



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:38 PM UTC

PDB ID : 6NOR / pdb_00006nor
Title : Crystal structure of GenD2 from gentamicin A biosynthesis in complex with NAD
Authors : Araujo, N.C.; Bury, P.S.; Huang, F.; Leadlay, P.F.; Dias, M.V.B.
Deposited on : 2019-01-16
Resolution : 2.40 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
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

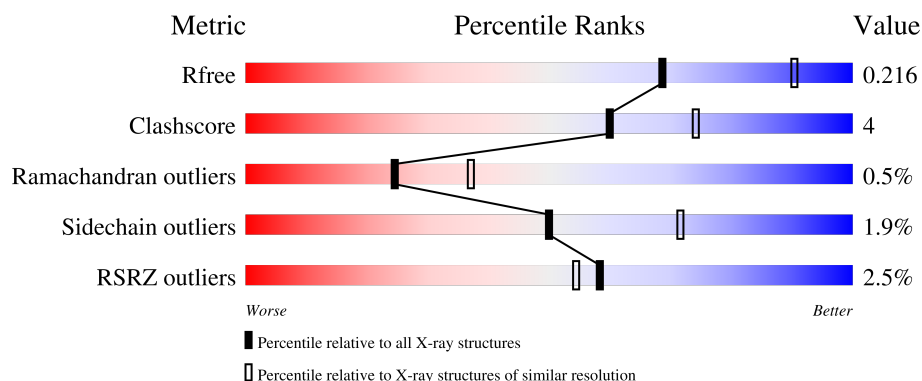
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	361	2% 88% 8% ..
1	B	361	2% 83% 10% .. 6%
1	C	361	2% 85% 8% • 6%
1	D	361	5% 81% 12% • 6%
1	E	361	0% 85% 7% • 6%

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Mol	Chain	Length	Quality of chain
1	F	361	% 87% 6% .. 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16105 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 Putative NAD dependent dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2618	1639	480	490	9			
1	B	341	Total	C	N	O	S	0	1	0
			2572	1610	471	482	9			
1	C	340	Total	C	N	O	S	0	0	0
			2553	1599	464	481	9			
1	D	341	Total	C	N	O	S	0	0	0
			2560	1603	468	480	9			
1	E	338	Total	C	N	O	S	0	0	0
			2547	1594	465	479	9			
1	F	340	Total	C	N	O	S	0	0	0
			2555	1600	467	479	9			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q70KD1
A	-18	GLY	-	expression tag	UNP Q70KD1
A	-17	SER	-	expression tag	UNP Q70KD1
A	-16	SER	-	expression tag	UNP Q70KD1
A	-15	HIS	-	expression tag	UNP Q70KD1
A	-14	HIS	-	expression tag	UNP Q70KD1
A	-13	HIS	-	expression tag	UNP Q70KD1
A	-12	HIS	-	expression tag	UNP Q70KD1
A	-11	HIS	-	expression tag	UNP Q70KD1
A	-10	HIS	-	expression tag	UNP Q70KD1
A	-9	SER	-	expression tag	UNP Q70KD1
A	-8	SER	-	expression tag	UNP Q70KD1
A	-7	GLY	-	expression tag	UNP Q70KD1
A	-6	LEU	-	expression tag	UNP Q70KD1
A	-5	VAL	-	expression tag	UNP Q70KD1
A	-4	PRO	-	expression tag	UNP Q70KD1
A	-3	ARG	-	expression tag	UNP Q70KD1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q70KD1
A	-1	SER	-	expression tag	UNP Q70KD1
A	0	HIS	-	expression tag	UNP Q70KD1
B	-19	MET	-	initiating methionine	UNP Q70KD1
B	-18	GLY	-	expression tag	UNP Q70KD1
B	-17	SER	-	expression tag	UNP Q70KD1
B	-16	SER	-	expression tag	UNP Q70KD1
B	-15	HIS	-	expression tag	UNP Q70KD1
B	-14	HIS	-	expression tag	UNP Q70KD1
B	-13	HIS	-	expression tag	UNP Q70KD1
B	-12	HIS	-	expression tag	UNP Q70KD1
B	-11	HIS	-	expression tag	UNP Q70KD1
B	-10	HIS	-	expression tag	UNP Q70KD1
B	-9	SER	-	expression tag	UNP Q70KD1
B	-8	SER	-	expression tag	UNP Q70KD1
B	-7	GLY	-	expression tag	UNP Q70KD1
B	-6	LEU	-	expression tag	UNP Q70KD1
B	-5	VAL	-	expression tag	UNP Q70KD1
B	-4	PRO	-	expression tag	UNP Q70KD1
B	-3	ARG	-	expression tag	UNP Q70KD1
B	-2	GLY	-	expression tag	UNP Q70KD1
B	-1	SER	-	expression tag	UNP Q70KD1
B	0	HIS	-	expression tag	UNP Q70KD1
C	-19	MET	-	initiating methionine	UNP Q70KD1
C	-18	GLY	-	expression tag	UNP Q70KD1
C	-17	SER	-	expression tag	UNP Q70KD1
C	-16	SER	-	expression tag	UNP Q70KD1
C	-15	HIS	-	expression tag	UNP Q70KD1
C	-14	HIS	-	expression tag	UNP Q70KD1
C	-13	HIS	-	expression tag	UNP Q70KD1
C	-12	HIS	-	expression tag	UNP Q70KD1
C	-11	HIS	-	expression tag	UNP Q70KD1
C	-10	HIS	-	expression tag	UNP Q70KD1
C	-9	SER	-	expression tag	UNP Q70KD1
C	-8	SER	-	expression tag	UNP Q70KD1
C	-7	GLY	-	expression tag	UNP Q70KD1
C	-6	LEU	-	expression tag	UNP Q70KD1
C	-5	VAL	-	expression tag	UNP Q70KD1
C	-4	PRO	-	expression tag	UNP Q70KD1
C	-3	ARG	-	expression tag	UNP Q70KD1
C	-2	GLY	-	expression tag	UNP Q70KD1
C	-1	SER	-	expression tag	UNP Q70KD1

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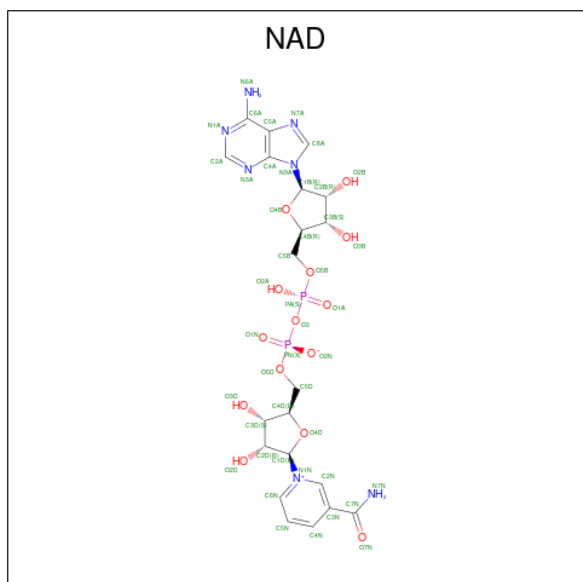
Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP Q70KD1
D	-19	MET	-	initiating methionine	UNP Q70KD1
D	-18	GLY	-	expression tag	UNP Q70KD1
D	-17	SER	-	expression tag	UNP Q70KD1
D	-16	SER	-	expression tag	UNP Q70KD1
D	-15	HIS	-	expression tag	UNP Q70KD1
D	-14	HIS	-	expression tag	UNP Q70KD1
D	-13	HIS	-	expression tag	UNP Q70KD1
D	-12	HIS	-	expression tag	UNP Q70KD1
D	-11	HIS	-	expression tag	UNP Q70KD1
D	-10	HIS	-	expression tag	UNP Q70KD1
D	-9	SER	-	expression tag	UNP Q70KD1
D	-8	SER	-	expression tag	UNP Q70KD1
D	-7	GLY	-	expression tag	UNP Q70KD1
D	-6	LEU	-	expression tag	UNP Q70KD1
D	-5	VAL	-	expression tag	UNP Q70KD1
D	-4	PRO	-	expression tag	UNP Q70KD1
D	-3	ARG	-	expression tag	UNP Q70KD1
D	-2	GLY	-	expression tag	UNP Q70KD1
D	-1	SER	-	expression tag	UNP Q70KD1
D	0	HIS	-	expression tag	UNP Q70KD1
E	-19	MET	-	initiating methionine	UNP Q70KD1
E	-18	GLY	-	expression tag	UNP Q70KD1
E	-17	SER	-	expression tag	UNP Q70KD1
E	-16	SER	-	expression tag	UNP Q70KD1
E	-15	HIS	-	expression tag	UNP Q70KD1
E	-14	HIS	-	expression tag	UNP Q70KD1
E	-13	HIS	-	expression tag	UNP Q70KD1
E	-12	HIS	-	expression tag	UNP Q70KD1
E	-11	HIS	-	expression tag	UNP Q70KD1
E	-10	HIS	-	expression tag	UNP Q70KD1
E	-9	SER	-	expression tag	UNP Q70KD1
E	-8	SER	-	expression tag	UNP Q70KD1
E	-7	GLY	-	expression tag	UNP Q70KD1
E	-6	LEU	-	expression tag	UNP Q70KD1
E	-5	VAL	-	expression tag	UNP Q70KD1
E	-4	PRO	-	expression tag	UNP Q70KD1
E	-3	ARG	-	expression tag	UNP Q70KD1
E	-2	GLY	-	expression tag	UNP Q70KD1
E	-1	SER	-	expression tag	UNP Q70KD1
E	0	HIS	-	expression tag	UNP Q70KD1
F	-19	MET	-	initiating methionine	UNP Q70KD1

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-18	GLY	-	expression tag	UNP Q70KD1
F	-17	SER	-	expression tag	UNP Q70KD1
F	-16	SER	-	expression tag	UNP Q70KD1
F	-15	HIS	-	expression tag	UNP Q70KD1
F	-14	HIS	-	expression tag	UNP Q70KD1
F	-13	HIS	-	expression tag	UNP Q70KD1
F	-12	HIS	-	expression tag	UNP Q70KD1
F	-11	HIS	-	expression tag	UNP Q70KD1
F	-10	HIS	-	expression tag	UNP Q70KD1
F	-9	SER	-	expression tag	UNP Q70KD1
F	-8	SER	-	expression tag	UNP Q70KD1
F	-7	GLY	-	expression tag	UNP Q70KD1
F	-6	LEU	-	expression tag	UNP Q70KD1
F	-5	VAL	-	expression tag	UNP Q70KD1
F	-4	PRO	-	expression tag	UNP Q70KD1
F	-3	ARG	-	expression tag	UNP Q70KD1
F	-2	GLY	-	expression tag	UNP Q70KD1
F	-1	SER	-	expression tag	UNP Q70KD1
F	0	HIS	-	expression tag	UNP Q70KD1

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $\text{C}_{21}\text{H}_{27}\text{N}_7\text{O}_{14}\text{P}_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

