



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:28 AM UTC

PDB ID : 1QG6 / pdb_00001qg6
Title : CRYSTAL STRUCTURE OF E. COLI ENOYL ACYL CARRIER PROTEIN
REDUCTASE IN COMPLEX WITH NAD AND TRICLOSAN
Authors : Rowsell, S.; Pauptit, R.A.
Deposited on : 1999-04-20
Resolution : 1.90 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

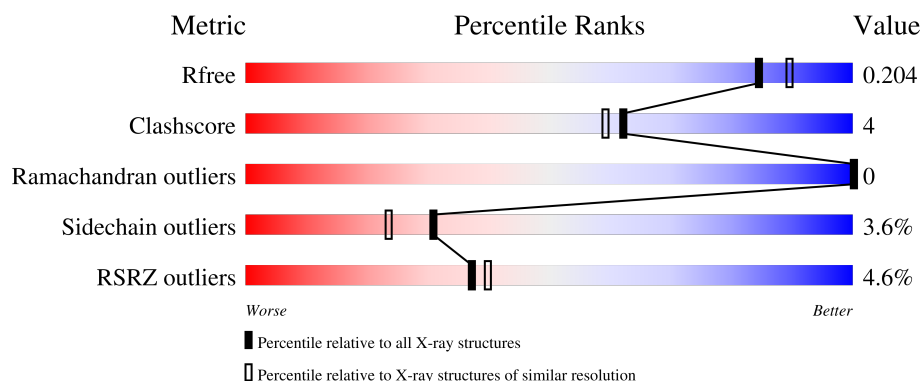
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	261	2% 89% 9% ..
1	B	261	4% 89% 9% ..
1	C	261	5% 87% 10% ..
1	D	261	7% 88% 10% ..

2 Entry composition [i](#)

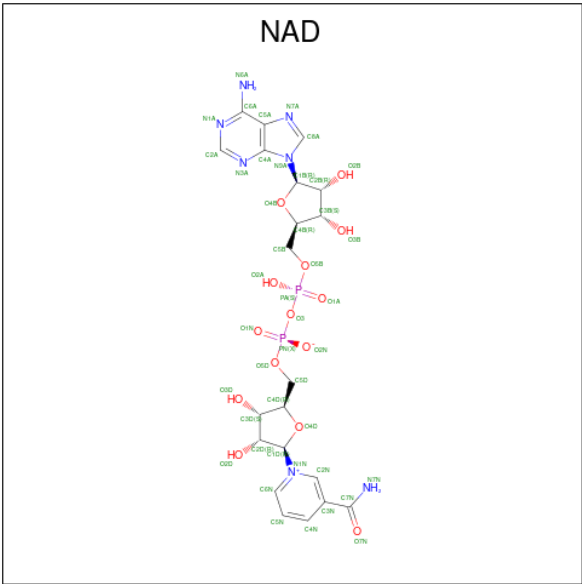
There are 4 unique types of molecules in this entry. The entry contains 8212 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (ENOYL-[ACYL-CARRIER PROTEIN] REDUCTASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			1904	1200	327	364	13			
1	B	257	Total	C	N	O	S	0	0	0
			1904	1200	327	364	13			
1	C	257	Total	C	N	O	S	0	0	0
			1904	1200	327	364	13			
1	D	257	Total	C	N	O	S	0	0	0
			1904	1200	327	364	13			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



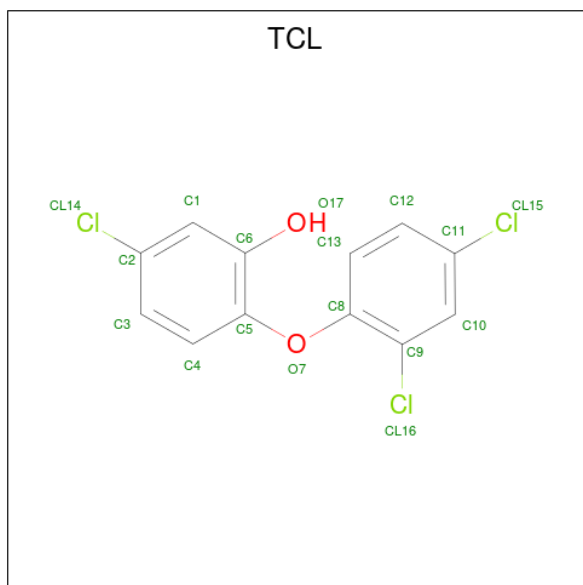
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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 TRICLOSAN (CCD ID: TCL) (formula: $C_{12}H_7Cl_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Cl	O	0	0
			17	12	3	2		
3	B	1	Total	C	Cl	O	0	0
			17	12	3	2		
3	C	1	Total	C	Cl	O	0	0
			17	12	3	2		
3	D	1	Total	C	Cl	O	0	0
			17	12	3	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	88	Total O 88 88	0	0
4	B	88	Total O 88 88	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	88	Total 88	O 88	0	0
4	D	88	Total 88	O 88	0	0

V213	R217	E243	H246	M256	N257	E258	LEU	GLU	LEU	LYS
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.16Å 80.29Å 82.75Å 90.00° 104.46° 90.00°	Depositor
Resolution (Å)	100.00 – 1.90 80.13 – 1.90	Depositor EDS
% Data completeness (in resolution range)	77.3 (100.00-1.90) 77.3 (80.13-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 1.90Å)	Xtriage
Refinement program	X-PLOR 98.1	Depositor
R, R_{free}	0.202 , 0.207 0.202 , 0.204	Depositor DCC
R_{free} test set	1717 reflections (3.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.4	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8212	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% 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: NAD, TCL

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	0.64	0/1936	0.95	6/2616 (0.2%)
1	B	0.64	0/1936	0.95	6/2616 (0.2%)
1	C	0.64	0/1936	0.95	6/2616 (0.2%)
1	D	0.64	0/1936	0.95	6/2616 (0.2%)
All	All	0.64	0/7744	0.95	24/10464 (0.2%)

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	86	ASP	N-CA-C	7.26	121.44	112.59
1	B	86	ASP	N-CA-C	7.25	121.43	112.59
1	C	86	ASP	N-CA-C	7.23	121.41	112.59
1	D	86	ASP	N-CA-C	7.22	121.40	112.59
1	B	13	GLY	N-CA-C	7.19	125.29	115.30
1	C	13	GLY	N-CA-C	7.18	125.28	115.30
1	D	13	GLY	N-CA-C	7.17	125.26	115.30
1	A	13	GLY	N-CA-C	7.16	125.26	115.30
1	A	217	ARG	N-CA-C	5.53	119.21	111.74
1	C	217	ARG	N-CA-C	5.52	119.20	111.74
1	B	217	ARG	N-CA-C	5.52	119.20	111.74
1	D	217	ARG	N-CA-C	5.52	119.19	111.74
1	B	100	LEU	N-CA-C	5.30	118.56	112.57
1	C	100	LEU	N-CA-C	5.29	118.55	112.57
1	A	100	LEU	N-CA-C	5.28	118.54	112.57
1	D	213	VAL	N-CA-C	5.26	119.16	113.43
1	C	213	VAL	N-CA-C	5.25	119.15	113.43
1	D	100	LEU	N-CA-C	5.24	118.49	112.57
1	A	213	VAL	N-CA-C	5.24	119.14	113.43
1	B	213	VAL	N-CA-C	5.23	119.13	113.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	PRO	N-CA-C	-5.19	102.95	111.21
1	D	137	PRO	N-CA-C	-5.19	102.95	111.21
1	B	137	PRO	N-CA-C	-5.18	102.97	111.21
1	C	137	PRO	N-CA-C	-5.18	102.97	111.21

