



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 3, 2023 – 10:35 AM EDT

PDB ID : 3RUA
Title : Specific recognition of N-acetylated substrates and domain flexibility in WbgU:
a UDP-GalNAc 4-epimerase
Authors : Bhatt, V.S.; Guan, W.; Wang, P.G.
Deposited on : 2011-05-04
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

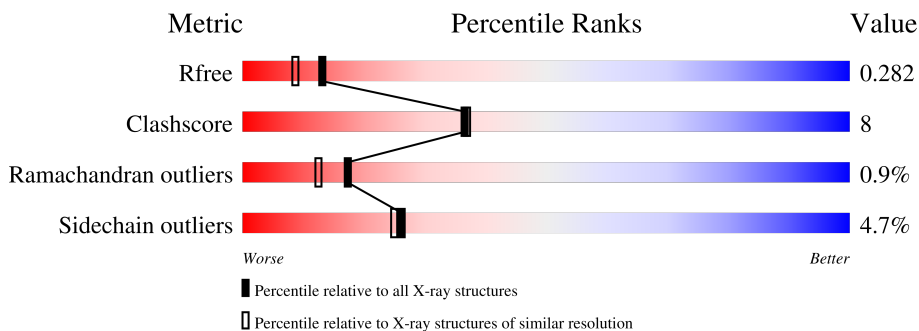
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	351	77% 15% . . .
1	B	351	77% 15% . . .
1	C	351	79% 14% . . .
1	D	351	81% 12% . . .

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 11365 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 WbgU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	336	2681	1712	459	502	8	0	0	0
1	B	336	2681	1712	459	502	8	0	0	0
1	C	336	2681	1712	459	502	8	0	0	0
1	D	336	2681	1712	459	502	8	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

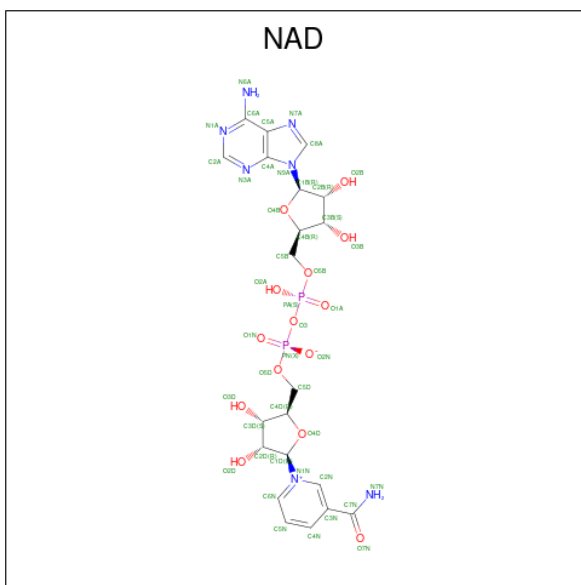
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	HIS	-	expression tag	UNP Q7BJX9
A	-7	HIS	-	expression tag	UNP Q7BJX9
A	-6	HIS	-	expression tag	UNP Q7BJX9
A	-5	HIS	-	expression tag	UNP Q7BJX9
A	-4	HIS	-	expression tag	UNP Q7BJX9
A	-3	HIS	-	expression tag	UNP Q7BJX9
B	-8	HIS	-	expression tag	UNP Q7BJX9
B	-7	HIS	-	expression tag	UNP Q7BJX9
B	-6	HIS	-	expression tag	UNP Q7BJX9
B	-5	HIS	-	expression tag	UNP Q7BJX9
B	-4	HIS	-	expression tag	UNP Q7BJX9
B	-3	HIS	-	expression tag	UNP Q7BJX9
C	-8	HIS	-	expression tag	UNP Q7BJX9
C	-7	HIS	-	expression tag	UNP Q7BJX9
C	-6	HIS	-	expression tag	UNP Q7BJX9
C	-5	HIS	-	expression tag	UNP Q7BJX9
C	-4	HIS	-	expression tag	UNP Q7BJX9
C	-3	HIS	-	expression tag	UNP Q7BJX9
D	-8	HIS	-	expression tag	UNP Q7BJX9
D	-7	HIS	-	expression tag	UNP Q7BJX9
D	-6	HIS	-	expression tag	UNP Q7BJX9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	HIS	-	expression tag	UNP Q7BJX9
D	-4	HIS	-	expression tag	UNP Q7BJX9
D	-3	HIS	-	expression tag	UNP Q7BJX9

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



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

- Molecule 3 is UNKNOWN LIGAND (three-letter code: UNL) (formula:).

