



# Full wwPDB X-ray Structure Validation Report ⓘ

May 31, 2022 – 04:05 pm BST

PDB ID : 6SY8  
Title : Mopeia Virus Exonuclease domain fully depleted of Manganese un ALD compound  
Authors : Nguyen, T.H.V.; Ferron, F.  
Deposited on : 2019-09-27  
Resolution : 2.08 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.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  
Xtrriage (Phenix) : 1.13  
EDS : 2.28.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.28.1

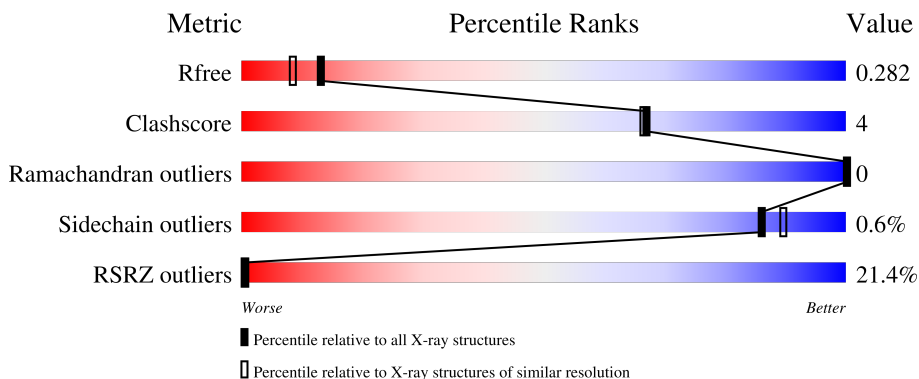
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.08 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	6189 (2.10-2.06)
Clashscore	141614	6738 (2.10-2.06)
Ramachandran outliers	138981	6663 (2.10-2.06)
Sidechain outliers	138945	6664 (2.10-2.06)
RSRZ outliers	127900	6057 (2.10-2.06)

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  $\leq 5\%$ . 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	206	
1	B	206	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3302 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 Nucleoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	198	1587	1000	275	302	10	0	0	0
1	B	199	1596	1005	276	305	10	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

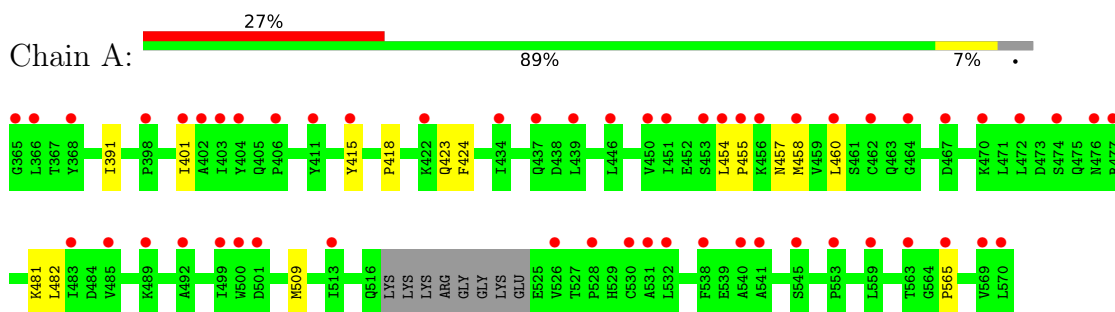
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	46	Total	O	0	0
			46	46		
3	B	71	Total	O	0	0
			71	71		