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	1904	0	1887	19	0
1	B	1904	0	1887	19	0
1	C	1904	0	1887	20	1
1	D	1904	0	1887	19	1
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	C	44	0	26	0	0
2	D	44	0	26	0	0
3	A	17	0	7	0	0
3	B	17	0	7	0	0
3	C	17	0	7	0	0
3	D	17	0	7	0	0
4	A	88	0	0	1	0
4	B	88	0	0	1	0
4	C	88	0	0	1	0
4	D	88	0	0	1	0
All	All	8212	0	7680	63	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (63) 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:114:LYS:HD3	1:B:114:LYS:HD3	1.12	1.11
1:C:114:LYS:HD3	1:D:114:LYS:HD3	1.10	1.07
1:B:256:MET:HE1	1:C:206:MET:HE3	1.51	0.92
1:A:206:MET:HE3	1:D:256:MET:HE1	1.53	0.90
1:B:206:MET:HE3	1:C:256:MET:HE1	1.54	0.90
1:C:114:LYS:CD	1:D:114:LYS:HD3	2.02	0.87
1:A:256:MET:HE1	1:D:206:MET:HE3	1.55	0.87
1:C:47:ARG:HH11	1:C:47:ARG:HB2	1.44	0.83
1:A:47:ARG:HH11	1:A:47:ARG:HB2	1.44	0.83
1:A:114:LYS:CD	1:B:114:LYS:HD3	2.05	0.83
1:B:47:ARG:HH11	1:B:47:ARG:HB2	1.44	0.83
1:D:47:ARG:HB2	1:D:47:ARG:HH11	1.44	0.80
1:C:114:LYS:HD3	1:D:114:LYS:CD	2.04	0.80
1:A:114:LYS:HD3	1:B:114:LYS:CD	2.05	0.77
1:D:150:GLU:OE2	1:D:246:HIS:HE1	1.70	0.74
1:C:150:GLU:OE2	1:C:246:HIS:HE1	1.70	0.74
1:A:150:GLU:OE2	1:A:246:HIS:HE1	1.70	0.72
1:B:150:GLU:OE2	1:B:246:HIS:HE1	1.70	0.72
1:D:185:ASN:HD22	1:D:243:GLU:H	1.51	0.59
1:A:185:ASN:HD22	1:A:243:GLU:H	1.51	0.58
1:C:185:ASN:HD22	1:C:243:GLU:H	1.51	0.58
1:B:38:THR:HA	1:B:61:LEU:O	2.05	0.57
1:C:38:THR:HA	1:C:61:LEU:O	2.05	0.57
1:B:185:ASN:HD22	1:B:243:GLU:H	1.51	0.57
1:C:150:GLU:OE2	1:C:246:HIS:CE1	2.57	0.57
1:D:38:THR:HA	1:D:61:LEU:O	2.05	0.57
1:A:38:THR:HA	1:A:61:LEU:O	2.05	0.56
1:B:150:GLU:OE2	1:B:246:HIS:CE1	2.57	0.54
1:B:47:ARG:HB2	1:B:47:ARG:NH1	2.21	0.54
1:D:47:ARG:HB2	1:D:47:ARG:NH1	2.21	0.54
1:D:150:GLU:OE2	1:D:246:HIS:CE1	2.57	0.53
1:A:150:GLU:OE2	1:A:246:HIS:CE1	2.57	0.53
1:C:47:ARG:HB2	1:C:47:ARG:NH1	2.21	0.52
1:A:47:ARG:HB2	1:A:47:ARG:NH1	2.21	0.51
1:A:108:VAL:O	1:B:129:LYS:HE3	2.11	0.50
1:B:185:ASN:ND2	1:B:243:GLU:H	2.10	0.50
1:A:185:ASN:ND2	1:A:243:GLU:H	2.10	0.49
1:C:185:ASN:ND2	1:C:243:GLU:H	2.10	0.48
1:D:185:ASN:ND2	1:D:243:GLU:H	2.10	0.48
1:C:108:VAL:O	1:D:129:LYS:HE3	2.13	0.47
1:A:129:LYS:HE3	1:B:108:VAL:O	2.15	0.47
1:D:193:ARG:HG2	1:D:193:ARG:NH1	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:ARG:HG2	1:A:193:ARG:HH11	1.80	0.47
1:D:193:ARG:HG2	1:D:193:ARG:HH11	1.80	0.47
1:B:256:MET:HA	1:B:258:GLU:OE2	2.15	0.47
1:C:193:ARG:HG2	1:C:193:ARG:NH1	2.30	0.47
1:D:256:MET:HA	1:D:258:GLU:OE2	2.15	0.46
1:C:193:ARG:HG2	1:C:193:ARG:HH11	1.80	0.46
1:A:256:MET:HA	1:A:258:GLU:OE2	2.15	0.46
1:A:193:ARG:HG2	1:A:193:ARG:NH1	2.30	0.46
1:B:193:ARG:HG2	1:B:193:ARG:HH11	1.80	0.46
1:B:193:ARG:HG2	1:B:193:ARG:NH1	2.30	0.45
1:A:114:LYS:HE3	1:A:114:LYS:HB2	1.55	0.45
1:C:256:MET:HA	1:C:258:GLU:OE2	2.15	0.45
1:B:114:LYS:HE3	1:B:114:LYS:HB2	1.54	0.45
1:C:129:LYS:HE3	1:D:108:VAL:O	2.17	0.44
1:C:114:LYS:HE3	1:C:114:LYS:HB2	1.55	0.43
1:C:257:ASN:HB2	4:C:651:HOH:O	2.18	0.42
1:D:257:ASN:HB2	4:D:655:HOH:O	2.18	0.42
1:A:257:ASN:HB2	4:A:645:HOH:O	2.19	0.42
1:B:257:ASN:HB2	4:B:649:HOH:O	2.19	0.42
1:C:122:TYR:CE2	1:C:126:ALA:HB2	2.56	0.40
1:D:122:TYR:CE2	1:D:126:ALA:HB2	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:ARG:O	1:D:43:LYS:NZ[2_645]	2.19	0.01

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	255/261 (98%)	249 (98%)	6 (2%)	0	100	100
1	B	255/261 (98%)	249 (98%)	6 (2%)	0	100	100
1	C	255/261 (98%)	249 (98%)	6 (2%)	0	100	100
1	D	255/261 (98%)	249 (98%)	6 (2%)	0	100	100
All	All	1020/1044 (98%)	996 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	195/200 (98%)	188 (96%)	7 (4%)	31	23
1	B	195/200 (98%)	188 (96%)	7 (4%)	31	23
1	C	195/200 (98%)	188 (96%)	7 (4%)	31	23
1	D	195/200 (98%)	188 (96%)	7 (4%)	31	23
All	All	780/800 (98%)	752 (96%)	28 (4%)	31	23

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	A	43	LYS
1	A	47	ARG
1	A	49	GLU
1	A	62	GLN
1	A	201	LYS
1	A	257	ASN
1	B	17	LYS
1	B	43	LYS
1	B	47	ARG
1	B	49	GLU
1	B	62	GLN
1	B	201	LYS

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Mol	Chain	Res	Type
1	B	257	ASN
1	C	17	LYS
1	C	43	LYS
1	C	47	ARG
1	C	49	GLU
1	C	62	GLN
1	C	201	LYS
1	C	257	ASN
1	D	17	LYS
1	D	43	LYS
1	D	47	ARG
1	D	49	GLU
1	D	62	GLN
1	D	201	LYS
1	D	257	ASN