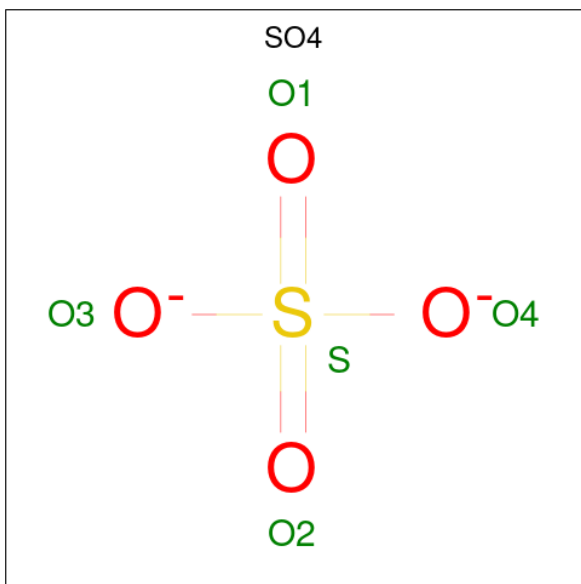
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	C	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	D	1	25	9	2	12	2	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	A	1	5	4	1	0	0
4	A	1	5	4	1	0	0

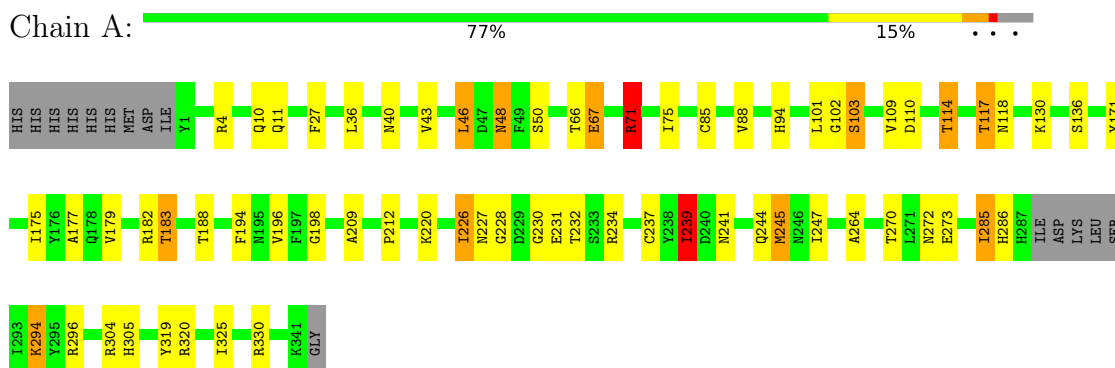
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	119	Total	O	0	0
			119	119		
5	B	72	Total	O	0	0
			72	72		
5	C	106	Total	O	0	0
			106	106		
5	D	58	Total	O	0	0
			58	58		

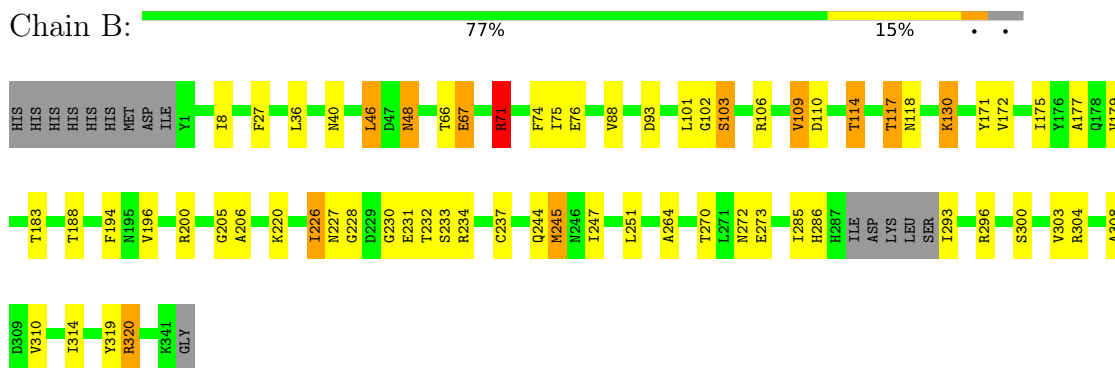
3 Residue-property plots [i](#)

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. 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. 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.

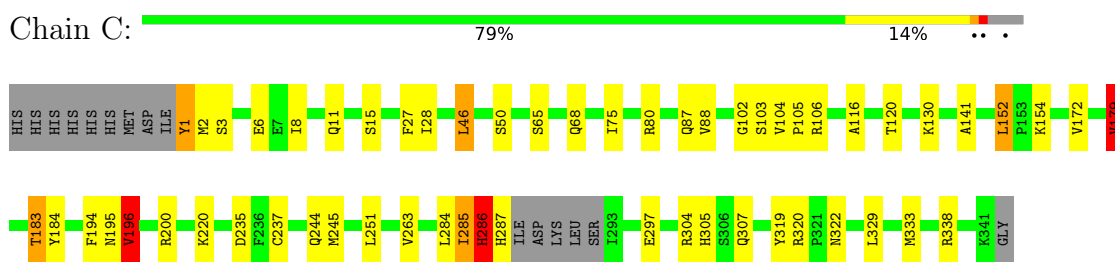
- Molecule 1: WbgU



- Molecule 1: WbgU



- Molecule 1: WbgU



- Molecule 1: WbgU

4 Data and refinement statistics i

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	77.44Å 77.44Å 224.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.10 49.92 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.10) 99.8 (49.92-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.180 , 0.234 0.255 , 0.282	Depositor DCC
R_{free} test set	4402 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	31.9	Xtrriage
Anisotropy	0.130	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 29.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.016 for -h,-k,l 0.477 for h,-h-k,-l 0.017 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11365	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UNL, NAD, SO4

