



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:52 PM UTC

PDB ID : 2G96 / pdb_00002g96
Title : Crystal Structure of Visfatin/Pre-B Cell Colony Enhancing Factor 1/Nicotinamide Phosphoribosyltransferase In Complex with Nicotinamide Mononucleotide
Authors : Eom, S.H.; Kim, M.-K.
Deposited on : 2006-03-05
Resolution : 2.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

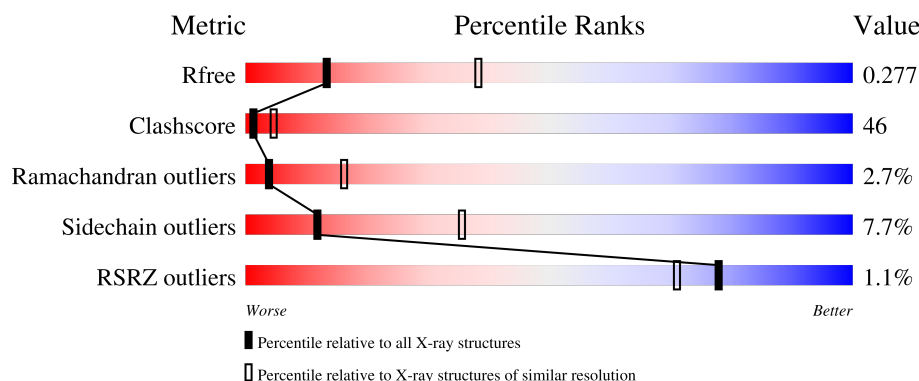
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	491	
1	B	491	

2 Entry composition [i](#)

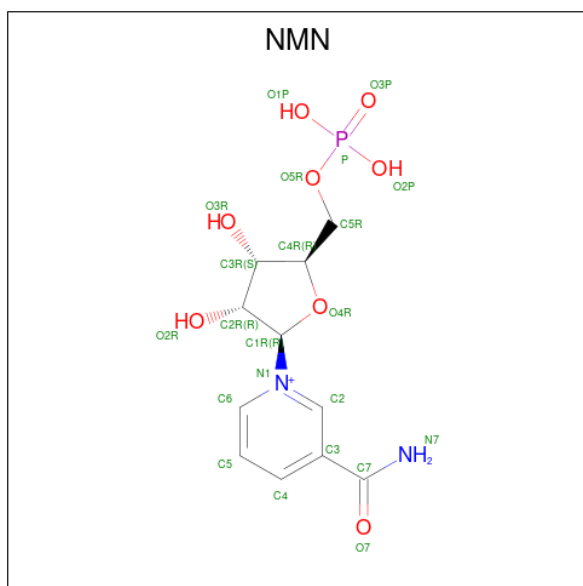
There are 3 unique types of molecules in this entry. The entry contains 7576 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Nicotinamide phosphoribosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	463	Total	C	N	O	S	0	0	0
			3700	2374	616	704	6			
1	B	463	Total	C	N	O	S	0	0	0
			3700	2374	616	704	6			

- Molecule 2 is BETA-NICOTINAMIDE RIBOSE MONOPHOSPHATE (CCD ID: NMN) (formula: $C_{11}H_{16}N_2O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	11	2	8	1		
2	B	1	Total	C	N	O	P	0	0
			22	11	2	8	1		

