Full wwPDB X-ray Structure Validation Report ⓘ

Feb 12, 2024 – 01:00 pm GMT

PDB ID	:	8CG2
Title	:	Crystal structure of S-adenosyl-L-homocysteine hydrolase from P. aeruginosa in complex with F2X-Entry library fragment B07
Authors	:	Malecki, P.H.; Gawel, M.; Stepniewska, M.; Brzezinski, K.
Deposited on	:	2023-02-03
Resolution	:	1.37 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:

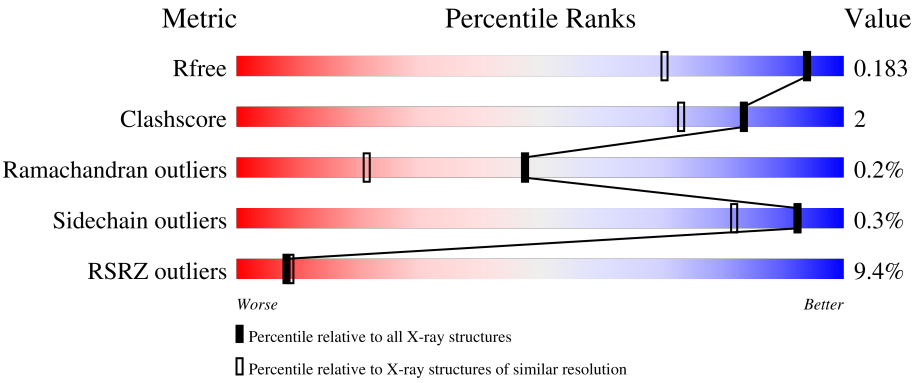
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.37 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	2907 (1.40-1.36)
Clashscore	141614	3037 (1.40-1.36)
Ramachandran outliers	138981	2970 (1.40-1.36)
Sidechain outliers	138945	2969 (1.40-1.36)
RSRZ outliers	127900	2846 (1.40-1.36)

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 <=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	472	13% 94%
1	C	472	6% 92% 6%

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	PO4	C	514	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 8532 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.

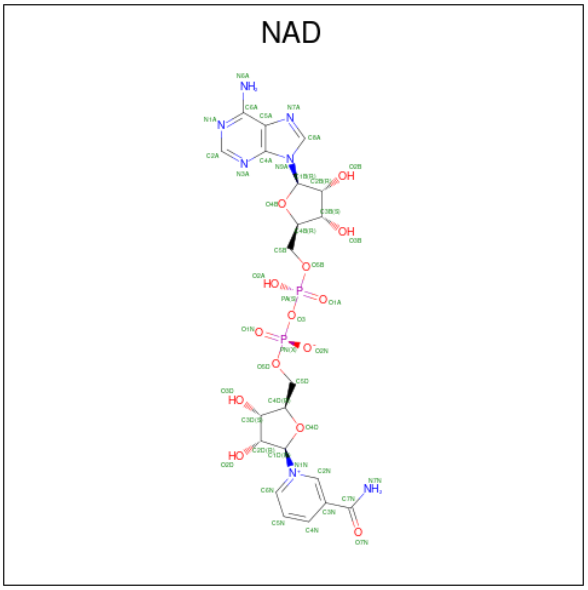
- Molecule 1 is a protein called Adenosylhomocysteinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	461	Total	C	N	O	S	0	9	0
			3615	2279	630	683	23			
1	C	461	Total	C	N	O	S	0	18	0
			3665	2316	633	691	25			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q9I685
A	-1	ASN	-	expression tag	UNP Q9I685
A	0	ALA	-	expression tag	UNP Q9I685
C	-2	SER	-	expression tag	UNP Q9I685
C	-1	ASN	-	expression tag	UNP Q9I685
C	0	ALA	-	expression tag	UNP Q9I685

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).

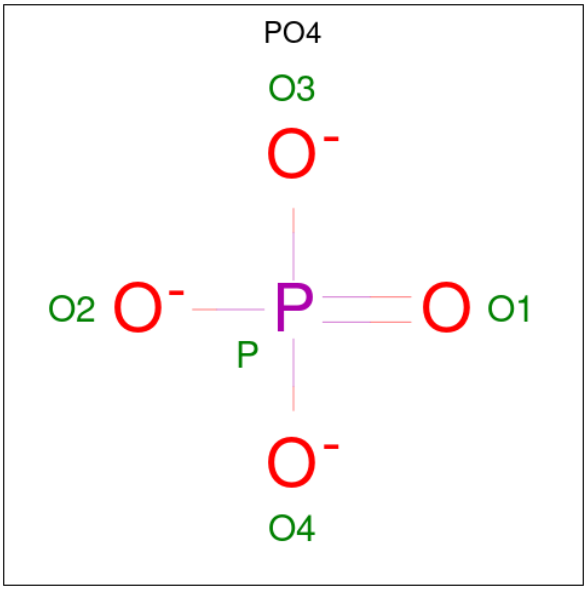


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O P 44 21 7 14 2	0	0
2	C	1	Total C N O P 44 21 7 14 2	0	0

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

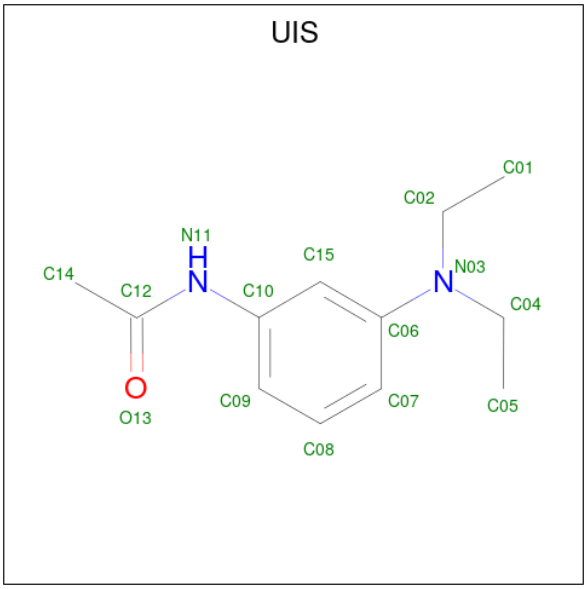
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total K 1 1	0	0
3	C	1	Total K 1 1	0	0

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



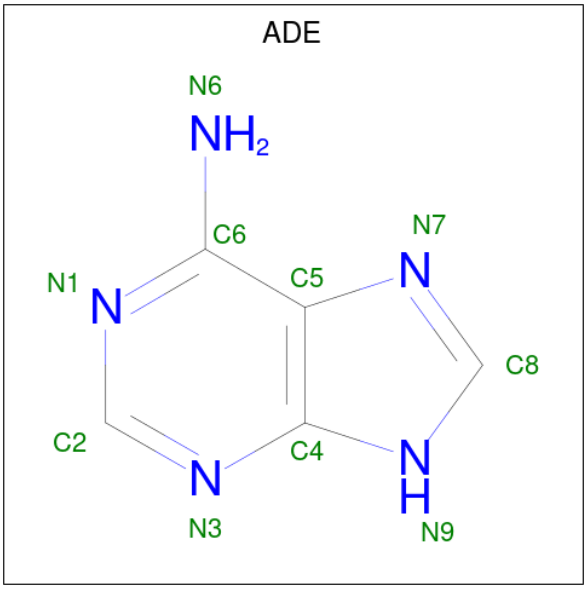
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0
4	A	1	Total O P 5 4 1	0	0
4	C	1	Total O P 5 4 1	0	0
4	C	1	Total O P 5 4 1	0	0
4	C	1	Total O P 5 4 1	0	0

- Molecule 5 is N-[3-(diethylamino)phenyl]ethanamide (three-letter code: UIS) (formula: $C_{12}H_{18}N_2O$) (labeled as "Ligand of Interest" by depositor).



