



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:54 PM UTC

PDB ID : 3RU9 / pdb_00003ru9
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 : 2.21 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

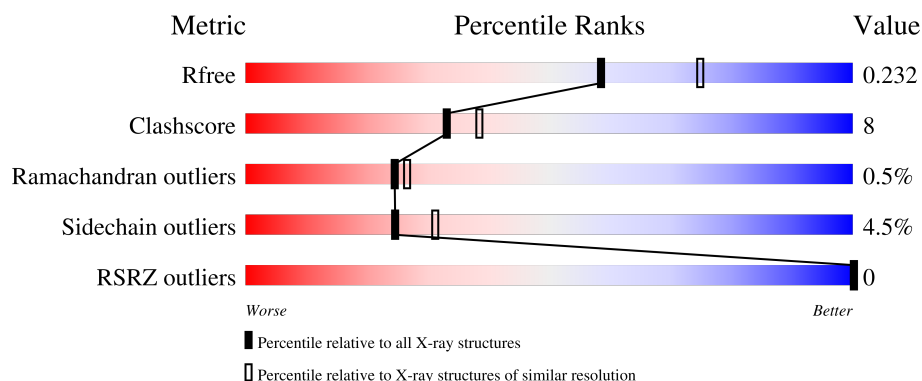
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

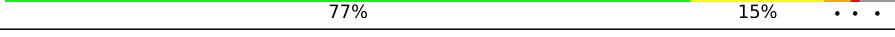
The reported resolution of this entry is 2.21 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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 $\leq 5\%$. 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	C	351	
1	D	351	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	346	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11333 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
1	A	336	Total	C	N	O	S	0	0	0
			2681	1712	459	502	8			
1	B	336	Total	C	N	O	S	0	0	0
			2681	1712	459	502	8			
1	C	336	Total	C	N	O	S	0	0	0
			2681	1712	459	502	8			
1	D	336	Total	C	N	O	S	0	0	0
			2681	1712	459	502	8			

There are 24 discrepancies between the modelled and reference sequences:

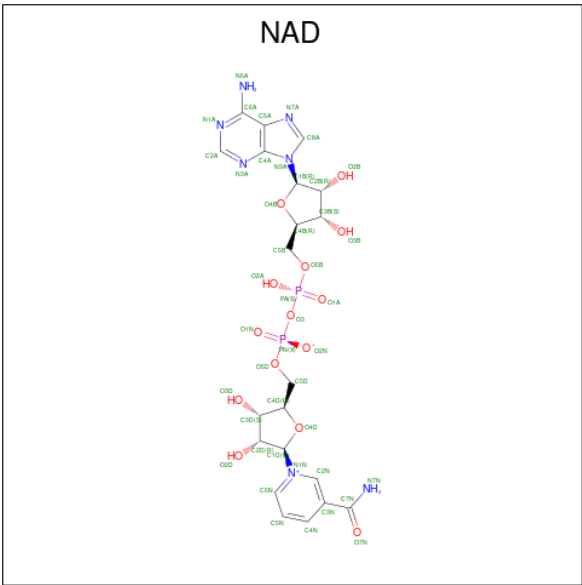
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	HIS	-	expression tag	UNP Q7BJX9
A	-7	HIS	-	expression tag	UNP Q7BJX9
A	-6	HIS	-	expression tag	UNP Q7BJX9
A	-5	HIS	-	expression tag	UNP Q7BJX9
A	-4	HIS	-	expression tag	UNP Q7BJX9
A	-3	HIS	-	expression tag	UNP Q7BJX9
B	-8	HIS	-	expression tag	UNP Q7BJX9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

Continued on next page...

Continued from previous page...

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 (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



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		
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 SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is UNKNOWN LIGAND (CCD ID: UNL) (formula:).

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

- Molecule 5 is GLYCINE (CCD ID: GLY) (formula: C₂H₅NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	0	0
			5	2	1	2		
5	D	1	Total	C	N	O	0	0
			5	2	1	2		

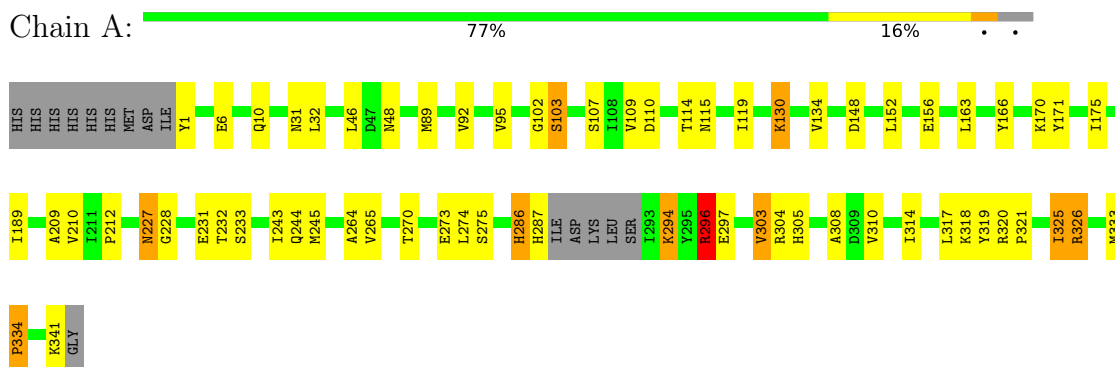
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	83	Total	O	0	0
			83	83		
6	B	71	Total	O	0	0
			71	71		
6	C	77	Total	O	0	0
			77	77		
6	D	82	Total	O	0	0
			82	82		

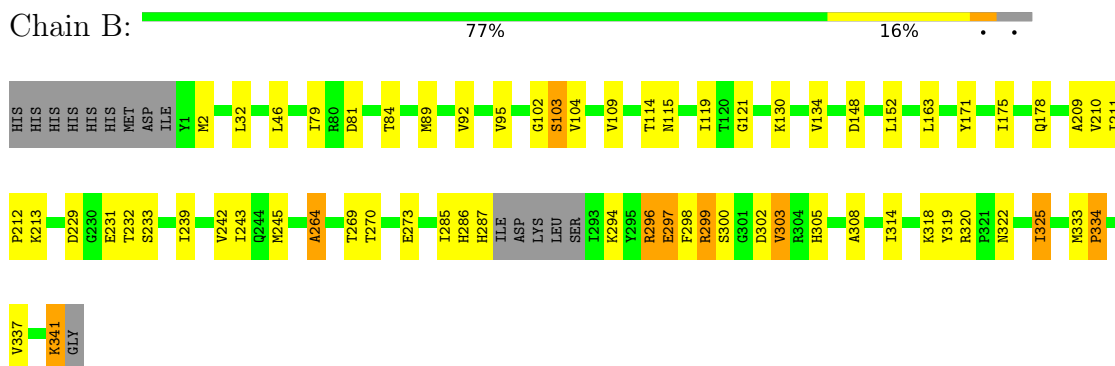
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

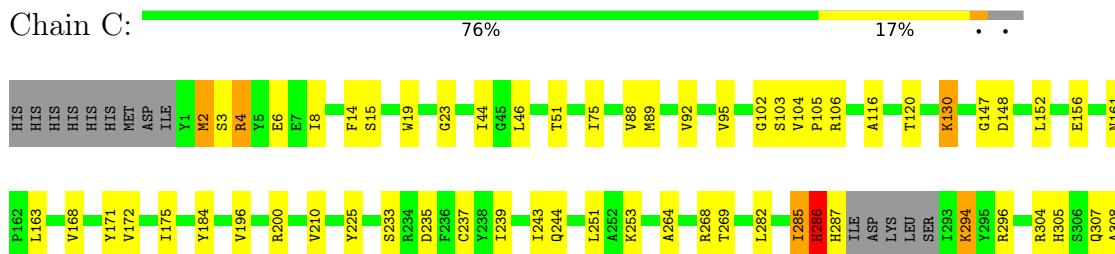
• Molecule 1: WbgU

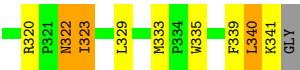


• Molecule 1: WbgU

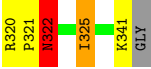
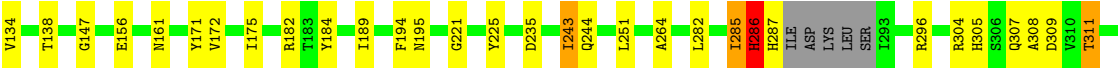


