

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

#### May 13, 2020 – 12:49 am BST

PDB ID 4RLZ

> Title : Crystal structure of Norovirus OIF P domain

Authors : Liu, W.; Chen, Y.; Tan, M.; Xia, M.; Li, X.; Jiang, X.; Rao, Z.

2014-10-18 Deposited on

1.19 Å(reported) Resolution

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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467

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

Xtriage (Phenix) 1.13 EDS 2.11

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

> Refmac 5.8.0158

CCP4 7.0.044 (Gargrove) Engh & Huber (2001)

Ideal geometry (proteins) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

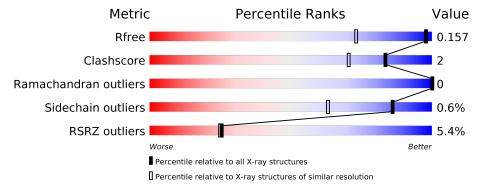
Validation Pipeline (wwPDB-VP) 2.11

## 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 1.19 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	130704	1223 (1.22-1.18)
Clashscore	141614	1286 (1.22-1.18)
Ramachandran outliers	138981	1240 (1.22-1.18)
Sidechain outliers	138945	1239 (1.22-1.18)
RSRZ outliers	127900	1200 (1.22-1.18)

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 on 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	316	93%	•	-
1	В	316	93%	•	-



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5636 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 Capsid protein.

$\mathbf{Mol}$	Chain	Residues		$\mathbf{At}$	oms			ZeroOcc	AltConf	Trace
1	Λ	306	Total	С	N	О	S	0	0	0
1	Α	300	2362	1500	404	453	5	0	U	0
1	D	307	Total	С	N	О	S	0	1	0
1	Ъ	307	2377	1510	407	455	5	0	1	U

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	212	GLY	-	EXPRESSION TAG	UNP Q6B7R3
A	213	PRO	-	EXPRESSION TAG	UNP Q6B7R3
A	214	LEU	-	EXPRESSION TAG	UNP Q6B7R3
A	215	GLY	-	EXPRESSION TAG	UNP Q6B7R3
A	216	SER	-	EXPRESSION TAG	UNP Q6B7R3
A	217	PRO	-	EXPRESSION TAG	UNP Q6B7R3
A	218	GLU	-	EXPRESSION TAG	UNP Q6B7R3
A	219	PHE	-	EXPRESSION TAG	UNP Q6B7R3
A	375	ASN	HIS	ENGINEERED MUTATION	UNP Q6B7R3
A	376	ILE	HIS	ENGINEERED MUTATION	UNP Q6B7R3
A	377	ALA	SER	ENGINEERED MUTATION	UNP Q6B7R3
A	378	SER	GLN	ENGINEERED MUTATION	UNP Q6B7R3
A	379	ASN	HIS	ENGINEERED MUTATION	UNP Q6B7R3
A	387	VAL	LEU	ENGINEERED MUTATION	UNP Q6B7R3
A	389	ILE	VAL	ENGINEERED MUTATION	UNP Q6B7R3
В	212	GLY	-	EXPRESSION TAG	UNP Q6B7R3
В	213	PRO	-	EXPRESSION TAG	UNP Q6B7R3
В	214	LEU	-	EXPRESSION TAG	UNP Q6B7R3
В	215	GLY	-	EXPRESSION TAG	UNP Q6B7R3
В	216	SER	-	EXPRESSION TAG	UNP Q6B7R3
В	217	PRO	-	EXPRESSION TAG	UNP Q6B7R3
В	218	GLU	-	EXPRESSION TAG	UNP Q6B7R3
В	219	PHE	-	EXPRESSION TAG	UNP Q6B7R3
В	375	ASN	HIS	ENGINEERED MUTATION	UNP Q6B7R3
В	376	ILE	HIS	ENGINEERED MUTATION	UNP Q6B7R3

