

Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2023 – 10:34 PM EDT

PDB ID : 3DT8

Title : Crystal Structure of Bovin Brain Platelet Activating Factor Acetylhydrolase

Covalently Inhibited by Sarin

Authors: Epstein, T.M.; Samanta, U.; Bahnson, B.J.

Deposited on : 2008-07-14

Resolution : 1.85 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.orgA 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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$

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

Xtriage (Phenix) : 1.13 EDS : 2.35

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

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

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

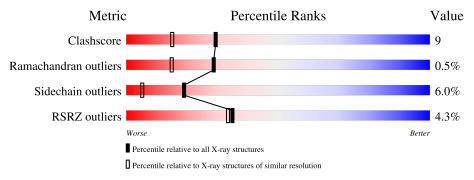
Validation Pipeline (wwPDB-VP) : 2.35

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 1.85 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	Similar resolution
Wiediic	$(\# {\rm Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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 <=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.

Mol	Chain	Length	Quality of chain			
			4%			
1	A	232	78%	9%	•	9%



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1787 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 Brain Platelet-activating factor acetylhydrolase IB subunit alpha.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	212	Total 1696	C 1070	N 321	O 300	P 1	S 4	0	0	0

There is a discrepancy between the modelled and reference sequences:

Cha	ain	Residue	Modelled	Actual	Comment	Reference
A	_	55	SER	CYS	engineered mutation	UNP Q29460

• Molecule 2 is water.

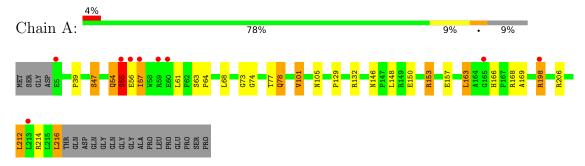
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	91	Total O 91 91	0	0



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 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.

• Molecule 1: Brain Platelet-activating factor acetylhydrolase IB subunit alpha





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	81.32Å 81.32Å 72.78Å	Donositon
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 - 1.85	Depositor
Resolution (A)	25.00 - 1.85	EDS
% Data completeness	92.2 (30.00-1.85)	Depositor
(in resolution range)	92.2 (25.00-1.85)	EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.16 (at 1.85Å)	Xtriage
Refinement program	REFMAC OF CCP4I FOR FINAL REFINEMENT, CNS	Depositor
D D	0.204 , 0.231	Depositor
R, R_{free}	0.203 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VI
Wilson B-factor (Å ²)	24.6	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.40 , 48.4	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.039 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1787	wwPDB-VF
Average B, all atoms (Å ²)	24.0	wwPDB-VF

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.53% 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.

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: SGB

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 $\mid \# Z > 5 \mid I$		RMSZ	# Z > 5	
1	A	0.67	0/1727	0.67	1/2347 (0.0%)	

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 maintain group or atoms of a sidechain that are expected to be planar.

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	101	VAL	CB-CA-C	-5.53	100.89	111.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	54	GLN	Peptide
1	A	55	SER	Peptide

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	1696	0	1677	32	0
2	A	91	0	0	0	0
All	All	1787	0	1677	32	0

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 9.

