



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 7, 2024 – 04:43 am GMT

PDB ID : 5O9F
Title : Crystal structure of *R. ruber* ADH-A, mutant Y294F, W295A, Y54F, F43S, H39Y
Authors : Dobritsch, D.; Maurer, D.; Hamnevik, E.; Enugala, T.R.; Widersten, M.
Deposited on : 2017-06-19
Resolution : 1.64 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 : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

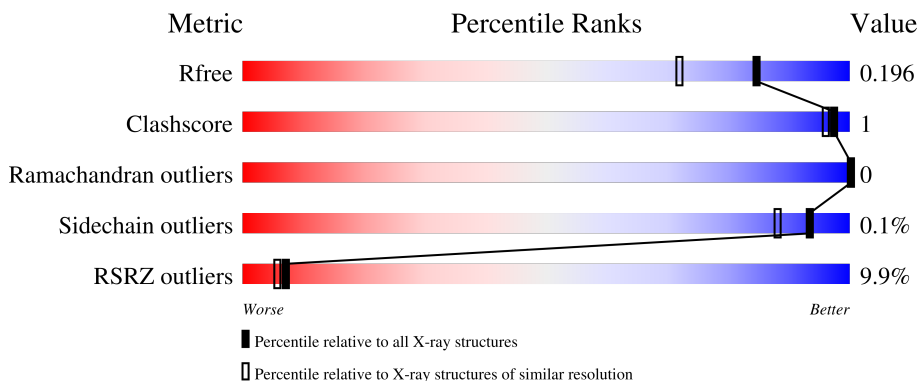
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

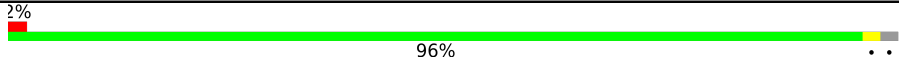
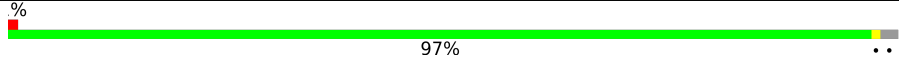
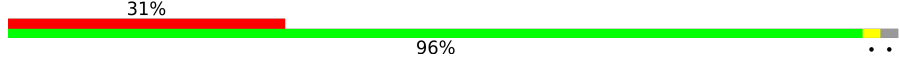
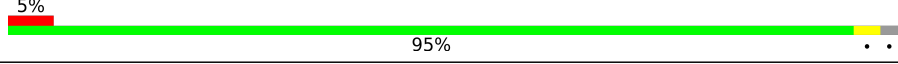
The reported resolution of this entry is 1.64 Å.

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	3122 (1.66-1.62)
Clashscore	141614	3268 (1.66-1.62)
Ramachandran outliers	138981	3215 (1.66-1.62)
Sidechain outliers	138945	3215 (1.66-1.62)
RSRZ outliers	127900	3079 (1.66-1.62)

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	352	 2% 96%
1	B	352	 % 97%
1	C	352	 31% 96%
1	D	352	 5% 95%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 11732 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 Alcohol dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	346	2480	1566	431	470	13	0	3	0
1	B	346	2475	1559	434	470	12	0	1	0
1	C	345	2462	1552	429	468	13	0	1	0
1	D	346	2483	1565	433	473	12	0	3	0

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	TYR	HIS	engineered mutation	UNP A0A1Q8I6M1
A	43	SER	PHE	engineered mutation	UNP A0A1Q8I6M1
A	294	PHE	TYR	engineered mutation	UNP A0A1Q8I6M1
A	295	ALA	TRP	engineered mutation	UNP A0A1Q8I6M1
A	346	THR	-	expression tag	UNP A0A1Q8I6M1
A	347	SER	-	expression tag	UNP A0A1Q8I6M1
A	348	HIS	-	expression tag	UNP A0A1Q8I6M1
A	349	HIS	-	expression tag	UNP A0A1Q8I6M1
A	350	HIS	-	expression tag	UNP A0A1Q8I6M1
A	351	HIS	-	expression tag	UNP A0A1Q8I6M1
A	352	HIS	-	expression tag	UNP A0A1Q8I6M1
B	39	TYR	HIS	engineered mutation	UNP A0A1Q8I6M1
B	43	SER	PHE	engineered mutation	UNP A0A1Q8I6M1
B	294	PHE	TYR	engineered mutation	UNP A0A1Q8I6M1
B	295	ALA	TRP	engineered mutation	UNP A0A1Q8I6M1
B	346	THR	-	expression tag	UNP A0A1Q8I6M1
B	347	SER	-	expression tag	UNP A0A1Q8I6M1
B	348	HIS	-	expression tag	UNP A0A1Q8I6M1
B	349	HIS	-	expression tag	UNP A0A1Q8I6M1
B	350	HIS	-	expression tag	UNP A0A1Q8I6M1
B	351	HIS	-	expression tag	UNP A0A1Q8I6M1