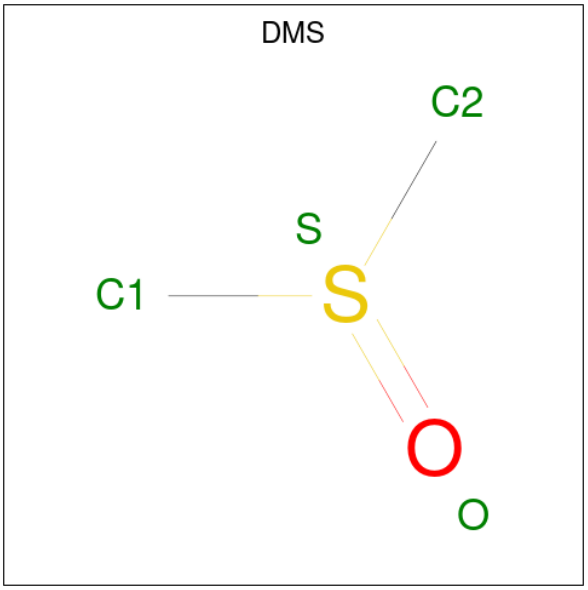
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			15	12	2	1		
5	C	1	Total	C	N	O	0	0
			15	12	2	1		

- Molecule 6 is ADENINE (three-letter code: ADE) (formula: $C_5H_5N_5$).



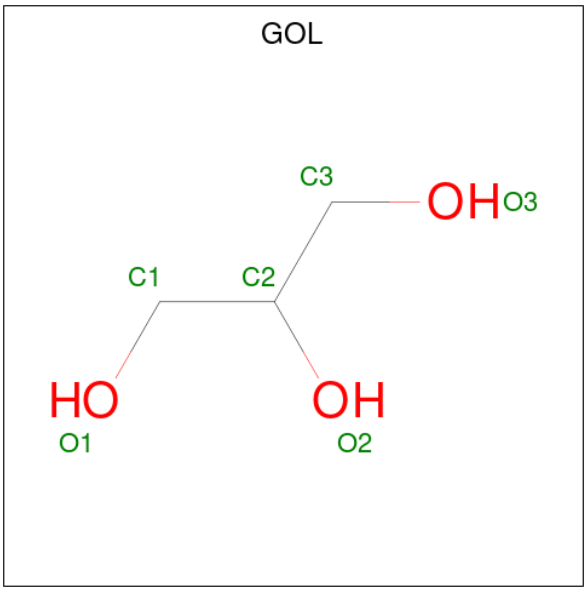
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C N 10 5 5	0	0
6	C	1	Total C N 10 5 5	0	0

- Molecule 7 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total C O S 4 2 1 1	0	0
7	C	1	Total C O S 4 2 1 1	0	0
7	C	1	Total C O S 4 2 1 1	0	0
7	C	1	Total C O S 4 2 1 1	0	0
7	C	1	Total C O S 4 2 1 1	0	0

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	C	1	Total C O 6 3 3	0	0
8	C	1	Total C O 6 3 3	0	0

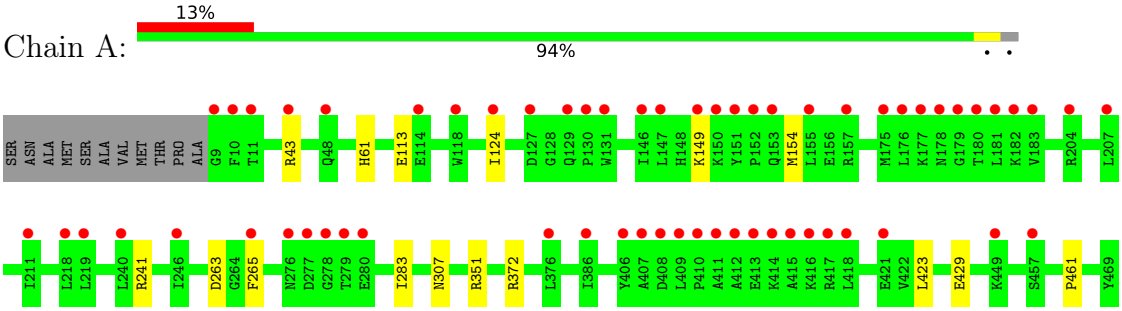
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	494	Total O 513 513	0	20
9	C	521	Total O 537 537	0	16

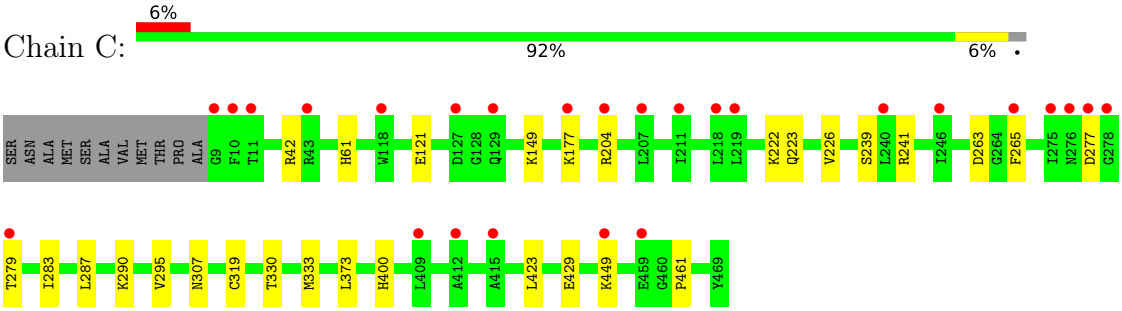
3 Residue-property plots (i)

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: Adenosylhomocysteinase



• Molecule 1: Adenosylhomocysteinase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	142.74Å 85.38Å 111.47Å 90.00° 122.25° 90.00°	Depositor
Resolution (Å)	41.72 – 1.37 47.14 – 1.37	Depositor EDS
% Data completeness (in resolution range)	99.5 (41.72-1.37) 99.5 (47.14-1.37)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.98 (at 1.37Å)	Xtriage
Refinement program	PHENIX 1.19.2-4158	Depositor
R, R_{free}	0.148 , 0.181 0.149 , 0.183	Depositor DCC
R_{free} test set	1184 reflections (0.50%)	wwPDB-VP
Wilson B-factor (Å^2)	16.6	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 56.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	8532	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: K, GOL, PO4, NAD, UIS, ADE, DMS

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	0.41	0/3696	0.62	0/4992
1	C	0.41	0/3767	0.62	0/5086
All	All	0.41	0/7463	0.62	0/10078

