

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

#### Aug 30, 2023 – 12:28 AM EDT

PDB ID : 3LYI

Title: PWWP Domain of Human Bromodomain-Containing Protein 1

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(SGC)

Deposited on : 2010-02-26

Resolution : 2.10 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: 4.02b-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)

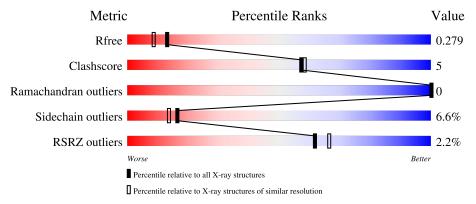
Validation Pipeline (wwPDB-VP) : 2.35

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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		
1	A	126	83%	13%	5%
1	В	126	71% 10%	17%	



## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1880 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.

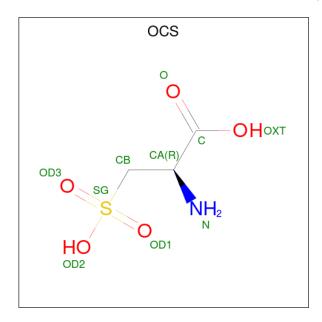
• Molecule 1 is a protein called Bromodomain-containing protein 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	120	Total 960	C 620	11	O 163	S 7	0	0	0
1	В	105	Total 832	C 539	- '	O 144	S 6	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference	
A	924	GLY	-	expression tag	UNP O95696	
В	924	GLY	-	expression tag	UNP O95696	

• Molecule 2 is CYSTEINESULFONIC ACID (three-letter code: OCS) (formula: C<sub>3</sub>H<sub>7</sub>NO<sub>5</sub>S).



Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf		
2	A	1	Total 10	C 3	N 1	O 5	S 1	0	0



### • Molecule 3 is water.

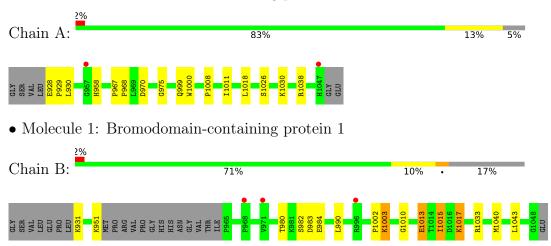
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	72	Total O 72 72	0	0
3	В	6	Total O 6 6	0	0



# 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: Bromodomain-containing protein 1





# 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	45.03Å 46.09Å 130.71Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor	
Resolution (Å)	37.66 - 2.10	Depositor	
resolution (A)	37.66 - 2.10	EDS	
% Data completeness	98.8 (37.66-2.10)	Depositor	
(in resolution range)	98.8 (37.66-2.10)	EDS	
$R_{merge}$	0.07	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.89  (at  2.10Å)	Xtriage	
Refinement program	REFMAC refmac_5.5.0109	Depositor	
$R, R_{free}$	0.234 , $0.276$	Depositor	
it, it free	0.234 , $0.279$	DCC	
$R_{free}$ test set	827 reflections $(5.04\%)$	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	37.9	Xtriage	
Anisotropy	0.104	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	$0.30 \; ,  46.6$	EDS	
L-test for twinning <sup>2</sup>	$< L > = 0.47, < L^2> = 0.31$	Xtriage	
Estimated twinning fraction	0.040 for k,h,-l	Xtriage	
$F_o, F_c$ correlation	0.94	EDS	
Total number of atoms	1880	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.31% 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.

## 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: OCS

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		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.66	0/986	0.70	1/1333 (0.1%)	
1	В	0.44	0/852	0.58	0/1148	
All	All	0.57	0/1838	0.65	1/2481 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
1	A	1038	ARG	NE-CZ-NH2	-5.18	117.71	120.30

There are no chirality outliers.

There are no planarity outliers.

#### 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	960	0	993	9	0
1	В	832	0	852	10	0
2	A	10	0	6	0	0
3	A	72	0	0	2	0
3	В	6	0	0	0	0
All	All	1880	0	1851	18	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 5.

