

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

#### Oct 2, 2023 – 01:07 PM EDT

PDB ID : 6NTK

Title : Crystal Structure of Recombinant Human Acetylcholinesterase Inhibited by

A-232

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Deposited on : 2019-01-29

Resolution : 2.41 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-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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 6 unique types of molecules in this entry. The entry contains 9275 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.

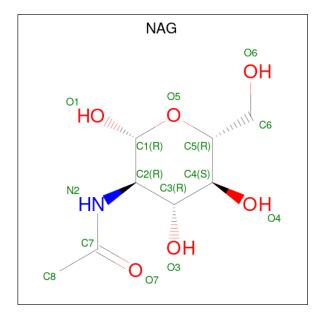
• Molecule 1 is a protein called Acetylcholinesterase.

Mol	Chain	Residues		At	oms		ZeroOcc	AltConf	Trace	
1	Δ	531	Total	С	N	О	S	0	0	0
1	11	551	4130	2651	722	744	13			
1	P	597	Total	С	N	Ο	S	0	0	0
1	Б	B 527	4104	2636	715	740	13	0	U	

• Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[al pha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	С	3	Total C N O 38 22 2 14	0	0	0
2	D	3	Total C N O 38 22 2 14	0	0	0

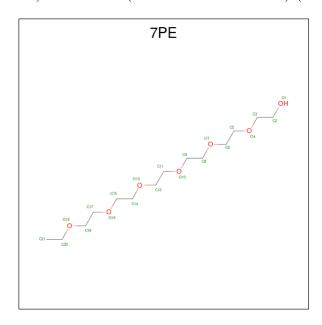
• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).





Mol	Chain	Residues	A	Atoms				AltConf
3	A	1	Total	С	N 1	O 5	0	0
	_	14	8	1	5			

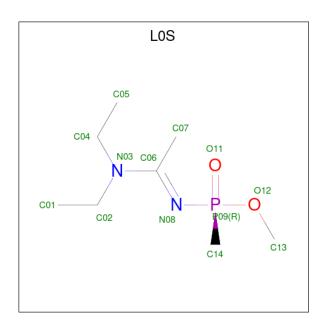
• Molecule 4 is 2-(2-(2-(2-(2-(2-ETHOXYETHOXY)ETHOXY



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 21 14 7	0	0
4	В	1	Total C O 21 14 7	0	0

• Molecule 5 is methyl (R)-N-[(1E)-1-(diethylamino)ethylidene]-P-methylphosphonamidate (three-letter code: L0S) (formula:  $C_8H_{19}N_2O_2P$ ).





Mol	Chain	Residues	${f Atoms}$					ZeroOcc	AltConf	
5	Λ	1	Total	С	N	О	Р	0	0	
3	Λ	1	12	7	2	2	1	0		
5	D	1	Total	С	N	О	Р	0	0	
5	D	$B \mid I \mid$		7	2	2	1	0	U	

#### • Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	418	Total O 418 418	0	0
6	В	467	Total O 467 467	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 31 2 1	Depositor
Cell constants	105.10Å 105.10Å 324.42Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	46.49 - 2.41	Depositor
% Data completeness	92.9 (46.49-2.41)	Depositor
(in resolution range)		1
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.71  (at  2.39Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
$R, R_{free}$	0.171 , 0.198	Depositor
Wilson B-factor $(Å^2)$	37.2	Xtriage
Anisotropy	0.004	Xtriage
L-test for twinning <sup>2</sup>	$< L > = 0.50, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
Total number of atoms	9275	wwPDB-VP
Average B, all atoms $(\mathring{A}^2)$	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.40% 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.

