



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:25 AM UTC

PDB ID : 1NNA / pdb_00001nna
Title : THREE-DIMENSIONAL STRUCTURE OF INFLUENZA A N9 NEURAMINIDASE AND ITS COMPLEX WITH THE INHIBITOR 2-DEOXY 2,3-DEHYDRO-N-ACETYL NEURAMINIC ACID
Authors : Bossart-Whitaker, P.; Carson, M.; Babu, Y.S.; Smith, C.D.; Laver, W.G.; Air, G.M.
Deposited on : 1993-03-08
Resolution : 2.50 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

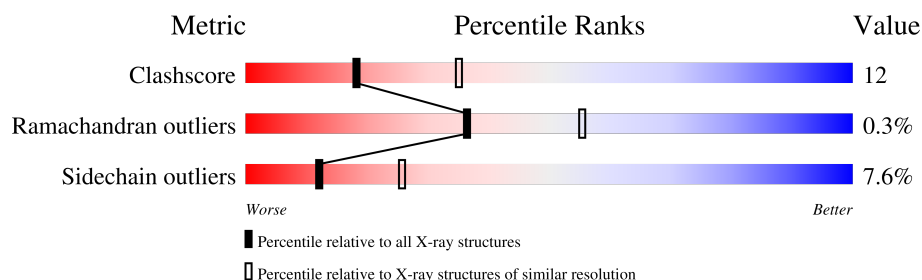
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	387	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3766 atoms, of which 709 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 NEURAMINIDASE.

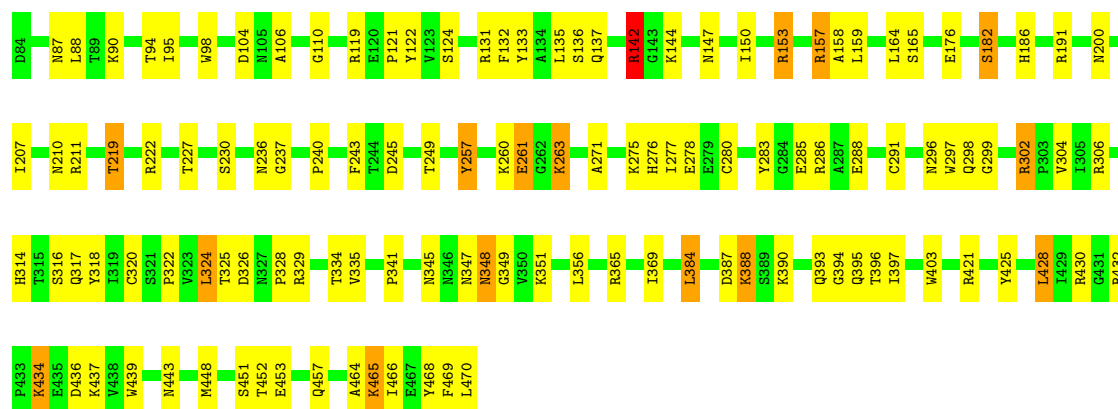
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	387	Total	C	H	N	O	S	0	0	0
			3765	1908	709	534	591	23			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

Note EDS was not executed.

Chain A: 68% 27% .



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 4 3 2	Depositor
Cell constants a, b, c, α , β , γ	183.78Å 183.78Å 183.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.193 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3766	wwPDB-VP
Average B, all atoms (Å ²)	10.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.67	1/3139 (0.0%)	0.88	3/4276 (0.1%)

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
1	A	0	11

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	296	ASN	CG-OD1	5.26	1.33	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	299	GLY	N-CA-C	7.12	120.99	111.03
1	A	436	ASP	N-CA-C	6.67	119.55	111.82
1	A	182	SER	N-CA-C	5.32	116.36	108.60

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	ARG	Sidechain
1	A	142	ARG	Sidechain
1	A	153	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	222	ARG	Sidechain
1	A	243	PHE	Sidechain
1	A	257	TYR	Sidechain
1	A	283	TYR	Sidechain
1	A	302	ARG	Sidechain
1	A	421	ARG	Sidechain
1	A	425	TYR	Sidechain
1	A	468	TYR	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	3056	709	2883	72	0
2	A	1	0	0	0	0
All	All	3057	709	2883	72	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 12.