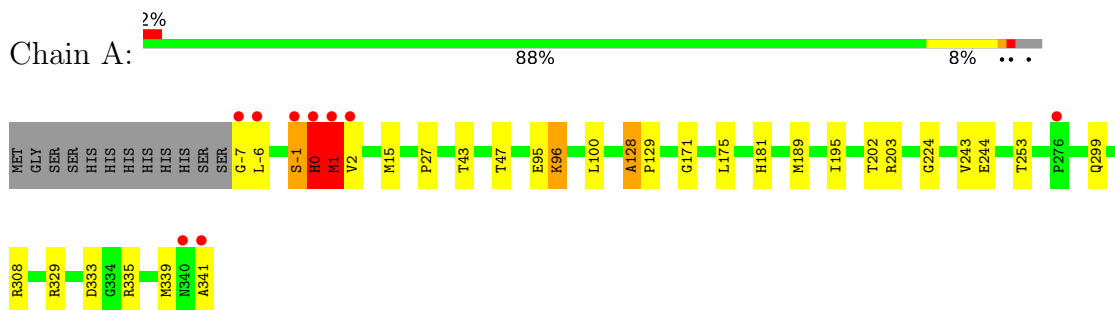
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	91	Total	O	0	0
			91	91		
3	B	66	Total	O	0	0
			66	66		
3	C	67	Total	O	0	0
			67	67		
3	D	50	Total	O	0	0
			50	50		
3	E	62	Total	O	0	0
			62	62		
3	F	100	Total	O	0	0
			100	100		

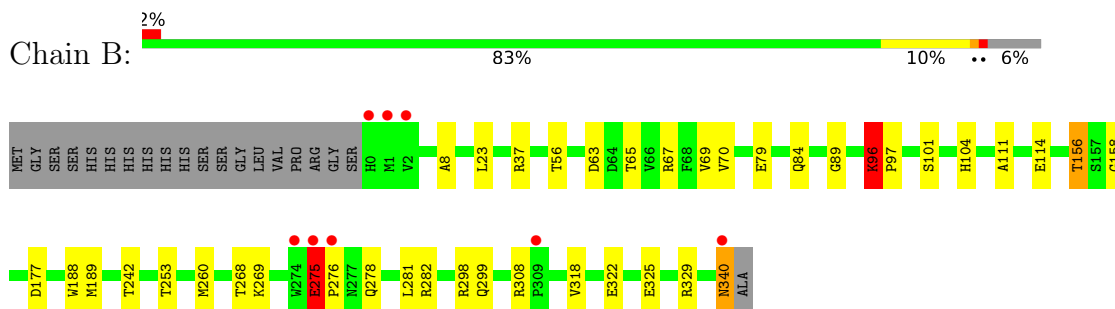
3 Residue-property plots [i](#)

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.

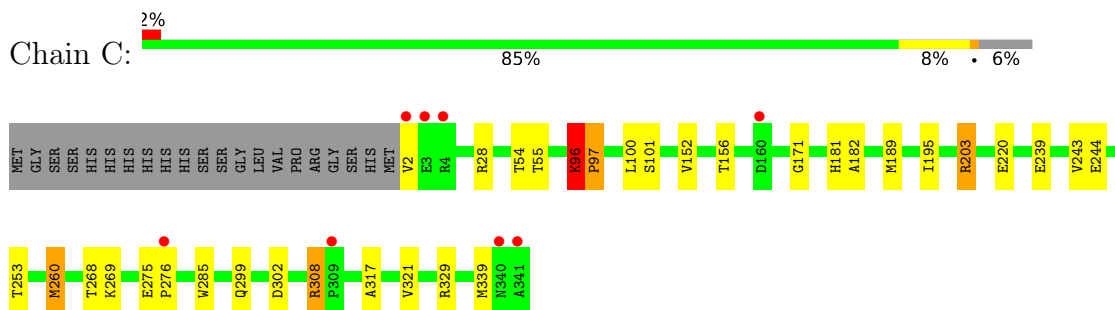
- Molecule 1: Putative NAD dependent dehydrogenase



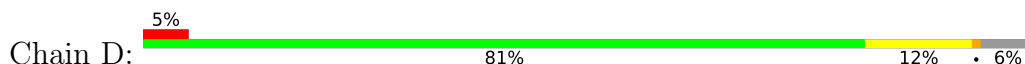
- Molecule 1: Putative NAD dependent dehydrogenase

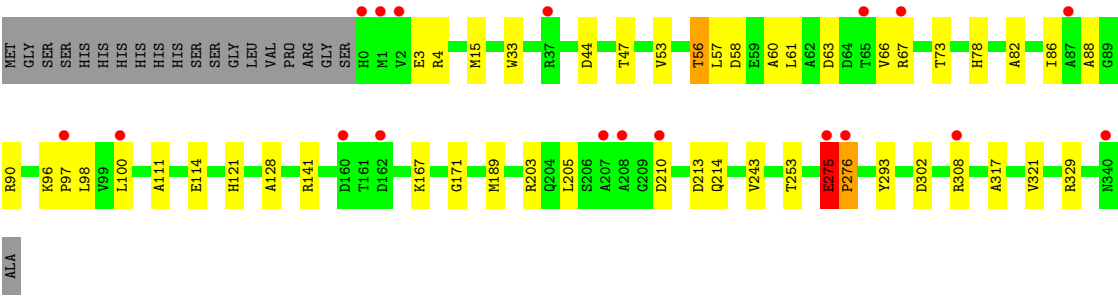


- Molecule 1: Putative NAD dependent dehydrogenase

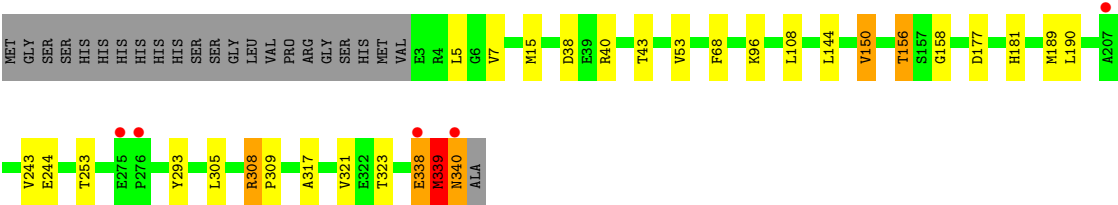
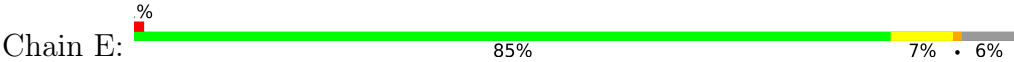


- Molecule 1: Putative NAD dependent dehydrogenase

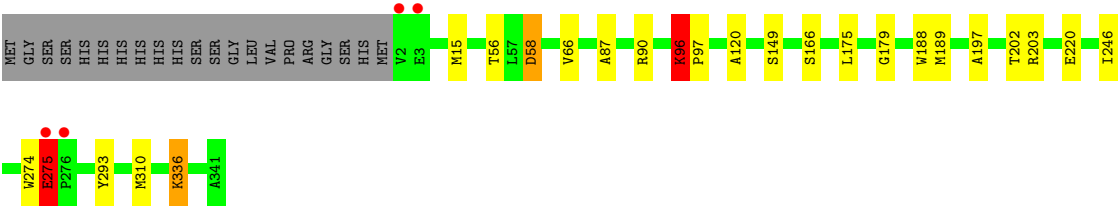
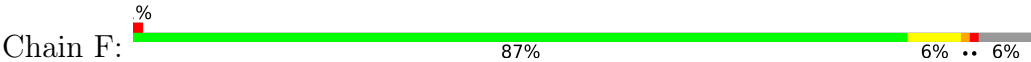




● Molecule 1: Putative NAD dependent dehydrogenase



● Molecule 1: Putative NAD dependent dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	124.00Å 124.00Å 272.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.95 – 2.40 49.95 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.95-2.40) 99.9 (49.95-2.40)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.39Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.175 , 0.223 (Not available) , 0.216	Depositor DCC
R_{free} test set	2007 reflections (2.10%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16105	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.36% 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

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

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	0.69	0/2674	0.89	5/3650 (0.1%)
1	B	0.62	0/2629	0.88	8/3588 (0.2%)
1	C	0.63	0/2607	0.87	5/3560 (0.1%)
1	D	0.59	0/2614	0.88	4/3569 (0.1%)
1	E	0.58	0/2601	0.83	3/3550 (0.1%)
1	F	0.67	0/2609	0.87	5/3562 (0.1%)
All	All	0.63	0/15734	0.87	30/21479 (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	1
1	B	0	2
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	3
All	All	0	9

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	96	LYS	CA-C-N	9.92	132.24	119.84
1	F	96	LYS	C-N-CA	9.92	132.24	119.84
1	A	-1	SER	CA-C-N	9.07	138.03	121.70
1	A	-1	SER	C-N-CA	9.07	138.03	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	96	LYS	CA-C-N	8.78	130.82	119.84
1	C	96	LYS	C-N-CA	8.78	130.82	119.84
1	D	275	GLU	CA-C-N	-7.84	110.05	119.84
1	D	275	GLU	C-N-CA	-7.84	110.05	119.84
1	F	275	GLU	CA-C-N	-7.33	110.68	119.84
1	F	275	GLU	C-N-CA	-7.33	110.68	119.84
1	A	0	HIS	N-CA-CB	7.12	122.60	110.50
1	C	308	ARG	CA-C-N	6.75	126.77	119.89
1	C	308	ARG	C-N-CA	6.75	126.77	119.89
1	F	96	LYS	C-N-CD	-6.63	97.80	125.00
1	B	96	LYS	CA-C-N	6.53	128.00	119.84
1	B	96	LYS	C-N-CA	6.53	128.00	119.84
1	A	128	ALA	CA-C-N	6.15	125.63	119.24
1	A	128	ALA	C-N-CA	6.15	125.63	119.24
1	E	338	GLU	N-CA-C	5.66	119.17	112.72
1	E	308	ARG	CA-C-N	5.62	125.57	119.78
1	E	308	ARG	C-N-CA	5.62	125.57	119.78
1	B	275	GLU	CA-C-N	-5.47	113.00	119.84
1	B	275	GLU	C-N-CA	-5.47	113.00	119.84
1	B	96	LYS	CD-CE-NZ	-5.46	94.44	111.90
1	C	96	LYS	C-N-CD	-5.45	102.64	125.00
1	D	128	ALA	CA-C-N	5.19	125.24	119.32
1	D	128	ALA	C-N-CA	5.19	125.24	119.32
1	B	282	ARG	CA-C-N	5.12	125.04	119.76
1	B	282	ARG	C-N-CA	5.12	125.04	119.76
1	B	96	LYS	C-N-CD	-5.11	104.05	125.00

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	MET	Peptide
1	B	275	GLU	Peptide
1	B	96	LYS	Peptide
1	C	96	LYS	Peptide
1	D	96	LYS	Peptide
1	E	339	MET	Peptide
1	F	274	TRP	Peptide
1	F	275	GLU	Peptide
1	F	96	LYS	Peptide

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	2618	0	2555	27	0
1	B	2572	0	2511	23	0
1	C	2553	0	2485	20	0
1	D	2560	0	2494	33	0
1	E	2547	0	2482	21	0
1	F	2555	0	2492	13	0
2	A	44	0	25	2	0
2	B	44	0	25	0	0
2	C	44	0	25	1	0
2	D	44	0	25	2	0
2	E	44	0	25	2	0
2	F	44	0	25	3	0
3	A	91	0	0	1	1
3	B	66	0	0	3	0
3	C	67	0	0	2	1
3	D	50	0	0	6	0
3	E	62	0	0	0	1
3	F	100	0	0	1	1
All	All	16105	0	15169	133	2

