wwPDB X-ray Structure Validation Summary Report (i)

Jun 23, 2022 – 04:16 pm BST

PDB ID	:	6TGW
Title	:	Crystal structure of human Aldehyde dehydrogenase 1A3 in complex with a selective inhibitor
Authors	:	Garavaglia, S.; Rizzi, M.
Deposited on	:	2019-11-18
Resolution	:	2.80 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:

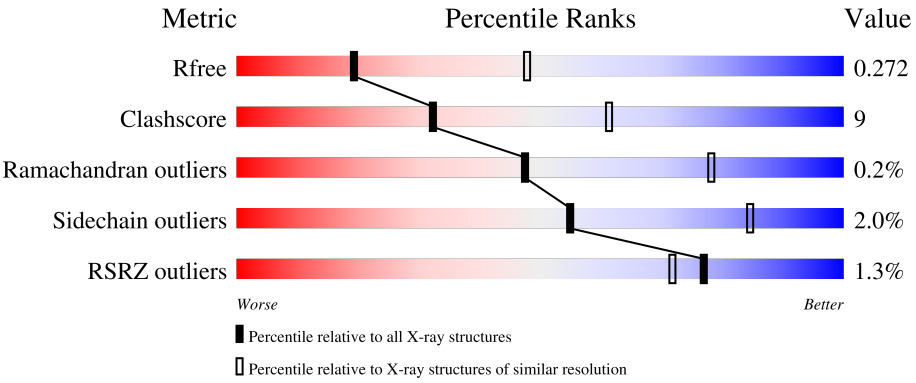
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

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 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	512	75% 17% • 7%
1	B	512	2% 73% 19% 7%
1	C	512	73% 21% 6%
1	D	512	76% 17% 7%

2 Entry composition

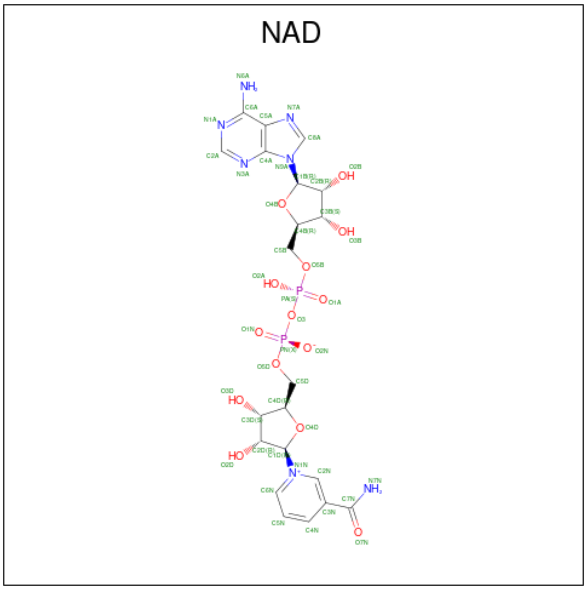
There are 4 unique types of molecules in this entry. The entry contains 15310 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 family 1 member A3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	478	Total	C	N	O	S	0	0	0
			3689	2354	627	688	20			
1	B	478	Total	C	N	O	S	0	0	0
			3689	2354	627	688	20			
1	C	479	Total	C	N	O	S	0	0	0
			3698	2358	629	691	20			
1	D	478	Total	C	N	O	S	0	0	0
			3689	2352	627	690	20			

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



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

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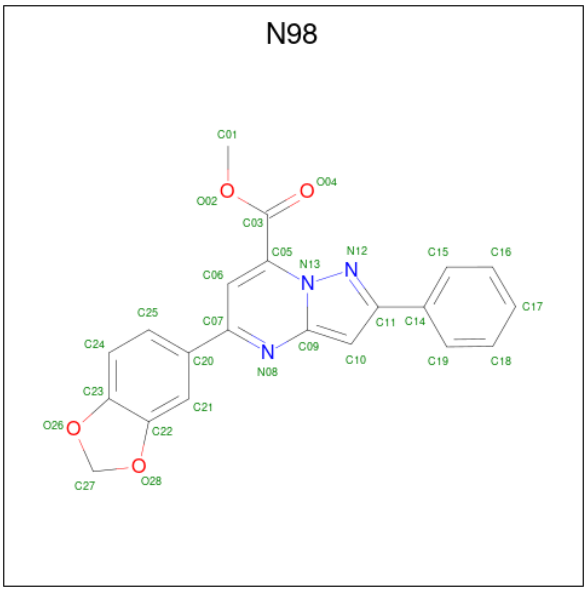
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total C N O P 44 21 7 14 2	0	0
2	D	1	Total C N O P 44 21 7 14 2	0	0

- Molecule 3 is methyl 5-(1,3-benzodioxol-5-yl)-2-phenyl-pyrazolo[1,5-a]pyrimidine-7-carboxylate (three-letter code: N98) (formula: $C_{21}H_{15}N_3O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 28 21 3 4	0	0
3	B	1	Total C N O 28 21 3 4	0	0
3	C	1	Total C N O 28 21 3 4	0	0
3	D	1	Total C N O 28 21 3 4	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	62	Total O 62 62	0	0
4	B	52	Total O 52 52	0	0

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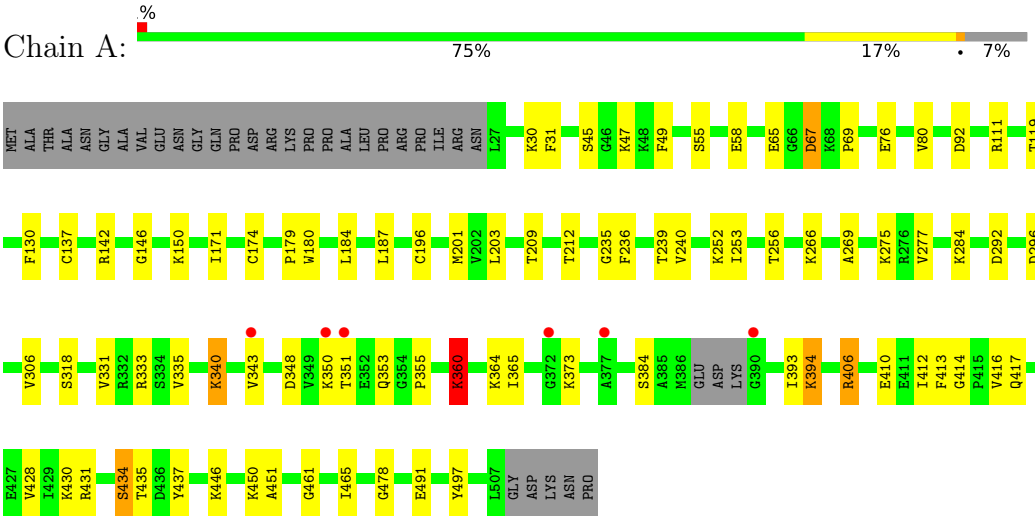
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	73	Total O 73 73	0	0
4	D	70	Total O 70 70	0	0

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.