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	1.09	5/2739 (0.2%)	0.92	8/3717 (0.2%)
1	B	1.07	4/2739 (0.1%)	0.99	10/3717 (0.3%)
1	C	1.00	2/2739 (0.1%)	0.90	6/3717 (0.2%)
1	D	0.99	3/2739 (0.1%)	0.87	6/3717 (0.2%)
All	All	1.04	14/10956 (0.1%)	0.92	30/14868 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	D	0	1
All	All	0	3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	117	THR	CB-CG2	-7.01	1.29	1.52
1	C	196	VAL	CB-CG2	-5.81	1.40	1.52
1	D	55	TYR	CD1-CE1	5.81	1.48	1.39
1	A	43	VAL	CB-CG2	5.59	1.64	1.52
1	D	55	TYR	CD2-CE2	5.58	1.47	1.39

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	200	ARG	NE-CZ-NH2	-17.95	111.32	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	200	ARG	NE-CZ-NH2	-13.32	113.64	120.30
1	B	200	ARG	NE-CZ-NH1	12.67	126.63	120.30
1	A	239	ILE	CG1-CB-CG2	9.58	132.47	111.40
1	C	200	ARG	NE-CZ-NH1	9.32	124.96	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	285	ILE	Peptide
1	C	285	ILE	Peptide
1	D	285	ILE	Peptide

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	2681	0	2658	49	0
1	B	2681	0	2658	58	0
1	C	2681	0	2658	40	0
1	D	2681	0	2658	34	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	C	44	0	26	0	0
2	D	44	0	26	0	0
3	A	25	0	0	0	0
3	B	25	0	0	0	0
3	C	25	0	0	0	0
3	D	25	0	0	0	0
4	A	10	0	0	0	0
5	A	119	0	0	0	0
5	B	72	0	0	0	0
5	C	106	0	0	2	0
5	D	58	0	0	0	0
All	All	11365	0	10736	171	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 8.

The worst 5 of 171 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:C:286:HIS:O	1:C:287:HIS:ND1	1.88	1.05
1:C:2:MET:HG3	1:C:322:ASN:HD21	1.25	1.01
1:D:2:MET:HG2	1:D:322:ASN:HD21	1.24	0.99
1:C:2:MET:CG	1:C:322:ASN:HD21	1.75	0.99
1:A:171:TYR:CE2	1:A:175:ILE:HD11	2.02	0.94

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	332/351 (95%)	319 (96%)	7 (2%)	6 (2%)	8 4
1	B	332/351 (95%)	313 (94%)	15 (4%)	4 (1%)	13 8
1	C	332/351 (95%)	324 (98%)	7 (2%)	1 (0%)	41 41
1	D	332/351 (95%)	322 (97%)	9 (3%)	1 (0%)	41 41
All	All	1328/1404 (95%)	1278 (96%)	38 (3%)	12 (1%)	17 12

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	227	ASN
1	A	286	HIS
1	B	227	ASN
1	C	286	HIS
1	D	286	HIS

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	290/304 (95%)	276 (95%)	14 (5%)	25	24
1	B	290/304 (95%)	279 (96%)	11 (4%)	33	34
1	C	290/304 (95%)	275 (95%)	15 (5%)	23	21
1	D	290/304 (95%)	276 (95%)	14 (5%)	25	24
All	All	1160/1216 (95%)	1106 (95%)	54 (5%)	26	25

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	15	SER
1	C	220	LYS
1	D	260	ILE
1	C	46	LEU
1	C	179	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	48	ASN
1	D	322	ASN
1	B	173	ASN
1	C	262	ASN
1	B	115	ASN

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 10 ligands modelled in this entry, 4 are unknown - leaving 6 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	NAD	A	343	-	42,48,48	1.45	7 (16%)	50,73,73	1.50	9 (18%)
2	NAD	D	343	-	42,48,48	1.62	5 (11%)	50,73,73	1.61	6 (12%)
2	NAD	C	343	-	42,48,48	1.84	9 (21%)	50,73,73	1.54	3 (6%)
2	NAD	B	343	-	42,48,48	1.39	5 (11%)	50,73,73	1.61	12 (24%)
4	SO4	A	345	-	4,4,4	0.33	0	6,6,6	0.45	0
4	SO4	A	346	-	4,4,4	0.13	0	6,6,6	0.70	0

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	A	343	-	-	8/26/62/62	0/5/5/5
2	NAD	B	343	-	-	6/26/62/62	0/5/5/5
2	NAD	D	343	-	-	5/26/62/62	0/5/5/5
2	NAD	C	343	-	-	5/26/62/62	0/5/5/5

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	343	NAD	C2N-N1N	5.98	1.42	1.35
2	D	343	NAD	C2N-N1N	5.84	1.42	1.35
2	C	343	NAD	O4B-C1B	5.38	1.48	1.41
2	A	343	NAD	C2N-N1N	4.33	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	343	NAD	C6N-N1N	3.82	1.44	1.35

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	343	NAD	N3A-C2A-N1A	-5.22	120.52	128.68
2	C	343	NAD	C3N-C2N-N1N	-5.06	115.48	120.43
2	D	343	NAD	N3A-C2A-N1A	-5.04	120.80	128.68
2	D	343	NAD	C2N-C3N-C4N	4.87	123.78	118.26
2	D	343	NAD	C3N-C2N-N1N	-4.63	115.90	120.43

There are no chirality outliers.