# 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)

6 monosaccharides 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	Tuno	Chain	Res	Link	Вс	ond leng	ths	Bond angles		
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	С	1	2,1	14,14,15	0.33	0	17,19,21	0.55	0
2	NAG	С	2	2	14,14,15	0.32	0	17,19,21	0.44	0
2	FUC	С	3	2	10,10,11	0.63	0	14,14,16	0.86	0
2	NAG	D	1	2,1	14,14,15	0.35	0	17,19,21	0.51	0
2	NAG	D	2	2	14,14,15	0.41	0	17,19,21	0.76	1 (5%)
2	FUC	D	3	2	10,10,11	0.48	0	14,14,16	0.92	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
2	NAG	С	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	С	2	2	-	2/6/23/26	0/1/1/1
2	FUC	С	3	2	-	-	0/1/1/1
2	NAG	D	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	FUC	D	3	2	-	-	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
2	D	2	NAG	C1-O5-C5	2.16	115.12	112.19

There are no chirality outliers.

All (10) torsion outliers are listed below:

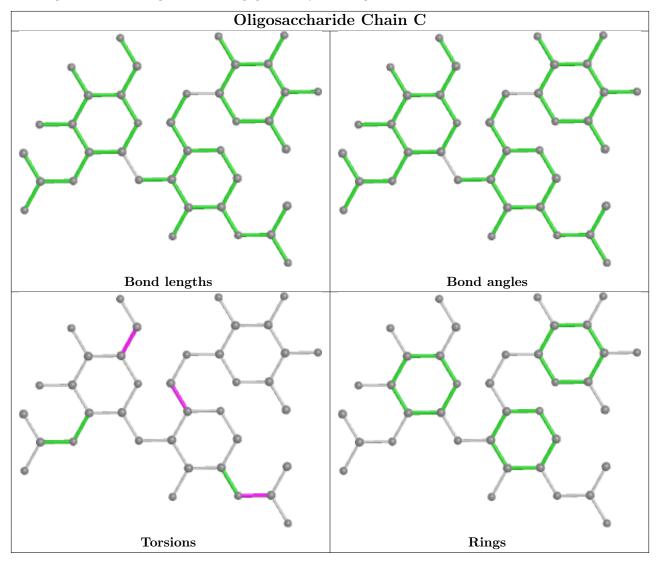
Mol	Chain	Res	Type	Atoms
2	С	2	NAG	O5-C5-C6-O6
2	С	2	NAG	C4-C5-C6-O6
2	С	1	NAG	C8-C7-N2-C2
2	С	1	NAG	O7-C7-N2-C2
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	С	1	NAG	C4-C5-C6-O6
2	С	1	NAG	O5-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6



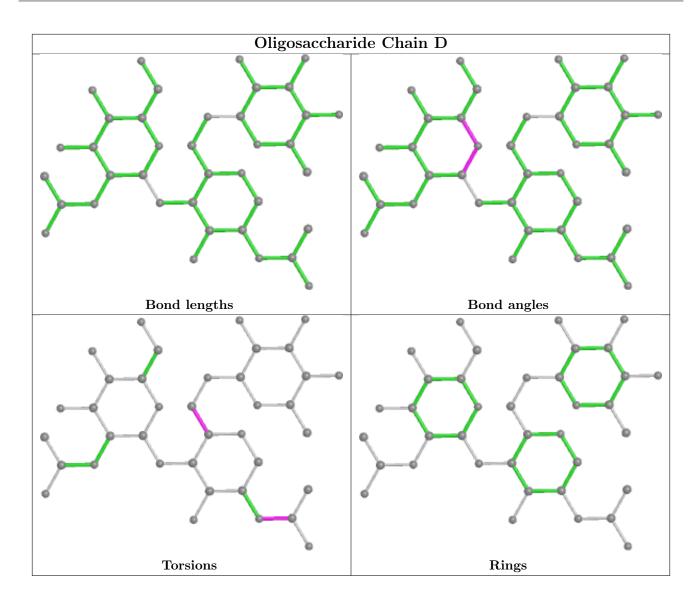
There are no ring outliers.

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 oligosaccharide.







