Full wwPDB X-ray Structure Validation Report ⓘ

Apr 11, 2022 – 10:12 am BST

PDB ID	:	7O5M
Title	:	Crystal structure of S-adenosyl-L-homocysteine hydrolase from Synechocystis sp. PCC 6803 cocrystallized with adenosine in the presence of Na+ cations
Authors	:	Malecki, P.H.; Imiolczyk, B.; Barciszewski, J.; Czyrko-Horczak, J.; Brzezinski, K.
Deposited on	:	2021-04-08
Resolution	:	2.20 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 following versions of software and data (see references ⓘ) were used in the production of this report:

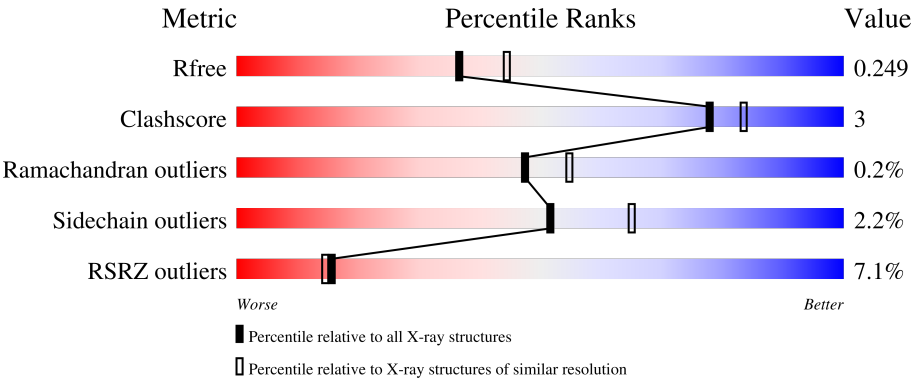
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	425	91% 7% .
1	C	425	14% 87% 10% .

2 Entry composition

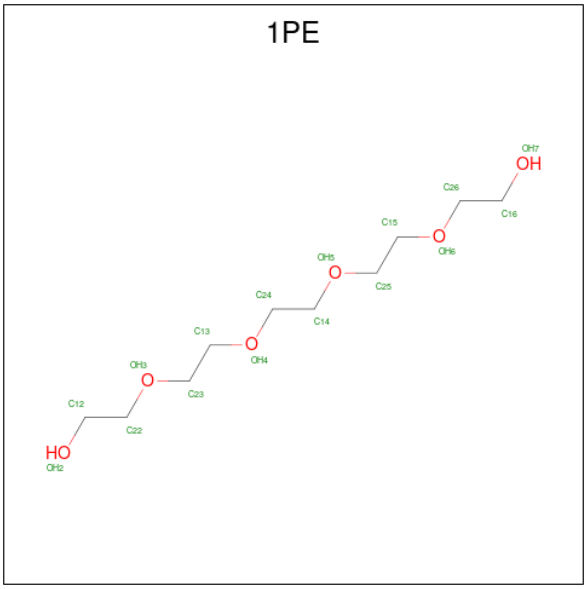
There are 6 unique types of molecules in this entry. The entry contains 6957 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

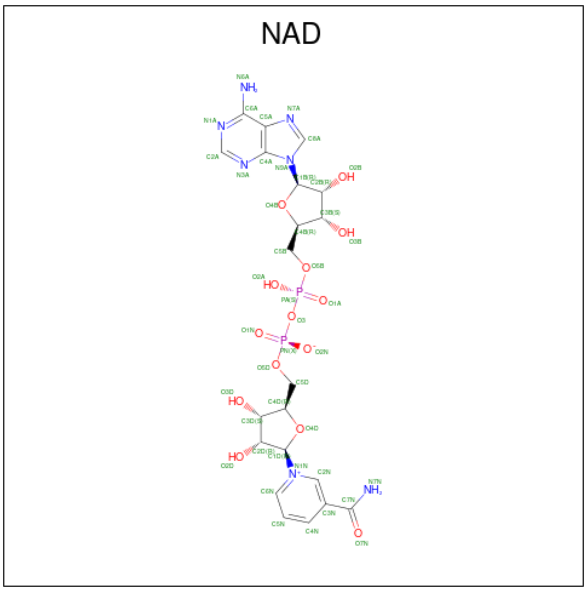
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	0	1	0
			3175	1993	560	603	19			
1	C	413	Total	C	N	O	S	0	0	0
			3159	1984	555	601	19			

