



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 11:24 pm BST

PDB ID : 1NM8  
Title : Structure of Human Carnitine Acetyltransferase: Molecular Basis for Fatty Acyl Transfer  
Authors : Wu, D.; Govindasamy, L.; Lian, W.; Gu, Y.; Kukar, T.; Agbandje-McKenna, M.; McKenna, R.  
Deposited on : 2003-01-09  
Resolution : 1.60 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](mailto: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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

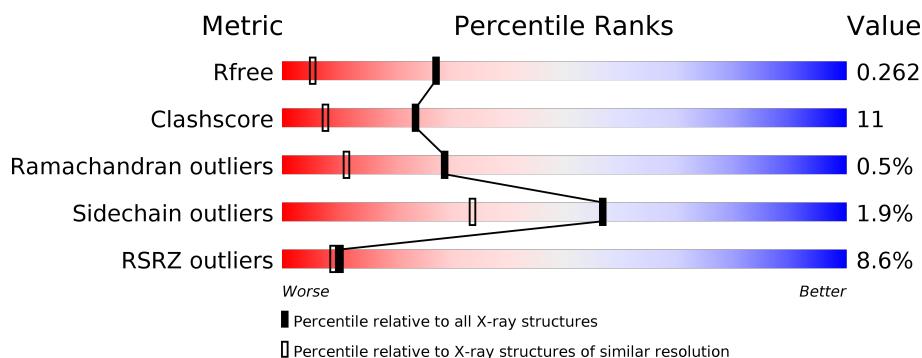
# 1 Overall quality at a glance

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))
$R_{free}$	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (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  $\geq 3$ , 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	616	<div> <div>8%</div> <div>77%</div> <div>17%</div> <div>• •</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5186 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 Carnitine O-acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	591	4714	3006	810	872	26	0	0	0

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	CLONING ARTIFACT	UNP P43155
A	2	ARG	-	CLONING ARTIFACT	UNP P43155
A	3	GLY	-	CLONING ARTIFACT	UNP P43155
A	4	SER	-	CLONING ARTIFACT	UNP P43155
A	5	HIS	-	CLONING ARTIFACT	UNP P43155
A	6	HIS	-	CLONING ARTIFACT	UNP P43155
A	7	HIS	-	CLONING ARTIFACT	UNP P43155
A	8	HIS	-	CLONING ARTIFACT	UNP P43155
A	9	HIS	-	CLONING ARTIFACT	UNP P43155
A	10	HIS	-	CLONING ARTIFACT	UNP P43155
A	11	THR	-	CLONING ARTIFACT	UNP P43155
A	12	ASP	-	CLONING ARTIFACT	UNP P43155
A	13	PRO	-	CLONING ARTIFACT	UNP P43155
A	67	GLU	GLY	VARIANT	UNP P43155
A	328	PRO	PHE	VARIANT	UNP P43155
A	496	ASP	GLY	VARIANT	UNP P43155
A	606	ILE	-	CLONING ARTIFACT	UNP P43155
A	607	SER	-	CLONING ARTIFACT	UNP P43155
A	608	GLU	-	CLONING ARTIFACT	UNP P43155
A	609	GLU	-	CLONING ARTIFACT	UNP P43155
A	610	ASP	-	CLONING ARTIFACT	UNP P43155
A	611	LEU	-	CLONING ARTIFACT	UNP P43155
A	612	SER	-	CLONING ARTIFACT	UNP P43155
A	613	LEU	-	CLONING ARTIFACT	UNP P43155
A	614	ILE	-	CLONING ARTIFACT	UNP P43155
A	615	SER	-	CLONING ARTIFACT	UNP P43155
A	616	GLY	-	CLONING ARTIFACT	UNP P43155

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	472	Total 472	O 472	0	0



- Molecule 1: Carnitine O-acetyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	137.50 Å 84.50 Å 57.50 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.60 27.22 – 1.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-1.60) 87.0 (27.22-1.60)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.70 (at 1.60 Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.208 , 0.232 0.242 , 0.262	Depositor DCC
$R_{free}$ test set	3914 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.0	Xtriage
Anisotropy	0.474	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 41.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5186	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.54% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.51	5/4829 (0.1%)	0.70	11/6550 (0.2%)

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 (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	302	PHE	N-CA	-12.39	1.21	1.46
1	A	448	ARG	N-CA	-12.36	1.21	1.46
1	A	35	PRO	CA-CB	9.01	1.71	1.53
1	A	296	ASN	N-CA	7.56	1.61	1.46
1	A	425	GLY	N-CA	-6.34	1.36	1.46

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	296	ASN	N-CA-CB	15.95	139.31	110.60
1	A	202	PRO	CA-N-CD	-8.75	99.25	111.50
1	A	35	PRO	N-CA-CB	-7.46	94.35	103.30
1	A	425	GLY	N-CA-C	-7.38	94.66	113.10
1	A	183	THR	N-CA-CB	6.29	122.25	110.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	295	LEU	Peptide

## 5.2 Too-close contacts

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	4714	0	4689	105	2
2	A	472	0	0	8	2
All	All	5186	0	4689	105	2

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 11.

The worst 5 of 105 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:81:TRP:CD2	1:A:497:ARG:NH2	2.14	1.16
1:A:280:ARG:NH1	1:A:392:VAL:HG21	1.65	1.10
1:A:81:TRP:CE2	1:A:497:ARG:NH2	2.19	1.10
1:A:280:ARG:HH12	1:A:392:VAL:HG21	1.21	1.04
1:A:274:VAL:HB	2:A:1045:HOH:O	0.86	1.03

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ARG:NH2	2:A:933:HOH:O[2_565]	1.74	0.46
1:A:351:MET:SD	2:A:880:HOH:O[4_556]	1.78	0.42

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	589/616 (96%)	574 (98%)	12 (2%)	3 (0%)	29	11

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	274	VAL
1	A	276	GLU
1	A	273	ARG

### 5.3.2 Protein sidechains ⓘ

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	521/543 (96%)	511 (98%)	10 (2%)	57	34

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	275	SER
1	A	306	LEU
1	A	509	ASP
1	A	272	PRO
1	A	483	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	289	HIS
1	A	299	ASN
1	A	527	HIS
1	A	282	HIS
1	A	529	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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	591/616 (95%)	0.86	51 (8%) 10 9	9, 15, 27, 44	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	274	VAL	13.0
1	A	279	TYR	11.1
1	A	273	ARG	8.3
1	A	351	MET	6.9
1	A	176	LYS	6.7

### 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.