Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 01:21 pm BST

PDB ID	:	4TVB
Title	:	Crystal Structure of the Homospermidine Synthase (HSS) from Blastochloris viridis in Complex with NAD, Putrescine and sym-Homospermidine
Authors	:	Krossa, S.
Deposited on	:	2014-06-26
Resolution	:	1.69 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:

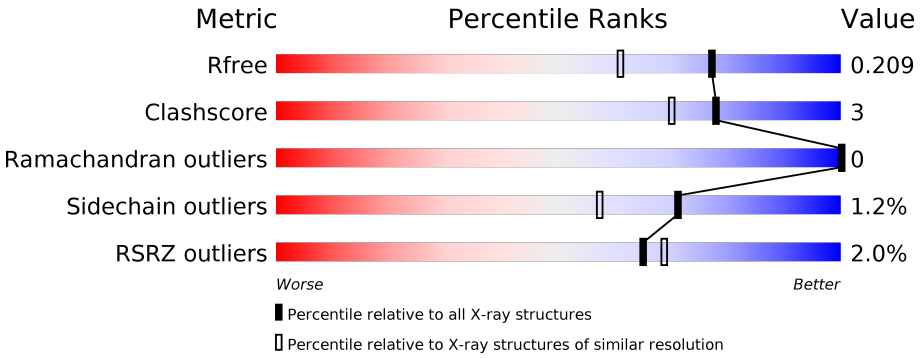
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.69 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	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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 on 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	479	2% 96%
1	B	479	2% 94% 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
3	37Z	A	502	-	-	X	-
6	PUT	B	502	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16180 atoms, of which 7307 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.

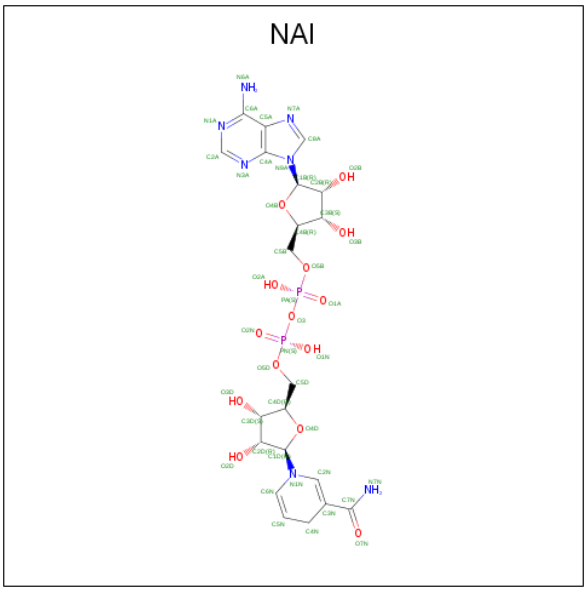
- Molecule 1 is a protein called Homospermidine synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	475	Total	C	H	N	O	S	0	2	0
			7332	2360	3605	651	700	16			
1	B	475	Total	C	H	N	O	S	0	3	0
			7336	2362	3606	649	702	17			

There are 4 discrepancies between the modelled and reference sequences:

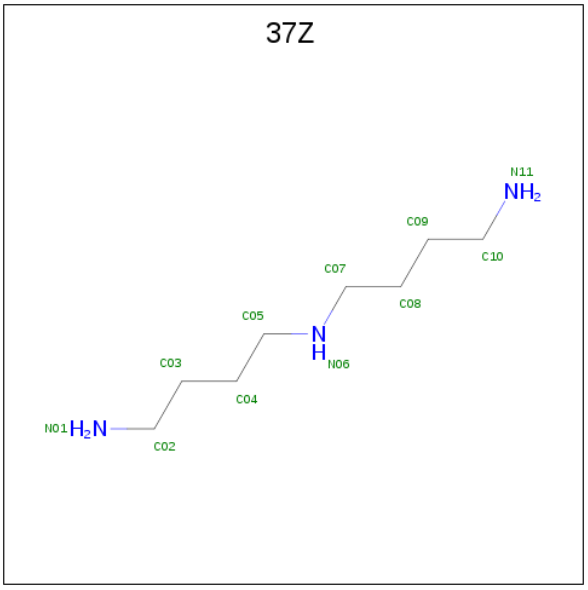
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP O32323
A	0	PRO	-	expression tag	UNP O32323
B	-1	GLY	-	expression tag	UNP O32323
B	0	PRO	-	expression tag	UNP O32323

- Molecule 2 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$).



