



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:59 PM UTC

PDB ID : 9L7W / pdb_00009l7w
Title : Crystal structure of monkeypox virus A30/H2 sub-complex at pH 4.0
Authors : Lin, S.; Jia, X.H.; Lu, G.W.
Deposited on : 2024-12-27
Resolution : 2.51 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

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>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

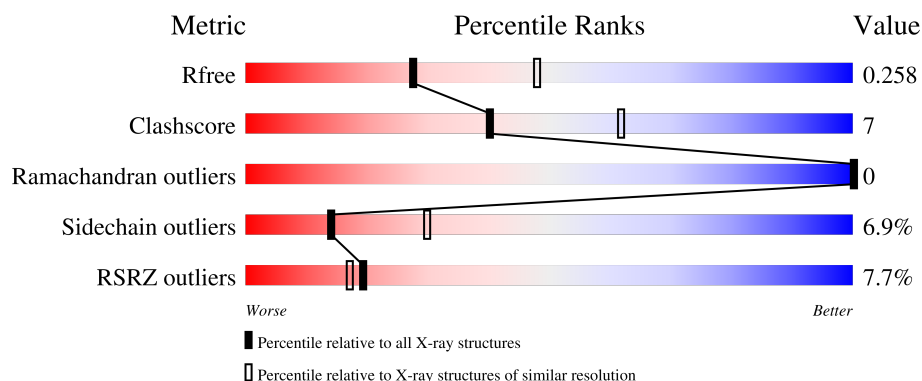
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 ≥ 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	168	4% 69% 10% • 20%
1	C	168	3% 61% 10% 29%
2	B	119	15% 61% 13% 5% 21%
2	D	119	3% 65% 11% • 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3611 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 MPXVgp092.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	134	Total	C	N	O	S	0	0	0
			1080	686	187	198	9			
1	C	119	Total	C	N	O	S	0	0	0
			951	605	164	174	8			

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	GLY	-	expression tag	UNP A0A7H0DN79
A	48	PRO	-	expression tag	UNP A0A7H0DN79
A	49	LEU	-	expression tag	UNP A0A7H0DN79
A	50	GLY	-	expression tag	UNP A0A7H0DN79
A	190	GLY	-	expression tag	UNP A0A7H0DN79
A	191	GLY	-	expression tag	UNP A0A7H0DN79
A	192	GLY	-	expression tag	UNP A0A7H0DN79
A	193	GLY	-	expression tag	UNP A0A7H0DN79
A	194	SER	-	expression tag	UNP A0A7H0DN79
A	195	GLY	-	expression tag	UNP A0A7H0DN79
A	196	GLY	-	expression tag	UNP A0A7H0DN79
A	197	GLY	-	expression tag	UNP A0A7H0DN79
A	198	GLY	-	expression tag	UNP A0A7H0DN79
A	199	SER	-	expression tag	UNP A0A7H0DN79
A	200	GLY	-	expression tag	UNP A0A7H0DN79
A	201	GLY	-	expression tag	UNP A0A7H0DN79
A	202	GLY	-	expression tag	UNP A0A7H0DN79
A	203	GLY	-	expression tag	UNP A0A7H0DN79
A	204	SER	-	expression tag	UNP A0A7H0DN79
A	205	GLY	-	expression tag	UNP A0A7H0DN79
A	206	GLY	-	expression tag	UNP A0A7H0DN79
A	207	GLY	-	expression tag	UNP A0A7H0DN79
A	208	GLY	-	expression tag	UNP A0A7H0DN79
A	209	SER	-	expression tag	UNP A0A7H0DN79
A	210	GLY	-	expression tag	UNP A0A7H0DN79

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Chain	Residue	Modelled	Actual	Comment	Reference
A	211	GLY	-	expression tag	UNP A0A7H0DN79
A	212	GLY	-	expression tag	UNP A0A7H0DN79
A	213	GLY	-	expression tag	UNP A0A7H0DN79
A	214	SER	-	expression tag	UNP A0A7H0DN79
C	47	GLY	-	expression tag	UNP A0A7H0DN79
C	48	PRO	-	expression tag	UNP A0A7H0DN79
C	49	LEU	-	expression tag	UNP A0A7H0DN79
C	50	GLY	-	expression tag	UNP A0A7H0DN79
C	190	GLY	-	expression tag	UNP A0A7H0DN79
C	191	GLY	-	expression tag	UNP A0A7H0DN79
C	192	GLY	-	expression tag	UNP A0A7H0DN79
C	193	GLY	-	expression tag	UNP A0A7H0DN79
C	194	SER	-	expression tag	UNP A0A7H0DN79
C	195	GLY	-	expression tag	UNP A0A7H0DN79
C	196	GLY	-	expression tag	UNP A0A7H0DN79
C	197	GLY	-	expression tag	UNP A0A7H0DN79
C	198	GLY	-	expression tag	UNP A0A7H0DN79
C	199	SER	-	expression tag	UNP A0A7H0DN79
C	200	GLY	-	expression tag	UNP A0A7H0DN79
C	201	GLY	-	expression tag	UNP A0A7H0DN79
C	202	GLY	-	expression tag	UNP A0A7H0DN79
C	203	GLY	-	expression tag	UNP A0A7H0DN79
C	204	SER	-	expression tag	UNP A0A7H0DN79
C	205	GLY	-	expression tag	UNP A0A7H0DN79
C	206	GLY	-	expression tag	UNP A0A7H0DN79
C	207	GLY	-	expression tag	UNP A0A7H0DN79
C	208	GLY	-	expression tag	UNP A0A7H0DN79
C	209	SER	-	expression tag	UNP A0A7H0DN79
C	210	GLY	-	expression tag	UNP A0A7H0DN79
C	211	GLY	-	expression tag	UNP A0A7H0DN79
C	212	GLY	-	expression tag	UNP A0A7H0DN79
C	213	GLY	-	expression tag	UNP A0A7H0DN79
C	214	SER	-	expression tag	UNP A0A7H0DN79

