



wwPDB EM Validation Summary Report ⓘ

Jul 9, 2025 – 01:37 PM JST

PDB ID : 9ILY / pdb_00009ily
EMDB ID : EMD-60676
Title : The Cryo-EM structure of MPXV E5 in the apo state
Authors : Cheng, Y.X.; Han, P.; Wang, H.
Deposited on : 2024-07-01
Resolution : 3.33 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

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>.

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

EMDB validation analysis : **FAILED**
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

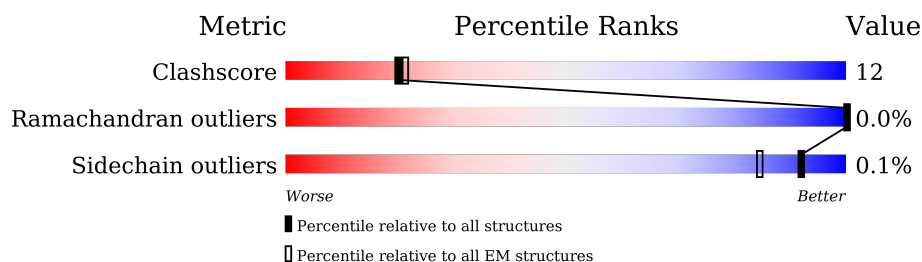
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.33 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	785	38% 15% 46%
1	B	785	38% 15% 46%
1	C	785	39% 14% 47%
1	D	785	38% 16% 46%
1	E	785	41% 13% 46%
1	F	785	38% 16% 46%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 20595 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

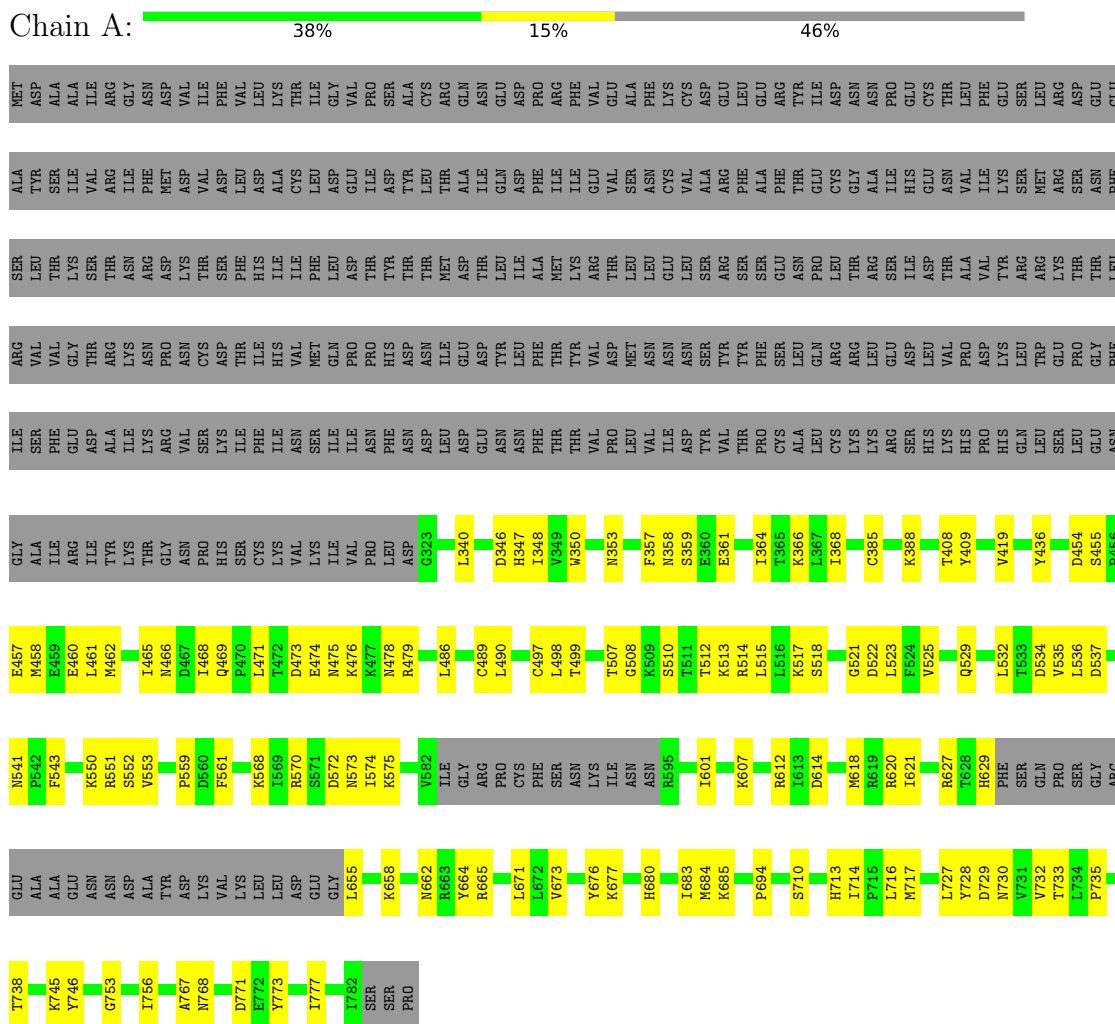
- Molecule 1 is a protein called Primase D5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	423	Total	C	N	O	S	0	0
			3441	2214	575	636	16		
1	F	423	Total	C	N	O	S	0	0
			3441	2214	575	636	16		
1	E	423	Total	C	N	O	S	0	0
			3441	2214	575	636	16		
1	D	423	Total	C	N	O	S	0	0
			3441	2214	575	636	16		
1	C	417	Total	C	N	O	S	0	0
			3390	2181	568	625	16		
1	B	423	Total	C	N	O	S	0	0
			3441	2214	575	636	16		