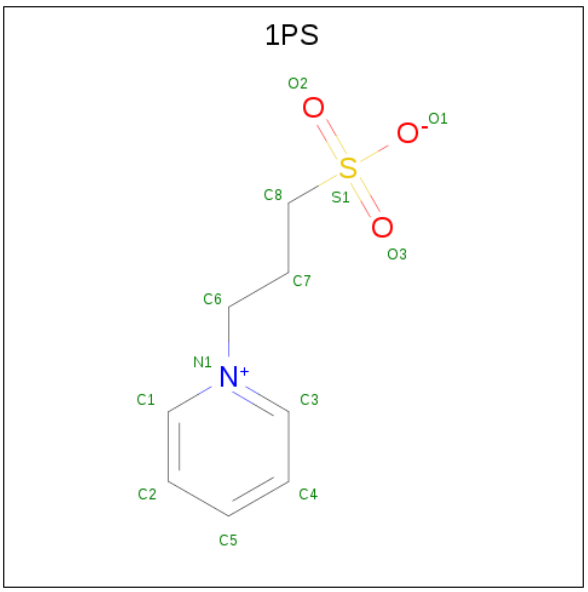
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			70	21	26	7	14	2		

- Molecule 3 is sym-homospermidine (three-letter code: 37Z) (formula: $C_8H_{21}N_3$).



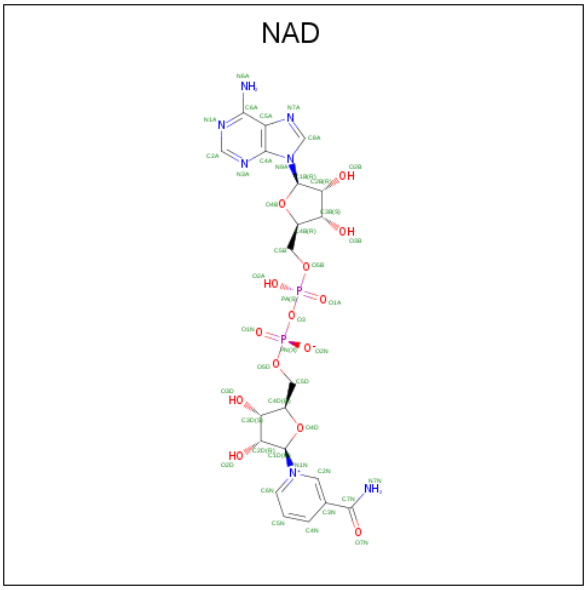
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	N	0	0
			31	8	20	3		

- Molecule 4 is 3-PYRIDINIUM-1-YLPROPANE-1-SULFONATE (three-letter code: 1PS) (formula: $C_8H_{11}NO_3S$).



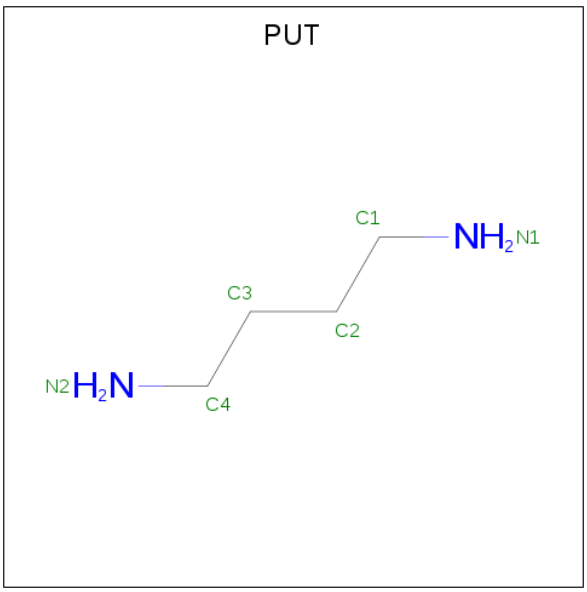
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	S	0	0
			24	8	11	1	3	1		

- Molecule 5 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	B	1	Total	C	H	N	O	P	0	0
			70	21	26	7	14	2		

- Molecule 6 is 1,4-DIAMINOBUTANE (three-letter code: PUT) (formula: $C_4H_{12}N_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	H	N	0	0
			19	4	13	2		

- Molecule 7 is water.