- Molecule 2 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



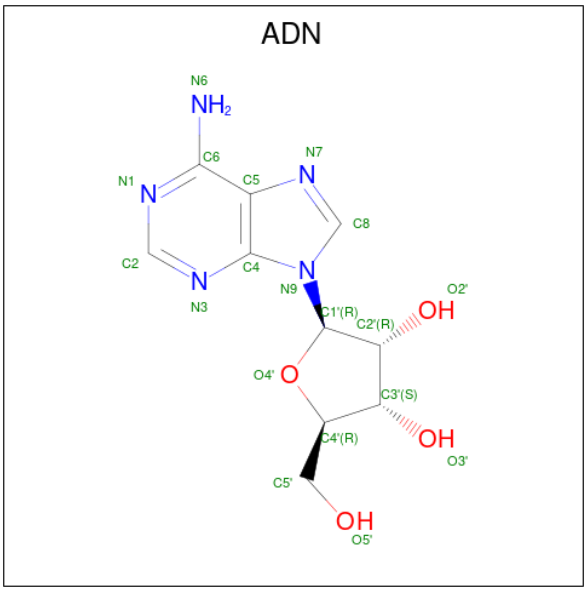
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O		0	0
			16	10	6			

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is ADENOSINE (three-letter code: ADN) (formula: $C_{10}H_{13}N_5O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			19	10	5	4		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 2 2	0	1
5	C	1	Total Cl 1 1	0	0

- Molecule 6 is water.

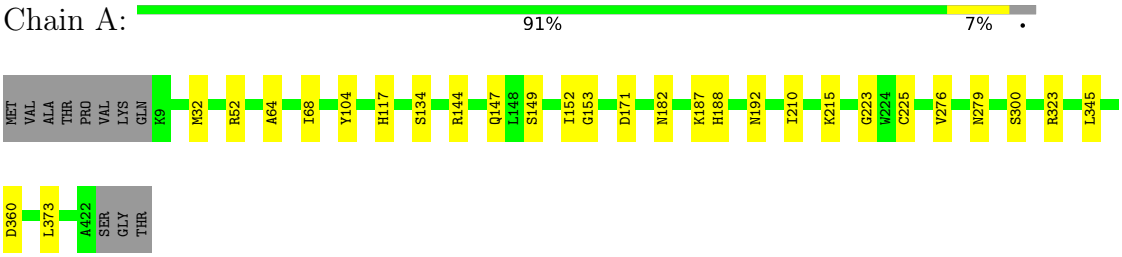
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	303	Total O 309 309	0	12
6	C	186	Total O 188 188	0	3

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.

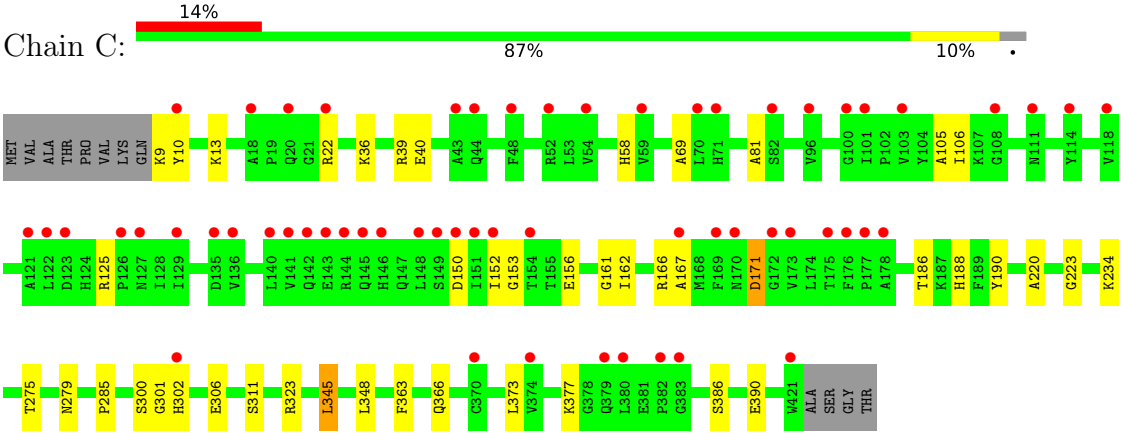
• Molecule 1: Adenosylhomocysteinase

Chain A:



• Molecule 1: Adenosylhomocysteinase

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	120.77Å 197.13Å 82.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.27 – 2.20 48.67 – 2.20	Depositor EDS
% Data completeness (in resolution range)	93.3 (42.27-2.20) 93.3 (48.67-2.20)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.22 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.19	Depositor
R, R_{free}	0.192 , 0.249 0.192 , 0.249	Depositor DCC
R_{free} test set	1033 reflections (2.20%)	wwPDB-VP
Wilson B-factor (Å^2)	22.6	Xtriage
Anisotropy	0.448	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.000 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.013 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6957	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.72% 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: ADN, 1PE, NAD, CL

