



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:17 AM UTC

PDB ID : 1Z0Z / pdb_00001z0z
Title : Crystal structure of a NAD kinase from Archaeoglobus fulgidus in complex with NAD
Authors : Liu, J.; Lou, Y.; Yokota, H.; Adams, P.D.; Kim, R.; Kim, S.H.; Berkeley Structural Genomics Center (BSGC)
Deposited on : 2005-03-02
Resolution : 2.85 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

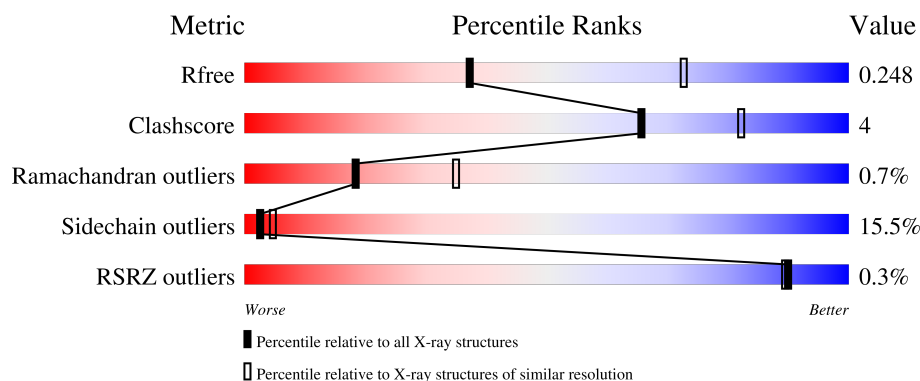
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	278	71% 15% • 10%
1	B	278	68% 19% • 10%
1	C	278	71% 17% • 10%
1	D	278	70% 18% • 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8150 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 Probable inorganic polyphosphate/ATP-NAD kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	0	0	0
			1964	1266	334	356	8			
1	B	249	Total	C	N	O	S	0	0	0
			1964	1266	334	356	8			
1	C	249	Total	C	N	O	S	0	0	0
			1964	1266	334	356	8			
1	D	249	Total	C	N	O	S	0	0	0
			1964	1266	334	356	8			

There are 116 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	cloning artifact	UNP O30297
A	-27	GLY	-	cloning artifact	UNP O30297
A	-26	SER	-	cloning artifact	UNP O30297
A	-25	SER	-	cloning artifact	UNP O30297
A	-24	HIS	-	cloning artifact	UNP O30297
A	-23	HIS	-	cloning artifact	UNP O30297
A	-22	HIS	-	cloning artifact	UNP O30297
A	-21	HIS	-	cloning artifact	UNP O30297
A	-20	HIS	-	cloning artifact	UNP O30297
A	-19	HIS	-	cloning artifact	UNP O30297
A	-18	ASP	-	cloning artifact	UNP O30297
A	-17	TYR	-	cloning artifact	UNP O30297
A	-16	ASP	-	cloning artifact	UNP O30297
A	-15	ILE	-	cloning artifact	UNP O30297
A	-14	PRO	-	cloning artifact	UNP O30297
A	-13	THR	-	cloning artifact	UNP O30297
A	-12	THR	-	cloning artifact	UNP O30297
A	-11	GLU	-	cloning artifact	UNP O30297
A	-10	ASN	-	cloning artifact	UNP O30297
A	-9	LEU	-	cloning artifact	UNP O30297
A	-8	TYR	-	cloning artifact	UNP O30297

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	PHE	-	cloning artifact	UNP O30297
A	-6	GLN	-	cloning artifact	UNP O30297
A	-5	GLY	-	cloning artifact	UNP O30297
A	-4	GLY	-	cloning artifact	UNP O30297
A	-3	GLY	-	cloning artifact	UNP O30297
A	-2	GLY	-	cloning artifact	UNP O30297
A	-1	GLY	-	cloning artifact	UNP O30297
A	0	GLY	-	cloning artifact	UNP O30297
B	-28	MET	-	cloning artifact	UNP O30297
B	-27	GLY	-	cloning artifact	UNP O30297
B	-26	SER	-	cloning artifact	UNP O30297
B	-25	SER	-	cloning artifact	UNP O30297
B	-24	HIS	-	cloning artifact	UNP O30297
B	-23	HIS	-	cloning artifact	UNP O30297
B	-22	HIS	-	cloning artifact	UNP O30297
B	-21	HIS	-	cloning artifact	UNP O30297
B	-20	HIS	-	cloning artifact	UNP O30297
B	-19	HIS	-	cloning artifact	UNP O30297
B	-18	ASP	-	cloning artifact	UNP O30297
B	-17	TYR	-	cloning artifact	UNP O30297
B	-16	ASP	-	cloning artifact	UNP O30297
B	-15	ILE	-	cloning artifact	UNP O30297
B	-14	PRO	-	cloning artifact	UNP O30297
B	-13	THR	-	cloning artifact	UNP O30297
B	-12	THR	-	cloning artifact	UNP O30297
B	-11	GLU	-	cloning artifact	UNP O30297
B	-10	ASN	-	cloning artifact	UNP O30297
B	-9	LEU	-	cloning artifact	UNP O30297
B	-8	TYR	-	cloning artifact	UNP O30297
B	-7	PHE	-	cloning artifact	UNP O30297
B	-6	GLN	-	cloning artifact	UNP O30297
B	-5	GLY	-	cloning artifact	UNP O30297
B	-4	GLY	-	cloning artifact	UNP O30297
B	-3	GLY	-	cloning artifact	UNP O30297
B	-2	GLY	-	cloning artifact	UNP O30297
B	-1	GLY	-	cloning artifact	UNP O30297
B	0	GLY	-	cloning artifact	UNP O30297
C	-28	MET	-	cloning artifact	UNP O30297
C	-27	GLY	-	cloning artifact	UNP O30297
C	-26	SER	-	cloning artifact	UNP O30297
C	-25	SER	-	cloning artifact	UNP O30297
C	-24	HIS	-	cloning artifact	UNP O30297

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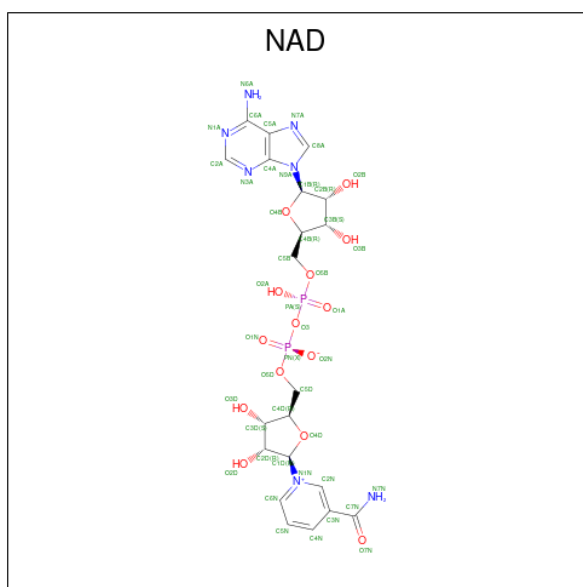
Chain	Residue	Modelled	Actual	Comment	Reference
C	-23	HIS	-	cloning artifact	UNP O30297
C	-22	HIS	-	cloning artifact	UNP O30297
C	-21	HIS	-	cloning artifact	UNP O30297
C	-20	HIS	-	cloning artifact	UNP O30297
C	-19	HIS	-	cloning artifact	UNP O30297
C	-18	ASP	-	cloning artifact	UNP O30297
C	-17	TYR	-	cloning artifact	UNP O30297
C	-16	ASP	-	cloning artifact	UNP O30297
C	-15	ILE	-	cloning artifact	UNP O30297
C	-14	PRO	-	cloning artifact	UNP O30297
C	-13	THR	-	cloning artifact	UNP O30297
C	-12	THR	-	cloning artifact	UNP O30297
C	-11	GLU	-	cloning artifact	UNP O30297
C	-10	ASN	-	cloning artifact	UNP O30297
C	-9	LEU	-	cloning artifact	UNP O30297
C	-8	TYR	-	cloning artifact	UNP O30297
C	-7	PHE	-	cloning artifact	UNP O30297
C	-6	GLN	-	cloning artifact	UNP O30297
C	-5	GLY	-	cloning artifact	UNP O30297
C	-4	GLY	-	cloning artifact	UNP O30297
C	-3	GLY	-	cloning artifact	UNP O30297
C	-2	GLY	-	cloning artifact	UNP O30297
C	-1	GLY	-	cloning artifact	UNP O30297
C	0	GLY	-	cloning artifact	UNP O30297
D	-28	MET	-	cloning artifact	UNP O30297
D	-27	GLY	-	cloning artifact	UNP O30297
D	-26	SER	-	cloning artifact	UNP O30297
D	-25	SER	-	cloning artifact	UNP O30297
D	-24	HIS	-	cloning artifact	UNP O30297
D	-23	HIS	-	cloning artifact	UNP O30297
D	-22	HIS	-	cloning artifact	UNP O30297
D	-21	HIS	-	cloning artifact	UNP O30297
D	-20	HIS	-	cloning artifact	UNP O30297
D	-19	HIS	-	cloning artifact	UNP O30297
D	-18	ASP	-	cloning artifact	UNP O30297
D	-17	TYR	-	cloning artifact	UNP O30297
D	-16	ASP	-	cloning artifact	UNP O30297
D	-15	ILE	-	cloning artifact	UNP O30297
D	-14	PRO	-	cloning artifact	UNP O30297
D	-13	THR	-	cloning artifact	UNP O30297
D	-12	THR	-	cloning artifact	UNP O30297
D	-11	GLU	-	cloning artifact	UNP O30297