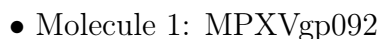
- Molecule 2 is a protein called Envelope protein OPG155.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	94	Total	C	N	O	S	0	0	0
			750	472	132	141	5			
2	D	94	Total	C	N	O	S	0	0	0
			750	472	132	141	5			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total 13	O 13	0	0
3	B	6	Total 6	O 6	0	0
3	C	20	Total 20	O 20	0	0
3	D	41	Total 41	O 41	0	0

- Molecule 1: MPXVgp092



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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	38.33Å 115.19Å 126.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.56 – 2.51 42.56 – 2.51	Depositor EDS
% Data completeness (in resolution range)	99.2 (42.56-2.51) 99.1 (42.56-2.51)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.210 , 0.258 0.215 , 0.258	Depositor DCC
R_{free} test set	998 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	46.1	Xtriage
Anisotropy	0.305	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 60.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3611	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	A	0.17	0/1104	0.44	0/1484
1	C	0.19	0/972	0.52	2/1306 (0.2%)
2	B	0.30	0/765	0.61	0/1036
2	D	0.29	0/765	0.63	0/1036
All	All	0.24	0/3606	0.54	2/4862 (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
2	D	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	182	CYS	CA-C-N	5.46	131.53	121.70
1	C	182	CYS	C-N-CA	5.46	131.53	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	101	ARG	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	A	1080	0	1064	10	0
1	C	951	0	938	16	0
2	B	750	0	731	22	0
2	D	750	0	731	9	0
3	A	13	0	0	1	0
3	B	6	0	0	0	0
3	C	20	0	0	2	0
3	D	41	0	0	1	0
All	All	3611	0	3464	46	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 7.

All (46) 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:B:120:VAL:HG13	1:C:116:LYS:HE3	1.69	0.74
1:C:156:SER:OG	3:C:301:HOH:O	2.08	0.71
2:D:122:ASN:ND2	3:D:202:HOH:O	2.27	0.67
2:B:70:LYS:HB3	2:B:88:ILE:HG23	1.81	0.63
2:B:101:ARG:NH1	2:B:125:ILE:O	2.32	0.62
1:A:142:PRO:O	1:A:146:GLN:HG3	2.01	0.61
2:D:81:ASN:N	2:D:81:ASN:OD1	2.34	0.60
1:C:142:PRO:O	1:C:146:GLN:HG3	2.02	0.60
2:B:119:ASP:H	1:C:116:LYS:HZ3	1.49	0.59
2:B:120:VAL:HG22	1:C:116:LYS:HE3	1.83	0.59
2:B:71:GLN:HG2	2:B:88:ILE:HD11	1.83	0.59
1:A:101:LYS:NZ	3:A:302:HOH:O	2.38	0.56
2:B:120:VAL:CG1	1:C:116:LYS:HE3	2.34	0.55
2:D:100:THR:HG22	2:D:133:ASN:HD21	1.72	0.55
2:B:97:PRO:O	2:B:98:ASN:HB2	2.08	0.54
2:D:81:ASN:HB2	2:D:105:LYS:HD3	1.89	0.53
2:B:120:VAL:HG13	1:C:116:LYS:CE	2.38	0.53
1:A:145:GLN:OE1	1:A:149:GLN:NE2	2.33	0.51
1:C:86:ARG:NH1	3:C:305:HOH:O	2.45	0.50
1:C:65:ILE:HG22	1:C:67:ASN:H	1.78	0.49
2:B:120:VAL:HG23	2:B:121:ILE:O	2.12	0.49
1:C:82:LEU:O	1:C:86:ARG:HG3	2.13	0.48
2:D:93:ALA:O	2:D:104:ARG:NH1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:100:THR:HG22	2:D:133:ASN:ND2	2.28	0.48
1:A:94:LYS:HD3	1:A:97:ILE:HD13	1.96	0.48
2:B:76:VAL:HG21	2:B:145:VAL:HG11	1.96	0.48
2:D:135:ASN:HB3	2:D:138:GLU:HB2	1.96	0.48
2:B:120:VAL:CG2	1:C:116:LYS:HE3	2.44	0.47
2:B:137:THR:HA	2:B:140:GLN:HG2	1.96	0.47
1:A:55:VAL:HG22	1:A:58:GLU:HG3	1.96	0.47
2:B:70:LYS:O	2:B:88:ILE:HG12	2.16	0.46
2:B:120:VAL:HG22	1:C:116:LYS:CE	2.45	0.46
2:B:120:VAL:HG23	2:B:121:ILE:C	2.41	0.45
1:A:137:ALA:HB3	2:B:69:VAL:HG22	1.98	0.45
2:B:123:ILE:H	2:B:123:ILE:HG12	1.30	0.45
2:B:131:ALA:O	2:B:134:ILE:HG23	2.19	0.43
1:C:115:ASP:OD1	1:C:116:LYS:N	2.51	0.43
1:C:153:LYS:HD3	1:C:153:LYS:HA	1.78	0.42
1:A:118:THR:O	1:A:119:TYR:HB2	2.19	0.42
1:A:138:ALA:HB2	2:B:69:VAL:HG21	2.01	0.42
2:B:137:THR:O	2:B:140:GLN:HG2	2.20	0.41
1:C:146:GLN:NE2	2:D:109:MET:HE1	2.34	0.41
2:D:101:ARG:NH1	2:D:125:ILE:H	2.18	0.41
1:A:128:THR:N	2:B:56:ASP:OD2	2.43	0.41
1:C:117:LYS:HD2	1:C:117:LYS:HA	1.91	0.40
1:A:145:GLN:HE21	1:A:145:GLN:HB2	1.73	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	Percentiles	
1	A	132/168 (79%)	129 (98%)	3 (2%)	0	100	100
1	C	117/168 (70%)	114 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	92/119 (77%)	85 (92%)	7 (8%)	0	100	100
2	D	92/119 (77%)	89 (97%)	3 (3%)	0	100	100
All	All	433/574 (75%)	417 (96%)	16 (4%)	0	100	100

