



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 24, 2021 – 11:07 AM GMT

PDB ID : 7BBO  
Title : Crystal Structure of the second bromodomain of Pleckstrin homology domain interacting protein (PHIP) in space group P212121  
Authors : Krojer, T.; Talon, R.; Fairhead, M.; Szykowska, A.; Burgess-Brown, N.A.; Brennan, P.E.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; von Delft, F.; Structural Genomics Consortium (SGC)  
Deposited on : 2020-12-18  
Resolution : 1.32 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](mailto: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 : 2.17.1.dev1  
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) : 2.17.1.dev1

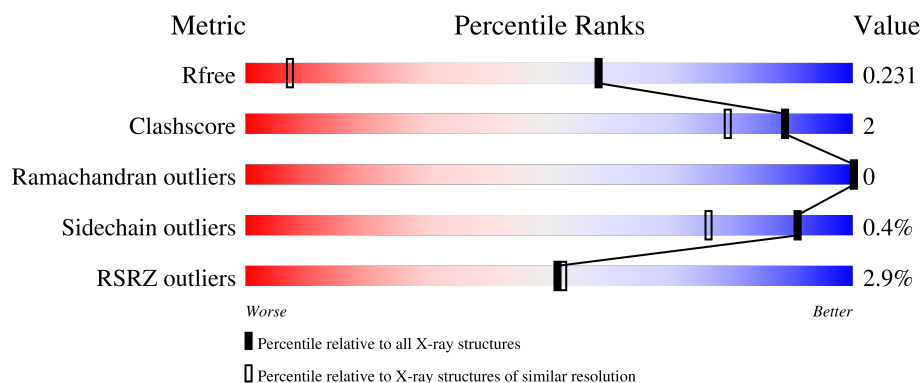
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.32 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	1611 (1.34-1.30)
Clashscore	141614	1667 (1.34-1.30)
Ramachandran outliers	138981	1615 (1.34-1.30)
Sidechain outliers	138945	1615 (1.34-1.30)
RSRZ outliers	127900	1580 (1.34-1.30)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	AAA	128	<div> <div>5%</div> <div>94%</div> <div>• •</div> </div>
1	BBB	128	<div> <div>%</div> <div>89%</div> <div>5% 5%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2279 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 PH-interacting protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	124	Total	C	N	O	S	0	0	0
			1029	653	171	198	7			
1	BBB	121	Total	C	N	O	S	0	2	0
			1015	645	166	197	7			

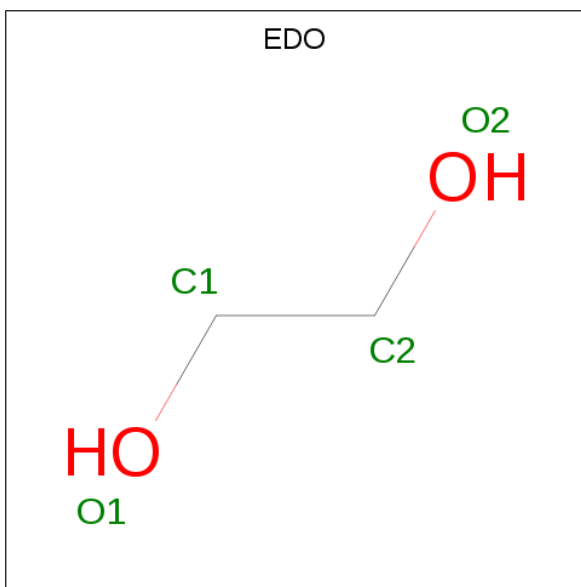
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	1313	SER	-	expression tag	UNP Q8WWQ0
AAA	1314	MET	-	expression tag	UNP Q8WWQ0
BBB	1313	SER	-	expression tag	UNP Q8WWQ0
BBB	1314	MET	-	expression tag	UNP Q8WWQ0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	1	Total	Ca	0	0
			1	1		
2	BBB	2	Total	Ca	0	0
			2	2		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AAA	1	Total C O 4 2 2	0	0
3	AAA	1	Total C O 4 2 2	0	0
3	BBB	1	Total C O 4 2 2	0	0
3	BBB	1	Total C O 4 2 2	0	0
3	BBB	1	Total C O 4 2 2	0	0
3	BBB	1	Total C O 4 2 2	0	0
3	BBB	1	Total C O 4 2 2	0	0
3	BBB	1	Total C O 4 2 2	0	0
3	BBB	1	Total C O 4 2 2	0	0

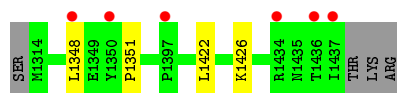
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	96	Total O 96 96	0	0
4	BBB	100	Total O 100 100	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: PH-interacting protein



- Molecule 1: PH-interacting protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	47.73Å 56.48Å 91.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.15 – 1.32 48.10 – 1.32	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.15-1.32) 99.7 (48.10-1.32)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.72 (at 1.32Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.186 , 0.226 0.191 , 0.231	Depositor DCC
$R_{free}$ test set	2843 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	11.5	Xtriage
Anisotropy	1.134	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 40.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2279	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	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 39.10 % 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 3.3376e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: EDO, CA

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	AAA	0.77	0/1052	0.79	0/1419
1	BBB	0.73	0/1038	0.79	0/1400
All	All	0.75	0/2090	0.79	0/2819

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	AAA	1029	0	1002	3	0
1	BBB	1015	0	984	6	0
2	AAA	1	0	0	0	0
2	BBB	2	0	0	0	0
3	AAA	8	0	11	0	0
3	BBB	28	0	30	0	0
4	AAA	96	0	0	1	0
4	BBB	100	0	0	2	0
All	All	2279	0	2027	8	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.

