

wwPDB X-ray Structure Validation Summary Report (i)

Aug 18, 2022 – 02:11 pm BST

PDB ID	:	7PQR
Title	:	LsAA9A expressed in E. coli
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Deposited on	:	2021-09-20
Resolution	:	1.30 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 (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:

MolProbity		FAILED
•		
Mogul	:	1.8.4, CSD as $541be(2020)$
Xtriage (Phenix)	:	1.13
EDS	:	2.29
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.30 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	Percentile Ranks	Value
Rfree		0.156
RSRZ outliers		0.4%
	Worse	Better
	Percentile relative to all X-ray structures	
	Percentile relative to X-ray structures of similar resolution	

Metric	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$				
R_{free}	130704	$1058 \ (1.30-1.30)$				
RSRZ outliers	127900	1029 (1.30-1.30)				

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

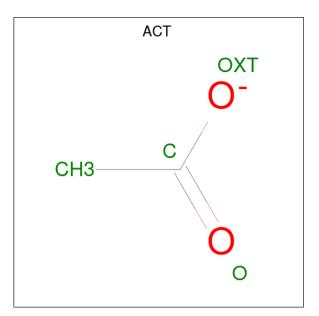
There are 6 unique types of molecules in this entry. The entry contains 2381 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Auxiliary activity 9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	235	Total 1885	C 1188	N 327	O 367	${ m S} { m 3}$	0	10	0

• Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 3 is COPPER (II) ION (three-letter code: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

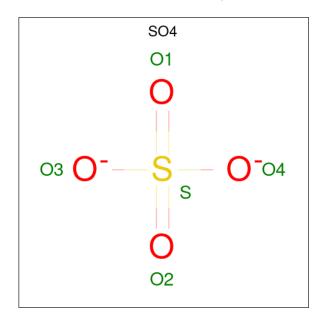


[Mol	Chain	Residues	Residues Atoms		AltConf
	3	А	1	Total Cu 1 1	0	0

• Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
4	А	7	Total Cl 7 7	0	0	

• Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
5	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
5	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
6	А	440	Total O 457 457	0	21	

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3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants	48.92Å 48.92Å 109.78Å	Deperitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.92 - 1.30	Depositor
Resolution (A)	48.92 - 1.30	EDS
% Data completeness	$99.8 \ (48.92 \text{-} 1.30)$	Depositor
(in resolution range)	99.8 (48.92-1.30)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.84 (at 1.30 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.133 , 0.153	Depositor
Π, Π_{free}	0.136 , 0.156	DCC
R_{free} test set	3124 reflections $(4.96%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	15.6	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$< L > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.045 for h,-k,-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	2381	wwPDB-VP
Average B, all atoms $(Å^2)$	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.82% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

Of 15 ligands modelled in this entry, 8 are monoatomic - leaving 7 for Mogul analysis.

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



	-						0 (0 /		
Mol	Turne	Chain	Res	Link	B	ond leng	gths	Bond angles		
NIOI	Type	Unann	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
5	SO4	А	314	-	4,4,4	0.33	0	$6,\!6,\!6$	0.12	0
2	ACT	А	302	-	3,3,3	1.07	0	$3,\!3,\!3$	0.60	0
2	ACT	А	315	-	3,3,3	0.90	0	$3,\!3,\!3$	0.81	0
2	ACT	А	303	-	3,3,3	1.41	0	$3,\!3,\!3$	1.52	1 (33%)
5	SO4	А	313	-	4,4,4	0.23	0	$6,\!6,\!6$	0.48	0
5	SO4	А	312	-	4,4,4	0.22	0	$6,\!6,\!6$	0.31	0
2	ACT	А	301	-	3,3,3	0.89	0	$3,\!3,\!3$	1.43	0

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).

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	303	ACT	O-C-CH3	-2.07	114.28	122.33

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 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.

Mol	Chain	Analysed	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	235/235~(100%)	-0.65	1 (0%) 92 91	12, 16, 22, 61	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	234	LEU	3.8

5.2 Non-standard residues in protein, DNA, RNA chains (i)

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

5.3 Carbohydrates (i)

There are no monosaccharides in this entry.

5.4 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	B-factors(Å ²)	$Q{<}0.9$
2	ACT	А	303	4/4	0.79	0.20	30,37,46,46	0
2	ACT	А	315	4/4	0.80	0.15	42,44,45,49	0
2	ACT	А	302	4/4	0.88	0.13	$61,\!61,\!61,\!62$	0
2	ACT	А	301	4/4	0.89	0.11	18,20,21,22	0
4	CL	A	306	1/1	0.89	0.04	46,46,46,46	0
4	CL	А	309	1/1	0.91	0.10	$52,\!52,\!52,\!52$	0

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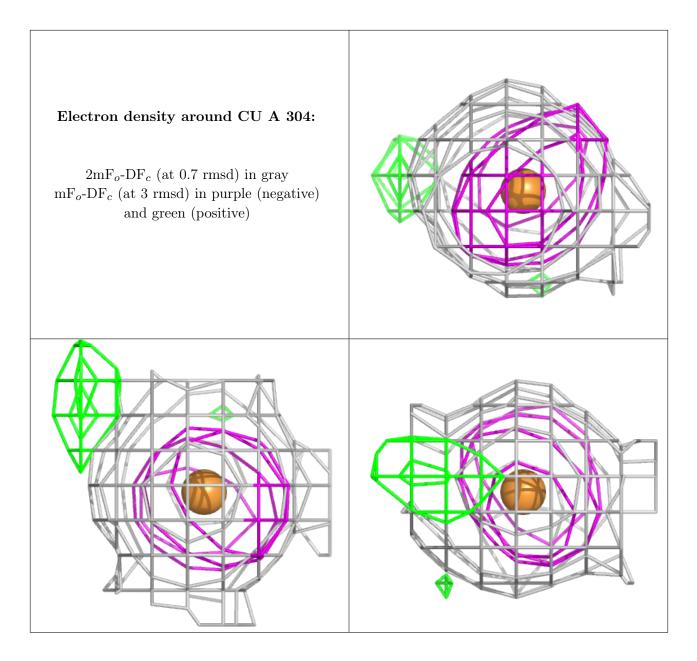


Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
5	SO4	А	313	5/5	0.91	0.19	$30,\!31,\!34,\!35$	5
5	SO4	А	314	5/5	0.91	0.27	47,50,55,57	5
4	CL	А	310	1/1	0.92	0.06	45,45,45,45	0
4	CL	А	307	1/1	0.93	0.06	41,41,41,41	0
4	CL	А	311	1/1	0.96	0.07	41,41,41,41	0
5	SO4	А	312	5/5	0.96	0.12	18,20,23,25	5
4	CL	А	308	1/1	0.98	0.13	29,29,29,29	0
4	CL	А	305	1/1	1.00	0.03	21,21,21,21	1
3	CU	А	304	1/1	1.00	0.02	16,16,16,16	0

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The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





5.5 Other polymers (i)

There are no such residues in this entry.

