

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

Mar 2, 2023 – 12:20 pm GMT

PDB ID : 8C3N

Title: Stapled peptide SP30 in complex with humanised RadA mutant HumRadA22

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Deposited on : 2022-12-27

Resolution : 1.21 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 : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.32.1 buster-report : 1.1.7 (2018)

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)

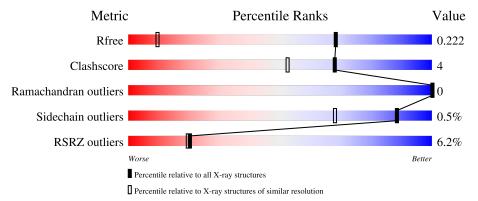
Validation Pipeline (wwPDB-VP) : 2.32.1

## 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 1.21 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	1232 (1.24-1.20)
Clashscore	141614	1294 (1.24-1.20)
Ramachandran outliers	138981	1251 (1.24-1.20)
Sidechain outliers	138945	1250 (1.24-1.20)
RSRZ outliers	127900	1209 (1.24-1.20)

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	A	231	83%	9%	• 7%
2	В	29	83%	14%	6 •



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2185 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 DNA repair and recombination protein RadA.

Mol	Chain	Residues		$\mathbf{At}$	oms			ZeroOcc	AltConf	Trace
1	A	214	Total	С	N	О	S	0	7	0
1	11		1725	1083	309	327	6		•	

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	MET	ARG	engineered mutation	UNP O74036
A	168	ALA	VAL	engineered mutation	UNP O74036
A	169	MET	ILE	engineered mutation	UNP O74036
A	170	TYR	TRP	engineered mutation	UNP O74036
A	182	LEU	ILE	engineered mutation	UNP O74036
A	198	ASP	LYS	engineered mutation	UNP O74036
A	199	ASN	HIS	engineered mutation	UNP O74036
A	200	VAL	ILE	engineered mutation	UNP O74036
A	201	ALA	TYR	engineered mutation	UNP O74036
A	202	TYR	VAL	engineered mutation	UNP O74036
A	213	GLN	LEU	engineered mutation	UNP O74036
A	215	LEU	VAL	engineered mutation	UNP O74036
A	216	TYR	GLN	engineered mutation	UNP O74036
A	219	SER	GLU	engineered mutation	UNP O74036
A	220	ALA	ASP	engineered mutation	UNP O74036
A	221	MET	LYS	engineered mutation	UNP O74036
A	222	MET	ILE	engineered mutation	UNP O74036
A	223	VAL	LYS	engineered mutation	UNP O74036
A	225	SER	LEU	engineered mutation	UNP O74036
A	232	TYR	VAL	engineered mutation	UNP O74036
A	263	ARG	LYS	engineered mutation	UNP O74036
A	264	PHE	HIS	engineered mutation	UNP O74036
A	266	ARG	ALA	engineered mutation	UNP O74036
A	267	MET	ASP	engineered mutation	UNP O74036
A	274	GLU	LEU	engineered mutation	UNP O74036
A	275	PHE	TYR	engineered mutation	UNP O74036
A	300	ASN	ARG	engineered mutation	UNP O74036

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	PRO	deletion	UNP O74036
A	?	-	ASP	deletion	UNP O74036
A	?	-	ALA	deletion	UNP O74036
A	?	-	PHE	deletion	UNP O74036
A	?	-	PHE	deletion	UNP O74036
A	?	-	GLY	deletion	UNP O74036
A	?	-	ASP	deletion	UNP O74036
A	?	-	PRO	deletion	UNP O74036
A	?	-	THR	deletion	UNP O74036
A	?	-	ARG	deletion	UNP O74036
A	?	-	PRO	deletion	UNP O74036
A	?	-	ILE	deletion	UNP O74036

• Molecule 2 is a protein called Breast cancer type 2 susceptibility protein.

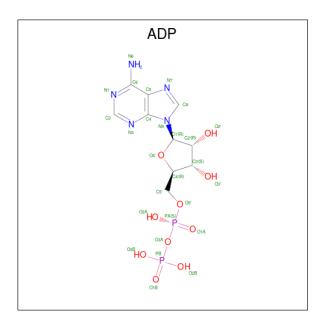
$\mathbf{Mol}$	Chain	Residues		$\mathbf{Atc}$	ms			ZeroOcc	AltConf	Trace
2	В	28	Total 198	C 122	N 35	O 39	S 2	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	2055	CYS	PHE	engineered mutation	UNP P51587
В	2056	SER	ARG	engineered mutation	UNP P51587
В	2059	SER	TYR	engineered mutation	UNP P51587
В	2060	THR	SER	engineered mutation	UNP P51587
В	2062	SER	HIS	engineered mutation	UNP P51587
В	2064	LYS	THR	engineered mutation	UNP P51587
В	1232	GLN	GLU	engineered mutation	UNP P51587
В	1234	CYS	LEU	engineered mutation	UNP P51587
В	1243	GLY	ASP	engineered mutation	UNP P51587

• Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



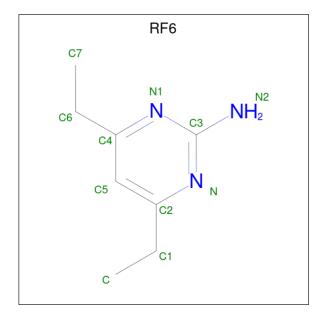


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total 27	4.0	N 5	O 10	P 2	0	0

• Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	$\begin{array}{cc} \text{Total} & \text{Mg} \\ 1 & 1 \end{array}$	0	0

• Molecule 5 is 4,6-diethylpyrimidin-2-amine (three-letter code: RF6) (formula:  $C_8H_{13}N_3$ ) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	Total C N 11 8 3	0	0

#### • Molecule 6 is water.

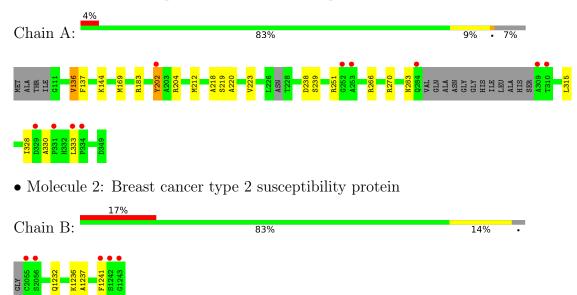
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	204	Total O 204 204	0	0
6	В	19	Total O 19 19	0	0



## 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: DNA repair and recombination protein RadA





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	143.02Å 37.96Å 43.93Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.43 - 1.21	Depositor
rtesolution (A)	37.43 - 1.21	EDS
% Data completeness	94.5 (37.43-1.21)	Depositor
(in resolution range)	94.5 (37.43-1.21)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.35 (at 1.21Å)	Xtriage
Refinement program	BUSTER, PHENIX 1.19.2_4158	Depositor
P.P.	0.211 , 0.218	Depositor
$R, R_{free}$	0.217 , $0.222$	DCC
$R_{free}$ test set	3419  reflections  (4.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.8	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.33, 40.8	EDS
L-test for twinning <sup>2</sup>	$  <  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	2185	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.66% 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, RF6, ADP

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		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.58	0/1750	0.64	0/2355	
2	В	0.61	0/199	0.76	0/262	
All	All	0.59	0/1949	0.65	0/2617	

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	#Planarity outliers
1	A	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	A	136[A]	VAL	Mainchain
1	A	183	ARG	Sidechain
1	A	251	ARG	Sidechain
1	A	270	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	1725	0	1725	14	0
2	В	198	0	202	3	0
3	A	27	0	12	0	0
4	A	1	0	0	0	0
5	В	11	0	0	0	0
6	A	204	0	0	2	0
6	В	19	0	0	0	0
All	All	2185	0	1939	15	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 4.

The worst 5 of 15 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:212:MET:SD	6:A:677:HOH:O	2.43	0.74
1:A:137:PHE:CZ	1:A:328:ILE:HG13	2.37	0.59
1:A:330:ALA:HB1	1:A:333:LEU:HD12	1.84	0.57
1:A:220:ALA:O	1:A:223[B]:VAL:HG22	2.13	0.49
1:A:219[A]:SER:HG	2:B:1241:PHE:HE2	1.59	0.49

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	ntiles
1	A	$215/231\ (93\%)$	214 (100%)	1 (0%)	0	100	100
2	В	26/29~(90%)	26 (100%)	0	0	100	100
All	All	241/260~(93%)	240 (100%)	1 (0%)	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	183/188 (97%)	181 (99%)	2 (1%)	73 41
2	В	22/22 (100%)	22 (100%)	0	100 100
All	All	205/210 (98%)	203 (99%)	2 (1%)	88 47

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	202[A]	TYR
1	A	202[B]	TYR

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)

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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	Tuno	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
IVIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	RF6	В	2301	2	11,11,11	0.55	0	12,14,14	0.56	0
3	ADP	A	401	4	24,29,29	0.67	0	29,45,45	0.80	1 (3%)

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
5	RF6	В	2301	2	-	2/4/4/4	0/1/1/1
3	ADP	A	401	4	-	2/12/32/32	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
3	A	401	ADP	C5-C6-N6	2.27	123.81	120.35

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	ADP	PA-O3A-PB-O3B
5	В	2301	RF6	C5-C4-C6-C7
3	A	401	ADP	PA-O3A-PB-O1B
5	В	2301	RF6	N1-C4-C6-C7