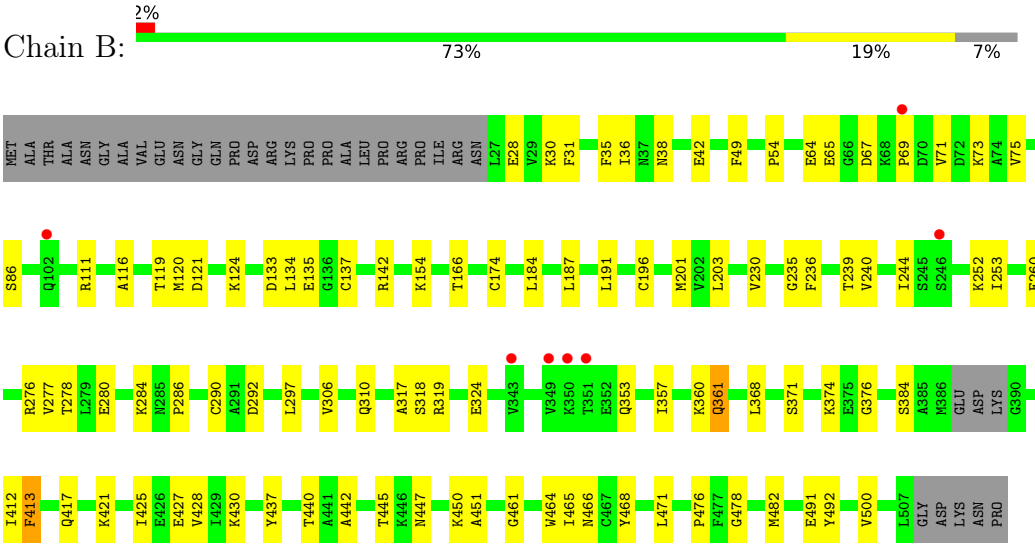
• Molecule 1: Aldehyde dehydrogenase family 1 member A3

Chain A:



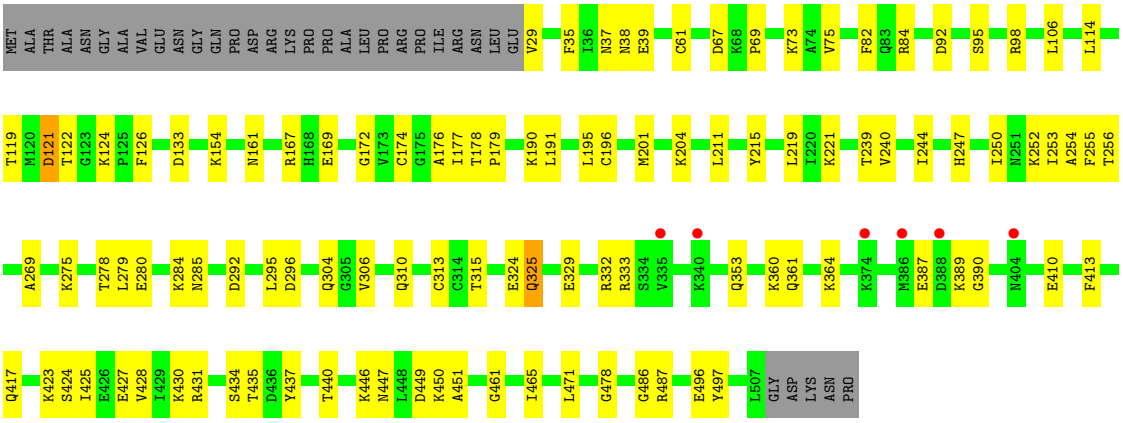
• Molecule 1: Aldehyde dehydrogenase family 1 member A3

Chain B:



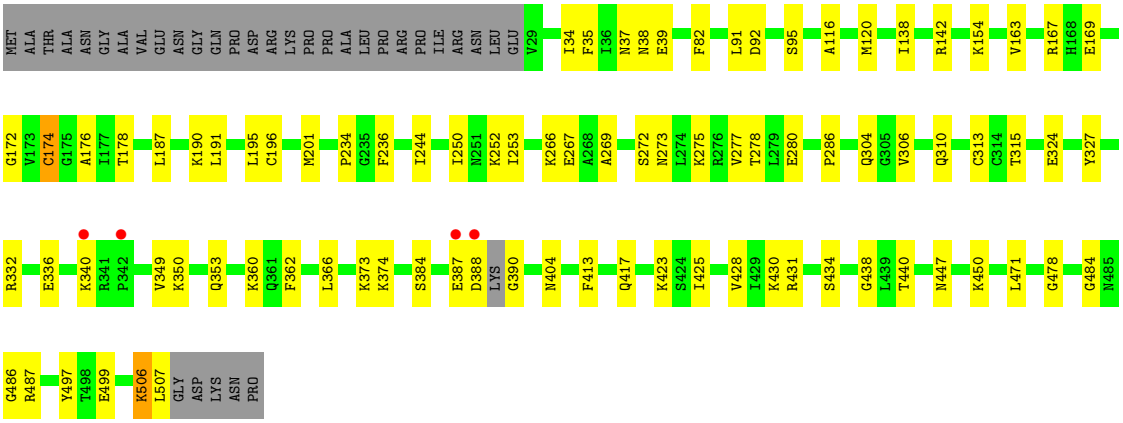
• Molecule 1: Aldehyde dehydrogenase family 1 member A3

Chain C:



• Molecule 1: Aldehyde dehydrogenase family 1 member A3

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.03Å 158.47Å 168.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.02 – 2.80 47.02 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.6 (47.02-2.80) 97.4 (47.02-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.18	Depositor
$< I/\sigma(I) >$ [1]	2.43 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.201 , 0.274 0.196 , 0.272	Depositor DCC
R_{free} test set	2634 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	30.4	Xtriage
Anisotropy	0.610	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.55$, $< L^2 > = 0.39$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	15310	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.78 % 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 3.0090e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAD, N98

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	0.56	4/3764 (0.1%)	0.64	2/5092 (0.0%)
1	B	0.53	1/3764 (0.0%)	0.68	1/5092 (0.0%)
1	C	0.46	0/3774	0.60	1/5106 (0.0%)
1	D	0.51	2/3764 (0.1%)	0.61	0/5092
All	All	0.52	7/15066 (0.0%)	0.63	4/20382 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	271	ARG	CB-CG	-10.60	1.24	1.52
1	A	360	LYS	CE-NZ	-9.91	1.24	1.49
1	A	58	GLU	CB-CG	-9.25	1.34	1.52
1	D	236	PHE	CB-CG	8.55	1.65	1.51
1	A	360	LYS	CD-CE	-8.33	1.30	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	271	ARG	CG-CD-NE	-15.70	78.84	111.80
1	A	58	GLU	CA-CB-CG	-10.32	90.70	113.40
1	C	325	GLN	CA-CB-CG	-6.03	100.13	113.40
1	A	393	ILE	C-N-CA	-5.25	108.56	121.70

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	3689	0	3716	61	0
1	B	3689	0	3716	85	1
1	C	3698	0	3723	69	1
1	D	3689	0	3706	64	0
2	A	44	0	25	3	0
2	B	44	0	25	1	0
2	C	44	0	24	1	0
2	D	44	0	23	3	0
3	A	28	0	0	0	0
3	B	28	0	0	1	0
3	C	28	0	0	3	0
3	D	28	0	0	3	0
4	A	62	0	0	2	0
4	B	52	0	0	2	0
4	C	73	0	0	0	0
4	D	70	0	0	1	0
All	All	15310	0	14958	263	1

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 9.