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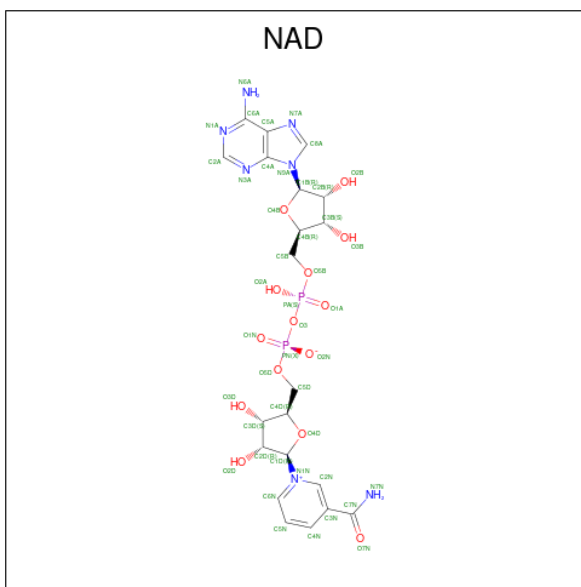
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Chain	Residue	Modelled	Actual	Comment	Reference
B	352	HIS	-	expression tag	UNP A0A1Q8I6M1
C	39	TYR	HIS	engineered mutation	UNP A0A1Q8I6M1
C	43	SER	PHE	engineered mutation	UNP A0A1Q8I6M1
C	294	PHE	TYR	engineered mutation	UNP A0A1Q8I6M1
C	295	ALA	TRP	engineered mutation	UNP A0A1Q8I6M1
C	346	THR	-	expression tag	UNP A0A1Q8I6M1
C	347	SER	-	expression tag	UNP A0A1Q8I6M1
C	348	HIS	-	expression tag	UNP A0A1Q8I6M1
C	349	HIS	-	expression tag	UNP A0A1Q8I6M1
C	350	HIS	-	expression tag	UNP A0A1Q8I6M1
C	351	HIS	-	expression tag	UNP A0A1Q8I6M1
C	352	HIS	-	expression tag	UNP A0A1Q8I6M1
D	39	TYR	HIS	engineered mutation	UNP A0A1Q8I6M1
D	43	SER	PHE	engineered mutation	UNP A0A1Q8I6M1
D	294	PHE	TYR	engineered mutation	UNP A0A1Q8I6M1
D	295	ALA	TRP	engineered mutation	UNP A0A1Q8I6M1
D	346	THR	-	expression tag	UNP A0A1Q8I6M1
D	347	SER	-	expression tag	UNP A0A1Q8I6M1
D	348	HIS	-	expression tag	UNP A0A1Q8I6M1
D	349	HIS	-	expression tag	UNP A0A1Q8I6M1
D	350	HIS	-	expression tag	UNP A0A1Q8I6M1
D	351	HIS	-	expression tag	UNP A0A1Q8I6M1
D	352	HIS	-	expression tag	UNP A0A1Q8I6M1

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

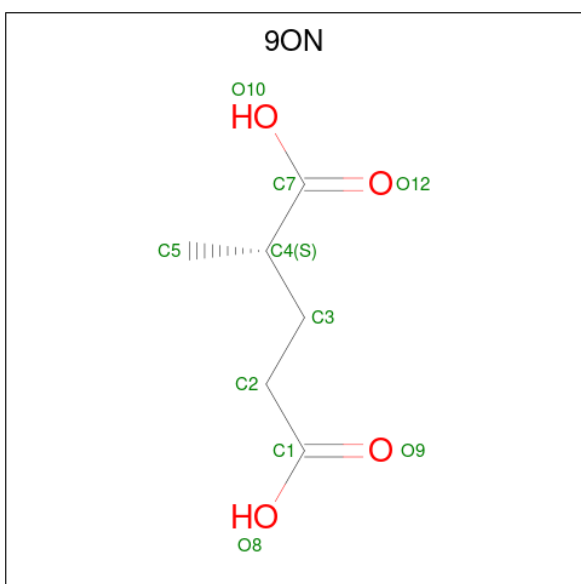
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Zn 2 2	0	0
2	B	2	Total Zn 2 2	0	0
2	C	2	Total Zn 2 2	0	0
2	D	2	Total Zn 2 2	0	0

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



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

- Molecule 4 is (2 {S})-2-methylpentanedioic acid (three-letter code: 9ON) (formula: $C_6H_{10}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 10 6 4	0	0
4	B	1	Total C O 10 6 4	0	0
4	D	1	Total C O 10 6 4	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	488	Total O 490 490	0	2
5	B	472	Total O 473 473	0	1
5	C	263	Total O 264 264	0	1
5	D	389	Total O 391 391	0	2

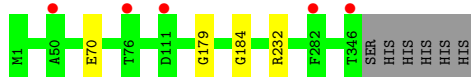
3 Residue-property plots

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.

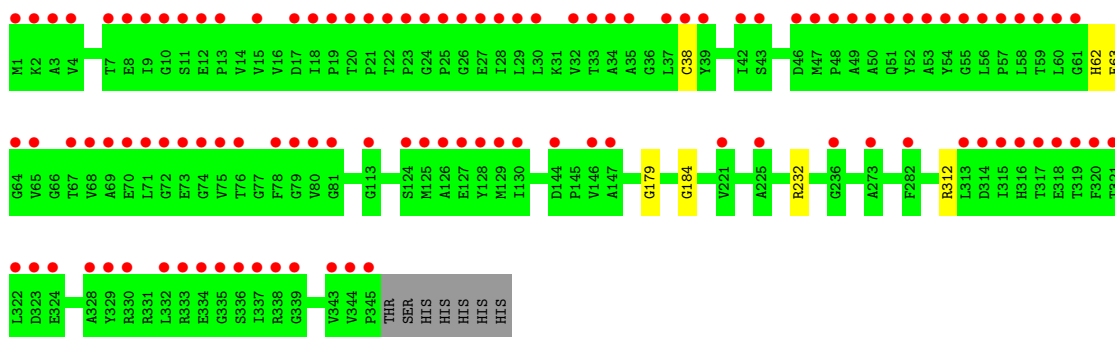
- Molecule 1: Alcohol dehydrogenase



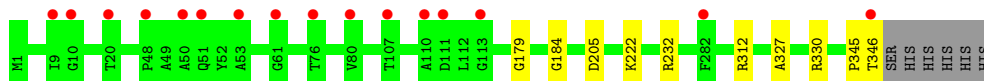
- Molecule 1: Alcohol dehydrogenase



- Molecule 1: Alcohol dehydrogenase



- Molecule 1: Alcohol dehydrogenase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.84Å 105.29Å 109.29Å 90.00° 91.36° 90.00°	Depositor
Resolution (Å)	29.50 – 1.64 28.49 – 1.64	Depositor EDS
% Data completeness (in resolution range)	97.3 (29.50-1.64) 97.3 (28.49-1.64)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 1.64Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.168 , 0.186 0.179 , 0.196	Depositor DCC
R_{free} test set	8693 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	20.9	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.001 for -h,l,k 0.017 for -h,-l,-k 0.024 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11732	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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: 9ON, NAD, ZN

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	0.49	0/2537	0.75	3/3465 (0.1%)
1	B	0.49	1/2526 (0.0%)	0.74	2/3448 (0.1%)
1	C	0.50	0/2513	0.76	2/3430 (0.1%)
1	D	0.47	0/2540	0.76	2/3467 (0.1%)
All	All	0.49	1/10116 (0.0%)	0.75	9/13810 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	70	GLU	CD-OE1	-5.38	1.19	1.25

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	232	ARG	NE-CZ-NH2	12.82	126.71	120.30
1	D	232	ARG	NE-CZ-NH2	-11.40	114.60	120.30
1	A	232	ARG	NE-CZ-NH1	9.33	124.97	120.30
1	D	232	ARG	NE-CZ-NH1	8.93	124.76	120.30
1	B	232	ARG	NE-CZ-NH2	-8.50	116.05	120.30
1	B	232	ARG	NE-CZ-NH1	8.42	124.51	120.30
1	C	232	ARG	NE-CZ-NH1	-8.00	116.30	120.30
1	A	232	ARG	NE-CZ-NH2	-6.95	116.83	120.30
1	A	153	ASP	CB-CG-OD2	-5.05	113.75	118.30

There are no chirality outliers.