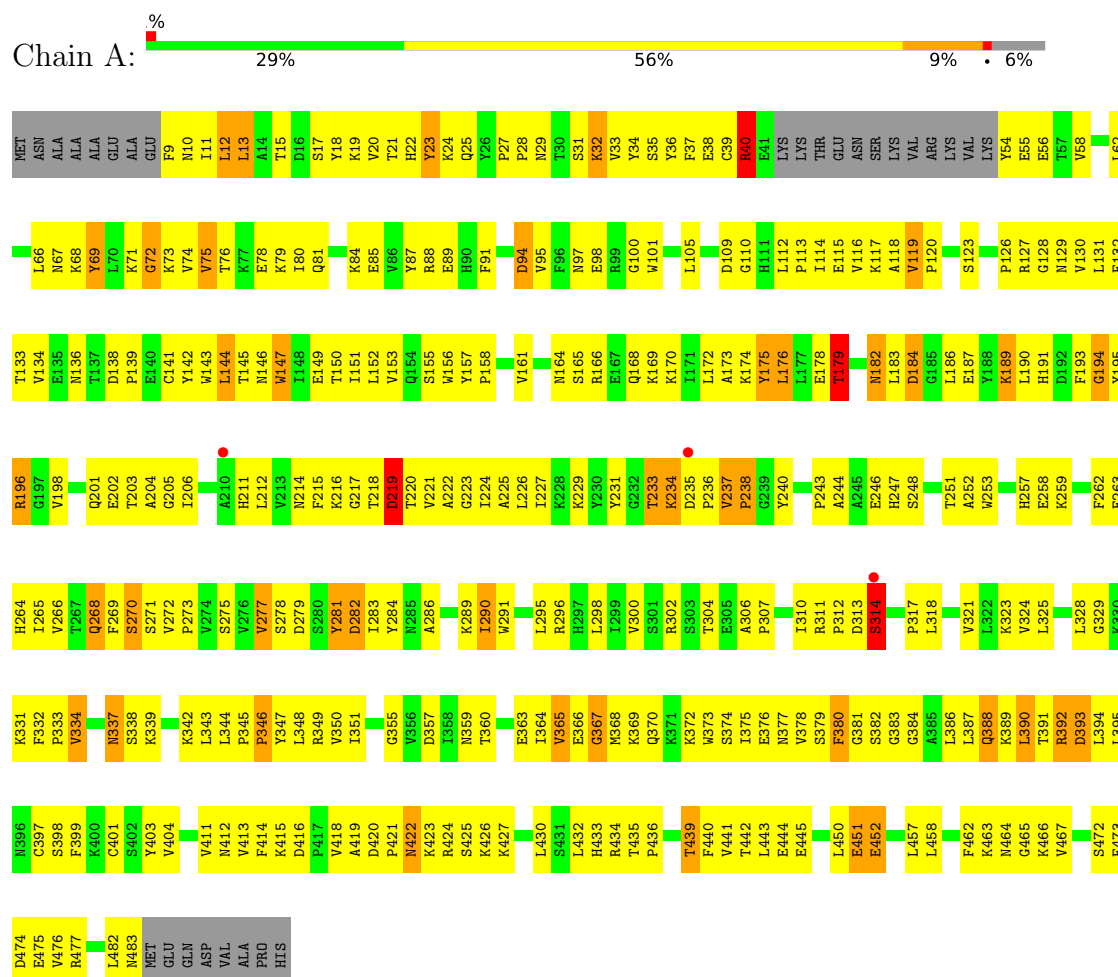
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	82	Total 82	O 82	0	0
3	B	50	Total 50	O 50	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: Nicotinamide phosphoribosyltransferase