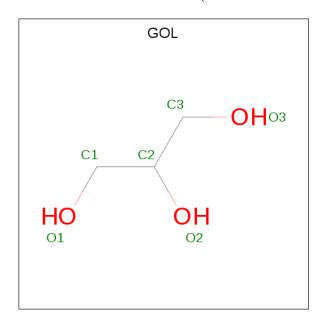
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Chain	Residue	Modelled	Actual	Comment	Reference
В	377	ALA	SER	ENGINEERED MUTATION	UNP Q6B7R3
В	378	SER	GLN	ENGINEERED MUTATION	UNP Q6B7R3
В	379	ASN	HIS	ENGINEERED MUTATION	UNP Q6B7R3
В	387	VAL	LEU	ENGINEERED MUTATION	UNP Q6B7R3
В	389	ILE	VAL	ENGINEERED MUTATION	UNP Q6B7R3

• Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



$oxed{N}$	/Iol	Chain	Residues	Atoms	ZeroOcc	AltConf
	2	A	1	Total C O 6 3 3	0	0
	2	В	1	Total C O 6 3 3	0	0

• Molecule 3 is water.

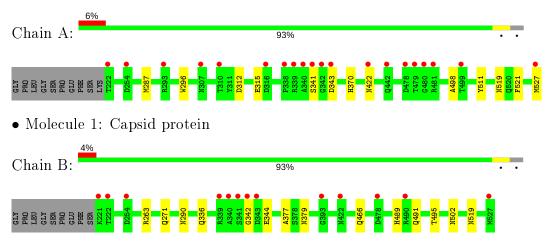
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	447	Total O 447 447	0	0
3	В	438	Total O 438 438	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Capsid protein





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	49.49Å 112.66Å 59.71Å	Danagitan
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 108.50° 90.00°	Depositor
Resolution (Å)	31.55 - 1.19	Depositor
Resolution (A)	31.55 - 1.19	EDS
% Data completeness	94.9 (31.55-1.19)	Depositor
(in resolution range)	94.9 (31.55-1.19)	EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.91 (at 1.19Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
D D	0.140 , 0.160	Depositor
$R, R_{free}$	0.137 , $0.157$	DCC
$R_{free}$ test set	9430 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	9.4	Xtriage
Anisotropy	0.498	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.39 , 48.1	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	0.97	EDS
Total number of atoms	5636	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.23% 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: GOL

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	Chain	Bond	lengths	Bond angles		
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.30	0/2430	0.53	0/3331	
1	В	0.30	0/2448	0.53	0/3354	
All	All	0.30	0/4878	0.53	0/6685	

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	A	2362	0	2274	11	0
1	В	2377	0	2295	12	0
2	A	6	0	8	0	0
2	В	6	0	8	0	0
3	A	447	0	0	4	0
3	В	438	0	0	5	0
All	All	5636	0	4585	22	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 2.

All (22) close contacts within the same asymmetric unit are listed below, sorted by their clash



magnitude.