The worst 5 of 263 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)
2:B:602:NAD:C1D	2:B:602:NAD:O4D	1.63	1.23
2:D:601:NAD:O4D	2:D:601:NAD:C1D	1.64	1.17
1:B:466:ASN:O	1:D:506:LYS:HE3	1.54	1.07
1:B:142:ARG:HD3	1:C:98:ARG:HH12	1.41	0.85
1:B:271:ARG:NH2	1:D:267:GLU:OE2	2.12	0.82

All (1) 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)
1:B:376:GLY:O	1:C:325:GLN:NE2[2_454]	1.68	0.52

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	474/512 (93%)	447 (94%)	27 (6%)	0	100	100
1	B	474/512 (93%)	451 (95%)	22 (5%)	1 (0%)	47	78
1	C	477/512 (93%)	456 (96%)	20 (4%)	1 (0%)	47	78
1	D	474/512 (93%)	446 (94%)	27 (6%)	1 (0%)	47	78
All	All	1899/2048 (93%)	1800 (95%)	96 (5%)	3 (0%)	47	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	196	CYS
1	B	374	LYS
1	D	438	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	395/422 (94%)	384 (97%)	11 (3%)	43	77
1	B	395/422 (94%)	387 (98%)	8 (2%)	55	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	396/422 (94%)	390 (98%)	6 (2%)	65 89
1	D	395/422 (94%)	389 (98%)	6 (2%)	65 89
All	All	1581/1688 (94%)	1550 (98%)	31 (2%)	55 84

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

Mol	Chain	Res	Type
1	B	196	CYS
1	D	388	ASP
1	B	361	GLN
1	D	434	SER
1	C	449	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	304	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)

8 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	602	-	42,48,48	5.56	18 (42%)	50,73,73	1.98	7 (14%)
2	NAD	D	601	-	42,48,48	5.54	15 (35%)	50,73,73	1.82	8 (16%)
3	N98	D	602	-	29,32,32	2.69	10 (34%)	36,46,46	2.86	12 (33%)
2	NAD	C	601	-	42,48,48	5.49	17 (40%)	50,73,73	1.73	6 (12%)
3	N98	A	602	-	29,32,32	2.56	9 (31%)	36,46,46	2.86	13 (36%)
3	N98	B	601	-	29,32,32	2.92	11 (37%)	36,46,46	3.11	14 (38%)
2	NAD	A	601	-	42,48,48	5.45	16 (38%)	50,73,73	1.99	6 (12%)
3	N98	C	602	-	29,32,32	2.76	10 (34%)	36,46,46	2.84	10 (27%)

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	602	-	-	7/26/62/62	0/5/5/5
2	NAD	D	601	-	-	14/26/62/62	0/5/5/5
3	N98	D	602	-	-	5/14/20/20	0/5/5/5
2	NAD	C	601	-	-	5/26/62/62	0/5/5/5
3	N98	A	602	-	-	0/14/20/20	0/5/5/5
3	N98	B	601	-	-	0/14/20/20	0/5/5/5
2	NAD	A	601	-	-	9/26/62/62	0/5/5/5
3	N98	C	602	-	-	4/14/20/20	0/5/5/5

The worst 5 of 106 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	NAD	C2D-C1D	-16.72	1.28	1.53
2	D	601	NAD	O4D-C1D	16.54	1.64	1.41
2	B	602	NAD	C2D-C1D	-16.44	1.28	1.53
2	D	601	NAD	C2B-C1B	-16.41	1.28	1.53
2	B	602	NAD	O4D-C1D	16.29	1.63	1.41

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	602	N98	O02-C03-C05	10.46	127.83	111.18
3	D	602	N98	O02-C03-C05	10.06	127.19	111.18
3	A	602	N98	O02-C03-C05	8.57	124.82	111.18
2	A	601	NAD	C5A-C6A-N6A	7.90	132.36	120.35
3	B	601	N98	C14-C11-N12	7.80	133.29	120.92

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	NAD	C5B-O5B-PA-O1A
2	A	601	NAD	C3D-C4D-C5D-O5D
2	A	601	NAD	C2D-C1D-N1N-C2N
2	A	601	NAD	C2D-C1D-N1N-C6N
2	B	602	NAD	PN-O3-PA-O5B

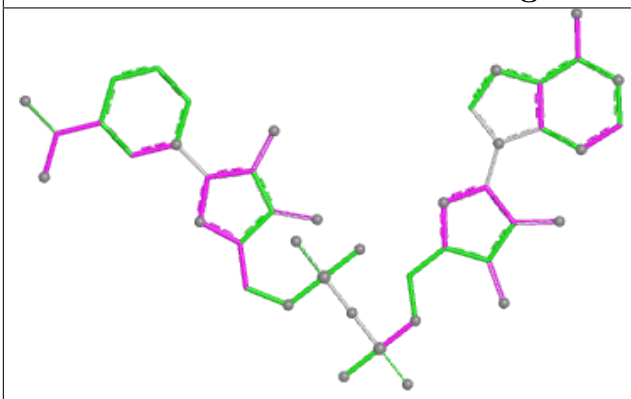
There are no ring outliers.

7 monomers are involved in 15 short contacts:

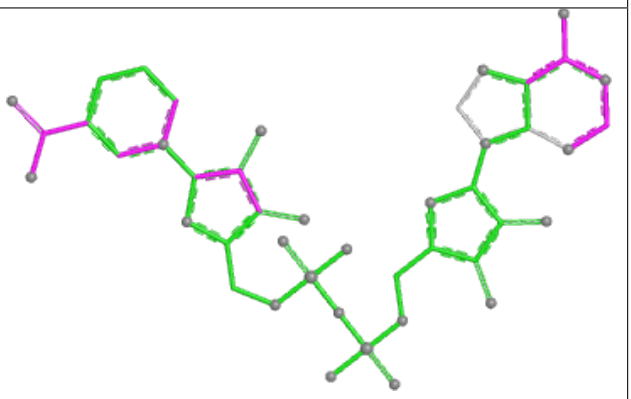
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	602	NAD	1	0
2	D	601	NAD	3	0
3	D	602	N98	3	0
2	C	601	NAD	1	0
3	B	601	N98	1	0
2	A	601	NAD	3	0
3	C	602	N98	3	0

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.