All (32) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
1 A FF CED HD9	1 A FC OLLI CA	distance (Å)	overlap (Å)
1:A:55:SER:HB3	1:A:56:GLU:CA	1.78	1.11
1:A:55:SER:CB	1:A:56:GLU:HA	1.81	1.10
1:A:55:SER:HB3	1:A:56:GLU:HA	0.90	0.88
1:A:56:GLU:O	1:A:56:GLU:HG3	1.74	0.85
1:A:166:HIS:HB3	1:A:169:ALA:HB3	1.61	0.81
1:A:78:GLN:H	1:A:78:GLN:HE21	1.30	0.78
1:A:214:ARG:HH11	1:A:214:ARG:HB3	1.52	0.73
1:A:56:GLU:O	1:A:56:GLU:CG	2.40	0.70
1:A:77:THR:H	1:A:105:ASN:HD21	1.38	0.70
1:A:78:GLN:H	1:A:78:GLN:NE2	2.00	0.58
1:A:146:ASN:HD22	1:A:148:LEU:H	1.52	0.58
1:A:57:ILE:HG23	1:A:198:ARG:HH12	1.69	0.57
1:A:57:ILE:HG23	1:A:198:ARG:NH1	2.18	0.57
1:A:214:ARG:HB3	1:A:214:ARG:NH1	2.19	0.57
1:A:54:GLN:O	1:A:55:SER:O	2.24	0.56
1:A:129:PRO:O	1:A:168:ARG:NH2	2.40	0.55
1:A:47:SGB:H4C2	1:A:73:GLY:CA	2.37	0.54
1:A:163:LEU:O	1:A:166:HIS:HB2	2.12	0.49
1:A:212:LEU:O	1:A:216:LEU:HB2	2.14	0.48
1:A:57:ILE:HG13	1:A:198:ARG:NH1	2.30	0.47
1:A:166:HIS:CB	1:A:169:ALA:HB3	2.37	0.47
1:A:47:SGB:H4C2	1:A:74:GLY:N	2.30	0.46
1:A:47:SGB:HBC1	1:A:47:SGB:H4C3	1.98	0.46
1:A:153:ARG:NE	1:A:157:GLU:OE2	2.50	0.45
1:A:57:ILE:HG13	1:A:198:ARG:HH12	1.82	0.43
1:A:146:ASN:ND2	1:A:148:LEU:H	2.14	0.43
1:A:39:PRO:HG3	1:A:68:LEU:HD12	2.01	0.42
1:A:55:SER:CB	1:A:56:GLU:CA	2.58	0.42
1:A:54:GLN:O	1:A:55:SER:C	2.58	0.42
1:A:63:SER:HB2	1:A:64:PRO:HD3	2.02	0.42
1:A:132:ARG:HD3	1:A:168:ARG:HD2	2.01	0.41
1:A:47:SGB:HBC1	1:A:47:SGB:C4	2.51	0.41



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	209/232 (90%)	199 (95%)	9 (4%)	1 (0%)	29 15

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	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	182/197 (92%)	171 (94%)	11 (6%)	19 5	

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	ILE
1	A	61	LEU
1	A	78	GLN
1	A	101	VAL
1	A	150	GLU
1	A	153	ARG
1	A	163	LEU

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type
1	A	198	ARG
1	A	206	ARG
1	A	212	LEU
1	A	216	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	28	HIS
1	A	78	GLN
1	A	105	ASN
1	A	143	GLN
1	A	146	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	Bo	ond leng	$_{ m ths}$	В	ond ang	gles
1	VIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
	1	SGB	A	47	1	10,12,13	2.69	4 (40%)	9,16,18	2.15	3 (33%)

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
1	SGB	A	47	1	-	1/10/13/15	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
1	A	47	SGB	P1-O1	5.31	1.55	1.47
1	A	47	SGB	O-C	5.29	1.41	1.19
1	A	47	SGB	P1-OG	2.66	1.61	1.58
1	A	47	SGB	P1-C1	2.39	1.83	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^o)$
1	A	47	SGB	P1-O2-C2	3.58	133.13	123.40
1	A	47	SGB	O2-C2-C4	3.31	119.28	107.69
1	A	47	SGB	C3-C2-C4	-2.59	99.71	113.47

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	47	SGB	C4-C2-O2-P1

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	47	SGB	4	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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)

In the following table, the column labelled '#RSRZ>2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	$\langle { m RSRZ} \rangle$	# RSRZ > 2		$OWAB(A^2)$	Q<0.9	
1	A	211/232 (90%)	0.05	9 (4%)	35	33	15, 22, 39, 50	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	56	GLU	5.0
1	A	5	GLU	4.8
1	A	59	ARG	3.5
1	A	55	SER	3.1
1	A	213	LEU	3.0
1	A	165	GLY	3.0
1	A	57	ILE	2.9
1	A	198	ARG	2.2
1	A	60	GLU	2.1

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	SGB	A	47	13/14	0.94	0.14	15,19,34,35	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.



6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.