Atom-1	Atom-2	$egin{array}{ll}  ext{Interatomic} \  ext{distance} \ ( ext{\AA}) \end{array}$	Clash overlap (Å)
1:B:336:GLN:HE22	1:B:377:ALA:H	1.18	0.87
1:A:341:SER:HB3	3:A:1070:HOH:O	1.84	0.75
1:B:290:ASN:HD21	1:B:379:ASN:HD21	1.35	0.70
1:A:370:HIS:HE1	1:B:344:GLU:OE2	1.75	0.69
1:B:290:ASN:ND2	1:B:379:ASN:HD21	1.92	0.68
1:A:519:ASN:HD22	1:A:521:PHE:H	1.46	0.63
1:B:263:ARG:HH21	1:B:491[A]:GLN:HE21	1.48	0.61
1:A:519:ASN:ND2	1:A:521:PHE:H	1.97	0.61
1:B:466:GLN:HG3	3:B:1013:HOH:O	2.00	0.60
1:A:296:TRP:O	1:A:370:HIS:HD2	1.85	0.59
1:B:489:HIS:HE1	1:B:495:THR:OG1	1.86	0.58
1:B:271:GLN:NE2	3:B:885:HOH:O	2.34	0.55
1:B:263:ARG:HH21	1:B:491[A]:GLN:NE2	2.06	0.54
1:B:519:ASN:HA	3:B:985:HOH:O	2.11	0.50
1:B:342:GLY:HA2	3:B:1006:HOH:O	2.12	0.49
1:B:466:GLN:HG3	3:B:955:HOH:O	2.14	0.47
1:A:296:TRP:O	1:A:370:HIS:CD2	2.68	0.47
1:A:498:ALA:HB2	1:A:527:MET:HG3	1.99	0.45
1:A:511:TYR:HB2	3:A:1052:HOH:O	2.17	0.43
1:A:315:GLU:HB2	3:A:949:HOH:O	2.19	0.42
1:A:287:MET:HE2	1:A:287:MET:HB3	1.90	0.40
1:A:422:ASN:ND2	3:A:872:HOH:O	2.54	0.40

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	304/316 (96%)	294 (97%)	10 (3%)	0	100	100
1	В	306/316 (97%)	299 (98%)	7 (2%)	0	100	100
All	All	610/632 (96%)	593 (97%)	17 (3%)	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	260/268 (97%)	258 (99%)	2 (1%)	81 55
1	В	$262/268 \; (98\%)$	261 (100%)	1 (0%)	91 76
All	All	522/536~(97%)	519 (99%)	3 (1%)	86 63

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	312	ASP
1	A	343	ASP
1	В	502	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	261	ASN
1	A	370	HIS
1	A	519	ASN
1	В	261	ASN
1	В	271	GLN
1	В	290	ASN
1	В	336	GLN
1	В	466	GLN
1	В	489	HIS

#### 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 carbohydrates in this entry.

#### 5.6 Ligand geometry (i)

2 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	Pos	Dog Link	Bond lengths			Bond angles		
MIOI	Type	Chain	m Res	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GOL	В	601	-	5,5,5	0.31	0	5, 5, 5	0.38	0
2	GOL	A	601	_	5,5,5	0.32	0	5,5,5	0.29	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.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	В	601	_	-	0/4/4/4	-
2	GOL	A	601	-	_	0/4/4/4	-

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	${f Analysed}$	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	306/316 (96%)	0.23	20 (6%) 18 18	6, 10, 22, 29	0
1	В	307/316 (97%)	0.16	13 (4%) 36 36	6, 10, 19, 30	0
All	All	613/632 (96%)	0.20	33 (5%) 25 25	6, 10, 21, 30	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	342	GLY	8.3
1	В	340	ALA	7.7
1	В	342	GLY	7.6
1	A	340	ALA	6.9
1	A	222	THR	6.7
1	A	341	SER	6.2
1	В	254	ASP	6.0
1	В	341	SER	5.0
1	В	221	LYS	4.7
1	A	339	ARG	4.5
1	A	293	ARG	4.2
1	В	478	ASP	3.9
1	В	222	THR	3.8
1	A	310	THR	3.7
1	В	339	ARG	3.5
1	В	343	ASP	3.2
1	A	481	ARG	3.1
1	A	338	PRO	2.9
1	A	343	ASP	2.8
1	A	478	ASP	2.8
1	A	422	ASN	2.7
1	A	480	GLY	2.6
1	В	527	MET	2.6
1	A	479	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	527	MET	2.5
1	В	422	ASN	2.5
1	A	442	GLN	2.4
1	A	499	THR	2.3
1	В	393	GLY	2.3
1	A	307	ASN	2.2
1	A	316	ASP	2.2
1	В	490	ARG	2.2
1	A	254	ASP	2.1

#### 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 carbohydrates 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	GOL	В	601	6/6	0.83	0.12	16,19,20,21	0
2	GOL	A	601	6/6	0.98	0.06	10,11,11,12	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