• Molecule 1: WbgU





● Molecule 1: WbgU



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	77.41Å 77.41Å 224.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.80 – 2.21 38.80 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.9 (38.80-2.21) 99.9 (38.80-2.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.22Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.181 , 0.232 0.184 , 0.232	Depositor DCC
R_{free} test set	3800 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 19.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l 0.478 for h,-h-k,-l 0.035 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11333	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% 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

5.1 Standard geometry

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	1.18	1/2739 (0.0%)	1.14	9/3717 (0.2%)
1	B	1.16	3/2739 (0.1%)	1.14	9/3717 (0.2%)
1	C	1.14	1/2739 (0.0%)	1.11	10/3717 (0.3%)
1	D	1.12	1/2739 (0.0%)	1.13	8/3717 (0.2%)
All	All	1.15	6/10956 (0.1%)	1.13	36/14868 (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	C	0	1
1	D	0	1
All	All	0	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	110	ASP	C-O	-7.33	1.15	1.24
1	B	239	ILE	CA-CB	5.58	1.61	1.54
1	C	19	TRP	CA-C	-5.53	1.46	1.52
1	B	264	ALA	C-O	-5.44	1.20	1.24
1	D	19	TRP	CA-C	-5.33	1.46	1.52
1	B	302	ASP	CA-C	5.01	1.58	1.52

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	3	SER	N-CA-C	10.04	124.04	111.69

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	3	SER	N-CA-C	8.61	122.28	111.69
1	D	156	GLU	N-CA-C	7.40	119.34	111.28
1	A	321	PRO	CA-C-N	7.20	130.15	120.65
1	A	321	PRO	C-N-CA	7.20	130.15	120.65
1	D	321	PRO	CA-C-N	6.90	129.83	120.44
1	D	321	PRO	C-N-CA	6.90	129.83	120.44
1	B	302	ASP	N-CA-C	6.86	120.08	108.90
1	A	303	VAL	N-CA-C	6.59	118.91	108.89
1	C	51	THR	N-CA-C	-6.52	105.90	114.31
1	A	210	VAL	N-CA-C	6.36	117.11	110.62
1	B	231	GLU	N-CA-C	6.07	117.90	111.28
1	B	294	LYS	N-CA-C	5.99	118.14	108.32
1	A	156	GLU	N-CA-C	5.96	118.26	111.11
1	B	303	VAL	N-CA-C	5.89	118.09	108.97
1	A	231	GLU	N-CA-C	5.88	118.64	111.82
1	C	156	GLU	N-CA-C	5.88	118.44	111.33
1	C	23	GLY	N-CA-C	-5.60	107.03	115.32
1	B	104	VAL	CA-C-N	-5.59	112.84	119.05
1	B	104	VAL	C-N-CA	-5.59	112.84	119.05
1	D	325	ILE	N-CA-C	5.57	116.30	110.62
1	B	229	ASP	N-CA-C	5.53	120.01	112.88
1	B	325	ILE	N-CA-C	5.47	115.67	110.42
1	D	322	ASN	N-CA-CB	-5.45	102.17	110.07
1	A	294	LYS	N-CA-C	5.43	117.34	108.76
1	C	239	ILE	N-CA-C	5.40	116.78	110.62
1	C	210	VAL	N-CA-C	5.30	115.51	110.42
1	A	233	SER	N-CA-C	5.29	117.43	109.23
1	C	14	PHE	CA-C-N	-5.27	117.64	122.28
1	C	14	PHE	C-N-CA	-5.27	117.64	122.28
1	D	221	GLY	N-CA-C	-5.21	108.08	115.43
1	C	130	LYS	N-CA-C	-5.17	105.73	111.36
1	A	189	ILE	N-CA-C	5.16	115.33	108.11
1	B	242	VAL	N-CA-C	5.14	115.86	110.62
1	C	323	ILE	N-CA-C	5.14	114.69	106.88
1	D	130	LYS	N-CA-C	-5.08	105.82	111.36

There are no chirality outliers.

All (2) planarity outliers are listed below:

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

5.2 Too-close contacts ⓘ

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	45	0
1	B	2681	0	2658	43	0
1	C	2681	0	2658	42	0
1	D	2681	0	2658	41	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	1	0
3	A	10	0	0	3	0
4	A	25	0	0	0	0
4	B	25	0	0	1	0
4	C	25	0	0	0	0
4	D	25	0	0	0	0
5	C	5	0	2	0	0
5	D	5	0	2	0	0
6	A	83	0	0	1	0
6	B	71	0	0	2	0
6	C	77	0	0	0	0
6	D	82	0	0	1	0
All	All	11333	0	10740	169	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.

