wwPDB X-ray Structure Validation Summary Report (i)

Feb 18, 2024 – 03:40 PM EST

PDB ID	:	4FR8
Title	:	Crystal structure of human aldehyde dehydrogenase-2 in complex with nitroglycerin
Authors	:	Lang, B.S.; Gruber, K.
Deposited on	:	2012-06-26
Resolution	:	2.20 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 (i) 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 (i)) were used in the production of this report:

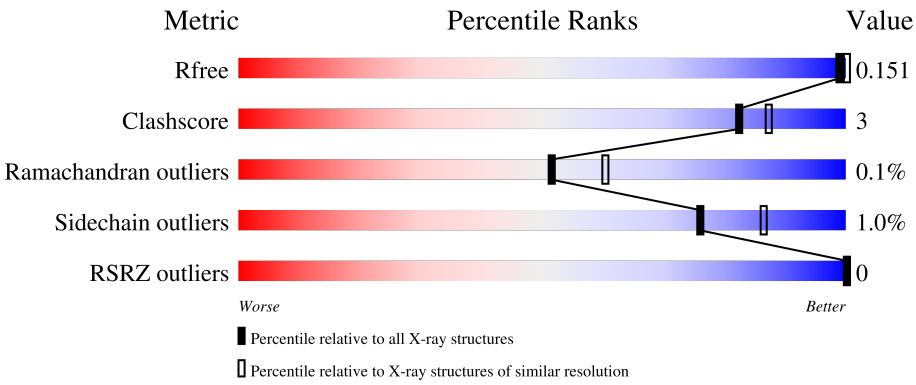
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	500	90% 9% •
1	B	500	93% 6% •
1	C	500	92% 7% •
1	D	500	92% 7% •
1	E	500	94% • •

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Mol	Chain	Length	Quality of chain
1	F	500	91% 8% •
1	G	500	94% 5% •
1	H	500	92% 7% •

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 33739 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 Aldehyde dehydrogenase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	493	3821	2428	652	724	17	0	4	0
1	B	493	3810	2422	651	720	17	0	2	0
1	C	496	3836	2437	656	726	17	0	3	0
1	D	493	3841	2438	657	729	17	0	6	0
1	E	493	3816	2425	652	721	18	0	3	0
1	F	493	3808	2420	651	720	17	0	2	0
1	G	494	3816	2425	653	722	16	0	2	0
1	H	493	3818	2426	652	723	17	0	3	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	268	GLN	GLU	engineered mutation	UNP P05091
A	301	SER	CYS	engineered mutation	UNP P05091
A	303	SER	CYS	engineered mutation	UNP P05091
B	268	GLN	GLU	engineered mutation	UNP P05091
B	301	SER	CYS	engineered mutation	UNP P05091
B	303	SER	CYS	engineered mutation	UNP P05091
C	268	GLN	GLU	engineered mutation	UNP P05091
C	301	SER	CYS	engineered mutation	UNP P05091
C	303	SER	CYS	engineered mutation	UNP P05091
D	268	GLN	GLU	engineered mutation	UNP P05091
D	301	SER	CYS	engineered mutation	UNP P05091
D	303	SER	CYS	engineered mutation	UNP P05091
E	268	GLN	GLU	engineered mutation	UNP P05091

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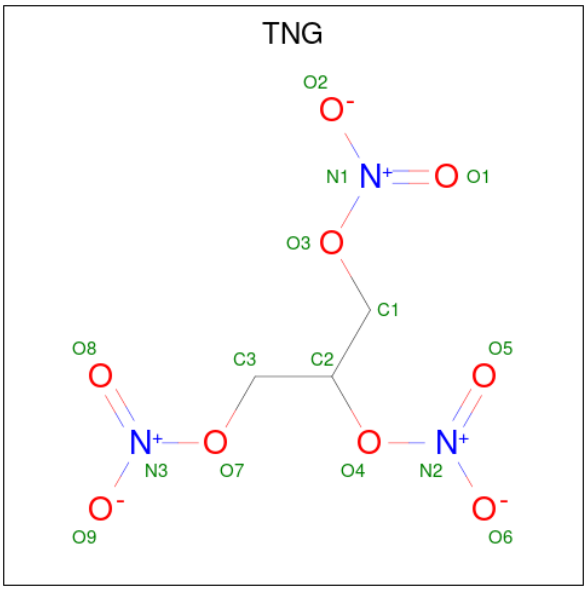
Chain	Residue	Modelled	Actual	Comment	Reference
E	301	SER	CYS	engineered mutation	UNP P05091
E	303	SER	CYS	engineered mutation	UNP P05091
F	268	GLN	GLU	engineered mutation	UNP P05091
F	301	SER	CYS	engineered mutation	UNP P05091
F	303	SER	CYS	engineered mutation	UNP P05091
G	268	GLN	GLU	engineered mutation	UNP P05091
G	301	SER	CYS	engineered mutation	UNP P05091
G	303	SER	CYS	engineered mutation	UNP P05091
H	268	GLN	GLU	engineered mutation	UNP P05091
H	301	SER	CYS	engineered mutation	UNP P05091
H	303	SER	CYS	engineered mutation	UNP P05091

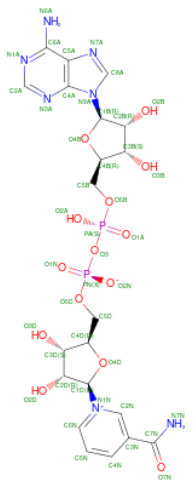
- Molecule 2 is propane-1,2,3-triyl trinitrate (three-letter code: TNG) (formula: $C_3H_5N_3O_9$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	15	3	3	9	0	0

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).

NAD

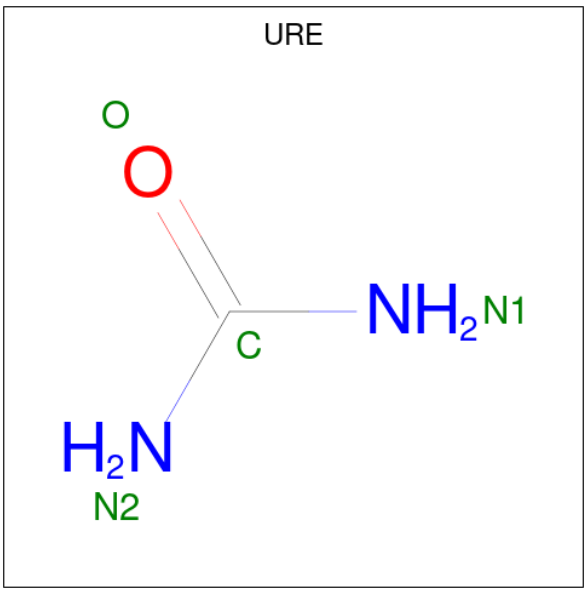


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	35	15	5	13	2	0	0
3	C	1	35	15	5	13	2	0	0
3	D	1	35	15	5	13	2	0	0
3	F	1	35	15	5	13	2	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	1	1	1	0	0
4	B	1	1	1	0	0
4	C	1	1	1	0	0
4	D	1	1	1	0	0
4	E	1	1	1	0	0
4	F	1	1	1	0	0
4	G	1	1	1	0	0
4	H	1	1	1	0	0

- Molecule 5 is UREA (three-letter code: URE) (formula: CH_4N_2O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	4	1	2	1	0	0
5	B	1	4	1	2	1	0	0
5	C	1	4	1	2	1	0	0
5	C	1	4	1	2	1	0	0
5	D	1	4	1	2	1	0	0
5	E	1	4	1	2	1	0	0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
6	A	1	1	1	0	0
6	B	1	1	1	0	0
6	C	1	1	1	0	0
6	D	1	1	1	0	0
6	E	1	1	1	0	0

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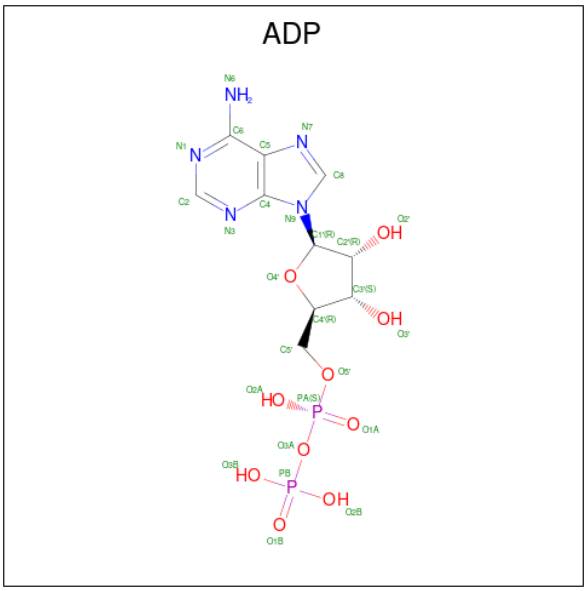
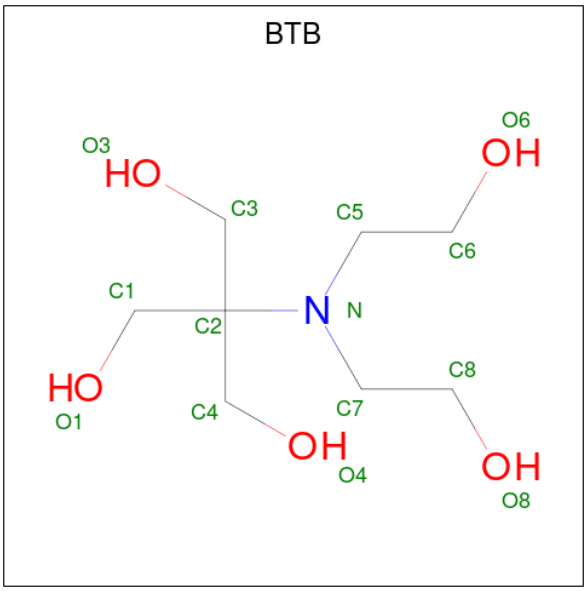
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
6	F	1	1	1	0	0
			Total	Na		
6	G	1	1	1	0	0
			Total	Na		
6	H	1	1	1	0	0

