



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 3, 2023 – 01:30 PM EDT

PDB ID : 3RUE
Title : Alternative analogs as viable substrates of UDP-hexose 4-epimerases
Authors : Bhatt, V.S.; Guan, W.; Wang, P.G.
Deposited on : 2011-05-05
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-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

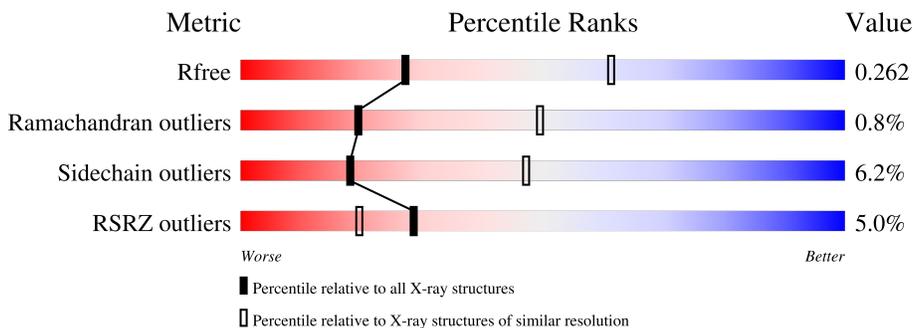
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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)
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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	351	
1	B	351	
1	S	351	
1	b	351	

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 11018 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	S	336	2681	1712	459	502	8	0	0	0
1	b	336	2681	1712	459	502	8	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

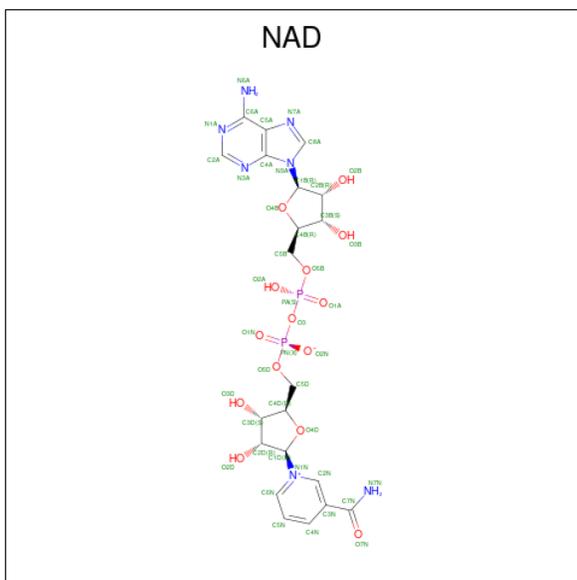
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	HIS	-	expression tag	UNP Q7BJX9
A	-7	HIS	-	expression tag	UNP Q7BJX9
A	-6	HIS	-	expression tag	UNP Q7BJX9
A	-5	HIS	-	expression tag	UNP Q7BJX9
A	-4	HIS	-	expression tag	UNP Q7BJX9
A	-3	HIS	-	expression tag	UNP Q7BJX9
B	-8	HIS	-	expression tag	UNP Q7BJX9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

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Chain	Residue	Modelled	Actual	Comment	Reference
b	-5	HIS	-	expression tag	UNP Q7BJX9
b	-4	HIS	-	expression tag	UNP Q7BJX9
b	-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	S	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		

- 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	S	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	b	1	25	9	2	12	2	0	0

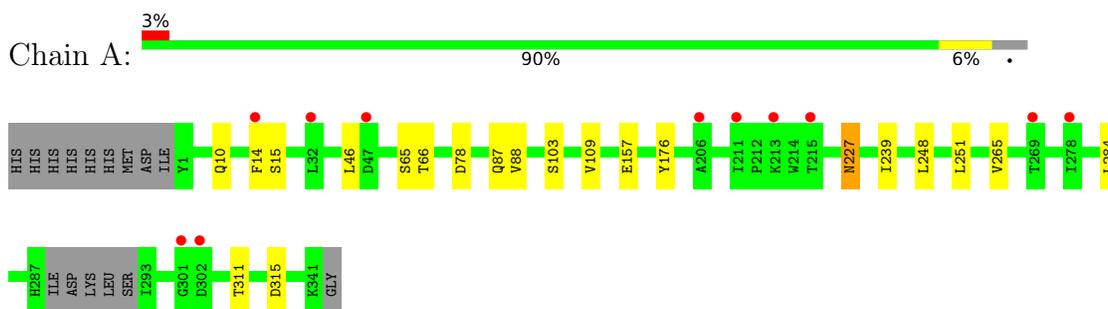
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	6	Total 6	O 6	0	0
4	B	6	Total 6	O 6	0	0
4	S	4	Total 4	O 4	0	0
4	b	2	Total 2	O 2	0	0

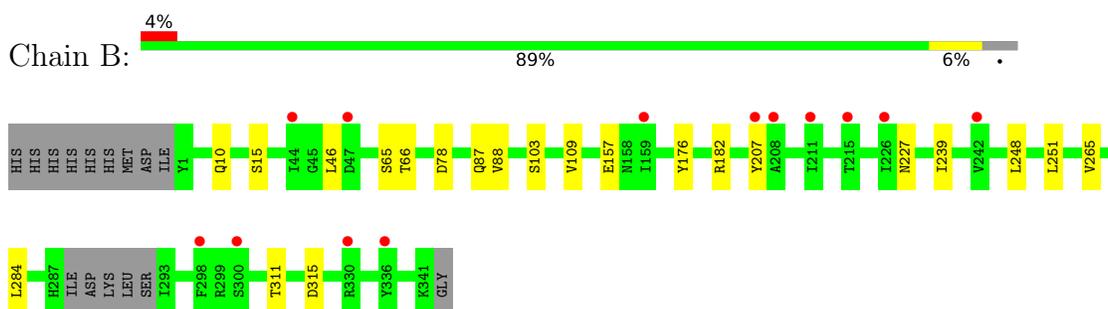
3 Residue-property plots [i](#)

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.