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3615	0	3643	11	0
1	C	3665	0	3716	24	0
2	A	44	0	26	0	0
2	C	44	0	26	1	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	15	0	0	1	0
4	C	15	0	0	0	0
5	A	15	0	0	2	0
5	C	15	0	0	2	0
6	A	10	0	4	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	10	0	4	0	0
7	C	20	0	30	1	0
8	C	12	0	16	0	0
9	A	513	0	0	1	0
9	C	537	0	0	6	0
All	All	8532	0	7465	36	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 (36) 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:C:223[B]:GLN:HE22	1:C:290:LYS:HE2	1.52	0.75
1:C:241[B]:ARG:HD2	9:C:924:HOH:O	1.95	0.65
1:A:351:ARG:NH2	4:A:506:PO4:O3	2.34	0.61
1:A:241[B]:ARG:NH1	1:A:263:ASP:O	2.28	0.59
1:C:223[B]:GLN:NE2	1:C:290:LYS:HE2	2.17	0.59
1:A:241[B]:ARG:HD2	9:A:917:HOH:O	2.02	0.59
1:C:373:LEU:HD22	2:C:501:NAD:N7N	2.20	0.56
1:C:423:LEU:HD22	5:C:510:UIS:C09	2.36	0.55
1:A:113:GLU:OE2	1:A:372[A]:ARG:NH2	2.40	0.55
1:C:449:LYS:NZ	9:C:603:HOH:O	2.42	0.53
1:C:241[B]:ARG:NH1	1:C:263:ASP:O	2.36	0.49
1:C:295[B]:VAL:HG12	1:C:319:CYS:SG	2.52	0.49
1:C:241[B]:ARG:HD3	1:C:265:PHE:CE1	2.48	0.48
1:A:423:LEU:HD22	5:A:504:UIS:C09	2.43	0.47
1:C:400:HIS:HB2	5:C:510:UIS:C08	2.44	0.46
1:C:149:LYS:HB3	1:C:149:LYS:HE3	1.58	0.45
1:A:241[B]:ARG:HD3	1:A:265:PHE:CE1	2.52	0.45
1:C:204[B]:ARG:HA	1:C:239:SER:HB2	2.00	0.44
1:C:223[B]:GLN:HE22	1:C:290:LYS:CE	2.28	0.44
1:C:287:LEU:O	1:C:290:LYS:HG2	2.17	0.44
1:C:177:LYS:HG3	9:C:931:HOH:O	2.18	0.43
1:C:283:ILE:HG13	1:C:307:ASN:HB3	1.99	0.43
7:C:504:DMS:H23	9:C:630:HOH:O	2.19	0.43
1:C:330:THR:HA	1:C:333[B]:MET:HE2	2.01	0.43
1:A:423:LEU:HD22	5:A:504:UIS:C08	2.49	0.42
1:C:277[B]:ASP:HB2	1:C:279:THR:H	1.84	0.42
1:A:149:LYS:HE3	1:A:149:LYS:HB3	1.73	0.42
1:A:124:ILE:HG23	1:A:154:MET:SD	2.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:VAL:HG22	1:C:295[B]:VAL:HG22	2.02	0.41
1:C:223[B]:GLN:OE1	1:C:290:LYS:HE2	2.21	0.41
1:C:429:GLU:OE1	1:C:461:PRO:HA	2.20	0.41
1:C:222[A]:LYS:HD3	9:C:734:HOH:O	2.21	0.41
1:A:283:ILE:HG13	1:A:307:ASN:HB3	2.02	0.41
1:A:429:GLU:OE1	1:A:461:PRO:HA	2.21	0.41
1:C:121[A]:GLU:HG2	9:C:884:HOH:O	2.21	0.40
1:C:204[A]:ARG:HA	1:C:239:SER:HB2	2.02	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	468/472 (99%)	458 (98%)	9 (2%)	1 (0%)	47	21
1	C	477/472 (101%)	468 (98%)	8 (2%)	1 (0%)	47	21
All	All	945/944 (100%)	926 (98%)	17 (2%)	2 (0%)	47	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	61	HIS
1	A	61	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	386/385 (100%)	385 (100%)	1 (0%)	92 82
1	C	395/385 (103%)	394 (100%)	1 (0%)	92 82
All	All	781/770 (101%)	779 (100%)	2 (0%)	92 82

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	ARG
1	C	42	ARG

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 21 ligands modelled in this entry, 2 are monoatomic - leaving 19 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	$\#\|Z\|>2$
7	DMS	C	507	-	3,3,3	0.67	0	3,3,3	0.39	0
4	PO4	A	503	-	4,4,4	0.68	0	6,6,6	0.50	0
8	GOL	C	505	-	5,5,5	1.01	0	5,5,5	0.95	0
6	ADE	A	505	-	9,11,11	0.93	0	7,15,15	1.07	0
6	ADE	C	512	-	9,11,11	0.84	0	7,15,15	1.14	1 (14%)
5	UIS	A	504	-	15,15,15	1.90	3 (20%)	19,19,19	1.42	3 (15%)
7	DMS	C	506	-	3,3,3	0.66	0	3,3,3	0.50	0
2	NAD	A	501	-	42,48,48	0.56	0	50,73,73	0.85	1 (2%)
4	PO4	C	503	-	4,4,4	0.70	0	6,6,6	0.32	0
4	PO4	A	507	-	4,4,4	0.58	0	6,6,6	1.22	0
4	PO4	C	513	-	4,4,4	1.03	0	6,6,6	0.64	0
8	GOL	C	509	-	5,5,5	0.76	0	5,5,5	1.23	0
2	NAD	C	501	-	42,48,48	0.53	0	50,73,73	0.80	2 (4%)
7	DMS	C	504	-	3,3,3	0.63	0	3,3,3	0.31	0
4	PO4	A	506	-	4,4,4	0.93	0	6,6,6	0.50	0
7	DMS	C	511	-	3,3,3	0.70	0	3,3,3	0.52	0
7	DMS	C	508	-	3,3,3	0.66	0	3,3,3	0.53	0
4	PO4	C	514	-	4,4,4	0.88	0	6,6,6	0.47	0
5	UIS	C	510	-	15,15,15	1.91	3 (20%)	19,19,19	1.64	5 (26%)

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
5	UIS	A	504	-	-	0/12/12/12	0/1/1/1
2	NAD	A	501	-	-	5/26/62/62	0/5/5/5
8	GOL	C	505	-	-	4/4/4/4	-
8	GOL	C	509	-	-	2/4/4/4	-
2	NAD	C	501	-	-	5/26/62/62	0/5/5/5
6	ADE	A	505	-	-	-	0/2/2/2
6	ADE	C	512	-	-	-	0/2/2/2
5	UIS	C	510	-	-	0/12/12/12	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	510	UIS	C12-N11	5.55	1.46	1.36
5	A	504	UIS	C12-N11	5.51	1.46	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	504	UIS	C06-N03	3.07	1.47	1.38
5	C	510	UIS	C10-N11	2.93	1.47	1.41
5	C	510	UIS	C06-N03	2.83	1.46	1.38
5	A	504	UIS	C10-N11	2.65	1.47	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	510	UIS	C07-C06-N03	-4.05	115.79	121.38
5	A	504	UIS	C07-C06-N03	-3.11	117.09	121.38
5	A	504	UIS	C14-C12-N11	2.45	118.58	114.98
5	C	510	UIS	C08-C09-C10	2.34	122.52	119.72
5	C	510	UIS	C04-N03-C02	2.21	120.58	116.34
6	C	512	ADE	C5-C6-N6	2.14	123.61	120.35
2	A	501	NAD	C5A-C6A-N6A	2.13	123.59	120.35
5	C	510	UIS	C15-C10-N11	2.12	127.12	120.18
2	C	501	NAD	C5A-C6A-N6A	2.11	123.57	120.35
5	A	504	UIS	C04-N03-C02	2.09	120.36	116.34
2	C	501	NAD	C2N-N1N-C1D	-2.09	114.49	119.14
5	C	510	UIS	C14-C12-N11	2.08	118.04	114.98

