1093 (90%)	893 (91%)	73 (7%)	18 (2%)	6	29
All	All	1942/2186 (89%)	1763 (91%)	137 (7%)	42 (2%)	5	24

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	200	LEU
1	A	520	ALA
1	A	712	GLU
1	B	360	ALA
1	B	520	ALA

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	718/796 (90%)	672 (94%)	46 (6%)	16	46
1	B	738/796 (93%)	694 (94%)	44 (6%)	17	48
All	All	1456/1592 (92%)	1366 (94%)	90 (6%)	16	47

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	241	GLU
1	B	672	VAL
1	B	319	GLU
1	B	442	ARG
1	B	764	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	397	GLN
1	B	904	HIS
1	B	514	GLN
1	B	670	GLN
1	B	1032	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

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	972/1093 (88%)	-0.11	18 (1%)	66 43	35, 63, 96, 139	0
1	B	1000/1093 (91%)	-0.10	28 (2%)	55 32	34, 61, 101, 138	0
All	All	1972/2186 (90%)	-0.10	46 (2%)	61 38	34, 62, 99, 139	0

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	479	PRO	4.7
1	B	195	LEU	4.4
1	B	470	ALA	4.0
1	B	482	VAL	3.8
1	A	1025	THR	3.4

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.