



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 3, 2026 – 01:21 AM JST

PDB ID : 21AW / pdb_000021aw
Title : Crystal structure of Nicotiana benthamiana importin alpha-Cucumber mosaic virus (strain FNY) suppressor of silencing 2b NLS peptide complex
Authors : Liu, Y.; Chen, Z.
Deposited on : 2025-12-05
Resolution : 2.00 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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

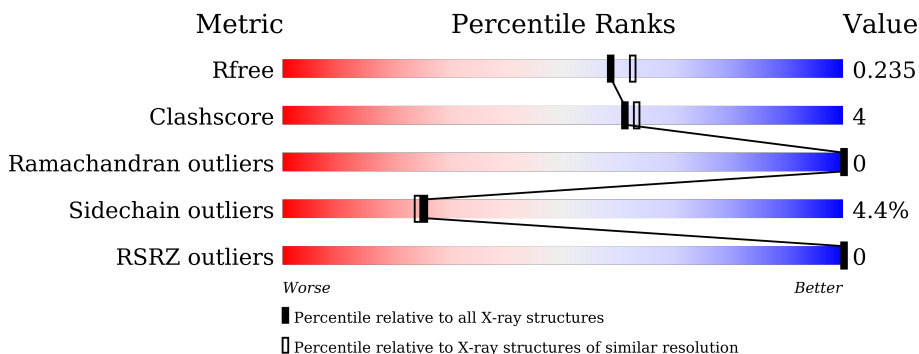
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	C	17	35% (green) 65% (grey)
1	D	17	35% (green) 65% (grey)
1	E	17	6% (red) 12% (orange) 12% (yellow) 71% (grey)
1	F	17	6% (red) 6% (orange) 88% (grey)
2	A	459	81% (green) 11% (yellow) 7% (orange) 7% (grey)
2	B	459	84% (green) 7% (yellow) 7% (orange) 7% (grey)

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7052 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 Suppressor of silencing 2b.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	C	6	Total	C	N	O	0	0	0
			54	32	15	7			
1	E	5	Total	C	N	O	0	0	0
			47	26	14	7			
1	D	6	Total	C	N	O	0	0	0
			54	32	15	7			
1	F	2	Total	C	N	O	0	0	0
			20	11	5	4			

- Molecule 2 is a protein called Importin subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	425	Total	C	N	O	S	0	0	0
			3269	2074	550	632	13			
2	B	425	Total	C	N	O	S	0	0	0
			3250	2064	547	626	13			

- Molecule 3 is water.

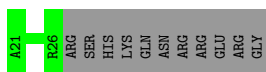
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	3	Total	O	0	0
			3	3		
3	E	1	Total	O	0	0
			1	1		
3	A	173	Total	O	0	0
			173	173		
3	D	7	Total	O	0	0
			7	7		
3	B	174	Total	O	0	0
			174	174		

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.

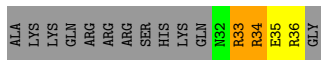
- Molecule 1: Suppressor of silencing 2b

Chain C: 



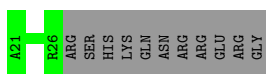
- Molecule 1: Suppressor of silencing 2b

Chain E: 



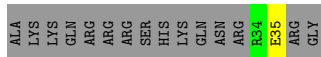
- Molecule 1: Suppressor of silencing 2b

Chain D: 




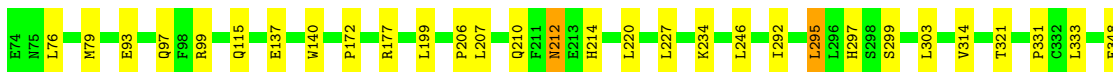
- Molecule 1: Suppressor of silencing 2b

Chain F: 



- Molecule 2: Importin subunit alpha

Chain A: 



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.93Å 77.53Å 98.58Å 90.00° 90.16° 90.00°	Depositor
Resolution (Å)	98.57 – 2.00 98.57 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (98.57-2.00) 98.9 (98.57-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.09 (at 2.00Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.187 , 0.223 0.201 , 0.235	Depositor DCC
R_{free} test set	3241 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtrriage
Anisotropy	0.044	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 30.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.419 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7052	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.38% 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	C	0.53	0/53	0.91	0/66
1	D	0.46	0/53	0.89	0/66
1	E	1.05	0/46	2.45	3/58 (5.2%)
1	F	0.81	0/19	1.14	0/23
2	A	1.12	6/3331 (0.2%)	1.13	3/4541 (0.1%)
2	B	1.06	7/3312 (0.2%)	1.08	4/4518 (0.1%)
All	All	1.08	13/6814 (0.2%)	1.11	10/9272 (0.1%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	235	PRO	N-CA	11.94	1.67	1.47
2	A	246	LEU	C-N	11.56	1.49	1.34
2	A	234	LYS	C-N	7.66	1.48	1.34
2	A	206	PRO	C-O	-6.80	1.15	1.24
2	B	234	LYS	C-O	-6.74	1.19	1.25
2	A	314	VAL	C-O	-6.36	1.16	1.24
2	B	172	PRO	C-O	-6.13	1.16	1.24
2	B	206	PRO	C-O	-5.67	1.17	1.24
2	B	205	ALA	C-O	-5.39	1.19	1.24
2	A	172	PRO	C-O	-5.36	1.17	1.24
2	A	331	PRO	C-O	-5.23	1.17	1.24
2	B	234	LYS	C-N	5.22	1.44	1.34
2	B	291	LEU	C-O	-5.14	1.18	1.24