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 (133) 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:96:LYS:NZ	1:B:177:ASP:O	1.96	0.97
1:E:156:THR:HG23	1:E:158:GLY:H	1.30	0.96
1:B:340:ASN:ND2	1:D:56:THR:HG21	1.91	0.85
1:A:203:ARG:HH21	1:C:220:GLU:HG3	1.41	0.82
1:E:340:ASN:H	1:E:340:ASN:HD22	1.25	0.81
1:A:224:GLY:O	1:C:203:ARG:NH1	2.15	0.78
1:A:1:MET:HA	1:A:27:PRO:HB2	1.66	0.77
1:B:67[B]:ARG:NH2	1:B:89:GLY:O	2.17	0.77
1:E:340:ASN:HD22	1:E:340:ASN:N	1.83	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:329:ARG:NH1	3:C:501:HOH:O	2.18	0.75
1:D:111:ALA:O	1:D:114:GLU:HB3	1.87	0.75
1:E:43:THR:HG22	1:E:53:VAL:HG11	1.69	0.72
1:B:156:THR:HG22	1:B:158:GLY:H	1.56	0.71
1:D:3:GLU:OE1	3:D:501:HOH:O	2.10	0.70
1:D:63:ASP:HB3	3:D:502:HOH:O	1.92	0.70
1:E:323:THR:HA	1:E:339:MET:HE1	1.74	0.69
1:A:341:ALA:HA	1:F:87:ALA:HB1	1.75	0.69
1:E:340:ASN:H	1:E:340:ASN:ND2	1.91	0.69
1:B:299:GLN:HG2	1:B:308:ARG:HH12	1.59	0.67
1:F:202:THR:O	1:F:203:ARG:NH1	2.28	0.67
1:B:325:GLU:OE2	1:B:329:ARG:NH1	2.28	0.66
1:C:189:MET:HE3	1:C:243:VAL:HG11	1.76	0.66
1:D:61:LEU:O	1:D:90:ARG:NH2	2.29	0.65
1:D:302:ASP:OD2	1:D:308:ARG:NH1	2.32	0.63
1:B:156:THR:CG2	1:B:158:GLY:H	2.12	0.63
1:D:4:ARG:O	1:D:67:ARG:NH2	2.32	0.63
1:B:63:ASP:OD1	1:B:65:THR:OG1	2.17	0.61
1:C:96:LYS:HD2	1:C:181:HIS:NE2	2.16	0.61
1:B:340:ASN:HD22	1:D:56:THR:HG21	1.63	0.61
1:D:100:LEU:HD22	1:D:171:GLY:HA3	1.83	0.61
1:E:156:THR:HG23	1:E:158:GLY:N	2.10	0.60
1:D:73:THR:O	1:D:78:HIS:NE2	2.35	0.58
1:D:203:ARG:HB2	1:D:214:GLN:HG3	1.86	0.58
1:D:60:ALA:O	3:D:502:HOH:O	2.18	0.57
1:A:-1:SER:HA	1:A:0:HIS:CG	2.40	0.56
1:B:318:VAL:O	1:B:322:GLU:HG3	2.05	0.56
1:A:202:THR:O	1:A:203:ARG:NH1	2.38	0.56
1:B:67[B]:ARG:NH1	3:B:501:HOH:O	2.20	0.56
1:D:33:TRP:NE1	3:D:502:HOH:O	2.37	0.56
1:F:56:THR:HG22	1:F:58:ASP:H	1.70	0.56
1:D:141:ARG:NE	1:D:141:ARG:HA	2.21	0.56
1:A:0:HIS:O	1:A:2:VAL:N	2.38	0.55
1:E:96:LYS:HD3	1:E:181:HIS:NE2	2.21	0.55
1:A:15:MET:HE3	2:A:401:NAD:C4N	2.36	0.55
1:C:100:LEU:HD22	1:C:171:GLY:HA3	1.88	0.55
1:A:203:ARG:NH2	1:C:220:GLU:HG3	2.17	0.55
1:B:101:SER:OG	1:B:104:HIS:ND1	2.39	0.55
1:D:88:ALA:O	1:D:90:ARG:NH1	2.40	0.55
1:C:268:THR:OG1	1:C:269:LYS:N	2.36	0.54
1:F:188:TRP:CZ3	1:F:189:MET:HE2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:ARG:HH21	1:A:335:ARG:HH22	1.54	0.53
1:A:244:GLU:HG3	1:A:253:THR:HG22	1.90	0.53
1:A:195:ILE:HG22	1:A:339:MET:HG3	1.90	0.53
1:F:293:TYR:OH	2:F:401:NAD:N7N	2.42	0.53
1:E:189:MET:HE3	1:E:243:VAL:HG11	1.90	0.53
1:B:268:THR:OG1	1:B:269:LYS:N	2.42	0.53
1:A:96:LYS:NZ	3:A:505:HOH:O	2.41	0.52
1:E:15:MET:HE3	2:E:401:NAD:C4N	2.41	0.51
1:C:317:ALA:O	1:C:321:VAL:HG23	2.11	0.51
1:E:150:VAL:HG21	1:E:190:LEU:HG	1.93	0.51
1:C:299:GLN:HG2	1:C:308:ARG:HH22	1.76	0.50
1:F:336:LYS:NZ	3:F:505:HOH:O	2.42	0.50
1:B:242:THR:HG22	3:B:548:HOH:O	2.11	0.50
1:A:299:GLN:HG2	1:A:308:ARG:HH12	1.77	0.50
1:E:96:LYS:HE2	1:E:177:ASP:O	2.12	0.50
1:E:293:TYR:OH	2:E:401:NAD:N7N	2.45	0.50
1:C:96:LYS:HG2	1:C:97:PRO:HD2	1.93	0.49
1:D:15:MET:HA	1:D:15:MET:HE2	1.94	0.49
1:D:205:LEU:HD12	1:D:213:ASP:HB2	1.95	0.48
1:C:260:MET:HG3	3:C:538:HOH:O	2.14	0.48
1:F:15:MET:HE3	2:F:401:NAD:C4N	2.44	0.48
1:D:98:LEU:HD13	1:D:121:HIS:HB3	1.94	0.48
1:B:268:THR:O	1:B:278:GLN:HG2	2.14	0.48
1:D:189:MET:HE3	1:D:243:VAL:HG11	1.96	0.48
1:D:141:ARG:HA	1:D:141:ARG:CZ	2.42	0.48
1:F:197:ALA:HB3	1:F:220:GLU:HB3	1.96	0.48
1:C:260:MET:HG2	1:C:285:TRP:NE1	2.29	0.47
1:C:152:VAL:HG11	1:C:182:ALA:HA	1.96	0.47
1:E:5:LEU:HB2	1:E:305:LEU:HD21	1.96	0.47
1:B:188:TRP:CZ3	1:B:189:MET:HE2	2.50	0.46
1:D:317:ALA:O	1:D:321:VAL:HG23	2.16	0.46
1:B:111:ALA:O	1:B:114:GLU:HB3	2.17	0.45
1:A:43:THR:O	1:A:47:THR:HG23	2.16	0.45
1:A:189:MET:HE3	1:A:243:VAL:HG11	1.99	0.45
1:D:33:TRP:CD1	3:D:502:HOH:O	2.69	0.45
1:A:333:ASP:OD2	1:A:335:ARG:NH1	2.49	0.45
1:E:244:GLU:HG3	1:E:253:THR:HG22	1.99	0.45
1:A:96:LYS:HD2	1:A:181:HIS:NE2	2.32	0.45
1:B:8:ALA:HB3	1:B:69:VAL:HG22	1.98	0.44
1:D:44:ASP:O	1:D:47:THR:HG22	2.17	0.44
1:C:275:GLU:HA	1:C:276:PRO:C	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:-7:GLY:HA3	1:A:-6:LEU:HA	1.54	0.43
1:A:299:GLN:HG2	1:A:308:ARG:NH1	2.33	0.43
1:D:15:MET:HE3	2:D:401:NAD:C4N	2.47	0.43
1:D:210:ASP:OD1	1:D:210:ASP:N	2.49	0.43
1:A:128:ALA:HA	1:A:129:PRO:HD3	1.85	0.43
1:D:293:TYR:OH	2:D:401:NAD:N7N	2.50	0.43
1:D:275:GLU:CB	1:D:276:PRO:HD3	2.49	0.43
1:E:308:ARG:HA	1:E:309:PRO:HD3	1.79	0.43
2:F:401:NAD:H6N	2:F:401:NAD:H2D	1.75	0.43
1:E:38:ASP:OD1	1:E:40:ARG:N	2.51	0.43
1:F:175:LEU:O	1:F:179:GLY:HA3	2.19	0.43
1:A:100:LEU:HD22	1:A:171:GLY:HA3	2.00	0.43
1:B:276:PRO:O	1:B:281:LEU:HD22	2.18	0.43
1:C:156:THR:HG22	1:C:239:GLU:HG3	2.01	0.43
1:C:28:ARG:NH1	1:C:302:ASP:OD1	2.43	0.43
1:A:189:MET:HG3	1:A:243:VAL:HG11	2.01	0.42
1:F:120:ALA:HB2	1:F:310:MET:HE1	2.01	0.42
1:A:95:GLU:OE1	2:A:401:NAD:H2N	2.20	0.42
1:C:244:GLU:HG3	1:C:253:THR:HG22	2.01	0.42
1:B:79:GLU:HG3	1:B:104:HIS:HB3	2.02	0.42
2:C:401:NAD:H6N	2:C:401:NAD:H2D	1.84	0.42
1:A:15:MET:HA	1:A:15:MET:HE2	2.02	0.42
1:E:7:VAL:HG22	1:E:68:PHE:HB3	2.02	0.42
1:A:2:VAL:H	1:A:2:VAL:HG22	1.46	0.41
1:F:58:ASP:N	1:F:58:ASP:OD1	2.52	0.41
1:D:66:VAL:HG21	3:D:502:HOH:O	2.20	0.41
1:E:96:LYS:HD3	1:E:181:HIS:CE1	2.56	0.41
1:C:54:THR:OG1	1:C:55:THR:N	2.54	0.41
1:D:82:ALA:O	1:D:86:ILE:HG13	2.20	0.41
1:F:66:VAL:O	1:F:90:ARG:HD2	2.21	0.41
1:D:203:ARG:HB2	1:D:214:GLN:CG	2.51	0.40
1:B:84:GLN:HG3	3:B:546:HOH:O	2.21	0.40
1:C:195:ILE:HG22	1:C:339:MET:HG3	2.03	0.40
1:E:317:ALA:O	1:E:321:VAL:HG23	2.21	0.40
1:A:175:LEU:HA	1:A:175:LEU:HD12	1.88	0.40
1:B:23:LEU:HD11	1:B:70:VAL:HG21	2.03	0.40
1:D:61:LEU:HD13	1:D:88:ALA:CB	2.51	0.40
1:D:61:LEU:HD23	1:D:61:LEU:HA	1.77	0.40
1:F:149:SER:HB2	1:F:246:ILE:HB	2.03	0.40
1:B:340:ASN:OD1	1:B:340:ASN:N	2.31	0.40
1:D:56:THR:OG1	1:D:58:ASP:OD1	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:7:VAL:HG22	1:E:68:PHE:HD2	1.87	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:545:HOH:O	3:F:545:HOH:O[4_655]	1.92	0.28
3:A:552:HOH:O	3:C:561:HOH:O[5_554]	2.09	0.11

