

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

### Aug 29, 2023 – 09:40 PM EDT

PDB ID : 3MJA

Title : Cricket Paralysis Virus IGR IRES Domain 3 RNA bound to selenate, structure

#2

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Deposited on : 2010-04-12

Resolution : 2.80 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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.35

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)

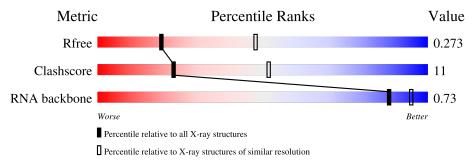
Validation Pipeline (wwPDB-VP) : 2.35

## 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 2.80 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	3140 (2.80-2.80)			
Clashscore	141614	3569 (2.80-2.80)			
RNA backbone	3102	1227 (3.10-2.50)			

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%

Mol	Chain	Length	Quality of chain						
1	В	29	45%	48%	7%				
2	С	14	57%	29%	14%				

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SE4	В	100	-	X	=	-
3	SE4	В	103	-	X	=	-
3	SE4	С	101	-	X	=	-
3	SE4	С	102	-	X	=	-



## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 937 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.

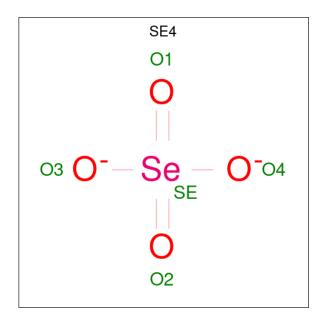
• Molecule 1 is a RNA chain called Domain 3 of the cricket paralysis virus intergenic region IRES RNA.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace
1	В	29	Total 621	C 277	N 110	O 205	P 29	0	0	0

• Molecule 2 is a RNA chain called RNA (5'-R(P\*UP\*AP\*AP\*AP\*AP\*AP\*AP\*UP\*UP\*UP\*AP\*CP\*CP\*U)-3').

Mol	Chain	Residues		Atoms			ZeroOcc	AltConf	Trace	
2	С	14	Total	C	N	0	P	0	0	0
			296	133	51	98	14			

• Molecule 3 is SELENATE ION (three-letter code: SE4) (formula: O<sub>4</sub>Se).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total O Se 5 4 1	0	0

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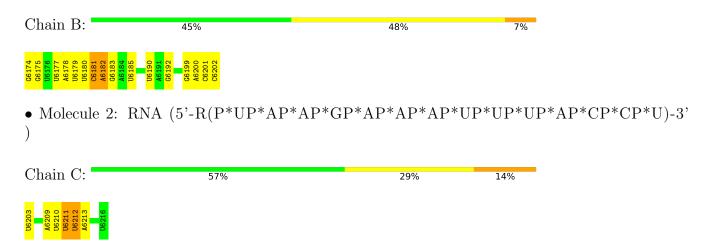
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total O Se 5 4 1	0	0
3	С	1	Total O Se 5 4 1	0	0
3	С	1	Total O Se 5 4 1	0	0



# 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. 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.

• Molecule 1: Domain 3 of the cricket paralysis virus intergenic region IRES RNA





# 4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 41 21 2	Depositor	
Cell constants	59.25Å 59.25Å 99.78Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	30.00 - 2.80	Depositor	
rtesolution (A)	29.00 - 2.30	EDS	
% Data completeness	99.9 (30.00-2.80)	Depositor	
(in resolution range)	99.7 (29.00-2.30)	EDS	
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.33 (at 2.31Å)	Xtriage	
Refinement program	CNS	Depositor	
P. P.	0.233 , 0.283	Depositor	
$R, R_{free}$	0.253 , $0.273$	DCC	
$R_{free}$ test set	1428 reflections (9.49%)	wwPDB-VP	
Wilson B-factor (Å <sup>2</sup> )	33.0	Xtriage	
Anisotropy	0.115	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.16 , -10.0	EDS	
L-test for twinning <sup>2</sup>	$ < L >=0.48, < L^2>=0.31$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
$F_o, F_c$ correlation	0.91	EDS	
Total number of atoms	937	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.66% 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: SE4

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	Bo	nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z >5	
1	В	0.54	1/694 (0.1%)	0.69	0/1078	
2	С	0.70	1/330 (0.3%)	0.80	1/509 (0.2%)	
All	All	0.60	2/1024~(0.2%)	0.73	1/1587 (0.1%)	

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	В	0	1

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	V I			$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
2	С	6203	U	OP3-P	-7.18	1.52	1.61
1	В	6174	G	OP3-P	-6.50	1.53	1.61

### All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	С	6203	U	OP1-P-OP2	-5.20	111.80	119.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	6180	U	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	В	621	0	311	13	0
2	С	296	0	150	6	0
3	В	10	0	0	0	0
3	С	10	0	0	0	0
All	All	937	0	461	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 11.

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:B:6177:U:H3	1:B:6199:G:H1	1.15	0.92
2:C:6211:U:O2'	2:C:6212:U:OP1	2.01	0.78
1:B:6181:C:H3'	1:B:6182:A:C5'	2.26	0.66
1:B:6175:G:N2	1:B:6202:C:H1'	2.11	0.65
1:B:6177:U:H2'	1:B:6178:A:C8	2.32	0.65

There are no symmetry-related clashes.

## 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

There are no protein molecules in this entry.

### 5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

#### 5.3.3 RNA (i)



Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	В	$28/29 \ (96\%)$	3 (10%)	0
2	С	13/14 (92%)	2 (15%)	2 (15%)
All	All	41/43 (95%)	5 (12%)	2 (4%)

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	В	6181	С
1	В	6182	A
1	В	6183	G
2	С	6211	U
2	С	6212	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	С	6210	U
2	С	6211	U

### 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)

4 ligands are 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			Bond angles		
IVIOI	Туре	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
3	SE4	В	103	-	4,4,4	4.70	4 (100%)	6,6,6	0.15	0



Mol	Type	Chain	Res	Link	В	ond len	$\overline{ m gths}$	В	ond ang	gles
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SE4	С	102	-	4,4,4	4.70	4 (100%)	6,6,6	0.14	0
3	SE4	В	100	-	4,4,4	4.78	4 (100%)	6,6,6	0.14	0
3	SE4	С	101	-	4,4,4	4.69	4 (100%)	6,6,6	0.13	0

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
3	С	102	SE4	SE-O4	-5.17	1.48	1.65
3	В	100	SE4	SE-O4	-5.17	1.48	1.65
3	С	101	SE4	SE-O3	-5.10	1.49	1.65
3	В	100	SE4	SE-O3	-5.06	1.49	1.65
3	С	101	SE4	SE-O4	-5.04	1.49	1.65

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

## 6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