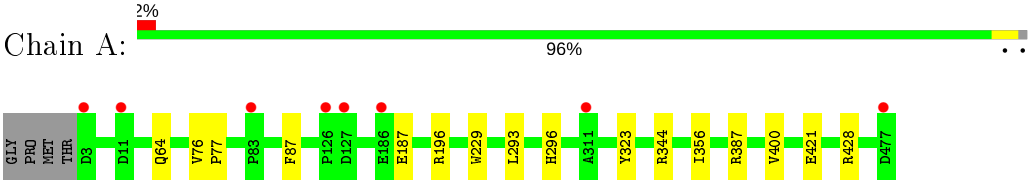
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	667	Total	O	0	0
			667	667		
7	B	631	Total	O	0	0
			631	631		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

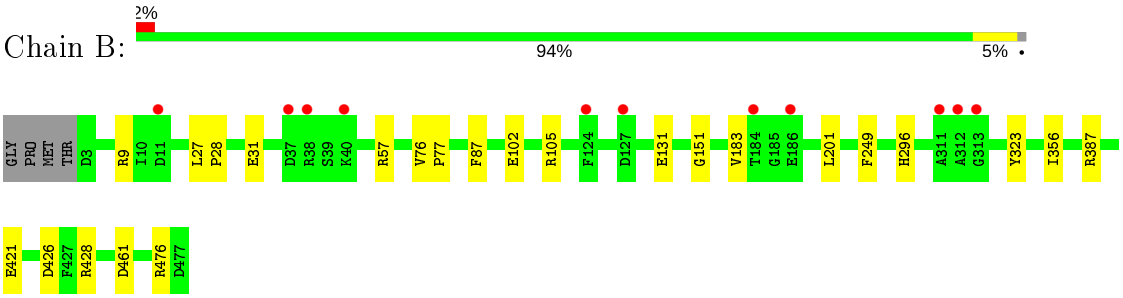
- Molecule 1: Homospermidine synthase

Chain A:



- Molecule 1: Homospermidine synthase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α, β, γ	59.51Å 109.25Å 157.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	9.99 – 1.69 89.72 – 1.69	Depositor EDS
% Data completeness (in resolution range)	97.9 (9.99-1.69) 87.7 (89.72-1.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.25	Depositor
$< I/\sigma(I) >$ [1]	0.64 (at 1.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.179 , 0.206 0.182 , 0.209	Depositor DCC
R_{free} test set	5690 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	14.9	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 40.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	16180	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 4.50% 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: 37Z, PUT, NAI, NAD, 1PS

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	0/3823	0.50	0/5210
1	B	0.29	0/3826	0.48	0/5214
All	All	0.30	0/7649	0.49	0/10424

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	3727	3605	3601	10	0
1	B	3730	3606	3601	14	0
2	A	44	26	27	12	0
3	A	11	20	21	13	0
4	A	13	11	11	0	0
5	B	44	26	26	8	0
6	B	6	13	12	8	0
7	A	667	0	0	4	4
7	B	631	0	0	7	1
All	All	8873	7307	7299	43	4