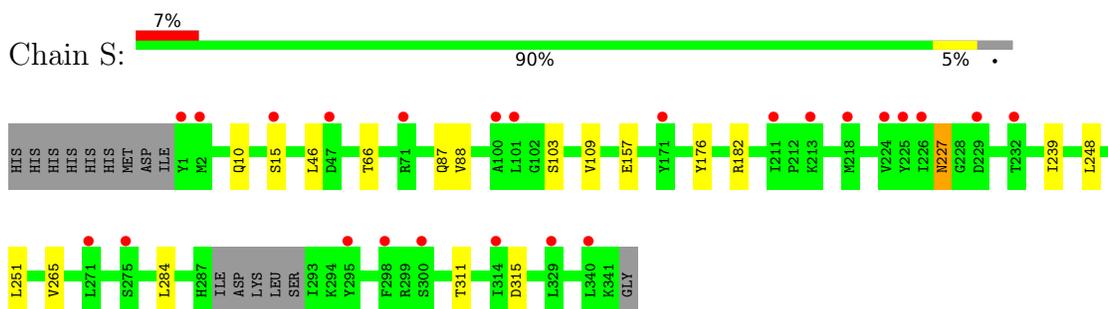
- Molecule 1: WbgU



- Molecule 1: WbgU

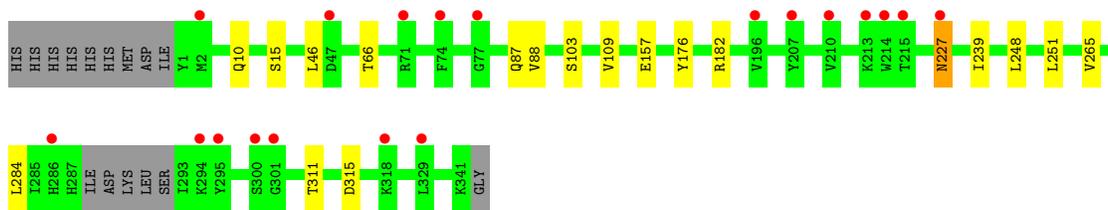


- Molecule 1: WbgU



- 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	78.45Å 78.45Å 226.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	75.50 – 2.80 43.50 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.4 (75.50-2.80) 99.4 (43.50-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 2.81Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.228 , 0.264 0.229 , 0.262	Depositor DCC
R_{free} test set	1900 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	67.1	Xtrriage
Anisotropy	0.097	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.014 for -h,-k,l 0.429 for h,-h-k,-l 0.017 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11018	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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: NAD, UNL

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	0.46	0/2739	0.58	0/3717
1	B	0.46	0/2739	0.58	0/3717
1	S	0.46	0/2739	0.57	0/3717
1	b	0.46	0/2739	0.57	0/3717
All	All	0.46	0/10956	0.58	0/14868

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](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	312 (94%)	17 (5%)	3 (1%)	17 46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	332/351 (95%)	312 (94%)	17 (5%)	3 (1%)	17	46
1	S	332/351 (95%)	309 (93%)	21 (6%)	2 (1%)	25	56
1	b	332/351 (95%)	310 (93%)	20 (6%)	2 (1%)	25	56
All	All	1328/1404 (95%)	1243 (94%)	75 (6%)	10 (1%)	19	49

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	SER
1	B	227	ASN
1	S	227	ASN
1	b	227	ASN
1	A	227	ASN
1	B	103	SER
1	A	103	SER
1	S	103	SER
1	b	103	SER
1	B	65	SER

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%)	272 (94%)	18 (6%)	18	47
1	B	290/304 (95%)	272 (94%)	18 (6%)	18	47
1	S	290/304 (95%)	272 (94%)	18 (6%)	18	47
1	b	290/304 (95%)	272 (94%)	18 (6%)	18	47
All	All	1160/1216 (95%)	1088 (94%)	72 (6%)	18	47

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	GLN

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Mol	Chain	Res	Type
1	A	15	SER
1	A	46	LEU
1	A	66	THR
1	A	78	ASP
1	A	87	GLN
1	A	88	VAL
1	A	109	VAL
1	A	157	GLU
1	A	176	TYR
1	A	227	ASN
1	A	239	ILE
1	A	248	LEU
1	A	251	LEU
1	A	265	VAL
1	A	284	LEU
1	A	311	THR
1	A	315	ASP
1	B	10	GLN
1	B	15	SER
1	B	46	LEU
1	B	66	THR
1	B	78	ASP
1	B	87	GLN
1	B	88	VAL
1	B	109	VAL
1	B	157	GLU
1	B	176	TYR
1	B	182	ARG
1	B	239	ILE
1	B	248	LEU
1	B	251	LEU
1	B	265	VAL
1	B	284	LEU
1	B	311	THR
1	B	315	ASP
1	S	10	GLN
1	S	15	SER
1	S	46	LEU
1	S	66	THR
1	S	87	GLN
1	S	88	VAL
1	S	109	VAL

