

# Full wwPDB X-ray Structure Validation Report (i)

#### Mar 18, 2024 – 05:07 PM JST

PDB ID : 6M3F

Title: Crystal structure of the mouse endonuclease EndoG(H138A/C110A), space

group P212121

Authors: Park, K.H.; Woo, E.J.

Deposited on : 2020-03-03

Resolution : 1.96 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:

 $\begin{array}{ccc} & Mol Probity & : & 4.02b\text{-}467 \\ Xtriage \left(Phenix\right) & : & 1.13 \end{array}$ 

EDS : 2.36

buster-report : 1.1.7 (2018)

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

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

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

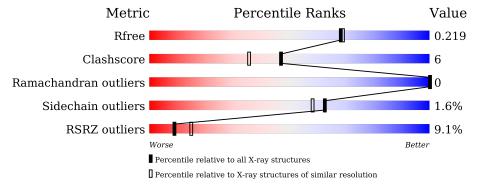
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.96 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
$R_{free}$	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)
RSRZ outliers	127900	2539 (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% 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				
1	В	249	76%	13%	• 10%		
1	С	249	7%	12%	14%		



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3803 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 Endonuclease G, mitochondrial.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	D	223	Total	С	N	О	S	0	0	0
1	Б	223	1784	1126	328	327	3	0	U	U
1	С	215	Total	С	N	О	S	1	0	0
1		210	1717	1089	311	314	3	1	U	U

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	110	ALA	CYS	engineered mutation	UNP O08600
В	138	ALA	HIS	engineered mutation	UNP 008600
С	110	ALA	CYS	engineered mutation	UNP O08600
С	138	ALA	HIS	engineered mutation	UNP O08600

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total Mg 1 1	0	0
2	С	1	Total Mg 1 1	0	0

• Molecule 3 is water.

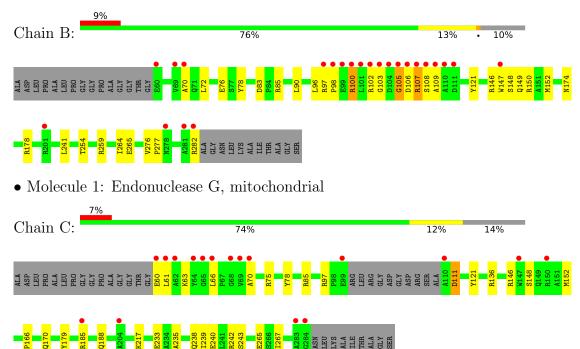
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	160	Total O 160 160	0	0
3	С	140	Total O 140 140	0	0



# 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 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: Endonuclease G, mitochondrial





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	53.69Å 68.88Å 127.19Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.24 - 1.96	Depositor
rtesolution (A)	33.24 - 1.96	EDS
% Data completeness	99.1 (33.24-1.96)	Depositor
(in resolution range)	99.1 (33.24-1.96)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.01	Depositor
$< I/\sigma(I) > 1$	4.82 (at 1.97Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
D D.	0.169 , 0.219	Depositor
$R, R_{free}$	0.169 , 0.219	DCC
$R_{free}$ test set	1697  reflections  (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.5	Xtriage
Anisotropy	0.548	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.38, 53.8	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3803	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.45% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: MG

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		lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	В	0.38	0/1828	0.58	0/2485	
1	С	0.38	0/1760	0.55	0/2394	
All	All	0.38	0/3588	0.57	0/4879	

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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	$\parallel$ #Planarity outliers	
1	В	0	4	

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	102	ARG	Peptide
1	В	105	GLY	Peptide
1	В	107	ARG	Peptide
1	В	108	SER	Peptide

## 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	В	1784	0	1745	28	1
1	С	1717	0	1678	22	1
2	В	1	0	0	0	0
2	С	1	0	0	0	0
3	В	160	0	0	3	0
3	С	140	0	0	6	0
All	All	3803	0	3423	43	1

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 6.

