

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

Dec 6, 2022 – 02:38 pm GMT

PDB ID : 7QQ0

Title: X-ray structure of the adduct obtained upon reaction of [cis-Rh2(OCOCH3)2

(OCOCF3)2] with RNase A (2)

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Deposited on : 2022-01-05

Resolution : 1.32 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.orgA 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 : FAILED

buster-report : 1.1.7 (2018)

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)

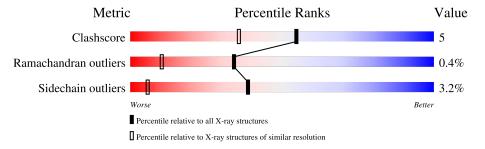
Validation Pipeline (wwPDB-VP) : 2.31.3

## 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 1.32 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	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
Clashscore	141614	1667 (1.34-1.30)
Ramachandran outliers	138981	1615 (1.34-1.30)
Sidechain outliers	138945	1615 (1.34-1.30)

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%

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain		
1	AAA	124	88%	11%	•
1	BBB	124	83%	16%	•



### 2 Entry composition (i)

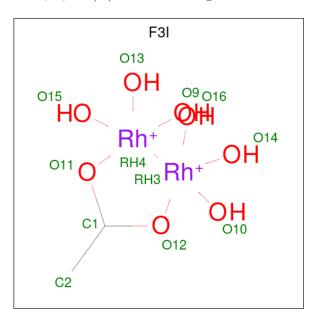
There are 4 unique types of molecules in this entry. The entry contains 2450 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ribonuclease pancreatic.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	AAA	124	Total 1006		N 182		S 12	0	7	0
1	BBB	124	Total 1027		N 185	O 209	S 12	0	8	0

• Molecule 2 is (mi2-acetato-O, O')-hexaaquo-dirhodium (II) (three-letter code: F3I) (formula: C<sub>2</sub>H<sub>10</sub>O<sub>8</sub>Rh<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf		
2	AAA	1	Total 12				0	1
2	BBB	1	Total 12	C 2	O 8	Rh 2	0	0

• Molecule 3 is RHODIUM(II) ION (three-letter code: RHF) (formula: Rh).



M	ol	Chain	Residues	Ator	ns	ZeroOcc	AltConf
٠	}	AAA	2	Total 2	Rh 2	0	0

#### • Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	178	Total O 179 179	0	8
4	BBB	209	Total O 212 212	0	23

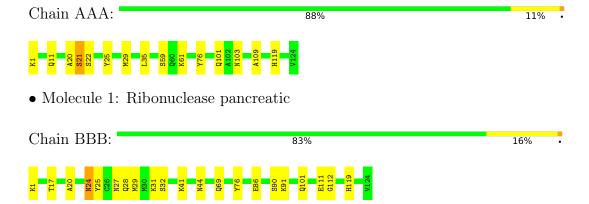


## 3 Residue-property plots (i)

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. 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. 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.

Note EDS failed to run properly.

• Molecule 1: Ribonuclease pancreatic





## 4 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	100.21Å 32.56Å 72.61Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.31^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	41.14 - 1.32	Depositor
% Data completeness	99.5 (41.14-1.32)	Depositor
(in resolution range)	, , ,	
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.35  (at  1.32Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
$R, R_{free}$	0.209 , $0.243$	Depositor
Wilson B-factor $(\mathring{A}^2)$	12.2	Xtriage
Anisotropy	0.031	Xtriage
L-test for twinning <sup>2</sup>	$< L > = 0.50, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	0.015 for -h,-k,l	Xtriage
Total number of atoms	2450	wwPDB-VP
Average B, all atoms $(\mathring{A}^2)$	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.90% 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: RHF, F3I

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		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	AAA	0.80	0/1023	0.88	1/1379 (0.1%)	
1	BBB	0.79	0/1043	0.89	1/1403 (0.1%)	
All	All	0.80	0/2066	0.89	2/2782 (0.1%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	BBB	76	TYR	CB-CG-CD2	-5.41	117.75	121.00
1	AAA	76	TYR	CB-CG-CD1	-5.03	117.98	121.00

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	AAA	1006	0	942	9	0
1	BBB	1027	0	980	10	0
2	AAA	12	0	0	1	0
2	BBB	12	0	0	2	0
3	AAA	2	0	0	0	0
4	AAA	179	0	0	4	0
4	BBB	212	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2450	0	1922	21	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 5.

All (21) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${\rm distance}({\rm \AA})$	overlap (Å)
1:BBB:32:SER:OG	4:BBB:301[B]:HOH:O	1.79	0.98
2:AAA:301[A]:F3I:O9	2:AAA:301[A]:F3I:O13	1.88	0.91
1:AAA:59[A]:SER:OG	4:AAA:401[A]:HOH:O	1.96	0.82
1:AAA:109:ALA:HB3	1:AAA:119[A]:HIS:HB3	1.62	0.81
2:BBB:201:F3I:O9	2:BBB:201:F3I:O13	2.07	0.73
1:AAA:101:GLN:HG3	4:AAA:408:HOH:O	1.92	0.69
1:AAA:11[A]:GLN:HG2	1:AAA:35:LEU:HD21	1.84	0.59
1:BBB:41:LYS:NZ	1:BBB:44:ASN:OD1	2.31	0.59
1:AAA:103:ASN:ND2	4:AAA:408:HOH:O	2.41	0.53
1:BBB:25:TYR:CZ	1:BBB:29:MET:HG3	2.48	0.48
1:AAA:61:LYS:HE3	4:AAA:561:HOH:O	2.13	0.47
1:BBB:20:ALA:HA	1:BBB:25:TYR:CD1	2.51	0.46
1:BBB:24:ASN:ND2	1:BBB:27:ASN:HD22	2.15	0.45
1:BBB:91[B]:LYS:HE3	1:BBB:91[B]:LYS:HB3	1.72	0.45
1:AAA:20:ALA:O	1:AAA:22:SER:N	2.50	0.45
1:AAA:25:TYR:CZ	1:AAA:29:MET:HG3	2.52	0.45
1:BBB:1[B]:LYS:O	1:BBB:1[B]:LYS:HG3	2.17	0.43
1:AAA:20:ALA:O	1:AAA:21:SER:C	2.57	0.42
1:BBB:119:HIS:HA	2:BBB:201:F3I:O10	2.20	0.41
1:BBB:86:GLU:HG2	1:BBB:90:SER:HB3	2.01	0.41
1:BBB:111[C]:GLU:CG	1:BBB:112:GLY:N	2.84	0.41

