



wwPDB X-ray Structure Validation Summary Report ⓘ

May 3, 2021 – 10:14 pm BST

PDB ID : 2VT6
Title : Native Torpedo californica acetylcholinesterase collected with a cumulated dose of 9400000 Gy
Authors : Colletier, J.P.; Bourgeois, D.; Sanson, B.; Fournier, D.; Sussman, J.L.; Silman, I.; Weik, M.
Deposited on : 2008-05-09
Resolution : 2.40 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.18
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.18

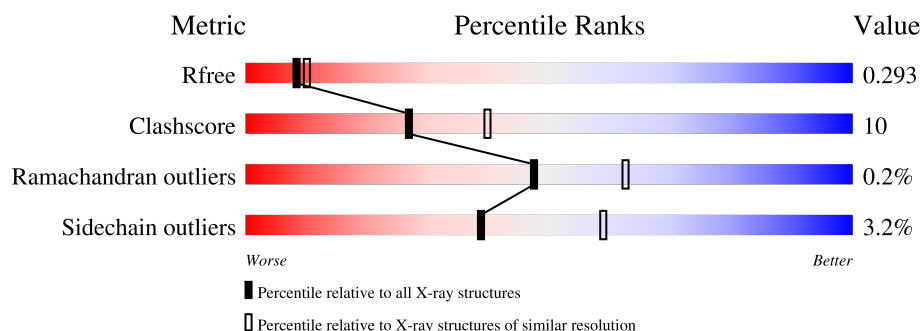
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	537	 78% 19% ..
1	B	537	 76% 21% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PGE	B	1540	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9558 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
1	A	529	Total	C	N	O	S	0	0	0
			4215	2705	714	774	22			
1	B	532	Total	C	N	O	S	0	0	0
			4242	2720	720	780	22			

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

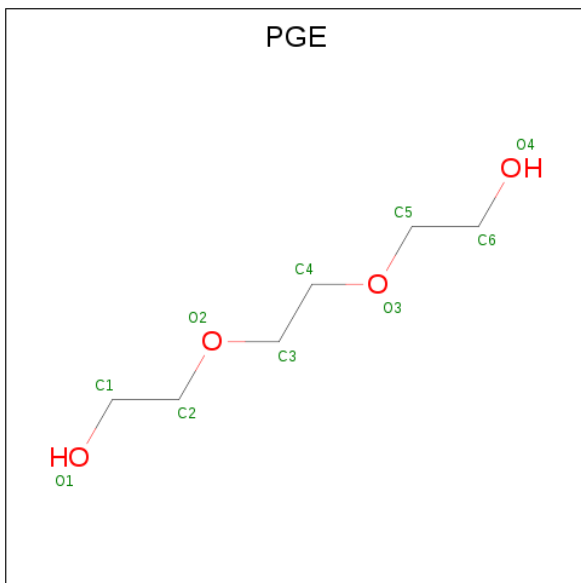


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		

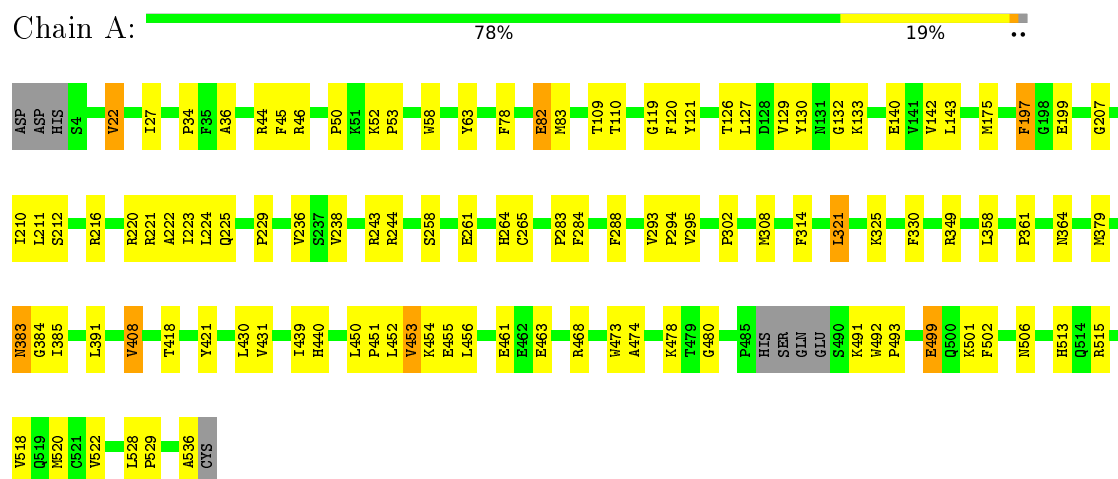
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	468	Total 468	O 468	0	0
5	B	495	Total 495	O 495	0	0

