

Full wwPDB X-ray Structure Validation Report (i)

Oct 2, 2023 – 05:50 AM EDT

PDB ID : 6MR4

Title : Crystal structure of the Sth1 bromodomain from S.cerevisiae Authors : Seo, H.S.; Hashimoto, H.; Krolak, A.; Debler, E.W.; Blus, B.J.

Deposited on : 2018-10-11

Resolution : 2.71 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 : FAILED Xtriage (Phenix) : 1.13 EDS : FAILED

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

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 2.71 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 10768 atoms, of which 5265 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 Nuclear protein STH1/NPS1.

Mol	Chain	Residues			Aton	ns			ZeroOcc	AltConf	Trace
1	Λ	109	Total	С	Н	N	О	S	0	0	0
1	A	109	1800	587	882	148	179	4	0	U	
1	В	106	Total	С	Н	N	О	S	0 0 0 0 0	0	0
1	Ъ	100	1765	576	867	143	175	4			
1	С	109	Total	С	Н	N	О	S	0	0	0
1		109	1799	587	881	148	179	4			
1	D	108	Total	С	Н	N	О	S	0	0	0
1	ט	100	1793	585	879	147	178	4	0	U	
1	Е	108	Total	С	Н	N	О	S	0	0	0
1	l Li	100	1792	585	878	147	178	4			
1	F	108	Total	С	Н	N	О	S	0	0	0
			1792	585	878	147	178	4			U

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1248	SER	-	expression tag	UNP P32597
A	1249	MET	-	expression tag	UNP P32597
В	1248	SER	-	expression tag	UNP P32597
В	1249	MET	-	expression tag	UNP P32597
С	1248	SER	-	expression tag	UNP P32597
С	1249	MET	-	expression tag	UNP P32597
D	1248	SER	-	expression tag	UNP P32597
D	1249	MET	-	expression tag	UNP P32597
Е	1248	SER	-	expression tag	UNP P32597
Е	1249	MET	-	expression tag	UNP P32597
F	1248	SER	-	expression tag	UNP P32597
F	1249	MET	-	expression tag	UNP P32597

• Molecule 2 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total O 3 3	0	0
2	В	5	Total O 5 5	0	0
2	С	3	Total O 3 3	0	0
2	E	3	Total O 3 3	0	0
2	F	13	Total O 13 13	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.



3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source	
Space group	C 1 2 1	Depositor	
Cell constants	$141.75 ext{Å}$ $74.62 ext{Å}$ $72.54 ext{Å}$	Depositor	
a, b, c, α , β , γ	90.00° 92.88° 90.00°		
Resolution (Å)	72.45 - 2.71	Depositor	
% Data completeness	98.3 (72.45-2.71)	Depositor	
(in resolution range)	· ,		
R_{merge}	0.08	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.81 (at 2.73Å)	Xtriage	
Refinement program	PHENIX	Depositor	
R, R_{free}	0.238 , 0.270	Depositor	
Wilson B-factor $(Å^2)$	48.0	Xtriage	
Anisotropy	0.395	Xtriage	
L-test for twinning ²	$< L > = 0.47, < L^2> = 0.30$	Xtriage	
Estimated twinning fraction	0.047 for -h,-k,l	Xtriage	
Total number of atoms	10768	wwPDB-VP	
Average B, all atoms (\mathring{A}^2)	55.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.33% 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.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

There are no ligands in this entry.

4.7 Other polymers (i)

There are no such residues in this entry.



4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