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	NAD	O4D-C1D-N1N-C2N
2	A	501	NAD	O4D-C1D-N1N-C6N
2	A	501	NAD	C2D-C1D-N1N-C2N
2	A	501	NAD	C2D-C1D-N1N-C6N
2	C	501	NAD	O4D-C1D-N1N-C2N
2	C	501	NAD	O4D-C1D-N1N-C6N
2	C	501	NAD	C2D-C1D-N1N-C2N
2	C	501	NAD	C2D-C1D-N1N-C6N
8	C	505	GOL	O1-C1-C2-O2
8	C	505	GOL	O1-C1-C2-C3
8	C	509	GOL	C1-C2-C3-O3
8	C	505	GOL	C1-C2-C3-O3
8	C	509	GOL	O2-C2-C3-O3
8	C	505	GOL	O2-C2-C3-O3
2	A	501	NAD	O4B-C4B-C5B-O5B
2	C	501	NAD	O4B-C4B-C5B-O5B

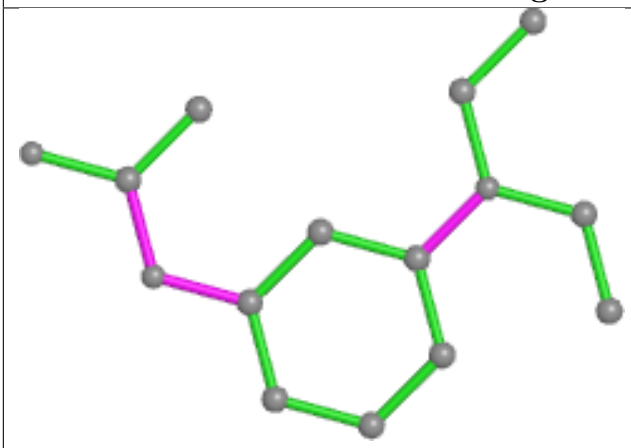
There are no ring outliers.

5 monomers are involved in 7 short contacts:

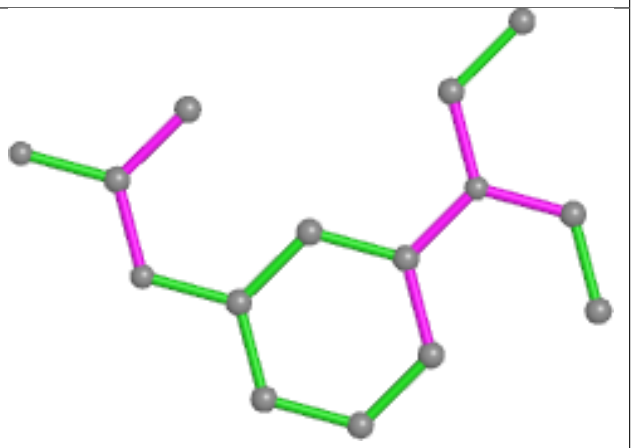
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	504	UIS	2	0
2	C	501	NAD	1	0
7	C	504	DMS	1	0
4	A	506	PO4	1	0
5	C	510	UIS	2	0

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 then 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.