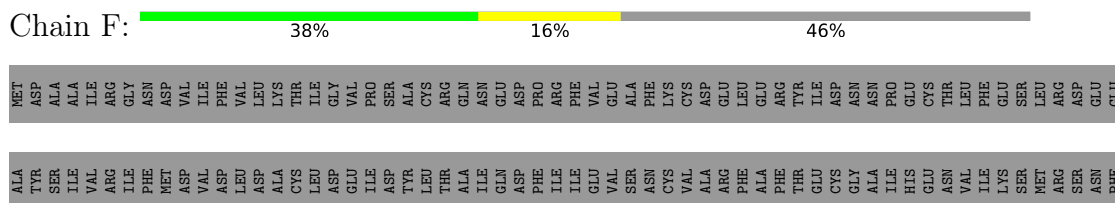
3 Residue-property plots

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: Primase D5

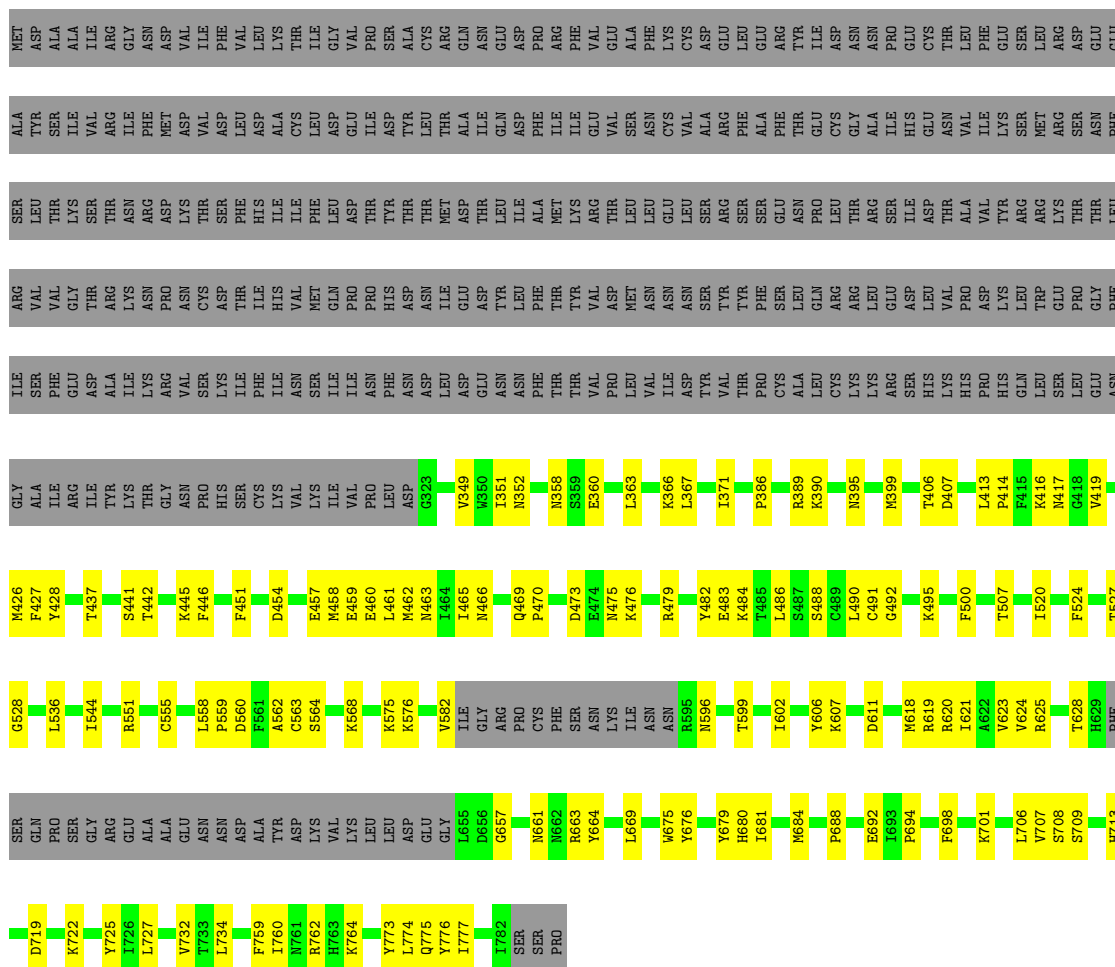


• Molecule 1: Primase D5



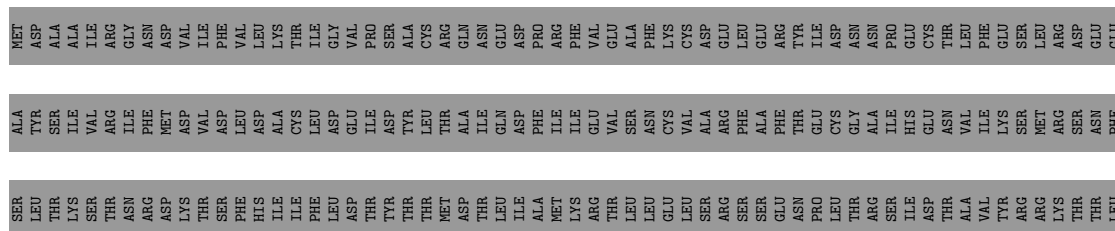
- Molecule 1: Primase D5

Chain D: 38% 16% 46%



- Molecule 1: Primase D5

Chain C: 39% 14% 47%







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94493	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor

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	A	0.10	0/3514	0.31	0/4744
1	B	0.11	0/3514	0.35	0/4744
1	C	0.11	0/3461	0.34	0/4669
1	D	0.09	0/3514	0.29	0/4744
1	E	0.10	0/3514	0.33	0/4744
1	F	0.14	0/3514	0.42	2/4744 (0.0%)
All	All	0.11	0/21031	0.34	2/28389 (0.0%)

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	B	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	362	PRO	CA-N-CD	-8.46	100.15	112.00
1	F	462	MET	CA-CB-CG	5.33	124.75	114.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	489	CYS	Peptide
1	B	490	LEU	Peptide

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	A	3441	0	3480	89	0
1	B	3441	0	3478	88	0
1	C	3390	0	3429	80	0
1	D	3441	0	3478	87	0
1	E	3441	0	3480	76	0
1	F	3441	0	3478	93	0
All	All	20595	0	20823	499	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 12.

The worst 5 of 499 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:F:681:ILE:HD12	1:F:682:PRO:HD3	1.54	0.89
