



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:36 AM UTC

PDB ID : 6IXT / pdb_00006ixt
Title : Crystal structure of isocitrate dehydrogenase from *Ostreococcus tauri* in complex with NAD⁺ and Mg²⁺
Authors : Zhu, G.P.; Tang, W.G.; Wang, P.
Deposited on : 2018-12-12
Resolution : 1.78 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

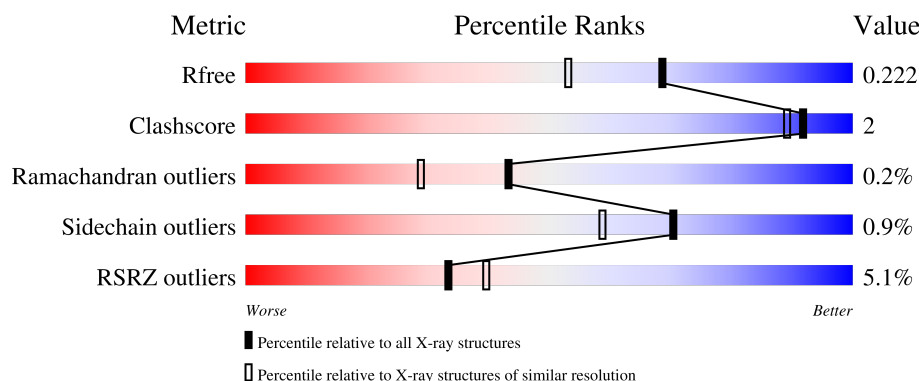
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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	418	92% 5%
1	B	418	8% 91% 6%
1	C	418	11% 93% • •
1	D	418	% 92% 5% •

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
4	GOL	D	501	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13850 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 Isocitrate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	0	0
			3153	1985	560	594	14			
1	B	405	Total	C	N	O	S	0	0	0
			3144	1980	553	597	14			
1	C	405	Total	C	N	O	S	0	0	0
			3144	1978	555	597	14			
1	D	405	Total	C	N	O	S	0	0	0
			3161	1989	560	598	14			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	GLY	-	expression tag	UNP A0A1Y5IEA9
A	13	HIS	-	expression tag	UNP A0A1Y5IEA9
A	14	HIS	-	expression tag	UNP A0A1Y5IEA9
A	15	HIS	-	expression tag	UNP A0A1Y5IEA9
A	16	HIS	-	expression tag	UNP A0A1Y5IEA9
A	17	HIS	-	expression tag	UNP A0A1Y5IEA9
A	18	HIS	-	expression tag	UNP A0A1Y5IEA9
A	19	HIS	-	expression tag	UNP A0A1Y5IEA9
B	12	GLY	-	expression tag	UNP A0A1Y5IEA9
B	13	HIS	-	expression tag	UNP A0A1Y5IEA9
B	14	HIS	-	expression tag	UNP A0A1Y5IEA9
B	15	HIS	-	expression tag	UNP A0A1Y5IEA9
B	16	HIS	-	expression tag	UNP A0A1Y5IEA9
B	17	HIS	-	expression tag	UNP A0A1Y5IEA9
B	18	HIS	-	expression tag	UNP A0A1Y5IEA9
B	19	HIS	-	expression tag	UNP A0A1Y5IEA9
C	12	GLY	-	expression tag	UNP A0A1Y5IEA9
C	13	HIS	-	expression tag	UNP A0A1Y5IEA9
C	14	HIS	-	expression tag	UNP A0A1Y5IEA9
C	15	HIS	-	expression tag	UNP A0A1Y5IEA9
C	16	HIS	-	expression tag	UNP A0A1Y5IEA9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	17	HIS	-	expression tag	UNP A0A1Y5IEA9
C	18	HIS	-	expression tag	UNP A0A1Y5IEA9
C	19	HIS	-	expression tag	UNP A0A1Y5IEA9
D	12	GLY	-	expression tag	UNP A0A1Y5IEA9
D	13	HIS	-	expression tag	UNP A0A1Y5IEA9
D	14	HIS	-	expression tag	UNP A0A1Y5IEA9
D	15	HIS	-	expression tag	UNP A0A1Y5IEA9
D	16	HIS	-	expression tag	UNP A0A1Y5IEA9
D	17	HIS	-	expression tag	UNP A0A1Y5IEA9
D	18	HIS	-	expression tag	UNP A0A1Y5IEA9
D	19	HIS	-	expression tag	UNP A0A1Y5IEA9