All (169) 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:B:296:ARG:HG3	1:B:297:GLU:N	1.52	1.05
1:A:296:ARG:HD3	1:A:297:GLU:H	1.20	1.04
1:B:296:ARG:CG	1:B:297:GLU:H	1.74	1.00
1:B:296:ARG:HG3	1:B:297:GLU:H	0.79	0.92
1:B:296:ARG:HD2	1:B:297:GLU:HB2	1.52	0.90
1:A:326:ARG:HG2	1:A:326:ARG:HH11	1.33	0.90
1:C:89:MET:HE3	1:C:89:MET:HA	1.55	0.88
1:A:89:MET:HE1	1:A:95:VAL:HG22	1.59	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:19:TRP:HE1	1:D:41:GLN:HE21	1.31	0.79
1:A:318:LYS:HE3	3:A:345:SO4:O1	1.84	0.77
1:B:89:MET:HE1	1:B:95:VAL:HG22	1.65	0.77
1:A:244:GLN:HE22	1:A:320:ARG:H	1.29	0.76
1:C:285:ILE:O	1:C:286:HIS:HB2	1.84	0.76
1:A:296:ARG:CD	1:A:297:GLU:H	1.99	0.75
1:B:171:TYR:CZ	1:B:175:ILE:HD11	2.22	0.74
1:B:296:ARG:CG	1:B:297:GLU:N	2.34	0.73
1:C:8:ILE:CG2	1:C:251:LEU:HD22	2.19	0.72
1:B:171:TYR:CE2	1:B:175:ILE:HD11	2.26	0.71
1:C:244:GLN:HE22	1:C:320:ARG:H	1.37	0.71
1:A:102:GLY:O	1:A:103:SER:HB3	1.89	0.70
1:D:89:MET:HE1	1:D:95:VAL:HG22	1.73	0.70
1:B:210:VAL:HG13	1:B:211:ILE:N	2.06	0.69
1:D:2:MET:SD	1:D:322:ASN:ND2	2.66	0.69
1:D:244:GLN:HE22	1:D:320:ARG:H	1.40	0.69
1:A:171:TYR:CE2	1:A:175:ILE:HD11	2.28	0.68
1:D:102:GLY:O	1:D:103:SER:HB3	1.92	0.68
1:D:2:MET:O	1:D:6:GLU:HG3	1.94	0.68
1:A:89:MET:CE	1:A:92:VAL:HG11	2.24	0.67
1:B:89:MET:CE	1:B:92:VAL:HG11	2.25	0.67
1:C:8:ILE:HG23	1:C:251:LEU:HD22	1.74	0.67
3:A:346:SO4:O3	1:B:318:LYS:HE2	1.96	0.66
1:B:2:MET:SD	1:B:322:ASN:OD1	2.55	0.65
1:D:8:ILE:HG23	1:D:251:LEU:HD22	1.76	0.65
1:D:285:ILE:O	1:D:286:HIS:HB2	1.93	0.65
1:B:102:GLY:O	1:B:103:SER:HB3	1.96	0.64
1:C:147:GLY:HA3	1:C:161:ASN:O	1.97	0.64
1:A:244:GLN:NE2	1:A:320:ARG:H	1.96	0.64
1:B:148:ASP:HB3	1:B:163:LEU:HD21	1.81	0.62
1:B:152:LEU:HD11	1:B:305:HIS:HB3	1.80	0.62
1:C:225:TYR:HB3	1:C:296:ARG:HE	1.64	0.61
1:A:296:ARG:HD3	1:A:297:GLU:N	2.05	0.61
1:B:337:VAL:O	1:B:341:LYS:HB2	1.99	0.61
1:B:341:LYS:NZ	1:B:341:LYS:HB3	2.16	0.60
1:D:8:ILE:CG2	1:D:251:LEU:HD22	2.32	0.60
1:C:106:ARG:NH1	1:D:14:PHE:O	2.35	0.59
1:C:2:MET:HG3	1:C:322:ASN:OD1	2.03	0.59
1:D:89:MET:HE3	1:D:89:MET:HA	1.84	0.59
1:A:148:ASP:HB3	1:A:163:LEU:HD21	1.84	0.59
1:B:270:THR:OG1	1:B:273:GLU:HG3	2.04	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2:MET:O	1:C:6:GLU:HG3	2.03	0.58
1:C:44:ILE:HD12	1:C:92:VAL:HG22	1.86	0.58
1:D:147:GLY:HA3	1:D:161:ASN:O	2.04	0.58
1:B:213:LYS:HE2	4:B:344:UNL:O4	2.03	0.58
1:C:339:PHE:HD2	1:C:340:LEU:HD23	1.69	0.57
1:C:102:GLY:O	1:C:103:SER:HB3	2.04	0.57
1:C:322:ASN:HD22	1:C:323:ILE:HG13	1.69	0.57
1:D:103:SER:OG	1:D:105:PRO:HD2	2.04	0.57
1:B:32:LEU:HD23	1:B:243:ILE:HD12	1.87	0.56
1:C:116:ALA:O	1:C:120:THR:HB	2.06	0.55
1:B:210:VAL:CG1	1:B:211:ILE:N	2.70	0.55
1:C:244:GLN:NE2	1:C:320:ARG:H	2.04	0.55
1:D:225:TYR:HB3	1:D:296:ARG:HE	1.72	0.55
1:D:2:MET:HB3	1:D:5:TYR:HB3	1.88	0.54
1:C:286:HIS:C	1:C:287:HIS:HD1	2.16	0.53
1:C:8:ILE:HG23	1:C:251:LEU:CD2	2.38	0.53
1:D:89:MET:HE2	1:D:134:VAL:HG11	1.90	0.53
1:A:130:LYS:NZ	1:D:67:GLU:OE2	2.41	0.52
1:B:210:VAL:HG13	1:B:211:ILE:HG13	1.91	0.52
1:A:270:THR:OG1	1:A:273:GLU:HG3	2.10	0.52
1:B:89:MET:HE2	1:B:134:VAL:HG11	1.92	0.52
1:D:309:ASP:OD1	1:D:311:THR:HB	2.09	0.52
1:D:119:ILE:HD13	1:D:172:VAL:HG11	1.92	0.51
1:B:115:ASN:OD1	1:B:119:ILE:HD12	2.10	0.51
1:C:89:MET:HE1	1:C:95:VAL:HG22	1.91	0.51
1:A:152:LEU:HD11	1:A:305:HIS:HB3	1.93	0.51
1:A:326:ARG:HH11	1:A:326:ARG:CG	2.14	0.51
1:D:244:GLN:NE2	1:D:320:ARG:H	2.06	0.51
1:A:333:MET:HB2	1:A:334:PRO:HD3	1.92	0.51
1:A:31:ASN:HB3	1:A:243:ILE:HD11	1.93	0.50
1:A:89:MET:HE1	1:A:95:VAL:CG2	2.36	0.50
1:C:8:ILE:HG21	1:C:251:LEU:HD22	1.92	0.50
1:A:314:ILE:HG23	1:A:320:ARG:NH1	2.27	0.50
1:B:314:ILE:HG23	1:B:320:ARG:NH1	2.27	0.49
1:A:326:ARG:HG2	1:A:326:ARG:NH1	2.11	0.49
1:B:245:MET:HG2	1:B:319:TYR:CE1	2.48	0.49
1:C:2:MET:O	1:C:6:GLU:N	2.36	0.49
1:C:171:TYR:CZ	1:C:175:ILE:HD11	2.48	0.48
1:A:227:ASN:OD1	1:A:296:ARG:HD2	2.12	0.48
1:C:286:HIS:C	1:C:287:HIS:ND1	2.71	0.48
1:D:117:THR:HG22	2:D:343:NAD:H61A	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:178:GLN:NE2	6:B:376:HOH:O	2.44	0.48
1:A:228:GLY:N	1:A:297:GLU:O	2.48	0.47
1:A:209:ALA:O	1:A:212:PRO:HD2	2.13	0.47
1:A:6:GLU:O	1:A:10:GLN:HG3	2.14	0.47
1:B:233:SER:HA	1:B:269:THR:O	2.15	0.47
1:B:89:MET:HA	1:B:89:MET:HE3	1.96	0.46
1:D:304:ARG:HG3	1:D:305:HIS:CD2	2.51	0.46
1:A:89:MET:HE2	1:A:134:VAL:HG11	1.97	0.46
1:A:245:MET:HE1	1:A:317:LEU:HD12	1.98	0.46
1:B:333:MET:HB2	1:B:334:PRO:HD3	1.98	0.46
1:A:245:MET:HG2	1:A:319:TYR:CE1	2.51	0.46
1:C:4:ARG:O	1:C:4:ARG:HG3	2.17	0.45
1:D:264:ALA:HB3	1:D:308:ALA:HB3	1.97	0.45
1:B:89:MET:CE	1:B:92:VAL:CG1	2.93	0.45
1:C:225:TYR:CD1	1:C:294:LYS:HG3	2.52	0.45
1:C:235:ASP:HB2	1:C:307:GLN:HA	1.98	0.45
1:B:89:MET:HE1	1:B:92:VAL:HG11	1.97	0.45
1:C:282:LEU:HD23	1:C:282:LEU:HA	1.84	0.45
1:C:329:LEU:O	1:C:333:MET:HG2	2.16	0.45
1:D:67:GLU:H	1:D:67:GLU:CD	2.25	0.45
1:D:130:LYS:HD2	1:D:184:TYR:CG	2.51	0.45
1:D:44:ILE:HD12	1:D:92:VAL:CG2	2.48	0.44
1:A:274:LEU:HD13	1:A:325:ILE:HD11	1.98	0.44
1:B:209:ALA:O	1:B:212:PRO:HD2	2.17	0.44
1:C:322:ASN:ND2	1:C:323:ILE:HG13	2.32	0.44
1:A:286:HIS:O	1:A:287:HIS:HB2	2.18	0.44
1:B:300:SER:HA	6:B:389:HOH:O	2.18	0.44
1:D:286:HIS:C	1:D:287:HIS:ND1	2.76	0.44
1:A:115:ASN:OD1	1:A:119:ILE:HD12	2.18	0.43
1:B:264:ALA:HB3	1:B:308:ALA:HB3	2.00	0.43
1:D:2:MET:HE3	1:D:5:TYR:CD2	2.53	0.43
1:D:235:ASP:HB2	1:D:307:GLN:HA	1.99	0.43
1:D:4:ARG:O	1:D:4:ARG:HG3	2.13	0.43
1:C:148:ASP:HB3	1:C:163:LEU:HD21	2.00	0.43
1:A:274:LEU:CD1	1:A:325:ILE:HD11	2.49	0.43
1:D:171:TYR:CZ	1:D:175:ILE:HD11	2.54	0.43
1:A:264:ALA:HB3	1:A:308:ALA:HB3	2.01	0.42
1:B:286:HIS:O	1:B:287:HIS:HB2	2.20	0.42
1:C:233:SER:HA	1:C:269:THR:O	2.20	0.42
1:A:265:VAL:O	1:A:265:VAL:CG1	2.67	0.42
3:A:346:SO4:O3	1:B:318:LYS:CE	2.66	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:81:ASP:OD2	1:B:84:THR:OG1	2.30	0.42
1:C:2:MET:HE2	1:C:2:MET:HB2	1.87	0.42
1:A:1:TYR:N	6:A:392:HOH:O	2.52	0.42
1:B:297:GLU:HB3	1:B:298:PHE:H	1.74	0.42
1:D:102:GLY:O	1:D:103:SER:CB	2.58	0.42
1:A:89:MET:HA	1:A:89:MET:HE3	2.01	0.42
1:B:232:THR:O	1:B:270:THR:HA	2.18	0.42
1:C:304:ARG:HG3	1:C:305:HIS:CD2	2.54	0.42
1:D:79:ILE:HD12	1:D:121:GLY:HA3	2.02	0.42
1:A:89:MET:CE	1:A:92:VAL:CG1	2.96	0.42
1:A:294:LYS:HE2	1:A:294:LYS:HB3	1.91	0.42
1:B:245:MET:HG2	1:B:319:TYR:CD1	2.55	0.42
1:A:310:VAL:HG23	1:A:314:ILE:HD11	2.02	0.42
1:B:299:ARG:CG	1:B:300:SER:H	2.33	0.41
1:A:107:SER:HB3	1:A:166:TYR:HB2	2.02	0.41
1:D:17:LYS:H	1:D:41:GLN:NE2	2.18	0.41
1:D:194:PHE:HB2	1:D:264:ALA:HB2	2.02	0.41
1:C:225:TYR:CE1	1:C:294:LYS:HG3	2.56	0.41
1:C:104:VAL:HB	1:C:105:PRO:HD3	2.02	0.41
1:C:196:VAL:HA	1:C:237:CYS:O	2.20	0.41
1:A:170:LYS:HD3	1:A:170:LYS:HA	1.90	0.41
1:A:171:TYR:CZ	1:A:175:ILE:HD11	2.54	0.41
1:A:232:THR:HG23	1:A:304:ARG:O	2.21	0.41
1:A:265:VAL:O	1:A:265:VAL:HG12	2.20	0.41
1:C:130:LYS:HD2	1:C:184:TYR:CG	2.56	0.41
1:C:168:VAL:O	1:C:172:VAL:HG23	2.20	0.41
1:C:200:ARG:HA	1:C:335:TRP:CH2	2.56	0.41
1:C:264:ALA:HB3	1:C:308:ALA:HB3	2.01	0.41
1:D:138:THR:HA	1:D:189:ILE:O	2.21	0.41
1:D:282:LEU:HD23	1:D:282:LEU:HA	1.84	0.41
1:D:79:ILE:HD12	1:D:121:GLY:C	2.46	0.40
1:C:75:ILE:HG13	1:C:88:VAL:HG12	2.02	0.40
1:D:8:ILE:HD11	6:D:359:HOH:O	2.19	0.40
1:A:32:LEU:HD23	1:A:243:ILE:HD12	2.04	0.40
1:C:268:ARG:HH11	1:C:268:ARG:HD3	1.64	0.40
1:D:194:PHE:O	1:D:195:ASN:C	2.65	0.40
1:B:79:ILE:HG13	1:B:121:GLY:HA3	2.03	0.40
1:D:32:LEU:HD23	1:D:243:ILE:HD12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	332/351 (95%)	317 (96%)	12 (4%)	3 (1%)	14	13
1	B	332/351 (95%)	319 (96%)	12 (4%)	1 (0%)	36	41
1	C	332/351 (95%)	322 (97%)	9 (3%)	1 (0%)	36	41
1	D	332/351 (95%)	320 (96%)	11 (3%)	1 (0%)	36	41
All	All	1328/1404 (95%)	1278 (96%)	44 (3%)	6 (0%)	24	26