- Molecule 7 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
7	B	1	27	10	5	10	2	0	0
			Total	C	N	O	P		
7	E	1	27	10	5	10	2	0	0
			Total	C	N	O	P		
7	G	1	27	10	5	10	2	0	0
			Total	C	N	O	P		
7	H	1	27	10	5	10	2	0	0

- Molecule 8 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: BTB) (formula: $C_8H_{19}NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
8	G	1	14	8	1	5	0	0

- Molecule 9 is water.

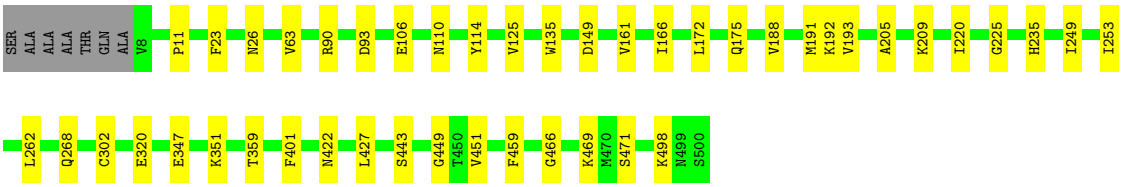
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	A	344	344	344	0	0
9	B	380	380	380	0	0
9	C	361	361	361	0	0
9	D	398	398	398	0	0
9	E	323	323	323	0	0
9	F	325	325	325	0	0
9	G	338	338	338	0	0
9	H	387	387	387	0	0

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.

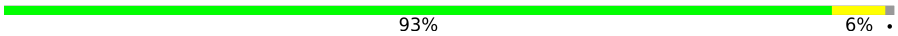
• Molecule 1: Aldehyde dehydrogenase, mitochondrial

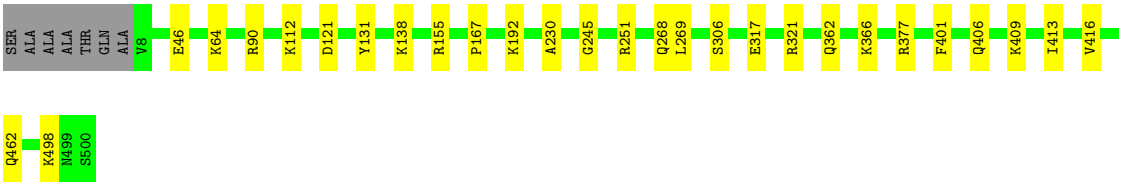
Chain A:



• Molecule 1: Aldehyde dehydrogenase, mitochondrial

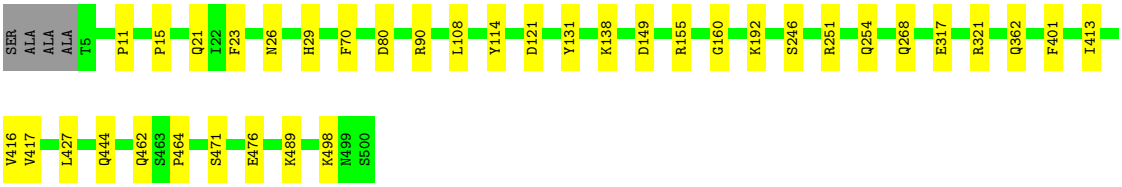
Chain B:





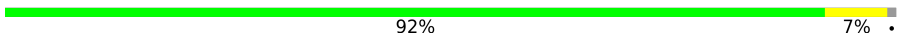
• Molecule 1: Aldehyde dehydrogenase, mitochondrial

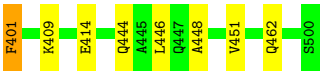
Chain C:



• Molecule 1: Aldehyde dehydrogenase, mitochondrial

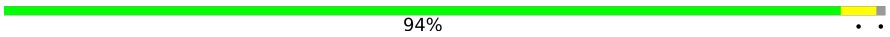
Chain D:





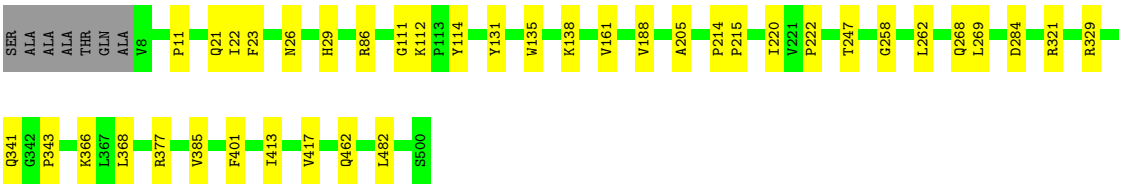
• Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain E:



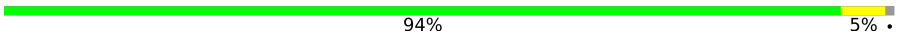
• Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain F:



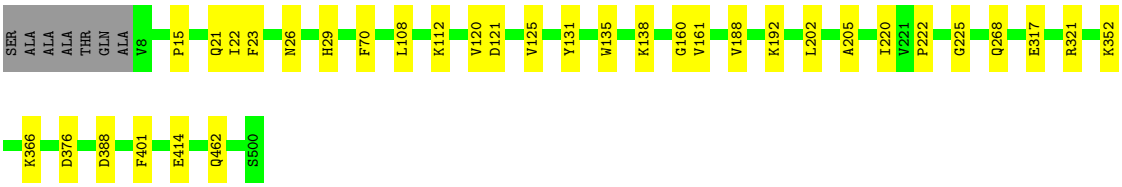
• Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain G:



• Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	101.66Å 175.92Å 102.30Å 90.00° 95.01° 90.00°	Depositor
Resolution (Å)	37.07 – 2.20 37.07 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (37.07-2.20) 95.3 (37.07-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	3.46 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.132 , 0.167 0.131 , 0.151	Depositor DCC
R_{free} test set	9049 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	17.8	Xtriage
Anisotropy	0.641	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 20.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	0.218 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	33739	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.57% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: TNG, BTB, NA, NAD, ADP, MG, URE

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	0.25	0/3905	0.43	0/5298
1	B	0.26	0/3894	0.42	0/5282
1	C	0.26	0/3920	0.44	0/5319
1	D	0.26	0/3925	0.43	0/5324
1	E	0.26	0/3900	0.42	0/5290
1	F	0.26	0/3892	0.42	0/5280
1	G	0.26	0/3900	0.43	0/5291
1	H	0.26	0/3902	0.43	0/5293
All	All	0.26	0/31238	0.43	0/42377

There are no bond length outliers.

There are no bond angle outliers.

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	3821	0	3763	30	0
1	B	3810	0	3757	16	0
1	C	3836	0	3781	25	0
1	D	3841	0	3776	23	0
1	E	3816	0	3760	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3808	0	3753	24	0
1	G	3816	0	3761	14	0
1	H	3818	0	3760	18	0
2	A	15	0	5	4	0
3	A	35	0	19	2	0
3	C	35	0	19	2	0
3	D	35	0	19	3	0
3	F	35	0	19	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	4	0	4	0	0
5	B	4	0	4	0	0
5	C	8	0	8	0	0
5	D	4	0	4	0	0
5	E	4	0	4	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
6	G	1	0	0	0	0
6	H	1	0	0	0	0
7	B	27	0	12	0	0
7	E	27	0	12	2	0
7	G	27	0	12	1	0
7	H	27	0	12	2	0
8	G	14	0	19	1	0
9	A	344	0	0	5	0
9	B	380	0	0	7	0
9	C	361	0	0	4	0
9	D	398	0	0	2	0
9	E	323	0	0	0	0
9	F	325	0	0	4	0
9	G	338	0	0	1	0
9	H	387	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	33739	0	30283	154	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 3.

