

Full wwPDB X-ray Structure Validation Report (i)

Oct 3, 2023 – 02:24 AM EDT

PDB ID : 6P0B

Title: Human DNA Ligase 1 (E346A/E592A) Bound to an Adenylated, dideoxy Ter-

minated DNA nick with 200 mM Mg2+

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Deposited on : 2019-05-16

Resolution : 2.20 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:

MolProbity : FAILED

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : FAILED

buster-report : 1.1.7 (2018)

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

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

Validation Pipeline (wwPDB-VP) : 2.35.1

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 2.20 Å.

There are no overall percentile quality scores available for this entry.

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



2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 11755 atoms, of which 5538 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 DNA ligase 1.

Mol	Chain	Residues			Atom	S			ZeroOcc	AltConf	Trace
1	A	642	Total	C	Н	N	0	S	0	2	0
			10121	3182	5098	880	944	17	-		

There are 4 discrepancies between the modelled and reference sequences:

C	hain	Residue	Modelled	Actual	Comment	Reference
	A	260	SER	-	expression tag	UNP P18858
	A	261	ASN	-	expression tag	UNP P18858
	A	346	ALA	GLU	engineered mutation	UNP P18858
	A	592	ALA	GLU	engineered mutation	UNP P18858

• Molecule 2 is a DNA chain called DNA (5'-D(*GP*CP*TP*GP*AP*TP*GP*CP*GP*TP*C)-3').

Mol	Chain	Residues		1	Atom	ıs			ZeroOcc	AltConf	Trace
2	В	11	Total 411	C 127	H 147	N 47	O 78	P 12	0	2	0

• Molecule 3 is a DNA chain called DNA (5'-D(P*GP*TP*CP*GP*GP*AP*C)-3').

Mol	Chain	Residues		A	\ton	ns			ZeroOcc	AltConf	Trace
2	C	7	Total	С	Н	N	О	Р	0	0	0
3		1	224	68	79	28	42	7	0	U	

• Molecule 4 is a DNA chain called DNA (5'-D(*GP*TP*CP*CP*GP*AP*CP*GP*AP*CP* GP*CP*AP*TP*CP*AP*GP*C)-3').

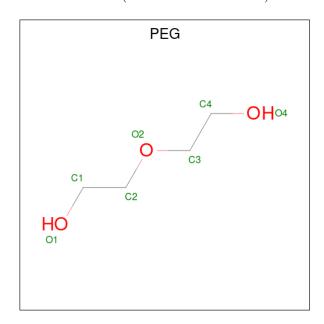
Mol	Chain	Residues			Aton	ıs			ZeroOcc	AltConf	Trace
4	D	18	Total 566	C 173	H 202	N 70	O 104	P 17	0	0	0

• Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).



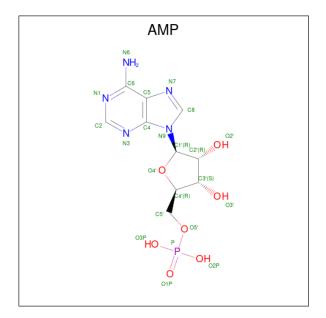
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	3	Total Mg 3 3	0	0
5	В	1	Total Mg 1 1	0	0

 $\bullet \ \ Molecule \ 6 \ is \ DI(HYDROXYETHYL)ETHER \ (three-letter \ code: \ PEG) \ (formula: \ C_4H_{10}O_3).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 7 4 3	0	0

 $\bullet \ \ Molecule\ 7\ is\ ADENOSINE\ MONOPHOSPHATE\ (three-letter\ code:\ AMP)\ (formula:\ C_{10}H_{14}N_5O_7P).$





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
7	C	1	Total	С	Н	N	О	Р	0	0
'		1	35	10	12	5	7	1	U	U

• Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	286	Total O 287 287	0	2
8	В	26	Total O 26 26	0	0
8	C	31	Total O 31 31	0	0
8	D	43	Total O 43 43	0	0

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



3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	71.87Å 101.40Å 115.61Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.43 - 2.20	Depositor
% Data completeness	99.1 (41.43-2.20)	Depositor
(in resolution range)	,	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.80 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155)	Depositor
R, R_{free}	0.170 , 0.206	Depositor
Wilson B-factor (\mathring{A}^2)	36.5	Xtriage
Anisotropy	0.380	Xtriage
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11755	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.18% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



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, 4 are monoatomic - leaving 2 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



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	Trino	Chain	Dag	Link	Во	ond leng	$ ag{ths}$	В	ond ang	les
IVIOI	Type	Chain	Res	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	AMP	С	101	3	22,25,25	0.54	0	25,38,38	1.05	1 (4%)
6	PEG	A	1004	-	6,6,6	0.58	0	5,5,5	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	AMP	С	101	3	-	1/6/26/26	0/3/3/3
6	PEG	A	1004	-	-	3/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

\mathbf{Mol}	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$ \ \mathbf{Ideal}(^o) $
7	С	101	AMP	O2P-P-O1P	2.49	120.45	110.68

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1004	PEG	O1-C1-C2-O2
6	A	1004	PEG	O2-C3-C4-O4
6	A	1004	PEG	C1-C2-O2-C3
7	С	101	AMP	C4'-C5'-O5'-P

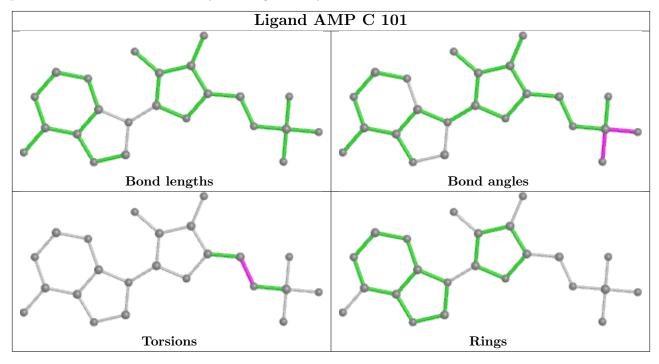
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring



in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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)

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

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

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

5.3 Carbohydrates (i)

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

5.4 Ligands (i)

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

5.5 Other polymers (i)

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