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Mol	Chain	Res	Type
1	S	157	GLU
1	S	176	TYR
1	S	182	ARG
1	S	227	ASN
1	S	239	ILE
1	S	248	LEU
1	S	251	LEU
1	S	265	VAL
1	S	284	LEU
1	S	311	THR
1	S	315	ASP
1	b	10	GLN
1	b	15	SER
1	b	46	LEU
1	b	66	THR
1	b	87	GLN
1	b	88	VAL
1	b	109	VAL
1	b	157	GLU
1	b	176	TYR
1	b	182	ARG
1	b	227	ASN
1	b	239	ILE
1	b	248	LEU
1	b	251	LEU
1	b	265	VAL
1	b	284	LEU
1	b	311	THR
1	b	315	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	11	GLN
1	A	149	HIS
1	A	161	ASN
1	A	244	GLN
1	A	287	HIS
1	B	10	GLN
1	B	11	GLN
1	B	149	HIS

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Mol	Chain	Res	Type
1	B	161	ASN
1	B	244	GLN
1	B	287	HIS
1	S	10	GLN
1	S	11	GLN
1	S	149	HIS
1	S	161	ASN
1	S	244	GLN
1	S	287	HIS
1	b	10	GLN
1	b	11	GLN
1	b	149	HIS
1	b	161	ASN
1	b	244	GLN
1	b	287	HIS

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 8 ligands modelled in this entry, 4 are unknown - leaving 4 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	b	343	-	42,48,48	0.80	0	50,73,73	1.25	3 (6%)
2	NAD	S	343	-	42,48,48	0.78	0	50,73,73	1.20	3 (6%)
2	NAD	A	344	-	42,48,48	1.85	15 (35%)	50,73,73	1.89	11 (22%)
2	NAD	B	343	-	42,48,48	0.81	0	50,73,73	1.27	4 (8%)

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	343	-	-	3/26/62/62	0/5/5/5
2	NAD	S	343	-	-	4/26/62/62	0/5/5/5
2	NAD	A	344	-	-	5/26/62/62	0/5/5/5
2	NAD	B	343	-	-	8/26/62/62	0/5/5/5

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	344	NAD	C2D-C1D	-4.68	1.46	1.53
2	A	344	NAD	PN-O5D	-3.12	1.46	1.59
2	A	344	NAD	O4B-C4B	-2.97	1.38	1.45
2	A	344	NAD	PA-O2A	-2.87	1.41	1.55
2	A	344	NAD	PN-O2N	-2.80	1.42	1.55
2	A	344	NAD	PN-O1N	-2.80	1.41	1.50
2	A	344	NAD	PA-O1A	-2.44	1.42	1.50
2	A	344	NAD	C4A-N3A	-2.42	1.32	1.35
2	A	344	NAD	PA-O5B	-2.41	1.49	1.59
2	A	344	NAD	C5A-N7A	-2.39	1.31	1.39
2	A	344	NAD	C2D-C3D	-2.39	1.46	1.53
2	A	344	NAD	O4D-C1D	-2.37	1.37	1.41
2	A	344	NAD	O5D-C5D	-2.17	1.36	1.44
2	A	344	NAD	C5A-C4A	-2.05	1.35	1.40
2	A	344	NAD	C2A-N1A	-2.01	1.30	1.33

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	344	NAD	O4D-C1D-C2D	-6.45	97.50	106.93
2	A	344	NAD	C3D-C2D-C1D	-5.14	93.23	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	344	NAD	N3A-C2A-N1A	-5.00	120.87	128.68
2	B	343	NAD	N3A-C2A-N1A	-4.69	121.35	128.68
2	b	343	NAD	N3A-C2A-N1A	-4.62	121.45	128.68
2	S	343	NAD	N3A-C2A-N1A	-4.52	121.61	128.68
2	A	344	NAD	C2N-C3N-C4N	3.61	122.35	118.26
2	S	343	NAD	PN-O3-PA	-3.52	120.75	132.83
2	b	343	NAD	PN-O3-PA	-3.44	121.03	132.83
2	B	343	NAD	PN-O3-PA	-3.35	121.32	132.83
2	A	344	NAD	O3D-C3D-C2D	-3.14	101.65	111.82
2	A	344	NAD	C4A-C5A-N7A	-2.36	106.94	109.40
2	b	343	NAD	C3D-C2D-C1D	2.32	104.48	100.98
2	A	344	NAD	O5B-C5B-C4B	2.31	116.96	108.99
2	A	344	NAD	C3N-C2N-N1N	-2.27	118.20	120.43
2	A	344	NAD	O4B-C4B-C3B	-2.23	100.69	105.11
2	B	343	NAD	C2N-C3N-C4N	2.23	120.79	118.26
2	A	344	NAD	C3N-C7N-N7N	-2.09	115.24	117.75
2	B	343	NAD	O4D-C1D-C2D	-2.08	103.89	106.93
2	A	344	NAD	O7N-C7N-N7N	2.02	125.44	122.58
2	S	343	NAD	C4A-C5A-N7A	-2.01	107.30	109.40