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	26	GLN
1	A	62	GLN
1	A	175	ASN
1	A	185	ASN
1	A	246	HIS
1	A	257	ASN
1	B	26	GLN
1	B	62	GLN
1	B	175	ASN
1	B	185	ASN
1	B	246	HIS
1	B	257	ASN
1	C	26	GLN
1	C	62	GLN
1	C	175	ASN
1	C	185	ASN
1	C	246	HIS
1	C	257	ASN
1	D	26	GLN
1	D	62	GLN
1	D	175	ASN
1	D	185	ASN
1	D	246	HIS

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Mol	Chain	Res	Type
1	D	257	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAD	D	504	-	46,48,48	2.31	18 (39%)	64,73,73	2.26	23 (35%)
2	NAD	B	502	-	46,48,48	2.31	18 (39%)	64,73,73	2.25	23 (35%)
3	TCL	B	602	-	18,18,18	0.71	0	25,25,25	0.46	0
2	NAD	C	503	-	46,48,48	2.32	18 (39%)	64,73,73	2.25	23 (35%)
3	TCL	D	604	-	18,18,18	0.72	0	25,25,25	0.47	0
3	TCL	C	603	-	18,18,18	0.71	0	25,25,25	0.47	0
2	NAD	A	501	-	46,48,48	2.32	18 (39%)	64,73,73	2.26	23 (35%)
3	TCL	A	601	-	18,18,18	0.72	0	25,25,25	0.47	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	D	504	-	-	8/30/62/62	0/5/5/5
2	NAD	B	502	-	-	8/30/62/62	0/5/5/5
3	TCL	B	602	-	-	0/4/4/4	0/2/2/2
2	NAD	C	503	-	-	8/30/62/62	0/5/5/5
3	TCL	D	604	-	-	0/4/4/4	0/2/2/2
3	TCL	C	603	-	-	0/4/4/4	0/2/2/2
2	NAD	A	501	-	-	8/30/62/62	0/5/5/5
3	TCL	A	601	-	-	0/4/4/4	0/2/2/2

All (72) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	503	NAD	C2N-N1N	5.85	1.41	1.35
2	D	504	NAD	C2N-N1N	5.82	1.41	1.35
2	A	501	NAD	C2N-N1N	5.80	1.41	1.35
2	B	502	NAD	C2N-N1N	5.76	1.41	1.35
2	A	501	NAD	C3N-C7N	5.54	1.58	1.50
2	C	503	NAD	C3N-C7N	5.53	1.58	1.50
2	D	504	NAD	C3N-C7N	5.51	1.58	1.50
2	B	502	NAD	C3N-C7N	5.50	1.58	1.50
2	A	501	NAD	C2A-N3A	4.77	1.42	1.33
2	B	502	NAD	C2A-N3A	4.76	1.42	1.33
2	C	503	NAD	C2A-N3A	4.76	1.42	1.33
2	D	504	NAD	C2A-N3A	4.71	1.42	1.33
2	C	503	NAD	O4D-C4D	4.08	1.54	1.45
2	D	504	NAD	O4D-C4D	4.07	1.54	1.45
2	B	502	NAD	O4D-C4D	4.07	1.54	1.45
2	A	501	NAD	O4D-C4D	4.06	1.54	1.45
2	D	504	NAD	C3D-C4D	3.41	1.61	1.53
2	B	502	NAD	C3D-C4D	3.40	1.61	1.53
2	A	501	NAD	C3D-C4D	3.39	1.61	1.53
2	C	503	NAD	C3D-C4D	3.38	1.61	1.53
2	D	504	NAD	O3B-C3B	3.32	1.51	1.43
2	B	502	NAD	O3B-C3B	3.31	1.51	1.43
2	A	501	NAD	O3B-C3B	3.31	1.51	1.43
2	C	503	NAD	O3B-C3B	3.30	1.51	1.43
2	B	502	NAD	C5A-C6A	3.25	1.50	1.41
2	C	503	NAD	C5A-C6A	3.25	1.50	1.41
2	A	501	NAD	C5A-C6A	3.24	1.50	1.41
2	D	504	NAD	C5A-C6A	3.22	1.50	1.41
2	D	504	NAD	O4B-C4B	3.13	1.52	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	503	NAD	O4B-C4B	3.13	1.51	1.45
2	A	501	NAD	O4B-C4B	3.12	1.51	1.45
2	B	502	NAD	O4B-C4B	3.12	1.51	1.45
2	C	503	NAD	C3B-C4B	3.11	1.60	1.53
2	A	501	NAD	C3B-C4B	3.11	1.60	1.53
2	B	502	NAD	C3B-C4B	3.09	1.60	1.53
2	D	504	NAD	C3B-C4B	3.08	1.60	1.53
2	C	503	NAD	C2N-C3N	3.07	1.43	1.39
2	B	502	NAD	C2N-C3N	3.03	1.43	1.39
2	A	501	NAD	C2N-C3N	3.01	1.43	1.39
2	D	504	NAD	C2N-C3N	3.00	1.43	1.39
2	C	503	NAD	C5A-N7A	-2.98	1.33	1.39
2	B	502	NAD	C5A-N7A	-2.96	1.33	1.39
2	A	501	NAD	C5A-N7A	-2.95	1.33	1.39
2	D	504	NAD	C5A-N7A	-2.95	1.33	1.39
2	A	501	NAD	PA-O3	-2.92	1.56	1.59
2	B	502	NAD	PA-O3	-2.92	1.56	1.59
2	D	504	NAD	PA-O3	-2.90	1.56	1.59
2	C	503	NAD	PA-O3	-2.88	1.56	1.59
2	D	504	NAD	C5N-C4N	2.87	1.43	1.38
2	B	502	NAD	C5N-C4N	2.84	1.43	1.38
2	A	501	NAD	C5N-C4N	2.82	1.43	1.38
2	C	503	NAD	C5N-C4N	2.79	1.43	1.38
2	C	503	NAD	C5B-C4B	-2.79	1.43	1.51
2	A	501	NAD	C5B-C4B	-2.77	1.43	1.51
2	B	502	NAD	C5B-C4B	-2.76	1.43	1.51
2	D	504	NAD	C5B-C4B	-2.75	1.43	1.51
2	D	504	NAD	C4A-N3A	2.57	1.39	1.34
2	B	502	NAD	C4A-N3A	2.56	1.39	1.34
2	A	501	NAD	C4A-N3A	2.55	1.39	1.34
2	C	503	NAD	C4A-N3A	2.51	1.39	1.34
2	B	502	NAD	O3D-C3D	-2.45	1.36	1.43
2	D	504	NAD	O3D-C3D	-2.44	1.36	1.43
2	A	501	NAD	O3D-C3D	-2.43	1.36	1.43
2	C	503	NAD	O3D-C3D	-2.42	1.37	1.43
2	A	501	NAD	C6A-N6A	-2.21	1.28	1.34
2	B	502	NAD	C6A-N6A	-2.20	1.28	1.34
2	D	504	NAD	C6A-N6A	-2.19	1.28	1.34
2	C	503	NAD	C6A-N6A	-2.18	1.28	1.34
2	D	504	NAD	C2B-C1B	2.17	1.60	1.53
2	A	501	NAD	C2B-C1B	2.15	1.60	1.53
2	B	502	NAD	C2B-C1B	2.14	1.60	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	503	NAD	C2B-C1B	2.13	1.60	1.53