### 4.6 Ligand geometry (i)

5 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	Chain	Pos	Res Link	Во	ond leng	$ ag{ths}$	Bond angles		
WIOI Typ	туре	Chain	rtes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	A	604	-	14,14,15	0.83	0	17,19,21	1.90	3 (17%)
4	7PE	В	601	-	20,20,20	0.46	0	19,19,19	0.27	0
4	7PE	A	605	-	20,20,20	0.47	0	19,19,19	0.27	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
MOI					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	LOS	A	606	-	8,11,12	2.33	3 (37%)	5,13,16	1.43	1 (20%)
5	LOS	В	605	-	8,11,12	2.35	3 (37%)	5,13,16	1.62	1 (20%)

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
3	NAG	A	604	-	-	1/6/23/26	0/1/1/1
4	7PE	В	601	-	-	10/18/18/18	-
4	7PE	A	605	-	-	9/18/18/18	-
5	LOS	A	606	-	-	0/8/14/16	-
5	LOS	В	605	-	-	0/8/14/16	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
5	A	606	LOS	C06-N03	4.24	1.45	1.34
5	В	605	LOS	C06-N03	4.21	1.45	1.34
5	В	605	LOS	C06-N08	-4.00	1.25	1.31
5	A	606	LOS	C06-N08	-3.79	1.25	1.31
5	A	606	LOS	C07-C06	2.56	1.53	1.49
5	В	605	LOS	C07-C06	2.47	1.53	1.49

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
3	A	604	NAG	C1-O5-C5	5.30	119.38	112.19
5	В	605	LOS	C07-C06-N08	-3.18	119.98	126.92
3	A	604	NAG	O5-C1-C2	-2.99	106.56	111.29
5	A	606	LOS	C07-C06-N08	-2.70	121.02	126.92
3	A	604	NAG	O3-C3-C4	-2.12	105.45	110.35

There are no chirality outliers.

All (20) torsion outliers are listed below:

$\mathbf{Mol}$	Chain	Res	Type	Atoms
4	A	605	7PE	O4-C5-C6-O7
4	В	601	7PE	O1-C2-C3-O4

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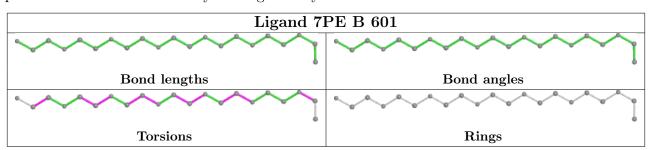
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Mol	Chain	Res	Type	Atoms
4	A	605	7PE	O10-C11-C12-O13
4	A	605	7PE	O16-C17-C18-O19
4	A	605	7PE	O13-C14-C15-O16
3	A	604	NAG	O5-C5-C6-O6
4	A	605	7PE	O7-C8-C9-O10
4	В	601	7PE	C5-C6-O7-C8
4	В	601	7PE	C8-C9-O10-C11
4	В	601	7PE	C14-C15-O16-C17
4	A	605	7PE	C2-C3-O4-C5
4	В	601	7PE	C11-C12-O13-C14
4	В	601	7PE	O7-C8-C9-O10
4	A	605	7PE	C9-C8-O7-C6
4	В	601	7PE	C21-C20-O19-C18
4	A	605	7PE	C21-C20-O19-C18
4	В	601	7PE	O4-C5-C6-O7
4	A	605	7PE	C18-C17-O16-C15
4	В	601	7PE	O13-C14-C15-O16
4	В	601	7PE	O10-C11-C12-O13

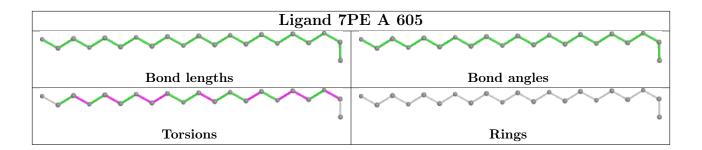
There are no ring outliers.

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.