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-10	ASN	-	cloning artifact	UNP O30297
D	-9	LEU	-	cloning artifact	UNP O30297
D	-8	TYR	-	cloning artifact	UNP O30297
D	-7	PHE	-	cloning artifact	UNP O30297
D	-6	GLN	-	cloning artifact	UNP O30297
D	-5	GLY	-	cloning artifact	UNP O30297
D	-4	GLY	-	cloning artifact	UNP O30297
D	-3	GLY	-	cloning artifact	UNP O30297
D	-2	GLY	-	cloning artifact	UNP O30297
D	-1	GLY	-	cloning artifact	UNP O30297
D	0	GLY	-	cloning artifact	UNP O30297

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



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

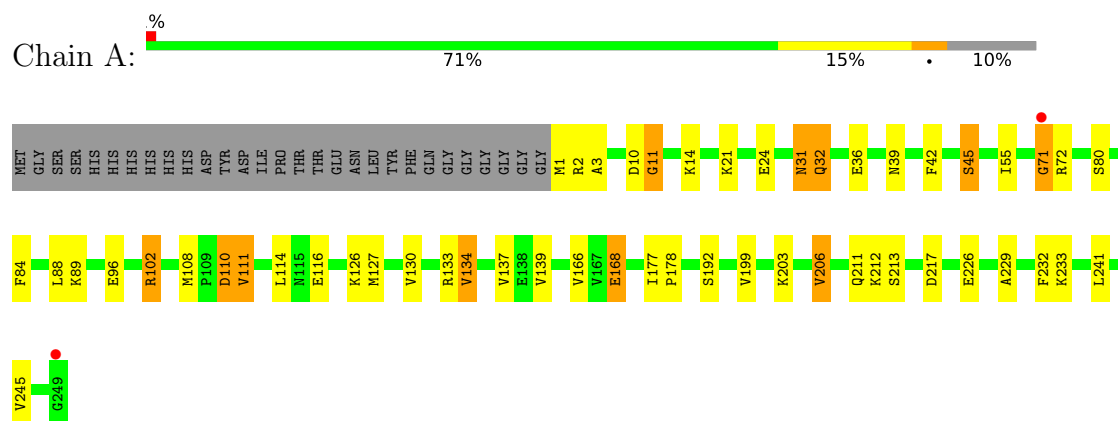
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	33	Total 33	O 33	0	0
3	B	31	Total 31	O 31	0	0
3	C	24	Total 24	O 24	0	0
3	D	30	Total 30	O 30	0	0

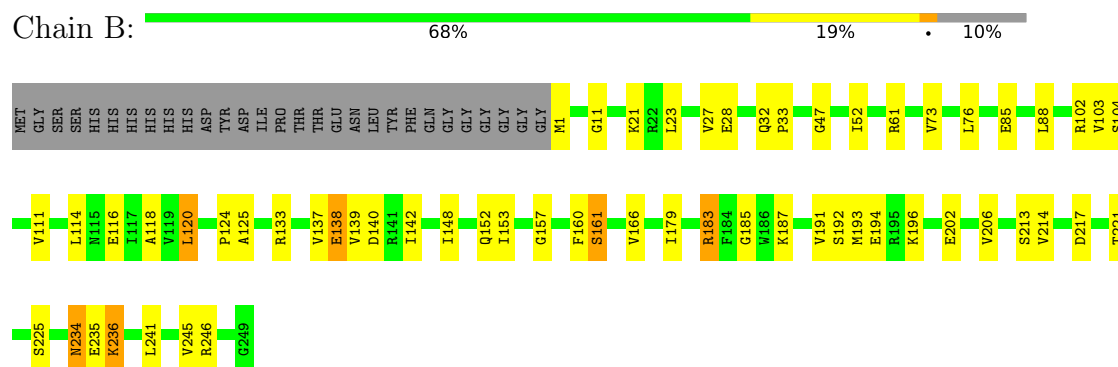
3 Residue-property plots

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.

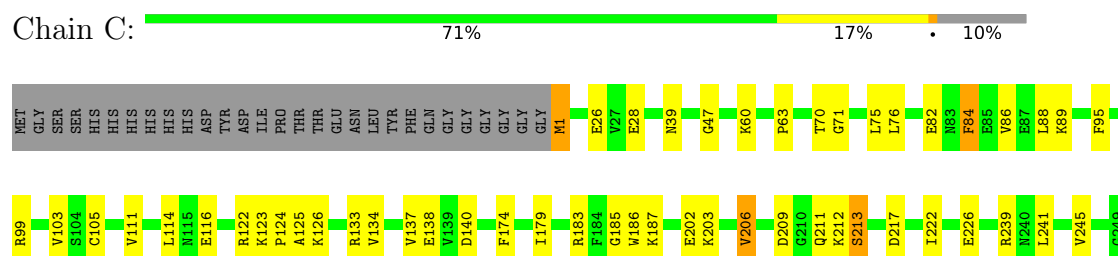
- Molecule 1: Probable inorganic polyphosphate/ATP-NAD kinase



- Molecule 1: Probable inorganic polyphosphate/ATP-NAD kinase

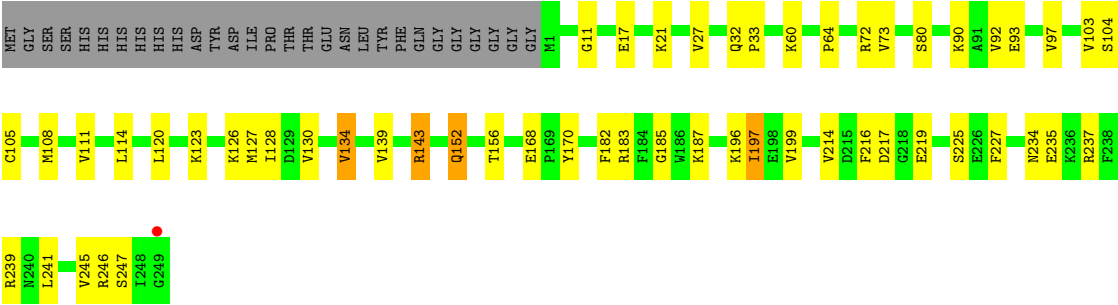


- Molecule 1: Probable inorganic polyphosphate/ATP-NAD kinase



- Molecule 1: Probable inorganic polyphosphate/ATP-NAD kinase

Chain D: 70% 18% 10%



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	122.41 Å 122.41 Å 201.87 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.85 20.00 – 2.85	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.85) 75.8 (20.00-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.83 Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.208 , 0.275 (Not available) , 0.248	Depositor DCC
R_{free} test set	1716 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	67.7	Xtrriage
Anisotropy	0.370	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8150	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.20 % 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 6.6888e-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 [i](#)