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	286	HIS
1	D	286	HIS
1	A	103	SER
1	A	296	ARG
1	B	103	SER
1	A	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%)	277 (96%)	13 (4%)	24	31
1	B	290/304 (95%)	278 (96%)	12 (4%)	27	35
1	C	290/304 (95%)	278 (96%)	12 (4%)	27	35
1	D	290/304 (95%)	275 (95%)	15 (5%)	21	25

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1160/1216 (95%)	1108 (96%)	52 (4%)	24	31

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LEU
1	A	48	ASN
1	A	109	VAL
1	A	114	THR
1	A	130	LYS
1	A	227	ASN
1	A	275	SER
1	A	296	ARG
1	A	303	VAL
1	A	325	ILE
1	A	326	ARG
1	A	334	PRO
1	A	341	LYS
1	B	46	LEU
1	B	109	VAL
1	B	114	THR
1	B	130	LYS
1	B	285	ILE
1	B	296	ARG
1	B	297	GLU
1	B	299	ARG
1	B	303	VAL
1	B	325	ILE
1	B	334	PRO
1	B	341	LYS
1	C	2	MET
1	C	4	ARG
1	C	15	SER
1	C	46	LEU
1	C	152	LEU
1	C	243	ILE
1	C	253	LYS
1	C	286	HIS
1	C	294	LYS
1	C	322	ASN
1	C	340	LEU
1	C	341	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	2	MET
1	D	3	SER
1	D	4	ARG
1	D	7	GLU
1	D	10	GLN
1	D	15	SER
1	D	46	LEU
1	D	109	VAL
1	D	182	ARG
1	D	243	ILE
1	D	286	HIS
1	D	311	THR
1	D	322	ASN
1	D	325	ILE
1	D	341	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	87	GLN
1	A	244	GLN
1	B	11	GLN
1	B	53	HIS
1	B	246	ASN
1	B	272	ASN
1	C	178	GLN
1	C	244	GLN
1	C	322	ASN
1	D	10	GLN
1	D	31	ASN
1	D	41	GLN
1	D	178	GLN
1	D	195	ASN
1	D	244	GLN
1	D	283	ASN
1	D	322	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are unknown - leaving 8 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	-	46,48,48	1.74	10 (21%)	64,73,73	1.76	12 (18%)
5	GLY	D	345	-	4,4,4	1.06	0	3,4,4	1.39	1 (33%)
2	NAD	C	343	-	46,48,48	1.78	7 (15%)	64,73,73	1.41	11 (17%)
2	NAD	D	343	-	46,48,48	2.14	10 (21%)	64,73,73	1.62	13 (20%)
3	SO4	A	345	-	4,4,4	0.44	0	6,6,6	0.86	0
3	SO4	A	346	-	4,4,4	0.23	0	6,6,6	0.86	0
5	GLY	C	345	-	4,4,4	1.12	1 (25%)	3,4,4	1.42	0
2	NAD	B	343	-	46,48,48	1.96	11 (23%)	64,73,73	1.68	12 (18%)

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	-	-	4/30/62/62	0/5/5/5
5	GLY	D	345	-	-	1/2/2/2	-
2	NAD	C	343	-	-	3/30/62/62	0/5/5/5
2	NAD	D	343	-	-	4/30/62/62	0/5/5/5
5	GLY	C	345	-	-	0/2/2/2	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	B	343	-	-	3/30/62/62	0/5/5/5

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	343	NAD	C2N-N1N	9.05	1.44	1.35
2	D	343	NAD	C2N-N1N	8.05	1.43	1.35
2	A	343	NAD	C2N-N1N	7.82	1.43	1.35
2	C	343	NAD	C2N-N1N	7.09	1.42	1.35
2	D	343	NAD	PA-O3	-6.63	1.52	1.59
2	C	343	NAD	C6N-N1N	4.14	1.44	1.35
2	D	343	NAD	C6N-N1N	4.14	1.44	1.35
2	B	343	NAD	O4D-C1D	4.12	1.46	1.40
2	D	343	NAD	C5A-N7A	-3.63	1.32	1.39
2	C	343	NAD	PA-O3	-3.47	1.55	1.59
2	C	343	NAD	C5A-N7A	-3.42	1.32	1.39
2	A	343	NAD	O4B-C1B	2.98	1.48	1.42
2	B	343	NAD	C6N-N1N	2.85	1.41	1.35
2	D	343	NAD	PN-O3	2.80	1.62	1.59
2	A	343	NAD	O4D-C1D	2.69	1.44	1.40
2	C	343	NAD	C1B-N9A	2.66	1.53	1.46
2	B	343	NAD	PA-O3	-2.65	1.56	1.59
2	A	343	NAD	C6N-N1N	2.52	1.41	1.35
2	D	343	NAD	C4A-N9A	-2.51	1.32	1.37
2	B	343	NAD	C5A-N7A	-2.43	1.34	1.39
2	A	343	NAD	PA-O2A	-2.43	1.44	1.55
2	D	343	NAD	C4N-C3N	2.41	1.43	1.39
2	B	343	NAD	PN-O2N	-2.41	1.44	1.55
2	B	343	NAD	C5B-C4B	2.40	1.58	1.51
2	D	343	NAD	PN-O2N	-2.38	1.44	1.55
2	C	343	NAD	C4A-N9A	-2.36	1.32	1.37
2	C	343	NAD	PN-O2N	-2.34	1.44	1.55
2	A	343	NAD	C5A-N7A	-2.27	1.34	1.39
2	A	343	NAD	C4A-N9A	-2.25	1.33	1.37
2	D	343	NAD	PA-O5B	2.21	1.68	1.59
2	A	343	NAD	O3B-C3B	2.18	1.48	1.43
2	A	343	NAD	PA-O1A	-2.16	1.43	1.50
2	A	343	NAD	O5D-C5D	-2.11	1.36	1.44
2	D	343	NAD	O4B-C1B	-2.06	1.37	1.42
2	B	343	NAD	PA-O1A	-2.03	1.43	1.50
5	C	345	GLY	OXT-C	-2.02	1.24	1.30
2	B	343	NAD	O4B-C1B	2.02	1.46	1.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	343	NAD	C4A-N9A	-2.01	1.33	1.37
2	B	343	NAD	C8A-N7A	2.01	1.35	1.31

