Full wwPDB X-ray Structure Validation Report ⓘ

Sep 19, 2023 – 01:28 pm BST

PDB ID	:	8BPT
Title	:	Crystal structure of the second bromodomain of BRD5 from Leishmania donovani
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Deposited on	:	2022-11-17
Resolution	:	1.60 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 ⓘ 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 ⓘ) were used in the production of this report:

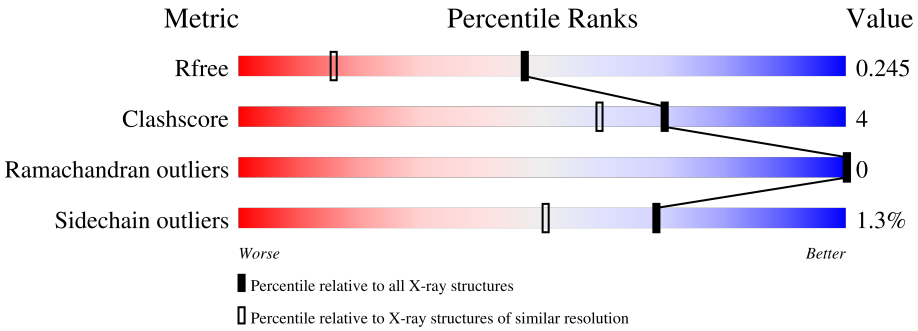
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)

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%

Mol	Chain	Length	Quality of chain
1	A	140	91% 9% .
1	B	140	83% 14% ..

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4569 atoms, of which 2194 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 Bromo domain-containing protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	139	Total	C	H	N	O	S	76	0	0
			2203	691	1097	202	207	6			
1	B	139	Total	C	H	N	O	S	76	0	0
			2203	691	1097	202	207	6			

- Molecule 2 is water.

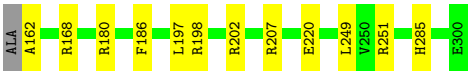
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	82	Total	O	0	0
			82	82		
2	B	81	Total	O	0	0
			81	81		

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. 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. 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.

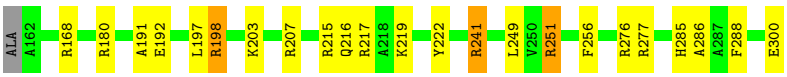
• Molecule 1: Bromo domain-containing protein

Chain A:



• Molecule 1: Bromo domain-containing protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	33.37Å 75.36Å 105.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.84 – 1.60 31.82 – 1.60	Depositor EDS
% Data completeness (in resolution range)	97.9 (31.84-1.60) 97.9 (31.82-1.60)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.39 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0352, REFMAC 5.8.0352	Depositor
R, R_{free}	0.162 , 0.215 0.208 , 0.245	Depositor DCC
R_{free} test set	1701 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å^2)	21.1	Xtriage
Anisotropy	0.643	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.45 , 39.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4569	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.09% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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.

5 Model quality

5.1 Standard geometry

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	0.42	0/1126	0.73	0/1522
1	B	0.47	0/1126	0.79	3/1522 (0.2%)
All	All	0.45	0/2252	0.76	3/3044 (0.1%)

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
1	B	0	6
All	All	0	8

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	251	ARG	NE-CZ-NH2	-8.24	116.18	120.30
1	B	276	ARG	NE-CZ-NH2	-6.84	116.88	120.30
1	B	241	ARG	NE-CZ-NH2	-5.02	117.79	120.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	180	ARG	Sidechain
1	A	202	ARG	Sidechain
1	B	180	ARG	Sidechain
1	B	198	ARG	Sidechain
1	B	217	ARG	Sidechain
1	B	241	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B	251	ARG	Sidechain
1	B	277	ARG	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	1106	1097	1094	8	0
1	B	1106	1097	1094	10	7
2	A	82	0	0	4	0
2	B	81	0	0	2	5
All	All	2375	2194	2188	16	7

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 4.

All (16) 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:207:ARG:HD3	2:A:476:HOH:O	1.87	0.74
1:A:197:LEU:HD11	1:B:256:PHE:CZ	2.22	0.74
1:A:162:ALA:N	2:A:401:HOH:O	2.22	0.71
1:A:186:PHE:CD1	1:A:249:LEU:HD21	2.29	0.68
1:A:220:GLU:HG2	2:A:431:HOH:O	1.94	0.68
1:B:191:ALA:HB1	1:B:198:ARG:HG2	1.80	0.63
1:B:168:ARG:HH12	1:B:219:LYS:HE3	1.64	0.62
1:A:168:ARG:HH11	1:A:168:ARG:HG3	1.78	0.49
1:B:249:LEU:C	1:B:249:LEU:HD23	2.34	0.48
1:B:168:ARG:HH22	1:B:219:LYS:NZ	2.14	0.44
1:B:207:ARG:NH2	2:B:404:HOH:O	2.52	0.43
1:A:285:HIS:HE1	2:A:472:HOH:O	2.01	0.42
1:A:197:LEU:HD22	1:B:197:LEU:HD22	2.02	0.42
1:B:285:HIS:HE1	2:B:475:HOH:O	2.02	0.42
1:B:286:ALA:HB1	1:B:288:PHE:CE1	2.56	0.41
1:B:192:GLU:HA	1:B:198:ARG:NH2	2.36	0.40

All (7) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:TYR:CB	2:B:479:HOH:O[4_565]	0.64	1.56
1:B:222:TYR:CG	2:B:479:HOH:O[4_565]	1.43	0.77
1:B:222:TYR:HB2	2:B:479:HOH:O[4_565]	0.93	0.67
1:B:222:TYR:HB3	2:B:479:HOH:O[4_565]	1.01	0.59
1:B:215:ARG:HH12	1:B:300:GLU:OE1[1_655]	1.46	0.14
1:B:207:ARG:NH1	1:B:216:GLN:HE22[4_465]	1.56	0.04
1:B:222:TYR:CA	2:B:479:HOH:O[4_565]	2.16	0.04

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	137/140 (98%)	135 (98%)	2 (2%)	0	100	100
1	B	137/140 (98%)	134 (98%)	3 (2%)	0	100	100
All	All	274/280 (98%)	269 (98%)	5 (2%)	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	117/117 (100%)	115 (98%)	2 (2%)	60	38
1	B	117/117 (100%)	116 (99%)	1 (1%)	78	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	234/234 (100%)	231 (99%)	3 (1%)	69 50

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

Mol	Chain	Res	Type
1	A	198	ARG
1	A	251	ARG
1	B	203	LYS

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

Mol	Chain	Res	Type
1	A	285	HIS
1	B	285	HIS

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

There are no ligands in this entry.

5.7 Other polymers

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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.