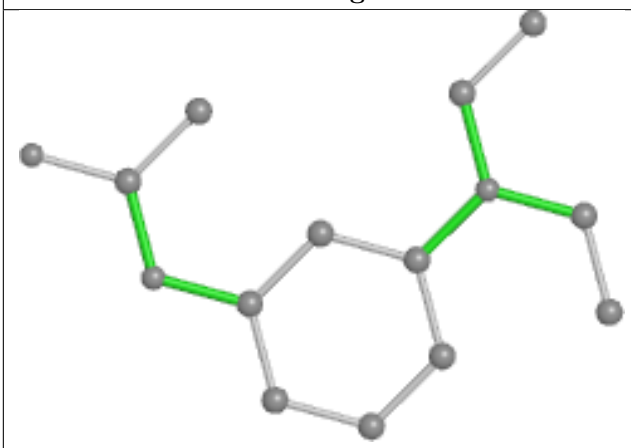
Ligand UIS A 504



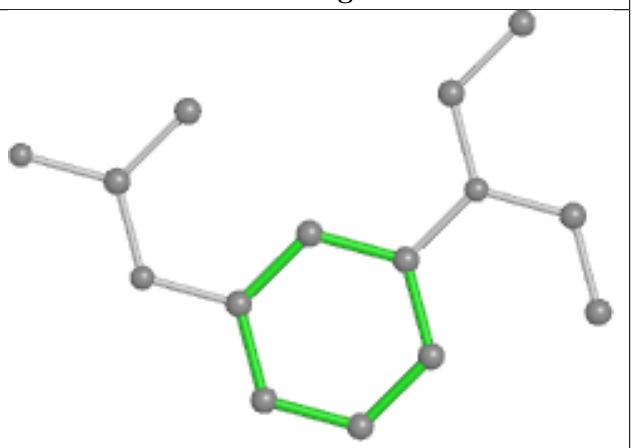
Bond lengths



Bond angles

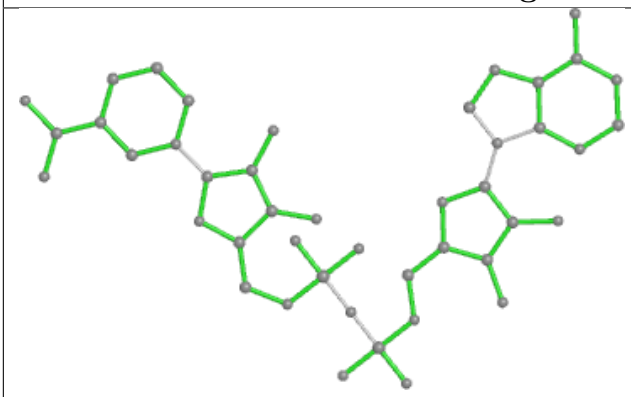


Torsions

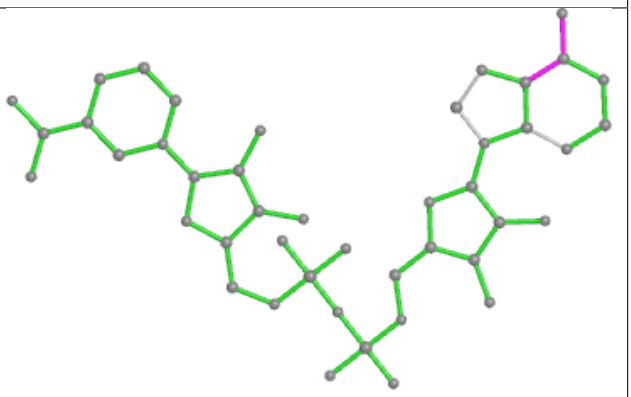


Rings

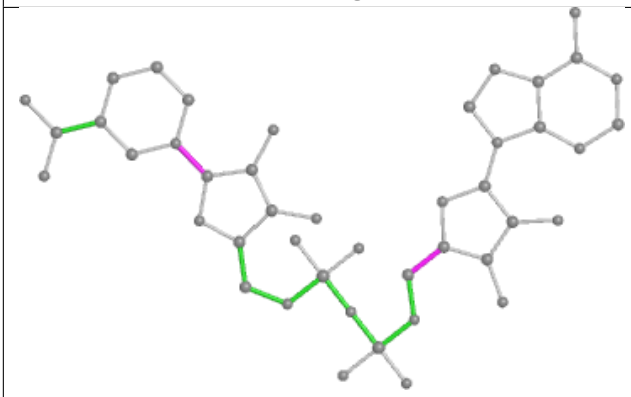
Ligand NAD A 501



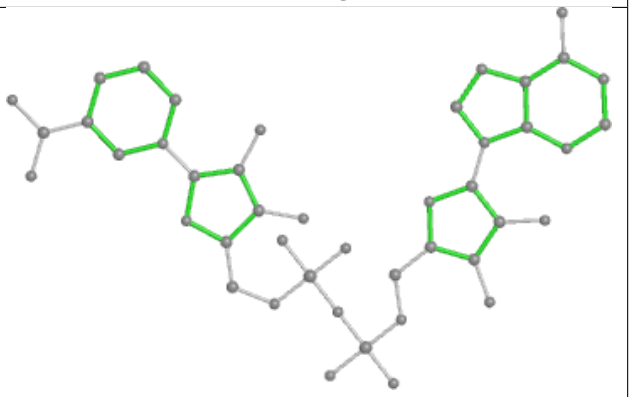
Bond lengths



Bond angles

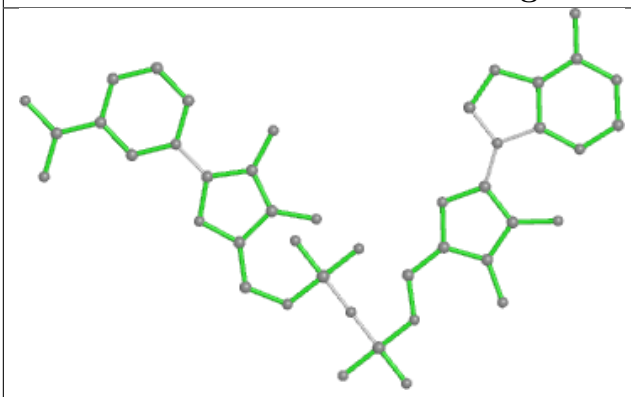


Torsions

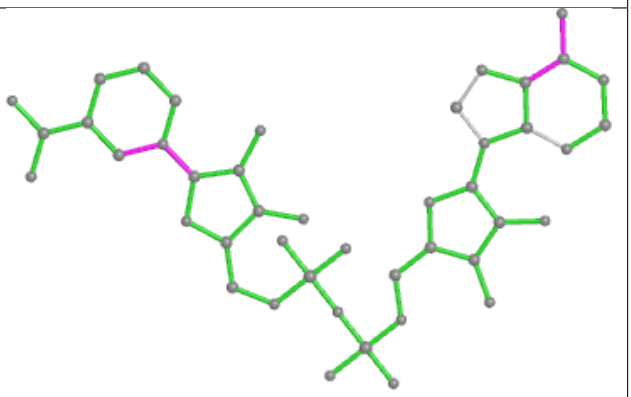


Rings

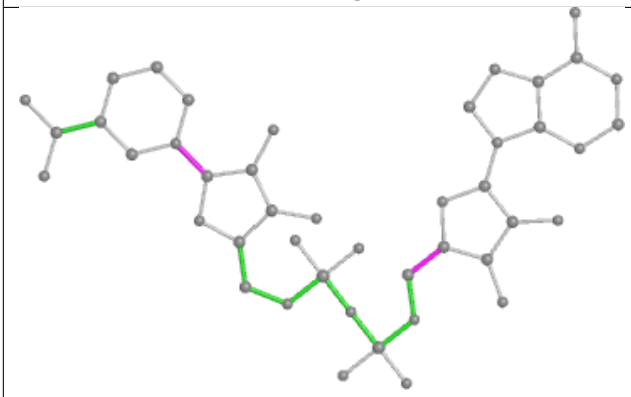
Ligand NAD C 501



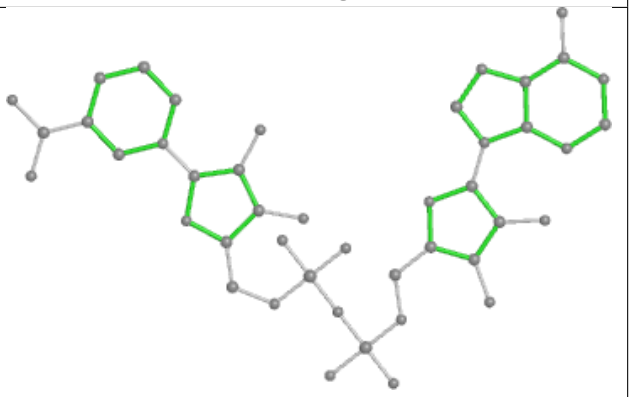
Bond lengths



Bond angles

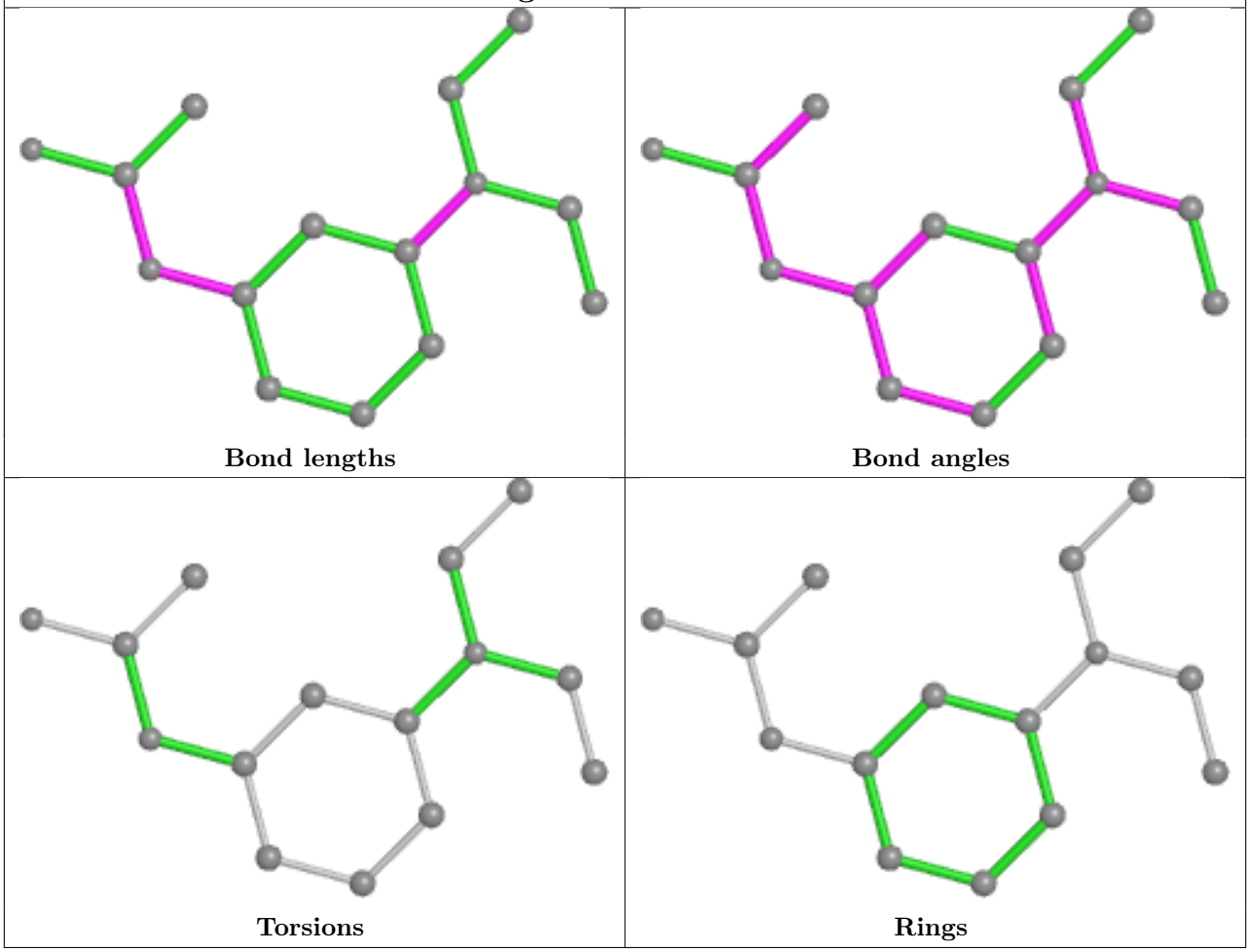


Torsions



Rings

Ligand UIS C 510



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, 95^{th} 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	461/472 (97%)	0.81	61 (13%) 3 3	13, 19, 38, 68	0
1	C	461/472 (97%)	0.44	26 (5%) 24 24	13, 18, 32, 52	0
All	All	922/944 (97%)	0.63	87 (9%) 8 9	13, 19, 35, 68	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	412	ALA	9.6
1	A	415	ALA	7.5
1	A	416	LYS	7.1
1	A	411	ALA	7.1
1	A	410	PRO	7.0
1	A	409	LEU	6.6
1	C	9	GLY	6.0
1	A	413	GLU	5.3
1	A	153	GLN	4.8
1	A	179	GLY	4.7
1	A	176	LEU	4.5
1	A	406	TYR	4.5
1	A	10	PHE	4.4
1	A	279	THR	4.4
1	A	9	GLY	4.0
1	C	277[A]	ASP	3.9
1	A	152	PRO	3.9
1	A	417	ARG	3.9
1	A	177	LYS	3.8
1	A	151	TYR	3.7
1	A	43	ARG	3.7