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	343	NAD	N3A-C2A-N1A	-5.42	120.38	128.58
2	A	343	NAD	C5A-C4A-N3A	-5.00	119.83	126.72
2	D	343	NAD	C5A-C4A-N3A	-4.67	120.29	126.72
2	B	343	NAD	C5A-C4A-N3A	-4.61	120.37	126.72
2	B	343	NAD	N3A-C2A-N1A	-4.58	121.64	128.58
2	D	343	NAD	N3A-C2A-N1A	-4.45	121.84	128.58
2	C	343	NAD	C5A-C4A-N3A	-4.10	121.07	126.72
2	B	343	NAD	N9A-C8A-N7A	-3.99	108.27	113.94
2	D	343	NAD	N9A-C8A-N7A	-3.84	108.49	113.94
2	C	343	NAD	N3A-C2A-N1A	-3.76	122.90	128.58
2	A	343	NAD	C6N-N1N-C2N	-3.72	118.71	121.88
2	D	343	NAD	C5A-N7A-C8A	3.71	109.28	103.45
2	A	343	NAD	C2A-N3A-C4A	3.70	120.86	111.83
2	A	343	NAD	N3A-C4A-N9A	3.57	133.24	127.17
2	A	343	NAD	N9A-C8A-N7A	-3.49	108.98	113.94
2	D	343	NAD	C4A-C5A-N7A	-3.46	106.63	110.58
2	B	343	NAD	C6N-N1N-C2N	-3.37	119.01	121.88
2	B	343	NAD	C2A-N3A-C4A	3.25	119.78	111.83
2	D	343	NAD	C2A-N3A-C4A	3.12	119.45	111.83
2	B	343	NAD	N3A-C4A-N9A	3.10	132.44	127.17
2	D	343	NAD	N3A-C4A-N9A	3.07	132.39	127.17
2	B	343	NAD	C5A-N7A-C8A	3.05	108.24	103.45
2	A	343	NAD	C4A-N9A-C8A	2.99	108.88	105.74
2	C	343	NAD	N9A-C8A-N7A	-2.93	109.77	113.94
2	B	343	NAD	C4A-N9A-C8A	2.91	108.79	105.74
2	B	343	NAD	C4A-C5A-N7A	-2.70	107.49	110.58
2	D	343	NAD	C6N-N1N-C2N	-2.69	119.58	121.88
2	C	343	NAD	N3A-C4A-N9A	2.65	131.68	127.17
2	C	343	NAD	C5A-N7A-C8A	2.60	107.53	103.45
2	A	343	NAD	C5A-N7A-C8A	2.53	107.43	103.45
2	C	343	NAD	C3N-C7N-N7N	-2.48	114.68	117.74
2	C	343	NAD	C2A-N3A-C4A	2.47	117.87	111.83
2	A	343	NAD	C4A-C5A-N7A	-2.47	107.76	110.58
2	D	343	NAD	C4A-N9A-C8A	2.41	108.27	105.74
2	D	343	NAD	O4B-C1B-N9A	-2.34	103.59	108.09
2	C	343	NAD	C2N-C3N-C4N	2.26	120.89	118.26

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	343	NAD	C2N-C3N-C4N	2.26	120.89	118.26
2	C	343	NAD	O7N-C7N-N7N	2.25	125.87	122.62
2	B	343	NAD	C5N-C4N-C3N	2.25	122.57	120.36
2	C	343	NAD	C4A-C5A-N7A	-2.24	108.02	110.58
2	D	343	NAD	C3N-C7N-N7N	-2.24	114.98	117.74
2	D	343	NAD	C2A-N1A-C6A	2.21	122.37	118.73
2	A	343	NAD	O4D-C4D-C5D	-2.20	102.30	109.33
2	A	343	NAD	C2N-C3N-C4N	2.16	120.77	118.26
2	C	343	NAD	C2A-N1A-C6A	2.11	122.20	118.73
2	A	343	NAD	O2N-PN-O1N	2.05	121.99	112.44
2	B	343	NAD	O4D-C4D-C5D	-2.05	102.77	109.33
2	B	343	NAD	O2N-PN-O1N	2.04	121.92	112.44
5	D	345	GLY	OXT-C-O	-2.02	118.15	123.33

There are no chirality outliers.

All (15) torsion outliers are listed below:

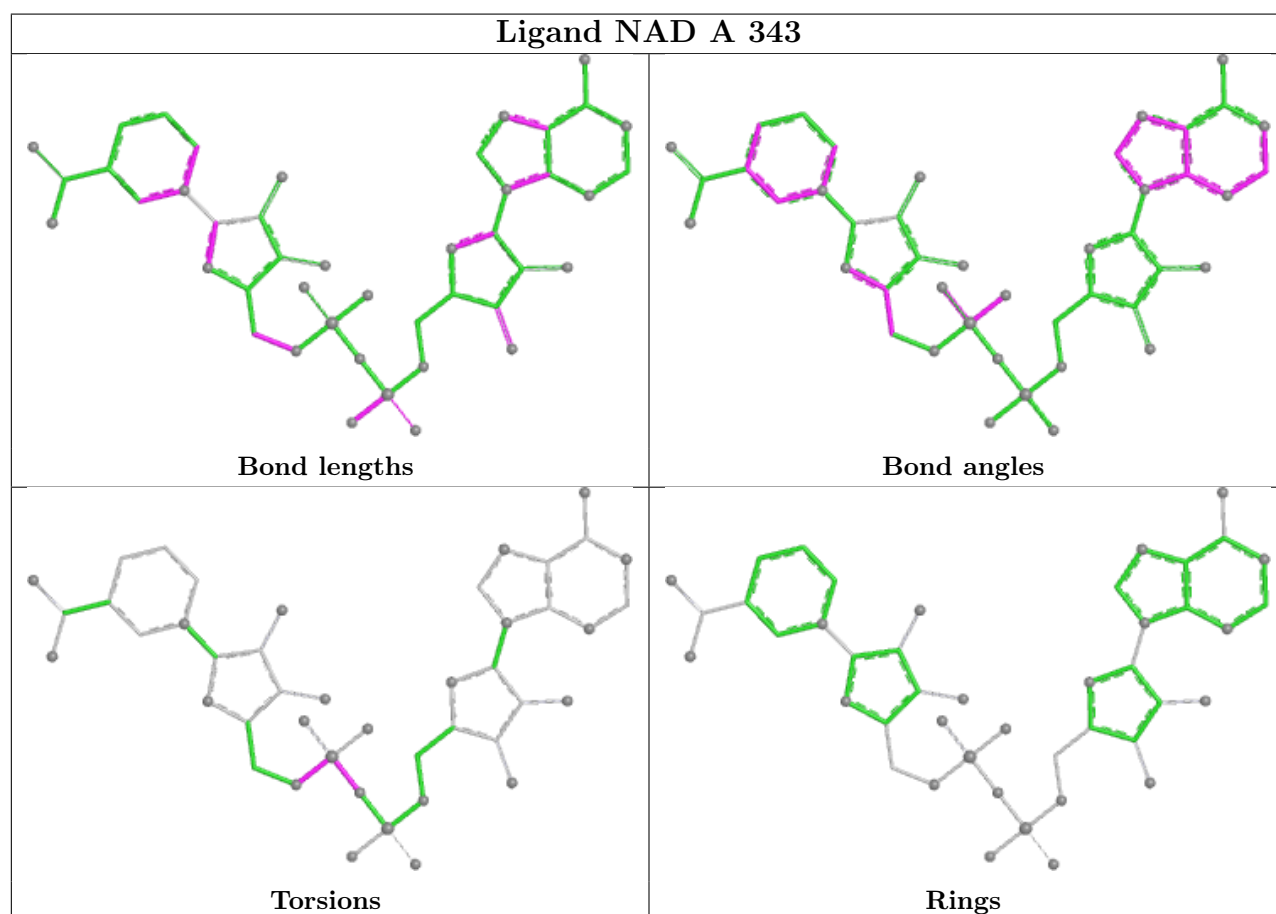
Mol	Chain	Res	Type	Atoms
2	A	343	NAD	C5D-O5D-PN-O3
2	A	343	NAD	C5D-O5D-PN-O1N
2	B	343	NAD	C5D-O5D-PN-O1N
2	C	343	NAD	C5D-O5D-PN-O3
2	C	343	NAD	C5D-O5D-PN-O1N
2	D	343	NAD	C5D-O5D-PN-O3
2	D	343	NAD	C5D-O5D-PN-O1N
2	A	343	NAD	C5D-O5D-PN-O2N
2	B	343	NAD	C5D-O5D-PN-O3
2	C	343	NAD	C5D-O5D-PN-O2N
2	D	343	NAD	C5D-O5D-PN-O2N
2	D	343	NAD	O4B-C4B-C5B-O5B
5	D	345	GLY	OXT-C-CA-N
2	A	343	NAD	PA-O3-PN-O2N
2	B	343	NAD	PA-O3-PN-O2N