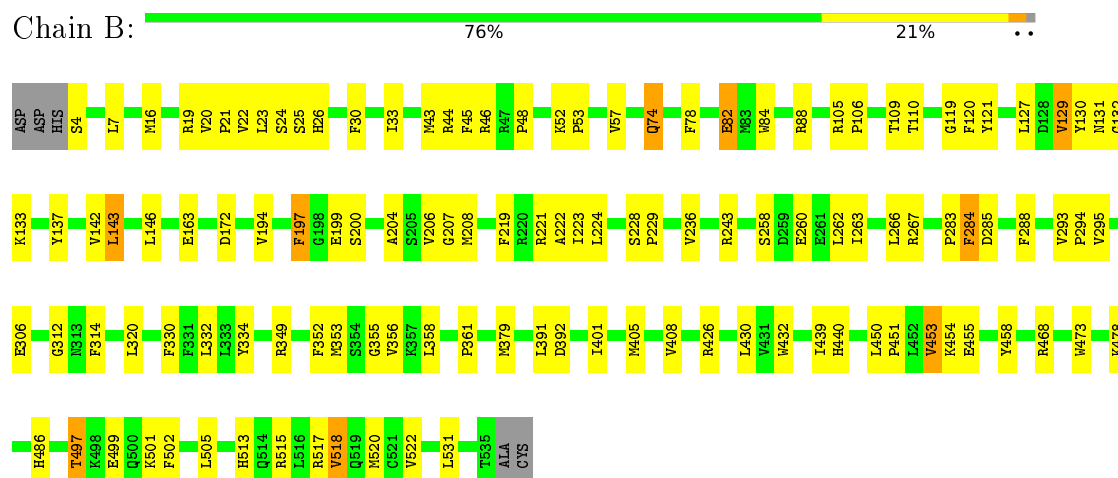
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: ACETYLCHOLINESTERASE



• Molecule 1: ACETYLCHOLINESTERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.66Å 106.08Å 150.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.40 19.96 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.4 (19.96-2.40) 98.5 (19.96-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.47 (at 2.41Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.193 , 0.234 0.280 , 0.293	Depositor DCC
R_{free} test set	2664 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	15.8	Xtriage
Anisotropy	1.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 71.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.27$, $\langle L^2 \rangle = 0.11$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	9558	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.97 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.1222e-03.*

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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, PGE, NAG

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 $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.36	0/4336	0.60	0/5886
1	B	0.36	0/4365	0.60	0/5926
All	All	0.36	0/8701	0.60	0/11812

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4215	0	4074	90	0
1	B	4242	0	4091	79	0
2	A	28	0	26	0	0
2	B	28	0	26	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	40	0	56	7	0
4	B	40	0	56	9	0
5	A	468	0	0	12	0
5	B	495	0	0	9	0
All	All	9558	0	8329	173	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 173 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:499:GLU:HG2	1:A:501:LYS:HE3	1.39	1.03
1:A:454:LYS:HA	1:A:454:LYS:HE2	1.56	0.88
1:B:194:VAL:HG12	5:B:2228:HOH:O	1.80	0.80
1:B:194:VAL:HG13	1:B:219:PHE:HA	1.61	0.80
1:B:48:PRO:HG3	1:B:172:ASP:OD1	1.80	0.79