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 (43) 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)
2:A:501:NAI:H42N	3:A:502:37Z:C05	1.24	1.63
5:B:501:NAD:C4N	6:B:502:PUT:H42	1.19	1.59
2:A:501:NAI:C4N	3:A:502:37Z:H1	1.39	1.52
5:B:501:NAD:C4N	6:B:502:PUT:C4	2.16	1.23
2:A:501:NAI:C5N	3:A:502:37Z:H1	1.74	1.17
5:B:501:NAD:H4N	6:B:502:PUT:H42	1.25	1.09
2:A:501:NAI:H42N	3:A:502:37Z:N06	1.77	1.00
2:A:501:NAI:C4N	3:A:502:37Z:C05	2.15	0.98
2:A:501:NAI:H42N	3:A:502:37Z:C04	1.97	0.94
5:B:501:NAD:C3N	6:B:502:PUT:H42	2.00	0.91
5:B:501:NAD:C5N	6:B:502:PUT:H42	2.08	0.81
2:A:501:NAI:H42N	3:A:502:37Z:H1	0.78	0.77
1:B:428:ARG:NH2	7:B:747:HOH:O	2.19	0.76
1:A:344:ARG:NH1	7:A:954:HOH:O	2.19	0.75
1:A:356:ILE:O	1:A:387:ARG:NH2	2.21	0.74
5:B:501:NAD:H4N	6:B:502:PUT:C4	2.02	0.74
2:A:501:NAI:C4N	3:A:502:37Z:N06	2.44	0.74
1:B:105:ARG:NH2	1:B:151:GLY:O	2.25	0.70
1:A:421:GLU:OE2	7:A:1259:HOH:O	2.11	0.68
1:B:131:GLU:OE1	7:B:1018:HOH:O	2.11	0.66
2:A:501:NAI:C3N	3:A:502:37Z:N06	2.60	0.64
1:B:461:ASP:OD2	7:B:981:HOH:O	2.15	0.60
1:A:187:GLU:OE2	1:A:428:ARG:NH2	2.36	0.57
1:A:64:GLN:NE2	7:A:604:HOH:O	2.36	0.57
1:B:31:GLU:OE1	1:B:57:ARG:NH2	2.38	0.57
1:B:426:ASP:OD1	7:B:920:HOH:O	2.18	0.56
1:B:356:ILE:O	1:B:387:ARG:NH2	2.33	0.56
2:A:501:NAI:C5N	3:A:502:37Z:C05	2.67	0.54
5:B:501:NAD:H4N	6:B:502:PUT:C3	2.37	0.54
1:A:229:TRP:CD2	3:A:502:37Z:H2	2.43	0.53
1:B:131:GLU:OE2	7:B:1074:HOH:O	2.19	0.51
1:A:400:VAL:HG21	2:A:501:NAI:H4N	1.94	0.50
1:B:183:VAL:HG21	1:B:201:LEU:HD23	1.96	0.48
1:B:461:ASP:O	1:B:476:ARG:NH2	2.48	0.47
2:A:501:NAI:C3N	3:A:502:37Z:H3	2.27	0.46
1:A:76:VAL:HB	1:A:77:PRO:HD3	1.98	0.45
1:A:196:ARG:NH2	7:A:608:HOH:O	2.50	0.45
5:B:501:NAD:C5N	6:B:502:PUT:C4	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:TRP:CE2	3:A:502:37Z:H2	2.52	0.44
1:B:76:VAL:HB	1:B:77:PRO:HD3	2.02	0.42
1:B:102:GLU:OE1	7:B:964:HOH:O	2.21	0.42
1:B:421:GLU:OE2	7:B:1191:HOH:O	2.21	0.41
1:B:27:LEU:N	1:B:28:PRO:HD2	2.35	0.41

All (4) 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)
7:A:649:HOH:O	7:A:695:HOH:O[3_555]	2.13	0.07
7:A:709:HOH:O	7:A:731:HOH:O[3_545]	2.14	0.06
7:A:716:HOH:O	7:B:641:HOH:O[4_555]	2.14	0.06
7:A:614:HOH:O	7:A:689:HOH:O[3_545]	2.18	0.02

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	475/479 (99%)	464 (98%)	11 (2%)	0	100	100
1	B	476/479 (99%)	461 (97%)	15 (3%)	0	100	100
All	All	951/958 (99%)	925 (97%)	26 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	391/392 (100%)	387 (99%)	4 (1%)	76	65
1	B	392/392 (100%)	387 (99%)	5 (1%)	69	54
All	All	783/784 (100%)	774 (99%)	9 (1%)	71	61

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	87	PHE
1	A	293	LEU
1	A	296	HIS
1	A	323	TYR
1	B	9	ARG
1	B	87	PHE
1	B	249	PHE
1	B	296	HIS
1	B	323	TYR

Some 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 carbohydrates in this entry.

5.6 Ligand geometry (i)

5 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	$\#\|Z\| > 2$
6	PUT	B	502	-	5,5,5	0.29	0	4,4,4	0.70	0
5	NAD	B	501	-	42,48,48	1.00	2 (4%)	50,73,73	1.39	5 (10%)
4	1PS	A	503	-	13,13,13	2.13	1 (7%)	17,17,17	1.28	2 (11%)
2	NAI	A	501	-	42,48,48	0.94	1 (2%)	47,73,73	1.22	4 (8%)
3	37Z	A	502	-	10,10,10	1.23	1 (10%)	9,9,9	2.25	3 (33%)

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
6	PUT	B	502	-	-	0/3/3/3	-
5	NAD	B	501	-	-	6/26/62/62	0/5/5/5
4	1PS	A	503	-	-	0/7/7/7	0/1/1/1
2	NAI	A	501	-	-	4/25/72/72	0/5/5/5
3	37Z	A	502	-	-	4/8/8/8	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	1PS	C8-S1	-7.31	1.67	1.77
5	B	501	NAD	C4N-C3N	4.14	1.46	1.39
3	A	502	37Z	C05-N06	-3.75	1.34	1.46
5	B	501	NAD	C5N-C4N	2.35	1.43	1.38
2	A	501	NAI	C4N-C5N	-2.00	1.43	1.48

