Full wwPDB X-ray Structure Validation Report (i)

Jun 21, 2016 – 01:44 PM EDT

PDB ID	:	1ACJ
Title	:	QUATERNARY LIGAND BINDING TO AROMATIC RESIDUES IN THE ACTIVE-SITE GORGE OF ACETYLCHOLINESTERASE
Authors	:	Sussman, J.L.; Harel, M.; Silman, I.
Deposited on	:	1993-08-18
Resolution	:	2.80 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

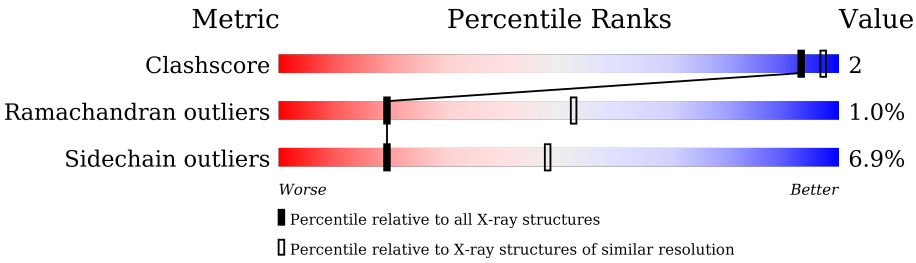
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027790

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 2.80 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))
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	537	85% 11% • •

2 Entry composition (i)

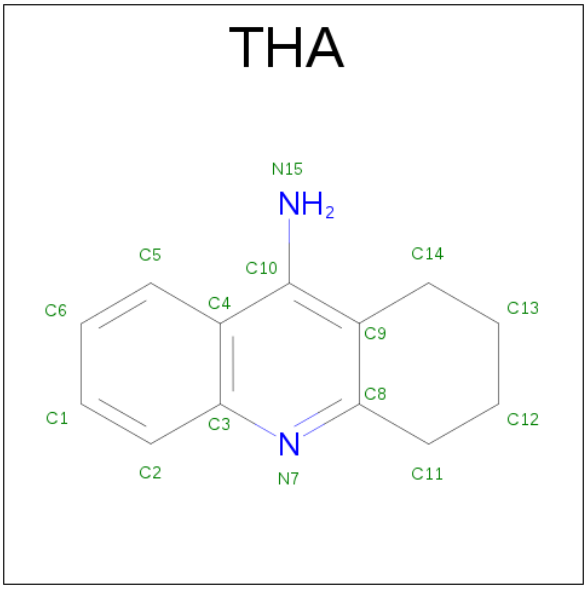
There are 3 unique types of molecules in this entry. The entry contains 4192 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	528	4095	2655	686	733	21	0	0	0

- Molecule 2 is TACRINE (three-letter code: THA) (formula: $C_{13}H_{14}N_2$).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	82	82	82	0	0

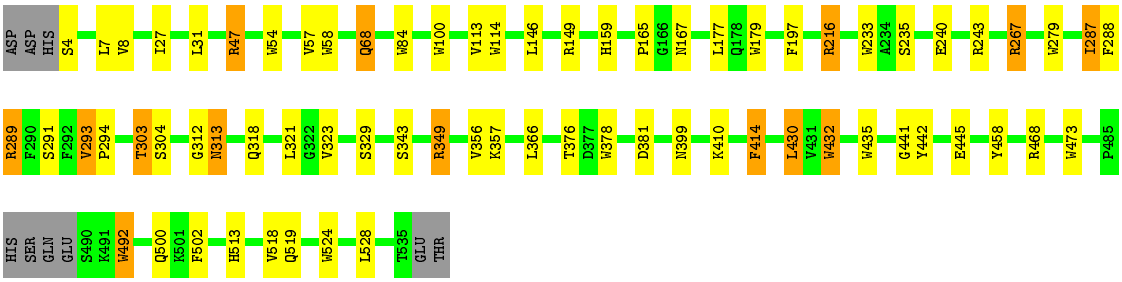
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

Note EDS was not executed.

- Molecule 1: ACETYLCHOLINESTERASE

Chain A:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	113.70Å 113.70Å 138.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.195 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4192	wwPDB-VP
Average B, all atoms ($Å^2$)	21.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: THA