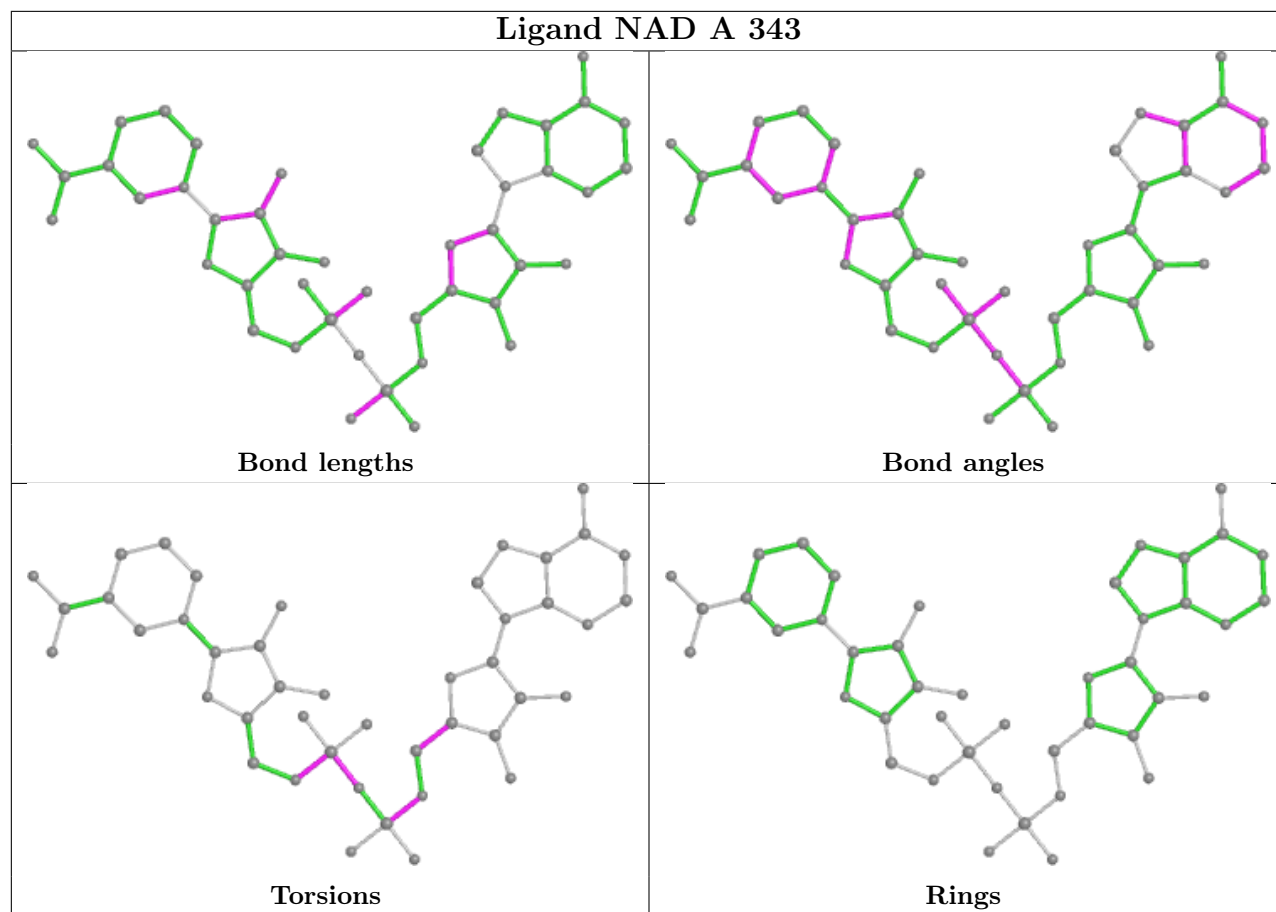
5 of 24 torsion outliers are listed below:

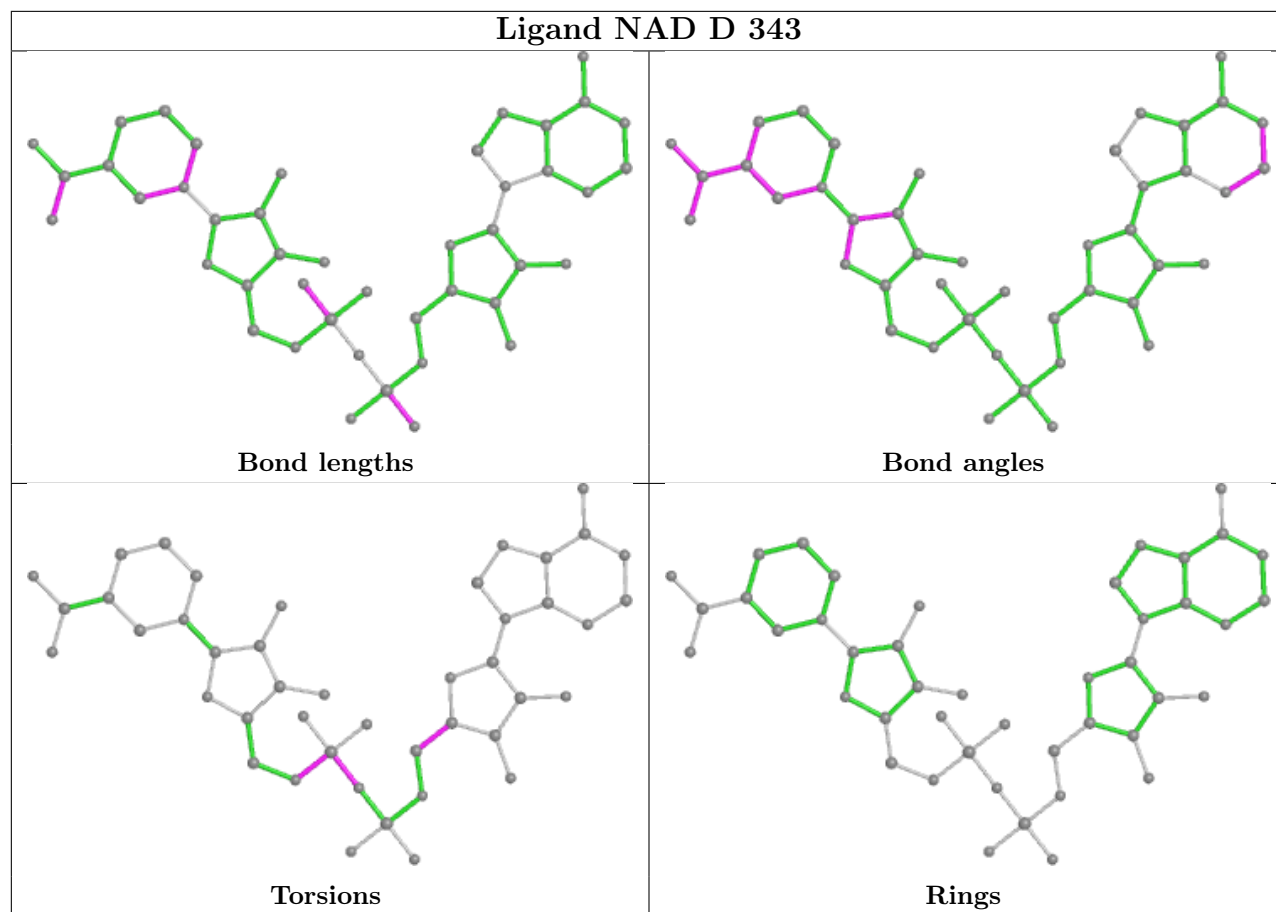
Mol	Chain	Res	Type	Atoms
2	A	343	NAD	C5B-O5B-PA-O2A
2	A	343	NAD	C5D-O5D-PN-O1N
2	B	343	NAD	C5B-O5B-PA-O2A
2	B	343	NAD	C5D-O5D-PN-O1N
2	C	343	NAD	C5D-O5D-PN-O1N

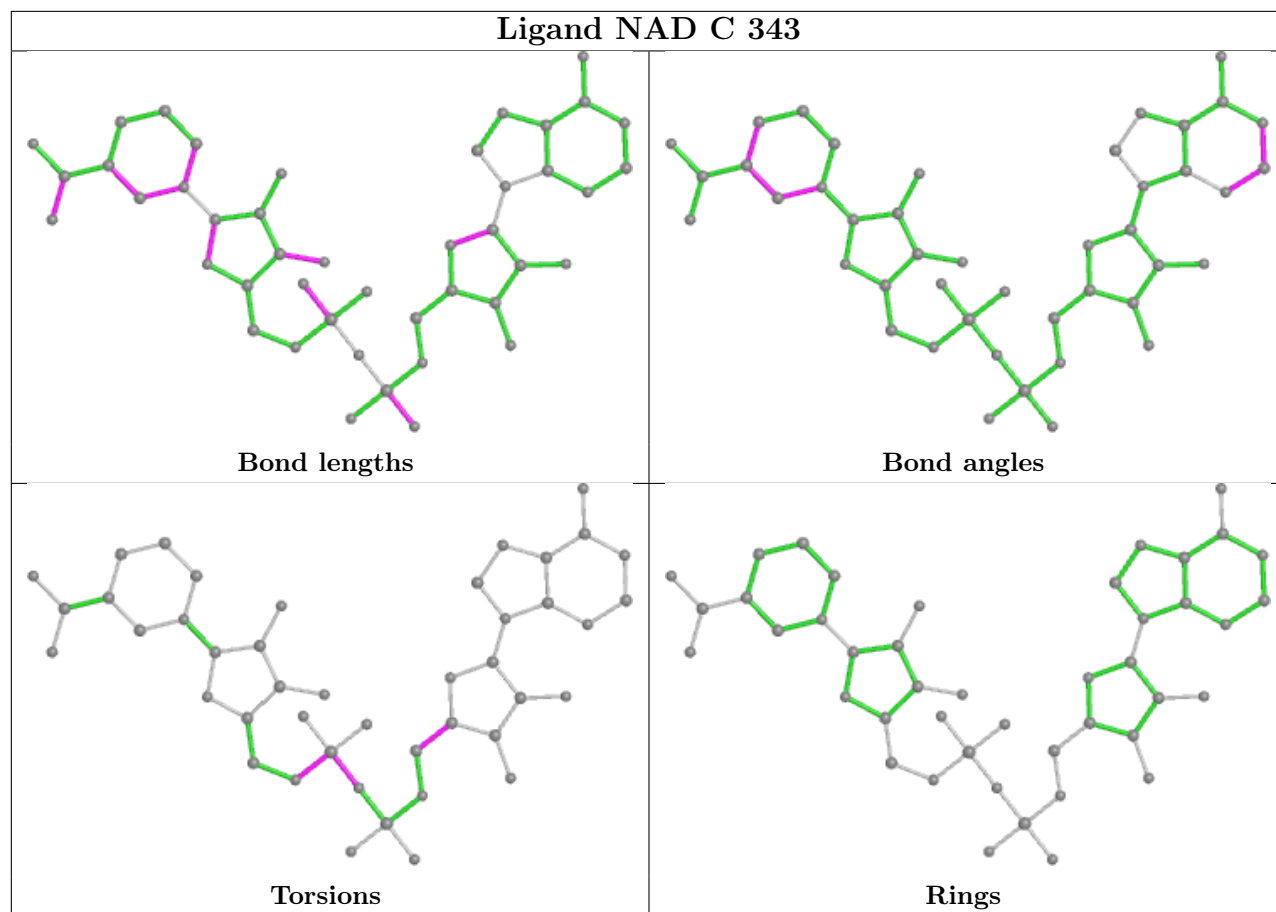
There are no ring outliers.