5.1 Standard geometry [i](#)

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	0.68	0/2002	1.08	6/2699 (0.2%)
1	B	0.70	0/2002	0.94	1/2699 (0.0%)
1	C	0.68	0/2002	0.89	1/2699 (0.0%)
1	D	0.67	0/2002	0.90	0/2699
All	All	0.68	0/8008	0.96	8/10796 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	110	ASP	CB-CA-C	-24.33	74.02	111.73
1	A	111	VAL	N-CA-C	-14.26	89.53	108.35
1	A	71	GLY	N-CA-C	12.73	143.35	113.18
1	B	140	ASP	N-CA-C	5.83	117.11	108.60
1	A	72	ARG	N-CA-C	-5.28	99.56	110.80
1	A	116	GLU	N-CA-C	5.17	116.16	108.60
1	A	110	ASP	N-CA-C	5.07	116.86	107.73
1	C	63	PRO	O-C-N	5.04	123.52	121.15

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	A	1964	0	2015	16	0
1	B	1964	0	2015	15	0
1	C	1964	0	2015	15	0
1	D	1964	0	2015	18	0
2	A	44	0	26	0	0
2	B	44	0	26	1	0
2	C	44	0	26	0	0
2	D	44	0	26	2	0
3	A	33	0	0	2	0
3	B	31	0	0	0	0
3	C	24	0	0	1	0
3	D	30	0	0	1	0
All	All	8150	0	8164	62	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 (62) 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:1:MET:N	3:A:3093:HOH:O	1.89	1.06
1:A:110:ASP:O	3:A:3100:HOH:O	1.86	0.92
1:D:183:ARG:HD2	1:D:185:GLY:O	1.85	0.76
1:A:166:VAL:HG23	1:B:187:LYS:HG2	1.79	0.64
1:C:70:THR:HG23	1:C:71:GLY:H	1.62	0.63
1:D:127:MET:HE1	1:D:182:PHE:HB2	1.80	0.62
1:C:209:ASP:O	1:C:211:GLN:HG2	2.00	0.62
1:D:123:LYS:NZ	3:D:3089:HOH:O	2.29	0.60
1:C:183:ARG:HD2	1:C:185:GLY:O	2.02	0.59
1:B:183:ARG:HD2	1:B:185:GLY:O	2.03	0.59
1:B:133:ARG:HG2	1:B:138:GLU:HA	1.87	0.57
1:A:31:ASN:HD22	1:A:32:GLN:HG2	1.70	0.56
1:D:143:ARG:HG3	1:D:143:ARG:HH11	1.69	0.56
1:D:152:GLN:H	1:D:152:GLN:HE21	1.52	0.55
1:C:1:MET:N	3:C:3078:HOH:O	2.39	0.55
1:A:134:VAL:HG13	1:A:139:VAL:HG21	1.89	0.54
1:C:124:PRO:O	1:C:125:ALA:HB3	2.08	0.54
1:A:232:PHE:O	1:A:233:LYS:C	2.50	0.54
1:B:234:ASN:HD22	1:B:234:ASN:C	2.17	0.52
1:D:32:GLN:HB2	1:D:33:PRO:CD	2.40	0.51
1:C:202:GLU:O	1:C:203:LYS:C	2.54	0.51
1:C:140:ASP:OD1	1:C:183:ARG:NH2	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:202:GLU:OE1	1:C:217:ASP:HB3	2.10	0.50
1:C:84:PHE:CD1	1:C:84:PHE:C	2.89	0.50
1:C:103:VAL:HG11	1:C:174:PHE:HE2	1.77	0.49
1:C:137:VAL:HG21	1:D:239:ARG:HA	1.94	0.49
1:B:234:ASN:HD22	1:B:236:LYS:H	1.60	0.48
1:A:206:VAL:O	1:A:213:SER:HA	2.13	0.48
1:A:45:SER:HB2	1:A:55:ILE:CD1	2.43	0.48
1:B:142:ILE:HD12	1:B:183:ARG:CZ	2.44	0.48
1:A:168:GLU:HG2	1:B:191:VAL:HA	1.96	0.47
1:C:186:TRP:O	1:C:187:LYS:HG2	2.13	0.47
1:A:102:ARG:HD3	1:A:229:ALA:HB2	1.96	0.46
1:A:2:ARG:NH1	1:A:39:ASN:O	2.48	0.46
1:D:134:VAL:CG1	1:D:139:VAL:HG11	2.46	0.45
1:A:80:SER:O	1:A:84:PHE:HB3	2.17	0.45
1:B:124:PRO:O	1:B:125:ALA:HB3	2.17	0.44
1:B:157:GLY:O	1:B:160:PHE:HB3	2.18	0.44
1:D:17:GLU:HG2	1:D:27:VAL:HG21	1.99	0.44
1:B:161:SER:OG	2:B:3076:NAD:N7N	2.51	0.43
1:D:197:ILE:CD1	1:D:197:ILE:N	2.82	0.43
1:D:168:GLU:HG2	1:D:170:TYR:H	1.82	0.43
1:B:61:ARG:CZ	1:B:61:ARG:HB3	2.48	0.43
1:D:72:ARG:NH2	1:D:247:SER:O	2.52	0.43
2:D:3078:NAD:H51N	2:D:3078:NAD:O2A	2.18	0.43
1:D:156:THR:O	2:D:3078:NAD:C2A	2.67	0.43
1:C:206:VAL:O	1:C:213:SER:HA	2.18	0.43
1:D:143:ARG:HH11	1:D:143:ARG:CG	2.31	0.43
1:D:234:ASN:HB3	1:D:237:ARG:HB2	2.00	0.42
1:A:10:ASP:O	1:A:11:GLY:C	2.62	0.42
1:A:3:ALA:HB2	1:A:42:PHE:CE2	2.54	0.42
1:D:152:GLN:H	1:D:152:GLN:NE2	2.17	0.42
1:A:130:VAL:HG13	1:A:199:VAL:HG13	2.01	0.41
1:C:1:MET:HE1	1:C:95:PHE:CD1	2.55	0.41
1:A:177:ILE:HG13	1:A:178:PRO:HD2	2.02	0.41
1:B:152:GLN:HG2	1:B:153:ILE:N	2.35	0.41
1:D:134:VAL:HA	1:D:196:LYS:O	2.19	0.41
1:B:32:GLN:HB2	1:B:33:PRO:HD2	2.02	0.41
1:B:148:ILE:HD11	1:B:179:ILE:HD11	2.02	0.40
1:B:118:ALA:HB1	1:B:120:LEU:HD21	2.04	0.40
1:D:130:VAL:HG13	1:D:199:VAL:HG13	2.04	0.40
1:C:47:GLY:HA2	1:C:70:THR:HG22	2.03	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	A	247/278 (89%)	226 (92%)	19 (8%)	2 (1%)	16	31
1	B	247/278 (89%)	228 (92%)	17 (7%)	2 (1%)	16	31
1	C	247/278 (89%)	224 (91%)	23 (9%)	0	100	100
1	D	247/278 (89%)	225 (91%)	19 (8%)	3 (1%)	10	22
All	All	988/1112 (89%)	903 (91%)	78 (8%)	7 (1%)	18	35

