



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:41 PM UTC

PDB ID : 8TN8 / pdb_00008tn8
Title : Crystal structure of the murine astrovirus capsid spike at 1.75 Å
Authors : Lanning, S.; DuBois, R.M.
Deposited on : 2023-08-01
Resolution : 1.75 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

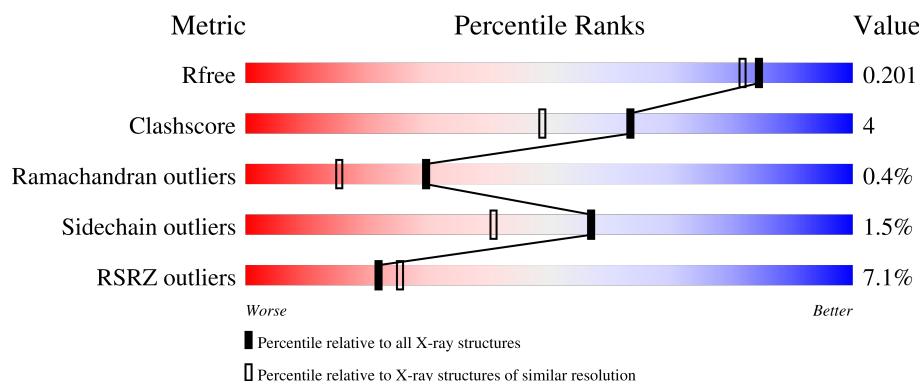
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

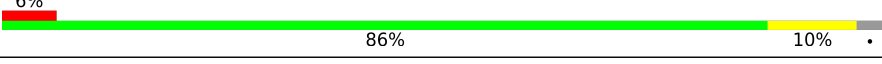
The reported resolution of this entry is 1.75 Å.

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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	261	 8% 84% 12% •
1	B	261	 6% 86% 10% •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4339 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 Capsid polypeptide VP90.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2005	1280	349	372	4			
1	B	253	Total	C	N	O	S	0	0	0
			2010	1283	350	373	4			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	426	MET	-	initiating methionine	UNP A0A482N9T7
A	427	GLY	-	expression tag	UNP A0A482N9T7
A	677	ALA	-	expression tag	UNP A0A482N9T7
A	678	ALA	-	expression tag	UNP A0A482N9T7
A	679	ALA	-	expression tag	UNP A0A482N9T7
A	680	GLU	-	expression tag	UNP A0A482N9T7
A	681	LEU	-	expression tag	UNP A0A482N9T7
A	682	ALA	-	expression tag	UNP A0A482N9T7
A	683	LEU	-	expression tag	UNP A0A482N9T7
A	684	VAL	-	expression tag	UNP A0A482N9T7
A	685	PRO	-	expression tag	UNP A0A482N9T7
A	686	ARG	-	expression tag	UNP A0A482N9T7
B	426	MET	-	initiating methionine	UNP A0A482N9T7
B	427	GLY	-	expression tag	UNP A0A482N9T7
B	677	ALA	-	expression tag	UNP A0A482N9T7
B	678	ALA	-	expression tag	UNP A0A482N9T7
B	679	ALA	-	expression tag	UNP A0A482N9T7
B	680	GLU	-	expression tag	UNP A0A482N9T7
B	681	LEU	-	expression tag	UNP A0A482N9T7
B	682	ALA	-	expression tag	UNP A0A482N9T7
B	683	LEU	-	expression tag	UNP A0A482N9T7
B	684	VAL	-	expression tag	UNP A0A482N9T7
B	685	PRO	-	expression tag	UNP A0A482N9T7
B	686	ARG	-	expression tag	UNP A0A482N9T7