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	0.31	0/3230	0.55	0/4379
1	C	0.31	0/3214	0.53	0/4358
All	All	0.31	0/6444	0.54	0/8737

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	3175	0	3172	12	0
1	C	3159	0	3155	24	0
2	A	16	0	22	1	0
3	A	44	0	26	3	0
3	C	44	0	26	2	0
4	A	19	0	13	1	0
5	A	2	0	0	0	0
5	C	1	0	0	0	0
6	A	309	0	0	1	0
6	C	188	0	0	0	0
All	All	6957	0	6414	37	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 3.

All (37) 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:39:ARG:HG3	1:C:69:ALA:HA	1.69	0.75
1:C:153:GLY:HA3	1:C:373:LEU:HD22	1.72	0.72
3:A:502:NAD:C4N	4:A:503:ADN:H3'	2.29	0.63
1:A:153:GLY:HA3	1:A:373:LEU:HD22	1.86	0.57
1:A:64:ALA:O	1:A:68:ILE:HG12	2.05	0.56
1:C:345:LEU:HD12	1:C:345:LEU:H	1.71	0.54
1:A:104:TYR:HB3	1:A:117:HIS:CD2	2.46	0.51
1:C:167:ALA:O	1:C:171:ASP:HB2	2.12	0.49
1:C:363:PHE:HA	1:C:366:GLN:HB2	1.94	0.49
1:C:39:ARG:HH21	1:C:40:GLU:HG3	1.77	0.48
1:A:210:ILE:HD11	1:A:215:LYS:HE2	1.95	0.48
1:C:152:ILE:HD12	1:C:377:LYS:HG3	1.94	0.48
1:C:302:HIS:O	1:C:345:LEU:HD11	2.14	0.48
1:A:152:ILE:HD11	2:A:501:1PE:H261	1.95	0.48
1:C:390:GLU:CD	1:C:390:GLU:H	2.16	0.47
1:A:192:ASN:O	1:A:225:CYS:HA	2.15	0.45
1:A:32:MET:HA	1:A:360:ASP:CG	2.37	0.45
1:C:345:LEU:HD23	3:C:501:NAD:N7N	2.32	0.45
1:C:279:ASN:O	1:C:306:GLU:HG2	2.17	0.45
1:C:81:ALA:HB2	1:C:105:ALA:HB1	1.99	0.44
1:A:279:ASN:ND2	3:A:502:NAD:N7A	2.65	0.44
1:A:52:ARG:NH2	6:A:614:HOH:O	2.50	0.44
1:C:301:GLY:HA3	1:C:306:GLU:OE2	2.17	0.44
1:A:144:ARG:HB3	1:A:147:GLN:HB2	2.00	0.43
1:C:186:THR:HA	1:C:190:TYR:CE2	2.52	0.43
1:C:13:LYS:HB2	1:C:106:ILE:HG23	2.01	0.43
1:C:162:ILE:O	1:C:166:ARG:HG3	2.19	0.42
1:C:220:ALA:HB3	1:C:275:THR:HA	2.01	0.42
1:A:182:ASN:HA	1:A:187:LYS:HD2	2.02	0.42
1:A:223:GLY:HA3	3:A:502:NAD:O5B	2.21	0.41
1:C:125:ARG:NE	1:C:150:ASP:OD2	2.52	0.41
1:C:9:LYS:HD2	1:C:10:TYR:CE2	2.56	0.41
1:C:285:PRO:HG3	1:C:311:SER:CB	2.51	0.41
1:C:58:HIS:CE1	1:C:348:LEU:HD13	2.55	0.41
1:C:156:GLU:CD	1:C:161:GLY:HA3	2.42	0.41
1:C:223:GLY:HA3	3:C:501:NAD:O5B	2.21	0.40
1:C:9:LYS:HG3	1:C:10:TYR:N	2.36	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	413/425 (97%)	400 (97%)	12 (3%)	1 (0%)	47 55
1	C	411/425 (97%)	395 (96%)	15 (4%)	1 (0%)	47 55
All	All	824/850 (97%)	795 (96%)	27 (3%)	2 (0%)	47 55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	345	LEU
1	A	345	LEU

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	336/344 (98%)	329 (98%)	7 (2%)	53 67
1	C	335/344 (97%)	327 (98%)	8 (2%)	49 62
All	All	671/688 (98%)	656 (98%)	15 (2%)	52 65