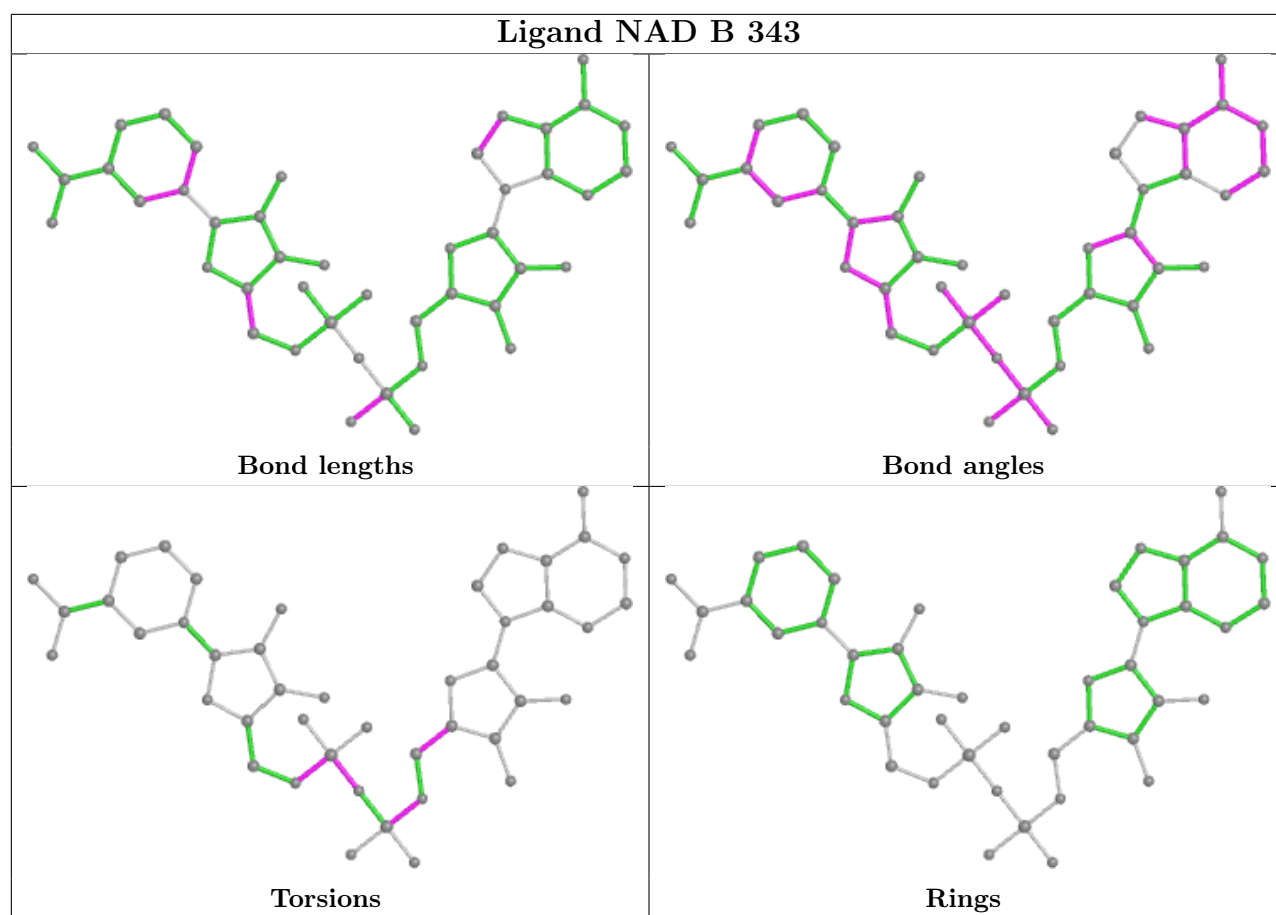
No monomer is involved in short contacts.