All (92) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	504	NAD	C2N-C3N-C4N	7.52	127.00	118.26
2	A	501	NAD	C2N-C3N-C4N	7.49	126.97	118.26
2	C	503	NAD	C2N-C3N-C4N	7.49	126.97	118.26
2	B	502	NAD	C2N-C3N-C4N	7.46	126.94	118.26
2	D	504	NAD	C5N-C4N-C3N	-7.05	113.44	120.36
2	A	501	NAD	C5N-C4N-C3N	-6.99	113.50	120.36
2	C	503	NAD	C5N-C4N-C3N	-6.96	113.53	120.36
2	B	502	NAD	C5N-C4N-C3N	-6.95	113.53	120.36
2	D	504	NAD	C6N-N1N-C2N	4.59	125.78	121.88
2	A	501	NAD	C6N-N1N-C2N	4.58	125.77	121.88
2	B	502	NAD	C6N-N1N-C2N	4.58	125.77	121.88
2	C	503	NAD	C6N-N1N-C2N	4.56	125.75	121.88
2	A	501	NAD	C6N-N1N-C1D	-4.43	111.04	119.73
2	D	504	NAD	C6N-N1N-C1D	-4.43	111.04	119.73
2	C	503	NAD	C6N-N1N-C1D	-4.42	111.05	119.73
2	B	502	NAD	C6N-N1N-C1D	-4.42	111.05	119.73
2	B	502	NAD	C2A-N1A-C6A	4.28	125.75	118.73
2	C	503	NAD	C2A-N1A-C6A	4.27	125.75	118.73
2	A	501	NAD	C2A-N1A-C6A	4.27	125.74	118.73
2	D	504	NAD	C2A-N1A-C6A	4.25	125.71	118.73
2	D	504	NAD	C4A-N9A-C8A	-3.78	101.77	105.74
2	A	501	NAD	C4A-N9A-C8A	-3.76	101.79	105.74
2	B	502	NAD	C4A-N9A-C8A	-3.76	101.79	105.74
2	C	503	NAD	C4A-N9A-C8A	-3.72	101.83	105.74
2	C	503	NAD	N3A-C2A-N1A	-3.57	123.18	128.58
2	D	504	NAD	N3A-C2A-N1A	-3.57	123.18	128.58
2	A	501	NAD	N3A-C2A-N1A	-3.56	123.19	128.58
2	B	502	NAD	N3A-C2A-N1A	-3.55	123.21	128.58
2	B	502	NAD	C5A-C4A-N3A	-3.43	121.99	126.72
2	D	504	NAD	C5A-C4A-N3A	-3.41	122.02	126.72
2	A	501	NAD	C5A-C4A-N3A	-3.41	122.03	126.72
2	C	503	NAD	C5A-C4A-N3A	-3.38	122.06	126.72
2	B	502	NAD	O2A-PA-O1A	2.66	124.82	112.44
2	C	503	NAD	O2A-PA-O1A	2.66	124.81	112.44
2	D	504	NAD	O2A-PA-O1A	2.66	124.81	112.44
2	A	501	NAD	O2A-PA-O1A	2.65	124.77	112.44
2	B	502	NAD	O4D-C4D-C3D	-2.59	100.02	105.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	NAD	O4D-C4D-C3D	-2.58	100.04	105.15
2	D	504	NAD	O4D-C4D-C3D	-2.58	100.04	105.15
2	C	503	NAD	O4D-C4D-C3D	-2.57	100.04	105.15
2	A	501	NAD	C1B-N9A-C8A	2.53	132.72	127.09
2	D	504	NAD	C1B-N9A-C8A	2.53	132.72	127.09
2	B	502	NAD	C1B-N9A-C8A	2.53	132.72	127.09
2	B	502	NAD	O2A-PA-O3	2.53	114.11	107.27
2	A	501	NAD	O2A-PA-O3	2.53	114.10	107.27
2	C	503	NAD	C1B-N9A-C8A	2.53	132.70	127.09
2	C	503	NAD	O2A-PA-O3	2.52	114.09	107.27
2	D	504	NAD	O2A-PA-O3	2.52	114.08	107.27
2	D	504	NAD	O3-PN-O1N	-2.43	103.40	110.70
2	A	501	NAD	O3-PN-O1N	-2.42	103.43	110.70
2	B	502	NAD	O3-PN-O1N	-2.42	103.43	110.70
2	C	503	NAD	O3-PN-O1N	-2.41	103.45	110.70
2	D	504	NAD	C5A-C4A-N9A	2.36	108.38	105.81
2	B	502	NAD	C5A-C4A-N9A	2.35	108.37	105.81
2	A	501	NAD	C5A-C4A-N9A	2.33	108.35	105.81
2	C	503	NAD	C5A-C4A-N9A	2.29	108.31	105.81
2	C	503	NAD	C6N-C5N-C4N	2.27	122.73	119.45
2	C	503	NAD	C2D-C3D-C4D	2.27	107.00	102.61
2	D	504	NAD	C6N-C5N-C4N	2.26	122.71	119.45
2	A	501	NAD	C2D-C3D-C4D	2.25	106.96	102.61
2	A	501	NAD	C6N-C5N-C4N	2.25	122.69	119.45
2	B	502	NAD	C2D-C3D-C4D	2.25	106.96	102.61
2	D	504	NAD	C2D-C3D-C4D	2.24	106.94	102.61
2	B	502	NAD	C6N-C5N-C4N	2.23	122.67	119.45
2	B	502	NAD	O2N-PN-O1N	2.20	122.70	112.44
2	C	503	NAD	O2N-PN-O1N	2.20	122.69	112.44
2	A	501	NAD	O2N-PN-O1N	2.20	122.68	112.44
2	D	504	NAD	O2N-PN-O1N	2.20	122.66	112.44
2	D	504	NAD	C4B-O4B-C1B	-2.15	104.72	109.47
2	C	503	NAD	C4B-O4B-C1B	-2.14	104.73	109.47
2	A	501	NAD	C4B-O4B-C1B	-2.14	104.74	109.47
2	C	503	NAD	O2B-C2B-C1B	2.14	117.47	110.10
2	B	502	NAD	C4B-O4B-C1B	-2.14	104.75	109.47
2	A	501	NAD	O2B-C2B-C1B	2.14	117.46	110.10
2	B	502	NAD	O2B-C2B-C1B	2.13	117.45	110.10
2	D	504	NAD	O2B-C2B-C1B	2.13	117.43	110.10
2	B	502	NAD	C2B-C3B-C4B	2.10	106.68	102.61
2	D	504	NAD	C2B-C3B-C4B	2.10	106.67	102.61
2	A	501	NAD	C2B-C3B-C4B	2.10	106.66	102.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	503	NAD	C2B-C3B-C4B	2.09	106.65	102.61
2	C	503	NAD	C5A-N7A-C8A	2.07	106.70	103.45
2	C	503	NAD	O3-PA-O1A	-2.07	104.48	110.70
2	B	502	NAD	O3-PA-O1A	-2.07	104.49	110.70
2	D	504	NAD	O3-PA-O1A	-2.07	104.49	110.70
2	D	504	NAD	C5A-N7A-C8A	2.06	106.69	103.45
2	A	501	NAD	O3-PA-O1A	-2.05	104.52	110.70
2	A	501	NAD	C5A-N7A-C8A	2.05	106.67	103.45
2	B	502	NAD	C5A-N7A-C8A	2.05	106.67	103.45
2	D	504	NAD	O3D-C3D-C4D	-2.03	105.26	111.08
2	C	503	NAD	O3D-C3D-C4D	-2.02	105.28	111.08
2	A	501	NAD	O3D-C3D-C4D	-2.02	105.29	111.08
2	B	502	NAD	O3D-C3D-C4D	-2.02	105.29	111.08