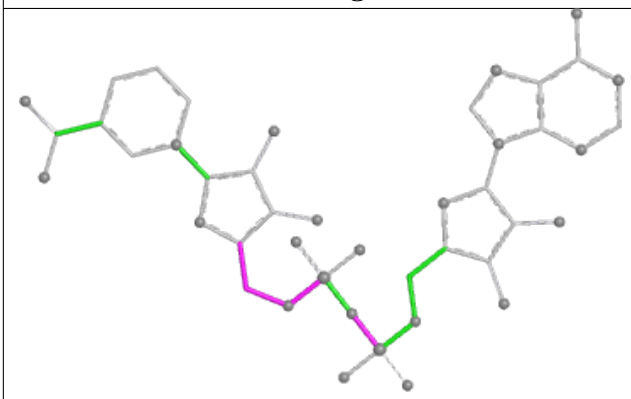
Ligand NAD B 602



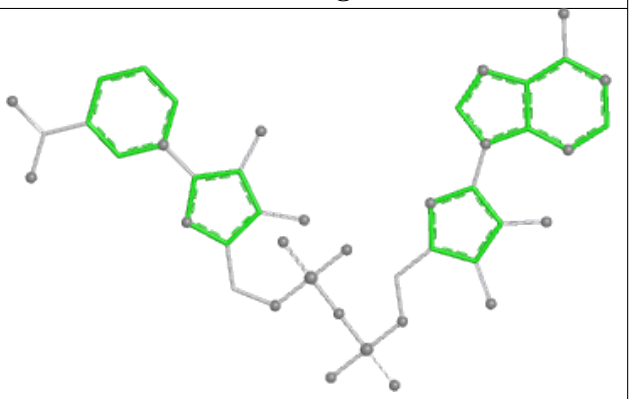
Bond lengths



Bond angles

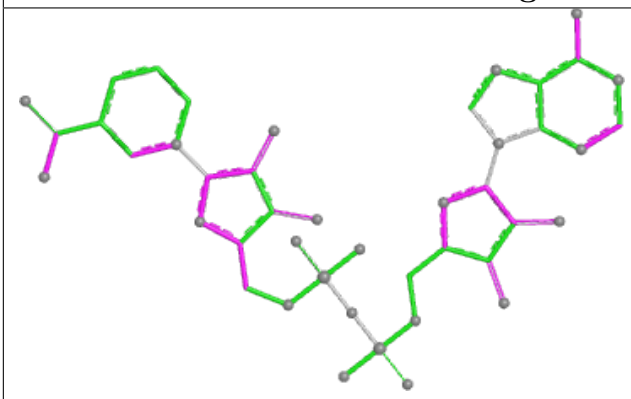


Torsions

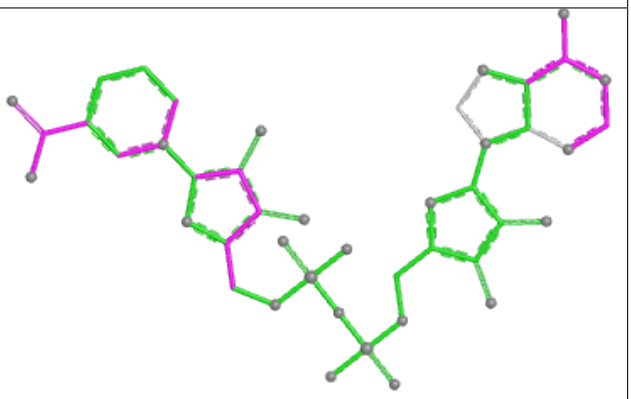


Rings

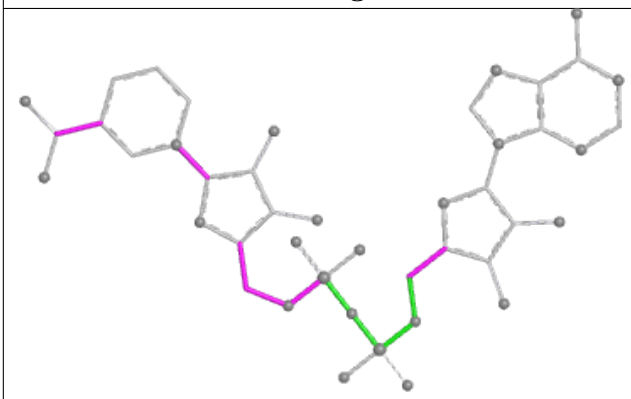
Ligand NAD D 601



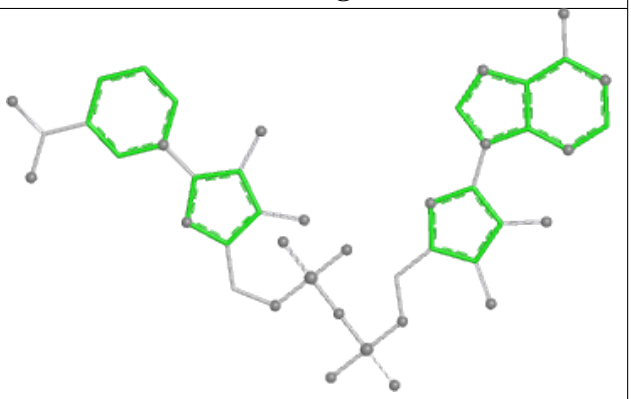
Bond lengths



Bond angles

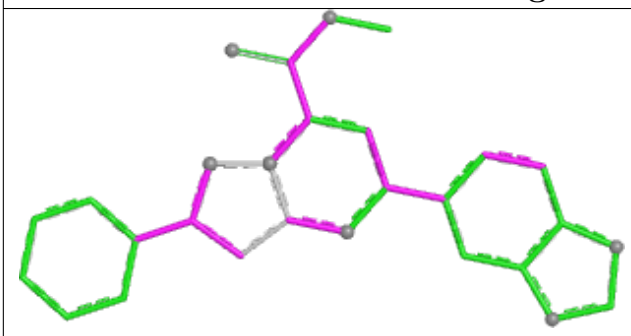


Torsions



Rings

Ligand N98 D 602



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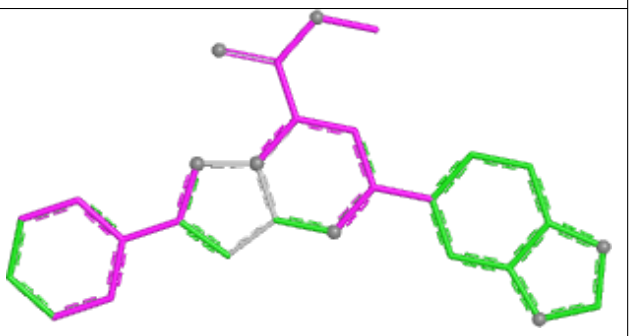

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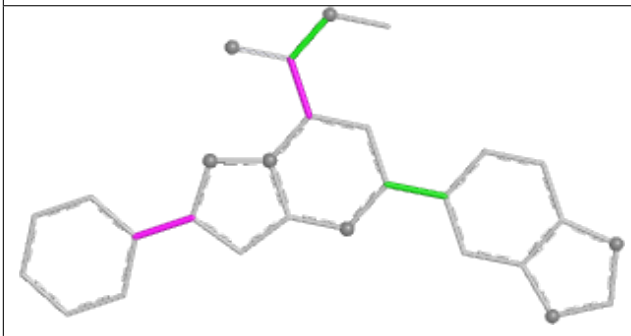

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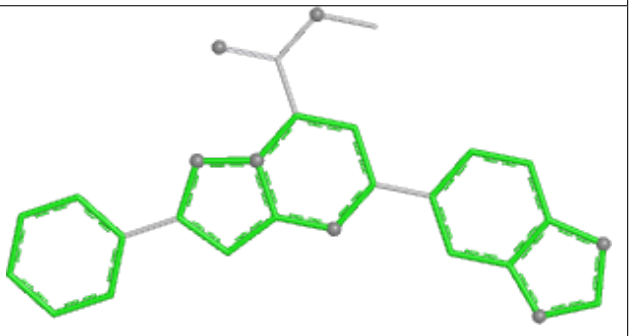
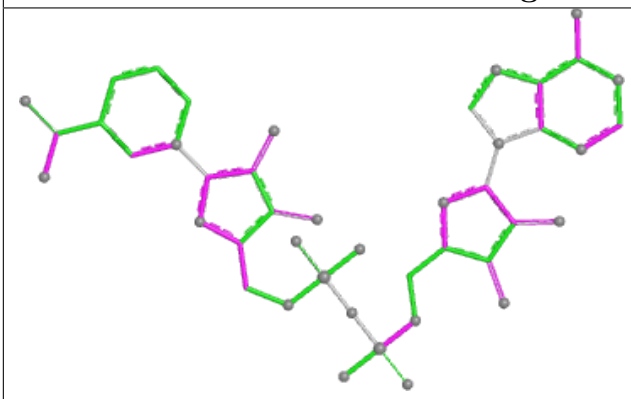