- # NAD

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

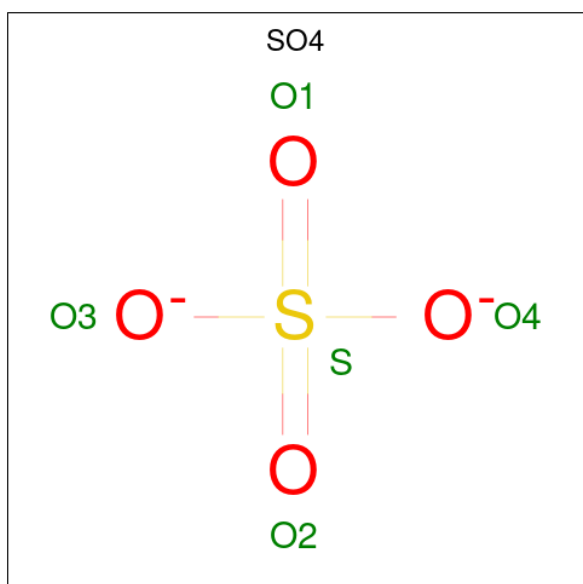


- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	335	Total O 335 335	0	0
6	B	273	Total O 273 273	0	0
6	C	254	Total O 254 254	0	0
6	D	267	Total O 267 267	0	0

3 Residue-property plots [i](#)

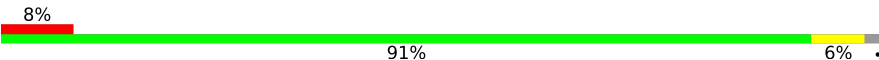
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

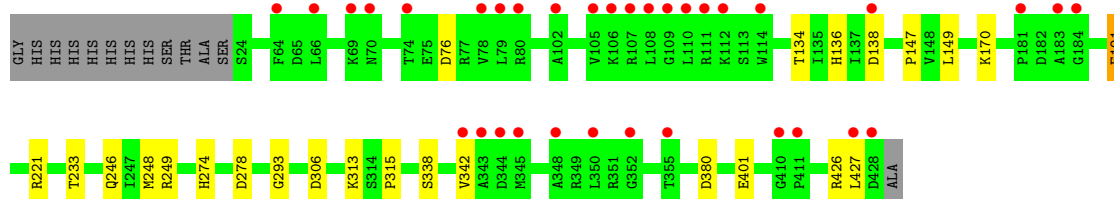
- Molecule 1: Isocitrate dehydrogenase

Chain A:  92% 5% .

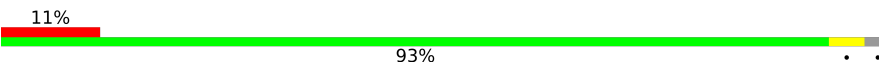


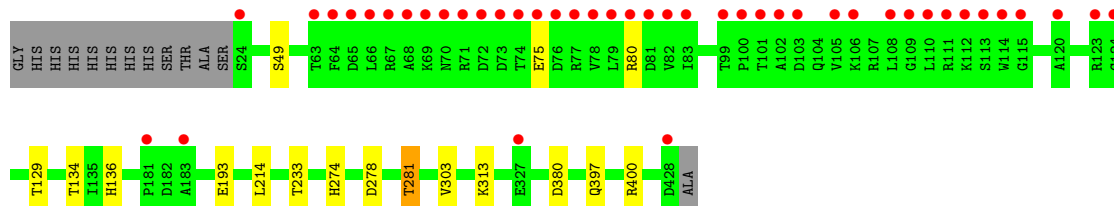
- Molecule 1: Isocitrate dehydrogenase

Chain B:  8% 91% 6% .

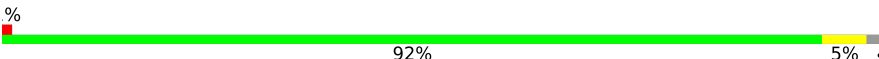


- Molecule 1: Isocitrate dehydrogenase

Chain C:  11% 93% . .



- Molecule 1: Isocitrate dehydrogenase

Chain D:  % 92% 5% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.39Å 79.18Å 112.10Å 90.27° 102.33° 112.52°	Depositor
Resolution (Å)	20.00 – 1.78 20.00 – 1.78	Depositor EDS
% Data completeness (in resolution range)	93.7 (20.00-1.78) 93.9 (20.00-1.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.190 , 0.216 0.199 , 0.222	Depositor DCC
R_{free} test set	9203 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	14.9	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 37.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13850	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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: GOL, SO4, MG, NAD

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	0.62	0/3220	0.81	0/4362
1	B	0.63	0/3211	0.83	2/4353 (0.0%)
1	C	0.61	0/3211	0.83	0/4354
1	D	0.62	0/3228	0.83	1/4372 (0.0%)
All	All	0.62	0/12870	0.82	3/17441 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	427	LEU	N-CA-C	6.82	119.73	111.82
1	B	221	ARG	CG-CD-NE	5.73	124.61	112.00
1	D	237	VAL	CB-CA-C	-5.09	106.60	111.44