The worst 5 of 154 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:459:PHE:CZ	2:A:601:TNG:H2	2.10	0.86
1:B:46:GLU:OE2	1:B:377:ARG:NH1	2.23	0.70
1:A:166:ILE:HD11	1:A:193:VAL:HG12	1.72	0.69
1:A:459:PHE:CE1	2:A:601:TNG:H2	2.29	0.67
7:E:1001:ADP:O1B	7:E:1001:ADP:O1A	2.12	0.65

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	495/500 (99%)	477 (96%)	18 (4%)	0	100	100
1	B	493/500 (99%)	478 (97%)	14 (3%)	1 (0%)	47	55
1	C	497/500 (99%)	480 (97%)	17 (3%)	0	100	100
1	D	497/500 (99%)	481 (97%)	16 (3%)	0	100	100
1	E	494/500 (99%)	475 (96%)	18 (4%)	1 (0%)	47	55
1	F	493/500 (99%)	477 (97%)	16 (3%)	0	100	100
1	G	494/500 (99%)	480 (97%)	14 (3%)	0	100	100
1	H	494/500 (99%)	479 (97%)	15 (3%)	0	100	100
All	All	3957/4000 (99%)	3827 (97%)	128 (3%)	2 (0%)	51	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	167	PRO
1	E	167	PRO

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	403/402 (100%)	399 (99%)	4 (1%)	76	86
1	B	401/402 (100%)	394 (98%)	7 (2%)	60	74
1	C	404/402 (100%)	398 (98%)	6 (2%)	65	78
1	D	405/402 (101%)	402 (99%)	3 (1%)	84	91
1	E	402/402 (100%)	400 (100%)	2 (0%)	88	94
1	F	401/402 (100%)	399 (100%)	2 (0%)	88	94
1	G	401/402 (100%)	399 (100%)	2 (0%)	88	94
1	H	402/402 (100%)	397 (99%)	5 (1%)	71	83
All	All	3219/3216 (100%)	3188 (99%)	31 (1%)	76	86

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	362	GLN
1	H	268	GLN
1	D	192	LYS
1	H	401	PHE
1	G	268	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	254	GLN
1	E	254	GLN
1	E	300	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 32 ligands modelled in this entry, 16 are monoatomic - leaving 16 for Mogul analysis.

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	TNG	A	601	-	8,14,14	0.95	0	4,17,17	0.55	0
3	NAD	F	1001	4	33,38,48	0.89	1 (3%)	37,58,73	1.41	6 (16%)
5	URE	E	1004	-	3,3,3	0.36	0	3,3,3	0.24	0
5	URE	B	1003	-	3,3,3	0.45	0	3,3,3	0.41	0
8	BTB	G	1004	-	13,13,13	0.35	0	7,16,16	0.57	0
7	ADP	E	1001	4	24,29,29	0.99	2 (8%)	29,45,45	1.40	4 (13%)
7	ADP	B	1001	4	24,29,29	0.98	1 (4%)	29,45,45	1.45	3 (10%)
5	URE	A	604	-	3,3,3	0.37	0	3,3,3	0.28	0
3	NAD	A	1001	4	33,38,48	0.87	1 (3%)	37,58,73	1.40	6 (16%)
5	URE	C	1003	-	3,3,3	0.43	0	3,3,3	0.37	0
5	URE	D	1003	-	3,3,3	0.45	0	3,3,3	0.52	0
3	NAD	C	1001	4	33,38,48	0.88	1 (3%)	37,58,73	1.37	5 (13%)
3	NAD	D	1001	4	33,38,48	0.88	1 (3%)	37,58,73	1.44	7 (18%)
5	URE	C	1005	-	3,3,3	0.39	0	3,3,3	0.24	0
7	ADP	H	1001	4	24,29,29	0.94	1 (4%)	29,45,45	1.34	3 (10%)
7	ADP	G	1001	4	24,29,29	0.97	1 (4%)	29,45,45	1.30	3 (10%)

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	TNG	A	601	-	-	5/8/14/14	-
3	NAD	F	1001	4	-	8/18/51/62	0/4/4/5
8	BTB	G	1004	-	-	4/21/21/21	-
7	ADP	B	1001	4	-	0/12/32/32	0/3/3/3
3	NAD	A	1001	4	-	7/18/51/62	0/4/4/5
3	NAD	C	1001	4	-	4/18/51/62	0/4/4/5
3	NAD	D	1001	4	-	6/18/51/62	0/4/4/5
7	ADP	E	1001	4	-	5/12/32/32	0/3/3/3
7	ADP	H	1001	4	-	3/12/32/32	0/3/3/3
7	ADP	G	1001	4	-	0/12/32/32	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	1001	ADP	C5-C4	2.57	1.47	1.40
7	E	1001	ADP	C5-C4	2.53	1.47	1.40
3	F	1001	NAD	C5A-C4A	2.51	1.47	1.40
7	H	1001	ADP	C5-C4	2.43	1.47	1.40
7	G	1001	ADP	C5-C4	2.42	1.47	1.40

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	B	1001	ADP	PA-O3A-PB	-4.19	118.44	132.83
3	D	1001	NAD	PN-O3-PA	-3.82	119.72	132.83
3	A	1001	NAD	PN-O3-PA	-3.82	119.72	132.83
3	F	1001	NAD	PN-O3-PA	-3.81	119.75	132.83
3	A	1001	NAD	N3A-C2A-N1A	-3.64	122.99	128.68

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	TNG	C2-C1-O3-N1
3	A	1001	NAD	C5D-O5D-PN-O1N
3	C	1001	NAD	C5D-O5D-PN-O1N

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Mol	Chain	Res	Type	Atoms
3	D	1001	NAD	C5D-O5D-PN-O1N
3	F	1001	NAD	C5D-O5D-PN-O1N

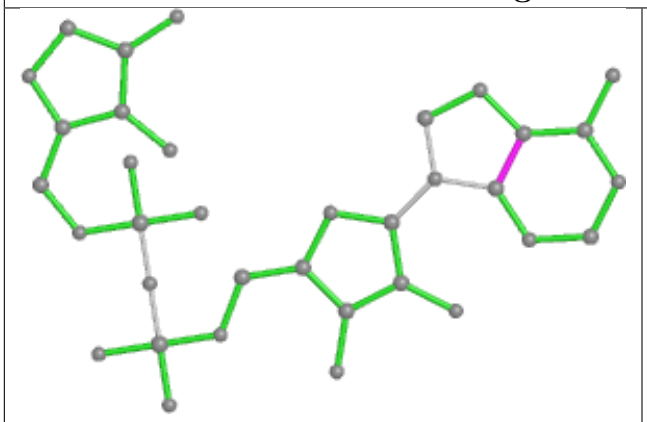
There are no ring outliers.

9 monomers are involved in 18 short contacts:

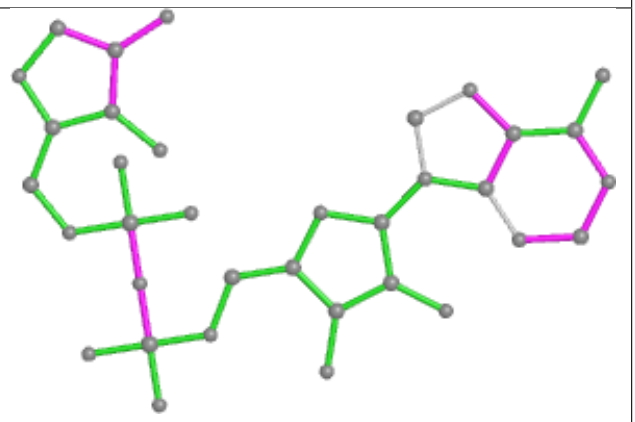
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	TNG	4	0
3	F	1001	NAD	1	0
8	G	1004	BTB	1	0
7	E	1001	ADP	2	0
3	A	1001	NAD	2	0
3	C	1001	NAD	2	0
3	D	1001	NAD	3	0
7	H	1001	ADP	2	0
7	G	1001	ADP	1	0

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 then 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.