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	502	37Z	C04-C05-N06	5.65	127.39	112.14
2	A	501	NAI	N3A-C2A-N1A	-4.35	121.88	128.68
5	B	501	NAD	N3A-C2A-N1A	-4.09	122.28	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	501	NAD	C5N-C4N-C3N	-3.96	115.65	120.34
4	A	503	1PS	O2-S1-C8	3.38	110.98	106.92
5	B	501	NAD	C3N-C7N-N7N	3.12	121.49	117.75
3	A	502	37Z	C08-C07-N06	-2.68	104.91	112.14
2	A	501	NAI	C1B-N9A-C4A	-2.62	122.04	126.64
5	B	501	NAD	N6A-C6A-N1A	2.49	123.74	118.57
5	B	501	NAD	C1B-N9A-C4A	-2.38	122.45	126.64
2	A	501	NAI	N6A-C6A-N1A	2.38	123.52	118.57
4	A	503	1PS	C7-C8-S1	-2.20	109.87	113.25
3	A	502	37Z	C07-N06-C05	2.06	123.17	113.45
2	A	501	NAI	C5A-C6A-N6A	-2.01	117.29	120.35

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	NAD	O4D-C1D-N1N-C2N
5	B	501	NAD	O4D-C1D-N1N-C6N
5	B	501	NAD	C2D-C1D-N1N-C2N
3	A	502	37Z	C04-C05-N06-C07
3	A	502	37Z	C03-C04-C05-N06
3	A	502	37Z	C07-C08-C09-C10
3	A	502	37Z	C02-C03-C04-C05
2	A	501	NAI	O4D-C1D-N1N-C2N
2	A	501	NAI	C2D-C1D-N1N-C2N
2	A	501	NAI	O4B-C4B-C5B-O5B
5	B	501	NAD	O4B-C4B-C5B-O5B
5	B	501	NAD	C2D-C1D-N1N-C6N
5	B	501	NAD	PN-O3-PA-O2A
2	A	501	NAI	PN-O3-PA-O2A

There are no ring outliers.

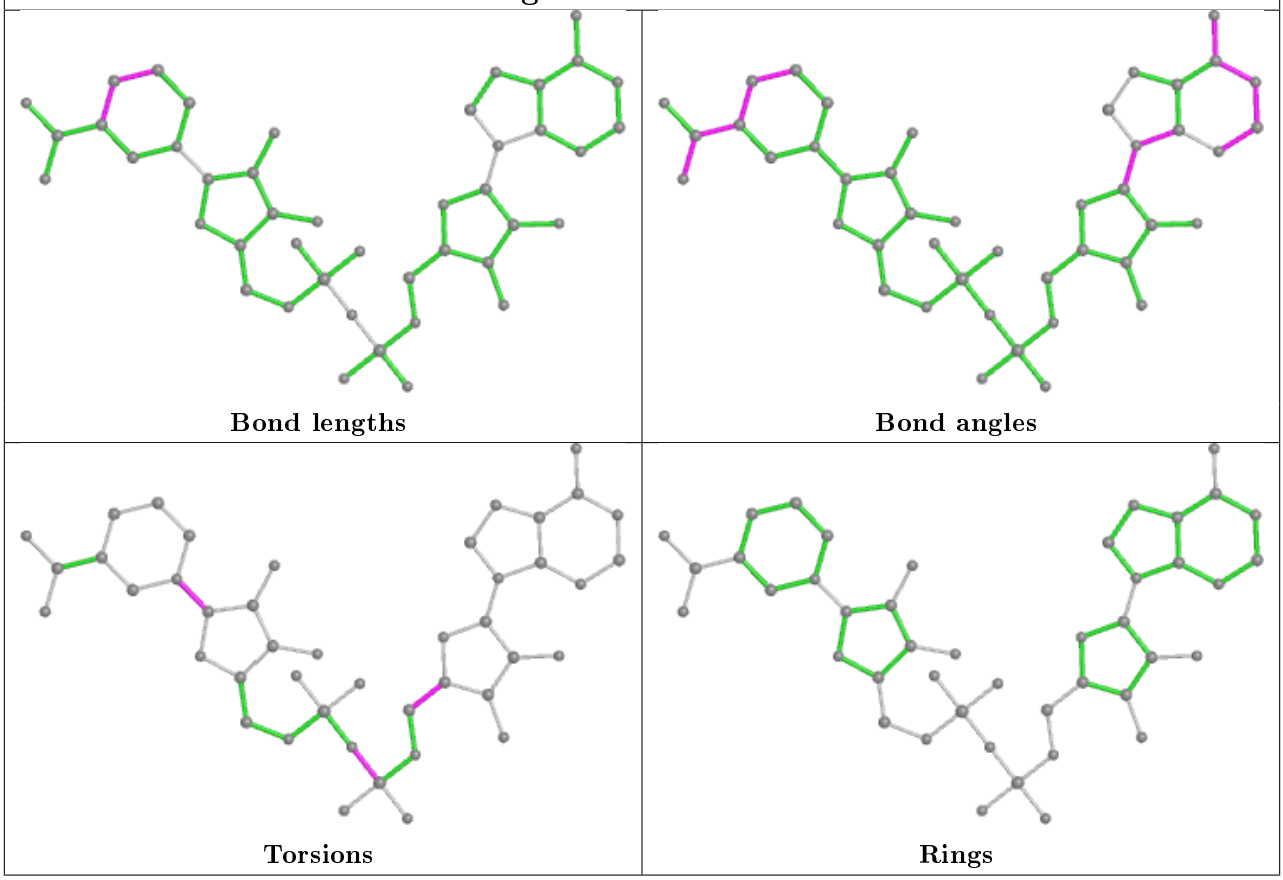
4 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	502	PUT	8	0
5	B	501	NAD	8	0
2	A	501	NAI	12	0
3	A	502	37Z	13	0