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	AAA	129/124 (104%)	123 (95%)	5 (4%)	1 (1%)	19	2
1	BBB	130/124 (105%)	127 (98%)	3 (2%)	0	100	100
All	All	259/248 (104%)	250 (96%)	8 (3%)	1 (0%)	34	10

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	21	SER

#### 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	AAA	116/109~(106%)	115 (99%)	1 (1%)	78 51		
1	BBB	118/109 (108%)	112 (95%)	6 (5%)	24 2		
All	All	$234/218 \; (107\%)$	227 (97%)	7 (3%)	39 6		

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

Mol	Chain	Res	Type
1	AAA	1	LYS
1	BBB	17	THR
1	BBB	24	ASN
1	BBB	28	GLN
1	BBB	31	LYS
1	BBB	69	GLN
1	BBB	101	GLN

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 4 ligands modelled in this entry, 2 are 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	Mol Type Chain Re		Chain Res Link		Bond lengths			Bond angles		
IVIOI	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	F3I	AAA	301[A]	1	1,12,12	1.66	0	0,25,25	-	-
2	F3I	BBB	201	4,1	1,12,12	1.75	0	0,25,25	-	-

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
2	F3I	AAA	301[A]	1	-	-	0/1/1/1
2	F3I	BBB	201	4,1	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.



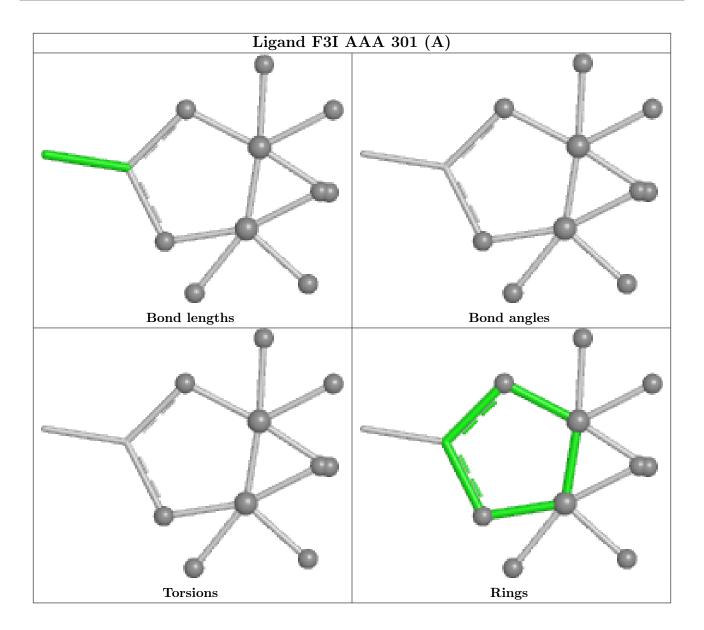
There are no ring outliers.

2 monomers are involved in 3 short contacts:

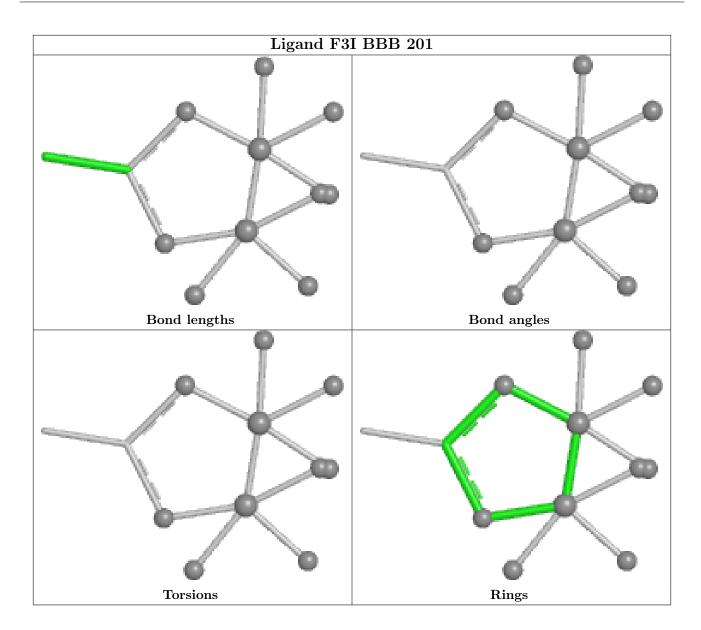
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	301[A]	F3I	1	0
2	BBB	201	F3I	2	0

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)

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

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

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

#### 6.3 Carbohydrates (i)

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

#### 6.4 Ligands (i)

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

### 6.5 Other polymers (i)

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