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

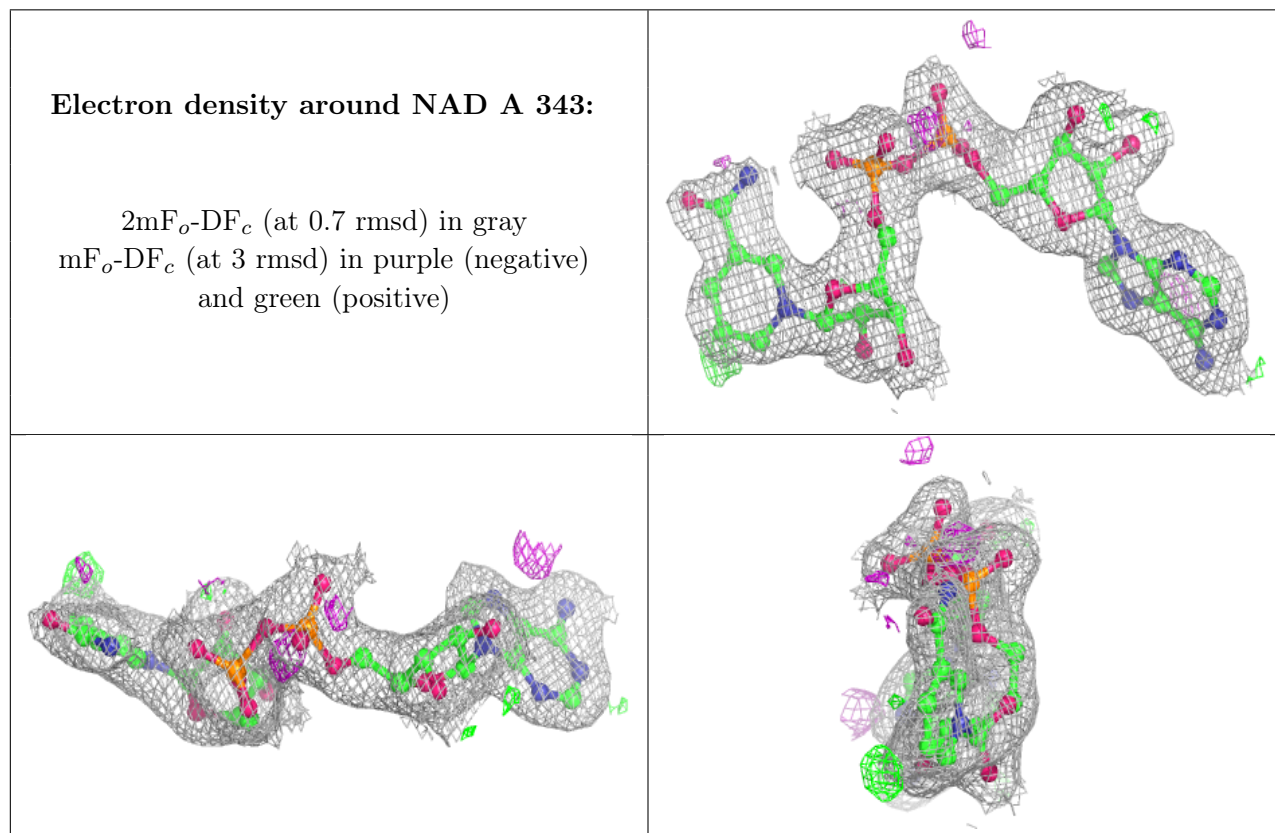
6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

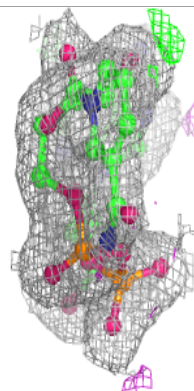
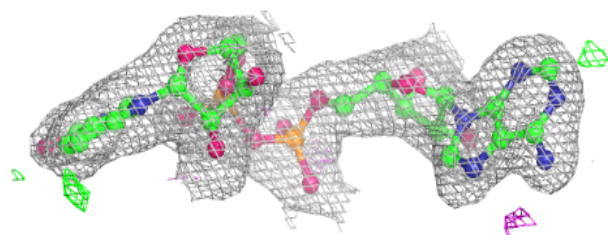
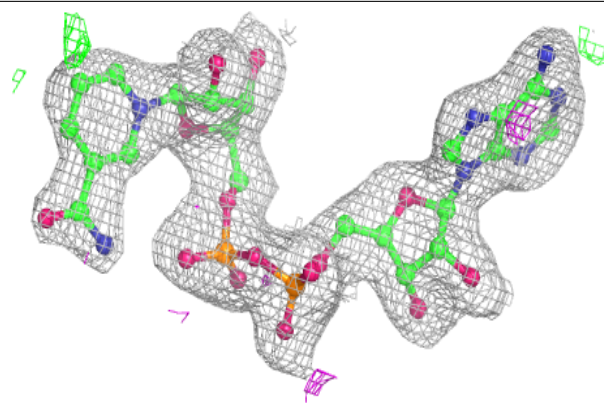
Unable to reproduce the depositors R factor - this section is therefore empty.

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.