1	C	10	PHE	3.6
1	A	130	PRO	3.6
1	C	219	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	178	ASN	3.5
1	A	414	LYS	3.4
1	A	240	LEU	3.4
1	C	246	ILE	3.3
1	C	275[A]	ILE	3.3
1	C	240	LEU	3.3
1	A	219	LEU	3.3
1	A	183	VAL	3.3
1	C	276[A]	ASN	3.3
1	A	147	LEU	3.3
1	C	278	GLY	3.1
1	A	157	ARG	3.1
1	A	155	LEU	3.1
1	C	415	ALA	3.0
1	A	182	LYS	3.0
1	A	129	GLN	3.0
1	A	204[A]	ARG	3.0
1	C	204[A]	ARG	3.0
1	A	276	ASN	3.0
1	A	127	ASP	2.9
1	C	127	ASP	2.9
1	A	180	THR	2.9
1	A	246	ILE	2.9
1	A	11	THR	2.8
1	C	11	THR	2.8
1	C	279	THR	2.8
1	A	181	LEU	2.8
1	A	118	TRP	2.8
1	C	218	LEU	2.7
1	C	409	LEU	2.7
1	C	177	LYS	2.7
1	A	418	LEU	2.6
1	A	407	ALA	2.6
1	A	386	ILE	2.5
1	A	408	ASP	2.5
1	A	207	LEU	2.5
1	C	211	ILE	2.5
1	A	278	GLY	2.4
1	C	449	LYS	2.4
1	C	265	PHE	2.4
1	C	129	GLN	2.4
1	A	218	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	149	LYS	2.3
1	A	146	ILE	2.3
1	A	131	TRP	2.3
1	A	277	ASP	2.3
1	A	175	MET	2.3
1	A	48	GLN	2.2
1	A	421	GLU	2.2
1	A	449	LYS	2.2
1	A	265	PHE	2.2
1	C	459	GLU	2.2
1	C	118	TRP	2.2
1	A	457	SER	2.2
1	C	43	ARG	2.1
1	A	150	LYS	2.1
1	C	412	ALA	2.1
1	A	211	ILE	2.1
1	A	376	LEU	2.0
1	C	207	LEU	2.0
1	A	124	ILE	2.0
1	A	114	GLU	2.0
1	A	280	GLU	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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	PO4	C	514	5/5	0.64	0.45	65,68,69,71	5
7	DMS	C	506	4/4	0.70	0.31	122,122,122,122	0