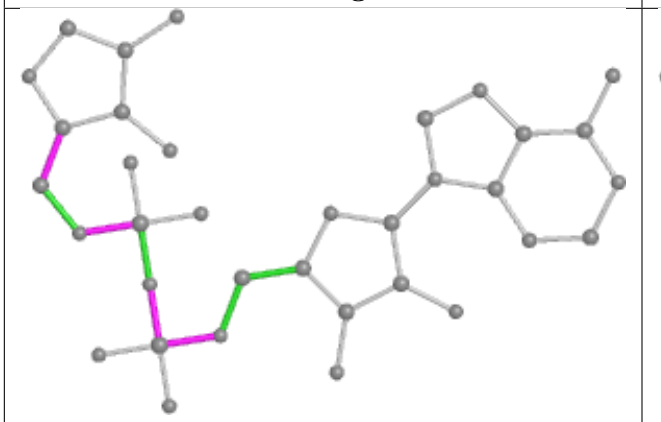
Ligand NAD F 1001



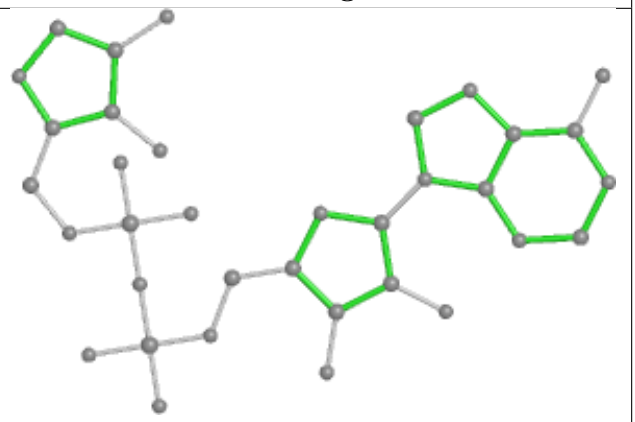
Bond lengths



Bond angles

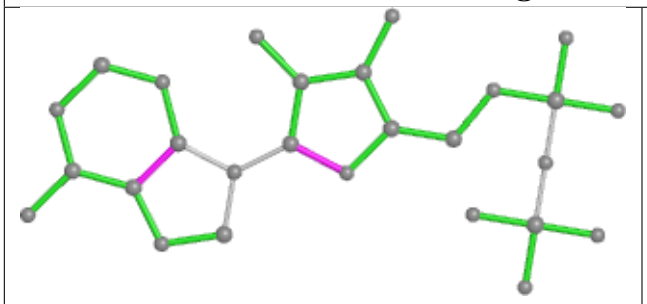


Torsions

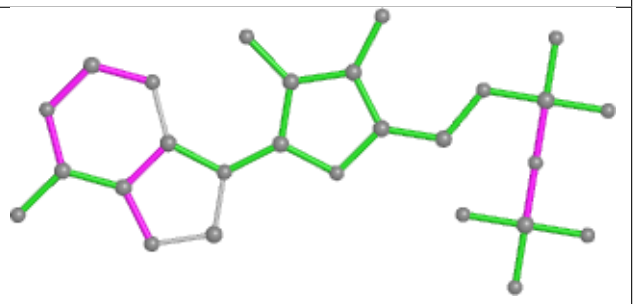


Rings

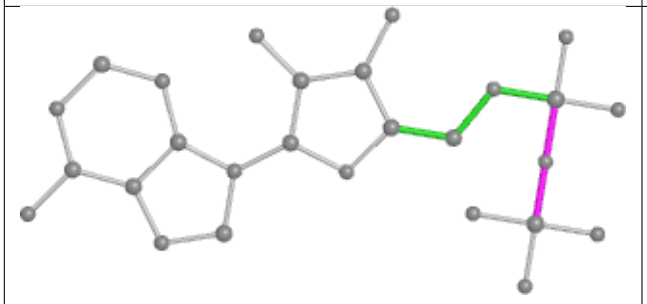
Ligand ADP E 1001



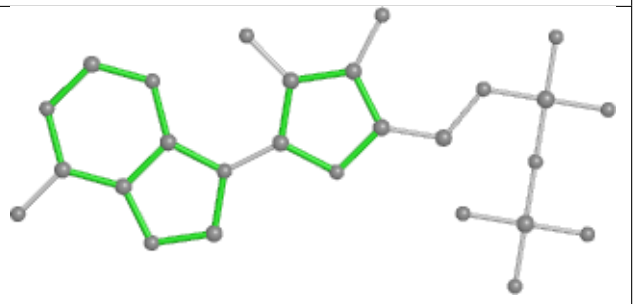
Bond lengths



Bond angles

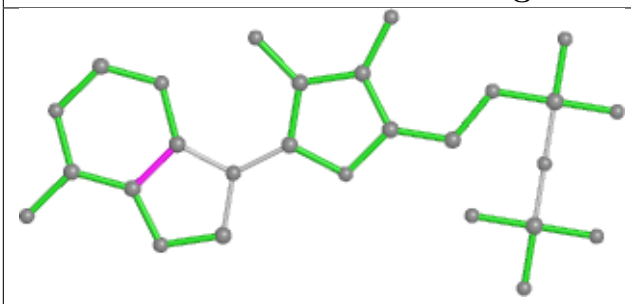


Torsions

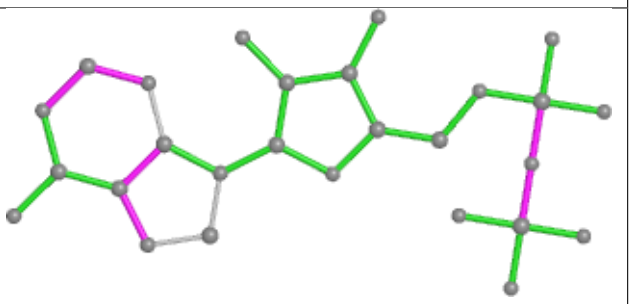


Rings

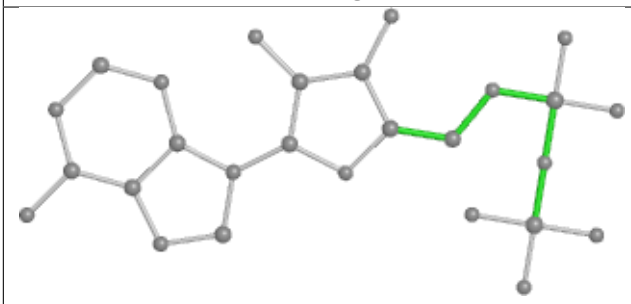
Ligand ADP B 1001



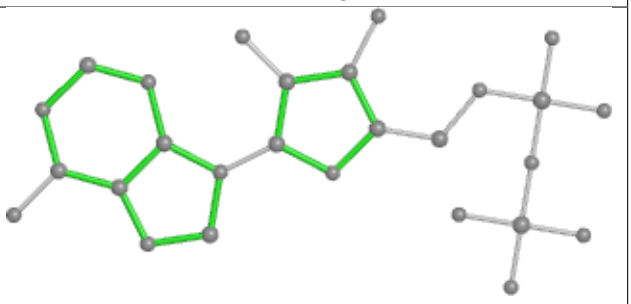
Bond lengths



Bond angles