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	NAD	C5D-O5D-PN-O3
2	A	501	NAD	C5D-O5D-PN-O1N
2	A	501	NAD	C5D-O5D-PN-O2N
2	A	501	NAD	O4D-C1D-N1N-C2N
2	B	502	NAD	C5D-O5D-PN-O3
2	B	502	NAD	C5D-O5D-PN-O1N
2	B	502	NAD	C5D-O5D-PN-O2N
2	B	502	NAD	O4D-C1D-N1N-C2N
2	C	503	NAD	C5D-O5D-PN-O3
2	C	503	NAD	C5D-O5D-PN-O1N
2	C	503	NAD	C5D-O5D-PN-O2N
2	C	503	NAD	O4D-C1D-N1N-C2N
2	D	504	NAD	C5D-O5D-PN-O3
2	D	504	NAD	C5D-O5D-PN-O1N
2	D	504	NAD	C5D-O5D-PN-O2N
2	D	504	NAD	O4D-C1D-N1N-C2N
2	A	501	NAD	PA-O3-PN-O1N
2	A	501	NAD	PA-O3-PN-O2N
2	B	502	NAD	PA-O3-PN-O1N
2	B	502	NAD	PA-O3-PN-O2N
2	C	503	NAD	PA-O3-PN-O1N
2	C	503	NAD	PA-O3-PN-O2N
2	D	504	NAD	PA-O3-PN-O1N
2	D	504	NAD	PA-O3-PN-O2N

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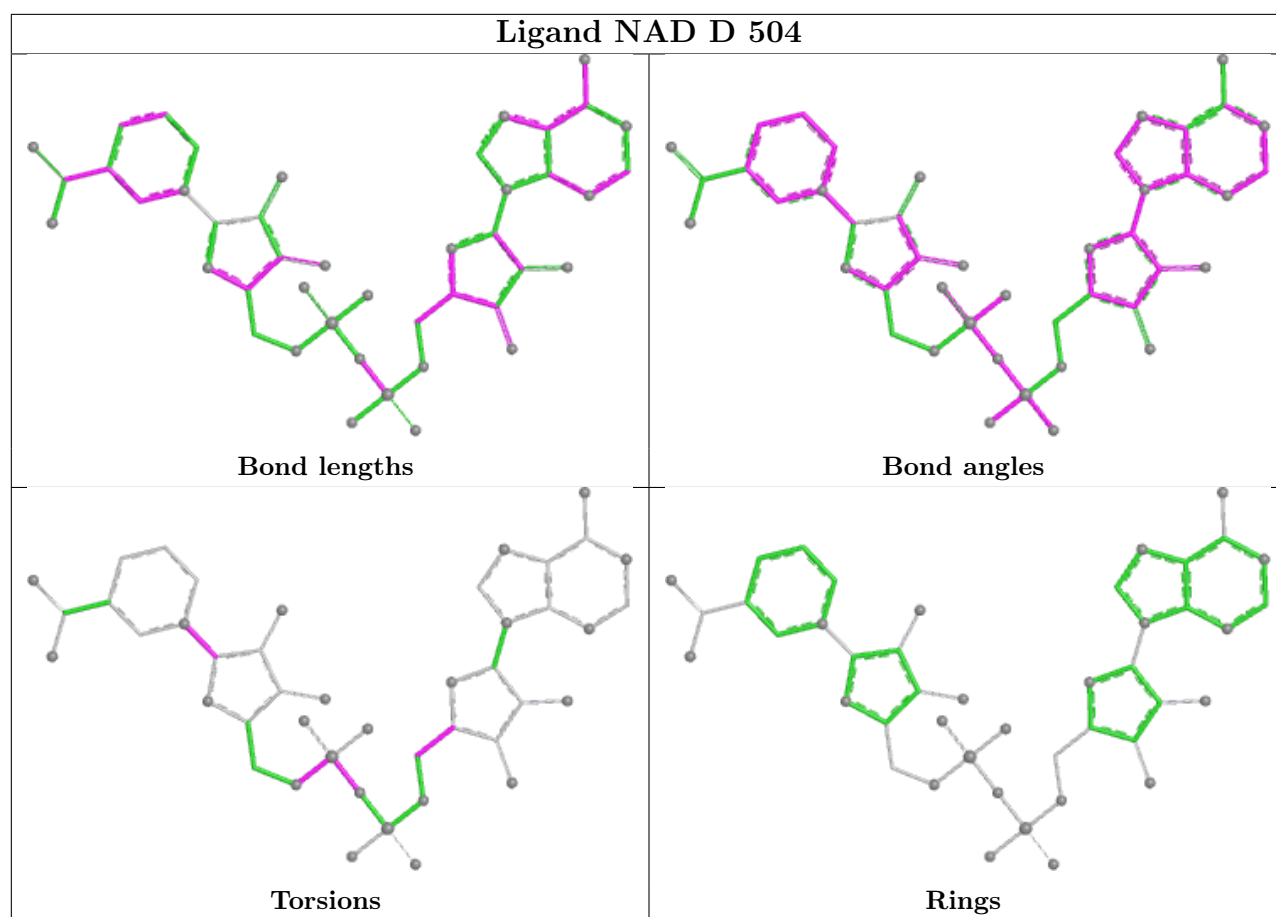
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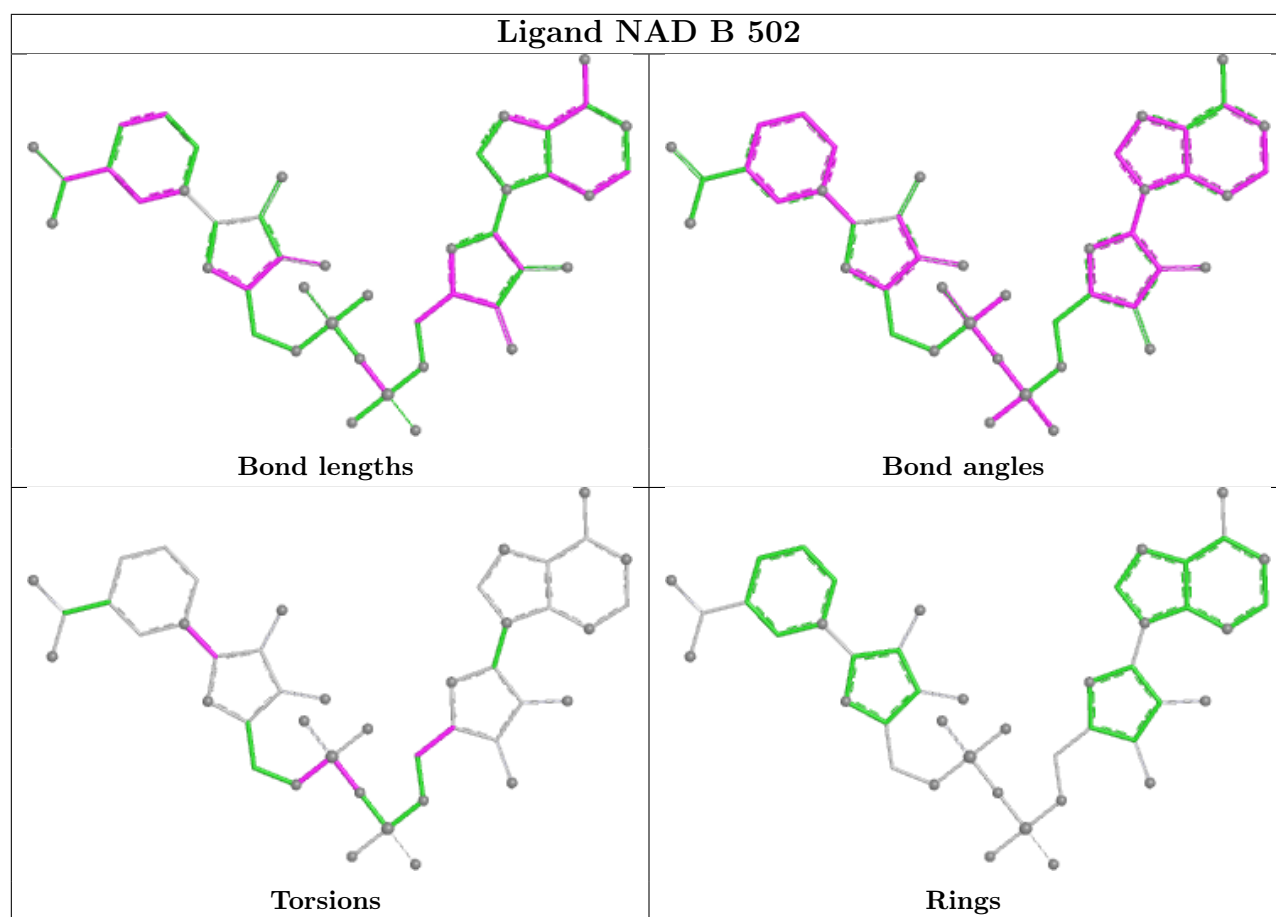
Mol	Chain	Res	Type	Atoms
2	A	501	NAD	O4D-C1D-N1N-C6N
2	B	502	NAD	O4D-C1D-N1N-C6N
2	C	503	NAD	O4D-C1D-N1N-C6N
2	D	504	NAD	O4D-C1D-N1N-C6N
2	A	501	NAD	O4B-C4B-C5B-O5B
2	B	502	NAD	O4B-C4B-C5B-O5B
2	C	503	NAD	O4B-C4B-C5B-O5B
2	D	504	NAD	O4B-C4B-C5B-O5B