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	GLY
1	A	71	GLY
1	B	11	GLY
1	D	64	PRO
1	D	128	ILE
1	B	47	GLY
1	D	11	GLY

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	213/235 (91%)	184 (86%)	29 (14%)	3	7
1	B	213/235 (91%)	173 (81%)	40 (19%)	1	2
1	C	213/235 (91%)	181 (85%)	32 (15%)	3	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	213/235 (91%)	182 (85%)	31 (15%)	3	5
All	All	852/940 (91%)	720 (84%)	132 (16%)	2	5

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LYS
1	A	21	LYS
1	A	24	GLU
1	A	31	ASN
1	A	32	GLN
1	A	36	GLU
1	A	45	SER
1	A	88	LEU
1	A	89	LYS
1	A	96	GLU
1	A	102	ARG
1	A	108	MET
1	A	111	VAL
1	A	114	LEU
1	A	126	LYS
1	A	127	MET
1	A	133	ARG
1	A	134	VAL
1	A	137	VAL
1	A	168	GLU
1	A	192	SER
1	A	203	LYS
1	A	206	VAL
1	A	211	GLN
1	A	212	LYS
1	A	217	ASP
1	A	226	GLU
1	A	241	LEU
1	A	245	VAL
1	B	1	MET
1	B	21	LYS
1	B	23	LEU
1	B	27	VAL
1	B	28	GLU
1	B	52	ILE
1	B	73	VAL

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Mol	Chain	Res	Type
1	B	76	LEU
1	B	85	GLU
1	B	88	LEU
1	B	102	ARG
1	B	103	VAL
1	B	104	SER
1	B	111	VAL
1	B	114	LEU
1	B	116	GLU
1	B	120	LEU
1	B	137	VAL
1	B	138	GLU
1	B	139	VAL
1	B	161	SER
1	B	166	VAL
1	B	183	ARG
1	B	192	SER
1	B	193	MET
1	B	194	GLU
1	B	196	LYS
1	B	202	GLU
1	B	206	VAL
1	B	213	SER
1	B	214	VAL
1	B	217	ASP
1	B	221	THR
1	B	225	SER
1	B	234	ASN
1	B	235	GLU
1	B	236	LYS
1	B	241	LEU
1	B	245	VAL
1	B	246	ARG
1	C	1	MET
1	C	26	GLU
1	C	28	GLU
1	C	39	ASN
1	C	60	LYS
1	C	75	LEU
1	C	76	LEU
1	C	82	GLU
1	C	84	PHE

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Mol	Chain	Res	Type
1	C	86	VAL
1	C	88	LEU
1	C	89	LYS
1	C	99	ARG
1	C	105	CYS
1	C	111	VAL
1	C	114	LEU
1	C	116	GLU
1	C	122	ARG
1	C	123	LYS
1	C	126	LYS
1	C	133	ARG
1	C	134	VAL
1	C	138	GLU
1	C	179	ILE
1	C	206	VAL
1	C	212	LYS
1	C	213	SER
1	C	222	ILE
1	C	226	GLU
1	C	239	ARG
1	C	241	LEU
1	C	245	VAL
1	D	21	LYS
1	D	60	LYS
1	D	73	VAL
1	D	80	SER
1	D	90	LYS
1	D	92	VAL
1	D	93	GLU
1	D	97	VAL
1	D	103	VAL
1	D	104	SER
1	D	105	CYS
1	D	108	MET
1	D	111	VAL
1	D	114	LEU
1	D	120	LEU
1	D	126	LYS
1	D	134	VAL
1	D	143	ARG
1	D	152	GLN

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Mol	Chain	Res	Type
1	D	187	LYS
1	D	197	ILE
1	D	214	VAL
1	D	216	PHE
1	D	217	ASP
1	D	219	GLU
1	D	225	SER
1	D	227	PHE
1	D	235	GLU
1	D	241	LEU
1	D	245	VAL
1	D	246	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	78	HIS
1	B	57	GLN
1	B	78	HIS
1	B	83	ASN
1	B	211	GLN
1	B	234	ASN
1	C	39	ASN
1	C	83	ASN
1	C	234	ASN
1	D	32	GLN
1	D	152	GLN

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

4 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	C	3077	-	46,48,48	1.92	7 (15%)	64,73,73	1.67	11 (17%)
2	NAD	A	3075	-	46,48,48	1.95	6 (13%)	64,73,73	1.72	14 (21%)
2	NAD	D	3078	-	46,48,48	1.99	6 (13%)	64,73,73	1.70	14 (21%)
2	NAD	B	3076	-	46,48,48	2.09	6 (13%)	64,73,73	1.76	14 (21%)

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	C	3077	-	-	4/30/62/62	0/5/5/5
2	NAD	A	3075	-	-	3/30/62/62	0/5/5/5
2	NAD	D	3078	-	-	8/30/62/62	0/5/5/5
2	NAD	B	3076	-	-	7/30/62/62	0/5/5/5

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3075	NAD	O7N-C7N	10.03	1.42	1.24
2	D	3078	NAD	O7N-C7N	9.86	1.42	1.24
2	C	3077	NAD	O7N-C7N	9.69	1.42	1.24
2	B	3076	NAD	O7N-C7N	9.36	1.41	1.24
2	B	3076	NAD	PA-O3	4.68	1.64	1.59
2	B	3076	NAD	PN-O3	4.53	1.64	1.59
2	B	3076	NAD	C2N-N1N	3.92	1.39	1.35
2	D	3078	NAD	PA-O3	3.77	1.63	1.59
2	D	3078	NAD	PN-O3	3.66	1.63	1.59
2	A	3075	NAD	C2A-N1A	3.49	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3076	NAD	C2A-N1A	3.45	1.40	1.33
2	B	3076	NAD	C2A-N3A	3.37	1.39	1.33
2	C	3077	NAD	C2A-N1A	3.32	1.39	1.33
2	A	3075	NAD	PN-O3	3.18	1.62	1.59
2	C	3077	NAD	C2N-N1N	3.11	1.38	1.35
2	D	3078	NAD	C2N-N1N	3.07	1.38	1.35
2	D	3078	NAD	C2A-N1A	3.01	1.39	1.33
2	C	3077	NAD	PA-O3	2.98	1.62	1.59
2	C	3077	NAD	C2A-N3A	2.89	1.39	1.33
2	A	3075	NAD	C2A-N3A	2.77	1.38	1.33
2	C	3077	NAD	PN-O3	2.70	1.62	1.59
2	A	3075	NAD	PA-O3	2.68	1.62	1.59
2	D	3078	NAD	C2A-N3A	2.65	1.38	1.33
2	C	3077	NAD	C8A-N7A	2.51	1.36	1.31
2	A	3075	NAD	C2N-N1N	2.34	1.37	1.35