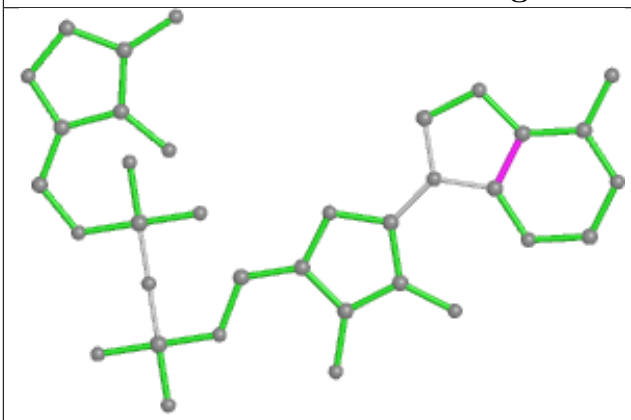


Torsions

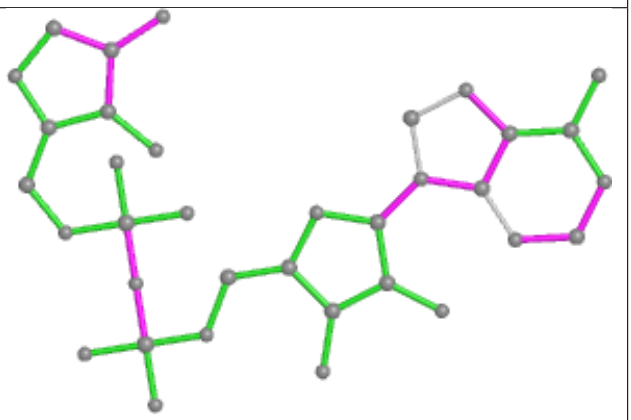


Rings

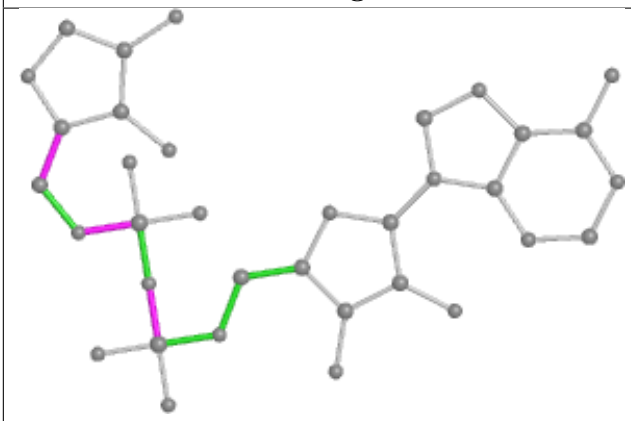
Ligand NAD A 1001



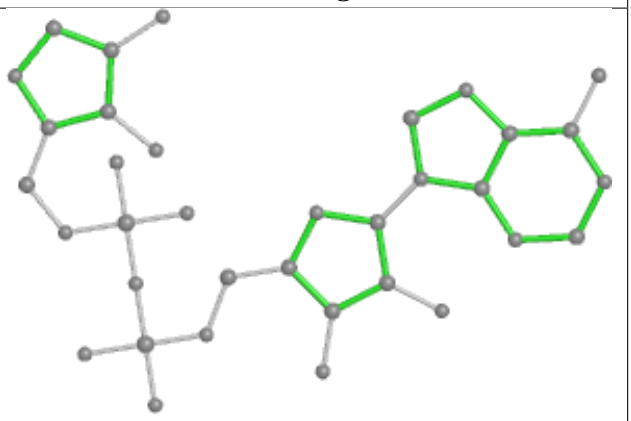
Bond lengths



Bond angles

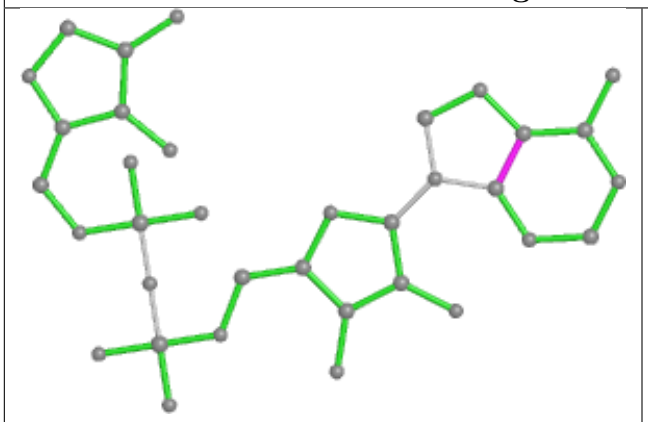


Torsions

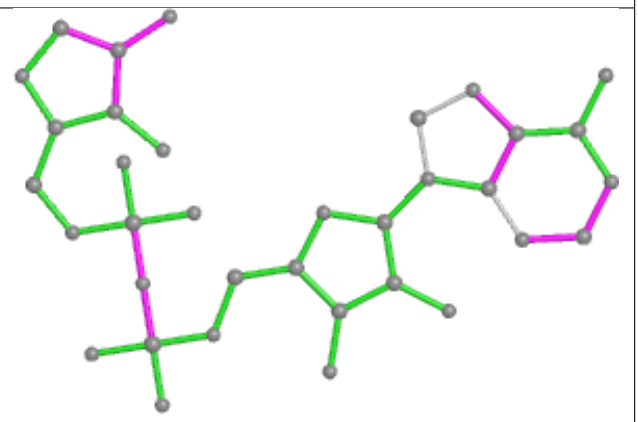


Rings

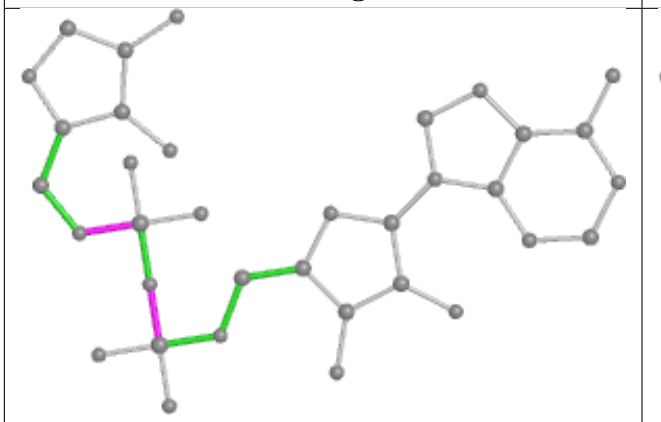
Ligand NAD C 1001



Bond lengths



Bond angles



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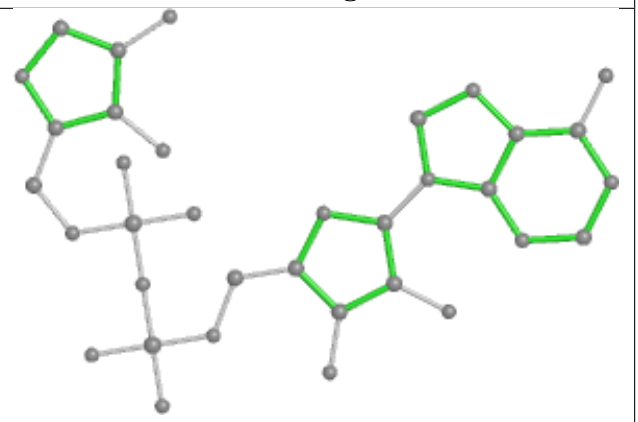
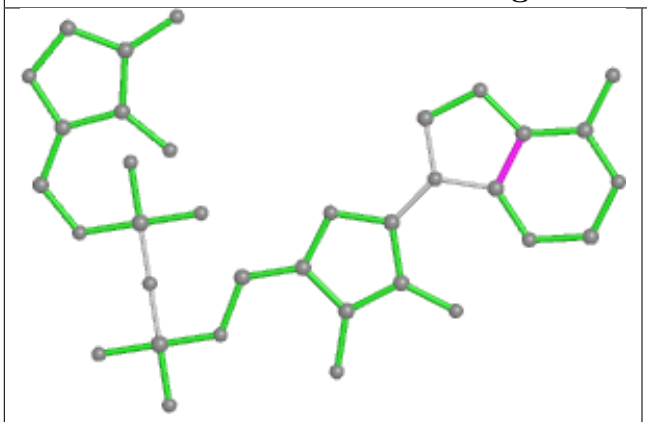
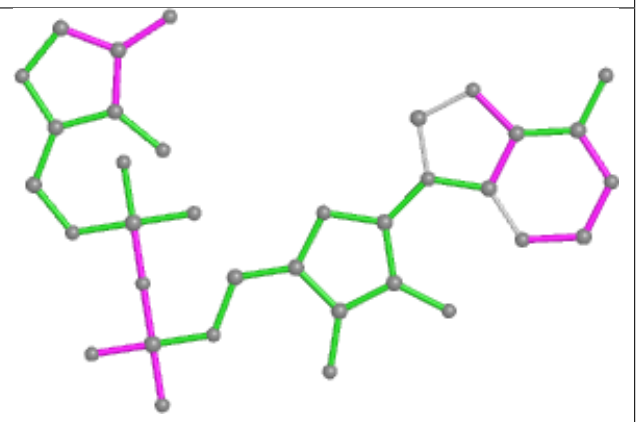