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	33	ARG	CG-CD-NE	-9.83	90.38	112.00
2	A	246	LEU	CA-C-N	8.51	128.50	119.05
2	A	246	LEU	C-N-CA	8.51	128.50	119.05
2	B	235	PRO	CA-N-CD	-7.74	100.66	111.50
2	A	246	LEU	O-C-N	-6.61	114.59	120.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	35	GLU	CB-CA-C	6.39	121.20	109.71
2	B	248	THR	CB-CA-C	5.10	119.52	110.85
2	B	234	LYS	CA-C-N	5.08	139.20	127.00
2	B	234	LYS	C-N-CA	5.08	139.20	127.00
1	E	34	ARG	CB-CA-C	-5.01	99.62	111.65

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	C	54	0	64	0	0
1	D	54	0	64	0	0
1	E	47	0	46	4	0
1	F	20	0	18	0	0
2	A	3269	0	3238	33	0
2	B	3250	0	3209	21	0
3	A	173	0	0	2	0
3	B	174	0	0	1	0
3	C	3	0	0	0	0
3	D	7	0	0	0	0
3	E	1	0	0	2	0
All	All	7052	0	6639	56	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 (56) 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:235:PRO:N	2:B:235:PRO:CA	1.67	1.39
2:A:99:ARG:HD3	2:A:137:GLU:OE1	1.77	0.85
1:E:34:ARG:HD3	3:E:101:HOH:O	1.79	0.81
2:A:297:HIS:CE1	2:A:299:SER:HB3	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:235:PRO:N	2:B:235:PRO:C	2.47	0.73
2:A:292:ILE:HA	2:A:295:LEU:HD22	1.71	0.73
2:A:115:GLN:CD	3:A:773:HOH:O	2.34	0.70
2:A:477:GLN:HE21	2:A:489:VAL:HG12	1.58	0.67
2:A:303:LEU:C	2:A:303:LEU:HD13	2.20	0.65
2:A:212:ASN:HD22	2:A:214:HIS:H	1.47	0.63
2:B:101:LEU:HD11	2:B:109:PRO:HG3	1.80	0.63
2:B:403:ASN:C	2:B:403:ASN:HD22	2.10	0.60
2:A:403:ASN:HD22	2:A:403:ASN:C	2.11	0.59
2:A:99:ARG:HD2	2:A:140:TRP:CE3	2.38	0.58
2:A:297:HIS:HE1	2:A:299:SER:HB3	1.73	0.53
2:B:417:LYS:HB3	2:B:418:PRO:HD3	1.91	0.53
2:B:389:LYS:HG2	2:B:430:ILE:HG13	1.92	0.52
2:A:479:HIS:HD2	2:A:481:ASN:HB3	1.74	0.52
2:A:374:ALA:HB3	2:A:375:PRO:HD3	1.91	0.51
2:B:99:ARG:HD2	2:B:140:TRP:CE3	2.45	0.50
2:A:348:GLU:HG3	3:A:719:HOH:O	2.10	0.50
2:A:497:LEU:HD12	2:A:497:LEU:N	2.27	0.50
2:B:343:LYS:HE3	2:B:344:SER:HA	1.93	0.50
1:E:34:ARG:H	2:A:355:ASN:HD21	1.59	0.49
2:A:454:THR:OG1	2:A:459:VAL:HG23	2.12	0.49
2:B:297:HIS:CE1	2:B:299:SER:HB3	2.48	0.48
2:A:439:GLU:OE1	2:A:487:LYS:HE3	2.14	0.48
2:B:462:GLN:CD	3:B:621:HOH:O	2.57	0.47
2:B:385:PHE:CE2	2:B:389:LYS:HD2	2.50	0.47
2:A:297:HIS:CE1	2:A:299:SER:CB	2.94	0.47
1:E:34:ARG:CD	3:E:101:HOH:O	2.52	0.46
2:B:297:HIS:ND1	2:B:299:SER:HB3	2.31	0.46
2:A:368:ILE:HG23	2:A:409:PHE:CE2	2.50	0.46
2:A:487:LYS:O	2:A:491:ILE:HD12	2.15	0.46
2:B:343:LYS:HE3	2:B:344:SER:CA	2.45	0.46
2:B:347:LYS:HE2	2:B:386:GLU:HB3	1.97	0.45
2:B:177:ARG:HE	2:B:210:GLN:HE22	1.63	0.45
2:B:374:ALA:HB3	2:B:375:PRO:HD3	1.98	0.45
2:A:297:HIS:ND1	2:A:299:SER:N	2.64	0.44
2:A:303:LEU:C	2:A:303:LEU:CD1	2.89	0.44
2:B:354:SER:HA	2:B:394:ALA:HA	1.99	0.44
2:B:347:LYS:CE	2:B:386:GLU:HB3	2.47	0.44
2:A:479:HIS:CD2	2:A:481:ASN:HB3	2.53	0.43
2:B:76:LEU:HB3	2:B:77:PRO:HD3	2.00	0.43
2:A:411:VAL:HG11	2:A:460:TYR:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:99:ARG:CD	2:A:137:GLU:OE1	2.56	0.43
2:A:297:HIS:HE1	2:A:299:SER:CB	2.32	0.42
2:B:148:GLY:HA3	2:B:152:ASN:HD22	1.85	0.42
2:A:76:LEU:HA	2:A:79:MET:HE2	2.02	0.42
1:E:33:ARG:NH1	2:A:321:THR:OG1	2.50	0.41
2:A:442:LEU:HD13	2:A:464:ILE:HD12	2.03	0.41
2:A:303:LEU:HD13	2:A:303:LEU:O	2.20	0.41
2:B:490:LYS:HD3	2:B:490:LYS:HA	1.83	0.41
2:A:297:HIS:CE1	2:A:299:SER:H	2.39	0.40
2:A:177:ARG:HE	2:A:210:GLN:HE22	1.68	0.40
2:A:442:LEU:HD12	2:A:442:LEU:HA	1.94	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	C	4/17 (24%)	4 (100%)	0	0	100	100
1	D	4/17 (24%)	4 (100%)	0	0	100	100
1	E	3/17 (18%)	3 (100%)	0	0	100	100
2	A	423/459 (92%)	418 (99%)	5 (1%)	0	100	100
2	B	423/459 (92%)	418 (99%)	5 (1%)	0	100	100
All	All	857/969 (88%)	847 (99%)	10 (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	C	5/15 (33%)	5 (100%)	0	100	100
1	D	5/15 (33%)	5 (100%)	0	100	100
1	E	4/15 (27%)	3 (75%)	1 (25%)	0	0
1	F	2/15 (13%)	1 (50%)	1 (50%)	0	0
2	A	357/393 (91%)	339 (95%)	18 (5%)	22	20
2	B	352/393 (90%)	340 (97%)	12 (3%)	32	33
All	All	725/846 (86%)	693 (96%)	32 (4%)	25	24