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	344	NAD	C5B-O5B-PA-O2A
2	B	343	NAD	C5B-O5B-PA-O1A
2	B	343	NAD	C5B-O5B-PA-O2A
2	B	343	NAD	C5B-O5B-PA-O3
2	b	343	NAD	C5D-O5D-PN-O1N
2	B	343	NAD	O4B-C4B-C5B-O5B
2	B	343	NAD	C3B-C4B-C5B-O5B
2	S	343	NAD	O4B-C4B-C5B-O5B
2	S	343	NAD	O4D-C4D-C5D-O5D
2	A	344	NAD	C5B-O5B-PA-O3
2	A	344	NAD	C5B-O5B-PA-O1A
2	S	343	NAD	C3B-C4B-C5B-O5B
2	b	343	NAD	O4B-C4B-C5B-O5B
2	A	344	NAD	C3B-C4B-C5B-O5B
2	B	343	NAD	O4D-C4D-C5D-O5D
2	B	343	NAD	C5D-O5D-PN-O3
2	b	343	NAD	C5D-O5D-PN-O3
2	S	343	NAD	C3D-C4D-C5D-O5D

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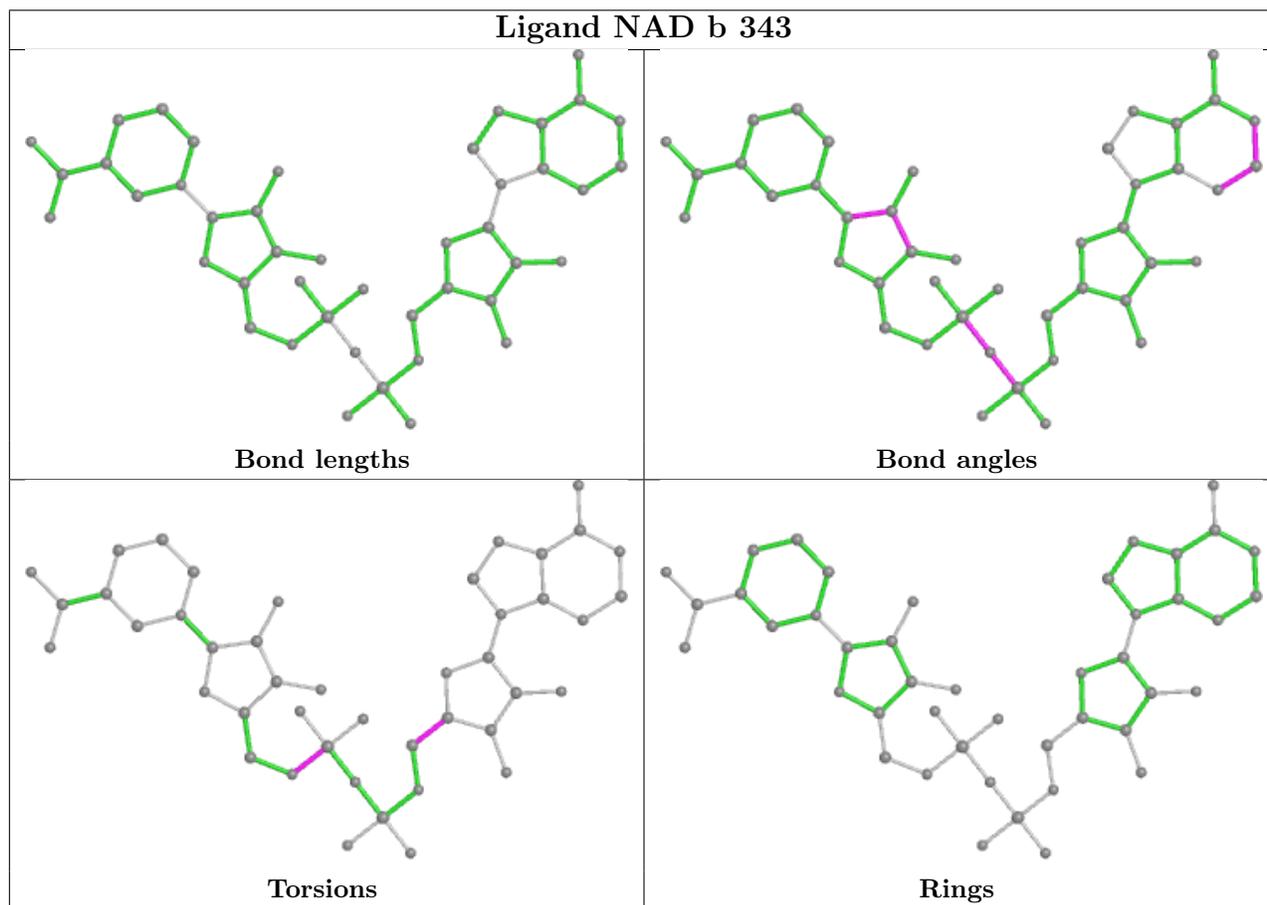
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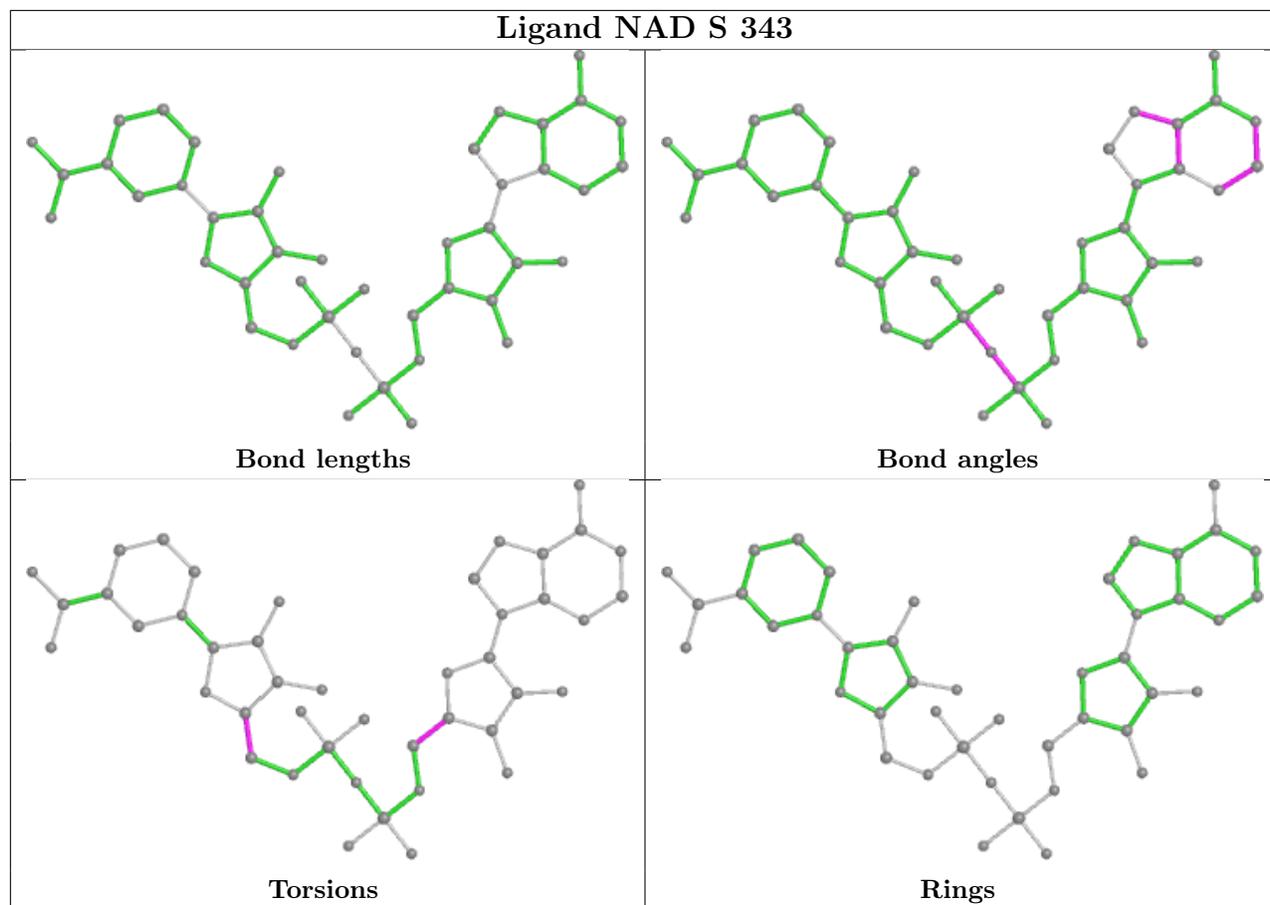
Mol	Chain	Res	Type	Atoms
2	B	343	NAD	C5D-O5D-PN-O1N
2	A	344	NAD	O4B-C4B-C5B-O5B