Rings

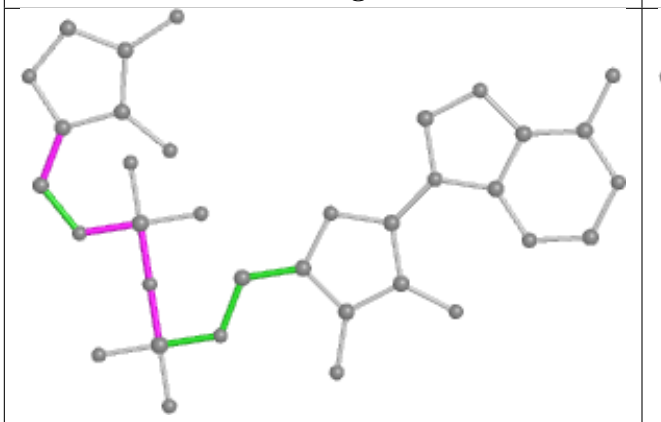
Ligand NAD D 1001



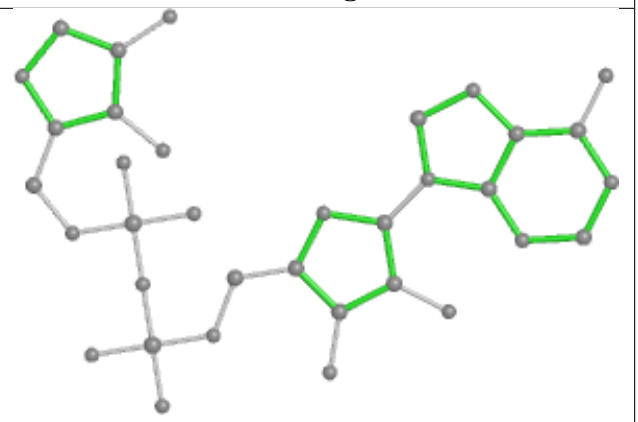
Bond lengths



Bond angles

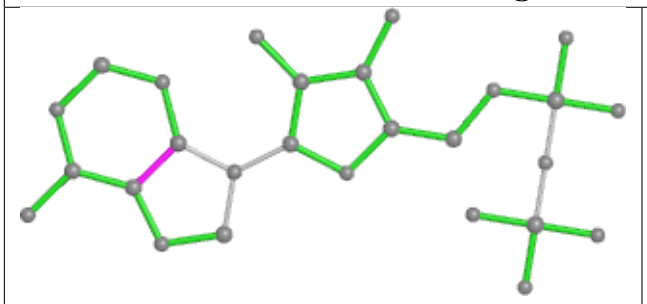


Torsions

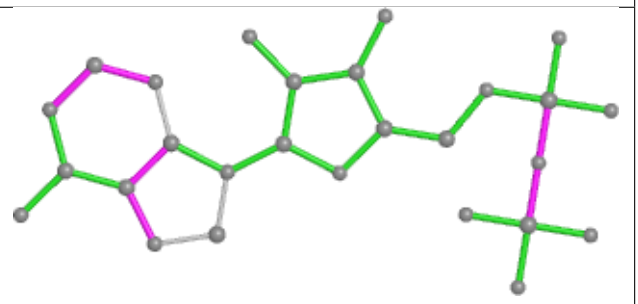


Rings

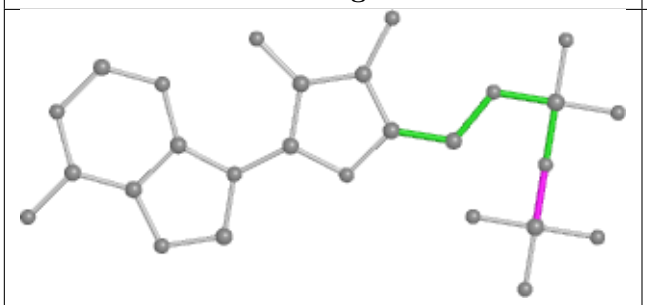
Ligand ADP H 1001



Bond lengths



Bond angles



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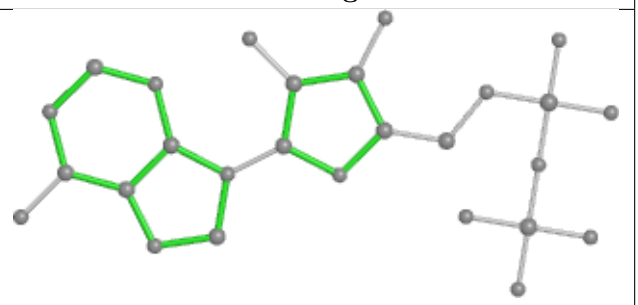
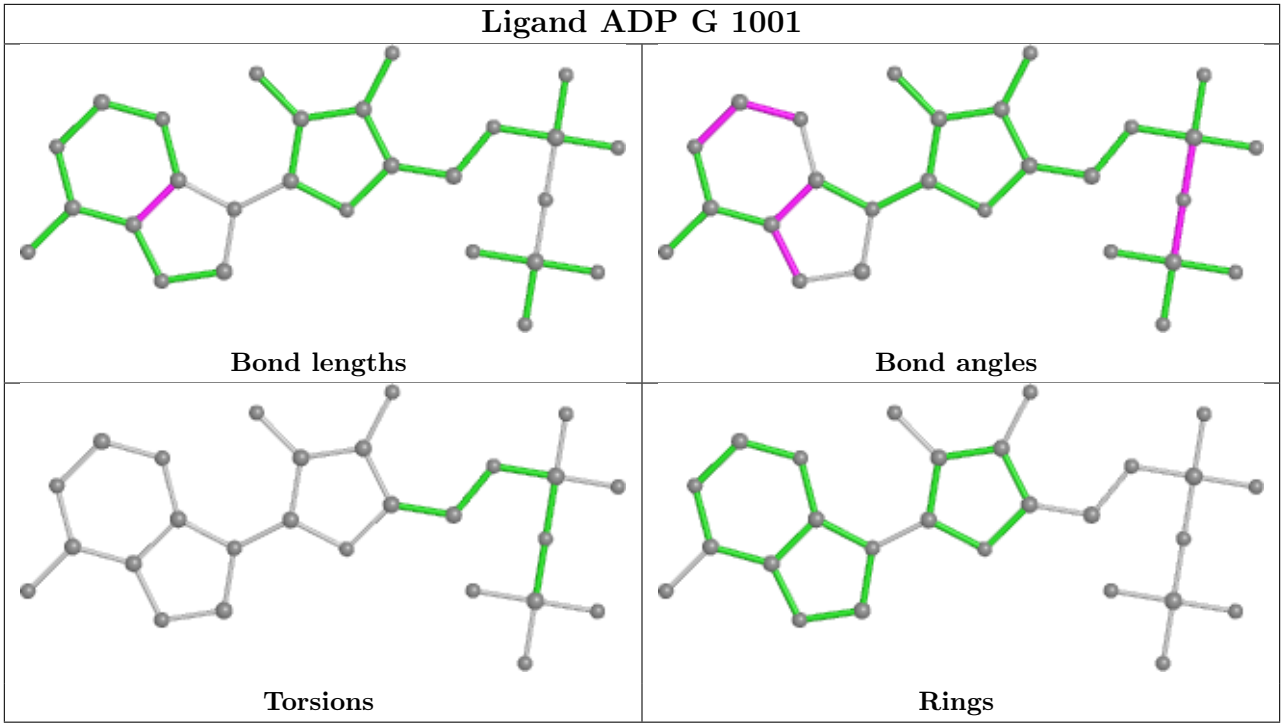


Rings



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	493/500 (98%)	-0.91	0	100	100	13, 21, 31, 45	0
1	B	493/500 (98%)	-0.92	0	100	100	12, 19, 29, 48	0
1	C	496/500 (99%)	-0.91	0	100	100	13, 19, 29, 42	0
1	D	493/500 (98%)	-0.96	0	100	100	11, 17, 26, 40	0
1	E	493/500 (98%)	-0.87	0	100	100	14, 21, 32, 55	0
1	F	493/500 (98%)	-0.84	0	100	100	13, 22, 33, 52	0
1	G	494/500 (98%)	-0.89	0	100	100	14, 20, 32, 46	0
1	H	493/500 (98%)	-0.95	0	100	100	12, 18, 27, 41	0
All	All	3948/4000 (98%)	-0.91	0	100	100	11, 20, 30, 55	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

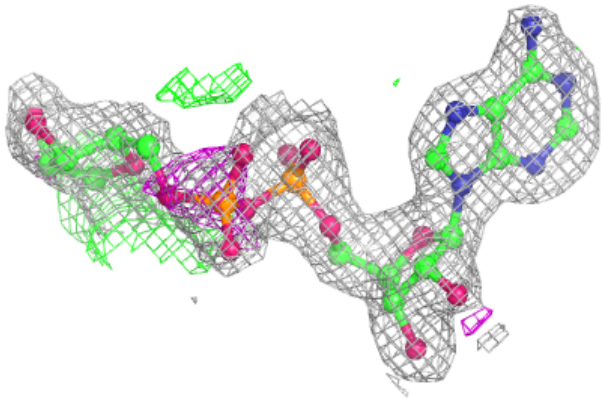
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

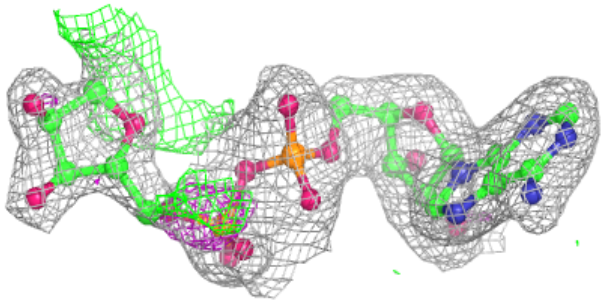
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	MG	C	1002	1/1	0.78	0.12	54,54,54,54	0
5	URE	E	1004	4/4	0.82	0.21	32,38,39,40	0
4	MG	F	1002	1/1	0.83	0.14	52,52,52,52	0
4	MG	D	1002	1/1	0.86	0.11	41,41,41,41	0
4	MG	B	1002	1/1	0.86	0.17	49,49,49,49	0
4	MG	A	603	1/1	0.86	0.13	44,44,44,44	0
2	TNG	A	601	15/15	0.88	0.24	22,26,29,29	15
6	NA	E	1003	1/1	0.90	0.11	28,28,28,28	0
4	MG	H	1002	1/1	0.93	0.13	45,45,45,45	0
5	URE	C	1005	4/4	0.93	0.10	33,40,41,41	0
3	NAD	F	1001	35/44	0.93	0.14	23,30,47,58	0
6	NA	A	605	1/1	0.93	0.12	27,27,27,27	0
4	MG	G	1002	1/1	0.93	0.07	50,50,50,50	0
5	URE	A	604	4/4	0.94	0.16	19,24,26,29	0
6	NA	F	1003	1/1	0.94	0.07	27,27,27,27	0
3	NAD	A	1001	35/44	0.95	0.12	20,28,44,51	0
3	NAD	D	1001	35/44	0.95	0.12	15,23,37,41	0
7	ADP	G	1001	27/27	0.95	0.10	20,25,43,54	0
3	NAD	C	1001	35/44	0.96	0.11	18,24,44,50	0
4	MG	E	1002	1/1	0.96	0.06	38,38,38,38	0
7	ADP	B	1001	27/27	0.96	0.11	17,23,45,57	0
7	ADP	E	1001	27/27	0.96	0.10	16,26,38,48	0
5	URE	C	1003	4/4	0.96	0.13	16,21,23,26	0
7	ADP	H	1001	27/27	0.96	0.10	18,22,44,49	0
5	URE	B	1003	4/4	0.97	0.12	17,20,24,27	0
6	NA	D	1004	1/1	0.97	0.07	25,25,25,25	0
6	NA	G	1003	1/1	0.97	0.06	27,27,27,27	0
6	NA	H	1003	1/1	0.97	0.07	15,15,15,15	0
6	NA	B	1004	1/1	0.98	0.06	23,23,23,23	0
5	URE	D	1003	4/4	0.98	0.10	16,24,28,29	0
8	BTB	G	1004	14/14	0.98	0.09	15,20,23,24	0
6	NA	C	1004	1/1	0.99	0.09	25,25,25,25	0