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	3153	0	3062	11	0
1	B	3144	0	3034	10	0
1	C	3144	0	3030	9	0
1	D	3161	0	3070	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	27	0	12	1	0
2	C	27	0	12	0	0
3	A	1	0	0	0	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
4	C	6	0	8	0	0
4	D	6	0	8	4	0
5	A	10	0	0	0	0
5	B	10	0	0	0	0
5	C	10	0	0	0	0
5	D	10	0	0	0	0
6	A	335	0	0	0	0
6	B	273	0	0	0	0
6	C	254	0	0	1	0
6	D	267	0	0	1	0
All	All	13850	0	12252	40	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 2.

All (40) 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:D:302:ASP:OD1	4:D:501:GOL:H12	1.81	0.81
1:C:278:ASP:O	1:C:281:THR:HG22	1.98	0.64
1:C:397:GLN:OE1	1:C:400:ARG:NH2	2.30	0.63
1:B:401:GLU:OE1	1:B:426:ARG:NH2	2.36	0.56
1:B:246:GLN:OE1	1:B:249:ARG:NH2	2.40	0.54
1:D:129:THR:HB	1:D:214:LEU:HD13	1.89	0.53
1:B:134:THR:OG1	1:B:136:HIS:HE1	1.93	0.52
1:A:342:VAL:HG13	2:A:501:NAD:H2B	1.92	0.51
1:C:233:THR:OG1	1:C:274:HIS:HE1	1.94	0.51
1:A:129:THR:HB	1:A:214:LEU:HD13	1.92	0.50
1:A:367:ILE:HG23	1:A:388:THR:HB	1.94	0.50
1:A:278:ASP:HB2	1:B:306:ASP:OD2	2.11	0.49
1:D:217:PHE:O	1:D:221:ARG:HG3	2.12	0.49
1:A:134:THR:OG1	1:A:136:HIS:HE1	1.96	0.48
1:A:233:THR:OG1	1:A:274:HIS:HE1	1.97	0.48
1:C:134:THR:OG1	1:C:136:HIS:HE1	1.96	0.48
1:D:233:THR:OG1	1:D:274:HIS:HE1	1.96	0.48
1:B:233:THR:OG1	1:B:274:HIS:HE1	1.99	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:HIS:CE1	1:D:147:PRO:HA	2.51	0.46
1:D:274:HIS:HD2	6:D:827:HOH:O	1.98	0.46
1:D:215:ALA:HA	1:D:248:MET:HE3	1.98	0.46
1:D:129:THR:HB	1:D:214:LEU:CD1	2.47	0.45
1:B:136:HIS:CE1	1:B:147:PRO:HA	2.51	0.45
1:B:315:PRO:O	1:B:338:SER:HB2	2.17	0.44
1:A:37:GLU:HB3	1:A:67:ARG:HG2	2.00	0.44
1:A:306:ASP:OD2	1:B:278:ASP:HB3	2.18	0.43
1:A:378:ASN:OD1	1:A:381:ARG:HD2	2.19	0.43
1:D:244:PHE:O	1:D:248:MET:HG3	2.19	0.43
1:C:75:GLU:O	1:C:80:ARG:NH2	2.51	0.42
1:A:136:HIS:CE1	1:A:147:PRO:HA	2.54	0.42
1:D:134:THR:OG1	1:D:136:HIS:HE1	2.03	0.42
1:B:170:LYS:CE	1:B:191:GLU:HG2	2.50	0.41
1:C:129:THR:HB	1:C:214:LEU:CD1	2.51	0.41
1:D:306:ASP:CG	4:D:501:GOL:H11	2.45	0.41
1:D:302:ASP:OD1	4:D:501:GOL:H31	2.20	0.41
1:C:278:ASP:OD2	4:D:501:GOL:H31	2.20	0.41
1:C:303:VAL:HA	1:D:278:ASP:HB3	2.03	0.41
1:C:193:GLU:HG3	6:C:710:HOH:O	2.21	0.40
1:B:149:LEU:O	1:B:293:GLY:HA2	2.21	0.40
1:A:121:MET:HE3	1:A:125:TRP:CZ3	2.56	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	403/418 (96%)	395 (98%)	7 (2%)	1 (0%)	43	29
1	B	403/418 (96%)	395 (98%)	7 (2%)	1 (0%)	43	29
1	C	403/418 (96%)	391 (97%)	11 (3%)	1 (0%)	43	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	403/418 (96%)	393 (98%)	9 (2%)	1 (0%)	43	29
All	All	1612/1672 (96%)	1574 (98%)	34 (2%)	4 (0%)	43	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	313	LYS
1	C	313	LYS
1	A	313	LYS
1	D	313	LYS

