



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2026 – 02:09 AM UTC

PDB ID : 9NIB / pdb_00009nib
Title : Black sea bass polyomavirus LTA NLS bound to improtin alpha 2
Authors : Hoad, M.; Forwood, J.K.; Alvisi, G.
Deposited on : 2025-02-25
Resolution : 2.20 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

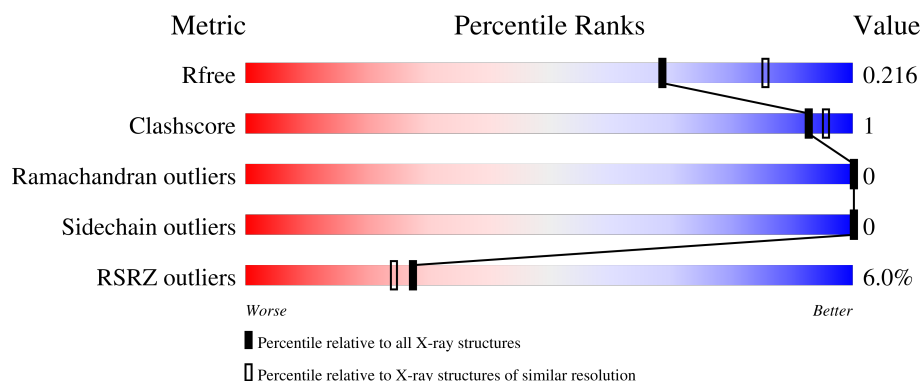
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	510	<div> <div>4%</div> <div>79%</div> <div>17%</div> </div>
2	B	24	<div> <div>17%</div> <div>46%</div> <div>50%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6874 atoms, of which 3444 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 Importin subunit alpha-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	424	Total	C	H	N	O	S	0	0	0
			6547	2061	3313	548	615	10			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	expression tag	UNP P52293
A	21	HIS	-	expression tag	UNP P52293
A	22	HIS	-	expression tag	UNP P52293
A	23	HIS	-	expression tag	UNP P52293
A	24	HIS	-	expression tag	UNP P52293
A	25	HIS	-	expression tag	UNP P52293
A	26	HIS	-	expression tag	UNP P52293
A	27	SER	-	expression tag	UNP P52293
A	28	SER	-	expression tag	UNP P52293
A	29	GLY	-	expression tag	UNP P52293
A	30	LEU	-	expression tag	UNP P52293
A	31	VAL	-	expression tag	UNP P52293
A	32	PRO	-	expression tag	UNP P52293
A	33	ARG	-	expression tag	UNP P52293
A	34	GLY	-	expression tag	UNP P52293
A	35	SER	-	expression tag	UNP P52293
A	36	GLY	-	expression tag	UNP P52293
A	37	MET	-	expression tag	UNP P52293
A	38	LEU	-	expression tag	UNP P52293
A	39	GLU	-	expression tag	UNP P52293
A	40	THR	-	expression tag	UNP P52293
A	41	ALA	-	expression tag	UNP P52293
A	42	ALA	-	expression tag	UNP P52293
A	43	ALA	-	expression tag	UNP P52293
A	44	LEU	-	expression tag	UNP P52293
A	45	PHE	-	expression tag	UNP P52293
A	46	GLU	-	expression tag	UNP P52293

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Chain	Residue	Modelled	Actual	Comment	Reference
A	47	ARG	-	expression tag	UNP P52293
A	48	ASN	-	expression tag	UNP P52293
A	49	HIS	-	expression tag	UNP P52293
A	50	MET	-	expression tag	UNP P52293
A	51	ASP	-	expression tag	UNP P52293
A	52	SER	-	expression tag	UNP P52293
A	53	PRO	-	expression tag	UNP P52293
A	54	ASP	-	expression tag	UNP P52293
A	55	LEU	-	expression tag	UNP P52293
A	56	GLY	-	expression tag	UNP P52293
A	57	THR	-	expression tag	UNP P52293
A	58	ASP	-	expression tag	UNP P52293
A	59	ASP	-	expression tag	UNP P52293
A	60	ASP	-	expression tag	UNP P52293
A	61	ASP	-	expression tag	UNP P52293
A	62	LEU	-	expression tag	UNP P52293
A	63	ALA	-	expression tag	UNP P52293
A	64	MET	-	expression tag	UNP P52293
A	65	ALA	-	expression tag	UNP P52293
A	66	ASP	-	expression tag	UNP P52293
A	67	ILE	-	expression tag	UNP P52293
A	68	GLY	-	expression tag	UNP P52293
A	69	SER	-	expression tag	UNP P52293

- Molecule 2 is a protein called Truncated large T antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	12	Total	C	H	N	O	S	0	0
			241	66	131	30	13	1		0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	660	ILE	TYR	conflict	UNP A0A0A1C723
B	661	ALA	ILE	conflict	UNP A0A0A1C723
B	662	GLU	SER	conflict	UNP A0A0A1C723
B	663	TYR	ILE	conflict	UNP A0A0A1C723
B	665	ARG	THR	conflict	UNP A0A0A1C723
B	667	HIS	TYR	conflict	UNP A0A0A1C723
B	668	ASN	ARG	conflict	UNP A0A0A1C723
B	671	SER	GLY	conflict	UNP A0A0A1C723
B	673	GLY	VAL	conflict	UNP A0A0A1C723

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Chain	Residue	Modelled	Actual	Comment	Reference
B	674	LEU	VAL	conflict	UNP A0A0A1C723
B	675	PRO	TRP	conflict	UNP A0A0A1C723
B	678	ARG	CYS	conflict	UNP A0A0A1C723
B	680	ARG	ALA	conflict	UNP A0A0A1C723
B	681	CYS	ILE	conflict	UNP A0A0A1C723
B	682	LEU	GLY	conflict	UNP A0A0A1C723
B	683	PHE	ALA	conflict	UNP A0A0A1C723