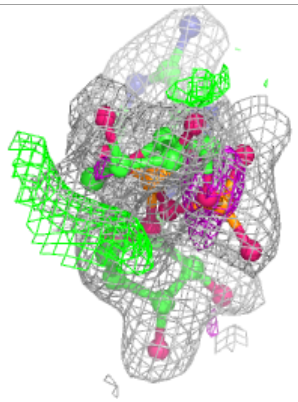
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAD F 1001:

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

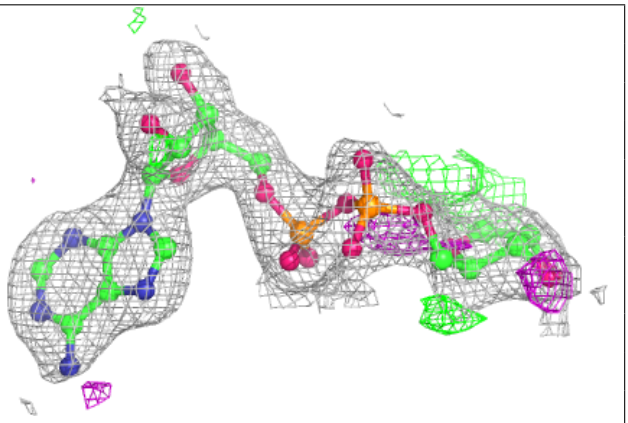


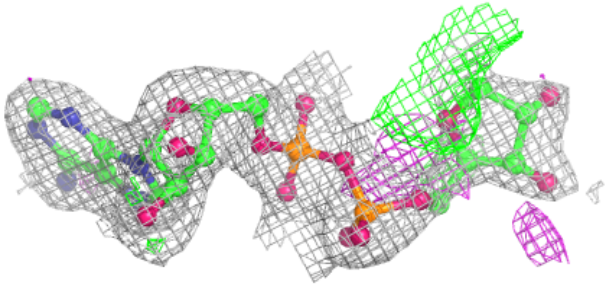


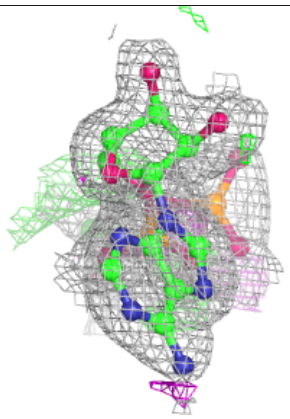


Electron density around NAD A 1001:

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

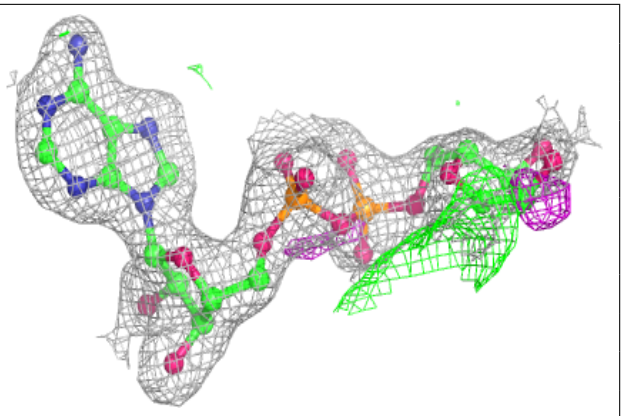


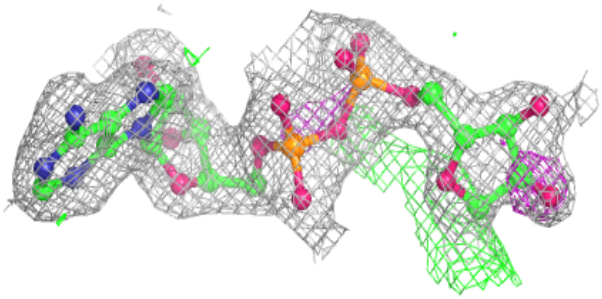


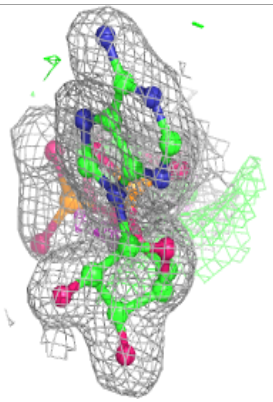


Electron density around NAD D 1001:

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

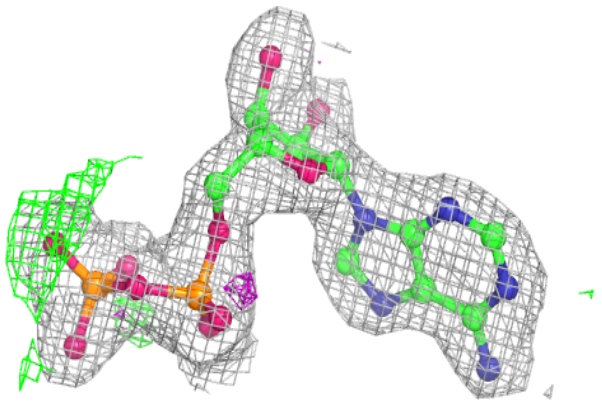


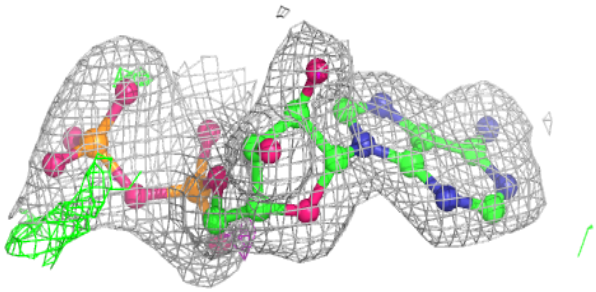


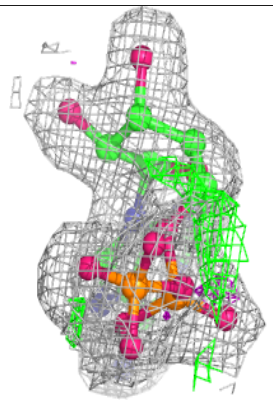


Electron density around ADP G 1001:

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

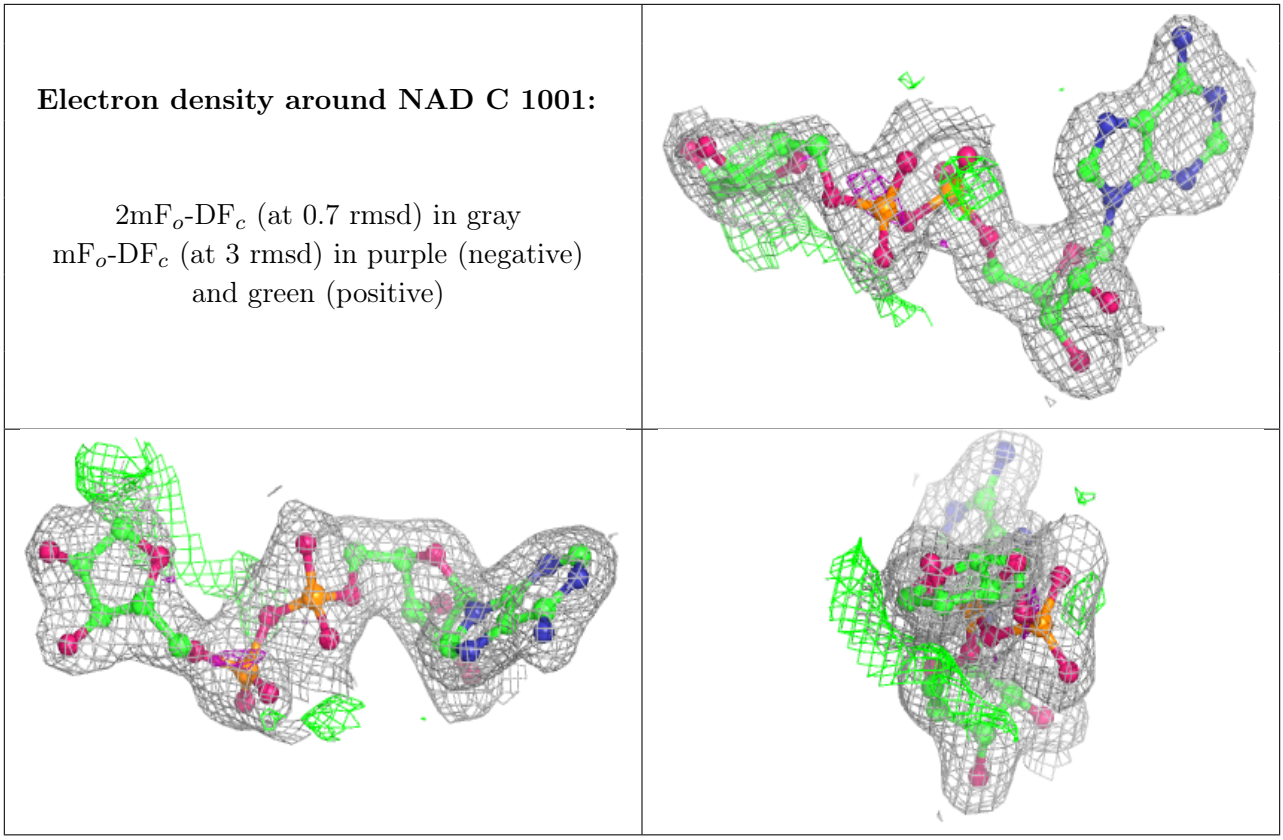






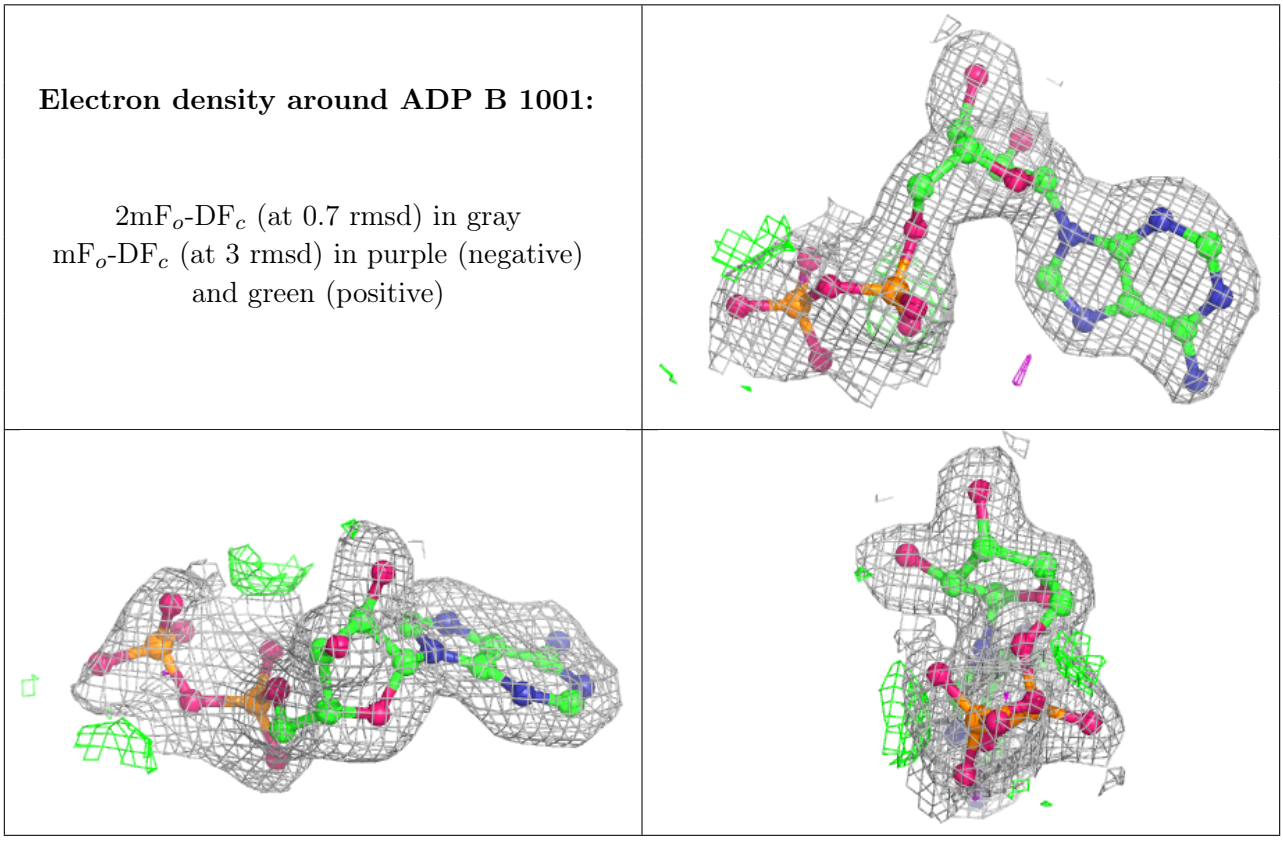
Electron density around NAD C 1001:

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



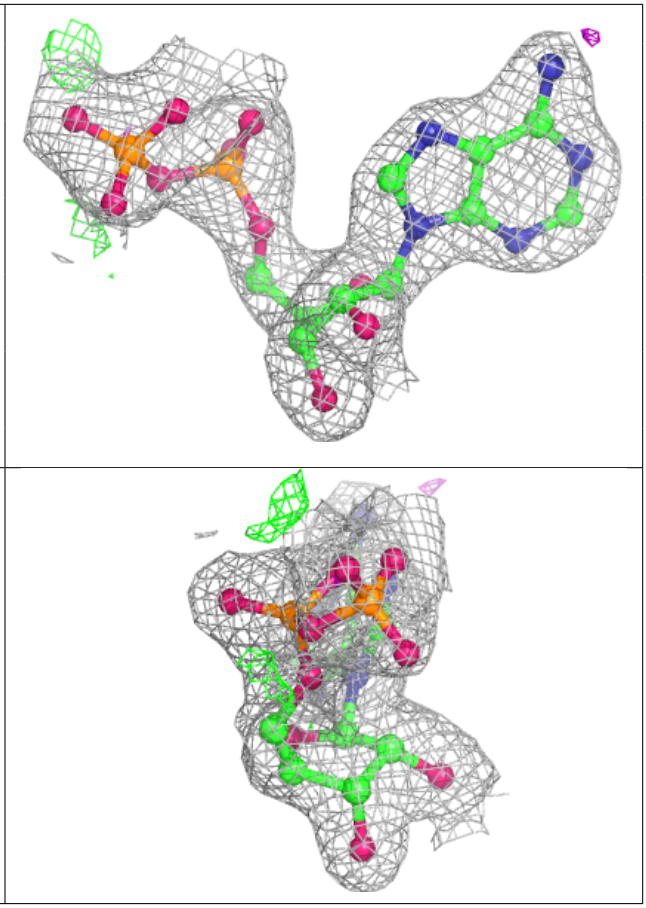
Electron density around ADP B 1001:

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



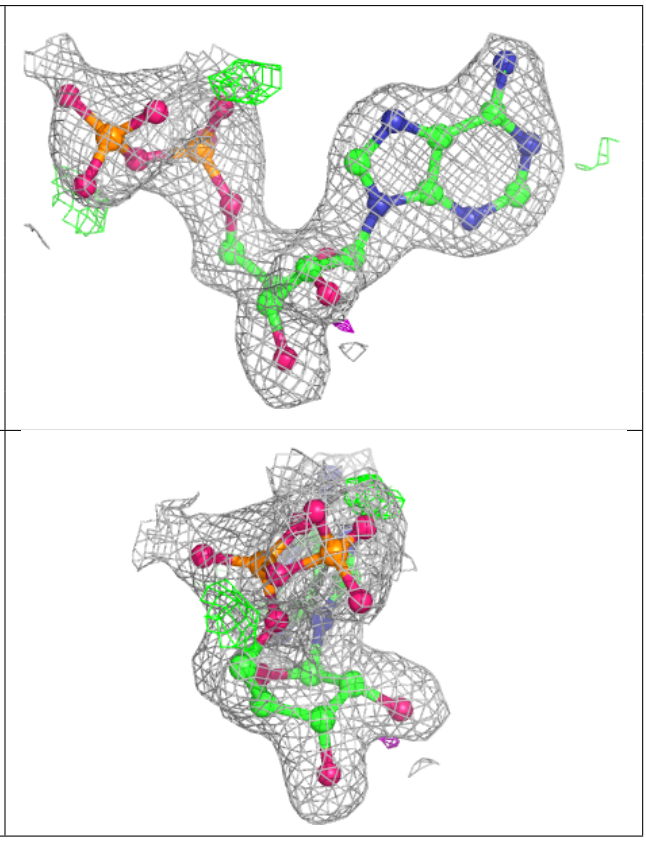
Electron density around ADP E 1001:

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



Electron density around ADP H 1001:

$2mF_o$-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.