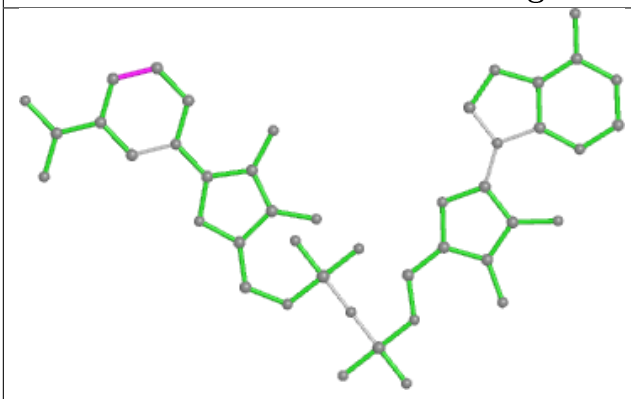
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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.

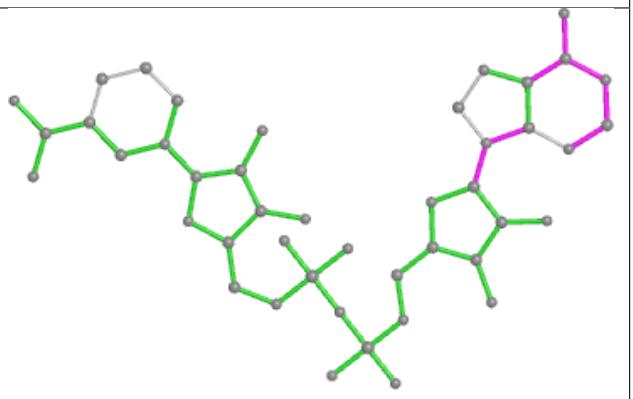
Ligand NAD B 501



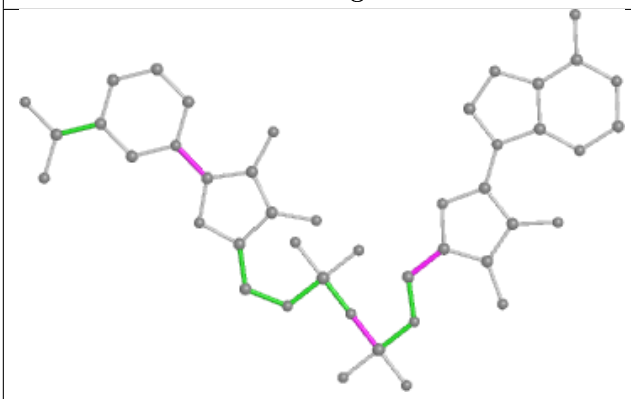
Ligand NAI A 501



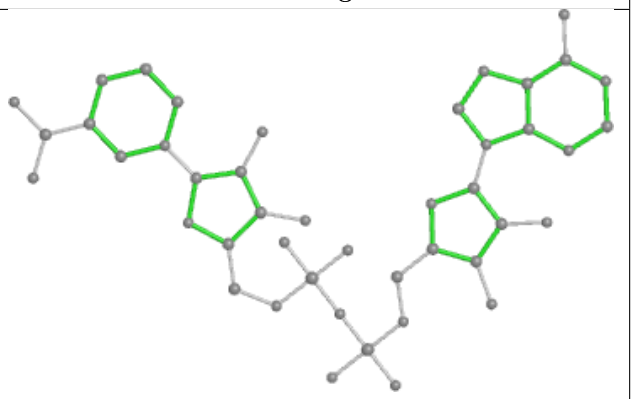
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	475/479 (99%)	-0.20	8 (1%)	70	74	12, 18, 29, 40	0
1	B	475/479 (99%)	-0.15	11 (2%)	60	64	13, 21, 32, 41	0
All	All	950/958 (99%)	-0.18	19 (2%)	65	69	12, 19, 31, 41	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	477	ASP	7.2
1	B	124	PHE	3.9
1	B	311	ALA	3.7
1	B	184	THR	2.9