GLN ASP VAL ALA PRO HIS	V411	L344	S275	G194	P126	Q63
	M412	P345	V276	R127	R127	M67
	F413	P346	V277	Y195	V130	K68
	F414	Y347	S278		L131	Y69
	K415	L348	D279	V198	F132	L70
	D416	R349	S280	S193	T133	K71
	P417	V350	Y281	S200	V134	G72
	V418	I351	D282	Q201	E135	K73
	A419	G355	I283	E202	N136	V74
	D420	V356	Y284	T203	T137	V75
	P421	D357	N285	A204	D138	T76
	N422	I358	G286	G205	P139	K77
	K423	N359	C287	I206	E140	
	R424	T360	E288		C141	E78
	S425	K361	K289	H211	Y142	K79
	K426	L361	I290		L143	I80
	K427	Q362	V291	N214	W143	Q81
	G428	E363	G292	F215	L144	E82
	R429	I364	E293	K216	T145	A83
	L430	V365	D294		N146	K84
	S431	E366	I295	D219	W147	E85
	L432	G367	R296	T220	I148	V86
	H433	N368	H297	V221	E149	Y87
		K369	L298		T150	R88
	T439	Q370	L299	I224	I151	E89
	F440	K371			L152	H90
	V441	K372	R302	Y230	V153	F91
	T442	W373	S303	Y231	Q154	Q92
	L443	K374	T304	G232	S155	D93
	E444	I375	E305	T233	W156	D94
	E445	E376	A306	K234	Y157	V95
	G446	N377	P307	D235	P158	F96
	K447	V378	L308	P236		N97
	G448	S379	I309	V237	V161	E98
	D449		R310	P238		R99
	L450	G384	R311	G239	N164	G100
	E451	A385	P312	Y240	S165	W101
	E452	L386		S241		N102
		L387	L318	V242	Q168	Y103
	L459	Q388	D319	P243	K169	I104
		K389	T320		L172	L105
	V461	L390		E246		E106
	F462	T391	K323		K107	K107
	K463	R392	V324	T249	Y108	Y108
		D393	L325	L250	L176	D109
	K466	L394	D326	T251	L177	G110
	V467	L395	I327	A252	E178	H111
		N396	L328	W253	T179	L112
	S472	C397	G329		S180	P113
	F473		K330	H257	G181	I114
	D474	K400	K331		N182	E115
	E475	C401	F332	F262	L183	V116
	V476	S402	P333	E263	D184	
	R477	Y403	V334	H264	G185	V119
		V404		I265	L186	P120
		V405	K337		E187	E121
	T406	T406		Q268	Y188	G122
	L482		Y341		K189	S123
	M483	L409	K342	P273	L190	V124
	GLU	G410	L343	V274	H191	I125

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.89Å 106.08Å 117.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90 20.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.90) 81.8 (20.00-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.84 (at 2.90Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.229 , 0.278 0.229 , 0.277	Depositor DCC
R_{free} test set	2030 reflections (9.81%)	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.808	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7576	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 58.91 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.9071e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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

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	0.51	0/3788	1.00	16/5136 (0.3%)
1	B	0.48	0/3788	0.97	16/5136 (0.3%)
All	All	0.49	0/7576	0.99	32/10272 (0.3%)

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	219	ASP	N-CA-C	-7.74	104.32	114.31
1	A	69	TYR	N-CA-C	7.47	123.30	114.04
1	A	378	VAL	N-CA-C	6.83	117.88	107.77
1	B	288	GLU	N-CA-C	6.66	118.62	111.36
1	B	180	SER	N-CA-C	-5.94	107.02	114.56

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	3700	0	3665	380	0
1	B	3700	0	3665	351	0
2	A	22	0	14	5	0
2	B	22	0	14	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	82	0	0	8	0
3	B	50	0	0	2	0
All	All	7576	0	7358	688	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 46.

The worst 5 of 688 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:318:LEU:HD23	1:B:364:ILE:HA	1.22	1.15
1:A:435:THR:HG22	1:A:441:VAL:HG23	1.24	1.09
1:B:400:LYS:HE2	1:B:401:CYS:H	1.08	1.08
1:A:318:LEU:HD23	1:A:364:ILE:HA	1.35	1.06
1:B:365:VAL:HG22	1:B:375:ILE:HD12	1.38	1.04

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	459/491 (94%)	387 (84%)	60 (13%)	12 (3%)	4	17
1	B	459/491 (94%)	399 (87%)	47 (10%)	13 (3%)	4	15
All	All	918/982 (94%)	786 (86%)	107 (12%)	25 (3%)	4	16

