



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:01 PM UTC

PDB ID : 7NXR / pdb_00007nrx
Title : Structure of the C-terminal domain of the pORF19 capsid protein from murid gammaherpesvirus 68 (MuHV-68)
Authors : Naniima, P.; Legrand, P.; Krey, T.
Deposited on : 2021-03-19
Resolution : 1.90 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

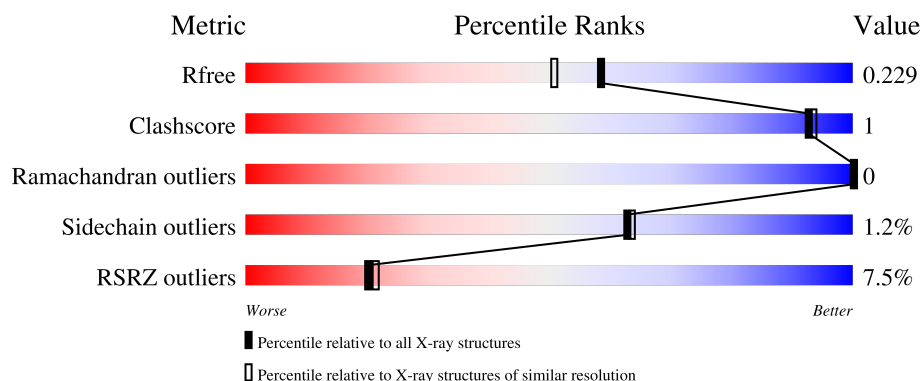
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	429	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3208 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 vertex component 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	385	Total	C	N	O	S	0	0	0
			3041	1960	511	558	12			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	MET	-	initiating methionine	UNP O41938
A	517	PRO	-	expression tag	UNP O41938
A	518	ALA	-	expression tag	UNP O41938
A	519	ALA	-	expression tag	UNP O41938
A	520	ALA	-	expression tag	UNP O41938
A	521	LEU	-	expression tag	UNP O41938
A	522	GLU	-	expression tag	UNP O41938
A	523	HIS	-	expression tag	UNP O41938
A	524	HIS	-	expression tag	UNP O41938
A	525	HIS	-	expression tag	UNP O41938
A	526	HIS	-	expression tag	UNP O41938
A	527	HIS	-	expression tag	UNP O41938
A	528	HIS	-	expression tag	UNP O41938
A	529	HIS	-	expression tag	UNP O41938
A	530	HIS	-	expression tag	UNP O41938
A	531	HIS	-	expression tag	UNP O41938

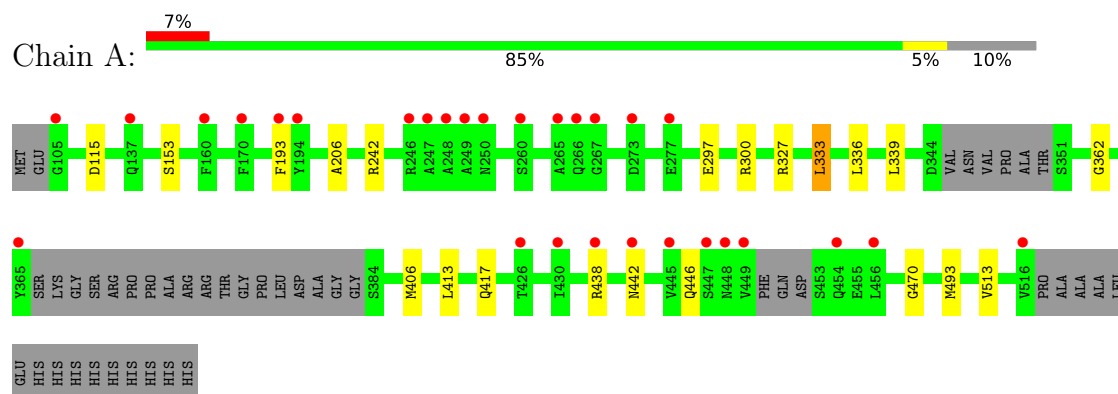
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	167	Total	O	0	0
			167	167		

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: Capsid vertex component 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	55.16Å 55.16Å 224.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.77 – 1.90 47.77 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.77-1.90) 100.0 (47.77-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 1.90Å)	Xtriage
Refinement program	BUSTER 2.10.4	Depositor
R, R_{free}	0.209 , 0.249 (Not available) , 0.229	Depositor DCC
R_{free} test set	1516 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	34.4	Xtriage
Anisotropy	0.489	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 31.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.079 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3208	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% 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

5.1 Standard geometry

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	0.68	1/3112 (0.0%)	1.02	5/4230 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	493	MET	SD-CE	-5.11	1.66	1.79

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	362	GLY	CA-C-N	5.18	127.94	120.38
1	A	362	GLY	C-N-CA	5.18	127.94	120.38
1	A	193	PHE	CA-CB-CG	5.00	118.81	113.80
1	A	327	ARG	CA-C-N	5.00	126.94	120.44
1	A	327	ARG	C-N-CA	5.00	126.94	120.44

There are no chirality outliers.

There are no planarity outliers.

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	3041	0	3046	9	0
2	A	167	0	0	2	0
All	All	3208	0	3046	9	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 1.

All (9) 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:A:339:LEU:HB2	1:A:413:LEU:HD11	1.86	0.56
1:A:206:ALA:HB1	1:A:333:LEU:HD13	1.89	0.53
1:A:336:LEU:HD13	1:A:406:MET:HE1	1.91	0.52
1:A:442:ASN:O	1:A:446:GLN:HG2	2.11	0.51
1:A:297:GLU:HG3	2:A:721:HOH:O	2.11	0.49
1:A:417:GLN:O	1:A:470:GLY:HA3	2.13	0.48
1:A:300:ARG:HG2	2:A:721:HOH:O	2.14	0.47
1:A:153:SER:HB2	1:A:438:ARG:CD	2.46	0.45
1:A:153:SER:HB2	1:A:438:ARG:NE	2.36	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	377/429 (88%)	372 (99%)	5 (1%)	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	337/371 (91%)	333 (99%)	4 (1%)	63	63

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	ASP
1	A	242	ARG
1	A	333	LEU
1	A	513	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	171	GLN
1	A	446	GLN

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 ⓘ

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	385/429 (89%)	0.61	29 (7%) 20 21	26, 38, 56, 67	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	265	ALA	3.7
1	A	193	PHE	3.4
1	A	194	TYR	3.2
1	A	449	VAL	3.2
1	A	438	ARG	3.2
1	A	260	SER	3.2
1	A	105	GLY	3.2
1	A	247	ALA	3.1
1	A	365	TYR	3.0
1	A	250	ASN	2.9
1	A	249	ALA	2.9
1	A	170	PHE	2.8
1	A	516	VAL	2.8
1	A	248	ALA	2.7
1	A	448	ASN	2.6
1	A	447	SER	2.5
1	A	137	GLN	2.4
1	A	273	ASP	2.4
1	A	266	GLN	2.3
1	A	445	VAL	2.3
1	A	442	ASN	2.2
1	A	160	PHE	2.1
1	A	454	GLN	2.1
1	A	430	ILE	2.1
1	A	246	ARG	2.1
1	A	277	GLU	2.1
1	A	267	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	456	LEU	2.0
1	A	426	THR	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.