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	347/361 (96%)	336 (97%)	9 (3%)	2 (1%)	21	32
1	B	340/361 (94%)	328 (96%)	10 (3%)	2 (1%)	21	32
1	C	338/361 (94%)	330 (98%)	7 (2%)	1 (0%)	36	50
1	D	339/361 (94%)	322 (95%)	14 (4%)	3 (1%)	14	22
1	E	336/361 (93%)	329 (98%)	6 (2%)	1 (0%)	36	50
1	F	338/361 (94%)	326 (96%)	10 (3%)	2 (1%)	21	32
All	All	2038/2166 (94%)	1971 (97%)	56 (3%)	11 (0%)	24	37

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	1	MET
1	B	97	PRO
1	C	97	PRO
1	D	97	PRO
1	D	275	GLU

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Mol	Chain	Res	Type
1	F	97	PRO
1	F	275	GLU
1	E	339	MET
1	B	275	GLU
1	D	276	PRO

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	260/274 (95%)	259 (100%)	1 (0%)	84	92
1	B	256/274 (93%)	249 (97%)	7 (3%)	39	62
1	C	254/274 (93%)	249 (98%)	5 (2%)	48	70
1	D	254/274 (93%)	248 (98%)	6 (2%)	43	65
1	E	254/274 (93%)	248 (98%)	6 (2%)	43	65
1	F	254/274 (93%)	250 (98%)	4 (2%)	55	76
All	All	1532/1644 (93%)	1503 (98%)	29 (2%)	50	71

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	LYS
1	B	37	ARG
1	B	56	THR
1	B	156	THR
1	B	253	THR
1	B	260	MET
1	B	298	ARG
1	B	340	ASN
1	C	2	VAL
1	C	96	LYS
1	C	101	SER
1	C	203	ARG
1	C	260	MET

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Mol	Chain	Res	Type
1	D	53	VAL
1	D	56	THR
1	D	57	LEU
1	D	167	LYS
1	D	253	THR
1	D	329	ARG
1	E	108	LEU
1	E	144	LEU
1	E	150	VAL
1	E	156	THR
1	E	338	GLU
1	E	340	ASN
1	F	58	ASP
1	F	96	LYS
1	F	166	SER
1	F	336	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	214	GLN
1	B	135	HIS
1	C	312	HIS
1	E	296	GLN
1	E	340	ASN
1	F	148	HIS

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

6 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	NAD	B	401	-	46,48,48	3.68	16 (34%)	64,73,73	1.69	13 (20%)
2	NAD	E	401	-	46,48,48	3.76	16 (34%)	64,73,73	1.61	10 (15%)
2	NAD	D	401	-	46,48,48	3.74	15 (32%)	64,73,73	1.70	12 (18%)
2	NAD	F	401	-	46,48,48	3.50	14 (30%)	64,73,73	1.76	12 (18%)
2	NAD	C	401	-	46,48,48	3.60	15 (32%)	64,73,73	1.71	12 (18%)
2	NAD	A	401	-	46,48,48	3.66	16 (34%)	64,73,73	1.78	12 (18%)

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	NAD	B	401	-	-	5/30/62/62	0/5/5/5
2	NAD	E	401	-	-	5/30/62/62	0/5/5/5
2	NAD	D	401	-	-	4/30/62/62	0/5/5/5
2	NAD	F	401	-	-	7/30/62/62	0/5/5/5
2	NAD	C	401	-	-	5/30/62/62	0/5/5/5
2	NAD	A	401	-	-	6/30/62/62	0/5/5/5

All (92) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	NAD	O4D-C1D	16.51	1.62	1.40
2	E	401	NAD	O4D-C1D	16.33	1.62	1.40
2	B	401	NAD	O4D-C1D	16.19	1.62	1.40
2	A	401	NAD	O4D-C1D	15.71	1.61	1.40
2	C	401	NAD	O4D-C1D	15.65	1.61	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	401	NAD	O4D-C1D	15.40	1.61	1.40
2	A	401	NAD	C2B-C1B	-8.24	1.27	1.53
2	E	401	NAD	C2B-C1B	-8.23	1.27	1.53
2	B	401	NAD	C2B-C1B	-8.12	1.28	1.53
2	C	401	NAD	C2B-C1B	-8.04	1.28	1.53
2	D	401	NAD	C2B-C1B	-8.02	1.28	1.53
2	D	401	NAD	O4B-C1B	7.80	1.60	1.42
2	E	401	NAD	O4B-C1B	7.75	1.59	1.42
2	F	401	NAD	C2B-C1B	-7.67	1.29	1.53
2	A	401	NAD	O4B-C1B	7.59	1.59	1.42
2	C	401	NAD	O4B-C1B	7.58	1.59	1.42
2	B	401	NAD	O4B-C1B	7.53	1.59	1.42
2	F	401	NAD	O4B-C1B	7.32	1.58	1.42
2	D	401	NAD	O4D-C4D	-6.97	1.29	1.45
2	B	401	NAD	O4D-C4D	-6.80	1.29	1.45
2	E	401	NAD	O4D-C4D	-6.60	1.30	1.45
2	C	401	NAD	O4D-C4D	-6.60	1.30	1.45
2	A	401	NAD	O4B-C4B	-6.45	1.30	1.45
2	A	401	NAD	O4D-C4D	-6.45	1.30	1.45
2	F	401	NAD	O4D-C4D	-6.42	1.30	1.45
2	E	401	NAD	O4B-C4B	-6.41	1.30	1.45
2	C	401	NAD	O4B-C4B	-6.34	1.30	1.45
2	D	401	NAD	O4B-C4B	-6.31	1.31	1.45
2	B	401	NAD	O4B-C4B	-6.27	1.31	1.45
2	F	401	NAD	O4B-C4B	-5.99	1.31	1.45
2	D	401	NAD	C7N-N7N	5.67	1.43	1.33
2	B	401	NAD	C7N-N7N	5.53	1.43	1.33
2	E	401	NAD	C7N-N7N	5.36	1.42	1.33
2	A	401	NAD	C7N-N7N	5.28	1.42	1.33
2	C	401	NAD	C7N-N7N	5.15	1.42	1.33
2	E	401	NAD	C2N-N1N	5.07	1.40	1.35
2	F	401	NAD	C7N-N7N	4.80	1.41	1.33
2	A	401	NAD	O3D-C3D	-4.56	1.31	1.43
2	E	401	NAD	O3D-C3D	-4.53	1.31	1.43
2	F	401	NAD	O3D-C3D	-4.51	1.31	1.43
2	B	401	NAD	O3D-C3D	-4.49	1.31	1.43
2	D	401	NAD	O3D-C3D	-4.44	1.32	1.43
2	C	401	NAD	O3D-C3D	-4.34	1.32	1.43
2	A	401	NAD	C2N-N1N	4.09	1.39	1.35
2	C	401	NAD	C2N-N1N	4.09	1.39	1.35
2	D	401	NAD	C2N-N1N	4.07	1.39	1.35
2	B	401	NAD	C2N-N1N	3.77	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	401	NAD	C2N-N1N	3.74	1.39	1.35
2	A	401	NAD	PA-O3	-3.60	1.55	1.59
2	E	401	NAD	PA-O3	-3.44	1.55	1.59
2	D	401	NAD	O2D-C2D	3.41	1.51	1.43
2	C	401	NAD	O7N-C7N	-3.38	1.17	1.24
2	A	401	NAD	O7N-C7N	-3.31	1.18	1.24
2	E	401	NAD	C3N-C7N	3.20	1.55	1.50
2	B	401	NAD	O7N-C7N	-3.15	1.18	1.24
2	D	401	NAD	C3N-C7N	3.15	1.55	1.50
2	E	401	NAD	O2D-C2D	3.12	1.50	1.43
2	E	401	NAD	O7N-C7N	-3.07	1.18	1.24
2	F	401	NAD	O7N-C7N	-3.07	1.18	1.24
2	D	401	NAD	O7N-C7N	-3.07	1.18	1.24
2	F	401	NAD	PA-O3	-2.97	1.56	1.59
2	A	401	NAD	C5A-N7A	-2.86	1.33	1.39
2	B	401	NAD	PA-O3	-2.75	1.56	1.59
2	D	401	NAD	O2B-C2B	2.69	1.49	1.43
2	C	401	NAD	O2D-C2D	2.65	1.49	1.43
2	A	401	NAD	O2D-C2D	2.64	1.49	1.43
2	F	401	NAD	O2D-C2D	2.61	1.49	1.43
2	B	401	NAD	C5A-N7A	-2.60	1.34	1.39
2	B	401	NAD	O2D-C2D	2.56	1.49	1.43
2	C	401	NAD	C3N-C7N	2.56	1.54	1.50
2	C	401	NAD	C5A-N7A	-2.56	1.34	1.39
2	E	401	NAD	C5A-N7A	-2.54	1.34	1.39
2	C	401	NAD	O2B-C2B	2.49	1.49	1.43
2	B	401	NAD	C3N-C7N	2.46	1.54	1.50
2	A	401	NAD	O3B-C3B	-2.45	1.36	1.43
2	A	401	NAD	C3N-C7N	2.44	1.54	1.50
2	B	401	NAD	O2B-C2B	2.42	1.49	1.43
2	D	401	NAD	PA-O3	-2.41	1.56	1.59
2	E	401	NAD	C5A-C4A	-2.37	1.34	1.39
2	E	401	NAD	O2B-C2B	2.35	1.48	1.43
2	F	401	NAD	C3N-C7N	2.33	1.54	1.50
2	B	401	NAD	O3B-C3B	-2.29	1.37	1.43
2	B	401	NAD	C5A-C4A	-2.25	1.35	1.39
2	A	401	NAD	C8A-N7A	2.25	1.36	1.31
2	C	401	NAD	C5A-C4A	-2.21	1.35	1.39
2	D	401	NAD	C5A-C4A	-2.20	1.35	1.39
2	E	401	NAD	O3B-C3B	-2.19	1.37	1.43
2	C	401	NAD	PA-O3	-2.14	1.57	1.59
2	F	401	NAD	C5A-C4A	-2.09	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	NAD	C5A-N7A	-2.09	1.35	1.39
2	A	401	NAD	C5A-C4A	-2.04	1.35	1.39
2	F	401	NAD	C5A-N7A	-2.04	1.35	1.39

