



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:44 PM GMT

PDB ID : 1UYV
Title : Acetyl-CoA carboxylase carboxyltransferase domain L1705I/V1967I mutant
Authors : Zhang, H.; Tweel, B.; Tong, L.
Deposited on : 2004-03-02
Resolution : 2.60 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
<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

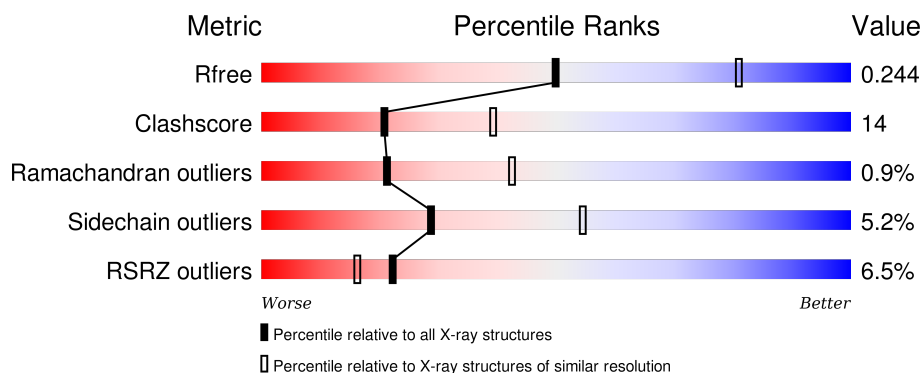
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	737	<div> <div>5%</div> <div> <div></div> <div>54%</div> <div>22%</div> <div>•</div> <div>22%</div> </div> </div>
1	B	737	<div> <div>4%</div> <div> <div></div> <div>51%</div> <div>23%</div> <div>•</div> <div>25%</div> </div> </div>
1	C	737	<div> <div>6%</div> <div> <div></div> <div>53%</div> <div>22%</div> <div>•</div> <div>23%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13666 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.

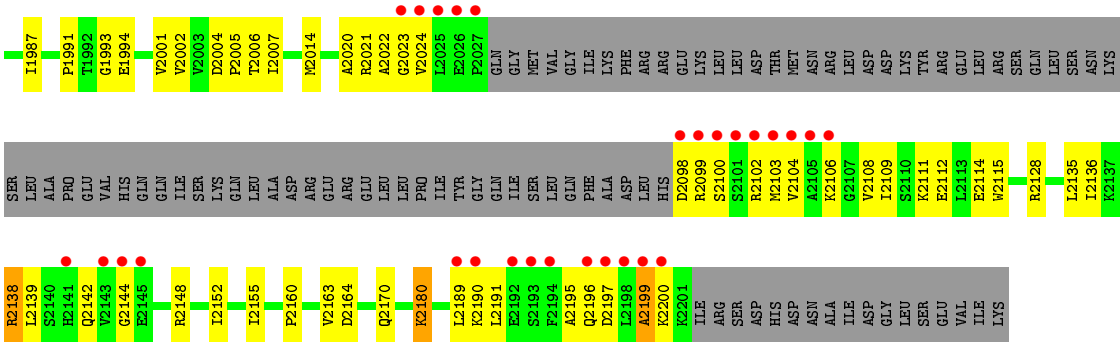
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	572	Total	C	N	O	S	0	0	1
			4542	2895	786	845	16			
1	B	553	Total	C	N	O	S	0	0	1
			4399	2805	759	821	14			
1	C	571	Total	C	N	O	S	0	0	1
			4533	2884	786	847	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1705	ILE	LEU	ENGINEERED MUTATION	UNP Q00955
A	1967	ILE	VAL	ENGINEERED MUTATION	UNP Q00955
B	1705	ILE	LEU	ENGINEERED MUTATION	UNP Q00955
B	1967	ILE	VAL	ENGINEERED MUTATION	UNP Q00955
C	1705	ILE	LEU	ENGINEERED MUTATION	UNP Q00955
C	1967	ILE	VAL	ENGINEERED MUTATION	UNP Q00955

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	75	Total	O	0	0
			75	75		
2	B	68	Total	O	0	0
			68	68		
2	C	49	Total	O	0	0
			49	49		



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	247.17Å 123.73Å 145.64Å 90.00° 94.20° 90.00°	Depositor
Resolution (Å)	27.56 – 2.60 27.56 – 2.52	Depositor EDS
% Data completeness (in resolution range)	87.2 (27.56-2.60) 88.8 (27.56-2.52)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.51Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.212 , 0.237 0.219 , 0.244	Depositor DCC
R_{free} test set	12751 reflections (11.39%)	DCC
Wilson B-factor (Å ²)	42.2	Xtriage
Anisotropy	0.349	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 135935 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	13666	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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	0.40	0/4647	0.58	0/6299
1	B	0.40	0/4503	0.58	0/6109
1	C	0.39	0/4635	0.56	0/6280
All	All	0.40	0/13785	0.57	0/18688

There are no bond length outliers.

There are no bond angle outliers.

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	4542	0	4484	128	0
1	B	4399	0	4326	137	0
1	C	4533	0	4467	137	0
2	A	75	0	0	0	0
2	B	68	0	0	1	0
2	C	49	0	0	2	0
All	All	13666	0	13277	386	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 14.

The worst 5 of 386 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:C:2144:GLY:HA3	1:C:2197:ASP:HB3	1.46	0.94
1:C:1759:ALA:H	1:C:1774:ASN:HD21	1.07	0.92
1:B:1815:ASN:H	1:B:1944:GLN:HE22	0.97	0.92
1:B:1730:CYS:HA	1:B:1752:GLN:HE21	1.36	0.90
1:A:1772:THR:H	1:A:1776:GLN:HE22	1.16	0.90

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	566/737 (77%)	527 (93%)	34 (6%)	5 (1%)	21	42
1	B	547/737 (74%)	507 (93%)	37 (7%)	3 (0%)	34	60
1	C	565/737 (77%)	521 (92%)	37 (6%)	7 (1%)	16	33
All	All	1678/2211 (76%)	1555 (93%)	108 (6%)	15 (1%)	21	42

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1529	ASP
1	A	1731	ARG
1	A	2142	GLN
1	B	2142	GLN
1	C	2199	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	480/628 (76%)	458 (95%)	22 (5%)	33	61
1	B	465/628 (74%)	440 (95%)	25 (5%)	27	52
1	C	479/628 (76%)	452 (94%)	27 (6%)	26	50
All	All	1424/1884 (76%)	1350 (95%)	74 (5%)	29	54

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1735	ILE
1	B	1961	ARG
1	C	2006	THR
1	B	1777	LEU
1	B	1797	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1752	GLN
1	B	1934	GLN
1	C	1941	ASN
1	B	1815	ASN
1	B	1944	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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](#)

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	572/737 (77%)	-0.15	35 (6%)	25	18	21, 41, 93, 100	0
1	B	553/737 (75%)	-0.21	29 (5%)	31	24	22, 42, 84, 100	0
1	C	571/737 (77%)	-0.04	47 (8%)	14	10	23, 45, 97, 100	0
All	All	1696/2211 (76%)	-0.13	111 (6%)	22	16	21, 43, 90, 100	0

The worst 5 of 111 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2027	PRO	6.9
1	C	2143	VAL	6.6
1	C	2197	ASP	6.4
1	A	1492	TRP	6.0
1	C	1702	VAL	5.7

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.