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	282	ASP
1	A	346	PRO

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Mol	Chain	Res	Type
1	B	282	ASP
1	B	394	LEU
1	B	419	ALA

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	408/431 (95%)	377 (92%)	31 (8%)	12	36
1	B	408/431 (95%)	376 (92%)	32 (8%)	11	35
All	All	816/862 (95%)	753 (92%)	63 (8%)	12	35

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	393	ASP
1	B	386	LEU
1	B	74	VAL
1	B	366	GLU
1	B	409	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	370	GLN
1	B	396	ASN
1	A	370	GLN
1	A	337	ASN
1	B	459	HIS

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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NMN	B	1002	-	21,23,23	3.22	10 (47%)	27,34,34	1.42	6 (22%)
2	NMN	A	1001	-	21,23,23	2.87	9 (42%)	27,34,34	1.38	7 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NMN	B	1002	-	-	0/14/30/30	0/2/2/2
2	NMN	A	1001	-	-	0/14/30/30	0/2/2/2

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1002	NMN	C2-N1	7.92	1.43	1.35
2	B	1002	NMN	C4-C3	7.10	1.50	1.39
2	A	1001	NMN	C4-C3	6.99	1.50	1.39
2	A	1001	NMN	C2-N1	6.19	1.41	1.35
2	B	1002	NMN	C6-N1	5.28	1.47	1.35

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1002	NMN	C3-C7-N7	3.13	121.59	117.74
2	B	1002	NMN	O7-C7-C3	-2.97	115.97	119.60
2	A	1001	NMN	O7-C7-C3	-2.71	116.29	119.60
2	A	1001	NMN	C3-C7-N7	2.68	121.04	117.74
2	B	1002	NMN	O2P-P-O5R	2.56	113.34	106.67

There are no chirality outliers.

There are no torsion outliers.

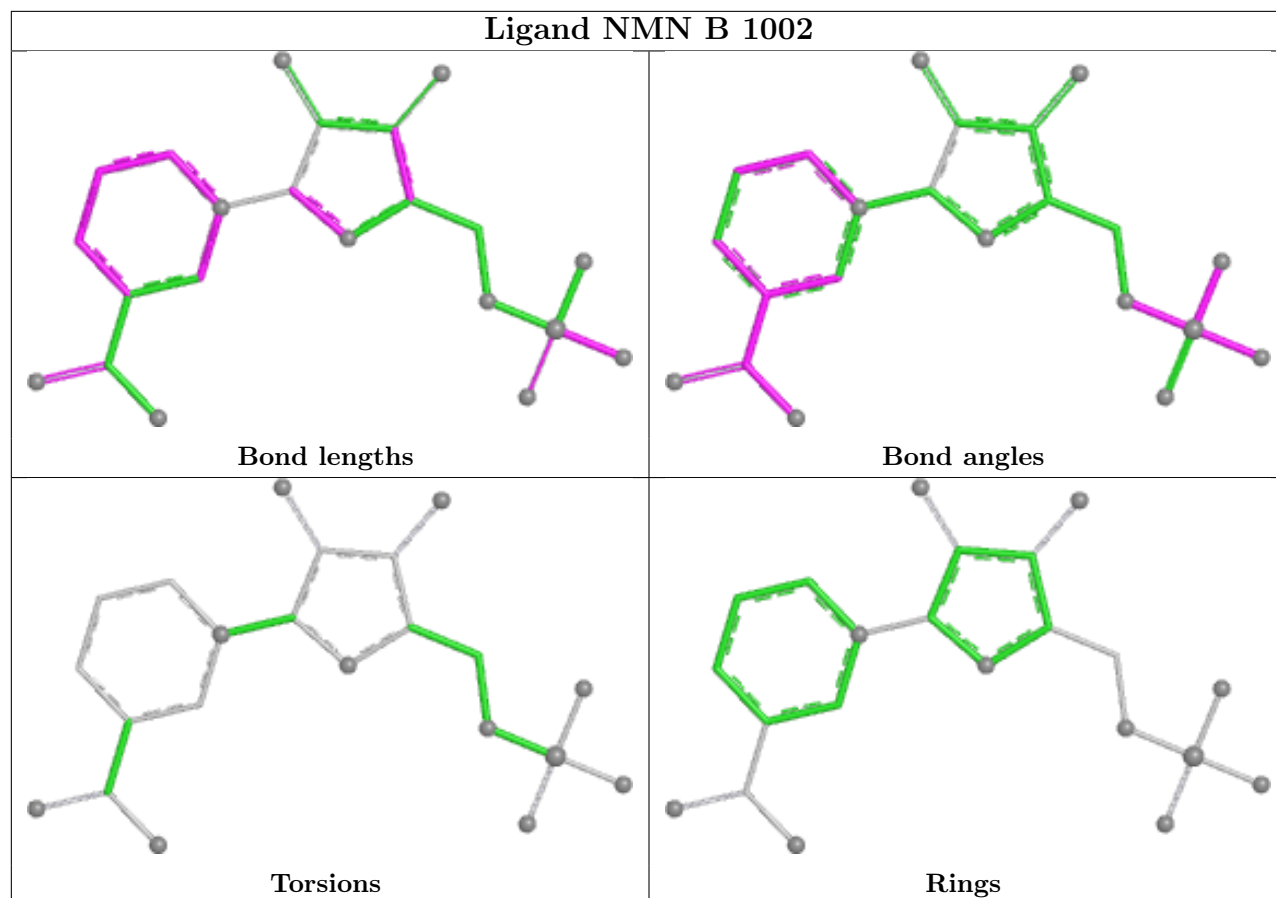
There are no ring outliers.