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	0.88	14/4214 (0.3%)	1.24	13/5730 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	TRP	CD2-CE2	6.62	1.49	1.41
1	A	279	TRP	CD2-CE2	6.62	1.49	1.41
1	A	233	TRP	CD2-CE2	6.43	1.49	1.41
1	A	54	TRP	CD2-CE2	6.29	1.49	1.41
1	A	435	TRP	CD2-CE2	6.22	1.48	1.41
1	A	432	TRP	CD2-CE2	6.15	1.48	1.41
1	A	473	TRP	CD2-CE2	6.01	1.48	1.41
1	A	378	TRP	CD2-CE2	5.76	1.48	1.41
1	A	492	TRP	CD2-CE2	5.68	1.48	1.41
1	A	84	TRP	CD2-CE2	5.50	1.48	1.41
1	A	524	TRP	CD2-CE2	5.38	1.47	1.41
1	A	100	TRP	CD2-CE2	5.35	1.47	1.41
1	A	114	TRP	CD2-CE2	5.31	1.47	1.41
1	A	58	TRP	CD2-CE2	5.02	1.47	1.41

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	47	ARG	NE-CZ-NH2	-15.36	112.62	120.30
1	A	414	PHE	CB-CG-CD1	11.39	128.77	120.80
1	A	414	PHE	CB-CG-CD2	-9.04	114.47	120.80
1	A	47	ARG	NE-CZ-NH1	8.57	124.58	120.30
1	A	216	ARG	NE-CZ-NH2	-6.63	116.98	120.30
1	A	343	SER	N-CA-CB	-6.32	101.02	110.50
1	A	267	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	A	293	VAL	N-CA-CB	-5.55	99.29	111.50
1	A	149	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	A	165	PRO	C-N-CA	-5.26	111.26	122.30
1	A	4	SER	CB-CA-C	5.14	119.87	110.10
1	A	492	TRP	N-CA-C	-5.07	97.32	111.00
1	A	303	THR	CA-CB-CG2	5.02	119.43	112.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	442	TYR	Sidechain
1	A	458	TYR	Sidechain

5.2 Too-close contacts (i)

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	4095	0	3909	15	0
2	A	15	0	14	1	0
3	A	82	0	0	1	0
All	All	4192	0	3923	15	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 2.

All (15) 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:216:ARG:HH22	1:A:313:ASN:ND2	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:THR:HG22	1:A:304:SER:H	1.76	0.50
1:A:68:GLN:HA	1:A:68:GLN:HE21	1.76	0.50
1:A:468:ARG:HB3	1:A:468:ARG:HH11	1.78	0.49
1:A:445:GLU:HG3	3:A:655:HOH:O	2.13	0.48
1:A:502:PHE:CZ	1:A:513:HIS:HB2	2.48	0.48
1:A:441:GLY:HA3	2:A:999:THA:H112	1.97	0.47
1:A:349:ARG:HH21	1:A:376:THR:HG21	1.81	0.44
1:A:7:LEU:HD13	1:A:8:VAL:N	2.34	0.43
1:A:235:SER:HA	1:A:294:PRO:O	2.19	0.42
1:A:289:ARG:NH2	1:A:399:ASN:OD1	2.53	0.42
1:A:312:GLY:HA3	1:A:414:PHE:CD2	2.53	0.41
1:A:430:LEU:HD12	1:A:432:TRP:H	1.85	0.41
1:A:287:ILE:HD13	1:A:287:ILE:HA	1.94	0.41
1:A:113:VAL:CG1	1:A:146:LEU:HD21	2.52	0.40

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	524/537 (98%)	485 (93%)	34 (6%)	5 (1%)	19 52

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	HIS
1	A	167	ASN
1	A	381	ASP
1	A	500	GLN
1	A	329	SER

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	423/470 (90%)	394 (93%)	29 (7%)	19 48

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ILE
1	A	31	LEU
1	A	47	ARG
1	A	57	VAL
1	A	68	GLN
1	A	177	LEU
1	A	197	PHE
1	A	240	GLU
1	A	243	ARG
1	A	267	ARG
1	A	287	ILE
1	A	288	PHE
1	A	289	ARG
1	A	291	SER
1	A	293	VAL
1	A	313	ASN
1	A	318	GLN
1	A	321	LEU
1	A	323	VAL
1	A	349	ARG
1	A	356	VAL
1	A	357	LYS
1	A	366	LEU
1	A	410	LYS
1	A	430	LEU
1	A	492	TRP
1	A	518	VAL
1	A	519	GLN
1	A	528	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	209	HIS
1	A	313	ASN
1	A	519	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	THA	A	999	-	17,17,17	1.71	3 (17%)	20,24,24	1.49	2 (10%)

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	THA	A	999	-	-	0/0/7/7	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	999	THA	C3-N7	-3.38	1.31	1.37
2	A	999	THA	C11-C8	2.88	1.55	1.50
2	A	999	THA	C14-C9	3.90	1.57	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	999	THA	C14-C9-C8	-3.34	118.45	120.95
2	A	999	THA	C8-N7-C3	4.35	122.60	117.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	999	THA	1	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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates (i)

EDS was not executed - this section will therefore be empty.

6.4 Ligands (i)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers (i)

EDS was not executed - this section will therefore be empty.