There are no planarity outliers.

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	2480	0	2492	4	0
1	B	2475	0	2478	1	0
1	C	2462	0	2459	5	0
1	D	2483	0	2485	5	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	44	0	26	0	0
3	B	44	0	26	0	0
3	C	44	0	26	0	0
3	D	44	0	26	0	0
4	A	10	0	0	0	0
4	B	10	0	0	0	0
4	D	10	0	0	0	0
5	A	490	0	0	1	0
5	B	473	0	0	0	0
5	C	264	0	0	1	0
5	D	391	0	0	2	0
All	All	11732	0	10018	15	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 1.

All (15) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:ASP:OD2	5:A:601:HOH:O	2.14	0.66
1:D:205[A]:ASP:OD2	5:D:601:HOH:O	2.17	0.57
1:C:38[B]:CYS:SG	1:C:62:HIS:NE2	2.78	0.56
1:D:312:ARG:NH1	5:D:603:HOH:O	2.33	0.55
1:C:38[B]:CYS:HG	1:C:62:HIS:CD2	2.26	0.54
1:A:34:ALA:HB3	1:A:65[A]:VAL:CG2	2.41	0.50
1:A:65[A]:VAL:HG22	1:A:149:ALA:HB2	1.99	0.45
1:D:345:PRO:O	1:D:346:THR:OG1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:312:ARG:NH1	5:C:607:HOH:O	2.50	0.44
1:C:38[B]:CYS:SG	1:C:63:GLU:HG3	2.59	0.42
1:A:179:GLY:O	1:A:184:GLY:HA3	2.20	0.41
1:D:327:ALA:HA	1:D:330:ARG:NH2	2.35	0.41
1:D:179:GLY:O	1:D:184:GLY:HA3	2.20	0.41
1:B:179:GLY:O	1:B:184:GLY:HA3	2.21	0.41
1:C:179:GLY:O	1:C:184:GLY:HA3	2.21	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	347/352 (99%)	340 (98%)	7 (2%)	0	100	100
1	B	345/352 (98%)	340 (99%)	5 (1%)	0	100	100
1	C	344/352 (98%)	339 (98%)	5 (2%)	0	100	100
1	D	347/352 (99%)	342 (99%)	5 (1%)	0	100	100
All	All	1383/1408 (98%)	1361 (98%)	22 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	251/254 (99%)	251 (100%)	0	100	100
1	B	249/254 (98%)	249 (100%)	0	100	100
1	C	247/254 (97%)	247 (100%)	0	100	100
1	D	250/254 (98%)	249 (100%)	1 (0%)	91	84
All	All	997/1016 (98%)	996 (100%)	1 (0%)	93	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	222	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 15 ligands modelled in this entry, 8 are monoatomic - leaving 7 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
4	9ON	D	504	2	9,9,9	0.88	0	10,11,11	0.81	0
3	NAD	A	503	-	42,48,48	0.78	1 (2%)	50,73,73	1.34	10 (20%)
4	9ON	A	504	2	9,9,9	0.97	0	10,11,11	0.78	0
3	NAD	C	503	-	42,48,48	0.78	1 (2%)	50,73,73	1.20	6 (12%)
3	NAD	D	503	-	42,48,48	0.80	2 (4%)	50,73,73	1.25	8 (16%)
3	NAD	B	503	-	42,48,48	0.85	3 (7%)	50,73,73	1.20	3 (6%)
4	9ON	B	504	2	9,9,9	0.88	0	10,11,11	0.96	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
4	9ON	D	504	2	-	2/9/9/9	-
3	NAD	A	503	-	-	8/26/62/62	0/5/5/5
4	9ON	A	504	2	-	4/9/9/9	-
3	NAD	C	503	-	-	8/26/62/62	0/5/5/5
3	NAD	D	503	-	-	8/26/62/62	0/5/5/5
3	NAD	B	503	-	-	8/26/62/62	0/5/5/5
4	9ON	B	504	2	-	4/9/9/9	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	503	NAD	O4D-C1D	2.33	1.44	1.41
3	B	503	NAD	C5A-C4A	2.32	1.47	1.40
3	A	503	NAD	C5A-C4A	2.29	1.47	1.40
3	B	503	NAD	C2A-N3A	2.24	1.35	1.32
3	C	503	NAD	C5A-C4A	2.16	1.46	1.40
3	D	503	NAD	O4D-C1D	2.13	1.44	1.41
3	D	503	NAD	C2A-N3A	2.02	1.35	1.32

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	NAD	N3A-C2A-N1A	-3.85	122.66	128.68
3	B	503	NAD	N3A-C2A-N1A	-3.85	122.67	128.68
3	C	503	NAD	N3A-C2A-N1A	-3.47	123.25	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	503	NAD	N3A-C2A-N1A	-3.30	123.53	128.68
3	C	503	NAD	C4A-C5A-N7A	-2.73	106.55	109.40
3	D	503	NAD	C4A-C5A-N7A	-2.65	106.64	109.40
3	C	503	NAD	C3N-C7N-N7N	2.62	120.89	117.75
3	A	503	NAD	C1B-N9A-C4A	-2.61	122.05	126.64
3	A	503	NAD	C6N-N1N-C2N	-2.57	119.63	121.97
3	A	503	NAD	C5N-C4N-C3N	-2.57	117.31	120.34
3	A	503	NAD	C3N-C2N-N1N	2.56	122.93	120.43
3	D	503	NAD	C6N-N1N-C2N	-2.43	119.76	121.97
3	D	503	NAD	O4D-C1D-C2D	-2.37	103.46	106.93
3	A	503	NAD	O2N-PN-O1N	2.34	123.79	112.24
3	D	503	NAD	C3N-C7N-N7N	2.33	120.54	117.75
3	B	503	NAD	C1B-N9A-C4A	-2.29	122.63	126.64
3	A	503	NAD	O2A-PA-O1A	2.27	123.48	112.24
3	B	503	NAD	C3N-C7N-N7N	2.23	120.43	117.75
3	D	503	NAD	C3N-C2N-N1N	2.22	122.59	120.43
3	D	503	NAD	C1B-N9A-C4A	-2.20	122.77	126.64
3	C	503	NAD	C1B-N9A-C4A	-2.18	122.81	126.64
3	D	503	NAD	O7N-C7N-N7N	-2.12	119.57	122.58
3	C	503	NAD	C6N-N1N-C2N	-2.09	120.07	121.97
3	A	503	NAD	C2A-N1A-C6A	2.07	122.29	118.75
3	C	503	NAD	PN-O3-PA	-2.06	125.77	132.83
3	A	503	NAD	C4A-C5A-N7A	-2.05	107.26	109.40
3	A	503	NAD	C3N-C7N-N7N	2.02	120.17	117.75