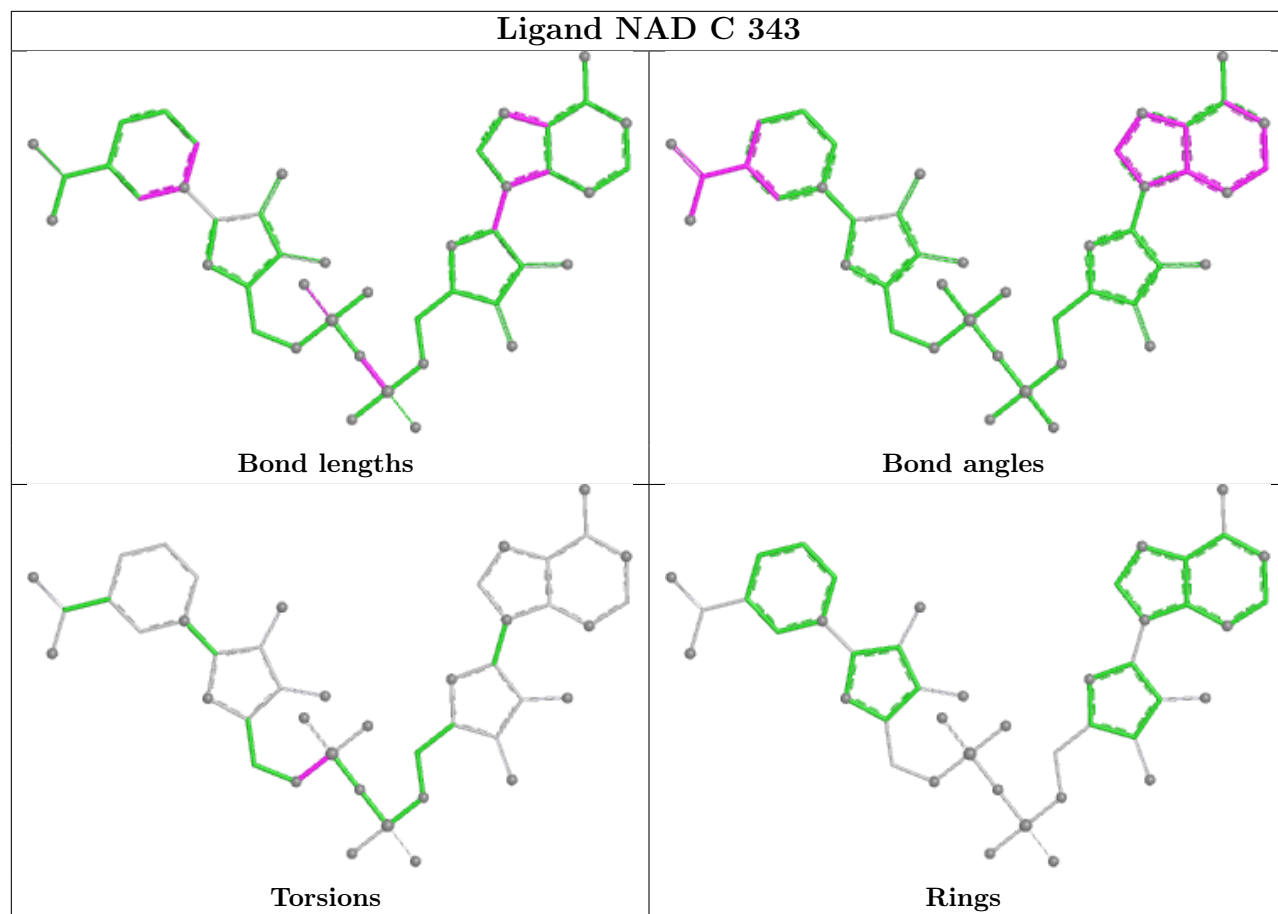
There are no ring outliers.

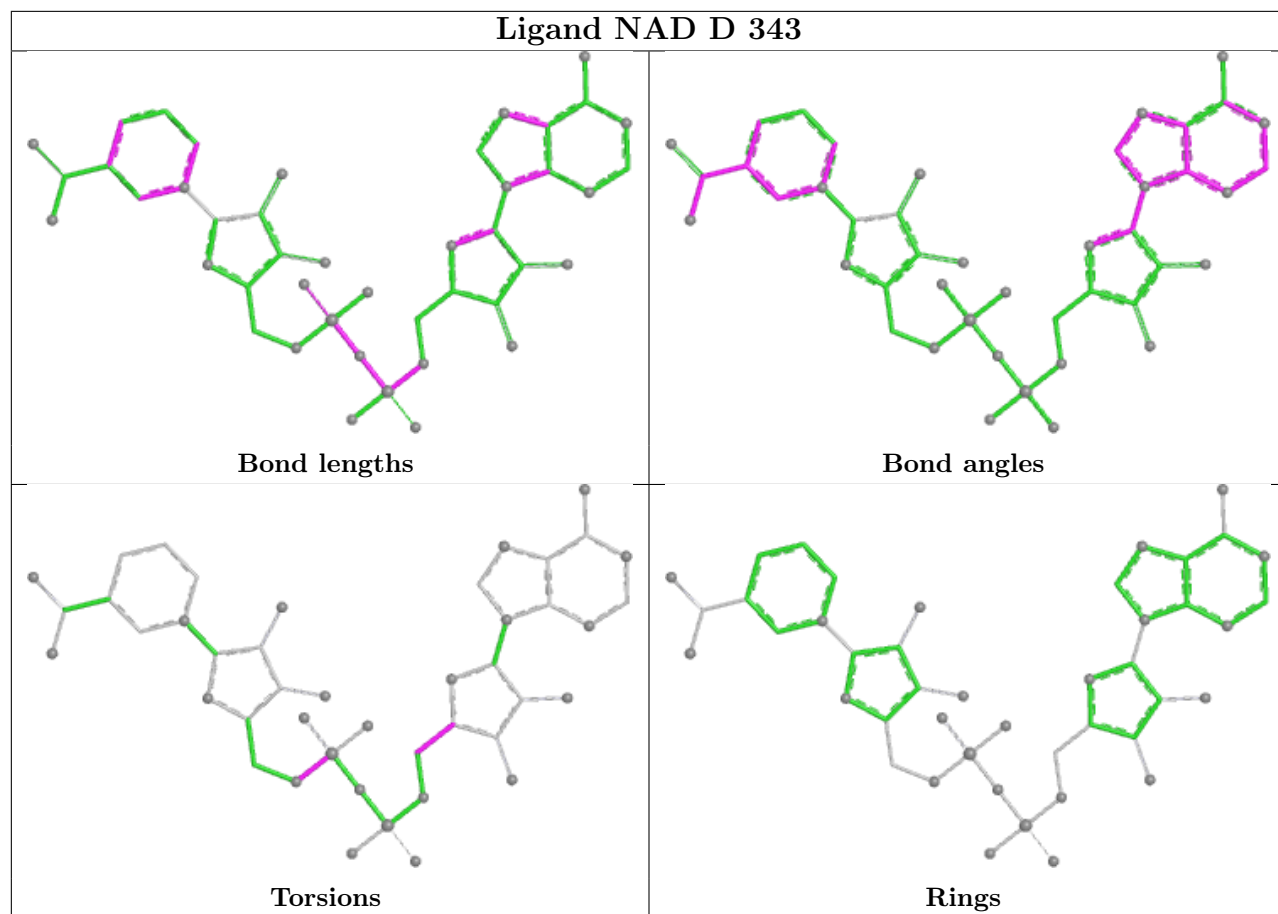
3 monomers are involved in 4 short contacts:

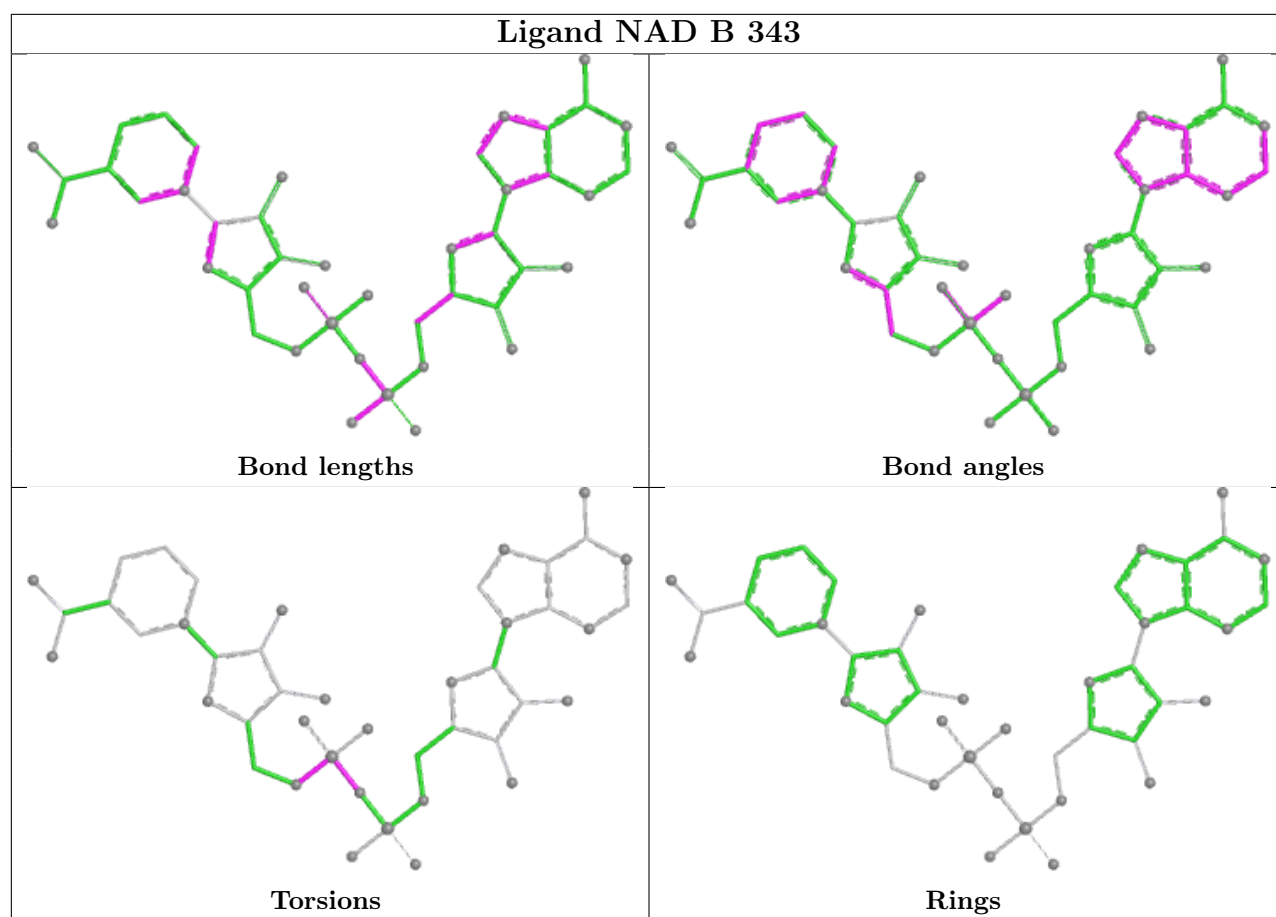
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	343	NAD	1	0
3	A	345	SO4	1	0
3	A	346	SO4	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	336/351 (95%)	-1.48	0 100 100	14, 26, 82, 100	0
1	B	336/351 (95%)	-1.49	0 100 100	14, 26, 81, 105	0
1	C	336/351 (95%)	-1.59	0 100 100	17, 27, 50, 75	0
1	D	336/351 (95%)	-1.59	0 100 100	17, 27, 51, 77	0
All	All	1344/1404 (95%)	-1.53	0 100 100	14, 27, 69, 105	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

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

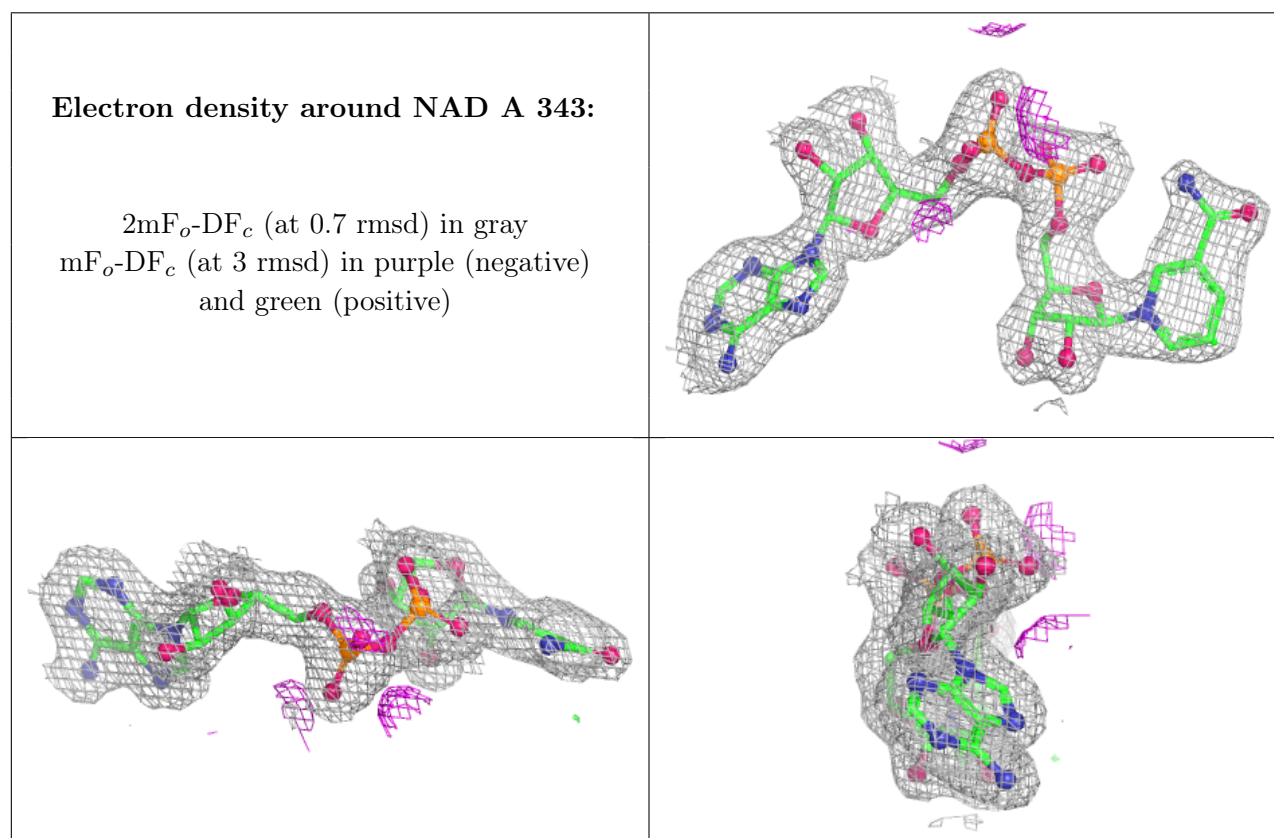
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	GLY	D	345	5/5	0.96	0.11	49,50,50,51	0
5	GLY	C	345	5/5	0.97	0.09	56,56,57,57	0
4	UNL	A	344	25/-	0.99	0.03	33,66,79,80	0
4	UNL	B	344	25/-	0.99	0.04	34,63,74,75	0

Continued on next page...