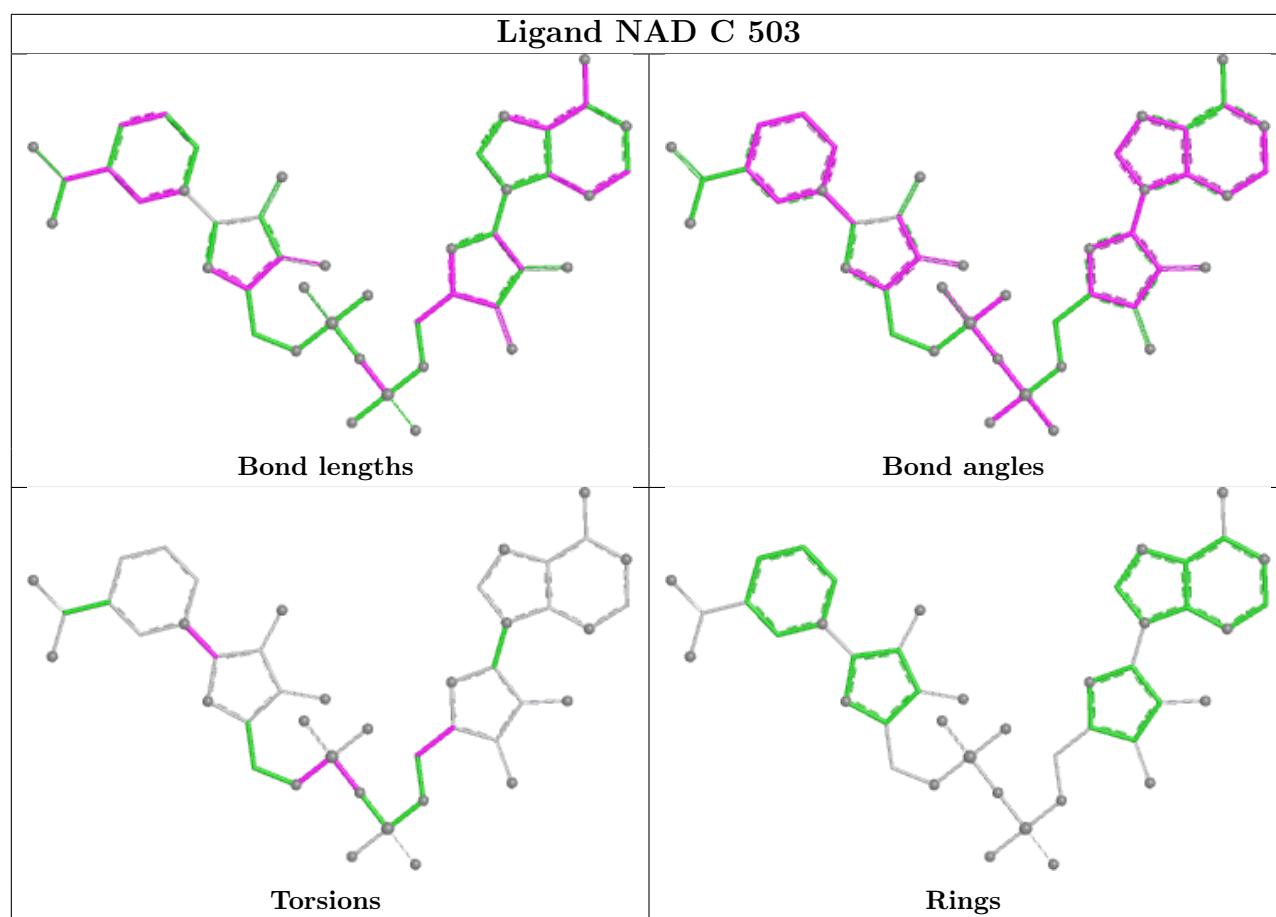
There are no ring outliers.