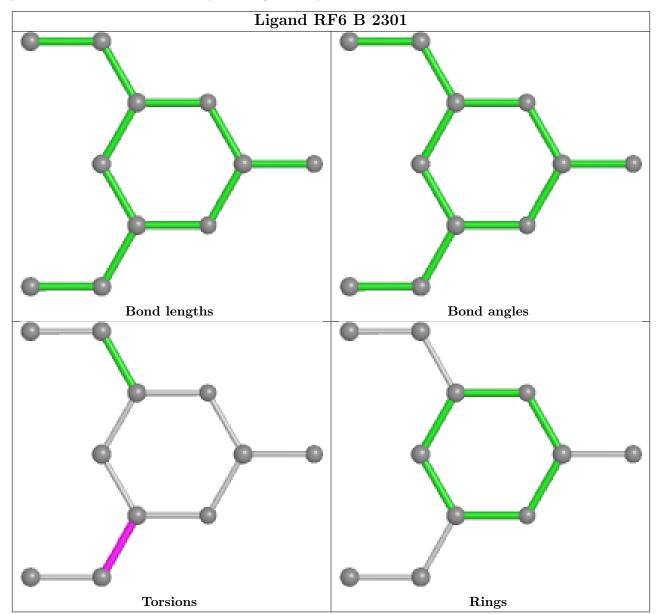
There are no ring outliers.

No monomer is involved in short contacts.

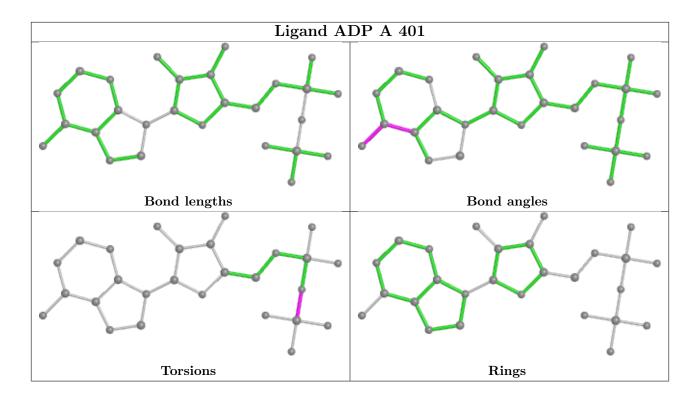
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be



highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







# 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	A	214/231 (92%)	0.38	10 (4%) 31 30	14, 23, 36, 50	0
2	В	$28/29 \ (96\%)$	1.23	5 (17%) 1 1	21, 31, 43, 68	0
All	All	242/260 (93%)	0.48	15 (6%) 20 19	14, 24, 39, 68	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	2055	CYS	9.8
1	A	310	THR	7.3
1	A	331	PRO	7.1
1	A	333	LEU	5.2
1	A	252	GLY	4.7

### 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.

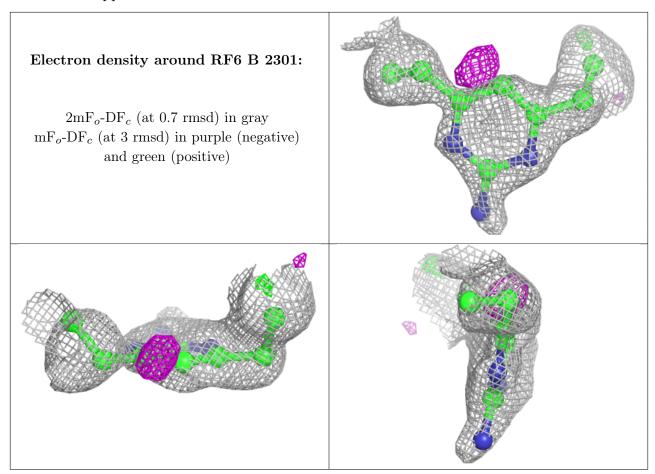
#### 6.4 Ligands (i)

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.

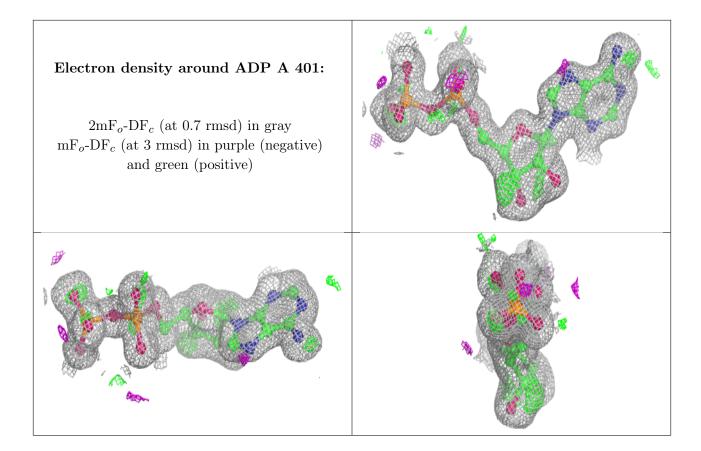


Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q<0.9
5	RF6	В	2301	11/11	0.68	0.29	31,43,50,59	0
3	ADP	A	401	27/27	0.97	0.09	14,21,27,32	0
4	MG	A	402	1/1	0.99	0.09	15,15,15,15	0

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.