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	36	ARG
2	A	93	GLU
2	A	97	GLN
2	A	199	LEU
2	A	207	LEU
2	A	212	ASN
2	A	220	LEU
2	A	227	LEU
2	A	295	LEU
2	A	333	LEU
2	A	403	ASN
2	A	410	LEU
2	A	425	CYS
2	A	431	VAL
2	A	442	LEU
2	A	476	LEU
2	A	482	THR
2	A	487	LYS
2	A	497	LEU
1	F	35	GLU
2	B	99	ARG
2	B	227	LEU
2	B	234	LYS
2	B	248	THR
2	B	259	GLU
2	B	343	LYS

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Mol	Chain	Res	Type
2	B	403	ASN
2	B	404	HIS
2	B	410	LEU
2	B	432	THR
2	B	490	LYS
2	B	497	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	152	ASN
2	A	179	GLN
2	A	201	HIS
2	A	210	GLN
2	A	212	ASN
2	A	236	GLN
2	A	256	ASN
2	A	327	HIS
2	A	340	ASN
2	A	355	ASN
2	A	362	ASN
2	A	403	ASN
2	A	477	GLN
2	A	479	HIS
2	B	152	ASN
2	B	179	GLN
2	B	210	GLN
2	B	236	GLN
2	B	254	HIS
2	B	340	ASN
2	B	355	ASN
2	B	381	GLN
2	B	403	ASN

5.3.3 RNA

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	C	6/17 (35%)	-0.71	0 100 100	40, 43, 49, 59	0
1	D	6/17 (35%)	-0.63	0 100 100	42, 43, 44, 58	0
1	E	5/17 (29%)	-0.35	0 100 100	55, 56, 61, 68	0
1	F	2/17 (11%)	-0.69	0 100 100	60, 60, 60, 70	0
2	A	425/459 (92%)	-1.04	0 100 100	23, 31, 52, 93	0
2	B	425/459 (92%)	-0.91	0 100 100	24, 33, 54, 92	0
All	All	869/986 (88%)	-0.97	0 100 100	23, 32, 56, 93	0

There are no RSRZ outliers to report.

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.