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	NAD	N3A-C2A-N1A	-6.01	119.48	128.58
2	F	401	NAD	N3A-C2A-N1A	-5.94	119.59	128.58
2	E	401	NAD	N3A-C2A-N1A	-5.73	119.91	128.58
2	F	401	NAD	C5A-C4A-N3A	-5.68	118.90	126.72
2	D	401	NAD	N3A-C2A-N1A	-5.57	120.15	128.58
2	C	401	NAD	N3A-C2A-N1A	-5.40	120.41	128.58
2	C	401	NAD	C5A-C4A-N3A	-5.32	119.39	126.72
2	B	401	NAD	C5A-C4A-N3A	-5.30	119.42	126.72
2	B	401	NAD	N3A-C2A-N1A	-5.28	120.58	128.58
2	A	401	NAD	C5A-C4A-N3A	-5.10	119.69	126.72
2	D	401	NAD	C5A-C4A-N3A	-4.94	119.92	126.72
2	E	401	NAD	C5A-C4A-N3A	-4.75	120.17	126.72
2	A	401	NAD	N9A-C8A-N7A	-4.39	107.71	113.94
2	D	401	NAD	N9A-C8A-N7A	-4.27	107.88	113.94
2	C	401	NAD	N9A-C8A-N7A	-3.98	108.29	113.94
2	E	401	NAD	N9A-C8A-N7A	-3.98	108.29	113.94
2	B	401	NAD	N9A-C8A-N7A	-3.95	108.33	113.94
2	F	401	NAD	C2A-N3A-C4A	3.85	121.23	111.83
2	A	401	NAD	C6N-N1N-C2N	-3.78	118.66	121.88
2	F	401	NAD	N9A-C8A-N7A	-3.77	108.58	113.94
2	A	401	NAD	C2A-N3A-C4A	3.56	120.52	111.83
2	C	401	NAD	C2A-N3A-C4A	3.43	120.22	111.83
2	B	401	NAD	C2A-N3A-C4A	3.34	119.99	111.83
2	F	401	NAD	N3A-C4A-N9A	3.34	132.84	127.17
2	D	401	NAD	C2A-N3A-C4A	3.33	119.97	111.83
2	F	401	NAD	N6A-C6A-N1A	-3.32	110.98	118.38
2	E	401	NAD	C2A-N3A-C4A	3.25	119.76	111.83
2	C	401	NAD	N3A-C4A-N9A	3.23	132.66	127.17
2	B	401	NAD	C5A-N7A-C8A	3.10	108.32	103.45
2	B	401	NAD	N6A-C6A-N1A	-3.10	111.48	118.38
2	D	401	NAD	N3A-C4A-N9A	3.05	132.36	127.17
2	A	401	NAD	C5A-N7A-C8A	3.05	108.25	103.45
2	D	401	NAD	C3N-C7N-N7N	3.04	121.49	117.74
2	E	401	NAD	N3A-C4A-N9A	3.02	132.30	127.17
2	E	401	NAD	O7N-C7N-N7N	-3.01	118.27	122.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	NAD	C5A-N7A-C8A	2.96	108.11	103.45
2	D	401	NAD	C5A-N7A-C8A	2.94	108.07	103.45
2	F	401	NAD	C5A-N7A-C8A	2.88	107.98	103.45
2	D	401	NAD	C6N-N1N-C2N	-2.83	119.47	121.88
2	D	401	NAD	N6A-C6A-N1A	-2.81	112.11	118.38
2	B	401	NAD	N3A-C4A-N9A	2.80	131.93	127.17
2	A	401	NAD	N3A-C4A-N9A	2.79	131.91	127.17
2	B	401	NAD	C4A-C5A-N7A	-2.77	107.42	110.58
2	C	401	NAD	C3N-C7N-N7N	2.68	121.04	117.74
2	A	401	NAD	N6A-C6A-N1A	-2.65	112.47	118.38
2	B	401	NAD	C3N-C7N-N7N	2.65	121.00	117.74
2	B	401	NAD	C5A-C4A-N9A	2.60	108.64	105.81
2	C	401	NAD	N6A-C6A-N1A	-2.57	112.66	118.38
2	A	401	NAD	C2N-C3N-C4N	2.55	121.22	118.26
2	E	401	NAD	C5A-N7A-C8A	2.41	107.23	103.45
2	C	401	NAD	O7N-C7N-N7N	-2.41	119.14	122.62
2	B	401	NAD	C6A-C5A-C4A	2.39	120.44	117.18
2	F	401	NAD	C4A-C5A-N7A	-2.37	107.87	110.58
2	C	401	NAD	C6A-C5A-C4A	2.36	120.40	117.18
2	A	401	NAD	C5A-C4A-N9A	2.36	108.38	105.81
2	A	401	NAD	C4A-C5A-N7A	-2.36	107.89	110.58
2	D	401	NAD	C4A-N9A-C8A	2.32	108.18	105.74
2	E	401	NAD	N6A-C6A-N1A	-2.31	113.22	118.38
2	A	401	NAD	C5N-C4N-C3N	-2.29	118.11	120.36
2	B	401	NAD	C5A-C6A-N6A	2.26	128.87	123.29
2	F	401	NAD	C5A-C4A-N9A	2.24	108.25	105.81
2	E	401	NAD	C4A-N9A-C8A	2.14	107.98	105.74
2	C	401	NAD	C4A-C5A-N7A	-2.13	108.14	110.58
2	D	401	NAD	C4A-C5A-N7A	-2.13	108.15	110.58
2	F	401	NAD	O7N-C7N-N7N	-2.12	119.55	122.62
2	F	401	NAD	C6N-N1N-C2N	-2.08	120.11	121.88
2	D	401	NAD	O7N-C7N-N7N	-2.07	119.62	122.62
2	F	401	NAD	C2N-C3N-C4N	2.07	120.66	118.26
2	E	401	NAD	C6A-C5A-C4A	2.05	119.98	117.18
2	B	401	NAD	C2N-C3N-C4N	2.01	120.59	118.26
2	C	401	NAD	C6N-N1N-C2N	-2.00	120.17	121.88

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	NAD	O4D-C1D-N1N-C2N

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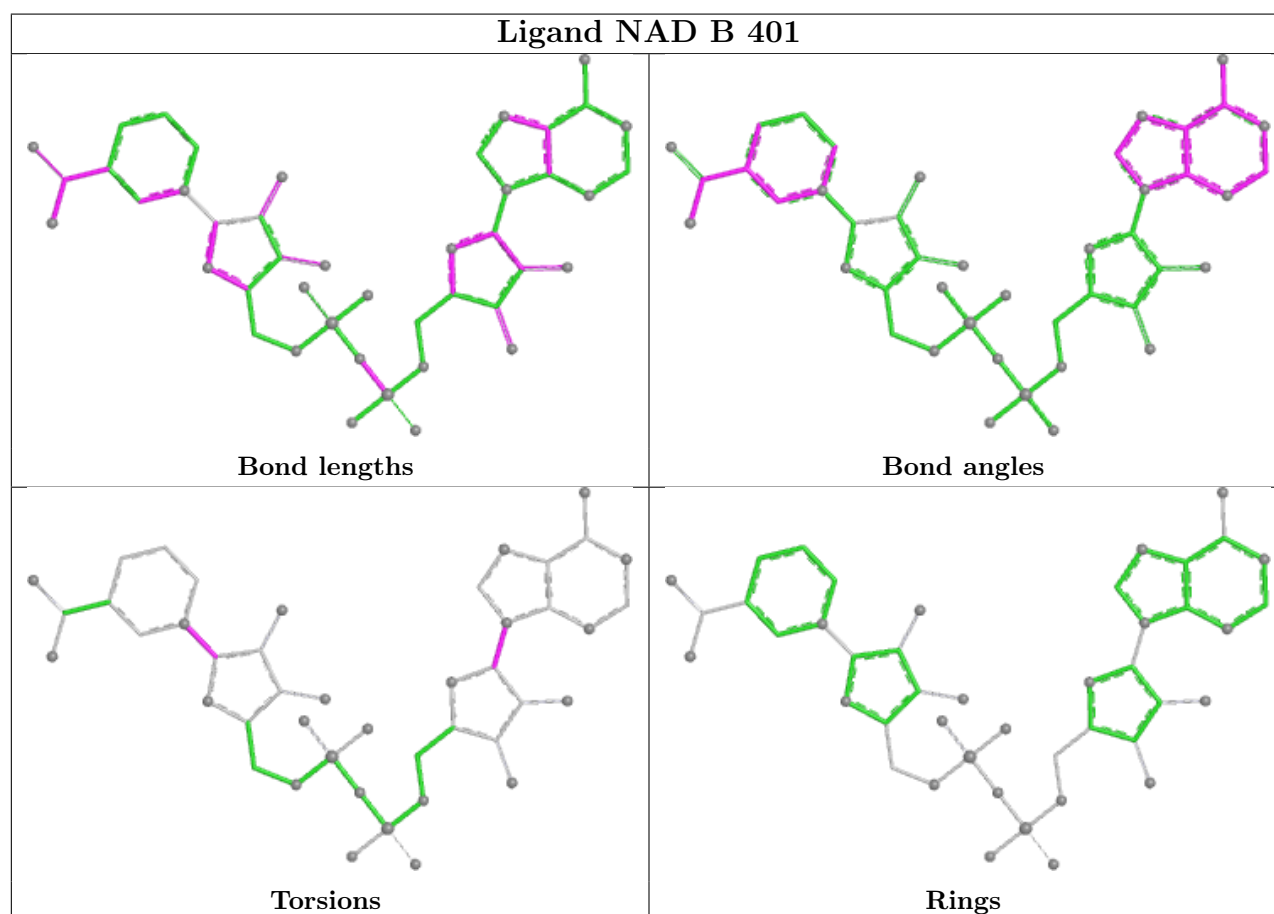
Mol	Chain	Res	Type	Atoms
2	A	401	NAD	O4D-C1D-N1N-C6N
2	A	401	NAD	C2D-C1D-N1N-C2N
2	A	401	NAD	C2D-C1D-N1N-C6N
2	B	401	NAD	O4D-C1D-N1N-C2N
2	B	401	NAD	O4D-C1D-N1N-C6N
2	B	401	NAD	C2D-C1D-N1N-C2N
2	B	401	NAD	C2D-C1D-N1N-C6N
2	C	401	NAD	O4D-C1D-N1N-C2N
2	C	401	NAD	O4D-C1D-N1N-C6N
2	C	401	NAD	C2D-C1D-N1N-C2N
2	C	401	NAD	C2D-C1D-N1N-C6N
2	D	401	NAD	O4D-C1D-N1N-C2N
2	D	401	NAD	O4D-C1D-N1N-C6N
2	E	401	NAD	O4D-C1D-N1N-C2N
2	E	401	NAD	O4D-C1D-N1N-C6N
2	E	401	NAD	C2D-C1D-N1N-C2N
2	F	401	NAD	O4D-C1D-N1N-C2N
2	F	401	NAD	O4D-C1D-N1N-C6N
2	F	401	NAD	C2D-C1D-N1N-C2N
2	F	401	NAD	C2D-C1D-N1N-C6N
2	B	401	NAD	C2B-C1B-N9A-C8A
2	E	401	NAD	C2B-C1B-N9A-C8A
2	F	401	NAD	C2B-C1B-N9A-C8A
2	C	401	NAD	C2B-C1B-N9A-C8A
2	D	401	NAD	C2D-C1D-N1N-C2N
2	E	401	NAD	C2D-C1D-N1N-C6N
2	A	401	NAD	C2B-C1B-N9A-C8A
2	A	401	NAD	O4B-C4B-C5B-O5B
2	D	401	NAD	C2B-C1B-N9A-C8A
2	F	401	NAD	PN-O3-PA-O2A
2	F	401	NAD	O4B-C4B-C5B-O5B

