



wwPDB X-ray Structure Validation Summary Report

Oct 3, 2023 – 02:36 AM EDT

PDB ID : 6O4X
Title : Binary complex of native hAChE with 9-aminoacridine
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Deposited on : 2019-03-01
Resolution : 2.30 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  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](#) ) were used in the production of this report:

MolProbity : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : **FAILED**
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

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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 5 unique types of molecules in this entry. The entry contains 8996 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	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	540	4188	2686	732	757	13	0	0	0
1	B	540	4188	2686	732	757	13	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

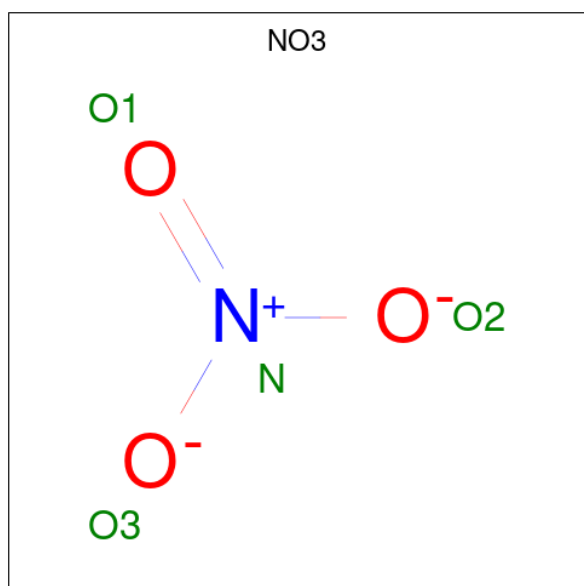
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P22303
A	-1	PRO	-	expression tag	UNP P22303
A	0	LEU	-	expression tag	UNP P22303
B	-2	GLY	-	expression tag	UNP P22303
B	-1	PRO	-	expression tag	UNP P22303
B	0	LEU	-	expression tag	UNP P22303

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



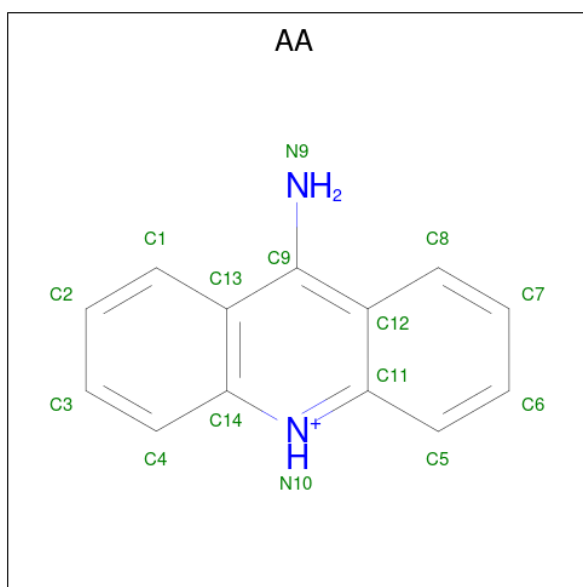
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is NITRATE ION (three-letter code: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	N	O	0	0
			4	1	3		

- Molecule 4 is 9-AMINOACRIDINE (three-letter code: AA) (formula: C₁₃H₁₁N₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			15	13	2		
4	B	1	Total	C	N	0	0
			15	13	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	278	Total	O	0	0
			278	278		
5	B	278	Total	O	0	0
			278	278		

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	Depositor
Cell constants a, b, c, α , β , γ	124.63Å 124.63Å 129.66Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	31.46 – 2.30	Depositor
% Data completeness (in resolution range)	73.2 (31.46-2.30)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.29Å)	Xtrriage
Refinement program	PHENIX (1.11_2567)	Depositor
R, R_{free}	0.190 , 0.223	Depositor
Wilson B-factor (Å ²)	33.4	Xtrriage
Anisotropy	0.009	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.057 for -h,-k,l 0.068 for h,-h-k,-l 0.480 for -k,-h,-l	Xtrriage
Total number of atoms	8996	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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](#)

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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](#)

8 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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	A	601	-	5,5,5	0.38	0	5,5,5	0.24	0
2	GOL	A	603	-	5,5,5	0.35	0	5,5,5	0.30	0
2	GOL	B	601	-	5,5,5	0.37	0	5,5,5	0.26	0
3	NO3	A	604	-	1,3,3	0.65	0	0,3,3	-	-
4	AA	A	605	-	17,17,17	1.54	3 (17%)	24,24,24	1.44	4 (16%)
2	GOL	A	602	-	5,5,5	0.37	0	5,5,5	0.19	0
2	GOL	B	602	-	5,5,5	0.37	0	5,5,5	0.11	0
4	AA	B	603	-	17,17,17	1.54	2 (11%)	24,24,24	1.51	6 (25%)

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	GOL	A	601	-	-	2/4/4/4	-
2	GOL	A	603	-	-	1/4/4/4	-
2	GOL	B	601	-	-	2/4/4/4	-
4	AA	A	605	-	-	-	0/3/3/3
2	GOL	A	602	-	-	2/4/4/4	-
2	GOL	B	602	-	-	3/4/4/4	-
4	AA	B	603	-	-	-	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	603	AA	C9-N9	2.53	1.42	1.33
4	A	605	AA	C9-N9	2.46	1.41	1.33
4	A	605	AA	C13-C14	-2.17	1.38	1.42
4	B	603	AA	C12-C11	-2.13	1.39	1.42
4	A	605	AA	C12-C11	-2.06	1.39	1.42

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	605	AA	C12-C11-N10	-3.36	120.21	123.35
4	A	605	AA	C14-N10-C11	3.29	122.50	117.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	603	AA	C12-C11-N10	-3.13	120.42	123.35
4	B	603	AA	C14-N10-C11	3.09	122.22	117.86
4	B	603	AA	C13-C14-N10	-2.68	120.84	123.35

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	GOL	O1-C1-C2-C3
2	A	601	GOL	O1-C1-C2-C3
2	A	602	GOL	O1-C1-C2-C3
2	A	603	GOL	C1-C2-C3-O3
2	B	602	GOL	O1-C1-C2-C3

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

5.1 Protein, DNA and RNA chains

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

5.2 Non-standard residues in protein, DNA, RNA chains

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

5.3 Carbohydrates

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

5.4 Ligands

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

5.5 Other polymers

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