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	326/346 (94%)	325 (100%)	1 (0%)	86	80
1	B	324/346 (94%)	318 (98%)	6 (2%)	50	32
1	C	324/346 (94%)	321 (99%)	3 (1%)	70	59
1	D	328/346 (95%)	326 (99%)	2 (1%)	78	70
All	All	1302/1384 (94%)	1290 (99%)	12 (1%)	70	59

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	380	ASP
1	B	76	ASP
1	B	138	ASP
1	B	191	GLU
1	B	248	MET
1	B	342	VAL
1	B	380	ASP
1	C	49	SER
1	C	281	THR
1	C	380	ASP

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Mol	Chain	Res	Type
1	D	76	ASP
1	D	380	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	136	HIS
1	A	165	ASN
1	A	212	HIS
1	A	274	HIS
1	A	371	ASN
1	B	136	HIS
1	B	212	HIS
1	B	274	HIS
1	B	286	GLN
1	C	126	ASN
1	C	136	HIS
1	C	212	HIS
1	C	274	HIS
1	C	371	ASN
1	D	136	HIS
1	D	165	ASN
1	D	274	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 1 is monoatomic - leaving 14 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	GOL	D	501	-	5,5,5	0.39	0	5,5,5	0.94	0
5	SO4	D	503	-	4,4,4	0.41	0	6,6,6	0.26	0
2	NAD	A	501	-	28,29,48	1.69	5 (17%)	43,45,73	1.99	10 (23%)
4	GOL	C	502	-	5,5,5	0.35	0	5,5,5	0.55	0
4	GOL	A	503	-	5,5,5	0.31	0	5,5,5	0.64	0
5	SO4	A	504	-	4,4,4	0.42	0	6,6,6	0.28	0
4	GOL	B	501	-	5,5,5	0.26	0	5,5,5	0.48	0
5	SO4	C	504	-	4,4,4	0.53	0	6,6,6	0.36	0
5	SO4	B	503	-	4,4,4	0.52	0	6,6,6	0.27	0
2	NAD	C	501	-	28,29,48	1.56	5 (17%)	43,45,73	1.90	9 (20%)
5	SO4	B	502	-	4,4,4	0.44	0	6,6,6	0.18	0
5	SO4	C	503	-	4,4,4	0.51	0	6,6,6	0.23	0
5	SO4	D	502	-	4,4,4	0.49	0	6,6,6	0.33	0
5	SO4	A	505	-	4,4,4	0.61	0	6,6,6	0.29	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	GOL	D	501	-	-	2/4/4/4	-
2	NAD	A	501	-	-	3/16/32/62	0/3/3/5
4	GOL	C	502	-	-	0/4/4/4	-
4	GOL	A	503	-	-	0/4/4/4	-
4	GOL	B	501	-	-	2/4/4/4	-
2	NAD	C	501	-	-	1/16/32/62	0/3/3/5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NAD	C5A-C4A	5.31	1.48	1.39
2	C	501	NAD	C5A-C4A	4.62	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NAD	PN-O1N	3.87	1.62	1.50
2	C	501	NAD	PN-O1N	3.70	1.62	1.50
2	A	501	NAD	C5A-C6A	2.94	1.49	1.41
2	A	501	NAD	PA-O3	2.82	1.62	1.59
2	C	501	NAD	C5A-C6A	2.70	1.48	1.41
2	A	501	NAD	C8A-N7A	2.46	1.36	1.31
2	C	501	NAD	C8A-N7A	2.34	1.36	1.31
2	C	501	NAD	C5A-N7A	-2.24	1.35	1.39

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	NAD	C5A-C4A-N3A	-6.22	118.16	126.72
2	C	501	NAD	C5A-C4A-N3A	-5.74	118.82	126.72
2	A	501	NAD	N3A-C4A-N9A	5.02	135.71	127.17
2	C	501	NAD	N3A-C4A-N9A	4.88	135.46	127.17
2	A	501	NAD	C2A-N3A-C4A	4.16	121.99	111.83
2	C	501	NAD	C2A-N3A-C4A	3.86	121.27	111.83
2	A	501	NAD	N3A-C2A-N1A	-3.80	122.83	128.58
2	C	501	NAD	N3A-C2A-N1A	-3.68	123.00	128.58
2	A	501	NAD	C4A-C5A-N7A	-3.34	106.77	110.58
2	C	501	NAD	C4A-N9A-C8A	3.27	109.18	105.74
2	A	501	NAD	O5D-PN-O2N	3.16	119.65	107.80
2	C	501	NAD	O5D-PN-O2N	3.10	119.41	107.80
2	C	501	NAD	C4A-C5A-N7A	-3.08	107.06	110.58
2	C	501	NAD	C5A-N7A-C8A	2.60	107.54	103.45
2	A	501	NAD	C5A-N7A-C8A	2.55	107.45	103.45
2	A	501	NAD	C4A-N9A-C8A	2.44	108.31	105.74
2	C	501	NAD	N9A-C8A-N7A	-2.43	110.49	113.94
2	A	501	NAD	C3B-C2B-C1B	2.27	105.76	101.46
2	A	501	NAD	C6A-C5A-N7A	2.17	136.28	132.09