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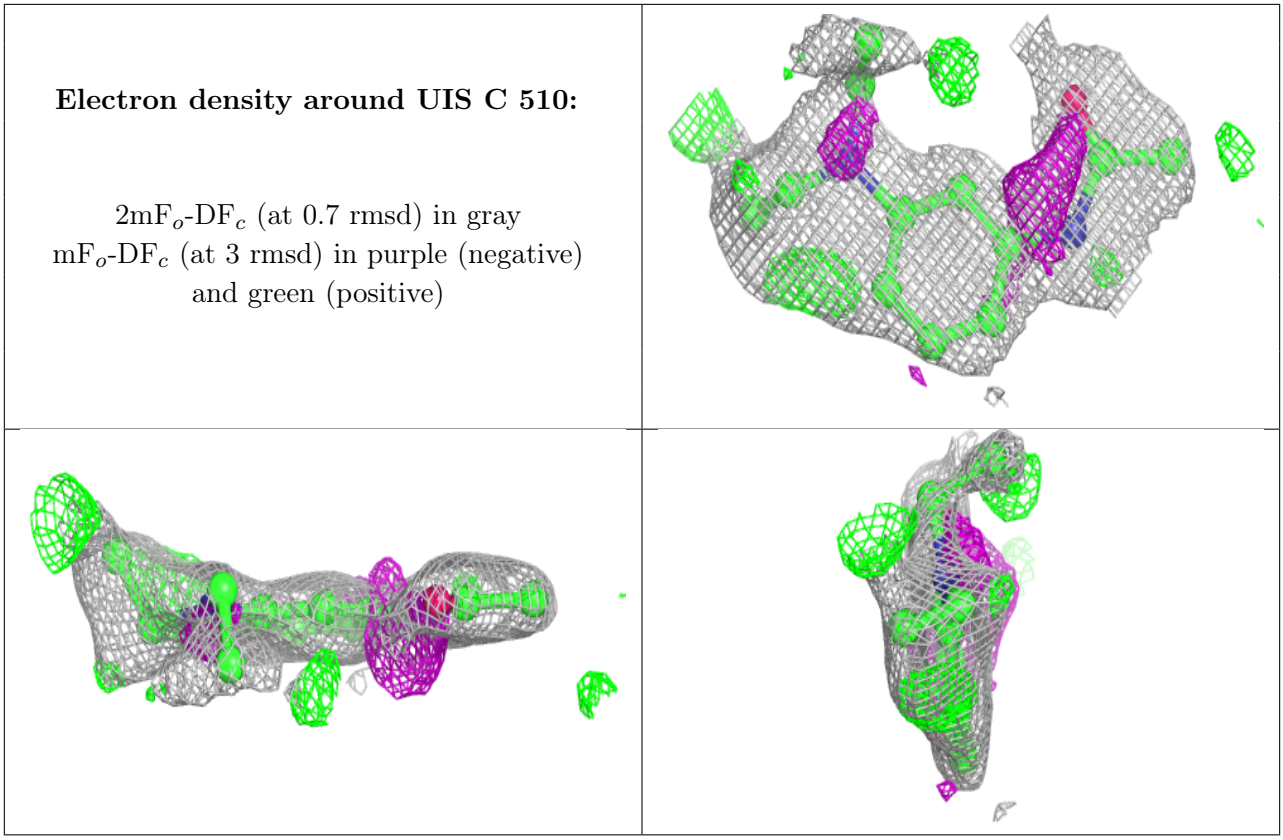
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	UIS	C	510	15/15	0.75	0.26	40,45,47,50	0
5	UIS	A	504	15/15	0.75	0.29	46,50,56,58	0
7	DMS	C	508	4/4	0.76	0.20	74,74,75,75	0
7	DMS	C	511	4/4	0.83	0.20	55,55,56,58	0
8	GOL	C	505	6/6	0.85	0.23	50,53,56,58	0
7	DMS	C	507	4/4	0.89	0.15	50,52,52,54	0
8	GOL	C	509	6/6	0.89	0.12	39,43,43,43	0
4	PO4	A	506	5/5	0.93	0.17	31,32,36,41	5
4	PO4	A	507	5/5	0.94	0.14	28,28,30,35	0
4	PO4	C	513	5/5	0.96	0.08	20,22,24,25	0
2	NAD	A	501	44/44	0.96	0.09	12,15,17,20	0
2	NAD	C	501	44/44	0.97	0.07	13,15,17,20	0
6	ADE	A	505	10/10	0.97	0.09	14,15,16,16	0
6	ADE	C	512	10/10	0.97	0.07	12,14,14,15	0
4	PO4	C	503	5/5	0.98	0.06	20,21,22,23	0
7	DMS	C	504	4/4	0.98	0.09	37,38,38,40	0
4	PO4	A	503	5/5	0.99	0.05	21,21,22,25	0
3	K	C	502	1/1	1.00	0.07	14,14,14,14	0
3	K	A	502	1/1	1.00	0.07	14,14,14,14	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.

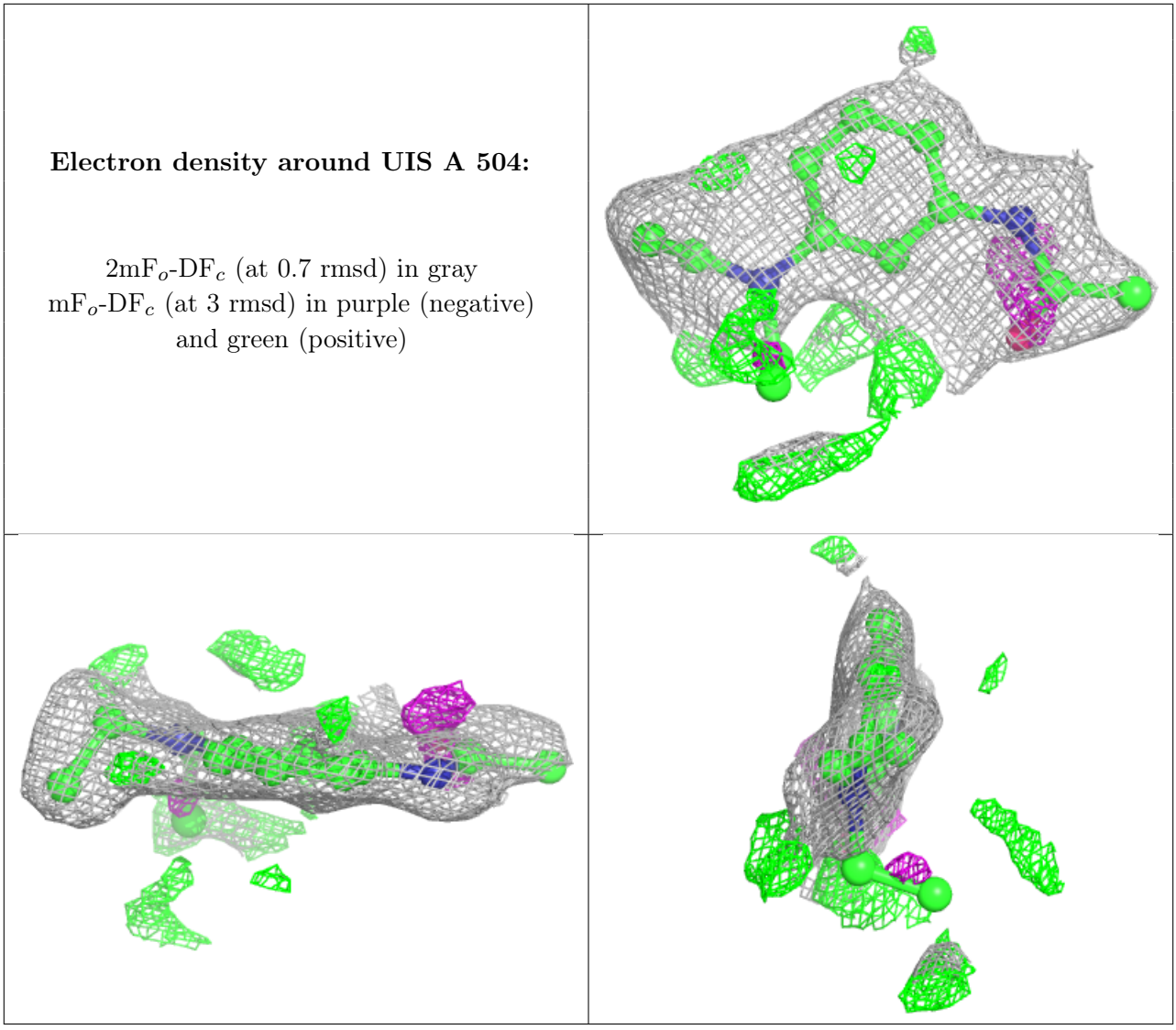
Electron density around UIS C 510:

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



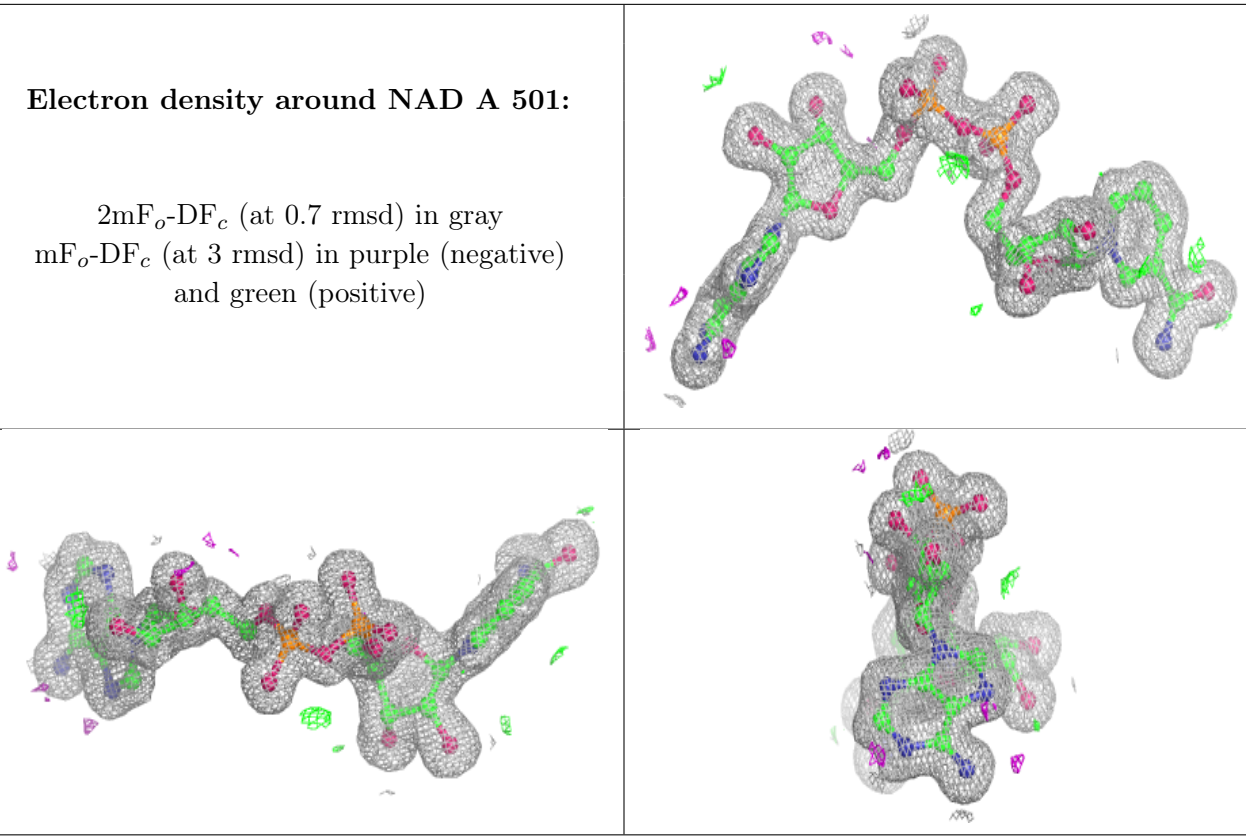
Electron density around UIS A 504:

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



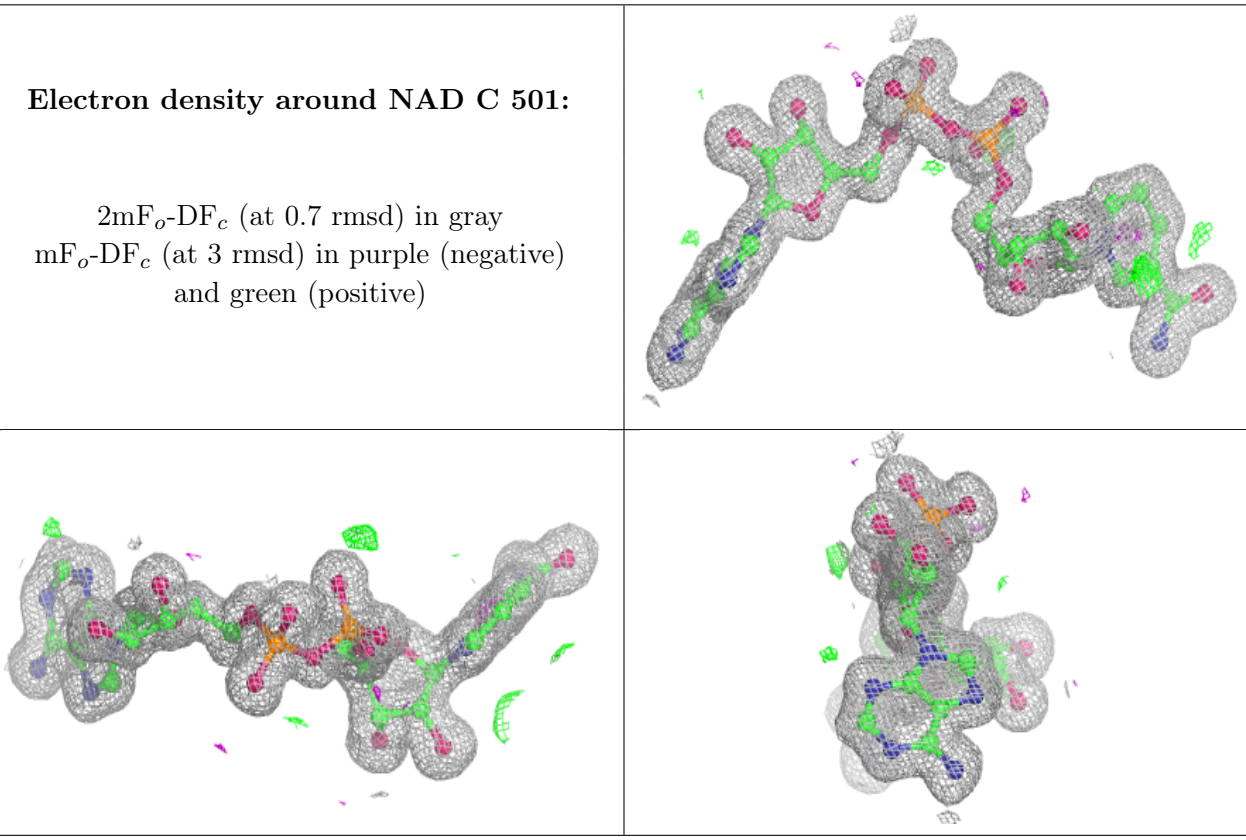
Electron density around NAD A 501:

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



Electron density around NAD C 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.