2 monomers are involved in 8 short contacts:

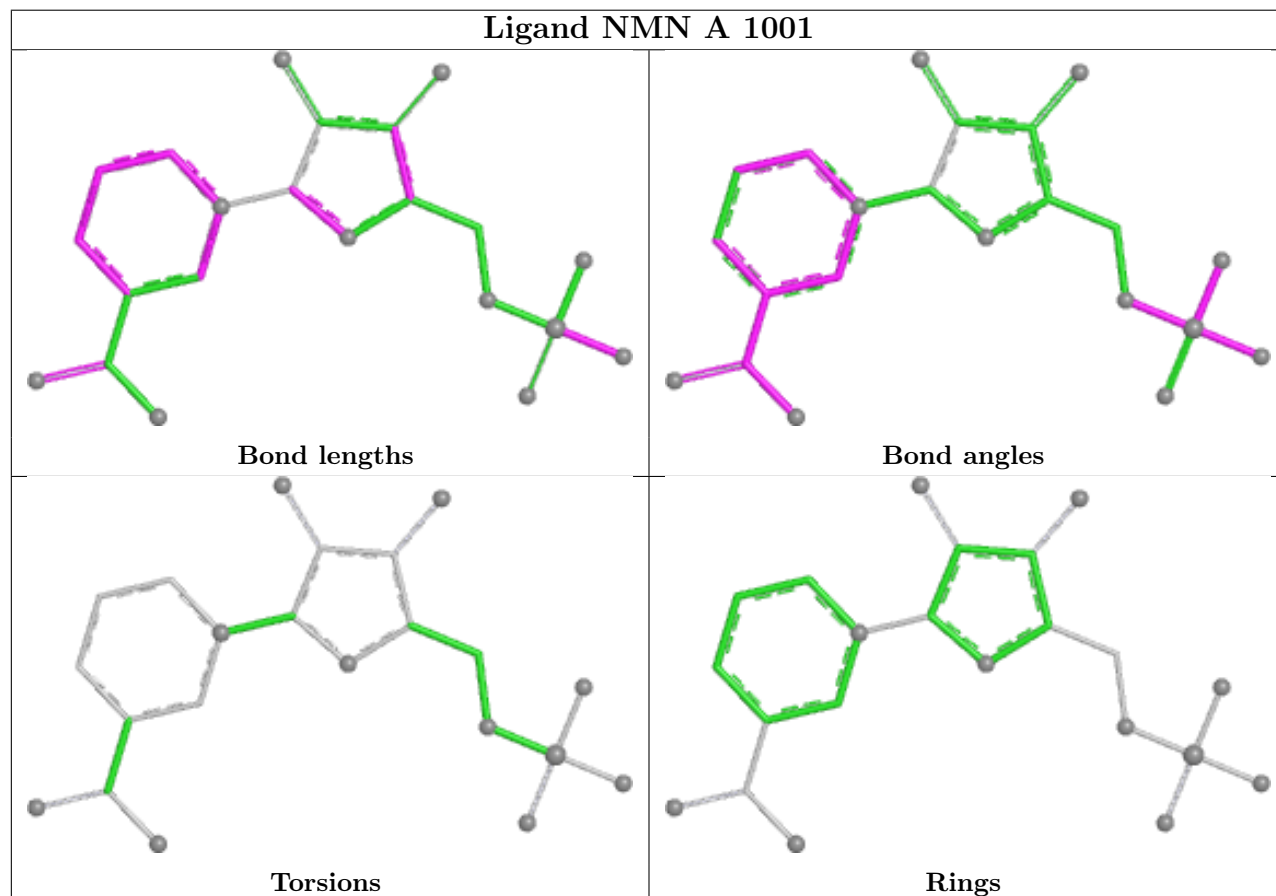
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1002	NMN	3	0
2	A	1001	NMN	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand NMN B 1002