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	NAD	C5B-O5B-PA-O1A
2	A	501	NAD	C5B-O5B-PA-O3
4	B	501	GOL	O1-C1-C2-C3
4	D	501	GOL	O1-C1-C2-O2
4	D	501	GOL	O1-C1-C2-C3
4	B	501	GOL	O1-C1-C2-O2

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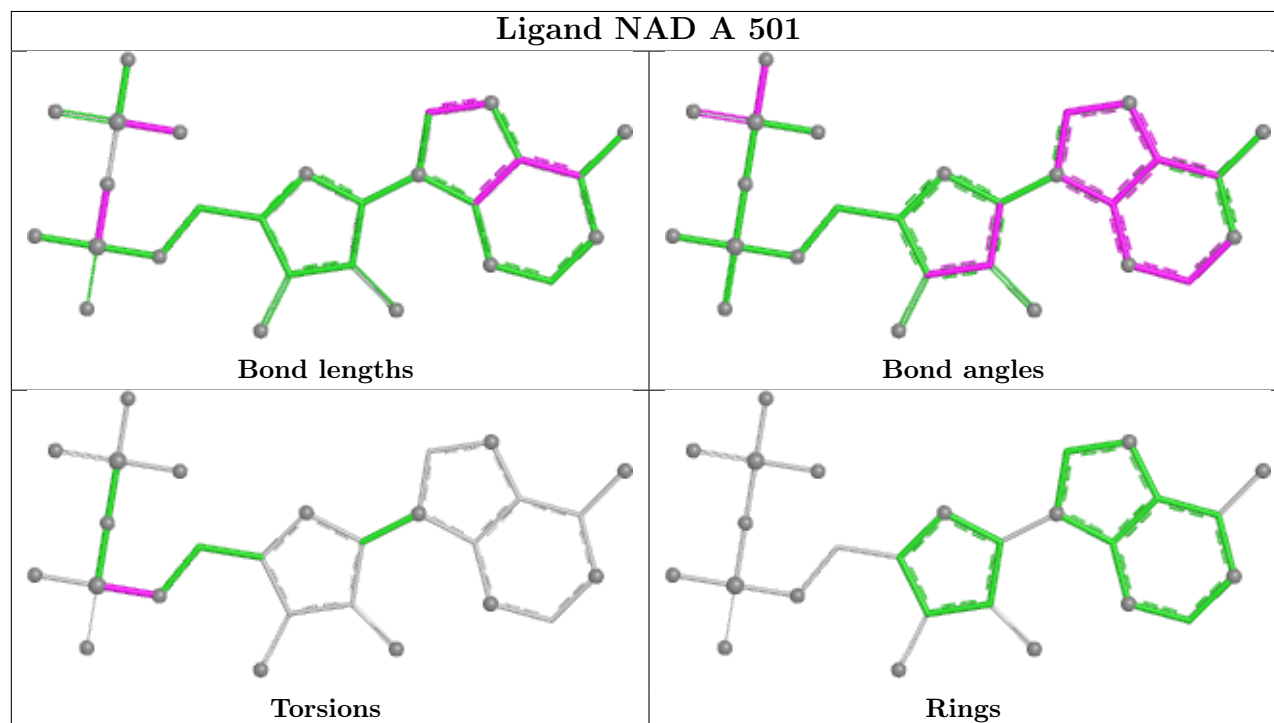
Mol	Chain	Res	Type	Atoms
2	A	501	NAD	C5B-O5B-PA-O2A
2	C	501	NAD	C5B-O5B-PA-O1A