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	NAD	O4D-C1D-N1N-C2N
3	A	503	NAD	O4D-C1D-N1N-C6N
3	A	503	NAD	C2D-C1D-N1N-C2N
3	A	503	NAD	C2D-C1D-N1N-C6N
3	B	503	NAD	O4D-C1D-N1N-C2N
3	B	503	NAD	O4D-C1D-N1N-C6N
3	B	503	NAD	C2D-C1D-N1N-C2N
3	C	503	NAD	O4D-C1D-N1N-C2N
3	C	503	NAD	O4D-C1D-N1N-C6N
3	C	503	NAD	C2D-C1D-N1N-C2N
3	C	503	NAD	C2D-C1D-N1N-C6N
3	D	503	NAD	O4D-C1D-N1N-C2N
3	D	503	NAD	O4D-C1D-N1N-C6N

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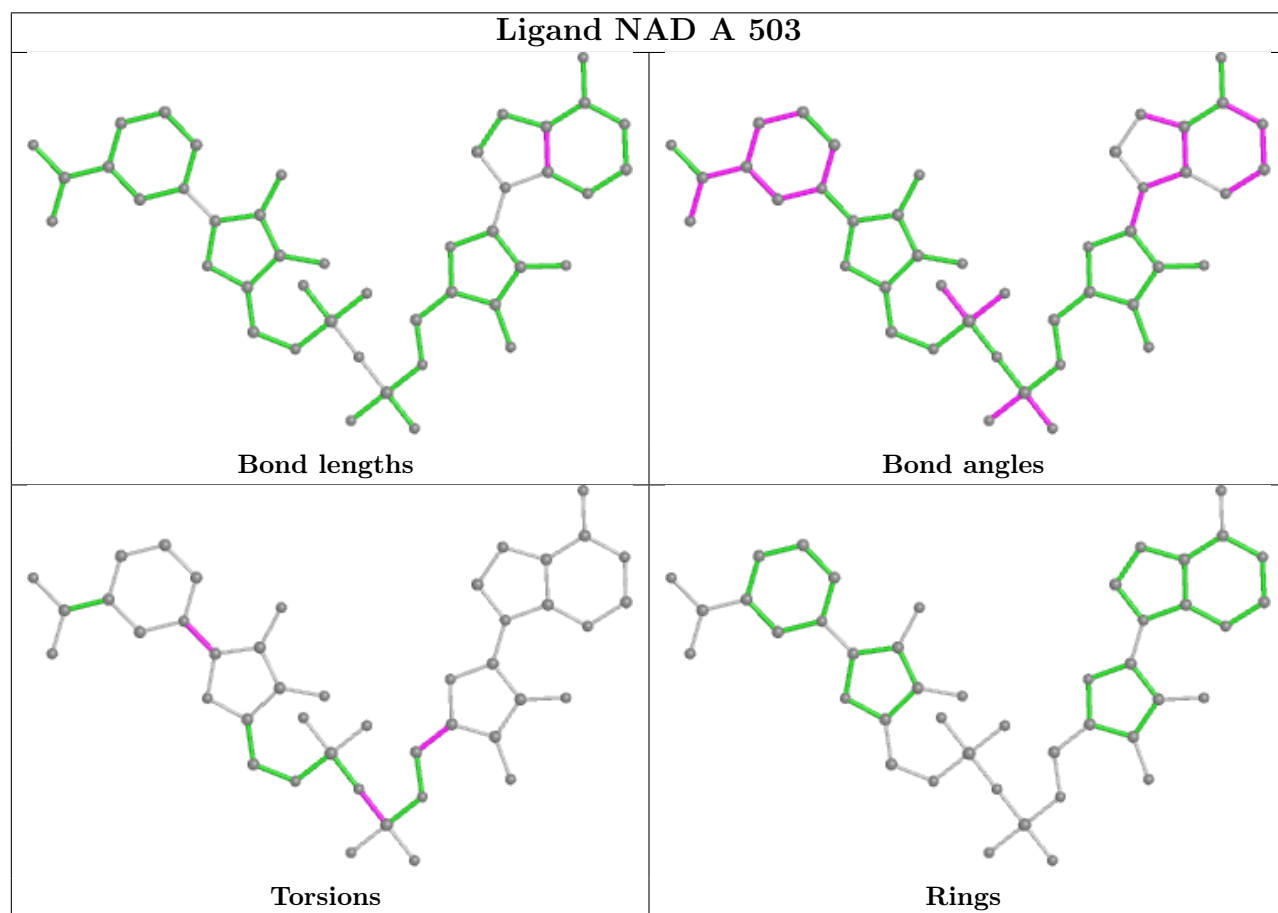
Mol	Chain	Res	Type	Atoms
3	D	503	NAD	C2D-C1D-N1N-C2N
3	D	503	NAD	C2D-C1D-N1N-C6N
3	A	503	NAD	O4B-C4B-C5B-O5B
3	B	503	NAD	O4B-C4B-C5B-O5B
3	A	503	NAD	C3B-C4B-C5B-O5B
3	D	503	NAD	O4B-C4B-C5B-O5B
3	B	503	NAD	C3B-C4B-C5B-O5B
3	C	503	NAD	O4B-C4B-C5B-O5B
3	A	503	NAD	PN-O3-PA-O1A
3	C	503	NAD	PN-O3-PA-O1A
4	A	504	9ON	C3-C4-C7-O12
4	B	504	9ON	C2-C3-C4-C5
4	B	504	9ON	C2-C3-C4-C7
3	D	503	NAD	C3B-C4B-C5B-O5B
3	A	503	NAD	PN-O3-PA-O2A
3	B	503	NAD	PN-O3-PA-O1A
3	B	503	NAD	PN-O3-PA-O2A
3	C	503	NAD	PN-O3-PA-O2A
3	D	503	NAD	PN-O3-PA-O1A
3	C	503	NAD	C3B-C4B-C5B-O5B
4	A	504	9ON	O9-C1-C2-C3
4	A	504	9ON	O8-C1-C2-C3
4	B	504	9ON	O8-C1-C2-C3
4	B	504	9ON	O9-C1-C2-C3
4	D	504	9ON	O9-C1-C2-C3
4	D	504	9ON	O8-C1-C2-C3
4	A	504	9ON	C3-C4-C7-O10
3	B	503	NAD	C2D-C1D-N1N-C6N
3	D	503	NAD	PN-O3-PA-O2A