All (43) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
	1100111 2	distance (Å)	overlap (Å)
1:B:85:ARG:HH21	1:C:85:ARG:HH22	1.12	0.90
1:B:106:ASP:HB3	1:B:146:ARG:HD3	1.56	0.87
1:C:111:ASP:OD1	3:C:401:HOH:O	2.10	0.69
1:B:85:ARG:NH1	3:B:404:HOH:O	2.27	0.68
1:B:97:ARG:HG3	3:B:401:HOH:O	1.94	0.68
1:B:85:ARG:HH21	1:C:85:ARG:NH2	1.92	0.66
1:B:107:ARG:HB3	1:B:149:GLN:NE2	2.11	0.66
1:C:97:ARG:NH2	3:C:404:HOH:O	2.28	0.65
1:B:103:GLY:HA2	1:B:146:ARG:HB3	1.81	0.63
1:C:179:TYR:OH	1:C:242:ARG:NH1	2.32	0.63
1:B:76:GLU:HG3	1:B:150:ARG:HG2	1.85	0.59
1:B:276:VAL:HG23	1:B:277:PRO:HD3	1.84	0.59
1:B:96:LEU:O	3:B:401:HOH:O	2.17	0.57
1:C:136:ARG:NH1	3:C:401:HOH:O	2.40	0.54
1:B:83:ASP:HB2	1:B:90:LEU:HG	1.90	0.54
1:C:240:GLU:OE1	3:C:402:HOH:O	2.18	0.53
1:C:240:GLU:OE2	3:C:403:HOH:O	2.19	0.52
1:B:241:LEU:HD21	1:B:264:ILE:HD13	1.93	0.51
1:B:106:ASP:OD1	1:B:106:ASP:N	2.42	0.50
1:B:276:VAL:CG2	1:B:277:PRO:HD3	2.43	0.47
1:B:72:LEU:HD21	1:C:66:LEU:HD13	1.95	0.47
1:B:259:ARG:HH11	1:B:259:ARG:HG3	1.79	0.47
1:B:78:TYR:HA	1:C:61:LEU:HD21	1.97	0.46
1:C:243:SER:HB3	1:C:267:ILE:HD12	1.96	0.46
1:C:217:LYS:HE3	3:C:465:HOH:O	2.16	0.44
1:B:105:GLY:O	1:B:149:GLN:NE2	2.50	0.44
1:C:60:GLU:OE1	1:C:63:LYS:HA	2.18	0.44
1:C:233:GLU:HA	1:C:239:ILE:HD13	2.00	0.43

Continued on next page...



Continued from previous page...

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap (Å)
1:B:100:ARG:HA	1:B:147:TRP:HB3	1.99	0.43
1:C:146:ARG:HA	1:C:152:MET:HE2	2.00	0.43
1:B:100:ARG:HA	1:B:100:ARG:HD2	1.78	0.43
1:B:174:ASN:O	1:B:178:ARG:HG3	2.19	0.43
1:B:107:ARG:HG2	1:B:109:ALA:H	1.84	0.43
1:B:121:TYR:CZ	1:C:265:GLU:HG3	2.55	0.42
1:B:70:ALA:HB2	1:C:70:ALA:HB2	2.01	0.42
1:C:235:ALA:O	1:C:238:GLN:HG3	2.19	0.42
1:B:97:ARG:HE	1:B:98:PRO:HD3	1.84	0.42
1:C:61:LEU:HD12	1:C:61:LEU:HA	1.93	0.41
1:B:105:GLY:N	1:B:146:ARG:O	2.53	0.41
1:C:75:ARG:HG3	1:C:78:TYR:CE1	2.56	0.40
1:B:265:GLU:HG3	1:C:121:TYR:CZ	2.56	0.40
1:B:146:ARG:HG2	1:B:152:MET:HE1	2.02	0.40
1:C:166:PRO:O	1:C:170:GLN:HG3	2.21	0.40

All (1) 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		$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:254:THR:OG1	1:C:185:ARG:NH2[2_555]	1.91	0.29

## 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	В	221/249 (89%)	213 (96%)	8 (4%)	0	100	100
1	С	211/249 (85%)	204 (97%)	7 (3%)	0	100	100
All	All	432/498 (87%)	417 (96%)	15 (4%)	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	В	186/199 (94%)	183 (98%)	3 (2%)	62 58	
1	С	179/199 (90%)	176 (98%)	3 (2%)	60 55	
All	All	$365/398 \; (92\%)$	359 (98%)	6 (2%)	62 58	