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	134	SER

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Mol	Chain	Res	Type
1	A	149	SER
1	A	171	ASP
1	A	188	HIS
1	A	276	VAL
1	A	300	SER
1	A	323	ARG
1	C	22	ARG
1	C	36	LYS
1	C	171	ASP
1	C	188	HIS
1	C	234	LYS
1	C	300	SER
1	C	323	ARG
1	C	386	SER

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 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	$\#\|Z\|>2$
3	NAD	A	502	-	42,48,48	0.54	0	50,73,73	0.72	1 (2%)
4	ADN	A	503	-	18,21,21	0.63	0	18,31,31	0.96	2 (11%)
2	1PE	A	501	-	15,15,15	0.18	0	14,14,14	0.07	0
3	NAD	C	501	-	42,48,48	0.55	0	50,73,73	0.65	1 (2%)

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
3	NAD	A	502	-	-	6/26/62/62	0/5/5/5
4	ADN	A	503	-	-	0/2/22/22	0/3/3/3
2	1PE	A	501	-	-	6/13/13/13	-
3	NAD	C	501	-	-	5/26/62/62	0/5/5/5

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	501	NAD	C5A-C6A-N6A	2.31	123.87	120.35
3	A	502	NAD	C5A-C6A-N6A	2.31	123.86	120.35
4	A	503	ADN	C5-C6-N6	2.29	123.84	120.35
4	A	503	ADN	C3'-C2'-C1'	2.13	104.18	100.98

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	NAD	O4D-C1D-N1N-C2N
3	A	502	NAD	O4D-C1D-N1N-C6N
3	A	502	NAD	C2D-C1D-N1N-C2N
3	A	502	NAD	C2D-C1D-N1N-C6N
3	C	501	NAD	O4D-C1D-N1N-C2N
3	C	501	NAD	O4D-C1D-N1N-C6N
3	C	501	NAD	C2D-C1D-N1N-C2N
3	C	501	NAD	C2D-C1D-N1N-C6N
2	A	501	1PE	OH5-C14-C24-OH4
2	A	501	1PE	OH4-C13-C23-OH3
2	A	501	1PE	C24-C14-OH5-C25

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Mol	Chain	Res	Type	Atoms
2	A	501	1PE	C23-C13-OH4-C24
2	A	501	1PE	C16-C26-OH6-C15
2	A	501	1PE	C15-C25-OH5-C14
3	A	502	NAD	O4B-C4B-C5B-O5B
3	C	501	NAD	O4B-C4B-C5B-O5B
3	A	502	NAD	C5B-O5B-PA-O1A

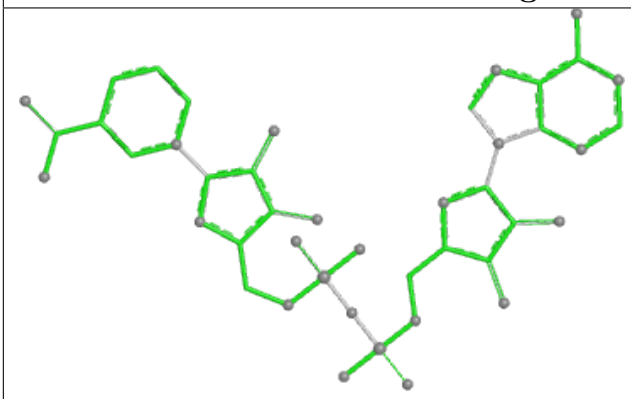
There are no ring outliers.

4 monomers are involved in 6 short contacts:

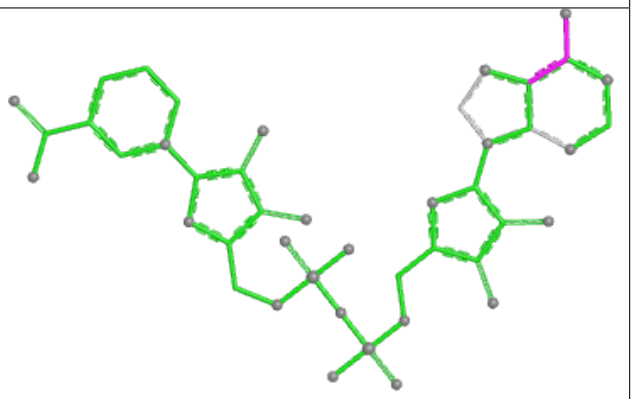
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	NAD	3	0
4	A	503	ADN	1	0
2	A	501	1PE	1	0
3	C	501	NAD	2	0

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.