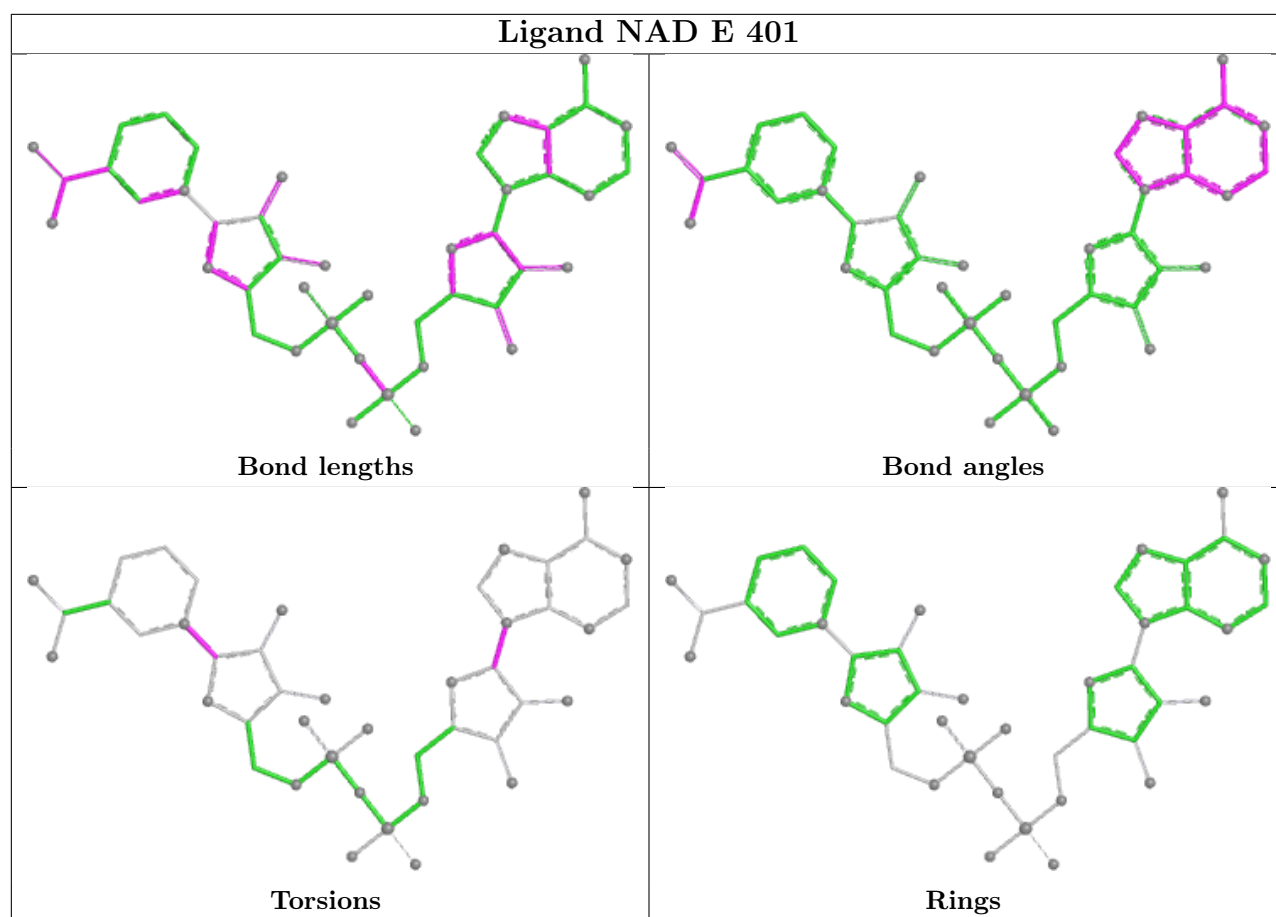
There are no ring outliers.

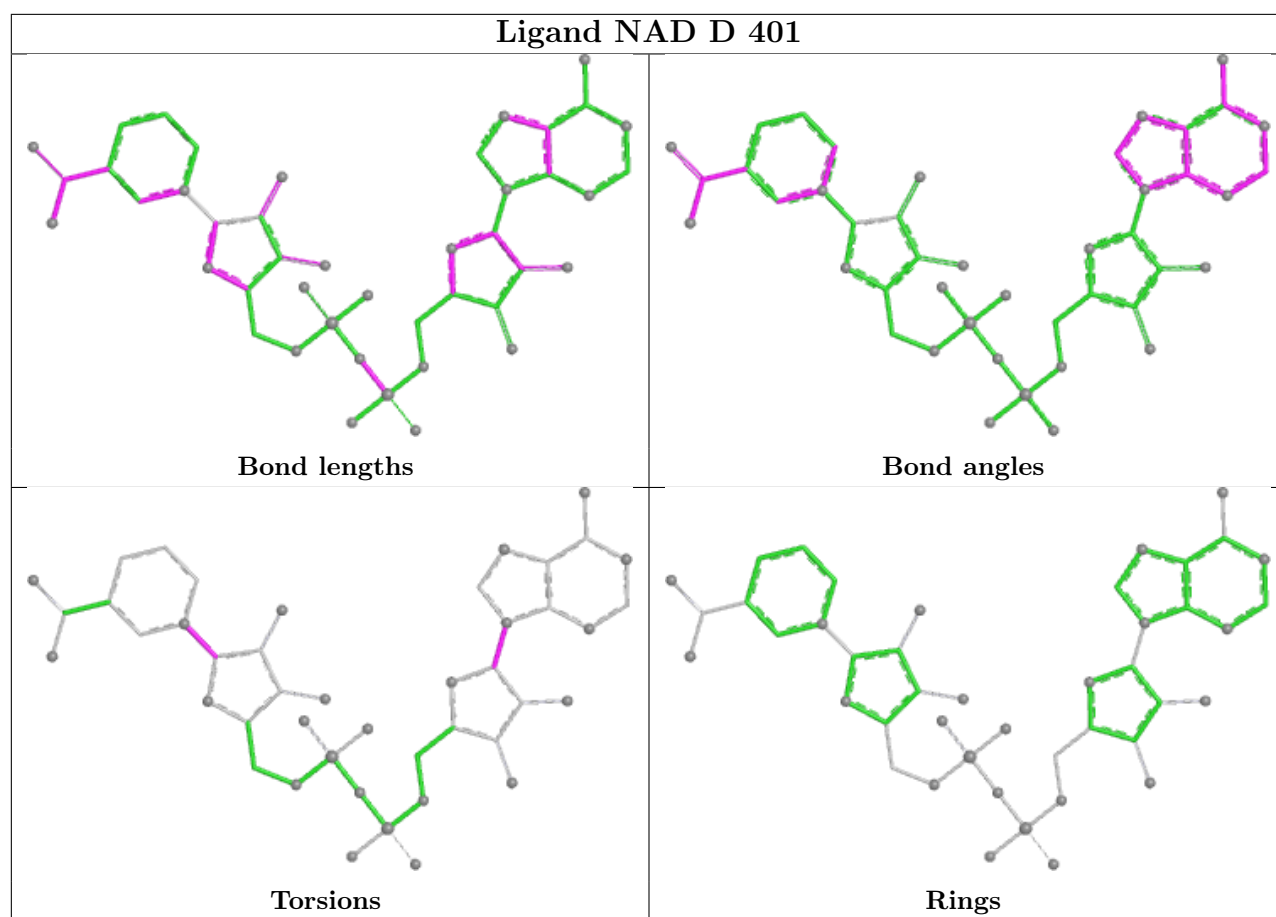
5 monomers are involved in 10 short contacts:

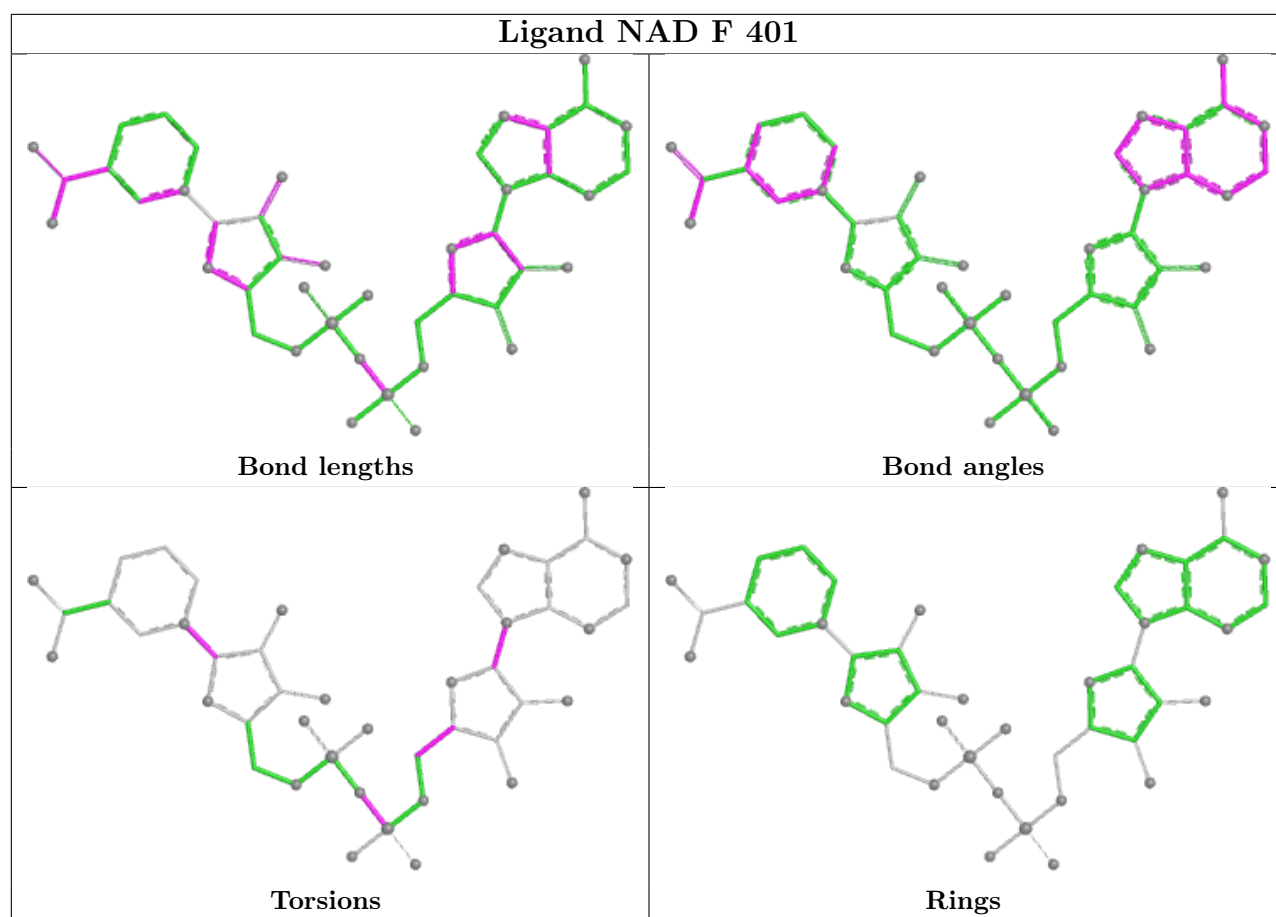
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	401	NAD	2	0
2	D	401	NAD	2	0
2	F	401	NAD	3	0
2	C	401	NAD	1	0
2	A	401	NAD	2	0

