

wwPDB X-ray Structure Validation Summary Report (i)

Aug 18, 2022 – 01:13 am BST

PDB ID	:	7PYO
Title	:	Structure of an LPMO (expressed in E.coli) at 2.31×10^{5} Gy
Authors	:	Tandrup, T.; Muderspach, S.J.; Banerjee, S.; Ipsen, J.O.; Rollan, C.H.;
		Norholm, M.H.H.; Johansen, K.S.; Lo Leggio, L.
Deposited on	:	2021-10-10
Resolution	:	1.40 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 as541be (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 1.40 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		0.166
RSRZ outliers		0
	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	1714 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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



7PYO

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2301 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.

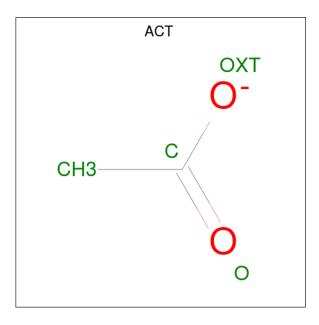
• Molecule 1 is a protein called Auxiliary activity 9.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	235	Total 1827	C 1157	N 312	O 355	${ m S} { m 3}$	0	8	0

• Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	А	1	Total 1	Cu 1	0	0

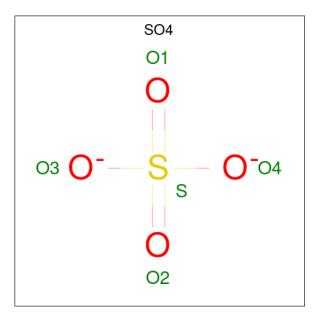
• Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	А	1	Total 4	$\begin{array}{c} \mathrm{C} \\ \mathrm{2} \end{array}$	O 2	0	0



• Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	444	Total O 449 449	0	5

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



3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants	48.86Å 48.86Å 108.96Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.62 - 1.40	Depositor
Resolution (A)	44.58 - 1.40	EDS
% Data completeness	99.5(44.62 - 1.40)	Depositor
(in resolution range)	99.6 (44.58 - 1.40)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.67 (at 1.40 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.138 , 0.163	Depositor
$10, 10_{free}$	0.147 , 0.166	DCC
R_{free} test set	2494 reflections $(5.01%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	13.7	Xtriage
Anisotropy	0.513	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$< L > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.053 for h,-k,-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	2301	wwPDB-VP
Average B, all atoms $(Å^2)$	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.46% 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 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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



4

0

10002	timbe is the root-mean-square of an 2 scores of the bond lengths (of angles).											
Mal	Mol Type	Chain	ain Dag		B	ond leng	gths	B	Sond ang	gles		
MIOI		Unam	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2		
3	ACT	А	302	-	3,3,3	0.89	0	3,3,3	0.59	0		
4	SO4	А	303[A]	-	4,4,4	0.41	0	6,6,6	0.19	0		
4	SO4	А	305	-	4,4,4	0.28	0	6,6,6	0.13	0		
4	SO4	А	304	-	4,4,4	0.26	0	$6,\!6,\!6$	0.53	0		

0.18

0

6, 6, 6

0.26

4,4,4

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.

А

306

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

SO4

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	<RSRZ $>$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q < 0.9
1	А	235/235~(100%)	-0.48	0 100 100	11, 14, 20, 36	0

There are no RSRZ outliers to report.

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)

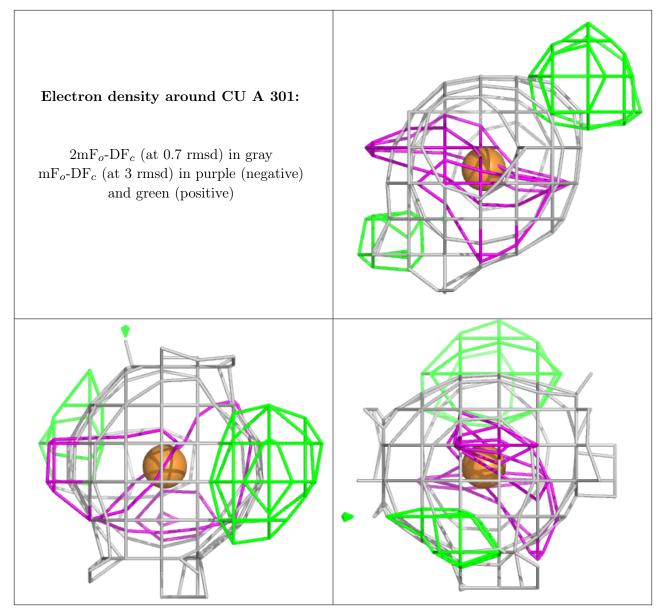
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
4	SO4	А	303[A]	5/5	0.85	0.16	$32,\!33,\!40,\!43$	0
3	ACT	А	302	4/4	0.86	0.12	34,34,35,36	0
4	SO4	А	306	5/5	0.90	0.19	$29,\!31,\!35,\!40$	5
4	SO4	А	305	5/5	0.94	0.21	$30,\!51,\!56,\!60$	0
4	SO4	А	304	5/5	0.98	0.09	$17,\!21,\!24,\!25$	0
2	CU	А	301	1/1	1.00	0.05	14, 14, 14, 14	0

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.