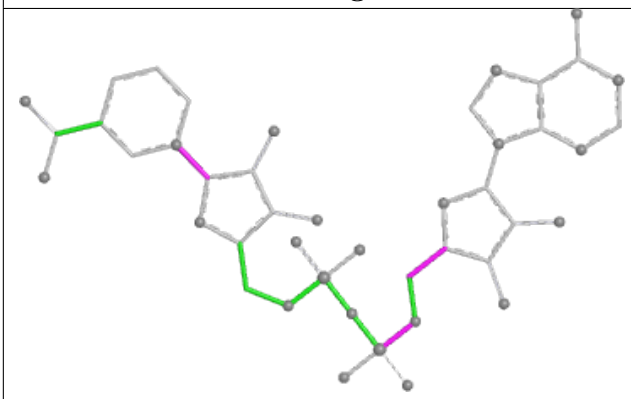
Ligand NAD A 502



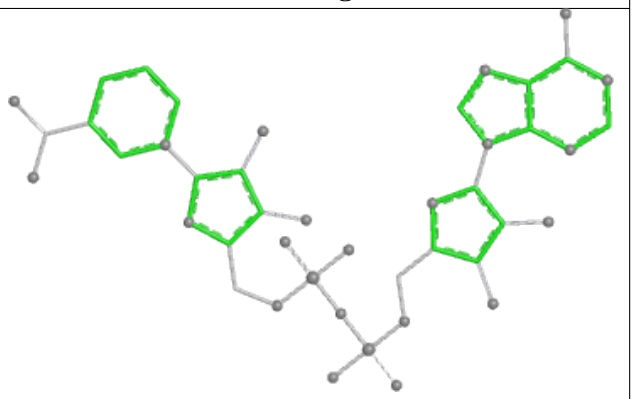
Bond lengths



Bond angles

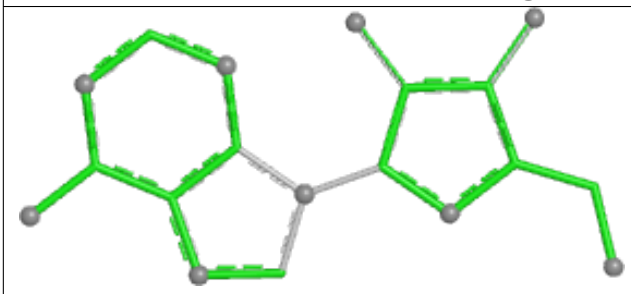


Torsions

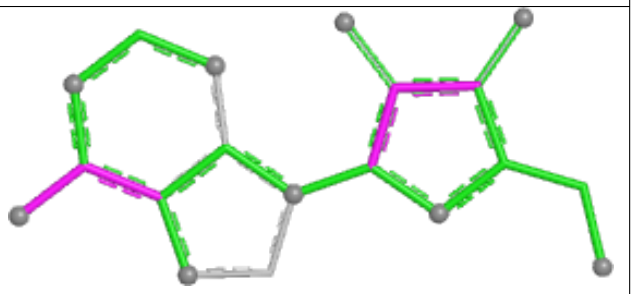


Rings

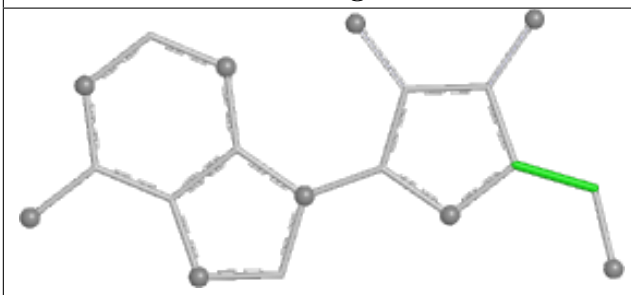
Ligand ADN A 503



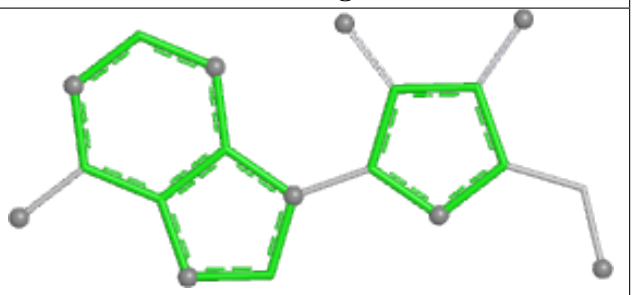
Bond lengths



Bond angles

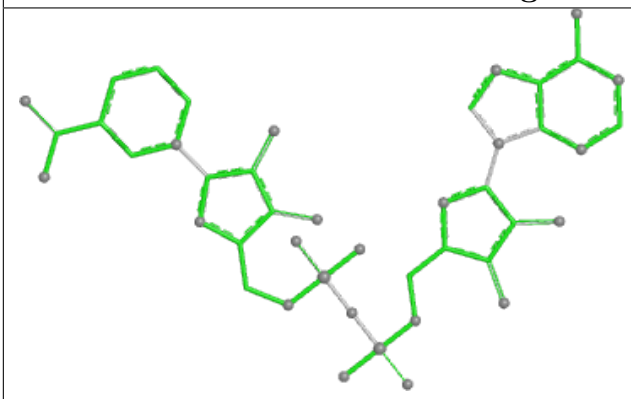


Torsions

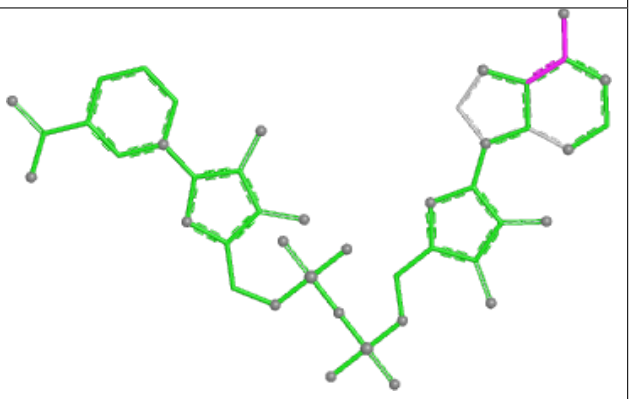


Rings

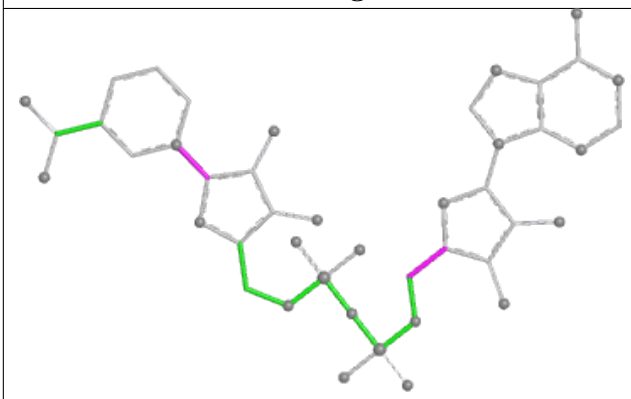
Ligand NAD C 501



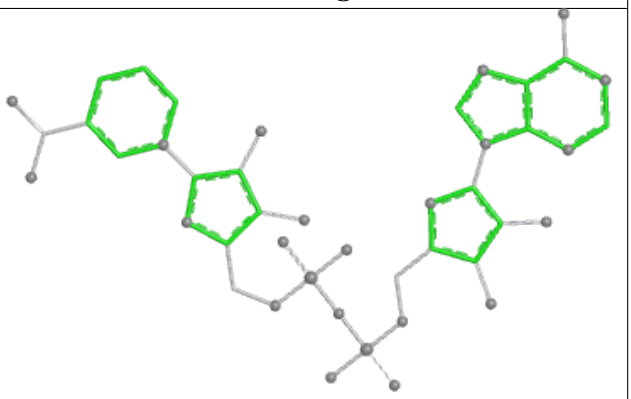
Bond lengths



Bond angles



Torsions



Rings

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	414/425 (97%)	-0.16	0 100 100	13, 22, 35, 51	0
1	C	413/425 (97%)	0.66	59 (14%) 2 2	13, 35, 60, 85	0
All	All	827/850 (97%)	0.25	59 (7%) 16 14	13, 24, 55, 85	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	118	VAL	6.4