All (72) 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:397:ILE:HD12	1:A:448:MET:HE2	1.58	0.83
1:A:403:TRP:CH2	1:A:434:LYS:HG2	2.15	0.82
1:A:237:GLY:HA3	1:A:260:LYS:HE2	1.67	0.75
1:A:153:ARG:HH11	1:A:200:ASN:HD21	1.37	0.73
1:A:277:ILE:O	1:A:278:GLU:HG2	1.97	0.65
1:A:119:ARG:HA	1:A:443:ASN:ND2	2.13	0.64
1:A:396:THR:H	1:A:457:GLN:HE22	1.45	0.64
1:A:395:GLN:HG3	1:A:457:GLN:HE21	1.62	0.64
1:A:261:GLU:CB	1:A:263:LYS:HE3	2.30	0.61
1:A:230:SER:HB3	1:A:351:LYS:HE2	1.82	0.61
1:A:164:LEU:O	1:A:165:SER:HB2	2.02	0.59
1:A:334:THR:O	1:A:388:LYS:HE3	2.03	0.58
1:A:286:ARG:HH11	1:A:286:ARG:HG2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:GLU:HB3	1:A:263:LYS:HE3	1.87	0.56
1:A:356:LEU:HD13	1:A:384:LEU:HG	1.89	0.55
1:A:348:ASN:HD22	1:A:349:GLY:H	1.54	0.54
1:A:240:PRO:HA	1:A:257:TYR:O	2.08	0.54
1:A:320:CYS:SG	1:A:384:LEU:O	2.66	0.54
1:A:98:TRP:HB3	1:A:448:MET:HE3	1.90	0.52
1:A:147:ASN:ND2	1:A:439:TRP:HB3	2.24	0.52
1:A:271:ALA:H	1:A:314:HIS:HE1	1.58	0.51
1:A:87:ASN:OD1	1:A:236:ASN:HB2	2.09	0.51
1:A:395:GLN:HG3	1:A:457:GLN:NE2	2.26	0.51
1:A:335:VAL:HG22	1:A:388:LYS:HG2	1.92	0.51
1:A:261:GLU:HB2	1:A:263:LYS:HE3	1.92	0.50
1:A:249:THR:HG22	1:A:347:ASN:HB3	1.93	0.50
1:A:317:GLN:HG2	1:A:318:TYR:H	1.76	0.50
1:A:95:ILE:HG21	1:A:98:TRP:CZ2	2.47	0.50
1:A:397:ILE:CD1	1:A:448:MET:HE2	2.36	0.49
1:A:142:ARG:NH2	1:A:469:PHE:HA	2.27	0.49
1:A:430:ARG:NH2	1:A:464:ALA:O	2.45	0.49
1:A:104:ASP:HB3	1:A:132:PHE:HE2	1.78	0.49
1:A:276:HIS:HB2	1:A:297:TRP:HE1	1.78	0.48
1:A:348:ASN:ND2	1:A:349:GLY:H	2.12	0.48
1:A:276:HIS:HB2	1:A:297:TRP:NE1	2.29	0.47
1:A:159:LEU:HD23	1:A:176:GLU:HB2	1.95	0.47
1:A:98:TRP:CB	1:A:448:MET:HE3	2.43	0.47
1:A:159:LEU:HD13	1:A:182:SER:OG	2.15	0.47
1:A:280:CYS:HB3	1:A:291:CYS:HB3	1.96	0.47
1:A:393:GLN:HG2	1:A:394:GLY:N	2.29	0.47
1:A:302:ARG:NH1	1:A:325:THR:O	2.48	0.47
1:A:207:ILE:HD12	1:A:207:ILE:N	2.30	0.46
1:A:124:SER:HB3	1:A:133:TYR:CE1	2.51	0.46
1:A:328:PRO:HG2	1:A:345:ASN:ND2	2.30	0.46
1:A:451:SER:OG	1:A:453:GLU:HB2	2.16	0.45
1:A:121:PRO:HA	1:A:133:TYR:O	2.15	0.45
1:A:186:HIS:HA	1:A:191:ARG:HA	1.98	0.45
1:A:286:ARG:HH11	1:A:286:ARG:CG	2.30	0.45