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

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

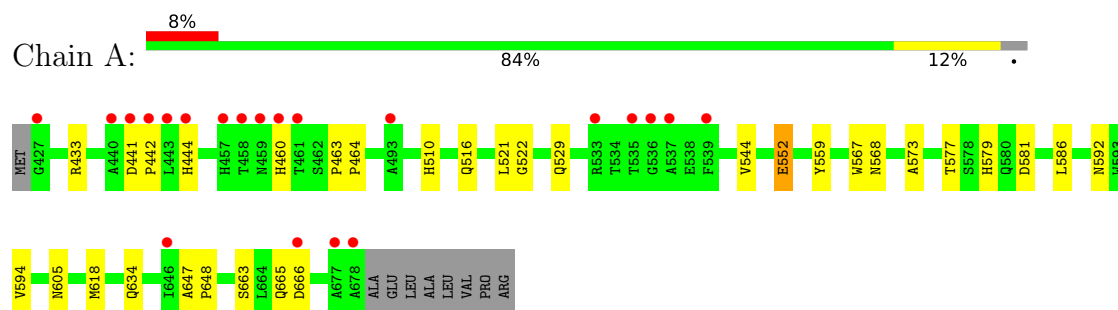
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	164	Total 164	O 164	0	0
3	B	158	Total 158	O 158	0	0

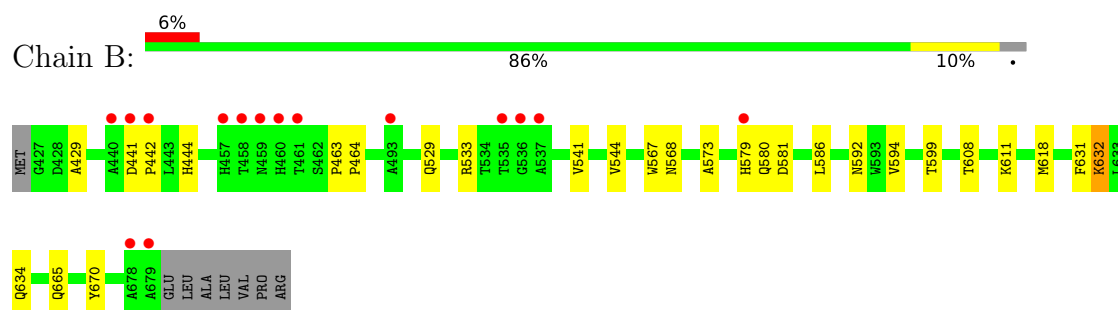
3 Residue-property plots

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 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: Capsid polyprotein VP90



• Molecule 1: Capsid polyprotein VP90



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	45.33Å 48.87Å 65.46Å 93.34° 102.91° 114.70°	Depositor
Resolution (Å)	43.75 – 1.75 43.75 – 1.75	Depositor EDS
% Data completeness (in resolution range)	92.8 (43.75-1.75) 89.4 (43.75-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.171 , 0.201 0.171 , 0.201	Depositor DCC
R_{free} test set	2294 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	18.4	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4339	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.36% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
K

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	0.27	0/2076	0.51	2/2855 (0.1%)
1	B	0.24	0/2081	0.50	2/2862 (0.1%)
All	All	0.26	0/4157	0.51	4/5717 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	594	VAL	CA-C-N	6.28	133.00	121.70
1	B	594	VAL	C-N-CA	6.28	133.00	121.70
1	A	594	VAL	CA-C-N	5.67	131.91	121.70
1	A	594	VAL	C-N-CA	5.67	131.91	121.70