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	100	ARG
1	В	148	SER
1	В	282	ARG
1	С	111	ASP
1	С	148	SER
1	С	188	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	В	149	GLN

#### 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 monosaccharides in this entry.



## 5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 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.

## 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	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	В	223/249 (89%)	0.51	23 (10%) 6 10	14, 23, 61, 124	0
1	С	215/249~(86%)	0.19	17 (7%) 12 19	15, 24, 54, 88	1 (0%)
All	All	438/498 (87%)	0.35	40 (9%) 9 15	14, 24, 56, 124	1 (0%)

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	106	ASP	10.8
1	В	109	ALA	9.5
1	В	104	ASP	7.9
1	В	107	ARG	7.7
1	В	105	GLY	7.7
1	В	108	SER	6.3
1	С	69	VAL	5.3
1	В	99	GLU	4.7
1	С	283	ALA	4.6
1	В	103	GLY	4.6
1	С	70	ALA	4.5
1	В	100	ARG	4.2
1	С	64	TYR	4.1
1	В	97	ARG	4.0
1	В	102	ARG	4.0
1	В	70	ALA	3.9
1	В	281	ALA	3.8
1	В	110	ALA	3.7
1	С	150	ARG	3.5
1	С	68	GLY	3.5
1	С	66	LEU	3.4
1	В	60	GLU	3.4
1	С	60	GLU	3.3
1	В	101	LEU	3.2

Continued on next page...



Continued from previous page...

Mol	Chain	Res Type		RSRZ
1	С	147   TRP		3.2
1	В	282	ARG	3.1
1	С	204	ALA	2.9
1	В	278	ASN	2.8
1	С	61	LEU	2.8
1	С	284	GLY	2.8
1	В	69	VAL	2.8
1	В	111	ASP	2.7
1	С	99	GLU	2.7
1	В	201	ARG	2.6
1	В	147	TRP	2.5
1	С	62	ALA	2.5
1	В	98	PRO	2.2
1	С	110	ALA	2.2
1	С	65	GLY	2.2
1	С	185	ARG	2.0

## 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 monosaccharides 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.

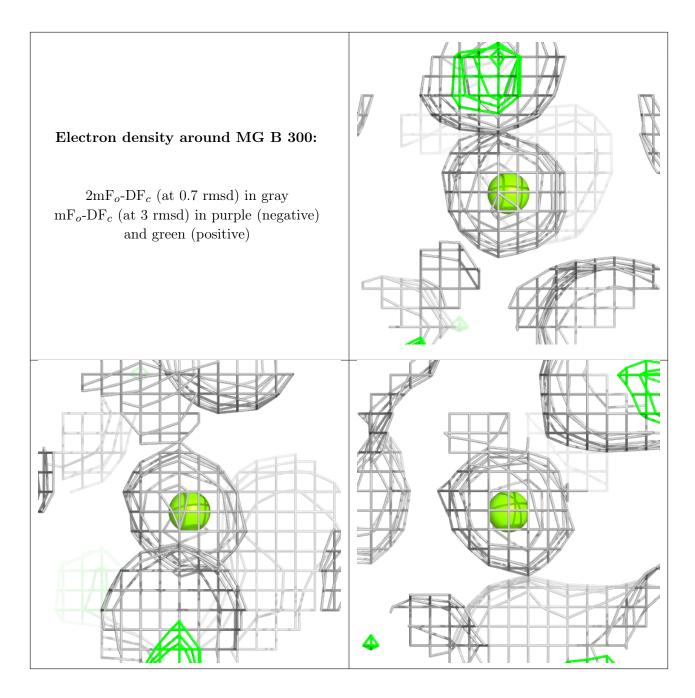
Mol	Type	Chain	$\operatorname{Res}$	Atoms	RSCC	RSR	${f B-factors}({f A}^2)$	Q<0.9
2	MG	С	300	1/1	0.98	0.08	42,42,42,42	0
2	MG	В	300	1/1	0.99	0.14	34,34,34,34	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



# 





## 6.5 Other polymers (i)

There are no such residues in this entry.