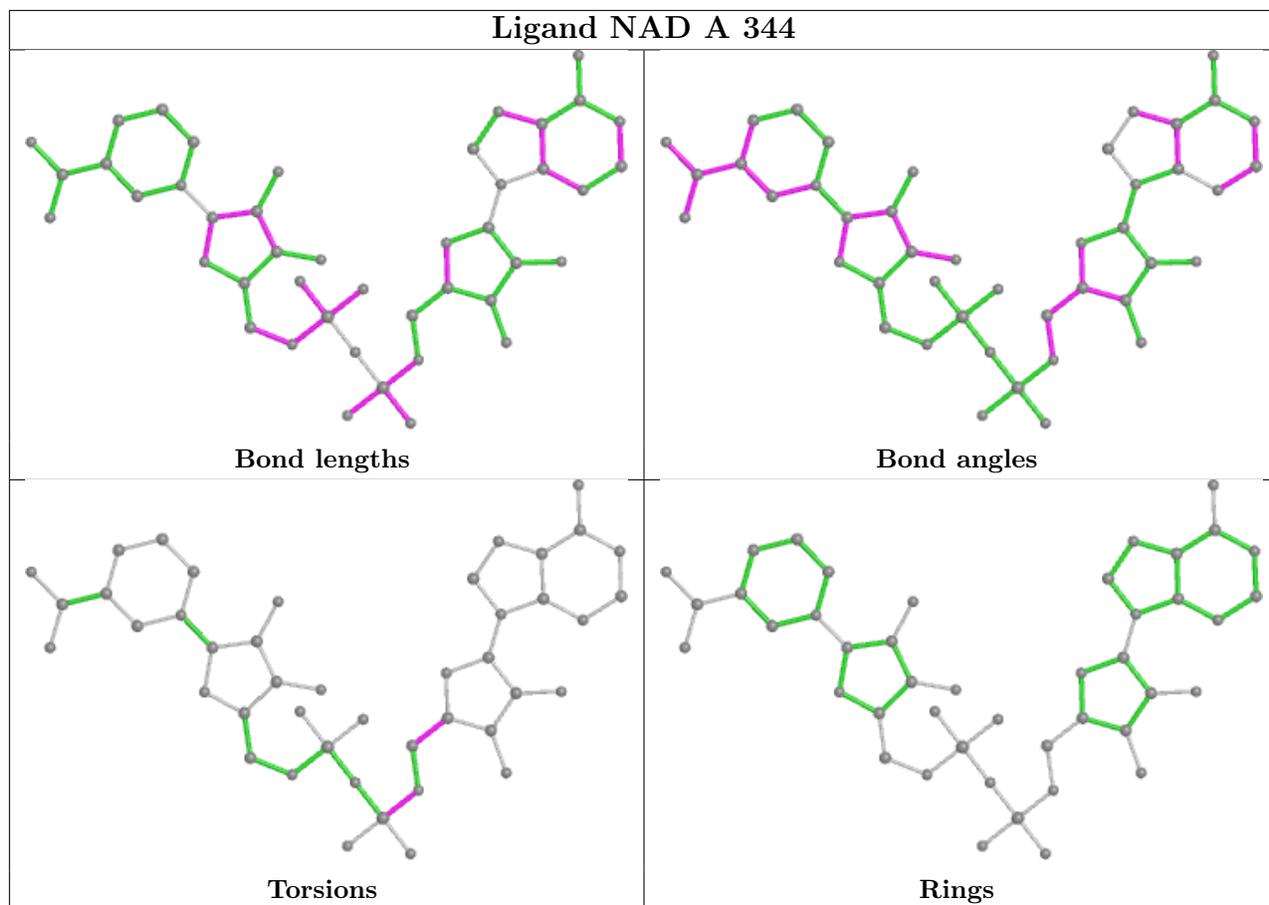
There are no ring outliers.