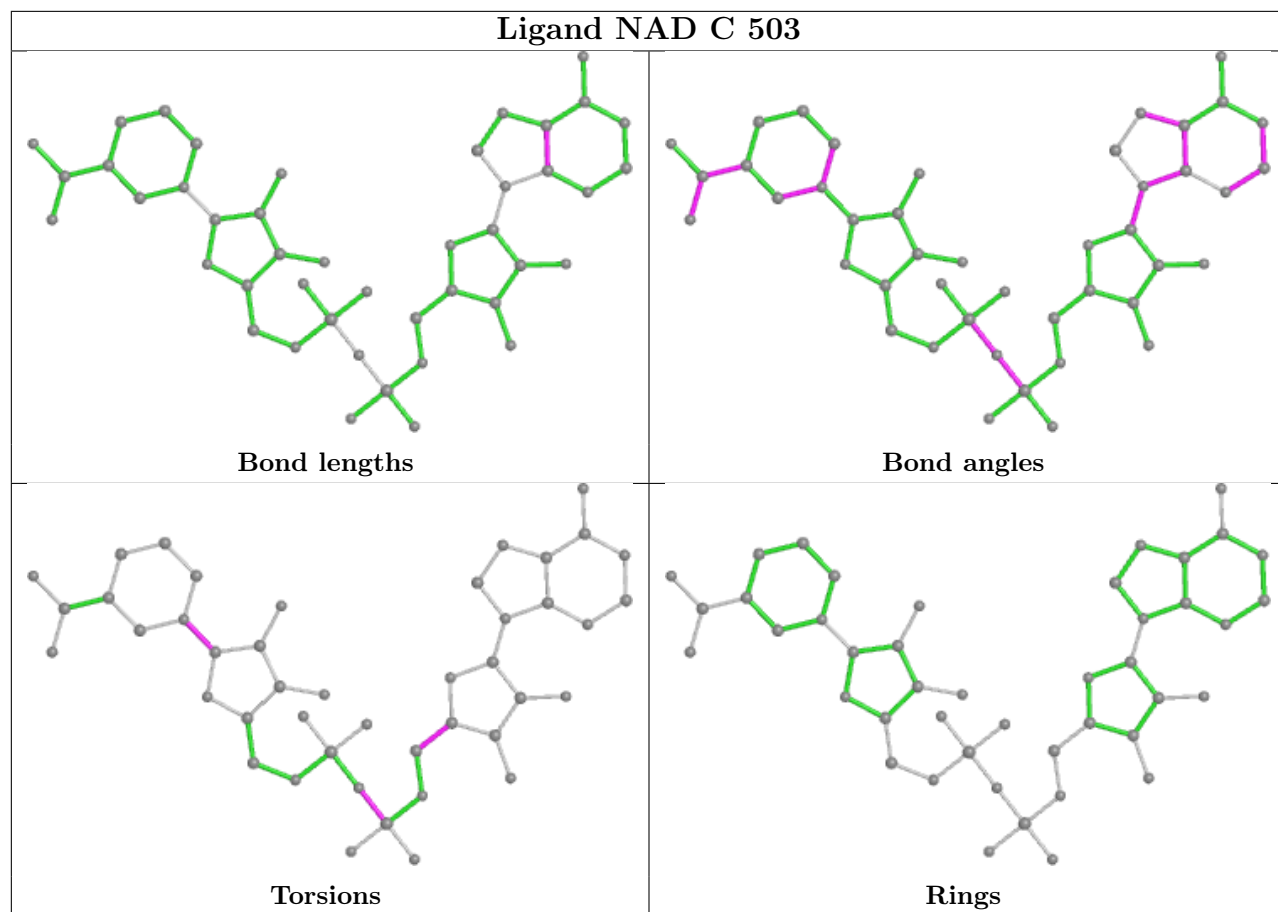
There are no ring outliers.