Ligand NMN A 1001



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	A	463/491 (94%)	0.01	3 (0%) 85 81	10, 27, 45, 58	0
1	B	463/491 (94%)	-0.03	7 (1%) 72 64	11, 27, 46, 67	0
All	All	926/982 (94%)	-0.01	10 (1%) 78 71	10, 27, 45, 67	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	237	VAL	5.1
1	B	236	PRO	3.4
1	A	314	SER	2.9
1	B	238	PRO	2.8
1	B	240	TYR	2.7

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](#)

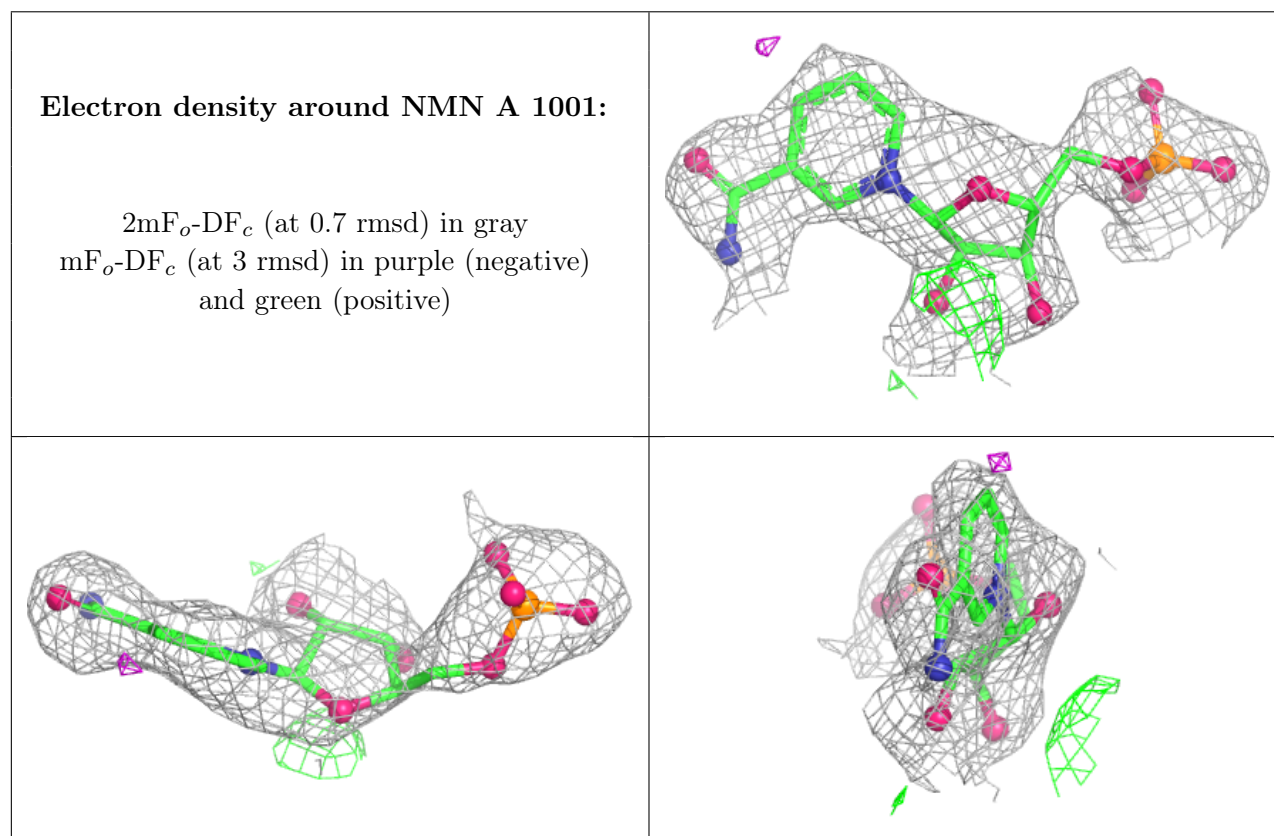