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	3078	NAD	N3A-C2A-N1A	-6.13	119.31	128.58
2	C	3077	NAD	N3A-C2A-N1A	-5.99	119.51	128.58
2	A	3075	NAD	N3A-C2A-N1A	-5.72	119.93	128.58
2	B	3076	NAD	N3A-C2A-N1A	-5.10	120.86	128.58
2	A	3075	NAD	N9A-C8A-N7A	-4.55	107.47	113.94
2	D	3078	NAD	N9A-C8A-N7A	-4.24	107.92	113.94
2	B	3076	NAD	C5A-C4A-N3A	-4.22	120.90	126.72
2	B	3076	NAD	N9A-C8A-N7A	-4.20	107.97	113.94
2	B	3076	NAD	C5A-N7A-C8A	3.99	109.72	103.45
2	C	3077	NAD	C5A-C4A-N3A	-3.91	121.34	126.72
2	C	3077	NAD	N9A-C8A-N7A	-3.86	108.46	113.94
2	D	3078	NAD	C5A-C4A-N3A	-3.82	121.46	126.72
2	A	3075	NAD	C4A-N9A-C8A	3.76	109.69	105.74
2	B	3076	NAD	O2A-PA-O3	3.71	117.31	107.27
2	D	3078	NAD	C5A-N7A-C8A	3.55	109.03	103.45
2	C	3077	NAD	O7N-C7N-N7N	-3.44	117.65	122.62
2	D	3078	NAD	C2A-N3A-C4A	3.40	120.14	111.83
2	C	3077	NAD	C5A-N7A-C8A	3.38	108.77	103.45
2	C	3077	NAD	C2A-N3A-C4A	3.31	119.91	111.83
2	A	3075	NAD	C5A-N7A-C8A	3.16	108.42	103.45
2	B	3076	NAD	C2A-N3A-C4A	3.13	119.48	111.83
2	B	3076	NAD	C6N-N1N-C2N	-3.13	119.21	121.88
2	B	3076	NAD	C4A-C5A-N7A	-3.11	107.03	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3076	NAD	O7N-C7N-N7N	-3.09	118.16	122.62
2	B	3076	NAD	O5B-PA-O1A	-3.07	96.77	108.94
2	A	3075	NAD	C3N-C7N-N7N	3.02	121.46	117.74
2	D	3078	NAD	O2A-PA-O3	2.86	115.01	107.27
2	D	3078	NAD	N3A-C4A-N9A	2.83	131.98	127.17
2	D	3078	NAD	C4A-N9A-C8A	2.81	108.69	105.74
2	A	3075	NAD	O2A-PA-O3	2.76	114.74	107.27
2	B	3076	NAD	N3A-C4A-N9A	2.76	131.87	127.17
2	A	3075	NAD	C2A-N3A-C4A	2.68	118.37	111.83
2	B	3076	NAD	O2A-PA-O5B	2.66	119.64	107.57
2	A	3075	NAD	C5A-C4A-N3A	-2.66	123.06	126.72
2	A	3075	NAD	O2N-PN-O1N	2.62	124.66	112.44
2	D	3078	NAD	O7N-C7N-N7N	-2.61	118.84	122.62
2	A	3075	NAD	N3A-C4A-N9A	2.58	131.55	127.17
2	A	3075	NAD	C4A-N9A-C1B	-2.56	120.65	126.63
2	C	3077	NAD	N3A-C4A-N9A	2.52	131.45	127.17
2	C	3077	NAD	O2N-PN-O1N	2.51	124.12	112.44
2	D	3078	NAD	C4A-C5A-N7A	-2.43	107.80	110.58
2	A	3075	NAD	O7N-C7N-N7N	-2.42	119.11	122.62
2	C	3077	NAD	C3N-C7N-N7N	2.42	120.72	117.74
2	D	3078	NAD	C6N-N1N-C2N	-2.37	119.86	121.88
2	D	3078	NAD	O2A-PA-O5B	2.34	118.16	107.57
2	C	3077	NAD	C6N-N1N-C2N	-2.30	119.92	121.88
2	C	3077	NAD	C4A-C5A-N7A	-2.30	107.95	110.58
2	B	3076	NAD	C4A-N9A-C8A	2.21	108.06	105.74
2	D	3078	NAD	C4A-N9A-C1B	-2.18	121.54	126.63
2	A	3075	NAD	C5A-C6A-N6A	-2.18	117.89	123.29
2	D	3078	NAD	O2N-PN-O1N	2.11	122.26	112.44
2	B	3076	NAD	O7N-C7N-C3N	2.06	122.11	119.60
2	A	3075	NAD	N6A-C6A-N1A	2.02	122.87	118.38

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	3075	NAD	O4D-C1D-N1N-C6N
2	B	3076	NAD	O4D-C1D-N1N-C6N
2	D	3078	NAD	O4D-C1D-N1N-C6N
2	A	3075	NAD	O4B-C4B-C5B-O5B
2	B	3076	NAD	C2B-C1B-N9A-C8A
2	D	3078	NAD	C2B-C1B-N9A-C8A
2	D	3078	NAD	O4B-C4B-C5B-O5B

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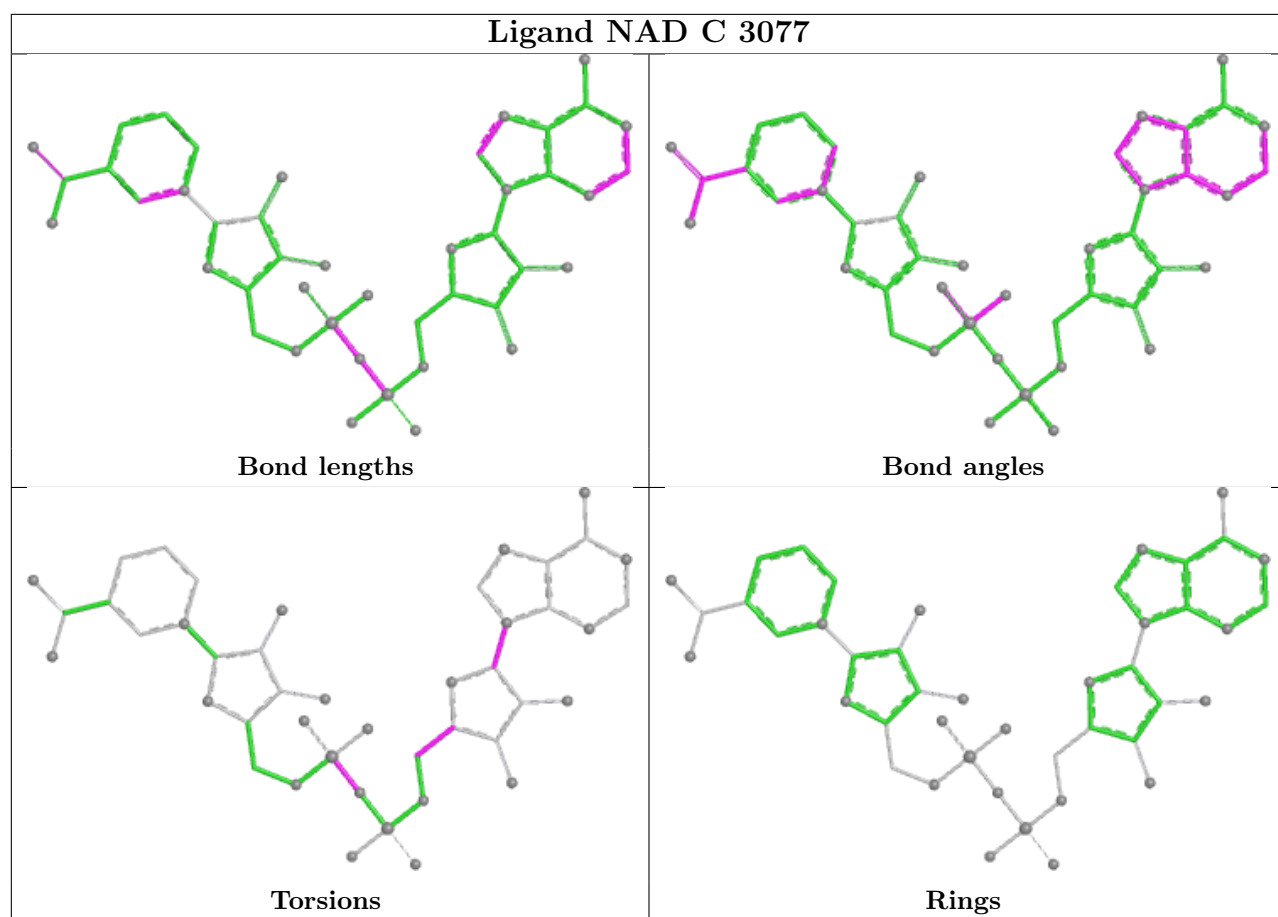
Mol	Chain	Res	Type	Atoms
2	C	3077	NAD	C2B-C1B-N9A-C8A
2	A	3075	NAD	O4D-C1D-N1N-C2N
2	B	3076	NAD	O4D-C1D-N1N-C2N
2	D	3078	NAD	O4D-C1D-N1N-C2N
2	B	3076	NAD	PN-O3-PA-O2A
2	D	3078	NAD	PN-O3-PA-O2A
2	D	3078	NAD	O4D-C4D-C5D-O5D
2	B	3076	NAD	O4B-C1B-N9A-C8A
2	D	3078	NAD	PN-O3-PA-O1A
2	D	3078	NAD	O4B-C1B-N9A-C8A
2	C	3077	NAD	O4B-C4B-C5B-O5B
2	C	3077	NAD	O4B-C1B-N9A-C8A
2	B	3076	NAD	PN-O3-PA-O1A
2	C	3077	NAD	PA-O3-PN-O2N
2	B	3076	NAD	O4B-C4B-C5B-O5B

