

Full wwPDB X-ray Structure Validation Report (i)

May 22, 2020 – 02:17 am BST

PDB ID : 5C85

> Title : Crystal structure of the human BRPF1 bromodomain in complex with SEED1

Authors : Zhu, J.; Caflisch, A.

2015-06-25 Deposited on

1.70 Å(reported)Resolution

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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467

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

Xtriage (Phenix) 1.13 EDS 2.11

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

> Refmac 5.8.0158

7.0.044 (Gargrove) CCP4

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

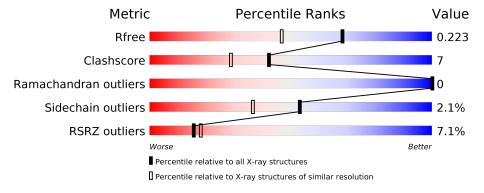
Validation Pipeline (wwPDB-VP) 2.11

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 1.70 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 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		
			7%		
1	A	116	83%	13%	



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1032 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.

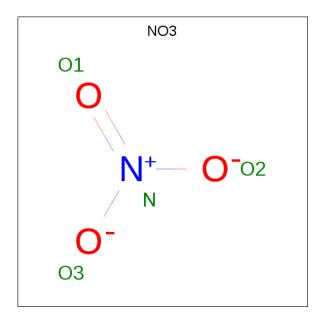
• Molecule 1 is a protein called Peregrin.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	110	Total	С	N	О	S	0	4	0
1	A	112	937	603	158	172	4	0	4	U

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	${f Comment}$	Reference
Α	625	SER	_	expression tag	UNP P55201

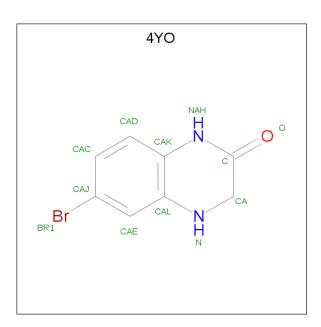
• Molecule 2 is NITRATE ION (three-letter code: NO3) (formula: NO₃).



\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
2	A	1	Total N O 4 1 3	0	0

• Molecule 3 is 6-bromo-3,4-dihydroquinoxalin-2(1H)-one (three-letter code: 4YO) (formula: C₈H₇BrN₂O).





Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf		
9	Λ	1	Total	Br	С	N	О	0	0
)	A	1	12	1	8	2	1	0	0

• Molecule 4 is water.

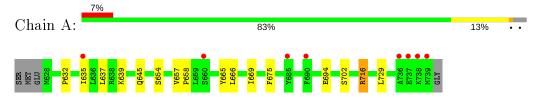
Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
4	A	79	Total O 79 79	0	0



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 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: Peregrin





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 32 2 1	Depositor	
Cell constants	60.72Å 60.72Å 61.87Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	40.07 - 1.70	Depositor	
rtesolution (A)	40.07 - 1.70	EDS	
% Data completeness	$100.0 \ (40.07 - 1.70)$	Depositor	
(in resolution range)	$100.0 \ (40.07 - 1.70)$	EDS	
R_{merge}	0.03	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	5.46 (at 1.70Å)	Xtriage	
Refinement program	PHENIX 1.9_1692	Depositor	
D D.	0.207 , 0.226	Depositor	
R, R_{free}	0.208 , 0.223	DCC	
R_{free} test set	731 reflections (4.91%)	wwPDB-VP	
Wilson B-factor (Å ²)	31.2	Xtriage	
Anisotropy	0.324	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34 , 56.2	EDS	
L-test for twinning ²	$< L >=0.48, < L^2>=0.31$	Xtriage	
Estimated twinning fraction	0.038 for -h,-k,l	Xtriage	
F_o, F_c correlation	0.96	EDS	
Total number of atoms	1032	wwPDB-VP	
Average B, all atoms (Å ²)	50.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.57% 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: 4YO, NO3

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).