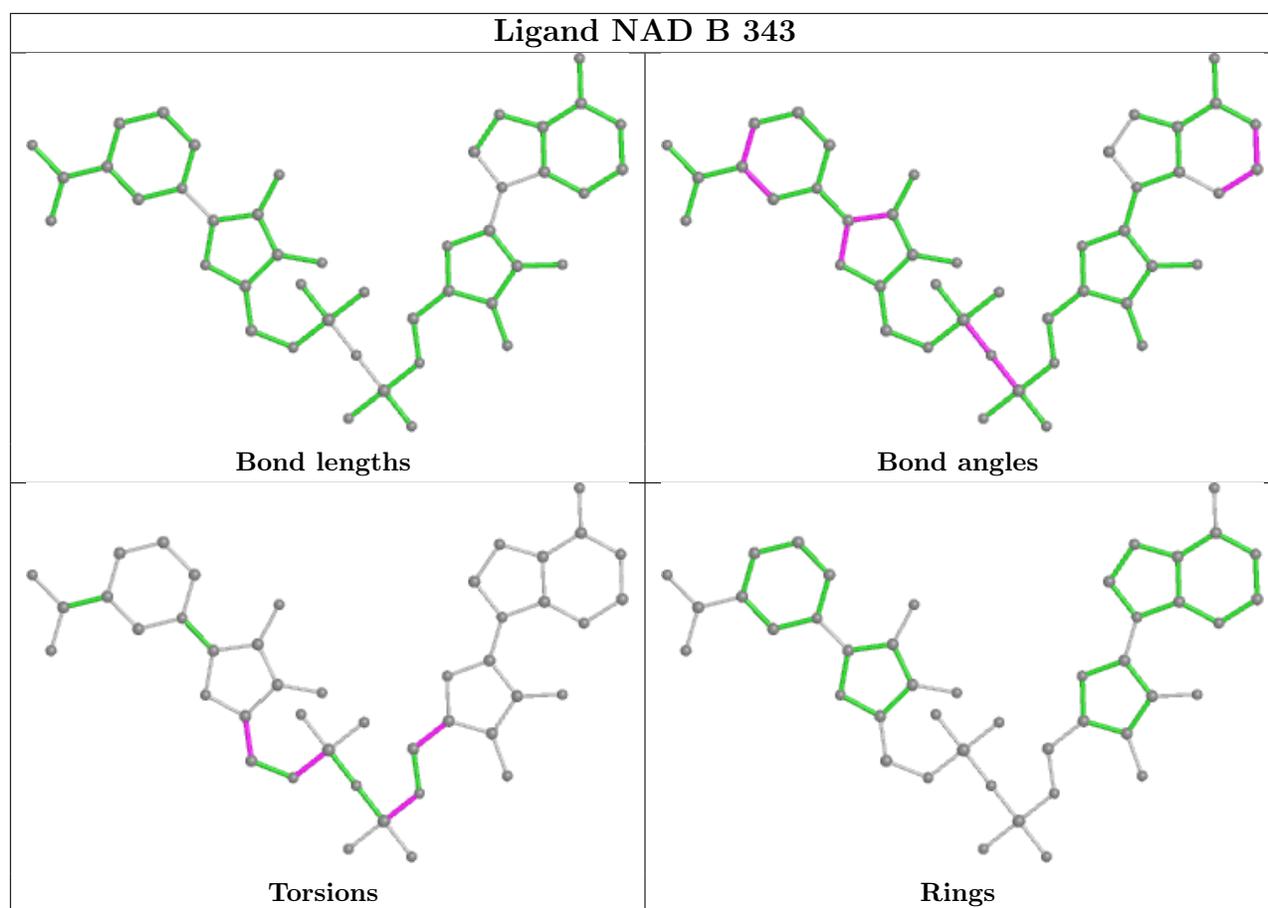
No monomer is involved in short contacts.