Rings

Ligand NAD C 601



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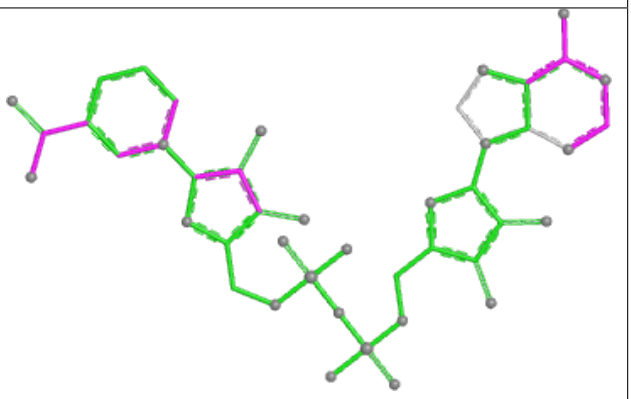
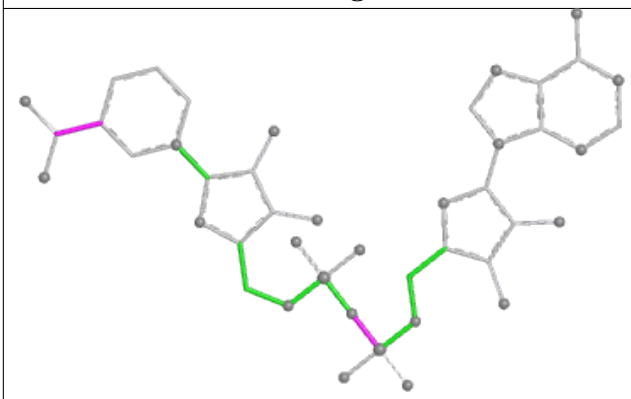
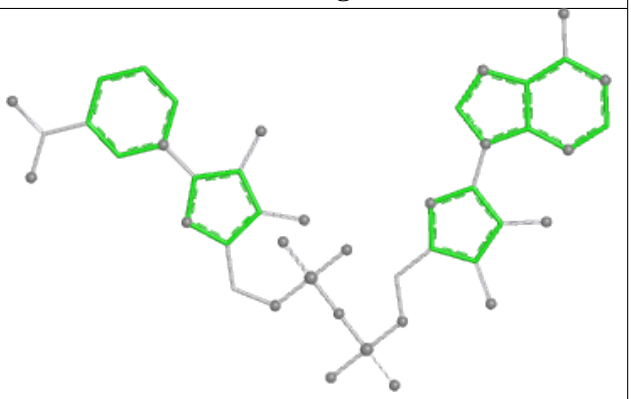


Bond angles

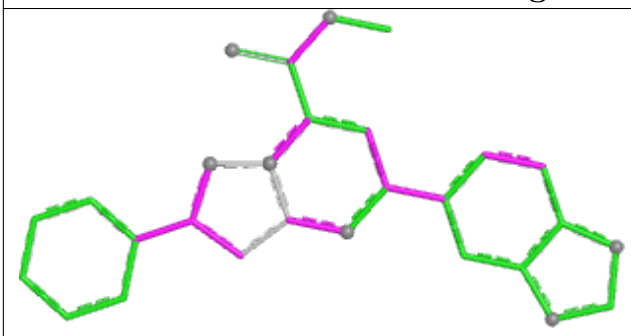


Torsions

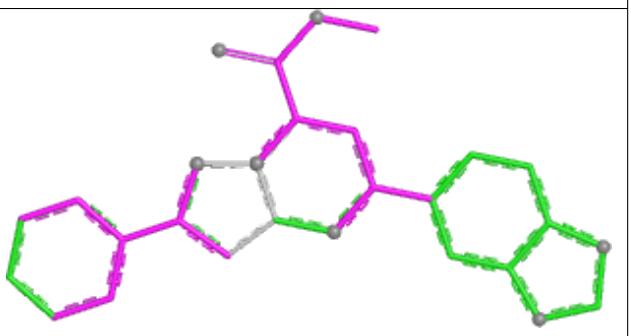


Rings

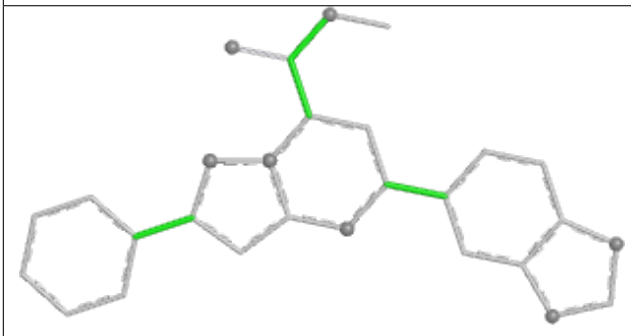
Ligand N98 A 602



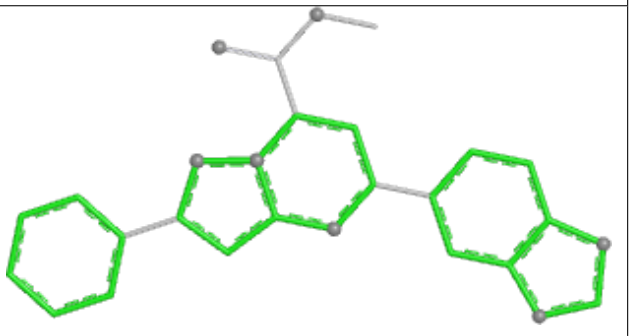
Bond lengths



Bond angles

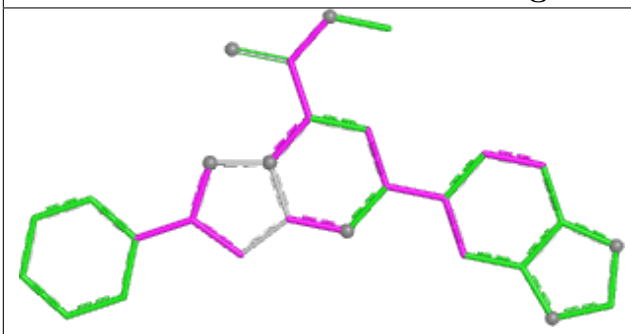


Torsions

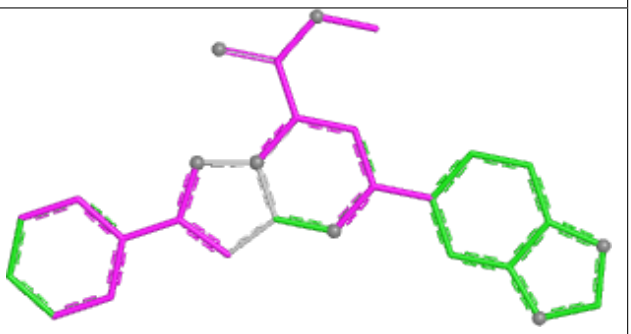


Rings

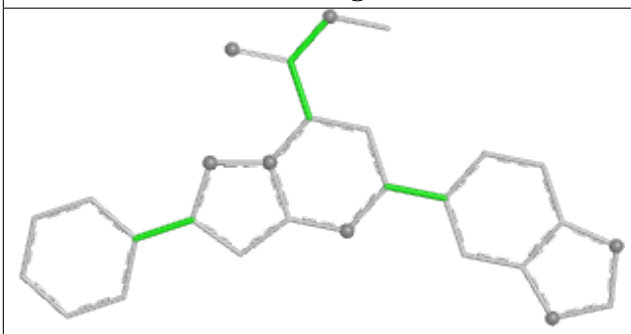
Ligand N98 B 601



Bond lengths



Bond angles



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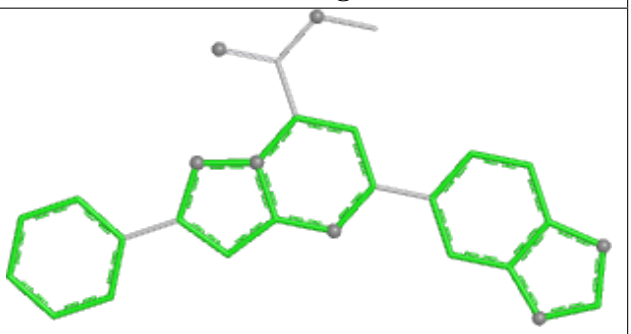
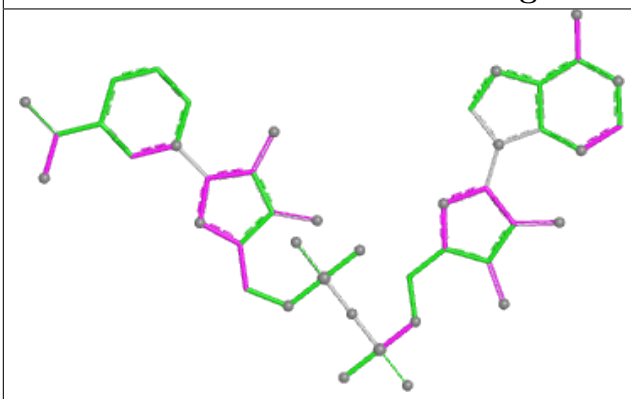
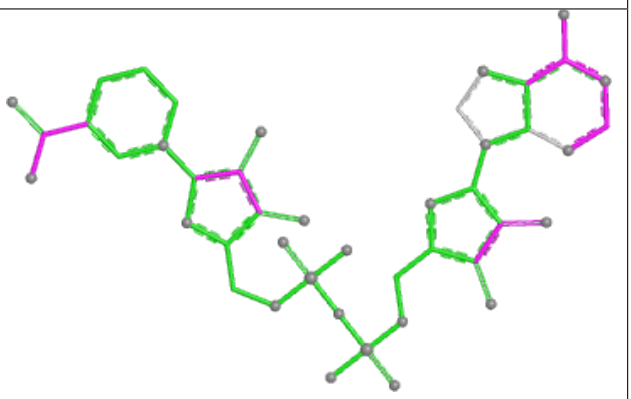