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	525/537 (98%)	504 (96%)	20 (4%)	1 (0%)	47	62
1	B	530/537 (99%)	506 (96%)	23 (4%)	1 (0%)	47	62
All	All	1055/1074 (98%)	1010 (96%)	43 (4%)	2 (0%)	47	62

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	486	HIS
1	A	22	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	461/469 (98%)	449 (97%)	12 (3%)	46	66
1	B	464/469 (99%)	446 (96%)	18 (4%)	32	50
All	All	925/938 (99%)	895 (97%)	30 (3%)	39	59

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	129	VAL
1	B	497	THR
1	B	221	ARG
1	B	518	VAL
1	B	453	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	457	ASN
1	B	514	GLN
1	A	514	GLN
1	B	68	GLN
1	B	74	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	1538	1	14,14,15	0.54	0	17,19,21	0.91	1 (5%)
4	PGE	A	1541	-	9,9,9	1.42	2 (22%)	8,8,8	1.37	1 (12%)
2	NAG	A	1544	1	14,14,15	0.61	0	17,19,21	0.75	1 (5%)
2	NAG	B	1537	1	14,14,15	0.68	0	17,19,21	0.57	0
4	PGE	A	1542	-	9,9,9	1.68	3 (33%)	8,8,8	0.95	0
4	PGE	A	1543	-	9,9,9	1.42	2 (22%)	8,8,8	1.15	1 (12%)
2	NAG	B	1536	1	14,14,15	0.54	0	17,19,21	0.75	1 (5%)
4	PGE	B	1540	-	9,9,9	2.24	5 (55%)	8,8,8	2.03	4 (50%)
4	PGE	A	1540	-	9,9,9	1.64	2 (22%)	8,8,8	1.82	1 (12%)
4	PGE	B	1541	-	9,9,9	0.89	0	8,8,8	1.25	1 (12%)
4	PGE	B	1539	-	9,9,9	1.37	2 (22%)	8,8,8	0.98	0
4	PGE	B	1542	-	9,9,9	1.40	1 (11%)	8,8,8	1.95	4 (50%)

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	A	1538	1	-	2/6/23/26	0/1/1/1
4	PGE	A	1541	-	-	1/7/7/7	-
2	NAG	A	1544	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1537	1	-	2/6/23/26	0/1/1/1
4	PGE	A	1542	-	-	3/7/7/7	-
4	PGE	A	1543	-	-	3/7/7/7	-
2	NAG	B	1536	1	-	0/6/23/26	0/1/1/1
4	PGE	B	1540	-	-	4/7/7/7	-
4	PGE	A	1540	-	-	3/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PGE	B	1541	-	-	2/7/7/7	-
4	PGE	B	1539	-	-	2/7/7/7	-
4	PGE	B	1542	-	-	4/7/7/7	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1540	PGE	O2-C2	3.70	1.58	1.42
4	B	1540	PGE	C4-C3	3.18	1.65	1.49
4	B	1540	PGE	O3-C5	2.93	1.54	1.42
4	B	1542	PGE	O3-C5	2.85	1.54	1.42
4	B	1540	PGE	O2-C3	2.51	1.52	1.42

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1540	PGE	C5-O3-C4	4.04	130.81	113.29
4	B	1540	PGE	O2-C2-C1	3.64	126.04	110.07
4	B	1540	PGE	O3-C4-C3	2.88	123.39	110.39
4	B	1541	PGE	O3-C4-C3	2.79	122.99	110.39
4	A	1541	PGE	O2-C3-C4	-2.70	98.20	110.39

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1538	NAG	C8-C7-N2-C2
2	A	1538	NAG	O7-C7-N2-C2
2	B	1537	NAG	O5-C5-C6-O6
2	B	1537	NAG	C4-C5-C6-O6
4	B	1542	PGE	C6-C5-O3-C4

There are no ring outliers.

7 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1541	PGE	1	0
4	A	1542	PGE	1	0
4	A	1543	PGE	5	0
4	B	1540	PGE	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1541	PGE	2	0
4	B	1539	PGE	1	0
4	B	1542	PGE	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.