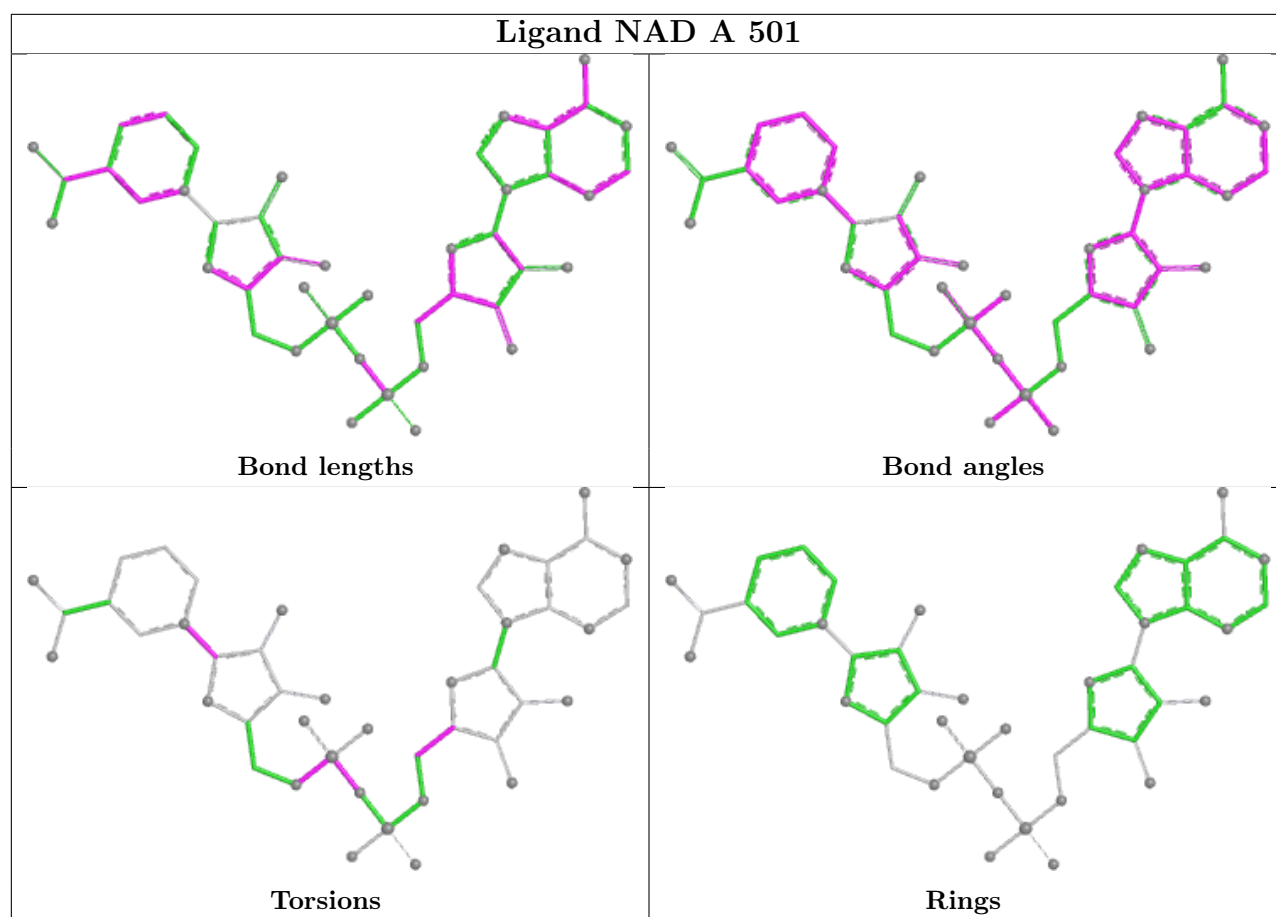
No monomer is involved in short contacts.

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	257/261 (98%)	0.41	5 (1%) 66 70	12, 23, 42, 63	0
1	B	257/261 (98%)	0.40	10 (3%) 43 46	12, 23, 42, 63	0
1	C	257/261 (98%)	0.47	14 (5%) 31 33	12, 23, 42, 63	0
1	D	257/261 (98%)	0.47	18 (7%) 22 24	12, 23, 42, 63	0
All	All	1028/1044 (98%)	0.44	47 (4%) 37 40	12, 23, 42, 63	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	43	LYS	6.7
1	D	46	GLY	5.9
1	D	44	LEU	5.8
1	B	46	GLY	4.7
1	D	47	ARG	4.5
1	C	43	LYS	3.8
1	C	46	GLY	3.7
1	D	195	LEU	3.6
1	B	81	VAL	3.5
1	C	51	PHE	3.3
1	D	45	LYS	3.2
1	C	54	GLN	3.2
1	C	44	LEU	3.2
1	D	42	ASP	3.2
1	B	198	SER	3.1
1	B	43	LYS	3.0
1	D	55	LEU	2.9
1	D	79	GLY	2.9
1	D	51	PHE	2.9
1	A	81	VAL	2.8
1	C	198	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	81	VAL	2.8
1	A	14	VAL	2.8
1	D	48	VAL	2.7
1	C	69	ALA	2.7
1	C	50	GLU	2.6
1	C	47	ARG	2.5
1	A	258	GLU	2.5
1	D	49	GLU	2.5
1	B	106	ASN	2.4
1	B	44	LEU	2.4
1	C	5	SER	2.4
1	B	210	CYS	2.4
1	D	197	ALA	2.3
1	D	210	CYS	2.3
1	D	2	GLY	2.3
1	A	66	ALA	2.2
1	D	198	SER	2.2
1	B	208	ALA	2.2
1	C	53	ALA	2.1
1	B	202	ASP	2.1
1	A	198	SER	2.1
1	D	205	LYS	2.0
1	B	112	GLY	2.0
1	D	54	GLN	2.0
1	C	76	ALA	2.0
1	C	58	ASP	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](#)

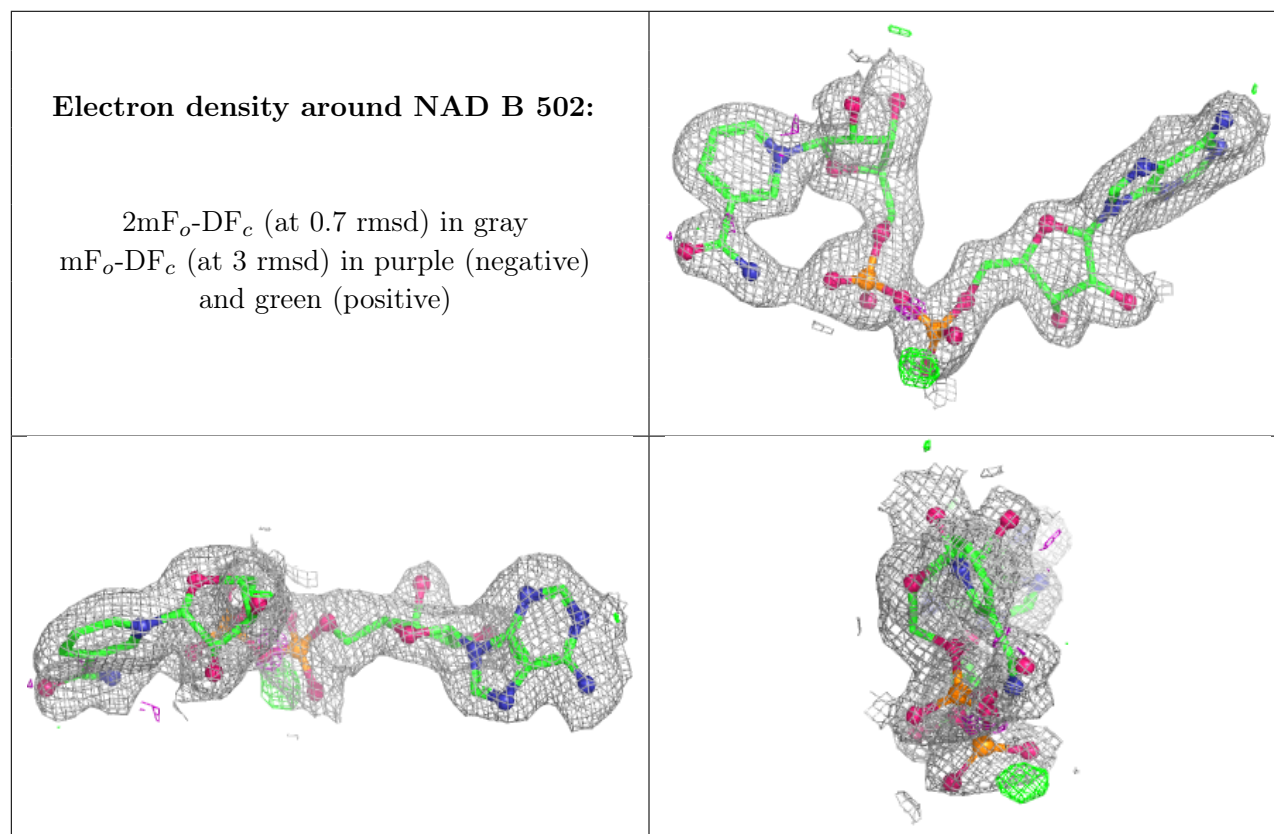
There are no oligosaccharides in this entry.