1	A	186	GLU	2.8
1	B	312	ALA	2.6
1	A	126	PRO	2.6
1	B	313	GLY	2.5
1	B	40	LYS	2.5
1	B	127	ASP	2.4
1	A	83	PRO	2.4
1	B	38	ARG	2.3
1	B	37	ASP	2.3
1	A	311	ALA	2.3
1	A	3	ASP	2.2
1	A	127	ASP	2.2
1	B	11	ASP	2.2
1	A	11	ASP	2.1
1	B	186	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

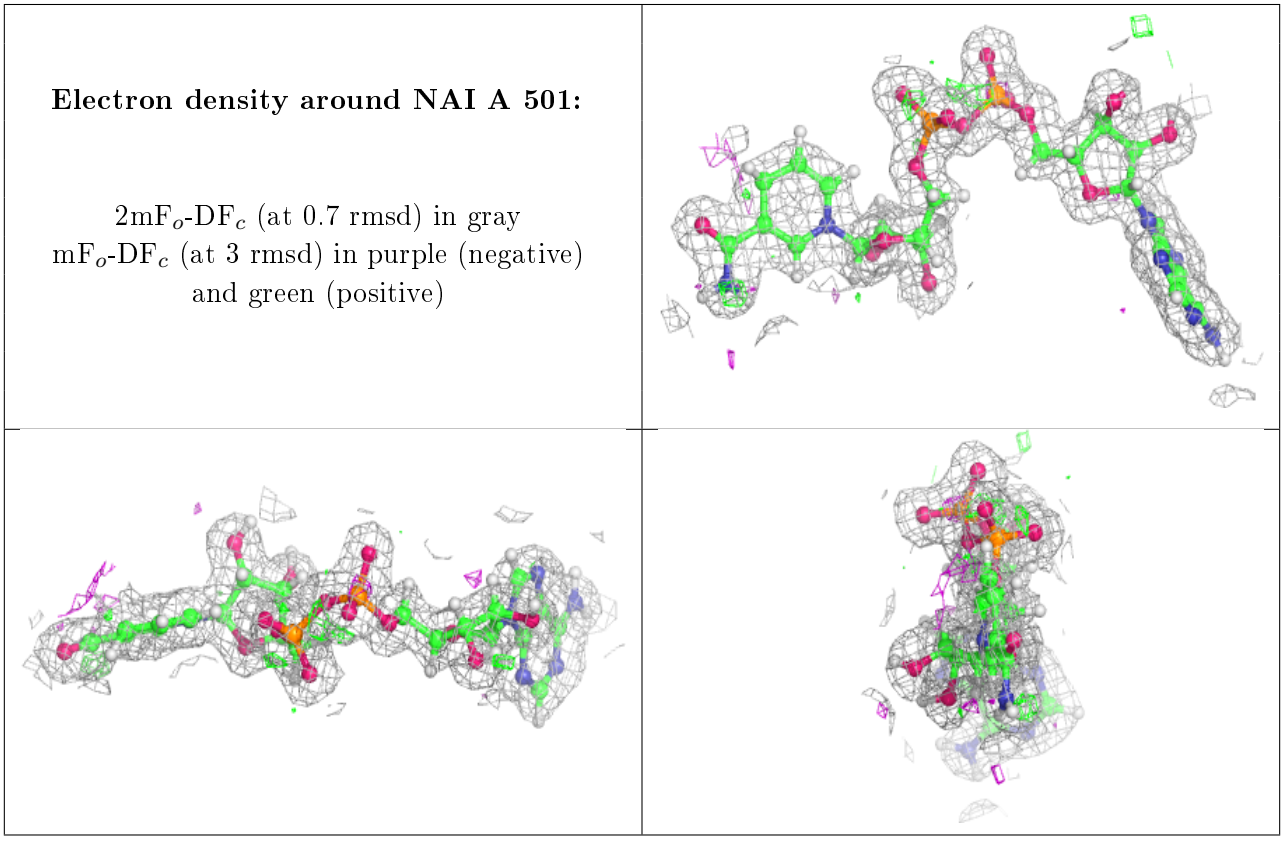
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
6	PUT	B	502	6/6	0.79	0.20	16,21,25,25	0
3	37Z	A	502	11/11	0.83	0.32	13,21,31,31	0
4	1PS	A	503	13/13	0.87	0.26	20,20,24,24	0
2	NAI	A	501	44/44	0.97	0.08	7,16,19,21	0
5	NAD	B	501	44/44	0.97	0.08	11,18,22,23	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.

