



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 12:19 am BST

PDB ID : 2MEV  
Title : STRUCTURAL REFINEMENT AND ANALYSIS OF MENO VIRUS  
Authors : Rossmann, M.G.  
Deposited on : 1989-04-21  
Resolution : 3.00 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](mailto: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 ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

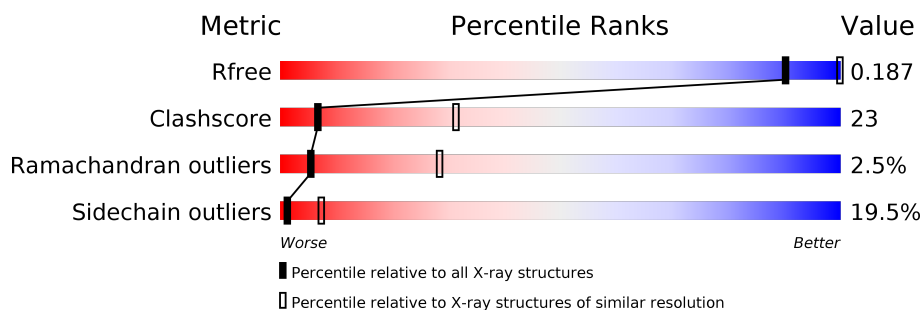
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	1	277	
2	2	256	
3	3	231	
4	4	70	

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
5	PO4	2	257	-	X	-	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6507 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 MENO VIRUS COAT PROTEIN (SUBUNIT VP1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	268	Total	C	N	O	S	0	0	0
			2091	1345	342	397	7			

- Molecule 2 is a protein called MENO VIRUS COAT PROTEIN (SUBUNIT VP2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	249	Total	C	N	O	S	0	0	0
			1973	1247	349	372	5			

- Molecule 3 is a protein called MENO VIRUS COAT PROTEIN (SUBUNIT VP3).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	3	231	Total	C	N	O	S	0	0	0
			1772	1153	283	326	10			

- Molecule 4 is a protein called MENO VIRUS COAT PROTEIN (SUBUNIT VP4).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	4	58	Total	C	N	O	S	0	0	0
			433	270	71	91	1			

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	2	1	Total	O	P	0	0
			5	4	1		

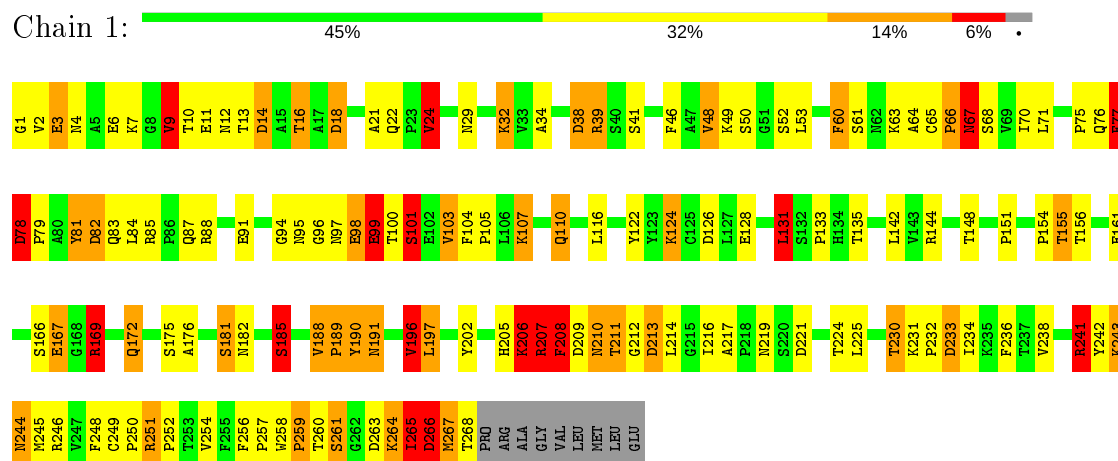
- Molecule 6 is water.

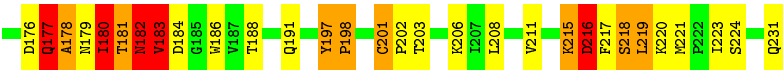
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	1	106	Total	O	0	0
			106	106		
6	2	69	Total	O	0	0
			69	69		
6	3	49	Total	O	0	0
			49	49		
6	4	9	Total	O	0	0
			9	9		

### 3 Residue-property plots

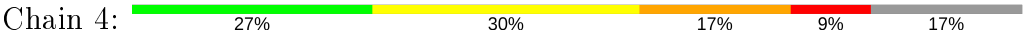
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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: MENGO VIRUS COAT PROTEIN (SUBUNIT VP1)





● Molecule 4: MENGU VIRUS COAT PROTEIN (SUBUNIT VP4)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	441.42Å 427.31Å 421.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 3.00 49.94 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-3.00) 36.8 (49.94-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.99 (at 2.61Å)	Xtriage
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.221 , (Not available) 0.202 , 0.187	Depositor DCC
$R_{free}$ test set	2516 reflections (0.25%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.8	Xtriage
Anisotropy	0.307	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 69.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.055 for k,h,-l 0.050 for -l,-k,-h 0.049 for -h,l,k 0.049 for l,h,k 0.049 for k,l,h	Xtriage
$F_o, F_c$ correlation	0.20	EDS
Total number of atoms	6507	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.92% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<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.