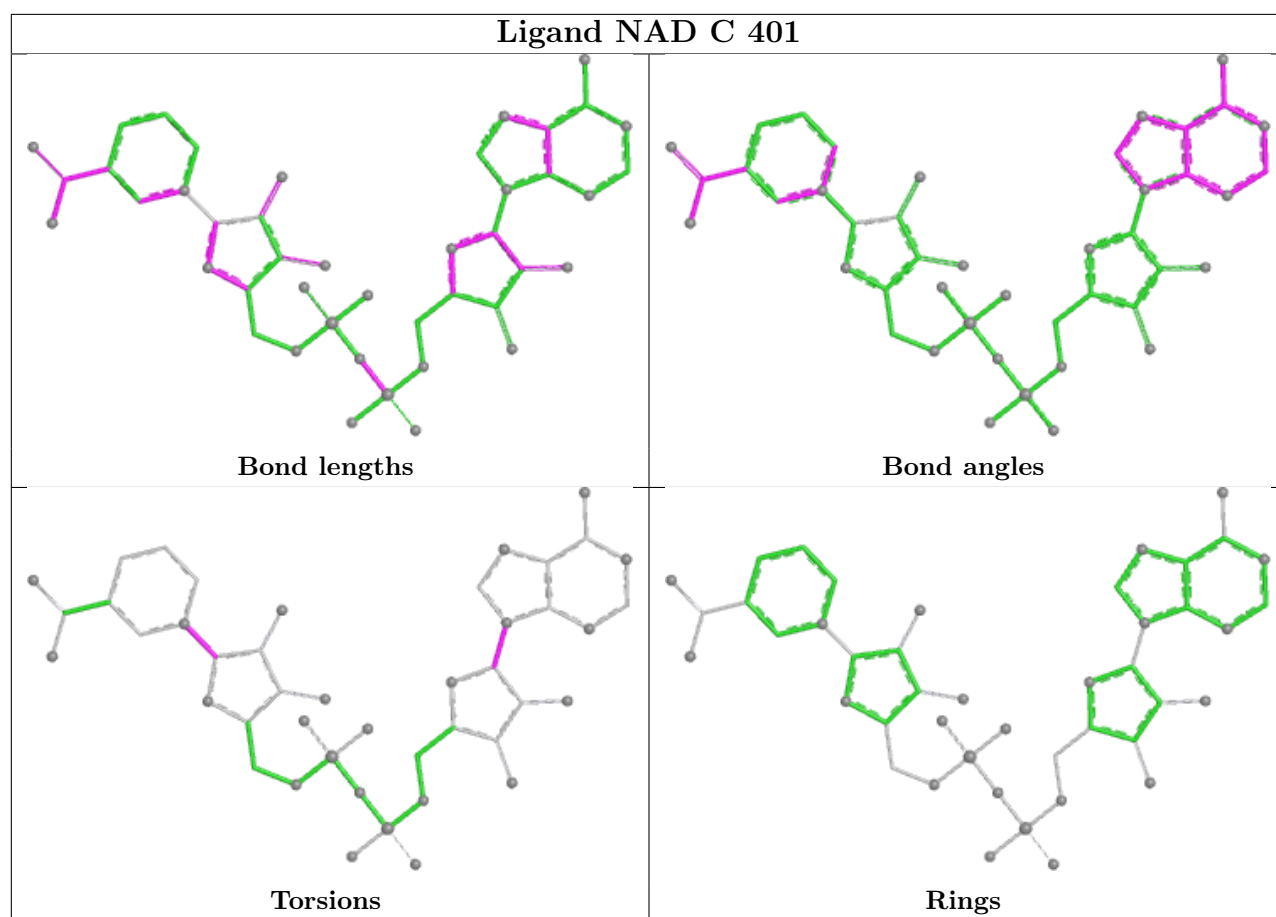
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

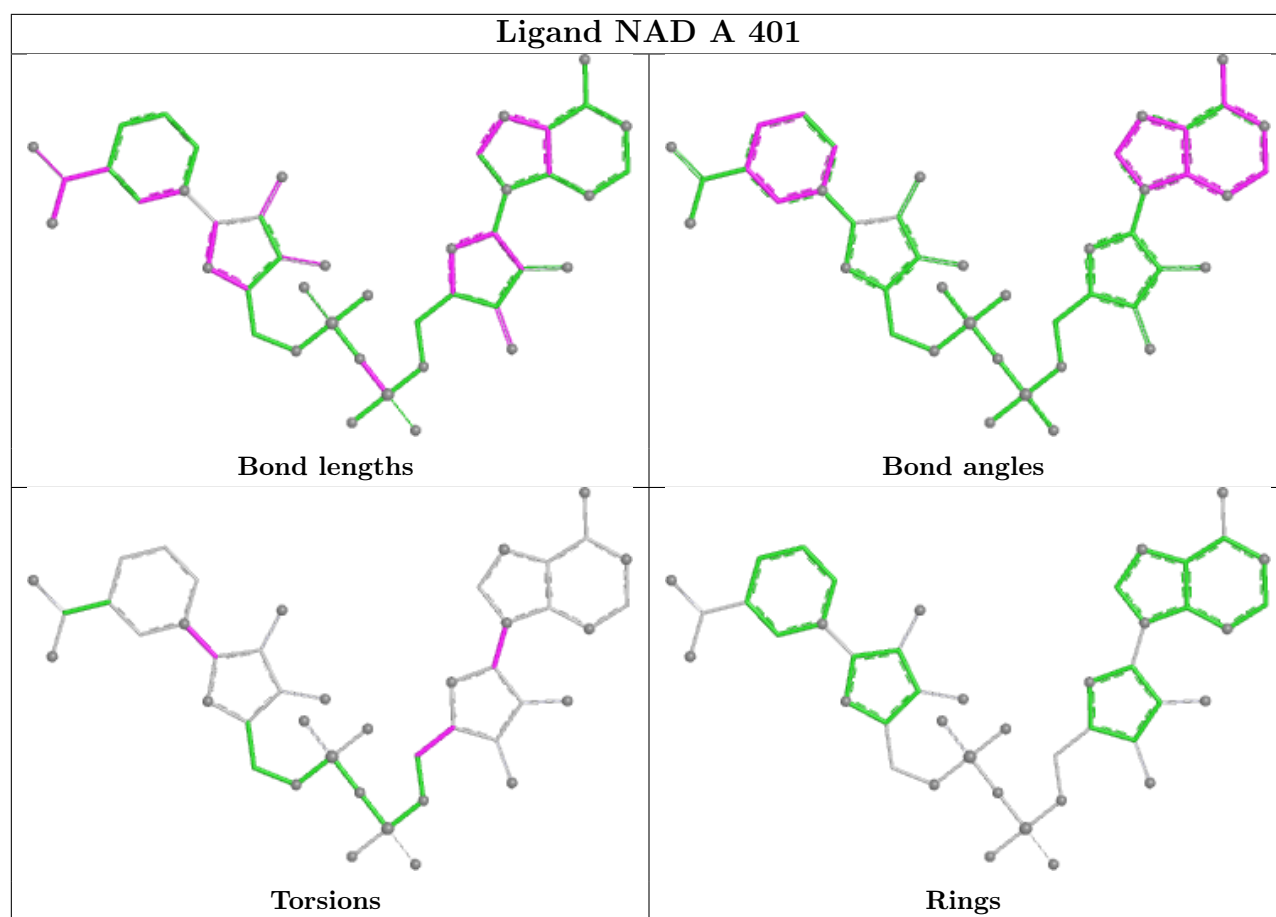












5.7 Other polymers [i](#)

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

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	349/361 (96%)	-0.38	9 (2%)	57	53	17, 23, 53, 119	1 (0%)
1	B	341/361 (94%)	-0.21	8 (2%)	61	57	18, 30, 60, 92	1 (0%)
1	C	340/361 (94%)	-0.30	8 (2%)	59	55	19, 29, 57, 88	0
1	D	341/361 (94%)	0.22	18 (5%)	32	28	21, 37, 69, 108	0
1	E	338/361 (93%)	-0.09	5 (1%)	72	68	21, 35, 62, 91	0
1	F	340/361 (94%)	-0.46	4 (1%)	76	73	18, 24, 47, 105	0
All	All	2049/2166 (94%)	-0.21	52 (2%)	58	54	17, 30, 61, 119	2 (0%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	10.0
1	A	341	ALA	5.8
1	A	340	ASN	5.6
1	F	2	VAL	5.6
1	D	0	HIS	5.2
1	D	2	VAL	5.0
1	B	276	PRO	4.7
1	C	2	VAL	4.3
1	B	0	HIS	4.3
1	B	340	ASN	4.1
1	F	276	PRO	3.9
1	B	1	MET	3.8
1	C	341	ALA	3.8
1	D	65	THR	3.7
1	A	-1	SER	3.7
1	F	275	GLU	3.6
1	A	0	HIS	3.3
1	D	97	PRO	3.1
1	A	2	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	E	275	GLU	2.9
1	E	207	ALA	2.9
1	E	340	ASN	2.9
1	D	207	ALA	2.8
1	D	160	ASP	2.8
1	D	275	GLU	2.8
1	A	-6	LEU	2.7
1	B	275	GLU	2.7
1	D	340	ASN	2.6
1	E	338	GLU	2.6
1	A	276	PRO	2.5
1	D	1	MET	2.5
1	D	210	ASP	2.5
1	C	3	GLU	2.5
1	D	37	ARG	2.5
1	D	208	ALA	2.5
1	C	309	PRO	2.4
1	A	-7	GLY	2.4
1	C	340	ASN	2.4
1	C	4	ARG	2.3
1	B	2	VAL	2.3
1	D	87	ALA	2.3
1	D	100	LEU	2.3
1	E	276	PRO	2.2
1	D	67	ARG	2.1
1	D	308	ARG	2.1
1	D	162	ASP	2.1
1	B	309	PRO	2.1
1	D	276	PRO	2.1
1	C	276	PRO	2.1
1	B	274	TRP	2.1
1	F	3	GLU	2.0
1	C	160	ASP	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](#)

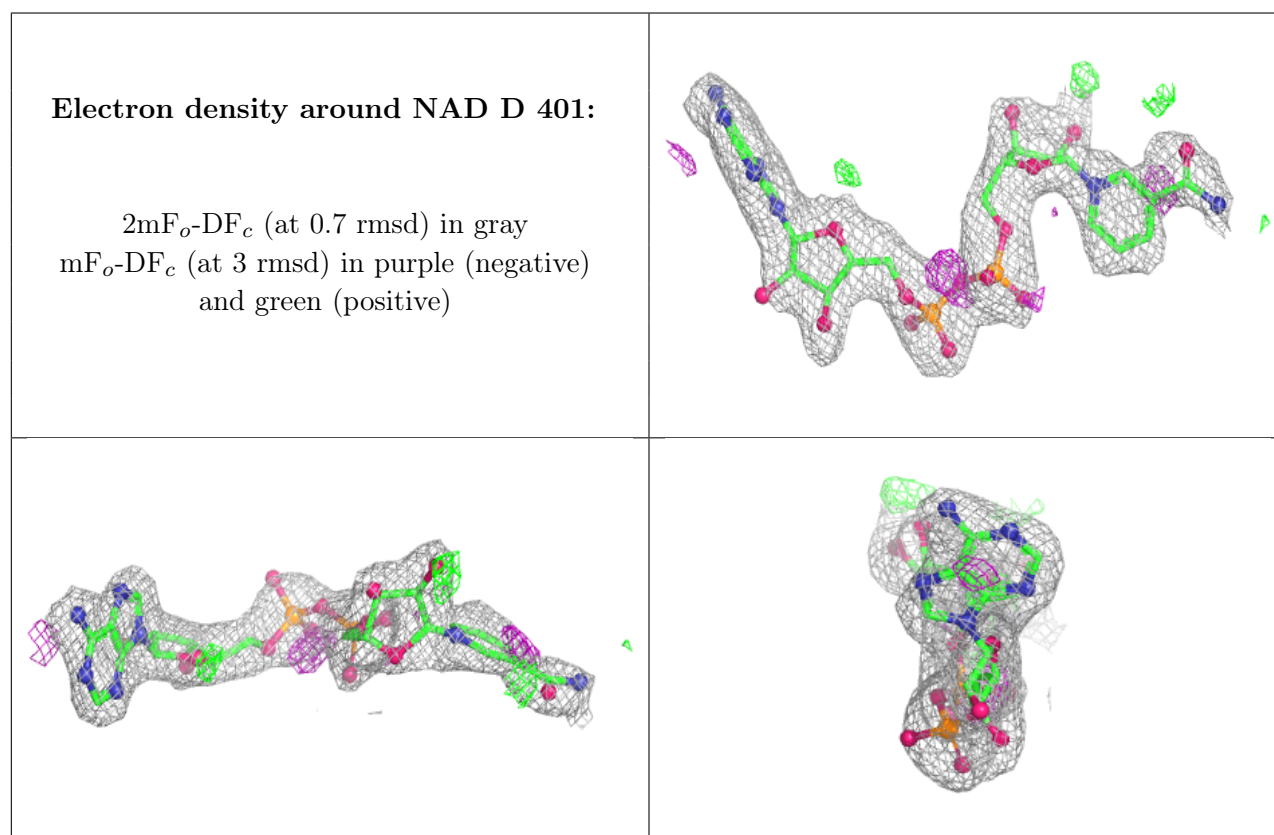
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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.

