



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2024 – 12:57 PM EDT

PDB ID : 5DDJ  
Title : Crystal structure of recombinant foot-and-mouth-disease virus O1M-S2093Y empty capsid  
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Deposited on : 2015-08-25  
Resolution : 3.50 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.37.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Rfmac : 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) : 2.37.1

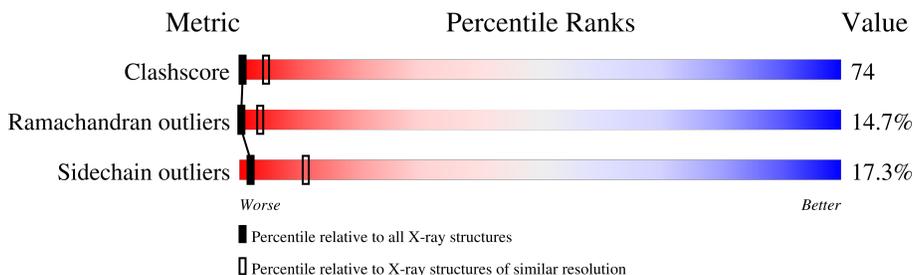
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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))
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)

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  $\geq 3$ , 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	211	16% (green), 48% (yellow), 21% (orange), 13% (grey), 2% (red)
2	2	218	21% (green), 52% (yellow), 22% (orange), 3% (grey), 2% (red)
3	3	220	29% (green), 52% (yellow), 18% (orange), 1% (red), 0% (grey)
4	4	85	16% (green), 32% (yellow), 6% (orange), 46% (grey), 0% (red)

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5131 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 Foot and mouth disease virus, VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	1	184	1437	910	258	266	3	0	0	0

- Molecule 2 is a protein called Foot and mouth disease virus, VP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	2	210	1656	1057	282	310	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	93	TYR	SER	engineered mutation	UNP Q6PMW3

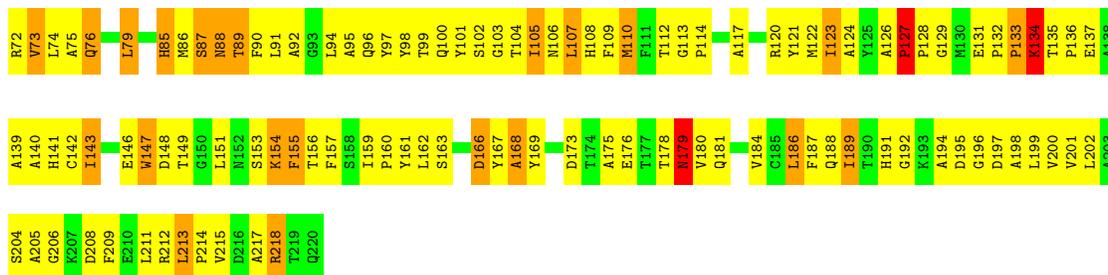
- Molecule 3 is a protein called Foot and mouth disease virus, VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	3	220	1685	1079	274	323	9	0	0	0

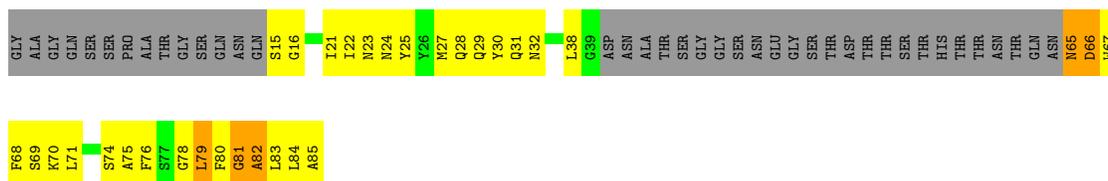
- Molecule 4 is a protein called Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	4	46	353	222	57	72	2	0	0	0





- Molecule 4: Genome polyprotein



## 4 Data and refinement statistics i

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	344.08Å 344.08Å 344.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.66 – 3.50 45.98 – 3.50	Depositor EDS
% Data completeness (in resolution range)	77.8 (49.66-3.50) 77.8 (45.98-3.50)	Depositor EDS
$R_{merge}$	0.43	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.28 (at 3.48Å)	Xtrriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.361 , (Not available) 0.361 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	65.1	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 87.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.21$	Xtrriage
Estimated twinning fraction	0.499 for -l,-k,-h	Xtrriage
$F_o, F_c$ correlation	0.70	EDS
Total number of atoms	5131	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.90% 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](#)

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	0.49	0/1471	0.82	1/2012 (0.0%)
2	2	0.52	0/1701	0.83	1/2323 (0.0%)
3	3	0.56	0/1735	0.83	2/2370 (0.1%)
4	4	0.59	0/359	0.73	0/481
All	All	0.53	0/5266	0.82	4/7186 (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	1	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	28	SER	N-CA-C	-5.67	95.70	111.00
3	3	213	LEU	CA-CB-CG	5.58	128.14	115.30
1	1	81	LYS	N-CA-C	-5.21	96.94	111.00
3	3	79	LEU	CA-CB-CG	5.06	126.95	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	107	TYR	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	1	1437	0	1443	268	0
2	2	1656	0	1610	295	0
3	3	1685	0	1610	217	0
4	4	353	0	324	35	0
All	All	5131	0	4987	746	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 74.

The worst 5 of 746 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)
2:2:32:VAL:HG22	2:2:33:THR:H	1.02	1.11
2:2:91:TYR:HA	2:2:94:LEU:HD22	1.12	1.10
2:2:78:CYS:HB2	2:2:180:VAL:HG23	1.26	1.07
1:1:94:PRO:HG2	1:1:97:ALA:HB2	1.37	1.04
1:1:34:PHE:HA	4:4:16:GLY:HA2	1.35	1.04

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	180/211 (85%)	108 (60%)	42 (23%)	30 (17%)	0 2
2	2	208/218 (95%)	124 (60%)	56 (27%)	28 (14%)	0 4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	218/220 (99%)	139 (64%)	50 (23%)	29 (13%)	0	4
4	4	42/85 (49%)	24 (57%)	10 (24%)	8 (19%)	0	2
All	All	648/734 (88%)	395 (61%)	158 (24%)	95 (15%)	0	3

5 of 95 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	15	VAL
1	1	16	GLU
1	1	38	ARG
1	1	39	PHE
1	1	45	LYS

### 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	153/173 (88%)	124 (81%)	29 (19%)	1	8
2	2	182/190 (96%)	149 (82%)	33 (18%)	1	9
3	3	176/176 (100%)	145 (82%)	31 (18%)	2	10
4	4	37/67 (55%)	35 (95%)	2 (5%)	22	55
All	All	548/606 (90%)	453 (83%)	95 (17%)	2	11

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	2	161	PRO
3	3	60	ASP
2	2	180	VAL
3	3	36	MET
3	3	85	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	3	191	HIS
4	4	23	ASN
2	2	19	ASN
2	2	103	ASN
2	2	149	ASN

### 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](#)

There are no ligands in this entry.

### 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.