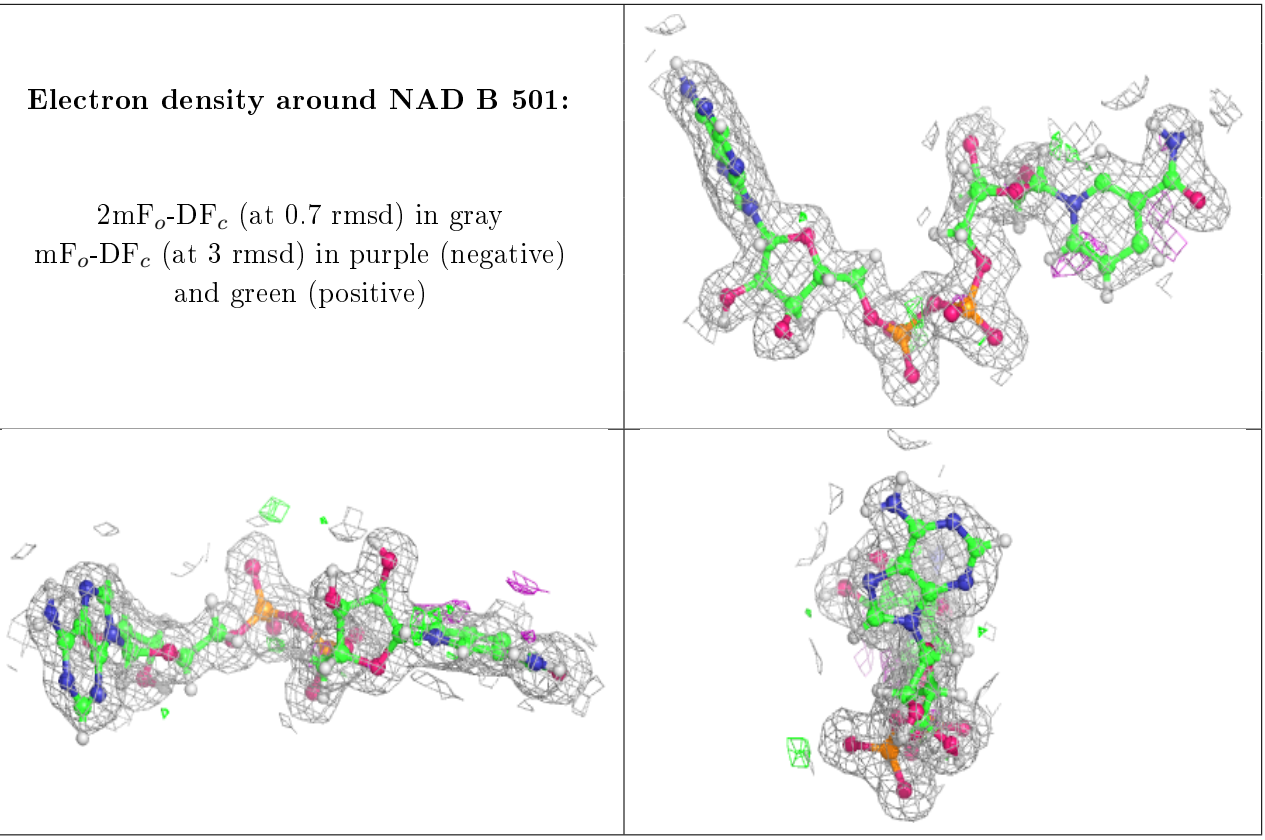
Electron density around NAI A 501:

$2mF_o$-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 B 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.