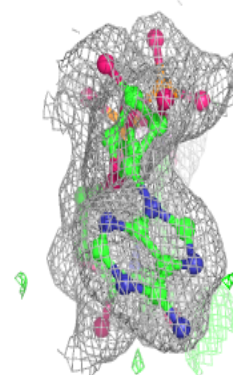
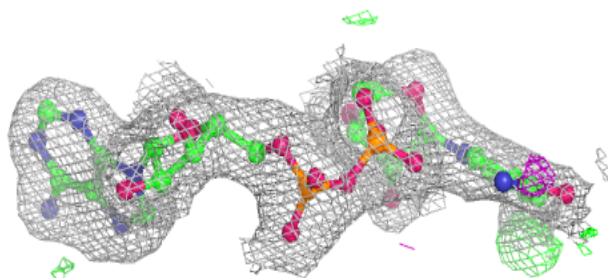
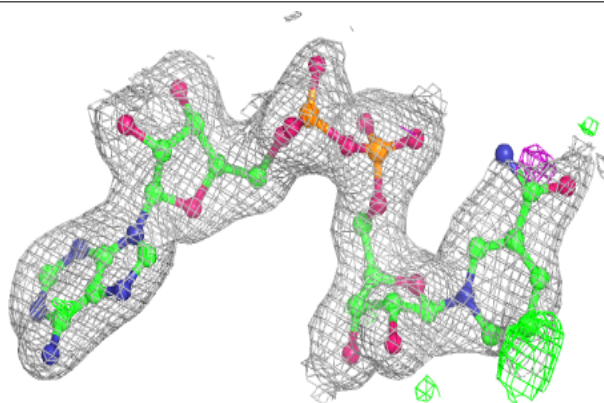


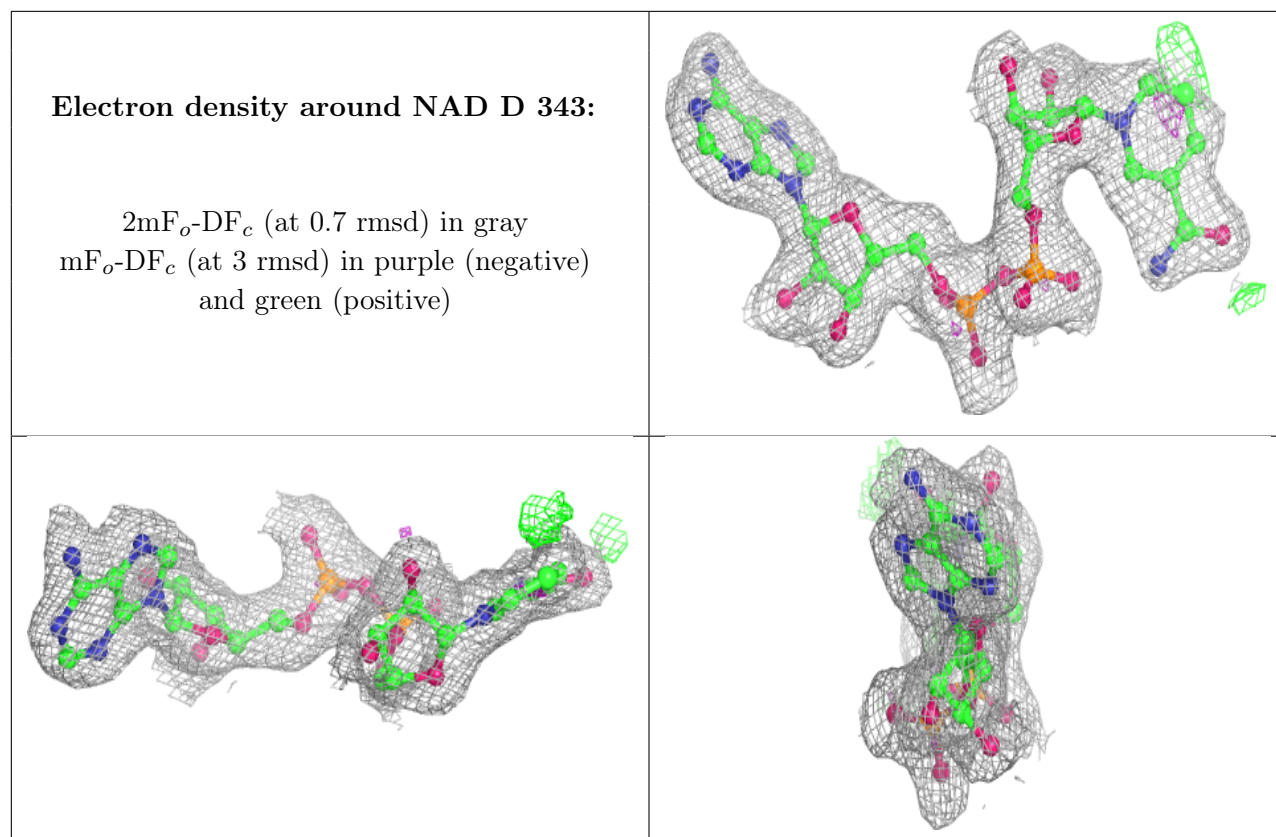
Electron density around NAD B 343:

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

**Electron density around NAD C 343:**

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





6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.