## 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: PO4

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	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	1	1.14	2/2159 (0.1%)	2.35	115/2952 (3.9%)
2	2	1.13	6/2028 (0.3%)	2.60	122/2776 (4.4%)
3	3	1.07	3/1829 (0.2%)	2.13	73/2512 (2.9%)
4	4	1.34	1/441 (0.2%)	2.99	52/600 (8.7%)
All	All	1.14	12/6457 (0.2%)	2.42	362/8840 (4.1%)

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
2	2	0	2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	20	GLY	N-CA	8.56	1.58	1.46
2	2	11	SER	CB-OG	7.89	1.52	1.42
2	2	254	SER	CB-OG	6.83	1.51	1.42
1	1	211	THR	CB-OG1	6.46	1.56	1.43
2	2	43	GLU	CD-OE2	6.13	1.32	1.25

The worst 5 of 362 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	102	ARG	NE-CZ-NH2	-21.77	109.42	120.30
2	2	61	ARG	NE-CZ-NH1	20.67	130.63	120.30
1	1	267	MET	C-N-CA	20.41	172.73	121.70
3	3	216	ASP	CB-CG-OD2	-19.35	100.88	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	161	ARG	CD-NE-CZ	18.62	149.67	123.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	2	255	ARG	Sidechain
2	2	81	ARG	Sidechain

## 5.2 Too-close contacts ⓘ

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	1	2091	0	2008	104	0
2	2	1973	0	1899	98	0
3	3	1772	0	1760	88	0
4	4	433	0	404	28	0
5	2	5	0	0	0	0
6	1	106	0	0	0	0
6	2	69	0	0	3	0
6	3	49	0	0	0	0
6	4	9	0	0	0	0
All	All	6507	0	6071	289	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 23.

The worst 5 of 289 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)
2:2:10:LEU:O	2:2:13:ARG:HB2	1.38	1.22
3:3:179:ASN:HB3	3:3:183:VAL:HG13	1.39	1.04
2:2:101:ARG:HD3	2:2:255:ARG:HB2	1.36	1.04
1:1:14:ASP:OD2	1:1:16:THR:HB	1.58	1.03
1:1:32:LYS:HE2	4:4:13:SER:HB2	1.41	1.02

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	Percentiles	
1	1	266/277 (96%)	238 (90%)	20 (8%)	8 (3%)	4	24
2	2	247/256 (96%)	227 (92%)	17 (7%)	3 (1%)	13	48
3	3	229/231 (99%)	208 (91%)	16 (7%)	5 (2%)	6	31
4	4	56/70 (80%)	46 (82%)	6 (11%)	4 (7%)	1	5
All	All	798/834 (96%)	719 (90%)	59 (7%)	20 (2%)	5	28

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	77	PHE
1	1	99	GLU
1	1	266	ASP
2	2	11	SER
2	2	253	LEU

### 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	1	233/240 (97%)	187 (80%)	46 (20%)	1	7
2	2	217/224 (97%)	177 (82%)	40 (18%)	1	9
3	3	195/195 (100%)	162 (83%)	33 (17%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	4	48/59 (81%)	32 (67%)	16 (33%)	0	1
All	All	693/718 (96%)	558 (80%)	135 (20%)	1	7

5 of 135 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	2	117	ASN
2	2	189	THR
4	4	27	ASN
2	2	120	GLN
2	2	158	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
2	2	158	GLN
2	2	184	ASN
4	4	50	GLN
2	2	160	ASN
2	2	181	GLN

### 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](#)

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			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	PO4	2	257	-	4,4,4	2.87	4 (100%)	6,6,6	0.28	0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	2	257	PO4	P-O4	-3.05	1.45	1.54
5	2	257	PO4	P-O3	-3.04	1.45	1.54
5	2	257	PO4	P-O2	-3.04	1.45	1.54
5	2	257	PO4	P-O1	-2.26	1.45	1.50

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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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

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

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

### 6.3 Carbohydrates ⓘ

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

### 6.4 Ligands ⓘ

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

### 6.5 Other polymers ⓘ

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