



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 4, 2022 – 08:19 PM EDT

PDB ID : 5K83  
Title : Crystal Structure of a Primate APOBEC3G N-Domain, in Complex with ss-DNA  
Authors : Xiao, X.; Li, S.-X.; Yang, H.; Chen, X.S.  
Deposited on : 2016-05-27  
Resolution : 2.39 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.

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The following versions of software and data (see [references ⓘ](#)) 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) : 2.27

## 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 2.39 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

There are 4 unique types of molecules in this entry. The entry contains 9837 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 Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G, Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	185	Total	C	N	O	S	0	0	0
			1551	1012	268	261	10			
1	C	191	Total	C	N	O	S	0	0	0
			1603	1045	279	268	11			
1	F	184	Total	C	N	O	S	0	0	0
			1543	1008	266	259	10			
1	E	191	Total	C	N	O	S	0	0	0
			1603	1045	279	268	11			
1	B	185	Total	C	N	O	S	0	0	0
			1551	1012	268	261	10			
1	A	191	Total	C	N	O	S	0	0	0
			1603	1045	279	268	11			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	GLY	-	expression tag	UNP M1GSK9
D	-3	PRO	-	expression tag	UNP M1GSK9
D	-2	ALA	-	expression tag	UNP M1GSK9
D	-1	GLY	-	expression tag	UNP M1GSK9
D	0	SER	-	expression tag	UNP M1GSK9
D	143	ALA	-	linker	UNP M1GSK9
D	144	GLU	-	linker	UNP M1GSK9
D	145	ALA	-	linker	UNP M1GSK9
D	146	GLY	-	linker	UNP M1GSK9
C	-4	GLY	-	expression tag	UNP M1GSK9
C	-3	PRO	-	expression tag	UNP M1GSK9
C	-2	ALA	-	expression tag	UNP M1GSK9
C	-1	GLY	-	expression tag	UNP M1GSK9
C	0	SER	-	expression tag	UNP M1GSK9
C	143	ALA	-	linker	UNP M1GSK9
C	144	GLU	-	linker	UNP M1GSK9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	145	ALA	-	linker	UNP M1GSK9
C	146	GLY	-	linker	UNP M1GSK9
F	-4	GLY	-	expression tag	UNP M1GSK9
F	-3	PRO	-	expression tag	UNP M1GSK9
F	-2	ALA	-	expression tag	UNP M1GSK9
F	-1	GLY	-	expression tag	UNP M1GSK9
F	0	SER	-	expression tag	UNP M1GSK9
F	143	ALA	-	linker	UNP M1GSK9
F	144	GLU	-	linker	UNP M1GSK9
F	145	ALA	-	linker	UNP M1GSK9
F	146	GLY	-	linker	UNP M1GSK9
E	-4	GLY	-	expression tag	UNP M1GSK9
E	-3	PRO	-	expression tag	UNP M1GSK9
E	-2	ALA	-	expression tag	UNP M1GSK9
E	-1	GLY	-	expression tag	UNP M1GSK9
E	0	SER	-	expression tag	UNP M1GSK9
E	143	ALA	-	linker	UNP M1GSK9
E	144	GLU	-	linker	UNP M1GSK9
E	145	ALA	-	linker	UNP M1GSK9
E	146	GLY	-	linker	UNP M1GSK9
B	-4	GLY	-	expression tag	UNP M1GSK9
B	-3	PRO	-	expression tag	UNP M1GSK9
B	-2	ALA	-	expression tag	UNP M1GSK9
B	-1	GLY	-	expression tag	UNP M1GSK9
B	0	SER	-	expression tag	UNP M1GSK9
B	143	ALA	-	linker	UNP M1GSK9
B	144	GLU	-	linker	UNP M1GSK9
B	145	ALA	-	linker	UNP M1GSK9
B	146	GLY	-	linker	UNP M1GSK9
A	-4	GLY	-	expression tag	UNP M1GSK9
A	-3	PRO	-	expression tag	UNP M1GSK9
A	-2	ALA	-	expression tag	UNP M1GSK9
A	-1	GLY	-	expression tag	UNP M1GSK9
A	0	SER	-	expression tag	UNP M1GSK9
A	143	ALA	-	linker	UNP M1GSK9
A	144	GLU	-	linker	UNP M1GSK9
A	145	ALA	-	linker	UNP M1GSK9
A	146	GLY	-	linker	UNP M1GSK9

- Molecule 2 is a DNA chain called DNA (5'-D(\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*TP\*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	3	Total	C	N	O	P	0	0	0
			34	17	2	13	2			
2	J	3	Total	C	N	O	P	0	0	0
			33	17	2	12	2			
2	H	3	Total	C	N	O	P	0	0	0
			34	17	2	13	2			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	Zn	0	0
			1	1		
3	C	1	Total	Zn	0	0
			1	1		
3	F	1	Total	Zn	0	0
			1	1		
3	E	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	30	Total	O	0	0
			30	30		
4	C	53	Total	O	0	0
			53	53		
4	I	3	Total	O	0	0
			3	3		
4	F	41	Total	O	0	0
			41	41		
4	E	62	Total	O	0	0
			62	62		
4	J	1	Total	O	0	0
			1	1		
4	B	30	Total	O	0	0
			30	30		
4	A	54	Total	O	0	0
			54	54		
4	H	2	Total	O	0	0
			2	2		

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

### 3 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.72Å 83.31Å 105.75Å 90.00° 120.00° 90.00°	Depositor
Resolution (Å)	45.79 – 2.39	Depositor
% Data completeness (in resolution range)	99.7 (45.79-2.39)	Depositor
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.02 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.186 , 0.251	Depositor
Wilson B-factor (Å <sup>2</sup> )	35.6	Xtriage
Anisotropy	0.219	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.486 for l,k,-h-l 0.486 for -h-l,k,h 0.044 for h,-k,-h-l 0.044 for l,-k,h 0.044 for -h-l,-k,l	Xtriage
Total number of atoms	9837	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% of the height of the origin peak. No significant pseudotranslation is detected.*

<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.

## 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](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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.

#### 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.