Rings

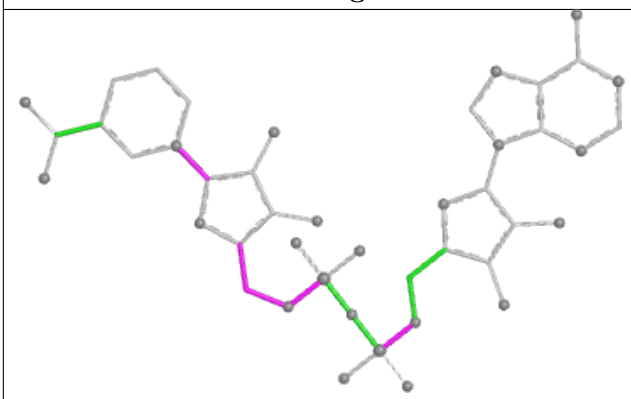
Ligand NAD A 601



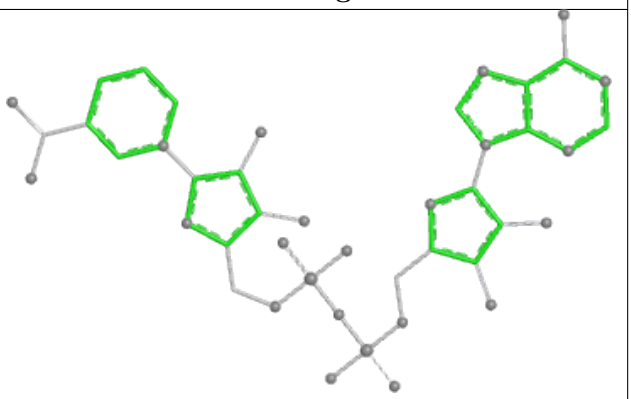
Bond lengths



Bond angles

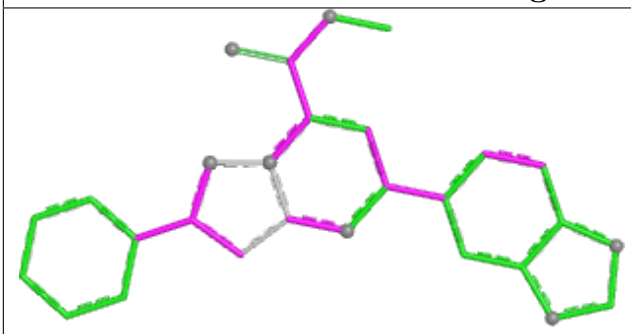


Torsions

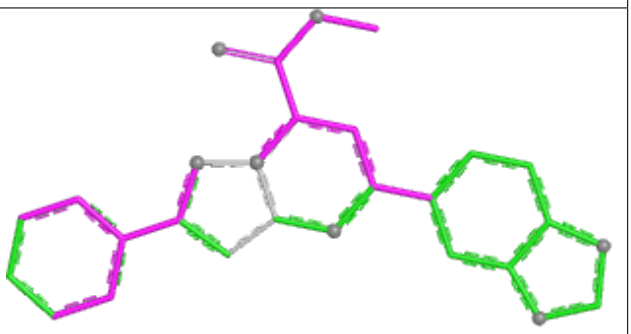


Rings

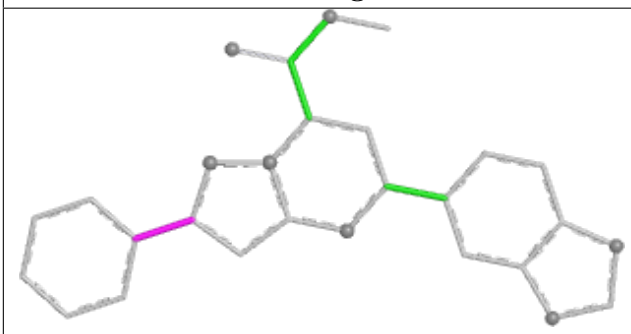
Ligand N98 C 602



Bond lengths



Bond angles



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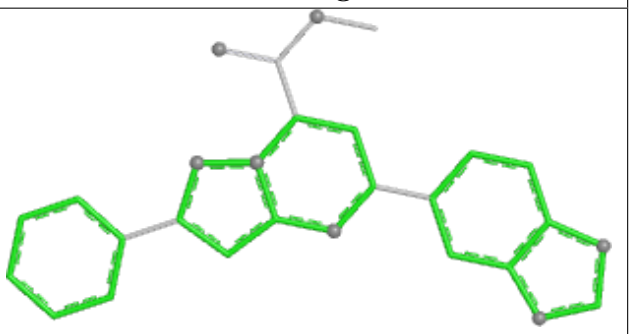


Rings

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

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, 95^{th} 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	478/512 (93%)	-0.07	6 (1%)	77	72	7, 20, 55, 65	0
1	B	478/512 (93%)	-0.15	8 (1%)	70	63	7, 19, 44, 56	0
1	C	479/512 (93%)	-0.16	6 (1%)	77	72	7, 19, 40, 81	0
1	D	478/512 (93%)	-0.23	4 (0%)	86	81	6, 19, 39, 75	0
All	All	1913/2048 (93%)	-0.15	24 (1%)	77	72	6, 19, 44, 81	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	350	LYS	3.3
1	A	351	THR	3.2
1	B	349	VAL	2.8
1	A	377	ALA	2.8
1	B	351	THR	2.5

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

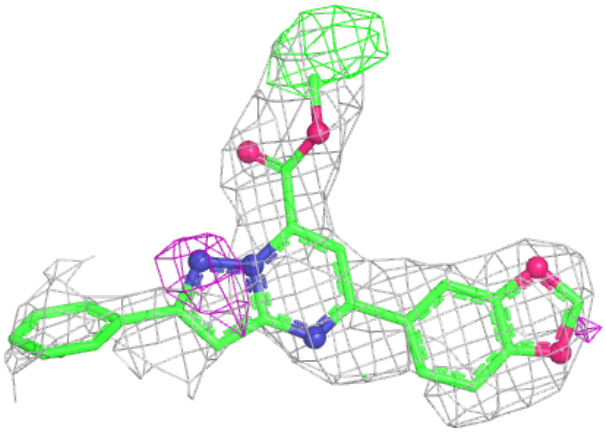
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