1	C	126	PRO	6.3
1	C	121	ALA	5.3
1	C	141	VAL	5.2
1	C	151	ILE	4.8
1	C	122	LEU	4.8
1	C	169	PHE	4.7
1	C	152	ILE	4.4
1	C	382	PRO	4.2
1	C	144	ARG	4.1
1	C	176	PHE	4.0
1	C	302	HIS	3.9
1	C	18	ALA	3.9
1	C	136	VAL	3.7
1	C	379	GLN	3.7
1	C	54	VAL	3.5
1	C	123	ASP	3.4
1	C	96	VAL	3.4
1	C	140	LEU	3.2
1	C	142	GLN	3.2
1	C	145	GLN	3.1
1	C	370	CYS	3.1
1	C	10	TYR	3.1
1	C	175	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	111	ASN	3.0
1	C	167	ALA	3.0
1	C	374	VAL	3.0
1	C	70	LEU	3.0
1	C	129	ILE	3.0
1	C	421	TRP	2.9
1	C	43	ALA	2.9
1	C	114	TYR	2.9
1	C	44	GLN	2.8
1	C	82	SER	2.7
1	C	48	PHE	2.7
1	C	149	SER	2.7
1	C	150	ASP	2.6
1	C	170	ASN	2.6
1	C	108	GLY	2.5
1	C	177	PRO	2.5
1	C	59	VAL	2.5
1	C	173	VAL	2.3
1	C	383	GLY	2.3
1	C	146	HIS	2.3
1	C	52	ARG	2.3
1	C	127	ASN	2.3
1	C	380	LEU	2.3
1	C	22	ARG	2.2
1	C	178	ALA	2.2
1	C	101	ILE	2.2
1	C	20	GLN	2.2