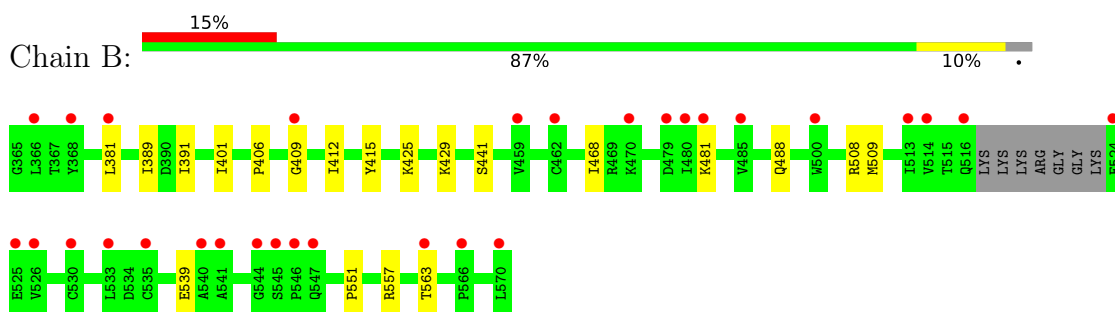
### 3 Residue-property plots [i](#)

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 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: Nucleoprotein



- Molecule 1: Nucleoprotein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	45.85Å 38.29Å 137.31Å 90.00° 92.63° 90.00°	Depositor
Resolution (Å)	68.58 – 2.08 68.59 – 2.08	Depositor EDS
% Data completeness (in resolution range)	99.5 (68.58-2.08) 99.5 (68.59-2.08)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.67 (at 2.08Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.248 , 0.283 0.256 , 0.282	Depositor DCC
$R_{free}$ test set	1346 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.3	Xtrriage
Anisotropy	1.132	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.029 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3302	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.66% 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:  
ZN

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	A	0.53	1/1620 (0.1%)	0.62	0/2193
1	B	0.50	0/1629	0.62	0/2205
All	All	0.51	1/3249 (0.0%)	0.62	0/4398

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	565	PRO	C-N	-7.11	1.20	1.34

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	1587	0	1577	9	0
1	B	1596	0	1583	16	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	46	0	0	0	0
3	B	71	0	0	2	0
All	All	3302	0	3160	25	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 4.

All (25) 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)
1:B:481:LYS:HE3	3:B:744:HOH:O	1.66	0.95
1:B:508:ARG:NH2	1:B:557:ARG:HH22	1.64	0.94
1:B:508:ARG:HH21	1:B:557:ARG:HH22	1.12	0.91
1:B:441:SER:HB2	1:B:563:THR:HG22	1.65	0.79
1:A:458:MET:HE3	1:A:460:LEU:HD21	1.72	0.71
1:A:455:PRO:HD2	1:A:458:MET:SD	2.35	0.66
1:B:381:LEU:HD11	1:B:412:ILE:HD11	1.80	0.63
1:A:458:MET:CE	1:A:460:LEU:HD21	2.30	0.61
1:B:406:PRO:HB3	1:B:539:GLU:HG2	1.88	0.56
1:B:391:ILE:HG22	1:B:401:ILE:HG12	1.87	0.55
1:B:425:LYS:O	1:B:429:LYS:HD3	2.07	0.55
1:B:488:GLN:HB3	3:B:745:HOH:O	2.08	0.53
1:A:454:LEU:HD22	1:A:458:MET:HE2	1.89	0.53
1:B:381:LEU:HD11	1:B:412:ILE:CD1	2.38	0.52
1:A:391:ILE:HG22	1:A:401:ILE:HG12	1.94	0.50
1:B:389:ILE:HG23	1:B:468:ILE:HD13	1.95	0.48
1:B:508:ARG:HH21	1:B:557:ARG:NH2	1.95	0.48
1:A:415:TYR:CE1	1:A:509:MET:HG3	2.50	0.46
1:A:481:LYS:HG3	1:A:482:LEU:N	2.32	0.45
1:B:508:ARG:NH2	1:B:557:ARG:NH2	2.48	0.43
1:B:508:ARG:HH22	1:B:557:ARG:HH12	1.65	0.43
1:B:409:GLY:O	1:B:551:PRO:HA	2.18	0.42
1:A:415:TYR:CZ	1:A:509:MET:HG3	2.55	0.42
1:B:415:TYR:CE1	1:B:509:MET:HG3	2.55	0.41
1:A:418:PRO:HG3	1:A:424:PHE:CD1	2.56	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	Percentiles	
1	A	194/206 (94%)	188 (97%)	6 (3%)	0	100	100
1	B	195/206 (95%)	191 (98%)	4 (2%)	0	100	100
All	All	389/412 (94%)	379 (97%)	10 (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	181/187 (97%)	179 (99%)	2 (1%)	73	78
1	B	182/187 (97%)	182 (100%)	0	100	100
All	All	363/374 (97%)	361 (99%)	2 (1%)	86	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	423	GLN
1	A	457	ASN