There are no oligosaccharides in this entry.

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.

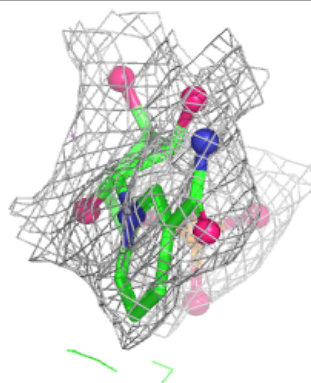
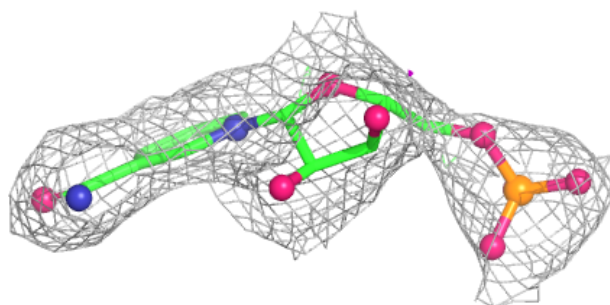
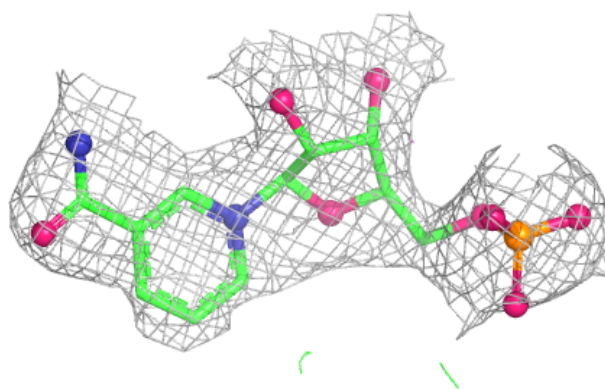
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NMN	A	1001	22/22	0.94	0.09	20,29,31,32	0
2	NMN	B	1002	22/22	0.94	0.10	19,22,25,26	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around NMN B 1002:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.