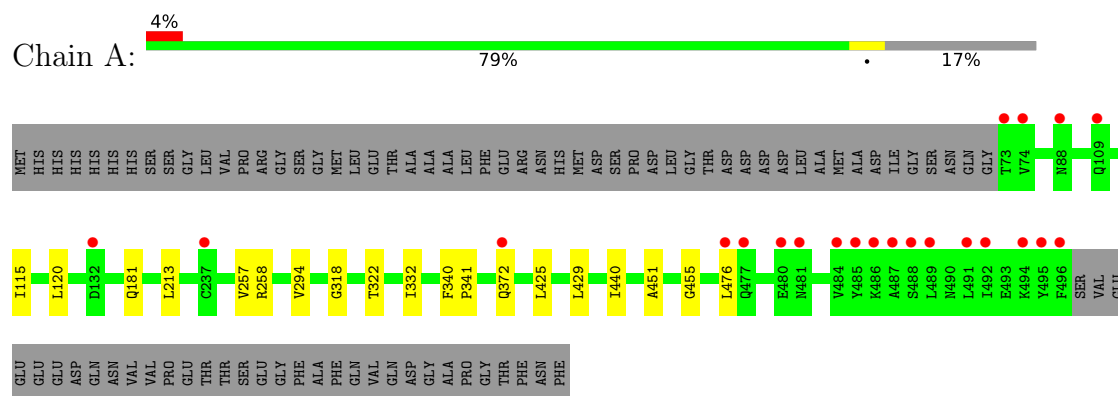
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	85	Total O 85 85	0	0
3	B	1	Total O 1 1	0	0

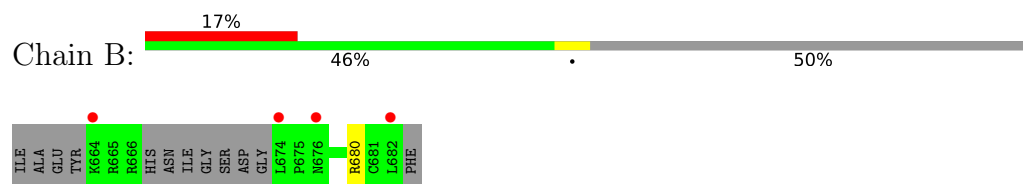
3 Residue-property plots [i](#)

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: Importin subunit alpha-1



- Molecule 2: Truncated large T antigen



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.80Å 89.19Å 99.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.20 – 2.20 29.20 – 2.20	Depositor EDS
% Data completeness (in resolution range)	93.9 (29.20-2.20) 93.9 (29.20-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.190 , 0.216 0.190 , 0.216	Depositor DCC
R_{free} test set	1708 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6874	wwPDB-VP
Average B, all atoms (Å ²)	59.0	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	0.11	0/3292	0.27	0/4487
2	B	0.10	0/109	0.29	0/139
All	All	0.11	0/3401	0.27	0/4626

There are no bond length outliers.

There are no bond angle outliers.

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	3234	3313	3312	10	0
2	B	110	131	129	1	0
3	A	85	0	0	0	0
3	B	1	0	0	0	0
All	All	3430	3444	3441	10	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 (10) 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:332:ILE:HG21	1:A:372:GLN:NE2	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:GLY:O	1:A:322:THR:HG23	2.07	0.55
1:A:451:ALA:O	1:A:455:GLY:N	2.46	0.49
1:A:213:LEU:O	1:A:258:ARG:NH2	2.46	0.47
1:A:340:PHE:N	1:A:341:PRO:CD	2.78	0.47
1:A:425:LEU:HG	1:A:440:ILE:HG23	1.98	0.46
1:A:115:ILE:HG23	1:A:120:LEU:HD12	1.98	0.45
1:A:429:LEU:HD22	1:A:476:LEU:HD11	1.99	0.45
1:A:181:GLN:OE1	2:B:680:ARG:NH1	2.44	0.44
1:A:257:VAL:HG22	1:A:294:VAL:CG1	2.50	0.42

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	422/510 (83%)	415 (98%)	7 (2%)	0	100	100
2	B	8/24 (33%)	8 (100%)	0	0	100	100
All	All	430/534 (80%)	423 (98%)	7 (2%)	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	356/426 (84%)	356 (100%)	0	100	100
2	B	12/21 (57%)	12 (100%)	0	100	100
All	All	368/447 (82%)	368 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no ligands in this entry.

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	424/510 (83%)	0.25	22 (5%) 33 29	38, 52, 100, 138	0
2	B	12/24 (50%)	1.39	4 (33%) 1 0	47, 70, 87, 93	0
All	All	436/534 (81%)	0.28	26 (5%) 27 24	38, 52, 100, 138	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	485	TYR	6.1
2	B	682	LEU	5.0
1	A	477	GLN	4.3
1	A	74	VAL	4.1
1	A	73	THR	3.0
1	A	489	LEU	2.9
1	A	88	ASN	2.9
1	A	484	VAL	2.8
1	A	491	LEU	2.7
2	B	664	LYS	2.6
1	A	480	GLU	2.5
1	A	487	ALA	2.5
1	A	109	GLN	2.5
1	A	496	PHE	2.4
1	A	237	CYS	2.4
1	A	481	ASN	2.4
1	A	492	ILE	2.3
1	A	476	LEU	2.3
1	A	132	ASP	2.3
1	A	488	SER	2.3
2	B	674	LEU	2.2
1	A	494	LYS	2.2
2	B	676	ASN	2.2
1	A	486	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	495	TYR	2.0
1	A	372	GLN	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.