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 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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

### 6.1 Protein, DNA and RNA chains

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<sup>th</sup> 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	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	198/206 (96%)	1.58	55 (27%) <b>0</b>   <b>0</b>	36, 56, 77, 93	0
1	B	199/206 (96%)	1.24	30 (15%) <b>2</b>   <b>2</b>	26, 48, 72, 101	0
All	All	397/412 (96%)	1.41	85 (21%) <b>0</b>   <b>0</b>	26, 52, 76, 101	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	524	GLU	7.7
1	A	500	TRP	7.2
1	A	455	PRO	5.7
1	A	462	CYS	5.1
1	B	526	VAL	4.6
1	A	501	ASP	4.6
1	A	489	LYS	4.5
1	B	525	GLU	4.3
1	A	464	GLY	4.1
1	B	516	GLN	3.9
1	A	404	TYR	3.9
1	A	454	LEU	3.8
1	A	485	VAL	3.7
1	A	446	LEU	3.7
1	A	541	ALA	3.6
1	A	563	THR	3.6
1	B	368	TYR	3.5
1	A	553	PRO	3.1
1	B	541	ALA	3.1
1	B	480	ILE	3.1
1	A	437	GLN	3.1
1	B	535	CYS	2.9
1	A	559	LEU	2.9
1	A	450	VAL	2.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	492	ALA	2.9
1	B	547	GLN	2.9
1	A	476	ASN	2.9
1	A	398	PRO	2.9
1	A	467	ASP	2.9
1	A	472	LEU	2.9
1	A	483	ILE	2.8
1	B	546	PRO	2.8
1	A	402	ALA	2.8
1	B	533	LEU	2.8
1	A	545	SER	2.8
1	A	458	MET	2.7
1	A	530	CYS	2.7
1	A	526	VAL	2.7
1	A	499	ILE	2.7
1	A	538	PHE	2.7
1	B	459	VAL	2.7
1	B	570	LEU	2.7
1	A	565	PRO	2.7
1	A	434	ILE	2.6
1	A	365	GLY	2.6
1	A	453	SER	2.5
1	B	514	VAL	2.5
1	A	513	ILE	2.5
1	B	500	TRP	2.5
1	A	406	PRO	2.5
1	A	540	ALA	2.5
1	B	462	CYS	2.5
1	B	540	ALA	2.4
1	A	422	LYS	2.4
1	A	451	ILE	2.4
1	B	545	SER	2.4
1	B	481	LYS	2.4
1	B	513	ILE	2.4
1	A	460	LEU	2.4
1	A	532	LEU	2.4
1	B	479	ASP	2.4
1	B	366	LEU	2.3
1	A	470	LYS	2.3
1	A	474	SER	2.3
1	A	403	ILE	2.3
1	B	470	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	381	LEU	2.3
1	A	477	ARG	2.3
1	A	401	ILE	2.2
1	B	530	CYS	2.2
1	A	366	LEU	2.2
1	A	528	PRO	2.2
1	B	544	GLY	2.2
1	A	415	TYR	2.2
1	A	439	LEU	2.2
1	A	456	LYS	2.2
1	B	409	GLY	2.1
1	A	368	TYR	2.1
1	A	411	TYR	2.1
1	B	566	PRO	2.1
1	A	569	VAL	2.1
1	B	563	THR	2.1
1	A	531	ALA	2.0
1	A	570	LEU	2.0
1	B	485	VAL	2.0

## 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 monosaccharides 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<sup>th</sup> 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZN	A	601	1/1	0.96	0.16	44,44,44,44	0
2	ZN	B	601	1/1	0.99	0.16	35,35,35,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.