	Tal	Chain	Bond	lengths	Bond angles		
10.	101	Chain	RMSZ	# Z >5	RMSZ	# Z > 5	
	1	A	0.34	0/961	0.49	0/1296	

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 (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	937	0	917	13	0
2	A	4	0	0	0	0
3	A	12	0	0	0	0
4	A	79	0	0	5	0
All	All	1032	0	917	13	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 7.

All (13) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$egin{array}{ll} ext{Interatomic} \ ext{distance} \ (ext{\AA}) \end{array}$	Clash overlap (Å)
1:A:645:GLN:OE1	4:A:901:HOH:O	2.08	0.69
1:A:645:GLN:NE2	4:A:904:HOH:O	2.29	0.65
1:A:694:GLU:HG3	1:A:729:LEU:HD13	1.84	0.60
1:A:639:LYS:HE3	4:A:911:HOH:O	2.10	0.52
1:A:632:PRO:O	1:A:635:ILE:HG13	2.10	0.52
1:A:654[A]:SER:HA	1:A:675:PHE:HB2	1.97	0.47
1:A:665:TYR:CZ	1:A:669:ILE:HG13	2.53	0.45
1:A:702[B]:SER:OG	4:A:902:HOH:O	2.21	0.42
1:A:716[A]:ARG:NH1	4:A:908:HOH:O	2.51	0.42
1:A:654[B]:SER:HA	1:A:675:PHE:HB2	2.02	0.42
1:A:637:LEU:HA	1:A:637:LEU:HD23	1.81	0.41
1:A:657:VAL:HA	1:A:658:PRO:HD3	1.94	0.41
1:A:716[B]:ARG:HD2	1:A:716[B]:ARG:HA	1.85	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	114/116 (98%)	113 (99%)	1 (1%)	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	98/105~(93%)	95 (97%)	3 (3%)	40 21	

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	666	LEU
1	A	716[A]	ARG
1	A	716[B]	ARG

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

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)

2 ligands are 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	Dog	Dog	Pos	Pos	Pos	Pos	Ros	Ros	Pos	Link	Bond lengths			Bond angles		
	туре	Chain		LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2									
2	NO3	A	801	-	1,3,3	6.15	1 (100%)	0,3,3	0.00	-									
3	4YO	A	802	-	13,13,13	4.13	3 (23%)	17,18,18	1.69	4 (23%)									



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.

\mathbf{Mol}	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	4YO	A	802	_	-	_	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$\operatorname{Ideal}(ext{\AA})$
3	A	802	4YO	CA-C	-14.13	1.40	1.50
2	A	801	NO3	O1-N	6.15	1.52	1.24
3	A	802	4YO	C-NAH	3.72	1.39	1.35
3	A	802	4YO	CA-N	2.00	1.48	1.45

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
3	A	802	4YO	CA-C-NAH	3.94	121.57	116.20
3	A	802	4YO	O-C-NAH	-3.91	117.98	121.43
3	A	802	4YO	CAK-NAH-C	-2.24	121.73	124.49
3	A	802	4YO	O-C-CA	2.22	120.41	118.67

There are no chirality outliers.

There are no torsion outliers.

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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$		$OWAB(A^2)$	Q < 0.9	
1	A	112/116 (96%)	0.55	8 (7%)	16	18	27, 50, 78, 89	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	739	MET	5.5
1	A	660	SER	5.4
1	A	690	PHE	3.1
1	A	736	ALA	3.0
1	A	635	ILE	2.9
1	A	737	GLU	2.9
1	A	685	TYR	2.8
1	A	738	LYS	2.6

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 carbohydrates 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
3	4YO	A	802	12/12	0.90	0.12	43,54,64,73	0
2	NO3	A	801	4/4	0.97	0.10	32,40,42,42	0

6.5 Other polymers (i)

There are no such residues in this entry.