The worst 5 of 8 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:BBB:1407[A]:SER:OG	4:BBB:1601:HOH:O	1.72	0.77
1:BBB:1376:GLU:OE1	4:BBB:1602:HOH:O	2.04	0.75
1:BBB:1318:ILE:HD11	1:BBB:1429:LEU:HD13	1.90	0.53
1:BBB:1347:LEU:N	1:BBB:1347:LEU:HD12	2.28	0.48
1:AAA:1351:PRO:HD2	4:AAA:1613:HOH:O	2.14	0.46

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	AAA	122/128 (95%)	121 (99%)	1 (1%)	0	100	100
1	BBB	121/128 (94%)	121 (100%)	0	0	100	100
All	All	243/256 (95%)	242 (100%)	1 (0%)	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	AAA	117/121 (97%)	116 (99%)	1 (1%)	78	51

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BBB	116/121 (96%)	116 (100%)	0	100	100
All	All	233/242 (96%)	232 (100%)	1 (0%)	91	76

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	1348	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 12 ligands modelled in this entry, 3 are monoatomic - leaving 9 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	$\# Z  > 2$
3	EDO	BBB	1505	2	3,3,3	0.20	0	2,2,2	0.41	0
3	EDO	AAA	1503	2	3,3,3	0.34	0	2,2,2	0.51	0
3	EDO	AAA	1502	-	3,3,3	0.68	0	2,2,2	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	BBB	1509	-	3,3,3	0.40	0	2,2,2	0.42	0
3	EDO	BBB	1504	2	3,3,3	0.25	0	2,2,2	0.34	0
3	EDO	BBB	1506	2	3,3,3	0.34	0	2,2,2	0.43	0
3	EDO	BBB	1508	2	3,3,3	0.06	0	2,2,2	0.40	0
3	EDO	BBB	1503	2	3,3,3	0.20	0	2,2,2	0.27	0
3	EDO	BBB	1507	2	3,3,3	0.12	0	2,2,2	0.29	0

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
3	EDO	BBB	1505	2	-	0/1/1/1	-
3	EDO	AAA	1503	2	-	0/1/1/1	-
3	EDO	AAA	1502	-	-	0/1/1/1	-
3	EDO	BBB	1509	-	-	1/1/1/1	-
3	EDO	BBB	1504	2	-	1/1/1/1	-
3	EDO	BBB	1506	2	-	0/1/1/1	-
3	EDO	BBB	1508	2	-	0/1/1/1	-
3	EDO	BBB	1503	2	-	0/1/1/1	-
3	EDO	BBB	1507	2	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	BBB	1509	EDO	O1-C1-C2-O2
3	BBB	1504	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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<sup>th</sup> 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>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	AAA	124/128 (96%)	-0.18	6 (4%) 30 31	12, 20, 39, 58	0
1	BBB	121/128 (94%)	-0.25	1 (0%) 86 86	11, 20, 39, 52	0
All	All	245/256 (95%)	-0.22	7 (2%) 51 52	11, 20, 39, 58	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	1348	LEU	5.2
1	AAA	1437	ILE	4.4
1	BBB	1313	SER	3.9
1	AAA	1436	THR	3.4
1	AAA	1350	TYR	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<sup>th</sup> 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	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	AAA	1503	4/4	0.92	0.10	23,25,29,29	0
3	EDO	BBB	1509	4/4	0.92	0.13	25,30,32,34	0
3	EDO	BBB	1504	4/4	0.95	0.06	17,21,22,24	0
3	EDO	BBB	1505	4/4	0.96	0.06	18,18,20,21	0
3	EDO	BBB	1508	4/4	0.96	0.10	19,20,24,26	0
3	EDO	AAA	1502	4/4	0.96	0.12	19,20,23,28	0
3	EDO	BBB	1507	4/4	0.97	0.05	18,19,20,21	0
3	EDO	BBB	1503	4/4	0.97	0.06	19,20,21,21	0
3	EDO	BBB	1506	4/4	0.97	0.07	19,19,19,21	0
2	CA	BBB	1501	1/1	0.99	0.07	15,15,15,15	0
2	CA	BBB	1502	1/1	1.00	0.05	16,16,16,16	0
2	CA	AAA	1501	1/1	1.00	0.04	24,24,24,24	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.