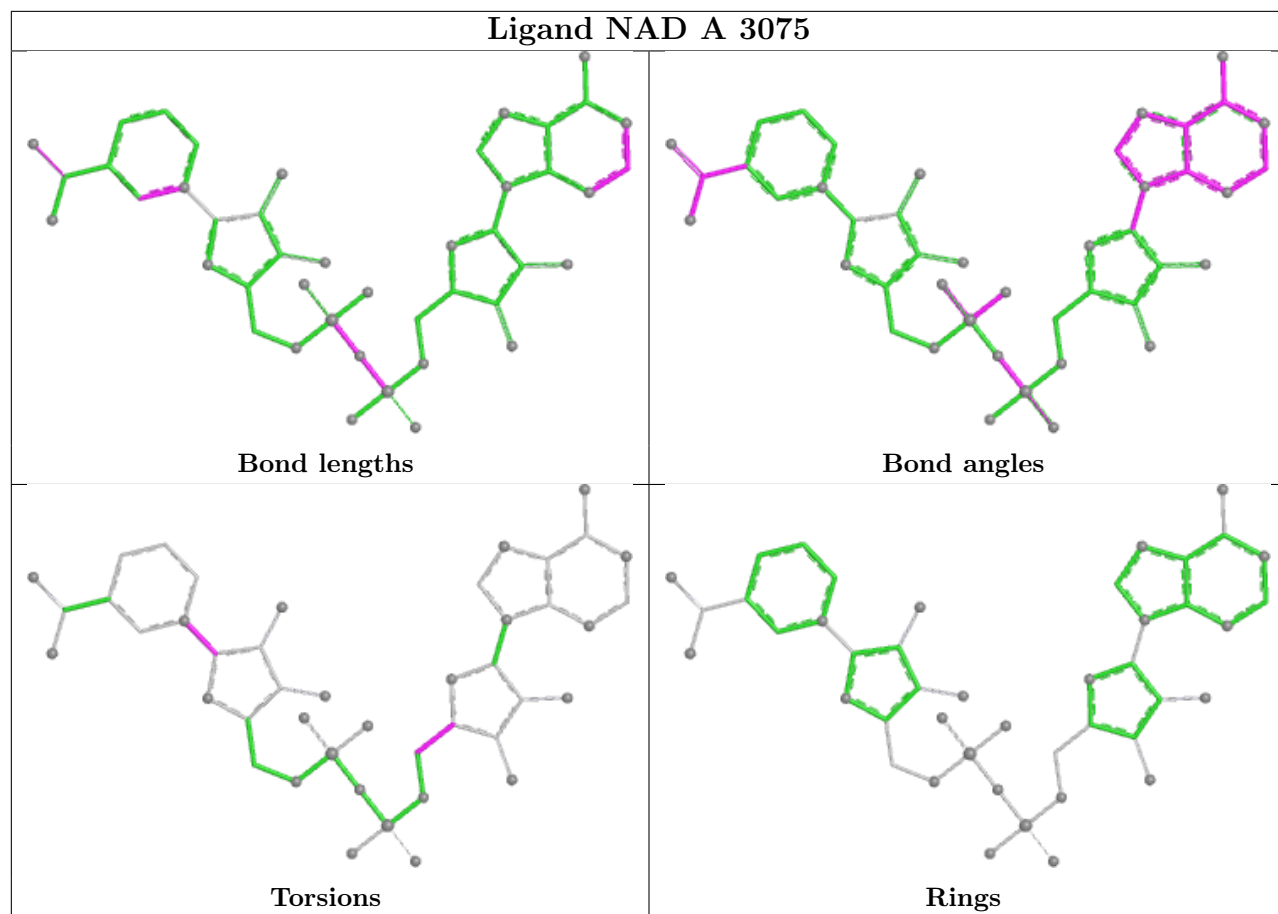
There are no ring outliers.

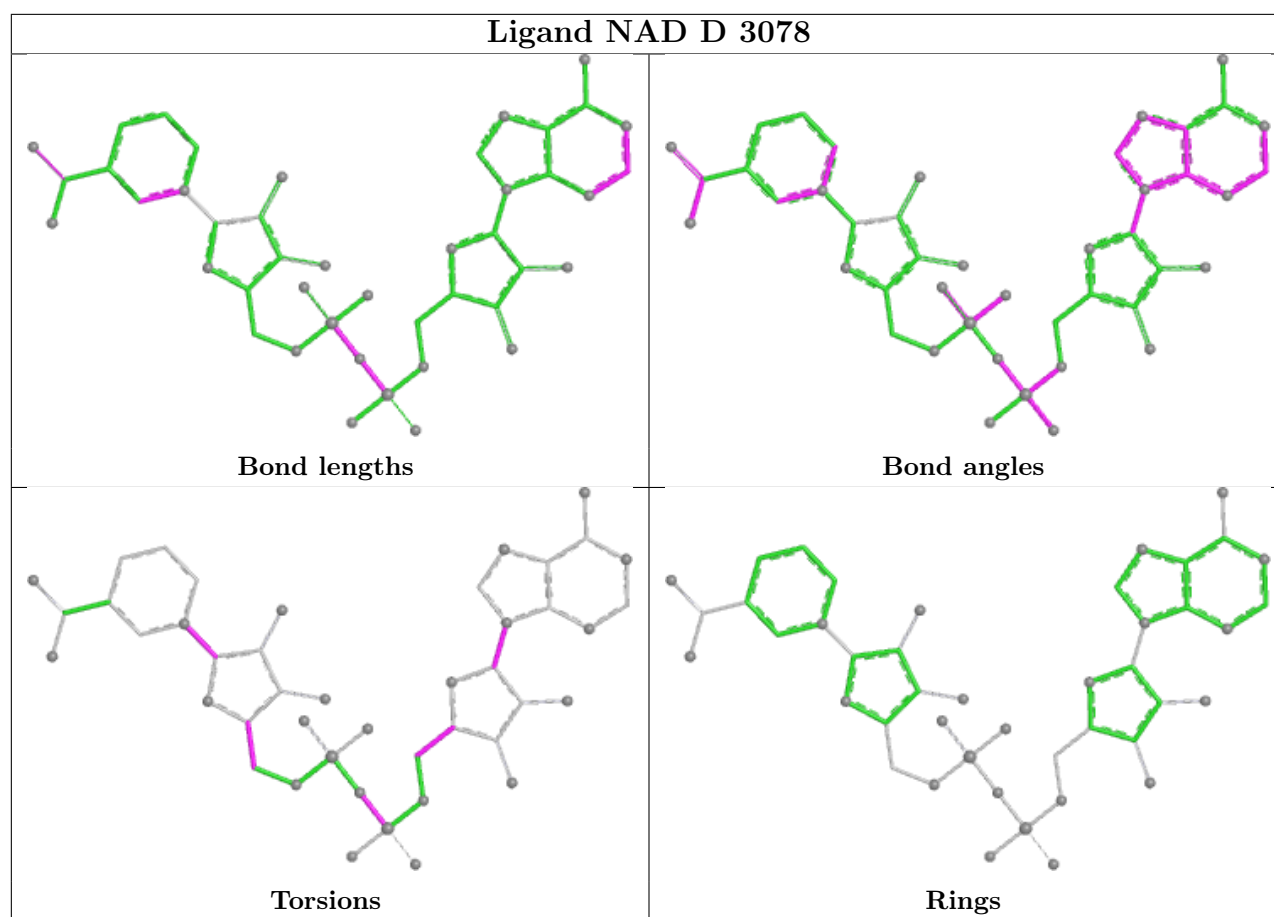
2 monomers are involved in 3 short contacts:

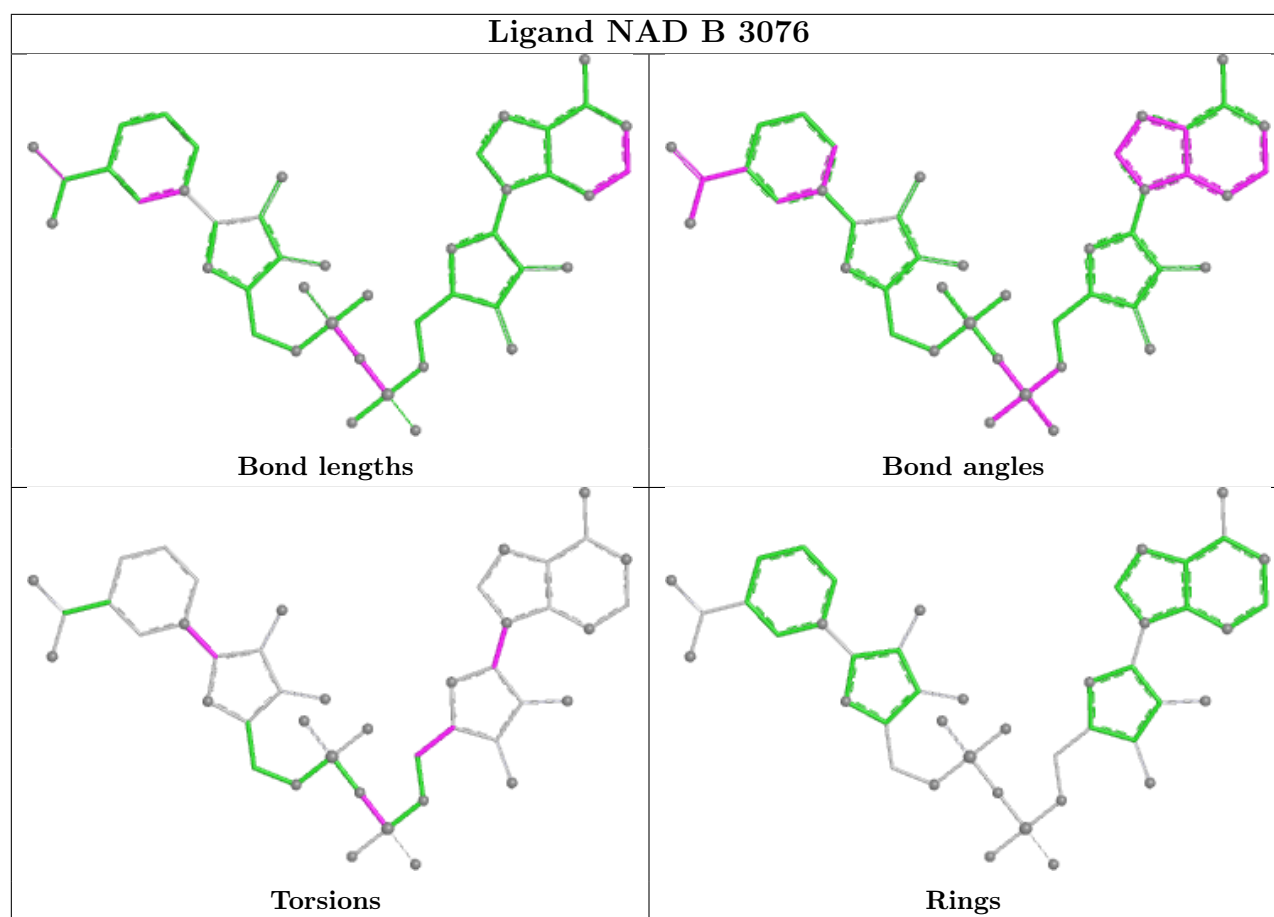
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	3078	NAD	2	0
2	B	3076	NAD	1	0

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 [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	249/278 (89%)	-0.11	2 (0%) 82 78	34, 38, 41, 44	0
1	B	249/278 (89%)	-0.19	0 100 100	34, 38, 41, 47	0
1	C	249/278 (89%)	-0.13	0 100 100	34, 39, 41, 44	0
1	D	249/278 (89%)	-0.17	1 (0%) 88 87	35, 38, 41, 45	0
All	All	996/1112 (89%)	-0.15	3 (0%) 90 89	34, 38, 41, 47	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	71	GLY	3.3
1	D	249	GLY	2.4
1	A	249	GLY	2.4

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](#)

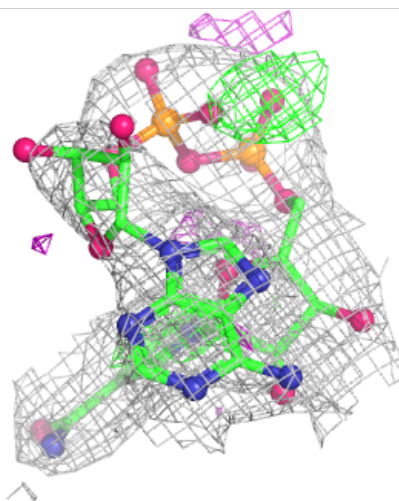
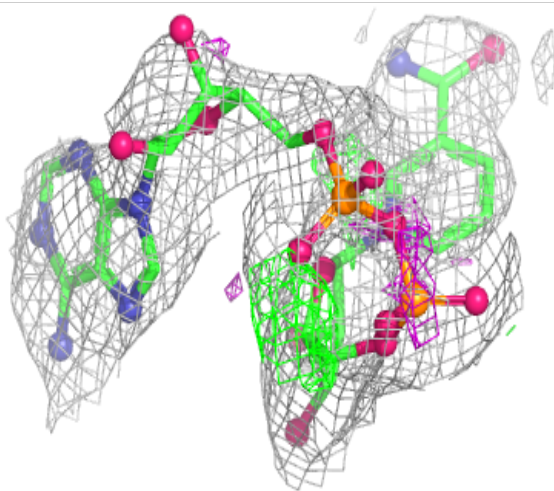
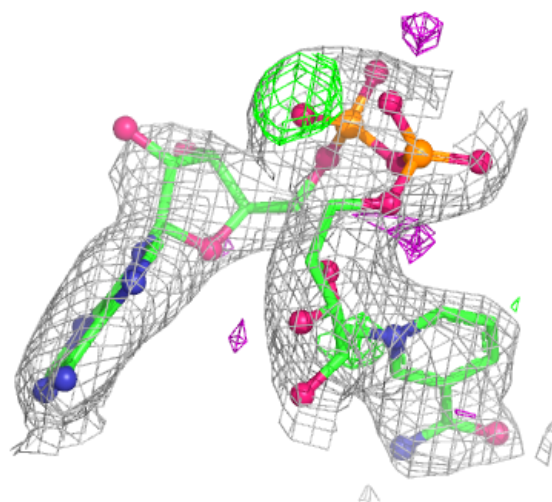
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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	NAD	C	3077	44/44	0.83	0.13	74,79,89,90	0
2	NAD	A	3075	44/44	0.86	0.13	75,79,89,92	0
2	NAD	D	3078	44/44	0.87	0.14	67,73,86,88	0
2	NAD	B	3076	44/44	0.89	0.13	67,73,80,81	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.