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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	336/351 (95%)	0.24	11 (3%) 46 36	51, 69, 117, 148	0
1	B	336/351 (95%)	0.24	13 (3%) 39 29	51, 69, 117, 148	0
1	S	336/351 (95%)	0.31	24 (7%) 16 9	51, 70, 118, 148	0
1	b	336/351 (95%)	0.40	19 (5%) 23 15	51, 69, 117, 149	0
All	All	1344/1404 (95%)	0.30	67 (4%) 28 19	51, 69, 118, 149	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	b	2	MET	7.9
1	b	300	SER	7.3
1	b	47	ASP	5.7
1	S	2	MET	5.5
1	S	226	ILE	4.6
1	S	47	ASP	4.1
1	A	47	ASP	4.1
1	b	295	TYR	3.9
1	A	32	LEU	3.8
1	A	14	PHE	3.7
1	S	224	VAL	3.6
1	S	1	TYR	3.6
1	b	301	GLY	3.5
1	S	232	THR	3.2
1	A	302	ASP	3.1
1	S	15	SER	3.1
1	S	275	SER	3.1
1	b	318	LYS	3.1
1	b	196	VAL	3.0
1	B	207	TYR	2.8
1	B	215	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	S	340	LEU	2.7
1	B	298	PHE	2.7
1	S	314	ILE	2.7
1	A	301	GLY	2.6
1	B	336	TYR	2.6
1	b	215	THR	2.6
1	S	71	ARG	2.6
1	A	211	ILE	2.6
1	S	211	ILE	2.5
1	b	71	ARG	2.5
1	B	208	ALA	2.5
1	A	269	THR	2.5
1	B	44	ILE	2.4
1	A	215	THR	2.4
1	A	206	ALA	2.4
1	b	286	HIS	2.3
1	B	47	ASP	2.3
1	b	213	LYS	2.3
1	S	101	LEU	2.3
1	S	225	TYR	2.3
1	b	210	VAL	2.3
1	S	218	MET	2.3
1	b	74	PHE	2.2
1	S	329	LEU	2.2
1	B	159	ILE	2.2
1	B	211	ILE	2.2
1	b	207	TYR	2.2
1	B	242	VAL	2.2
1	B	300	SER	2.2
1	S	271	LEU	2.2
1	b	227	ASN	2.2
1	b	77	GLY	2.1
1	S	295	TYR	2.1
1	S	213	LYS	2.1
1	b	294	LYS	2.1
1	S	229	ASP	2.1
1	b	329	LEU	2.1
1	S	100	ALA	2.1
1	B	330	ARG	2.1
1	A	213	LYS	2.1
1	S	300	SER	2.1
1	b	214	TRP	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	278	ILE	2.0
1	B	226	ILE	2.0
1	S	298	PHE	2.0
1	S	171	TYR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

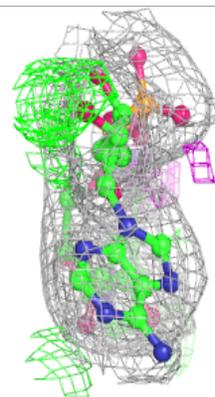
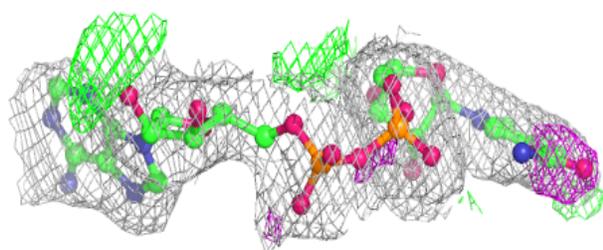
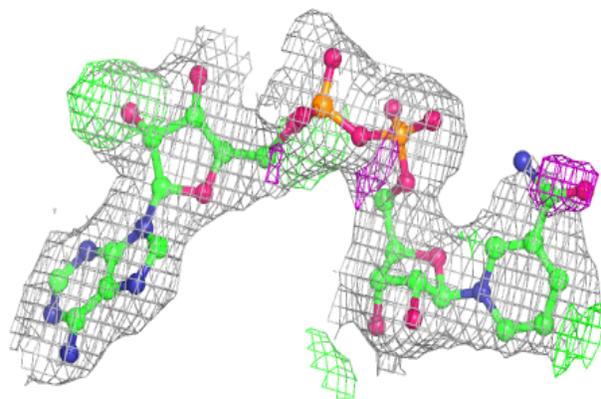
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	UNL	S	344	25/-	0.85	0.18	77,79,80,80	0
3	UNL	b	344	25/-	0.86	0.21	75,78,79,79	0
2	NAD	A	344	44/44	0.91	0.17	54,58,64,66	0
3	UNL	A	343	25/-	0.91	0.14	80,85,86,87	0
2	NAD	b	343	44/44	0.92	0.20	61,63,70,70	0
2	NAD	B	343	44/44	0.92	0.18	59,60,65,66	0
3	UNL	B	344	25/-	0.93	0.18	78,83,84,85	0
2	NAD	S	343	44/44	0.94	0.16	59,62,68,68	0