1:B:489:CYS:HA	1:B:491:CYS:HB3	1.56	0.87
1:F:568:LYS:HE3	1:F:568:LYS:HA	1.59	0.83
1:B:477:LYS:HA	1:B:480:GLU:HG2	1.64	0.79
1:F:454:ASP:H	1:F:458:MET:HE3	1.50	0.75

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	417/785 (53%)	393 (94%)	24 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	417/785 (53%)	378 (91%)	39 (9%)	0	100	100
1	C	409/785 (52%)	360 (88%)	49 (12%)	0	100	100
1	D	417/785 (53%)	390 (94%)	27 (6%)	0	100	100
1	E	417/785 (53%)	397 (95%)	20 (5%)	0	100	100
1	F	417/785 (53%)	389 (93%)	27 (6%)	1 (0%)	44	72
All	All	2494/4710 (53%)	2307 (92%)	186 (8%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	683	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	391/725 (54%)	391 (100%)	0	100	100
1	B	391/725 (54%)	391 (100%)	0	100	100
1	C	385/725 (53%)	384 (100%)	1 (0%)	91	94
1	D	391/725 (54%)	391 (100%)	0	100	100
1	E	391/725 (54%)	391 (100%)	0	100	100
1	F	391/725 (54%)	389 (100%)	2 (0%)	86	91
All	All	2340/4350 (54%)	2337 (100%)	3 (0%)	92	96

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

Mol	Chain	Res	Type
1	F	462	MET
1	F	755	ASP
1	C	491	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15

such sidechains are listed below:

Mol	Chain	Res	Type
1	E	475	ASN
1	D	605	ASN
1	E	713	HIS
1	C	763	HIS
1	D	358	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 oligosaccharides 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.