

wwPDB X-ray Structure Validation Summary Report (i)

Nov 5, 2023 – 12:58 AM EDT

PDB ID	:	7RJN
Title	:	Crystal structure of human bromodomain containing protein 3 (BRD3) in
		complex with BCLTF1
Authors	:	Fedorov, E.; Islam, K.; Ghosh, A.
Deposited on	:	2021-07-21
Resolution	:	1.95 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 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:

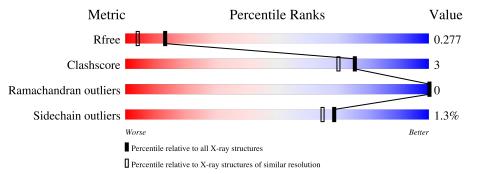
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.95 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)

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	А	123		92%	7% ••		
1	В	123		90%	7% •		
2	С	10	40%	60%			
2	D	10	40%	60%			



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2250 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 3.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	122	Total	С	Ν	0	\mathbf{S}	0	2	0
1			1023	661	169	183	10			
1	В	120	Total	С	Ν	Ο	\mathbf{S}	0	9	0
1	D	120	1007	651	167	179	10	0	2	0

There are 4 discrepancies between the modelled and reference sequences:

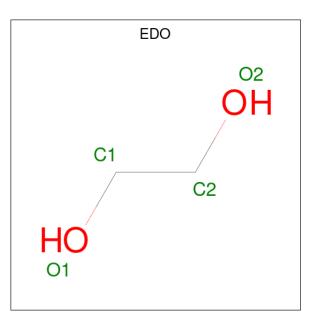
Chain	Residue	Modelled	Actual	Comment	Reference
А	22	SER	-	expression tag	UNP Q15059
А	23	MET	-	expression tag	UNP Q15059
В	22	SER	-	expression tag	UNP Q15059
В	23	MET	-	expression tag	UNP Q15059

• Molecule 2 is a protein called Bcl-2-associated transcription factor 1.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	С	4	Total C N O 34 23 5 6	0	0	0
2	D	4	Total C N O 34 23 5 6	0	0	0

• Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	79	Total O 79 79	0	0
4	В	58	Total O 59 59	0	1
4	С	1	Total O 1 1	0	0
4	D	1	Total O 1 1	0	0



TH AL AL T3 LEC LEC LYS AR(

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: Bromodomain-containing protein 3

Chain A:		92%		7% ••
822 K35 K 40 K 52 K 52 A 56	K67 K88 L129 L134 L134 C134 GLU			
• Molecule 1: I	Bromodomain-conta	ining protein 3		
Chain B:		90%		7% •
SER M23 K35 K35 K44 K48 K48 K52	W57 P58 X88 M106 GLU GLU GLU			
• Molecule 2: I	Bcl-2-associated tran	nscription factor 1		
Chain C:	40%		60%	
THR ALA ALY T333 F336 LEU LEU LEU ARG				
• Molecule 2: I	Bcl-2-associated tran	nscription factor 1		
Chain D:	40%		60%	
<mark></mark>				



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	42.73Å 54.79Å 122.24Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 - 1.95	Depositor
Resolution (A)	29.49 - 1.95	EDS
% Data completeness	99.7 (20.00-1.95)	Depositor
(in resolution range)	$100.0\ (29.49-1.95)$	EDS
R _{merge}	0.13	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.79 (at 1.95 Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
D D.	0.183 , 0.234	Depositor
R, R_{free}	0.238 , 0.277	DCC
R_{free} test set	1074 reflections $(4.97%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	19.5	Xtriage
Anisotropy	0.499	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35, 43.3	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2250	wwPDB-VP
Average B, all atoms $(Å^2)$	25.0	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 49.05 % 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 7.8813e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical 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.



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: ALY, EDO

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.38	0/1057	0.51	0/1432	
1	В	0.37	0/1041	0.53	0/1412	
2	С	0.49	0/21	0.58	0/25	
2	D	0.50	0/21	0.55	0/25	
All	All	0.37	0/2140	0.52	0/2894	

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	А	1023	0	1022	8	0
1	В	1007	0	1004	8	0
2	С	34	0	32	0	0
2	D	34	0	32	0	0
3	А	4	0	6	0	0
3	В	8	0	12	0	0
4	А	79	0	0	0	0
4	В	59	0	0	1	0
4	С	1	0	0	0	0

Continued on next page...



Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1	0	0	0	0
All	All	2250	0	2108	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 3.

The worst 5 of 13 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:44:ASN:HA	1:B:48:LYS:HD2	1.67	0.76
1:B:23:MET:SD	4:B:352:HOH:O	2.55	0.65
1:A:56:ALA:HA	1:A:129:LEU:HD11	1.82	0.62
1:B:52:LYS:HD3	1:B:52:LYS:N	2.25	0.52
1:A:134:LEU:CD1	1:B:106:ASN:HB2	2.40	0.51

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	Perce	entiles
1	А	122/123~(99%)	120 (98%)	2(2%)	0	100	100
1	В	120/123~(98%)	119 (99%)	1 (1%)	0	100	100
2	С	1/10 (10%)	1 (100%)	0	0	100	100
2	D	1/10 (10%)	1 (100%)	0	0	100	100
All	All	244/266~(92%)	241 (99%)	3~(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	А	116/115~(101%)	114 (98%)	2(2%)	60	55	
1	В	114/115~(99%)	113~(99%)	1 (1%)	78	77	
2	С	2/6~(33%)	2~(100%)	0	100	100	
2	D	2/6~(33%)	2(100%)	0	100	100	
All	All	234/242~(97%)	231~(99%)	3 (1%)	69	65	

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

Mol	Chain	Res	Type
1	А	52	LYS
1	А	67	LYS
1	В	35	LYS

Sometimes 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)

2 non-standard protein/DNA/RNA residues 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).



Mal	Mol Type	Type Chain Res		Link	Bond lengths			Bond angles		
10101	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	ALY	С	335	2	10,11,12	0.79	0	7,12,14	0.72	0
2	ALY	D	335	2	10,11,12	0.83	0	7,12,14	0.78	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
2	ALY	С	335	2	-	1/9/10/12	-
2	ALY	D	335	2	-	2/9/10/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	С	335	ALY	O-C-CA-CB
2	D	335	ALY	O-C-CA-CB
2	D	335	ALY	CG-CD-CE-NZ

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

3 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	Dec	Link	B	Bond lengths			Bond angles		
INIOI	Moi Type C	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
3	EDO	В	201	-	$3,\!3,\!3$	0.56	0	$2,\!2,\!2$	0.23	0	
3	EDO	А	201	-	3,3,3	0.48	0	2,2,2	0.24	0	
3	EDO	В	202	-	3,3,3	0.53	0	2,2,2	0.30	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	В	201	-	-	0/1/1/1	-
3	EDO	А	201	-	-	0/1/1/1	-
3	EDO	В	202	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

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)

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

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

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

6.3 Carbohydrates (i)

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

6.4 Ligands (i)

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

6.5 Other polymers (i)

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