There are no Ramachandran outliers to report.

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 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	117/129 (91%)	111 (95%)	6 (5%)	21	43
1	C	102/129 (79%)	97 (95%)	5 (5%)	22	45
2	B	86/105 (82%)	78 (91%)	8 (9%)	8	18
2	D	86/105 (82%)	78 (91%)	8 (9%)	8	18
All	All	391/468 (84%)	364 (93%)	27 (7%)	14	30

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	VAL
1	A	60	THR
1	A	95	ASP
1	A	117	LYS
1	A	145	GLN
1	A	168	ASN
2	B	69	VAL
2	B	81	ASN
2	B	118	SER
2	B	119	ASP
2	B	120	VAL
2	B	121	ILE
2	B	123	ILE
2	B	145	VAL

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Mol	Chain	Res	Type
1	C	66	LYS
1	C	69	VAL
1	C	74	SER
1	C	101	LYS
1	C	145	GLN
2	D	57	ARG
2	D	62	VAL
2	D	67	SER
2	D	81	ASN
2	D	95	VAL
2	D	98	ASN
2	D	100	THR
2	D	104	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	GLN
1	A	149	GLN
1	C	70	ASN
2	D	122	ASN
2	D	133	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.

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, 95th 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 ²)	Q<0.9
1	A	134/168 (79%)	0.62	7 (5%) 33 29	33, 62, 87, 100	0
1	C	119/168 (70%)	0.23	5 (4%) 40 36	22, 46, 91, 107	0
2	B	94/119 (78%)	1.08	18 (19%) 3 2	36, 64, 116, 140	0
2	D	94/119 (78%)	0.01	4 (4%) 40 35	20, 34, 76, 106	0
All	All	441/574 (76%)	0.48	34 (7%) 19 17	20, 54, 93, 140	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	93	GLY	5.2
2	B	122	ASN	5.0
2	B	97	PRO	4.5
1	C	65	ILE	4.2
2	B	121	ILE	4.2
2	B	123	ILE	4.0
2	B	131	ALA	3.8
2	B	95	VAL	3.6
1	A	176	PHE	3.6
2	D	123	ILE	3.3
2	B	120	VAL	3.2
2	B	96	GLY	3.0
2	D	122	ASN	3.0
1	C	69	VAL	2.9
2	B	132	PRO	2.8
1	A	89	LEU	2.8
2	B	145	VAL	2.7
1	C	183	SER	2.7
2	B	141	PHE	2.6
1	A	54	PRO	2.6
2	B	98	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	175	TYR	2.4
2	D	99	ASN	2.4
2	D	95	VAL	2.4
2	B	144	SER	2.3
1	C	116	LYS	2.3
1	A	119	TYR	2.2
1	A	62	TYR	2.2
2	B	130	ILE	2.2
2	B	133	ASN	2.2
2	B	146	LEU	2.2
2	B	78	TYR	2.1
2	B	53	PRO	2.1
1	A	59	LEU	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.