1	C	154	THR	2.1
1	C	148	LEU	2.1
1	C	103	VAL	2.1
1	C	71	HIS	2.0
1	C	100	GLY	2.0
1	C	172	GLY	2.0
1	C	143	GLU	2.0
1	C	135	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 monosaccharides in this entry.

6.4 Ligands (i)

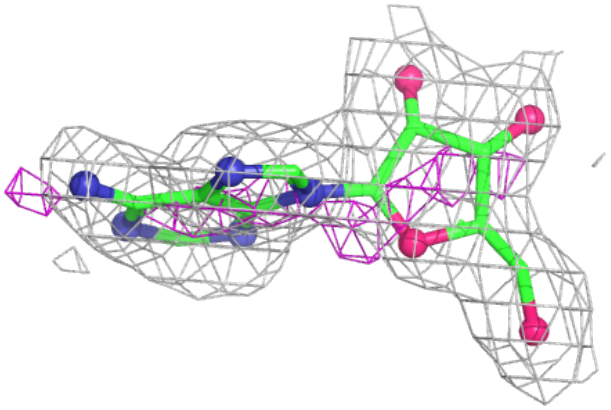
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

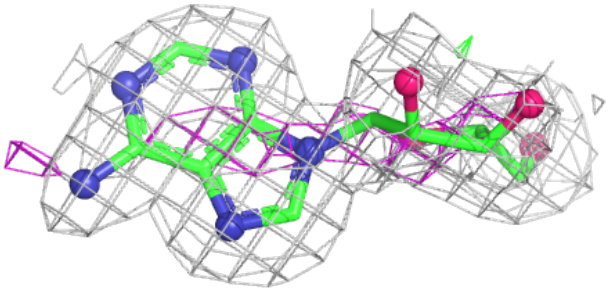
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	ADN	A	503	19/19	0.80	0.20	14,25,35,36	0
5	CL	C	502	1/1	0.82	0.16	65,65,65,65	0
2	1PE	A	501	16/16	0.83	0.22	29,35,41,42	16
5	CL	A	504[B]	1/1	0.95	0.22	26,26,26,26	1
5	CL	A	504[A]	1/1	0.95	0.22	39,39,39,39	1
3	NAD	A	502	44/44	0.96	0.13	11,18,23,24	0
3	NAD	C	501	44/44	0.96	0.12	11,19,23,27	0

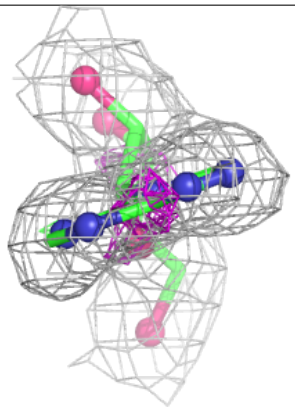
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADN 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)