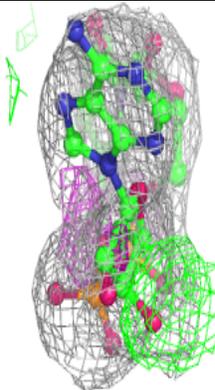
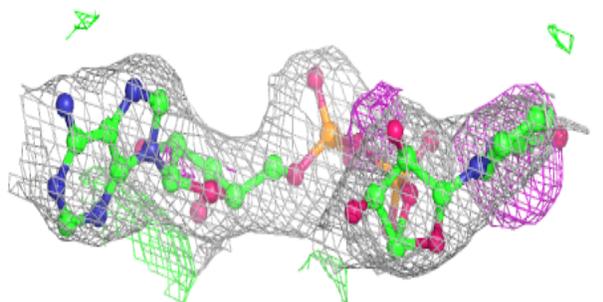
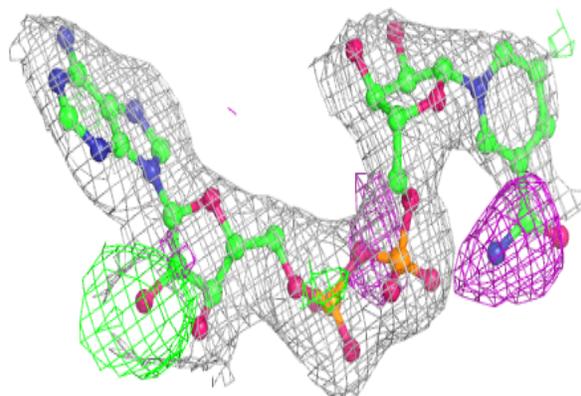
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAD A 344:

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

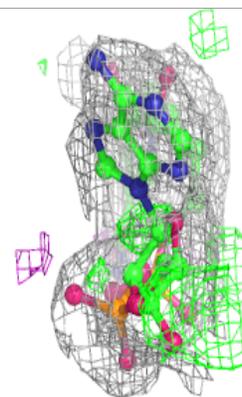
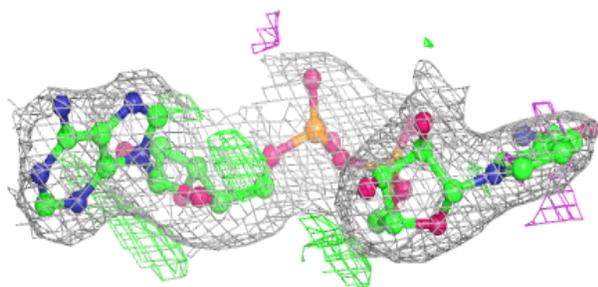
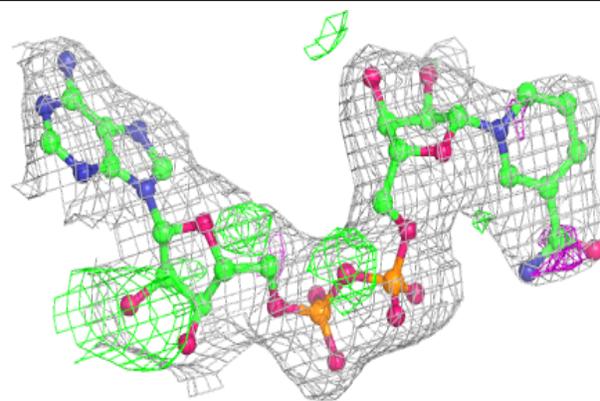
**Electron density around NAD b 343:**

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

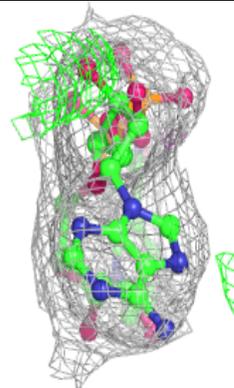
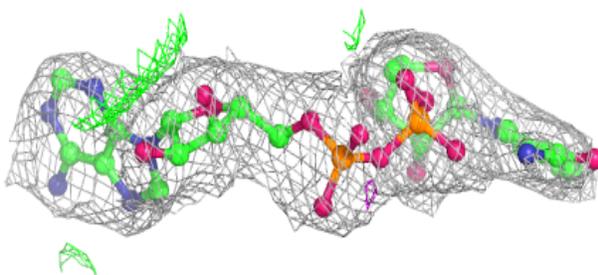
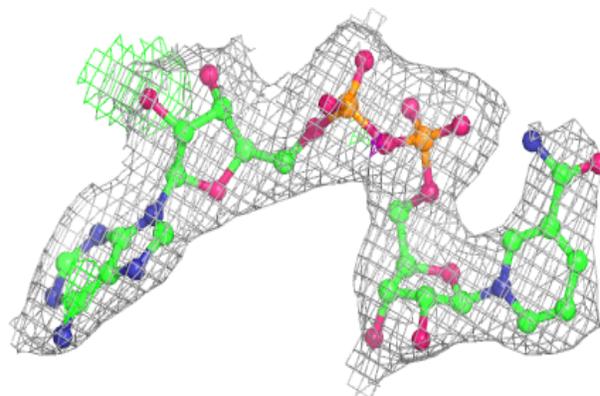


Electron density around NAD B 343:

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

**Electron density around NAD S 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](#)

There are no such residues in this entry.