

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

#### Oct 15, 2023 – 04:10 PM EDT

PDB ID	:	7UDP
Title	:	Crystal structure of COQ8A-CA157 inhibitor complex in space group C2
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Deposited on	:	2022-03-20
Resolution	:	2.01 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:

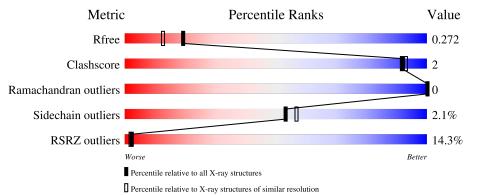
Xtriage (Phenix) EDS buster-report Percentile statistics Refmac CCP4 Ideal geometry (proteins) Ideal geometry (DNA, RNA)	:::::::::::::::::::::::::::::::::::::::	20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove) Engh & Huber (2001) Parkinson et al. (1996)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 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 2.01 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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		
			14%		
1	А	393	90%	7%	•



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# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6150 atoms, of which 3054 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.

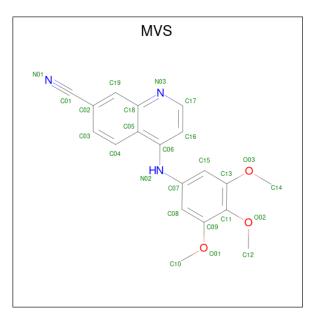
• Molecule 1 is a protein called Atypical kinase COQ8A, mitochondrial.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	А	378	Total 6090	C 1941	Н 3037	N 534	O 554	S 24	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	255	SER	-	expression tag	UNP Q8NI60

• Molecule 2 is 4-[(3,4,5-trimethoxyphenyl)amino]quinoline-7-carbonitrile (three-letter code: MVS) (formula:  $C_{19}H_{17}N_3O_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	Δ	1	Total	С	Η	Ν	0	0	0
	11	Ĩ	42	19	17	3	3	0	0

• Molecule 3 is water.



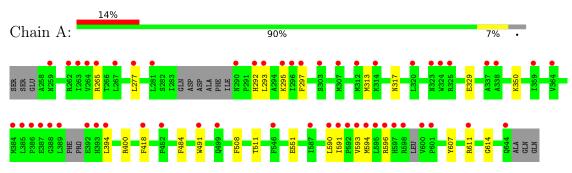
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	18	Total O 18 18	0	0



## 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: Atypical kinase COQ8A, mitochondrial





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	151.21Å 56.38Å 48.68Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $98.39^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	37.40 - 2.01	Depositor
Resolution (A)	37.40 - 2.01	EDS
% Data completeness	99.9 (37.40-2.01)	Depositor
(in resolution range)	94.4 (37.40-2.01)	EDS
R <sub>merge</sub>	0.03	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.64 (at 2.00 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.20.1-4487	Depositor
D D.	0.240 , $0.279$	Depositor
$R, R_{free}$	0.236 , $0.272$	DCC
$R_{free}$ test set	2130 reflections $(7.79\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	61.7	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.37, 61.1	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6150	wwPDB-VP
Average B, all atoms $(Å^2)$	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.75% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<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: MVS

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		
NIOI	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.24	0/3116	0.47	0/4198	

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	3053	3037	3036	10	1
2	А	25	17	0	0	0
3	А	18	0	0	0	0
All	All	3096	3054	3036	10	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 2.

All (10) 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:A:313:MET:O	1:A:317:ASN:ND2	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:593:VAL:HG23	1:A:594:MET:HG2	1.97	0.45
1:A:591:ILE:HD13	1:A:611:ARG:HH22	1.82	0.45
1:A:484:PHE:CE2	1:A:511:THR:HG21	2.52	0.45
1:A:293:LEU:HD21	1:A:297:PHE:CE1	2.51	0.45
1:A:484:PHE:CZ	1:A:511:THR:HG21	2.51	0.45
1:A:607:TYR:CZ	1:A:611:ARG:NE	2.87	0.43
1:A:329:GLU:HG3	1:A:350:LYS:HA	2.01	0.42
1:A:277:LEU:CD1	1:A:394:LEU:HD11	2.51	0.41
1:A:590:LEU:HD13	1:A:614:GLY:HA2	2.02	0.40

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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	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:ARG:NH1	1:A:551:GLU:O[4_546]	2.13	0.07

## 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	Percentile	$\mathbf{s}$
1	А	370/393~(94%)	349~(94%)	21 (6%)	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	330/343~(96%)	323~(98%)	7~(2%)	53 57

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	265	ARG
1	А	292	HIS
1	А	295	LYS
1	А	418	PHE
1	А	491	TRP
1	А	508	PHE
1	А	596	ARG

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)

1 ligand is 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	Res	Link Bond lengths		Link	Bond lengths		В	ond ang	les
	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
2	MVS	А	701	-	27,27,27	0.26	0	37,37,37	0.32	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.