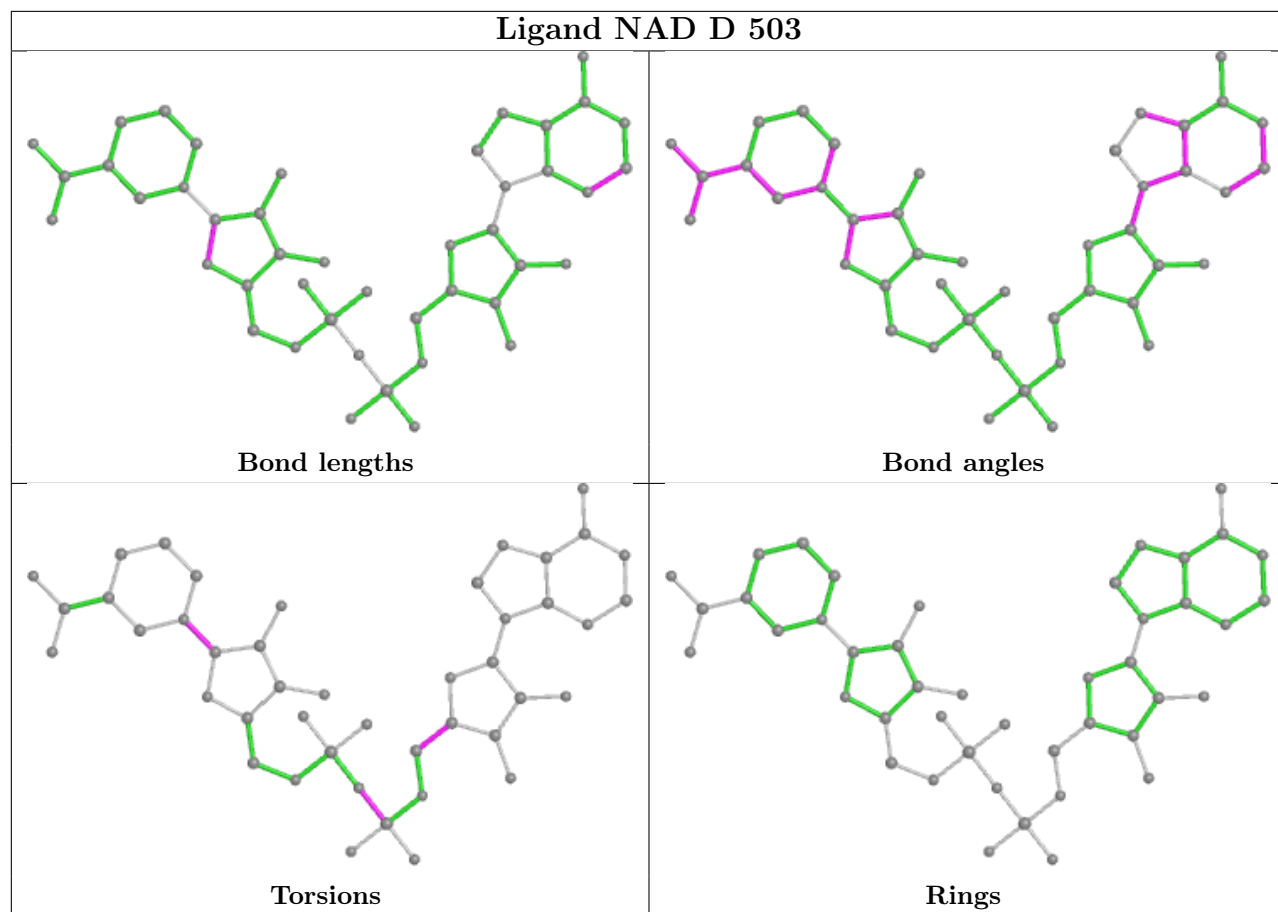
No monomer is involved in short contacts.

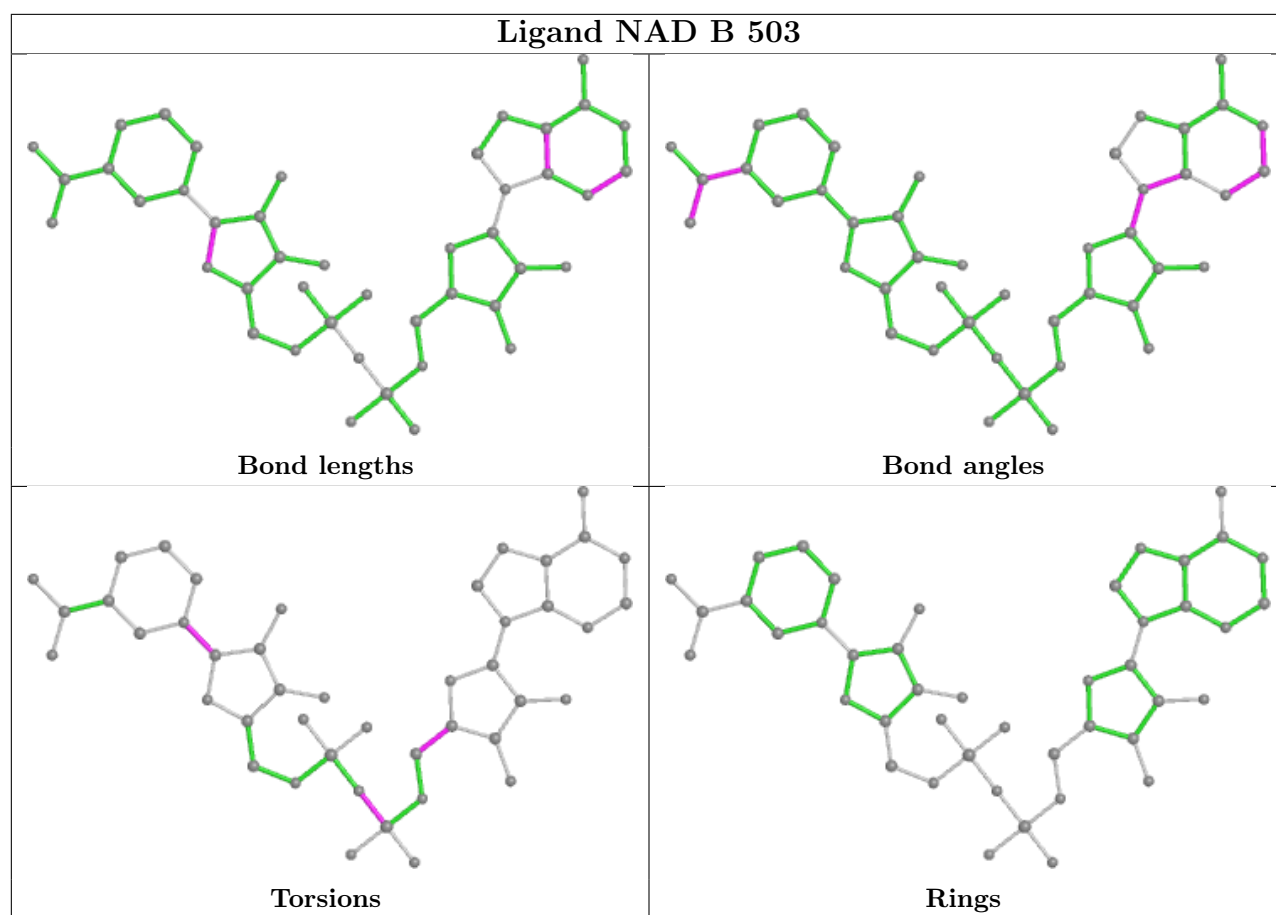
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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](#)

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	346/352 (98%)	-0.03	7 (2%) 65 65	13, 20, 35, 48	0
1	B	346/352 (98%)	-0.09	5 (1%) 75 76	13, 20, 34, 49	0
1	C	345/352 (98%)	1.38	109 (31%) 0 0	14, 30, 59, 79	0
1	D	346/352 (98%)	0.33	16 (4%) 32 30	14, 25, 44, 55	0
All	All	1383/1408 (98%)	0.40	137 (9%) 7 6	13, 22, 49, 79	0