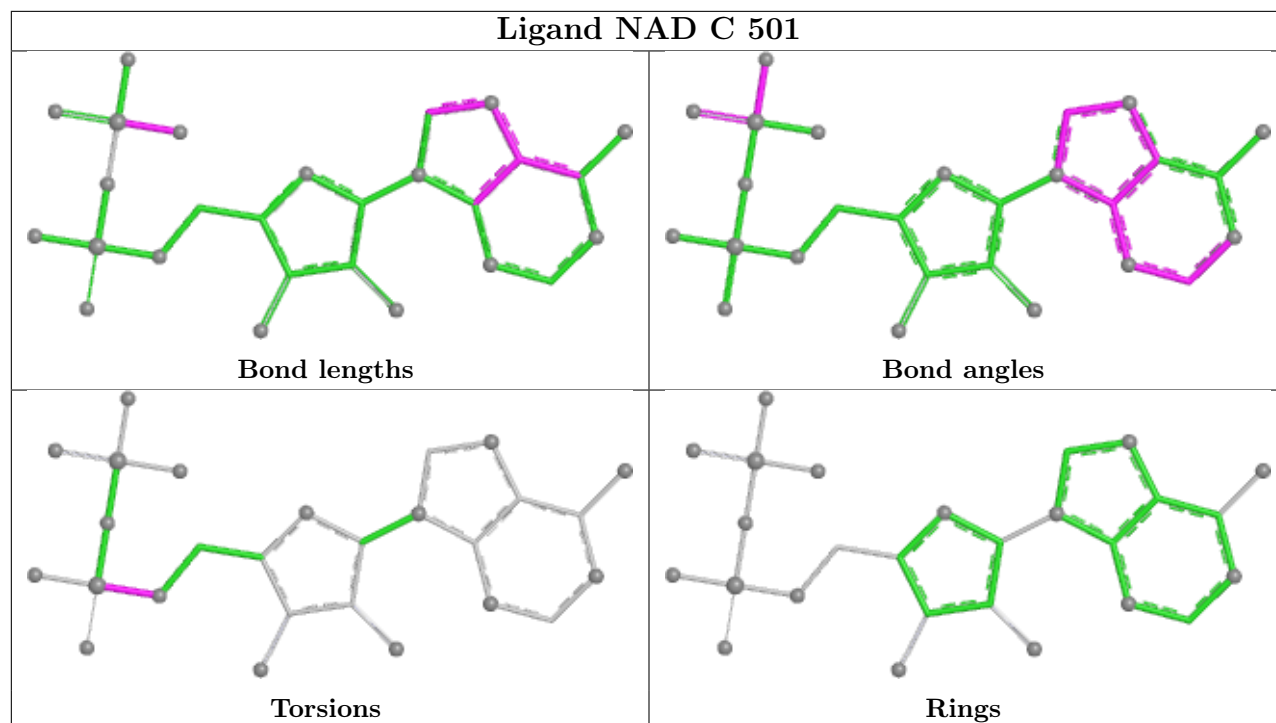
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	501	GOL	4	0
2	A	501	NAD	1	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 ⓘ

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	405/418 (96%)	-0.22	2 (0%) 87 91	6, 13, 26, 44	0
1	B	405/418 (96%)	0.35	34 (8%) 17 20	7, 17, 39, 64	0
1	C	405/418 (96%)	0.37	44 (10%) 10 12	9, 17, 40, 56	0
1	D	405/418 (96%)	-0.06	3 (0%) 84 88	8, 16, 29, 43	0
All	All	1620/1672 (96%)	0.11	83 (5%) 33 39	6, 16, 34, 64	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	110	LEU	8.3
1	C	114	TRP	6.9
1	C	105	VAL	6.6
1	C	102	ALA	5.2
1	C	74	THR	4.9
1	B	108	LEU	4.9
1	C	111	ARG	4.7
1	C	108	LEU	4.5
1	C	109	GLY	4.4
1	B	105	VAL	4.3
1	B	411	PRO	4.2
1	B	110	LEU	4.1
1	B	183	ALA	3.8
1	C	113	SER	3.6
1	B	350	LEU	3.5
1	C	80	ARG	3.4
1	C	72	ASP	3.4
1	C	64	PHE	3.4
1	B	352	GLY	3.4
1	C	67	ARG	3.4
1	C	78	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	68	ALA	3.3
1	C	75	GLU	3.2
1	C	70	ASN	3.2
1	C	120	ALA	3.2
1	B	428	ASP	3.2
1	B	112	LYS	3.1
1	C	81	ASP	3.1
1	B	343	ALA	3.1
1	C	79	LEU	3.0
1	C	69	LYS	3.0
1	C	73	ASP	2.9
1	C	112	LYS	2.9
1	C	115	GLY	2.9
1	B	348	ALA	2.9
1	B	106	LYS	2.8
1	C	77	ARG	2.8
1	B	138	ASP	2.8
1	B	107	ARG	2.8
1	C	82	VAL	2.8
1	C	65	ASP	2.7
1	B	74	THR	2.7
1	C	103	ASP	2.7
1	B	355	THR	2.7
1	B	114	TRP	2.6
1	B	111	ARG	2.6
1	B	109	GLY	2.6
1	B	80	ARG	2.6
1	B	78	VAL	2.5
1	B	184	GLY	2.5
1	C	63	THR	2.5
1	B	427	LEU	2.5
1	C	66	LEU	2.5
1	C	181	PRO	2.5
1	C	83	ILE	2.5
1	C	24	SER	2.4
1	C	428	ASP	2.4
1	C	106	LYS	2.4
1	B	79	LEU	2.4
1	D	327	GLU	2.4
1	C	100	PRO	2.4
1	B	342	VAL	2.4
1	B	102	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	76	ASP	2.3
1	C	71	ARG	2.3
1	B	344	ASP	2.3
1	C	99	THR	2.3
1	B	69	LYS	2.3
1	C	124	GLY	2.3
1	D	344	ASP	2.2
1	B	70	ASN	2.2
1	C	183	ALA	2.2
1	A	108	LEU	2.2
1	D	350	LEU	2.2
1	C	101	THR	2.2
1	C	123	ARG	2.1
1	B	181	PRO	2.1
1	C	327	GLU	2.1
1	B	410	GLY	2.1
1	B	66	LEU	2.1
1	B	345	MET	2.1
1	B	64	PHE	2.1
1	A	428	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.