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	2005	0	1867	17	0
1	B	2010	0	1872	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	164	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	158	0	0	1	0
All	All	4339	0	3739	31	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 (31) 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:608:THR:HB	1:B:611:LYS:HD3	1.63	0.80
1:B:579:HIS:CD2	1:B:581:ASP:H	2.08	0.71
1:A:522:GLY:HA2	1:A:552:GLU:HG2	1.73	0.71
1:A:579:HIS:CD2	1:A:581:ASP:H	2.15	0.64
1:A:568:ASN:ND2	1:B:573:ALA:H	2.03	0.56
1:A:573:ALA:H	1:B:568:ASN:ND2	2.02	0.56
1:A:559:TYR:OH	1:A:605:ASN:ND2	2.38	0.56
1:A:544:VAL:HG23	1:A:618:MET:HG2	1.90	0.52
1:A:433:ARG:NH1	1:A:666:ASP:OD1	2.40	0.51
1:B:544:VAL:HG23	1:B:618:MET:HG2	1.93	0.51
1:B:567:TRP:HA	1:B:592:ASN:O	2.11	0.49
1:A:567:TRP:HA	1:A:592:ASN:O	2.13	0.49
1:B:568:ASN:ND2	1:B:592:ASN:HD22	2.12	0.48
1:A:573:ALA:HA	1:A:586:LEU:O	2.15	0.47
1:A:647:ALA:N	1:A:648:PRO:HD2	2.30	0.47
1:B:441:ASP:HA	1:B:444:HIS:CE1	2.50	0.47
1:A:510:HIS:HD2	3:A:854:HOH:O	1.97	0.46
1:B:429:ALA:HB2	1:B:670:TYR:CE2	2.51	0.46
1:B:631:PHE:C	1:B:632:LYS:HG3	2.41	0.46
1:B:580:GLN:NE2	3:B:811:HOH:O	2.49	0.45
1:A:463:PRO:HA	1:A:464:PRO:HD3	1.84	0.45
1:A:529:GLN:OE1	1:A:634:GLN:HG2	2.17	0.44
1:B:529:GLN:OE1	1:B:634:GLN:HG2	2.17	0.44
1:A:441:ASP:HA	1:A:444:HIS:CE1	2.53	0.43
1:A:510:HIS:HB2	1:A:521:LEU:HD11	2.01	0.42
1:B:573:ALA:HA	1:B:586:LEU:O	2.20	0.42
1:B:463:PRO:HA	1:B:464:PRO:HD3	1.83	0.41
1:B:533:ARG:HG2	1:B:541:VAL:HG22	2.01	0.41
1:A:663:SER:OG	1:A:665:GLN:HB3	2.20	0.41
1:A:665:GLN:HB2	1:B:665:GLN:CD	2.46	0.41
1:B:579:HIS:CG	1:B:580:GLN:N	2.89	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	250/261 (96%)	245 (98%)	4 (2%)	1 (0%)	30	15
1	B	251/261 (96%)	244 (97%)	6 (2%)	1 (0%)	30	15
All	All	501/522 (96%)	489 (98%)	10 (2%)	2 (0%)	30	15

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	442	PRO
1	A	442	PRO

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	205/212 (97%)	201 (98%)	4 (2%)	48	29
1	B	205/212 (97%)	203 (99%)	2 (1%)	68	56
All	All	410/424 (97%)	404 (98%)	6 (2%)	57	41

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	460	HIS

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Mol	Chain	Res	Type
1	A	516	GLN
1	A	552	GLU
1	A	577	THR
1	B	599	THR
1	B	632	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	444	HIS
1	A	510	HIS
1	A	568	ASN
1	A	579	HIS
1	A	580	GLN
1	A	605	ASN
1	A	665	GLN
1	B	444	HIS
1	B	494	GLN
1	B	568	ASN
1	B	579	HIS
1	B	580	GLN
1	B	592	ASN
1	B	605	ASN
1	B	630	GLN
1	B	674	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	252/261 (96%)	0.51	21 (8%) 17 20	14, 23, 44, 83	0
1	B	253/261 (96%)	0.50	15 (5%) 28 32	17, 26, 50, 72	0
All	All	505/522 (96%)	0.50	36 (7%) 22 25	14, 24, 50, 83	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	678	ALA	4.9
1	A	443	LEU	4.7
1	A	461	THR	4.5
1	B	441	ASP	4.4
1	B	458	THR	4.2
1	A	458	THR	4.1
1	B	442	PRO	4.0
1	A	441	ASP	4.0
1	A	442	PRO	3.9
1	B	679	ALA	3.8
1	A	460	HIS	3.8
1	B	536	GLY	3.6
1	A	459	ASN	3.4
1	A	539	PHE	3.4
1	B	461	THR	3.3
1	A	535	THR	3.3
1	B	460	HIS	3.3
1	A	537	ALA	3.2
1	A	677	ALA	3.1
1	B	493	ALA	2.8
1	B	535	THR	2.8
1	A	457	HIS	2.7
1	A	493	ALA	2.6
1	B	537	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	678	ALA	2.5
1	B	459	ASN	2.3
1	A	427	GLY	2.3
1	A	536	GLY	2.3
1	A	666	ASP	2.3
1	B	457	HIS	2.3
1	B	579	HIS	2.2
1	A	533	ARG	2.2
1	A	440	ALA	2.1
1	A	444	HIS	2.1
1	A	646	ILE	2.1
1	B	440	ALA	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 oligosaccharides 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, 95th 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($\text{\AA}^2$)	Q<0.9
2	K	A	701	1/1	0.99	0.07	29,29,29,29	0
2	K	B	701	1/1	0.99	0.07	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.