Continued from previous page...

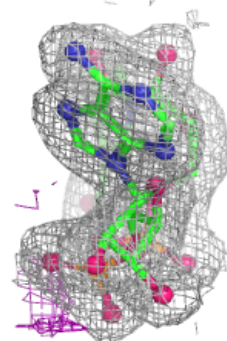
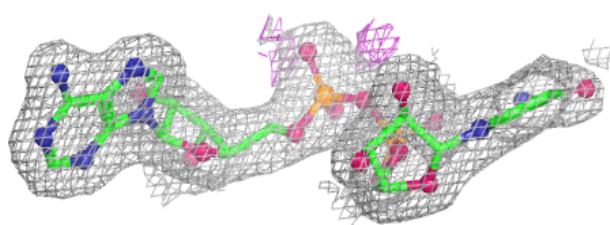
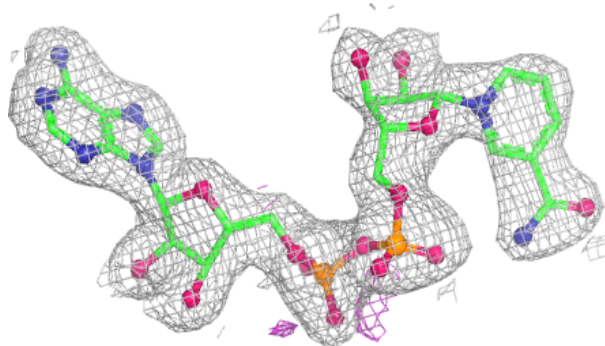
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	A	345	5/5	1.00	0.02	26,28,29,29	0
3	SO4	A	346	5/5	1.00	0.01	24,25,28,29	0
2	NAD	A	343	44/44	1.00	0.02	12,20,38,44	0
2	NAD	B	343	44/44	1.00	0.02	15,20,39,44	0
4	UNL	C	344	25/-	1.00	0.02	28,34,37,38	0
4	UNL	D	344	25/-	1.00	0.02	30,35,37,41	0
2	NAD	C	343	44/44	1.00	0.02	18,23,44,47	0
2	NAD	D	343	44/44	1.00	0.02	15,22,44,46	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.

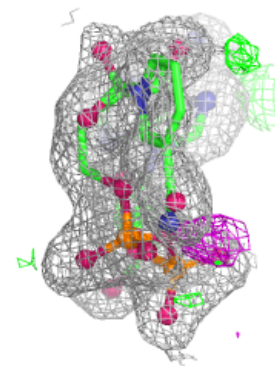
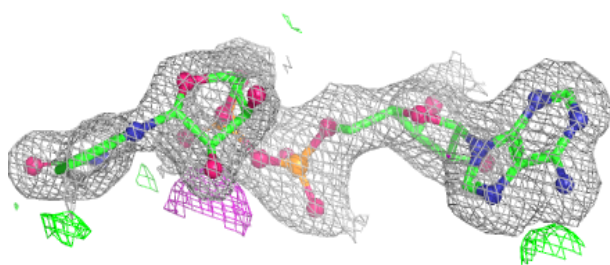
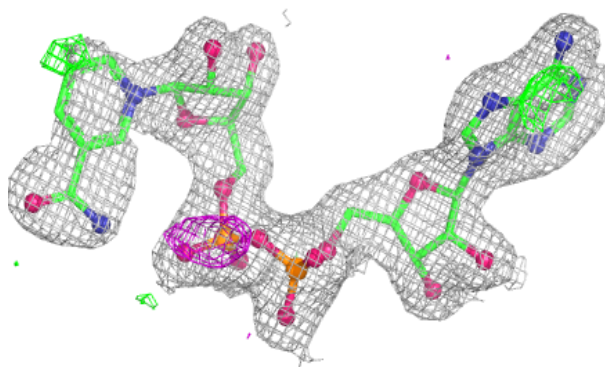


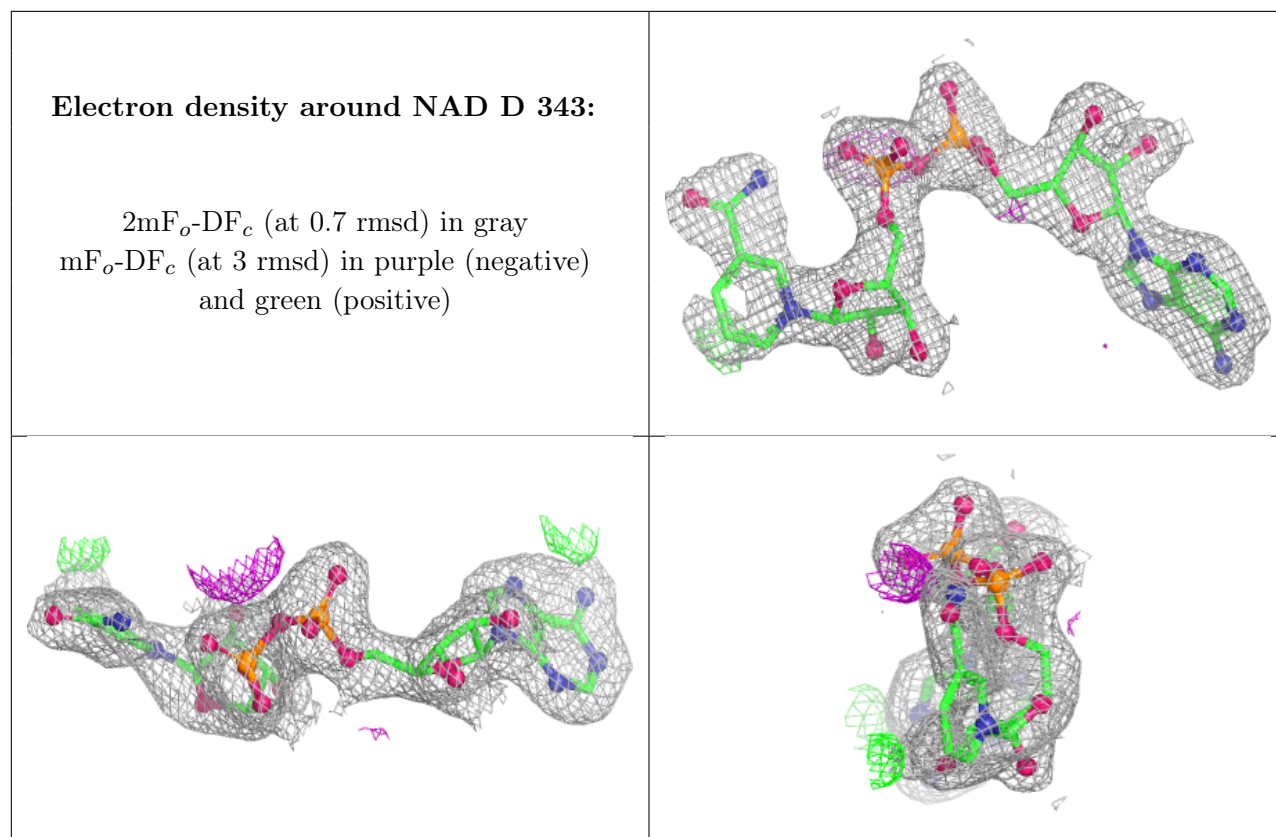
Electron density around NAD B 343:

$2mF_o-DF_c$ (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 ⓘ

There are no such residues in this entry.