

# Full wwPDB X-ray Structure Validation Report (i)

#### Jan 3, 2024 – 04:27 pm GMT

PDB ID : 5AGH

Title : Crystal structure of the LeuRS editing domain of Candida albicans Mutant

K510A

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Deposited on : 2015-02-02

Resolution : 1.81 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

 $Mol Probity \quad : \quad 4.02b\text{-}467$ 

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

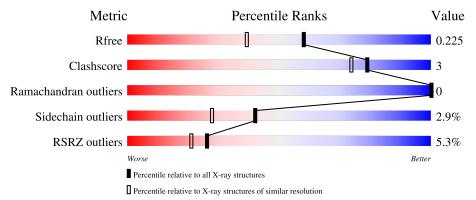
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.81 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
$R_{free}$	130704	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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 <=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		
			5%		
1	A	261	86%	8%	6%



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2100 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 POTENTIAL CYTOSOLIC LEUCYL TRNA SYNTHETASE.

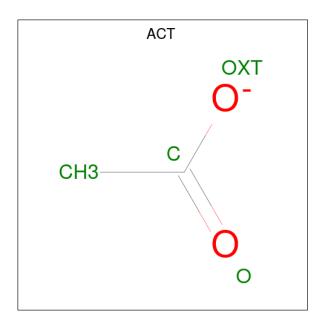
$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	246	Total 1945	C 1249	N 312	O 375	S 9	0	3	1

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	278	MET	-	expression tag	UNP Q5A9A4
A	279	GLY	-	expression tag	UNP Q5A9A4
A	531	LEU	-	expression tag	UNP Q5A9A4
A	532	GLU	-	expression tag	UNP Q5A9A4
A	533	HIS	-	expression tag	UNP Q5A9A4
A	534	HIS	-	expression tag	UNP Q5A9A4
A	535	HIS	-	expression tag	UNP Q5A9A4
Α	536	HIS	-	expression tag	UNP Q5A9A4
A	537	HIS	-	expression tag	UNP Q5A9A4
A	538	HIS	-	expression tag	UNP Q5A9A4
A	360	GLU	GLN	conflict	UNP Q5A9A4
A	510	ALA	LYS	engineered mutation	UNP Q5A9A4

• Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0

### • Molecule 3 is water.

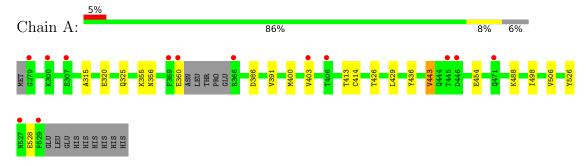
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	147	Total O 147 147	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: POTENTIAL CYTOSOLIC LEUCYL TRNA SYNTHETASE





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	89.35Å 41.10Å 67.26Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $106.71^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	64.42 - 1.81	Depositor
rtesolution (A)	25.96 - 1.81	EDS
% Data completeness	90.4 (64.42-1.81)	Depositor
(in resolution range)	90.5 (25.96-1.81)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.06 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
D D.	0.165 , 0.218	Depositor
$R, R_{free}$	0.176 , $0.225$	DCC
$R_{free}$ test set	998 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.2	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.39, 56.2	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2100	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.37% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 5 Model quality (i)

## 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ACT

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).

Mal	Chain	Boı	nd lengths	Bond	angles
IVIOI	Mol Chain RMSZ		# Z  > 5	RMSZ	# Z >5
1	A	0.57	1/1993~(0.1%)	0.70	0/2698

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
1	A	528	GLU	C-N	-5.51	1.23	1.34

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	1945	0	1943	11	0
2	A	8	0	6	0	0
3	A	147	0	0	2	0
All	All	2100	0	1949	11	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 (11) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance}  (\mathring{\rm A}) \end{array}$	Clash overlap (Å)
1:A:391:VAL:HG11	1:A:498:ILE:HD11	1.61	0.82
1:A:315:ALA:O	3:A:2025:HOH:O	2.04	0.75
1:A:426:THR:HG23	1:A:443:VAL:HG23	1.79	0.64
1:A:400:MET:HB3	1:A:403:VAL:HG23	1.82	0.61
1:A:429:LEU:HD23	1:A:436:TYR:CG	2.39	0.57
1:A:320:GLU:HG3	1:A:506:VAL:HG13	1.93	0.51
1:A:426:THR:HG23	1:A:443:VAL:CG2	2.43	0.45
1:A:356:ASN:HB2	1:A:526:TYR:HE1	1.83	0.44
1:A:391:VAL:HG11	1:A:498:ILE:CD1	2.42	0.43
1:A:488:LYS:NZ	3:A:2124:HOH:O	2.46	0.41
1:A:325:GLN:HA	1:A:414:CYS:O	2.22	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	245/261 (94%)	241 (98%)	4 (2%)	0	100 100

There are no Ramachandran outliers to report.

### 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	Analysed Rotameric		Percentiles	
1	A	213/226 (94%)	206 (97%)	7 (3%)	38 23	



A 11	$\langle \neg \rangle$	• 1	• . 1	, .	. 1 1 .	1. , 1.1	1
$A\Pi$	(1)	residues	with a	non-rotameric	sidechain	are listed b	oelow:

Mol	Chain	Res	Type
1	A	355	LYS
1	A	360	GLU
1	A	386[A]	ASP
1	A	386[B]	ASP
1	A	413	THR
1	A	443	VAL
1	A	454	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Type	Chain	Chain	Res	Link	$\mathbf{B}_{0}$	ond leng	$\operatorname{gths}$	В	ond ang	gles
	IVIOI	туре		nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2	
	2	ACT	A	1530	-	3,3,3	0.72	0	3,3,3	0.88	0	
	2	ACT	A	1529	-	3,3,3	0.68	0	3,3,3	1.11	0	



There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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,  $95^{th}$  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.

Mo	Chain	Analysed	<RSRZ $>$	# RSRZ > 2	$OWAB(A^2)$	Q<0.9
1	A	246/261 (94%)	-0.02	13 (5%) 26 21	14, 23, 53, 76	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	359	PHE	7.1
1	A	406	THR	5.2
1	A	445	THR	4.2
1	A	279	GLY	3.9
1	A	446	ASP	3.5
1	A	360	GLU	3.4
1	A	403	VAL	3.1
1	A	307	GLU	2.6
1	A	300	LYS	2.5
1	A	366	ARG	2.4
1	A	527	ASN	2.2
1	A	471	GLN	2.2
1	A	529	PRO	2.1

### 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 monosaccharides in this entry.



## 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q<0.9
2	ACT	A	1530	4/4	0.76	0.17	39,43,43,45	0
2	ACT	A	1529	4/4	0.77	0.21	42,43,44,45	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