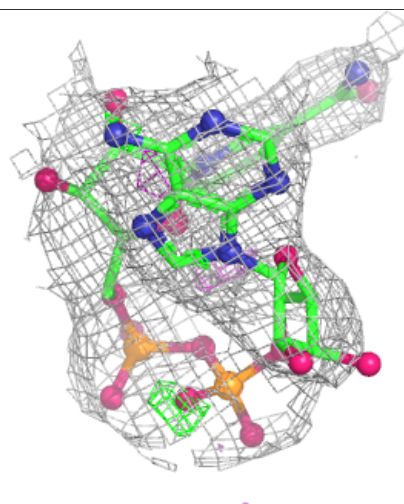
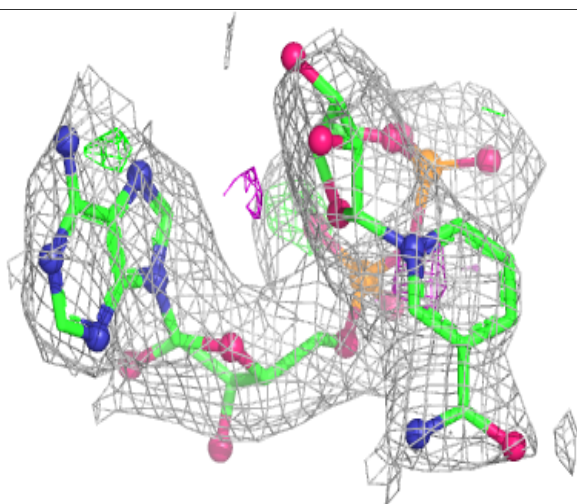
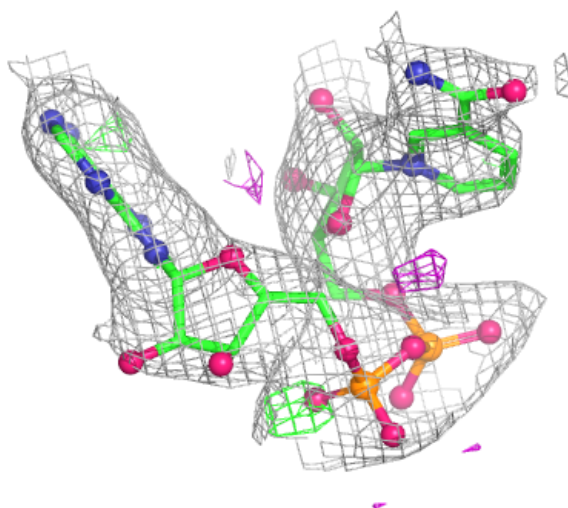
Electron density around NAD C 3077:

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



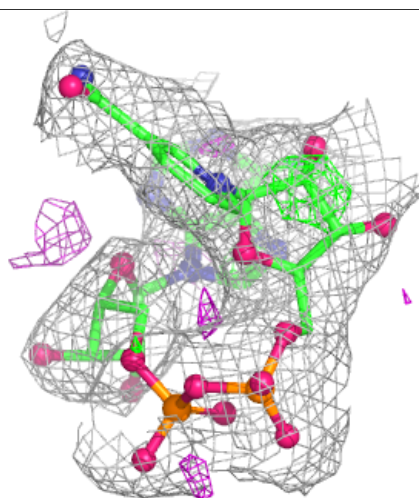
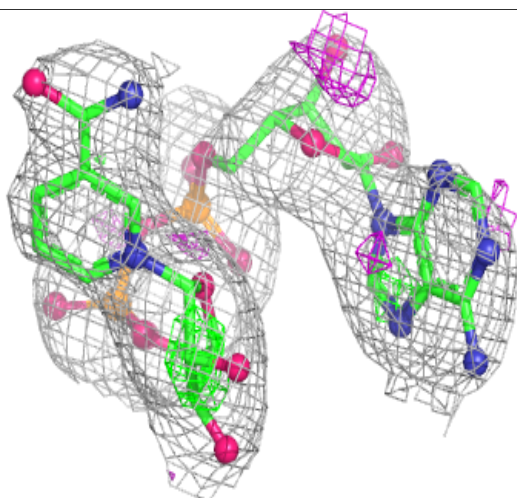
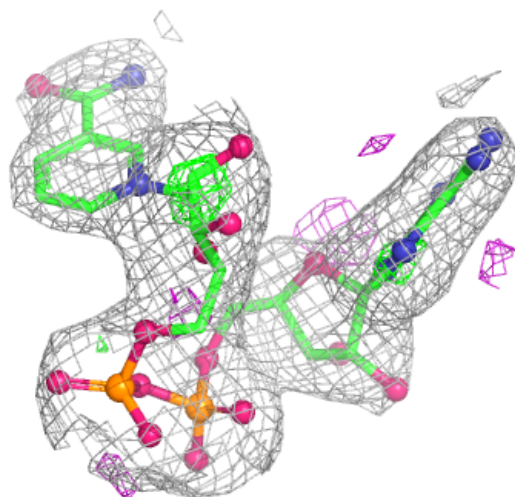
Electron density around NAD A 3075:

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



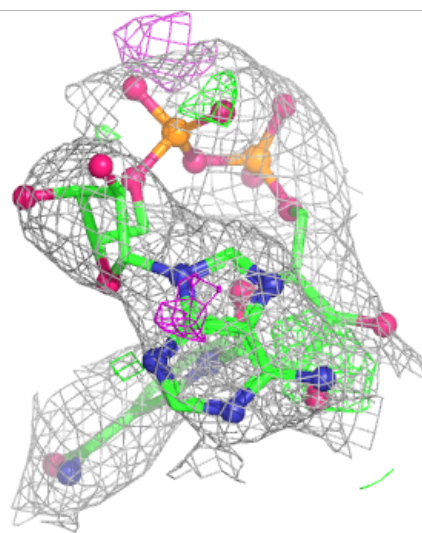
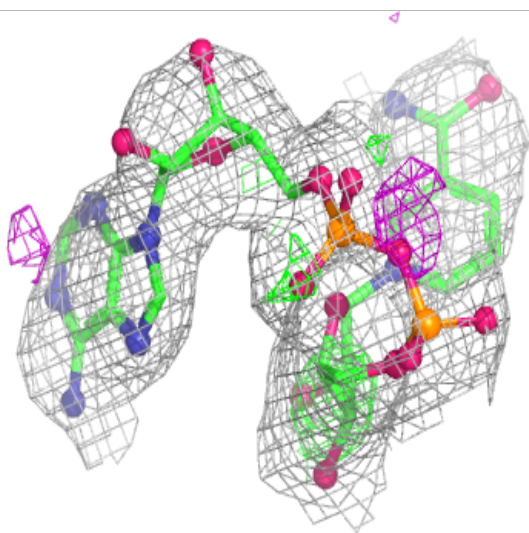
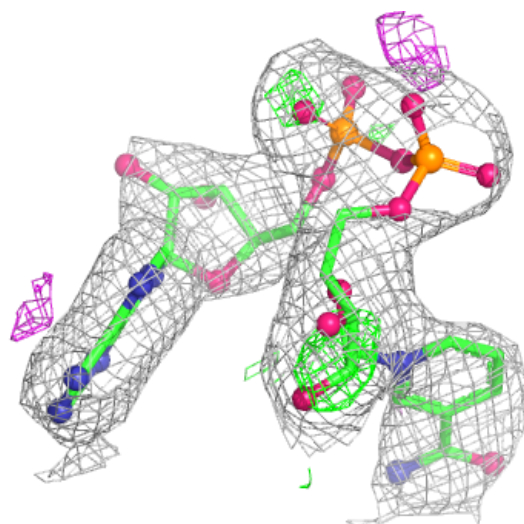
Electron density around NAD D 3078:

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



Electron density around NAD B 3076:

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 ⓘ

There are no such residues in this entry.