All (137) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	75	VAL	10.1
1	C	344	VAL	9.1
1	C	50	ALA	7.6
1	C	58	LEU	7.3
1	C	48	PRO	7.1
1	C	80	VAL	7.1
1	D	76	THR	7.0
1	C	23	PRO	6.6
1	C	9	ILE	6.5
1	D	346	THR	6.3
1	C	51	GLN	6.1
1	C	56	LEU	6.0
1	C	321	THR	5.9
1	C	128	TYR	5.8
1	C	71	LEU	5.8
1	C	18	ILE	5.7
1	C	11	SER	5.6
1	C	320	PHE	5.5
1	C	53	ALA	5.5
1	C	22	THR	5.5
1	C	78	PHE	5.4

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Mol	Chain	Res	Type	RSRZ
1	C	337	ILE	5.4
1	C	76	THR	5.3
1	C	47	MET	5.3
1	C	38[A]	CYS	5.2
1	C	334	GLU	5.2
1	A	50	ALA	4.9
1	C	25	PRO	4.8
1	C	10	GLY	4.8
1	C	42	ILE	4.6
1	C	57	PRO	4.6
1	C	24	GLY	4.6
1	A	346	THR	4.6
1	C	73	GLU	4.5
1	C	4	VAL	4.5
1	B	282	PHE	4.5
1	C	333	ARG	4.4
1	C	69	ALA	4.4
1	C	60	LEU	4.2
1	B	346	THR	4.1
1	D	50	ALA	4.1
1	C	49	ALA	4.0
1	C	124	SER	4.0
1	C	21	PRO	4.0
1	C	37	LEU	3.9
1	C	332	LEU	3.9
1	C	315	ILE	3.9
1	C	55	GLY	3.8
1	C	3	ALA	3.8
1	C	330	ARG	3.8
1	C	19	PRO	3.8
1	C	43	SER	3.7
1	C	125	MET	3.7
1	C	32	VAL	3.7
1	C	329	TYR	3.6
1	C	28	ILE	3.6
1	C	81	GLY	3.6
1	C	52	TYR	3.6
1	C	323	ASP	3.6
1	C	34	ALA	3.6
1	C	17	ASP	3.5
1	C	54	TYR	3.5
1	A	113	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	339	GLY	3.5
1	C	336	SER	3.5
1	A	282	PHE	3.4
1	C	46	ASP	3.4
1	C	113	GLY	3.4
1	C	127	GLU	3.4
1	C	61	GLY	3.4
1	C	20	THR	3.3
1	C	1	MET	3.2
1	C	13	PRO	3.2
1	C	335	GLY	3.2
1	C	15	VAL	3.2
1	C	2	LYS	3.2
1	D	111	ASP	3.2
1	C	318	GLU	3.2
1	D	110	ALA	3.2
1	C	12	GLU	3.2
1	C	26	GLY	3.2
1	C	322	LEU	3.2
1	C	314	ASP	3.1
1	D	113	GLY	3.1
1	C	130	ILE	3.1
1	C	7	THR	3.0
1	C	29	LEU	3.0
1	C	30	LEU	3.0
1	D	53	ALA	2.9
1	B	76	THR	2.9
1	C	72	GLY	2.9
1	D	20	THR	2.9
1	C	147	ALA	2.9
1	D	107	THR	2.8
1	C	126	ALA	2.8
1	C	338	ARG	2.8
1	C	65	VAL	2.7
1	D	80	VAL	2.7
1	C	74	GLY	2.7
1	C	67	THR	2.7
1	C	146	VAL	2.6
1	C	68	VAL	2.6
1	B	111	ASP	2.6
1	C	35	ALA	2.5
1	C	129	MET	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	59	THR	2.5
1	C	319	THR	2.4
1	C	8	GLU	2.4
1	B	50	ALA	2.4
1	D	9	ILE	2.4
1	A	107	THR	2.4
1	C	317	THR	2.4
1	D	51	GLN	2.4
1	C	27	GLU	2.3
1	A	111	ASP	2.3
1	C	345	PRO	2.3
1	D	10	GLY	2.3
1	C	328	ALA	2.3
1	C	282	PHE	2.3
1	A	53	ALA	2.2
1	C	343	VAL	2.2
1	D	48	PRO	2.2
1	D	282	PHE	2.2
1	C	79	GLY	2.2
1	C	225	ALA	2.1
1	C	313	LEU	2.1
1	C	64	GLY	2.1
1	C	39	TYR	2.1
1	C	273	ALA	2.1
1	C	324	GLU	2.1
1	C	144	ASP	2.1
1	C	316	HIS	2.1
1	C	70	GLU	2.0
1	D	61	GLY	2.0
1	C	221	VAL	2.0
1	C	236	GLY	2.0
1	C	33	THR	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

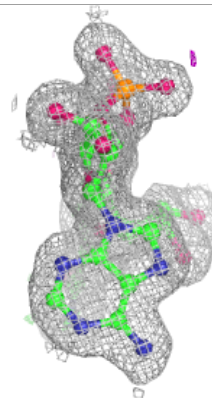
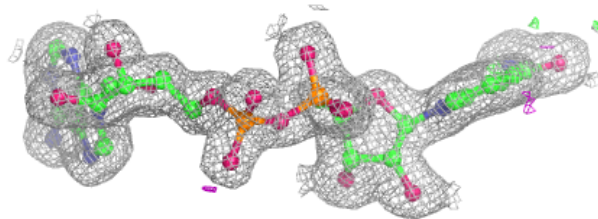
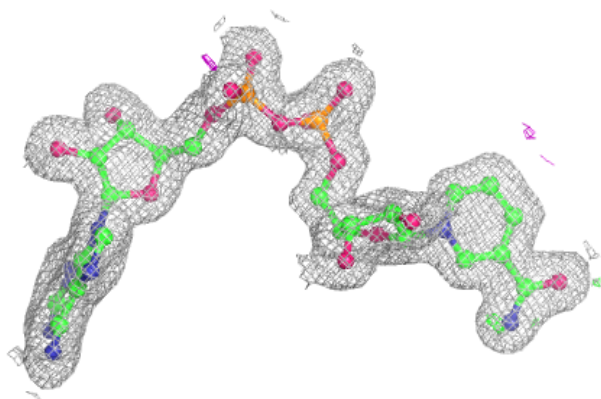
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	9ON	B	504	10/10	0.88	0.16	26,40,48,52	0
4	9ON	A	504	10/10	0.89	0.15	24,41,55,56	0
4	9ON	D	504	10/10	0.89	0.18	28,46,59,59	0
3	NAD	C	503	44/44	0.96	0.07	19,20,21,22	0
3	NAD	B	503	44/44	0.97	0.08	15,16,17,18	0
3	NAD	A	503	44/44	0.97	0.08	14,15,16,17	0
3	NAD	D	503	44/44	0.97	0.06	17,18,20,21	0
2	ZN	D	502	1/1	0.99	0.04	24,24,24,24	0
2	ZN	A	502	1/1	0.99	0.03	20,20,20,20	0
2	ZN	C	501	1/1	0.99	0.04	17,17,17,17	0
2	ZN	C	502	1/1	0.99	0.03	21,21,21,21	1
2	ZN	B	502	1/1	1.00	0.03	21,21,21,21	0
2	ZN	A	501	1/1	1.00	0.03	17,17,17,17	0
2	ZN	B	501	1/1	1.00	0.03	17,17,17,17	0
2	ZN	D	501	1/1	1.00	0.03	17,17,17,17	0