1:A:430:ARG:NH1	1:A:466:ILE:HG12	2.31	0.45
1:A:322:PRO:O	1:A:324:LEU:HD13	2.17	0.45
1:A:403:TRP:CZ3	1:A:434:LYS:HG2	2.52	0.45
1:A:135:LEU:HA	1:A:158:ALA:O	2.17	0.44
1:A:304:VAL:O	1:A:316:SER:HA	2.17	0.44
1:A:393:GLN:HG2	1:A:394:GLY:H	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:HIS:HB2	1:A:297:TRP:CD1	2.54	0.43
1:A:317:GLN:HG2	1:A:318:TYR:N	2.34	0.43
1:A:465:LYS:HE3	1:A:465:LYS:HB3	1.93	0.43
1:A:219:THR:HG22	1:A:245:ASP:OD2	2.20	0.42
1:A:430:ARG:HH12	1:A:466:ILE:HG12	1.84	0.42
1:A:428:LEU:O	1:A:443:ASN:HA	2.20	0.42
1:A:122:TYR:CG	1:A:230:SER:HA	2.55	0.42
1:A:322:PRO:HG2	1:A:390:LYS:HE2	2.01	0.41
1:A:329:ARG:O	1:A:369:ILE:HD12	2.20	0.41
1:A:94:THR:O	1:A:452:THR:HG22	2.19	0.41
1:A:275:LYS:HD3	1:A:341:PRO:HD3	2.02	0.41
1:A:277:ILE:C	1:A:278:GLU:HG2	2.45	0.41
1:A:106:ALA:O	1:A:110:GLY:N	2.53	0.41
1:A:271:ALA:H	1:A:314:HIS:CE1	2.36	0.41
1:A:317:GLN:NE2	1:A:318:TYR:O	2.54	0.41
1:A:326:ASP:O	1:A:329:ARG:HD3	2.21	0.40
1:A:136:SER:O	1:A:157:ARG:CD	2.70	0.40
1:A:437:LYS:HE3	1:A:470:LEU:HD21	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	385/387 (100%)	359 (93%)	25 (6%)	1 (0%)	36 55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	LEU

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	340/340 (100%)	314 (92%)	26 (8%)	12	26

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	90	LYS
1	A	137	GLN
1	A	142	ARG
1	A	144	LYS
1	A	150	ILE
1	A	157	ARG
1	A	210	ASN
1	A	211	ARG
1	A	219	THR
1	A	227	THR
1	A	261	GLU
1	A	263	LYS
1	A	285	GLU
1	A	288	GLU
1	A	298	GLN
1	A	306	ARG
1	A	324	LEU
1	A	348	ASN
1	A	365	ARG
1	A	384	LEU
1	A	387	ASP
1	A	388	LYS
1	A	428	LEU
1	A	432	ARG
1	A	434	LYS
1	A	465	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	99	HIS
1	A	105	ASN
1	A	137	GLN
1	A	147	ASN
1	A	172	ASN
1	A	200	ASN
1	A	210	ASN
1	A	228	GLN
1	A	314	HIS
1	A	317	GLN
1	A	345	ASN
1	A	348	ASN
1	A	393	GLN
1	A	443	ASN
1	A	457	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](#)

Of 1 ligands modelled in this entry, 1 is 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 [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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.