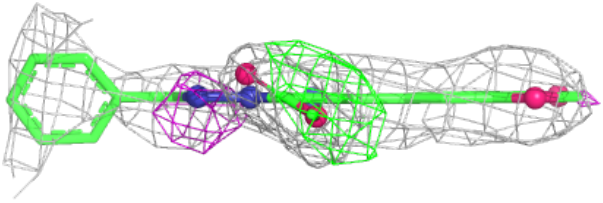
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	N98	C	602	28/28	0.79	0.31	12,35,50,57	0
3	N98	B	601	28/28	0.81	0.29	17,30,56,58	0
3	N98	A	602	28/28	0.82	0.28	13,30,59,64	0
3	N98	D	602	28/28	0.83	0.29	15,34,57,60	0
2	NAD	D	601	44/44	0.92	0.19	8,28,81,87	0
2	NAD	C	601	44/44	0.93	0.19	10,22,82,88	0
2	NAD	B	602	44/44	0.94	0.17	7,20,67,72	0
2	NAD	A	601	44/44	0.95	0.16	9,19,72,77	0

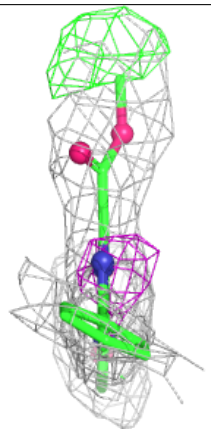
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around N98 C 602:

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

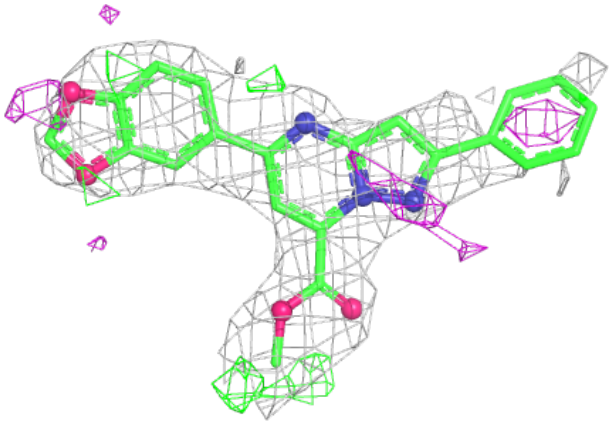


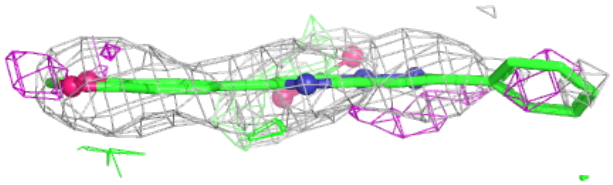


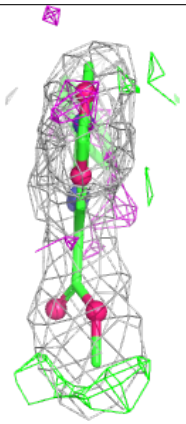


Electron density around N98 B 601:

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

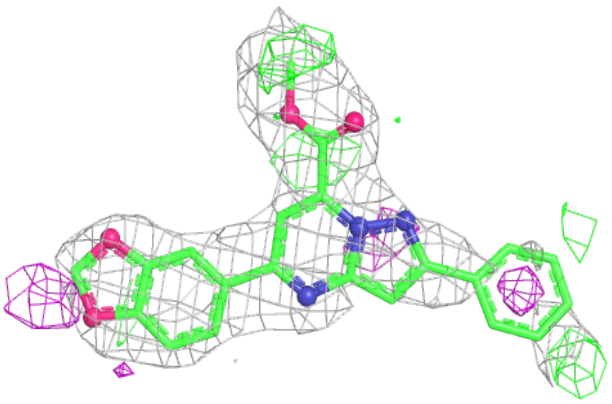


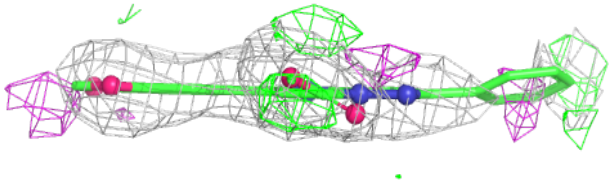


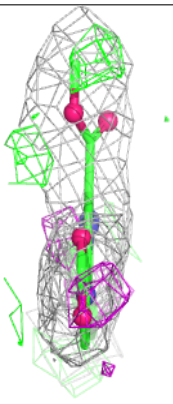


Electron density around N98 A 602:

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

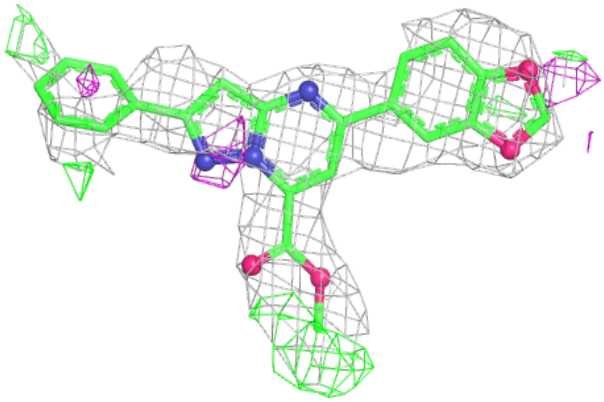


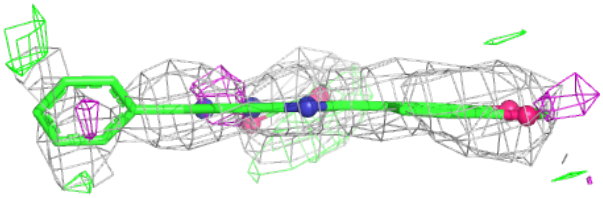


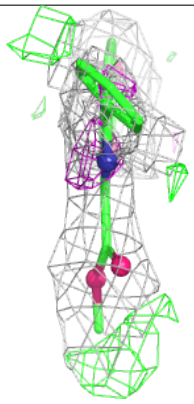


Electron density around N98 D 602:

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

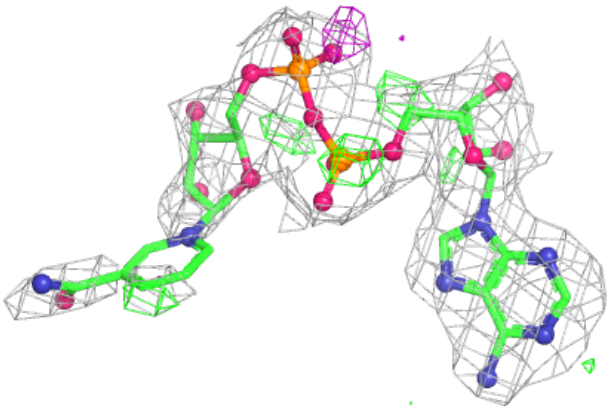


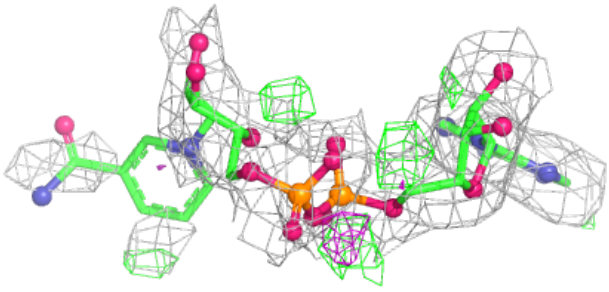


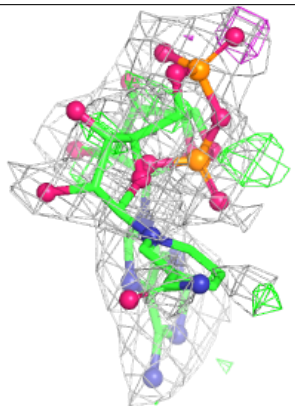


Electron density around NAD D 601:

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

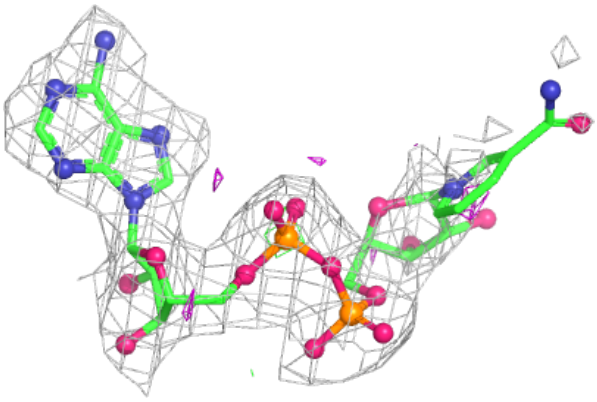


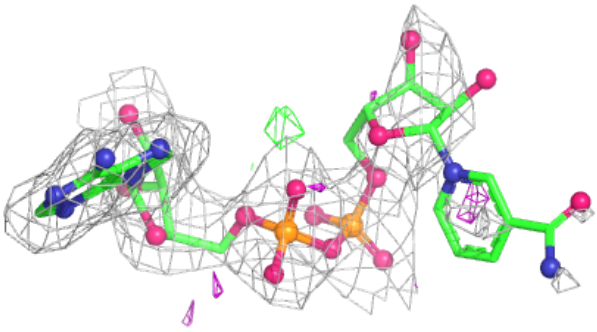


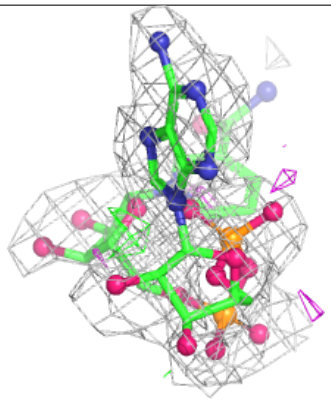


Electron density around NAD C 601:

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

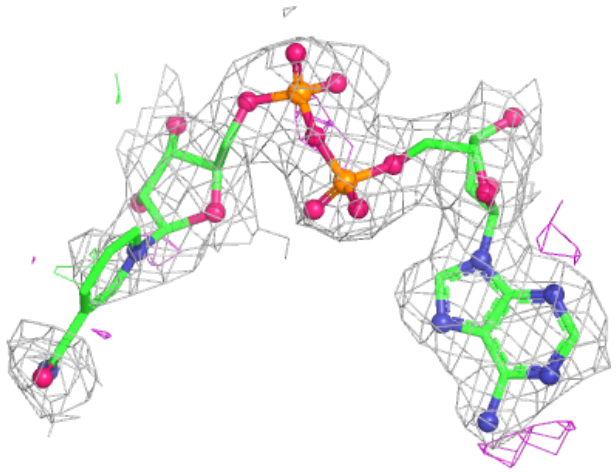


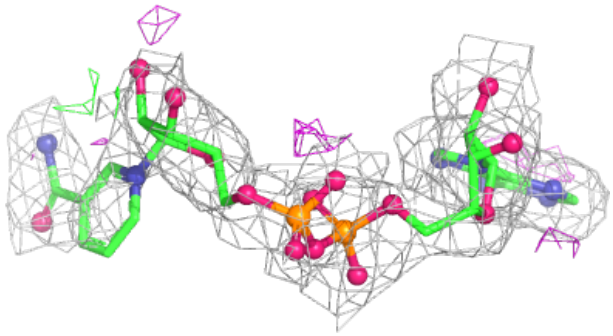


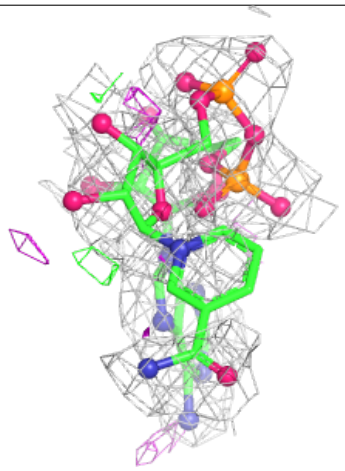


Electron density around NAD B 602:

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

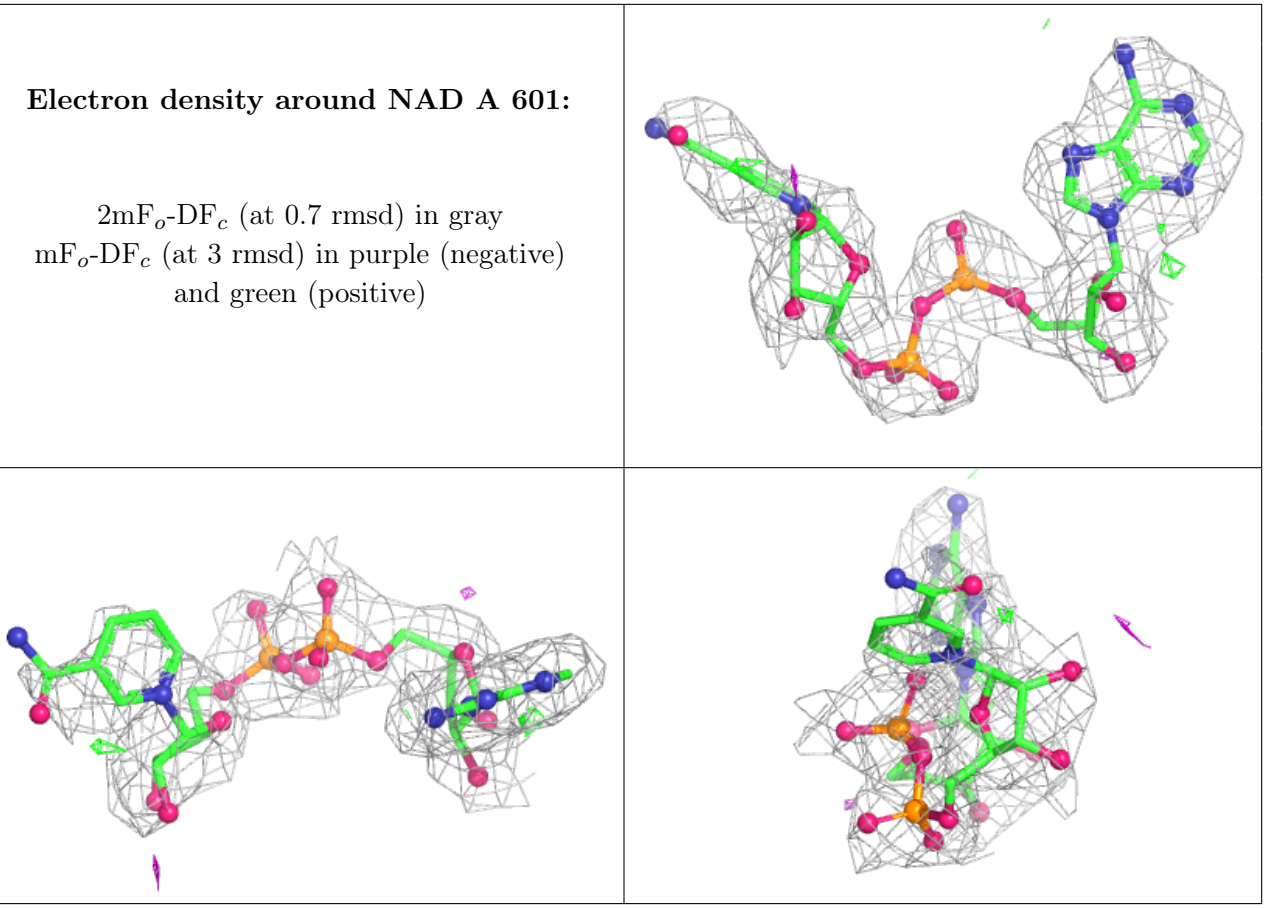






Electron density around NAD A 601:

$2mF_o$-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.