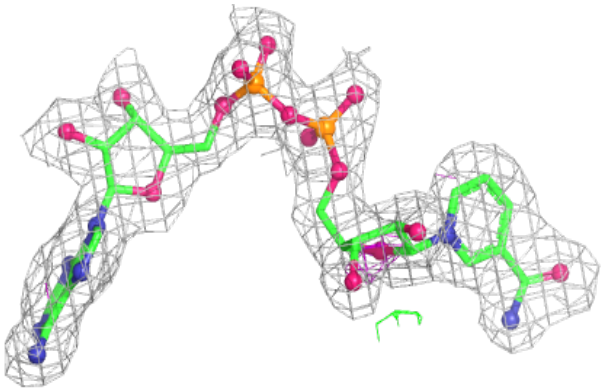


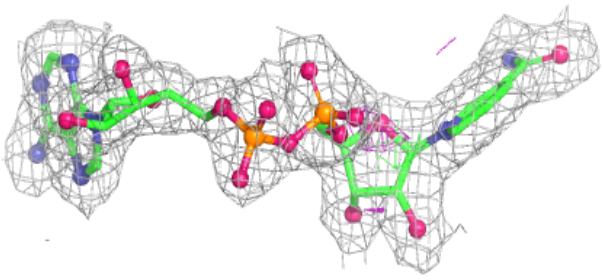


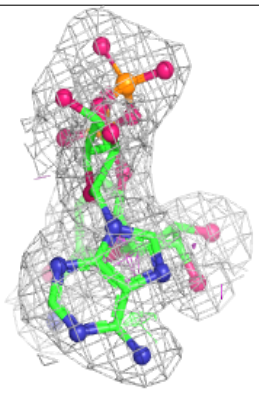


Electron density around NAD A 502:

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

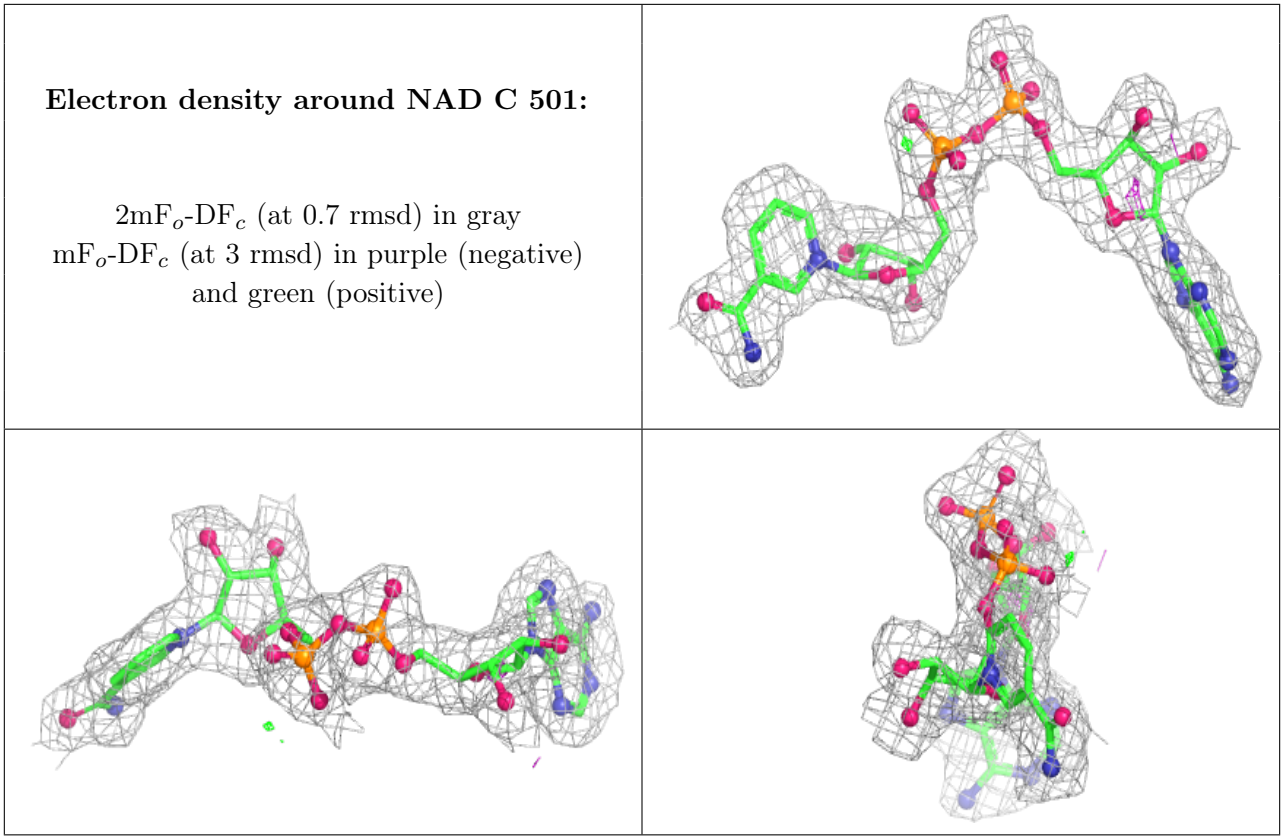






Electron density around NAD C 501:

$2mF_o$-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.