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.

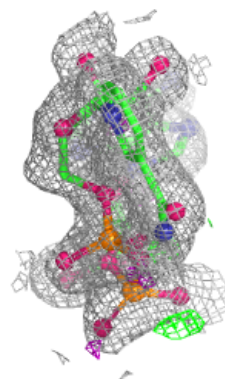
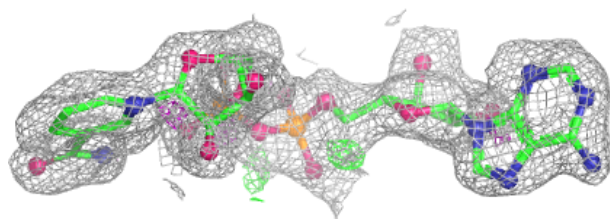
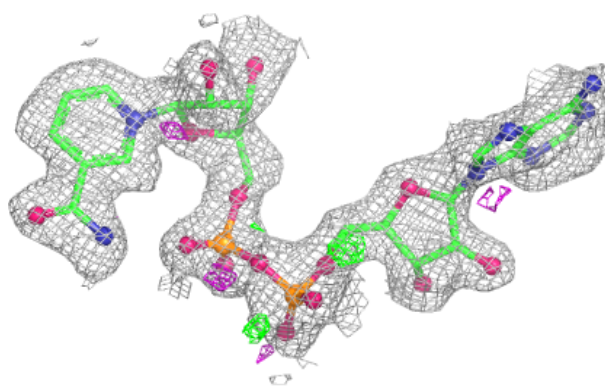
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAD	B	502	44/44	0.94	0.08	16,23,25,30	0
2	NAD	C	503	44/44	0.94	0.07	16,23,25,30	0
2	NAD	A	501	44/44	0.95	0.08	16,23,25,30	0
3	TCL	B	602	17/17	0.95	0.07	17,22,28,31	0
3	TCL	A	601	17/17	0.96	0.07	17,22,28,31	0
2	NAD	D	504	44/44	0.96	0.07	16,23,25,30	0
3	TCL	C	603	17/17	0.96	0.08	17,22,28,31	0
3	TCL	D	604	17/17	0.97	0.08	17,22,28,31	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.

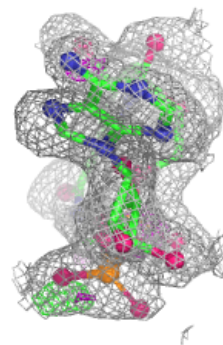
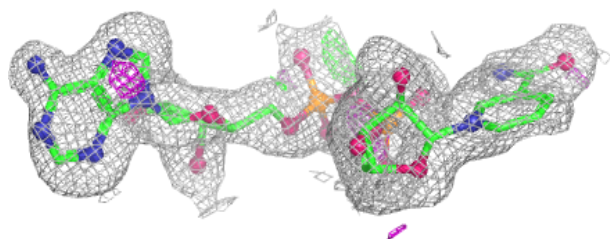
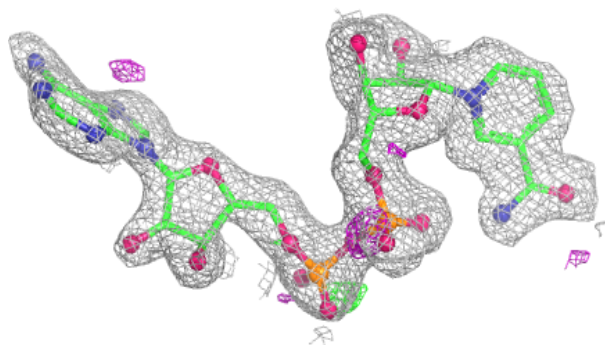


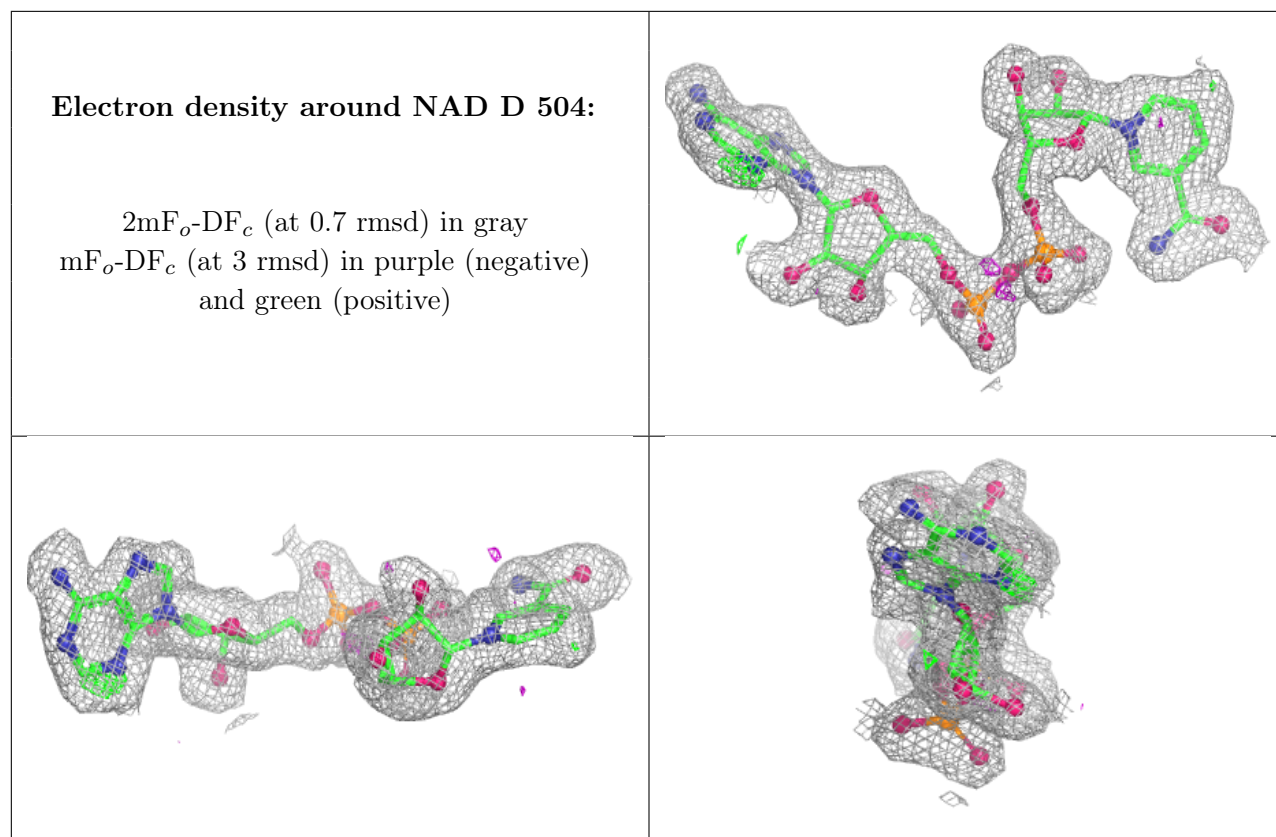
Electron density around NAD C 503:

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

**Electron density around NAD A 501:**

$2mF_o-DF_c$ (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.