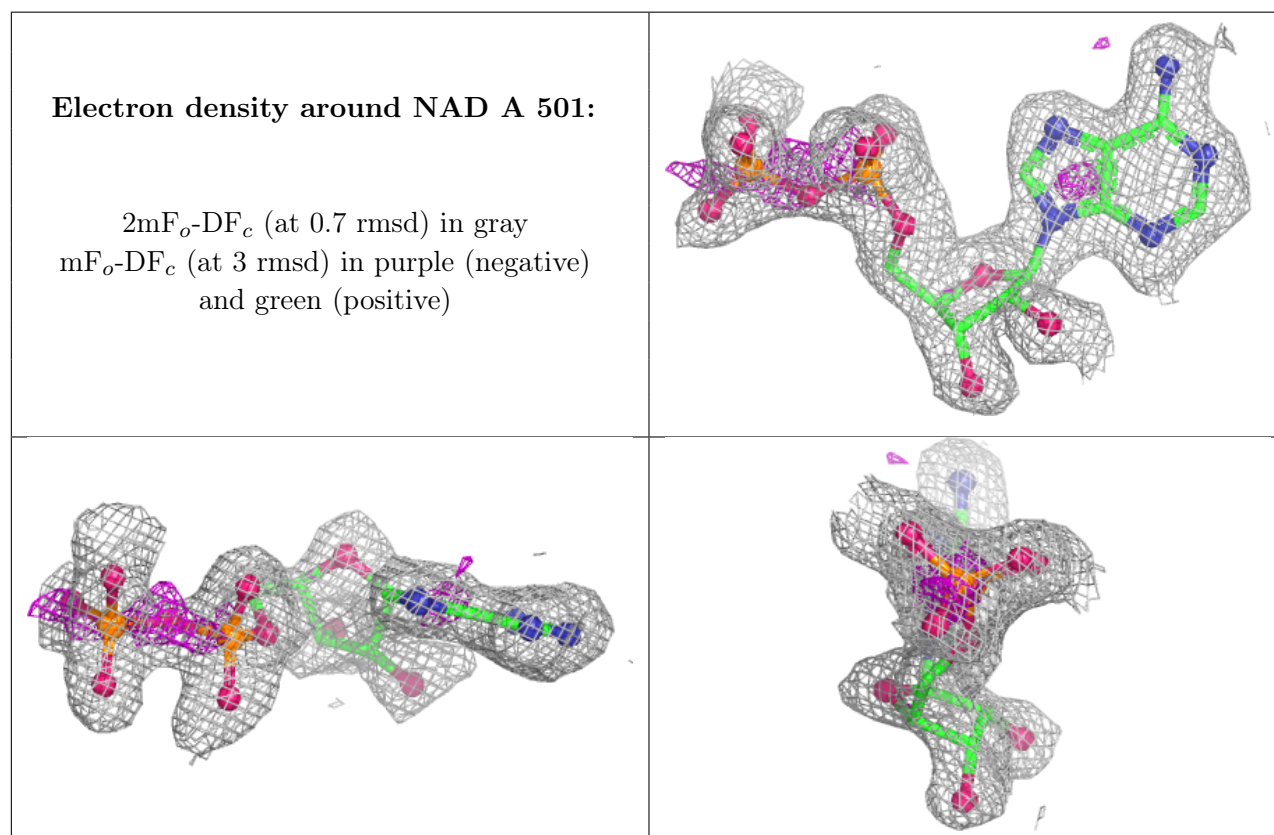
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	D	501	6/6	0.67	0.24	28,32,35,39	0
5	SO4	D	503	5/5	0.81	0.17	51,52,54,55	0
5	SO4	C	503	5/5	0.85	0.16	39,39,44,45	0