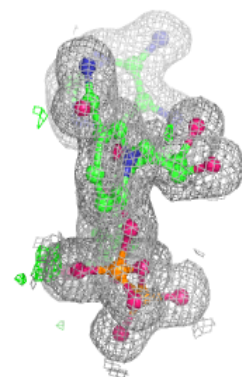
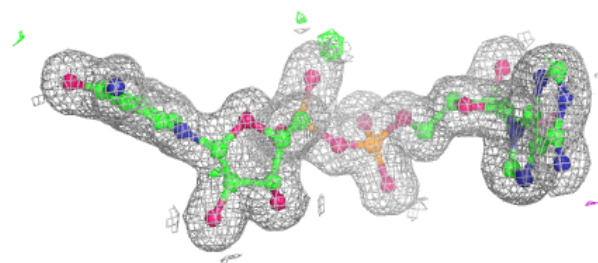
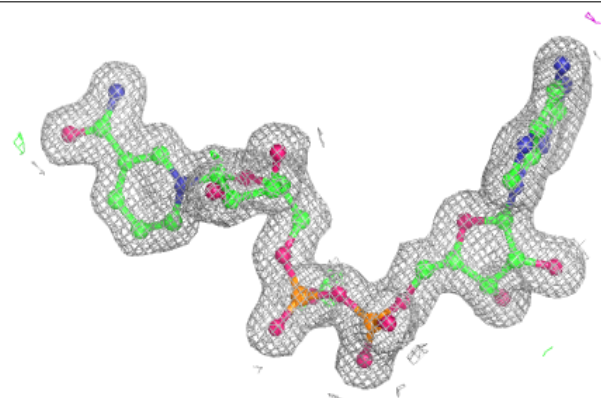
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAD C 503:

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

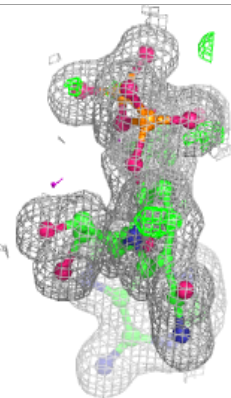
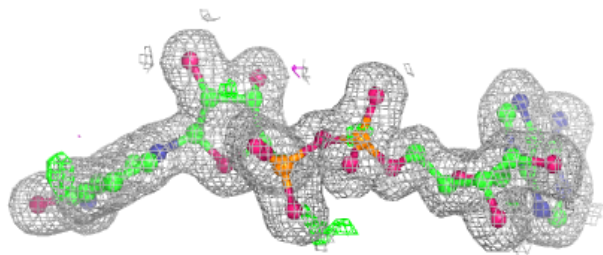
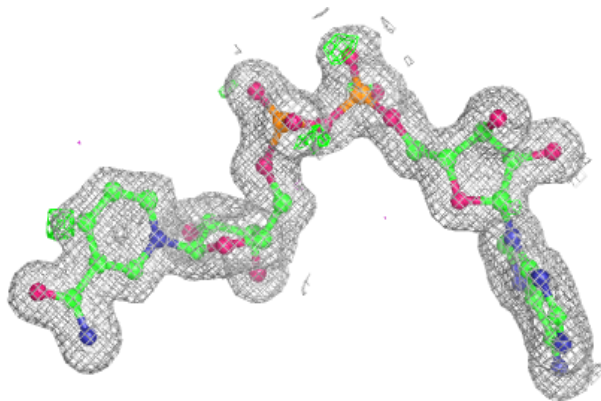
**Electron density around NAD B 503:**

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

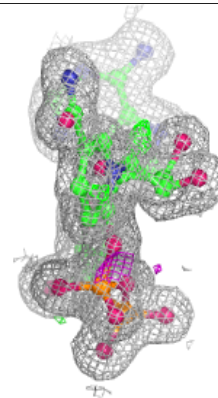
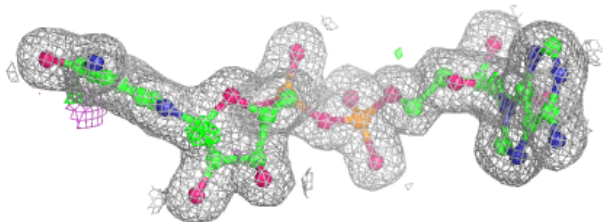
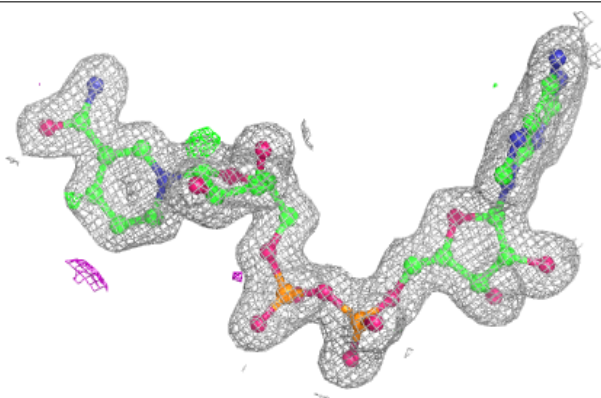


Electron density around NAD A 503:

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

**Electron density around NAD D 503:**

$2mF_o-DF_c$ (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.