I	Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
	2	MVS	А	701	-	-	0/12/12/12	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

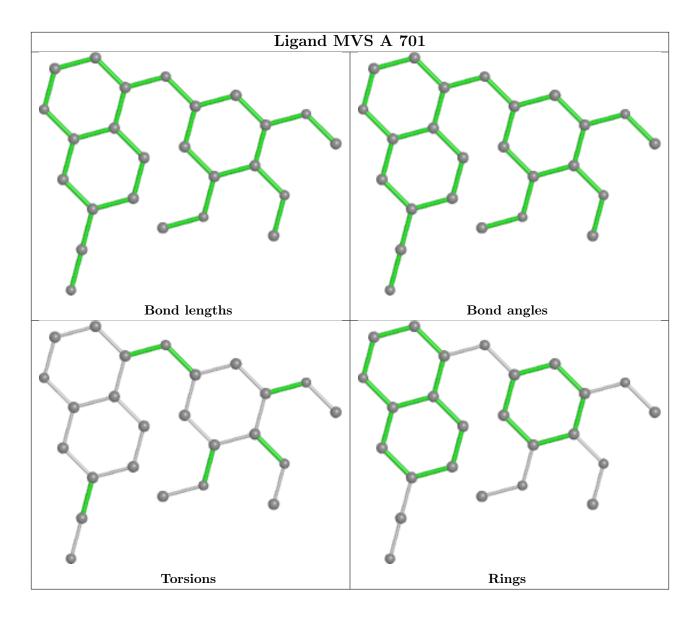
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 $>$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	А	378/393~(96%)	0.83	54 (14%) 2 2	53, 79, 144, 201	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	600	VAL	8.3
1	А	598	ARG	5.9
1	А	590	LEU	5.1
1	А	320	LEU	4.9
1	А	387	GLU	4.7
1	А	593	VAL	4.4
1	А	597	HIS	4.2
1	А	265	ARG	4.0
1	А	384	MET	4.0
1	А	392	GLU	3.9
1	А	290	ASN	3.8
1	А	389	LEU	3.7
1	А	324	TRP	3.7
1	А	546	PHE	3.5
1	А	259	ASN	3.4
1	А	314	LYS	3.4
1	А	281	LEU	3.4
1	А	385	LEU	3.1
1	А	263	ILE	2.9
1	А	323	ASN	2.9
1	А	393	HIS	2.9
1	А	293	LEU	2.9
1	А	388	GLY	2.9
1	А	307	MET	2.8
1	А	296	ILE	2.8
1	А	594	MET	2.8
1	A	644	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	А	303	SER	2.7
1	А	312	MET	2.7
1	А	592	PRO	2.6
1	А	297	PHE	2.6
1	А	264	VAL	2.6
1	А	595	LEU	2.6
1	А	295	LYS	2.5
1	А	292	HIS	2.5
1	А	499	GLN	2.4
1	А	267	LEU	2.3
1	А	262	ARG	2.3
1	А	587	ILE	2.3
1	А	418	PHE	2.3
1	А	325	ARG	2.3
1	А	591	ILE	2.3
1	А	596	ARG	2.2
1	А	601	PRO	2.2
1	А	611	ARG	2.2
1	А	337	ALA	2.2
1	А	338	ALA	2.2
1	А	359	ILE	2.1
1	А	394	LEU	2.1
1	А	452	PRO	2.1
1	А	364	VAL	2.1
1	А	277	LEU	2.0
1	А	386	PRO	2.0
1	А	491	TRP	2.0

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## 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)

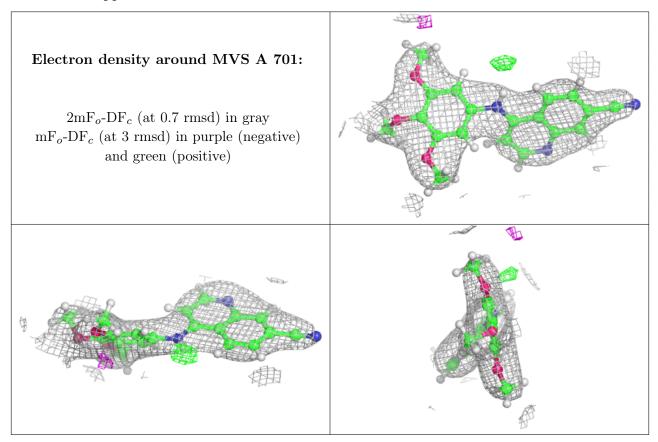
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,



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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
2	MVS	А	701	25/25	0.95	0.15	$60,\!68,\!81,\!87$	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.