All (18) 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:B:1013:GLU:O	1:B:1017:LYS:HG2	1.91	0.70
1:A:928:GLU:HB3	1:A:929:PRO:HD3	1.75	0.69
1:B:1040:MET:CE	1:B:1040:MET:HA	2.25	0.66
1:B:1010:GLY:HA3	1:B:1040:MET:HE1	1.83	0.61
1:B:1040:MET:CE	1:B:1043:LEU:HD12	2.31	0.59
1:B:1040:MET:HE1	1:B:1043:LEU:HD12	1.90	0.54
1:B:1040:MET:HA	1:B:1040:MET:HE3	1.89	0.53
3:A:72:HOH:O	1:B:1003:LYS:HE2	2.09	0.53
1:A:930:LEU:HD21	1:A:1008:PRO:HD3	1.91	0.51
1:A:999:GLN:OE1	3:A:3:HOH:O	2.19	0.51
1:A:975:GLY:HA3	1:A:1000:TRP:CE2	2.46	0.51
1:A:1026:SER:O	1:A:1030:LYS:HG3	2.17	0.45
1:A:968:PRO:HB2	1:A:970:ASP:OD1	2.18	0.44
1:B:1040:MET:HA	1:B:1040:MET:HE2	1.98	0.43
1:A:928:GLU:HB3	1:A:929:PRO:CD	2.47	0.42
1:B:984:GLU:CD	1:B:1002:PRO:HB2	2.40	0.41
1:A:967:PRO:HA	1:A:968:PRO:HD3	1.95	0.41
1:A:1018:LEU:HD22	1:B:1015:ILE:HD12	2.03	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	118/126 (94%)	113 (96%)	5 (4%)	0	100	100
1	В	101/126 (80%)	96 (95%)	5 (5%)	0	100	100
All	All	219/252 (87%)	209 (95%)	10 (5%)	0	100	100



There are no Ramachandran outliers to report.

#### 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	107/112 (96%)	105 (98%)	2 (2%)	57 63		
1	В	91/112 (81%)	80 (88%)	11 (12%)	5 2		
All	All	198/224 (88%)	185 (93%)	13 (7%)	16 14		

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	958	HIS
1	A	1011	ILE
1	В	931	LYS
1	В	951	LYS
1	В	980	THR
1	В	982	SER
1	В	983	ASP
1	В	990	LEU
1	В	1003	LYS
1	В	1013	GLU
1	В	1015	ILE
1	В	1017	LYS
1	В	1033	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	$\operatorname{Res}$	Type
1	A	994	ASN
1	В	979	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 monosaccharides 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	$\mathbf{B}_{0}$	ond leng	$\operatorname{gths}$	В	ond ang	les
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2 Counts $ RMSZ  # Z $		# Z  > 2	
2	OCS	A	1500	-	8,9,9	1.68	2 (25%)	10,13,13	2.04	2 (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
2	OCS	A	1500	-	-	7/9/9/9	-

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(\mathbf{\mathring{A}})$	Ideal(A)
2	A	1500	OCS	CB-CA	2.81	1.56	1.53
2	A	1500	OCS	CB-SG	2.59	1.86	1.77

#### All (2) bond angle outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^o)$
2	A	1500	OCS	OD3-SG-CB	3.91	111.59	106.94
2	A	1500	OCS	OD2-SG-CB	3.43	111.21	105.74



There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1500	OCS	C-CA-CB-SG
2	A	1500	OCS	O-C-CA-N
2	A	1500	OCS	CA-CB-SG-OD1
2	A	1500	OCS	CA-CB-SG-OD2
2	A	1500	OCS	CA-CB-SG-OD3
2	A	1500	OCS	OXT-C-CA-N
2	A	1500	OCS	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

## 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	<RSRZ $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	120/126 (95%)	-0.15	2 (1%) 70 74	29, 41, 67, 73	0
1	В	105/126 (83%)	0.25	3 (2%) 51 57	55, 74, 109, 117	0
All	All	225/252 (89%)	0.03	5 (2%) 62 66	29, 57, 102, 117	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1047	HIS	3.7
1	A	957	GLY	3.3
1	В	971	VAL	2.5
1	В	996	ARG	2.5
1	В	968	PRO	2.5

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

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

### 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

### 6.4 Ligands (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
	2	OCS	A	1500	10/10	0.87	0.13	54,60,67,68	0

# 6.5 Other polymers (i)

There are no such residues in this entry.