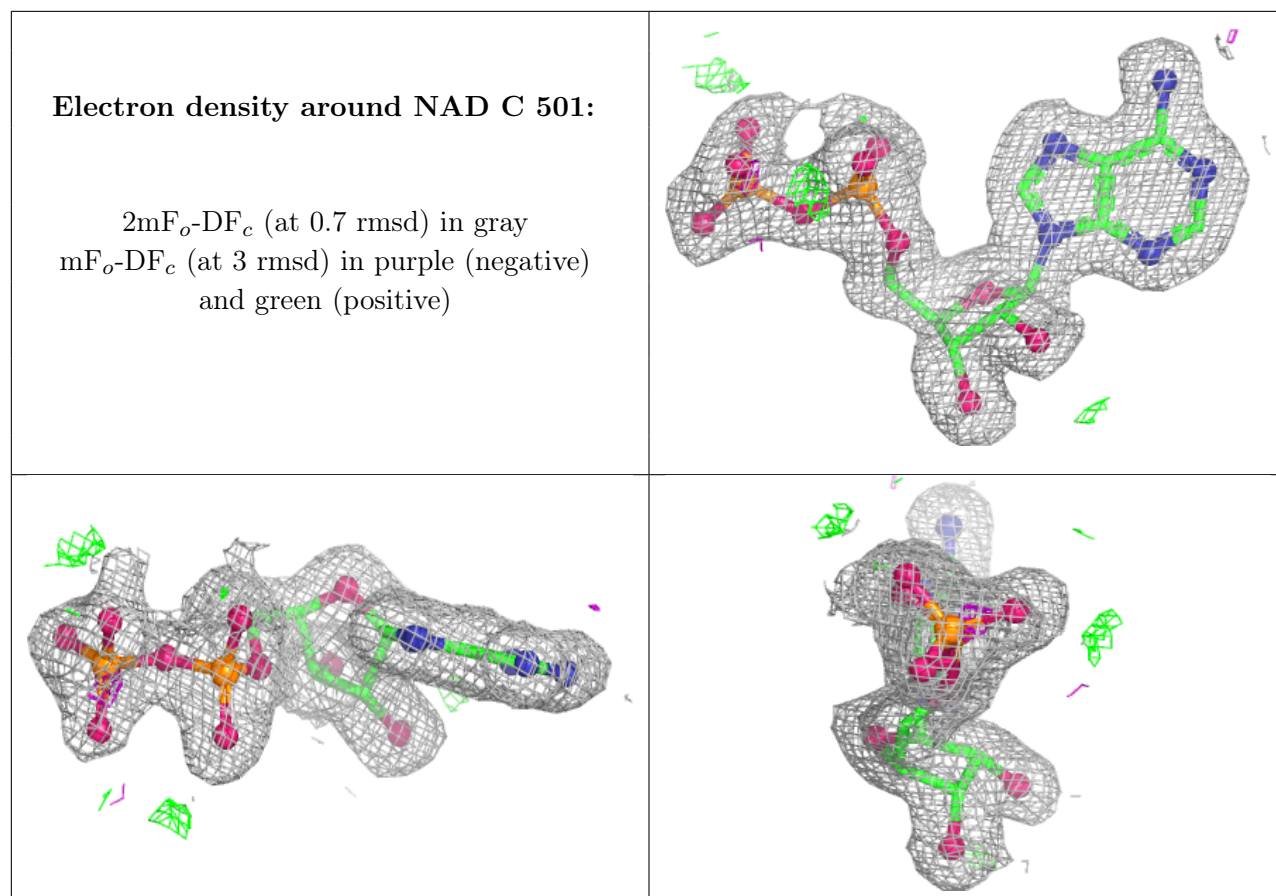
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	C	502	6/6	0.85	0.14	28,29,30,32	0
5	SO4	C	504	5/5	0.86	0.21	38,40,40,41	0
5	SO4	B	502	5/5	0.87	0.10	50,52,53,55	0
4	GOL	B	501	6/6	0.87	0.12	26,27,28,30	0
5	SO4	D	502	5/5	0.88	0.14	31,33,35,35	0
2	NAD	A	501	27/44	0.88	0.11	27,32,36,37	0
5	SO4	B	503	5/5	0.89	0.11	39,41,41,42	0
4	GOL	A	503	6/6	0.90	0.11	24,26,27,28	0
5	SO4	A	505	5/5	0.91	0.16	30,31,35,36	0
5	SO4	A	504	5/5	0.92	0.14	40,42,43,44	0
3	MG	A	502	1/1	0.92	0.17	27,27,27,27	0
2	NAD	C	501	27/44	0.95	0.07	17,22,36,36	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.





6.5 Other polymers ⓘ

There are no such residues in this entry.