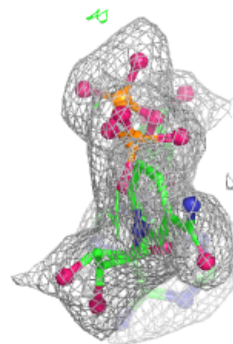
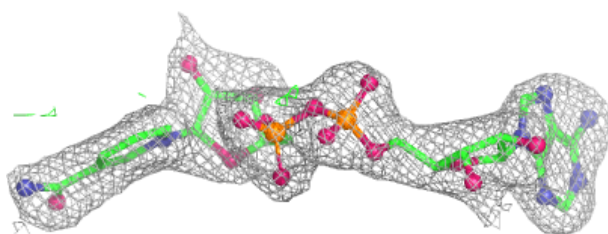
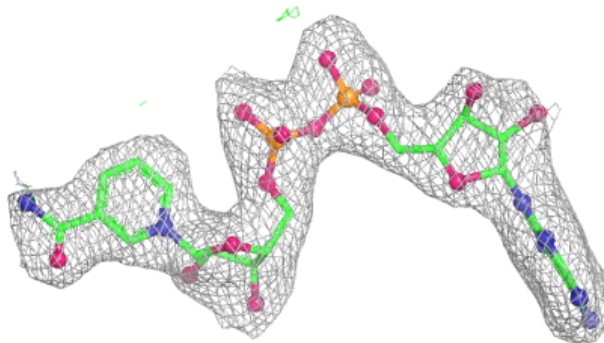
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAD	D	401	44/44	0.86	0.12	49,57,73,99	0
2	NAD	E	401	44/44	0.96	0.08	30,44,57,61	0
2	NAD	C	401	44/44	0.97	0.06	24,32,42,47	0
2	NAD	B	401	44/44	0.98	0.06	20,30,37,45	0
2	NAD	A	401	44/44	0.98	0.05	17,20,26,34	0
2	NAD	F	401	44/44	0.98	0.05	18,21,29,33	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.

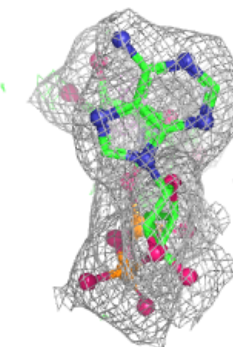
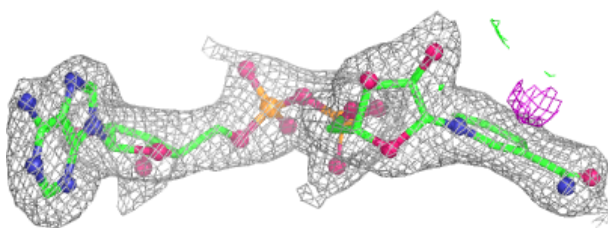
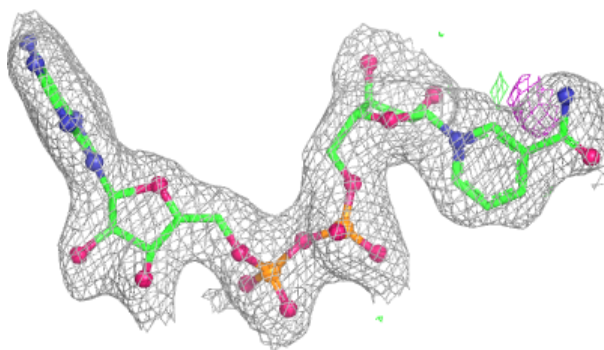


Electron density around NAD E 401:

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

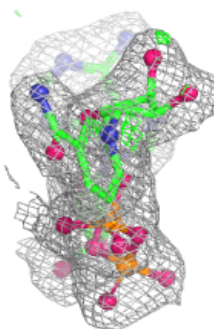
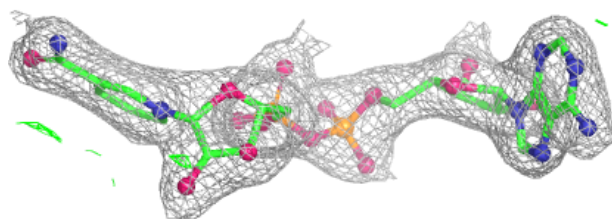
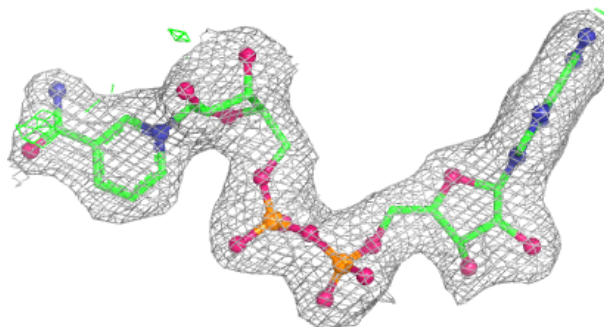
**Electron density around NAD C 401:**

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

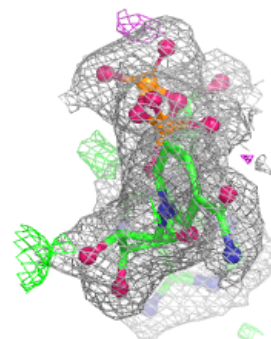
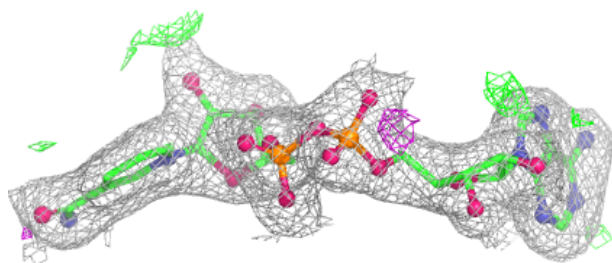
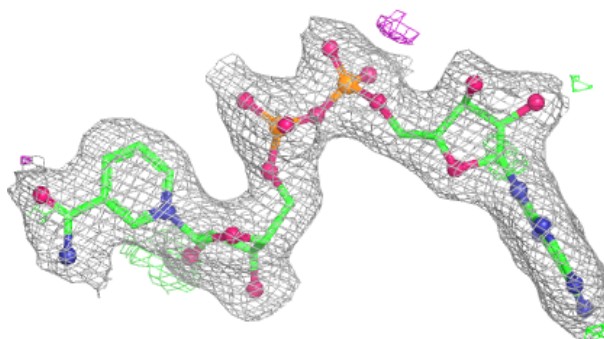


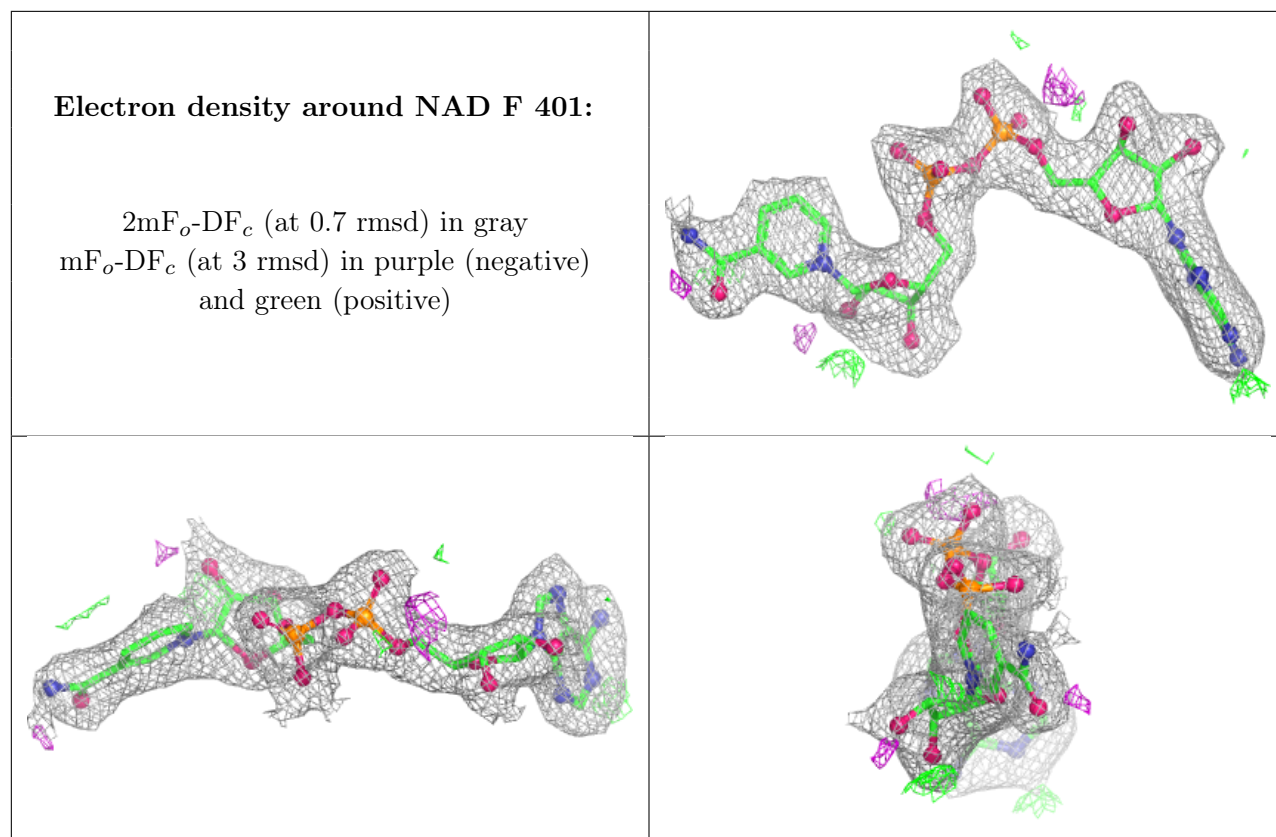
Electron density around NAD B 401:

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

**Electron density around NAD A 401:**

$2mF_o-DF_c$ (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.