Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 07:30 pm BST

PDB ID	:	4A7P
Title	:	Se-Met derivatized UgdG, UDP-glucose dehydrogenase from Sphingomonas elodea
Authors	:	Rocha, J.; Granja, A.T.; Sa-Correia, I.; Fialho, A.M.; Frazao, C.
Deposited on	:	2011-11-14
Resolution	:	3.40 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:

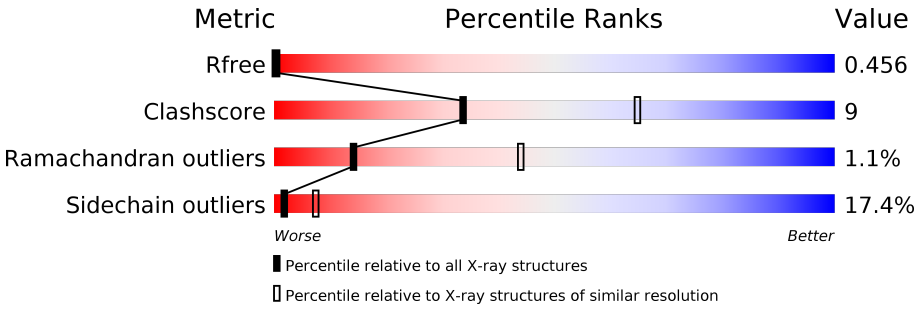
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 3.40 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)

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%

Mol	Chain	Length	Quality of chain
1	A	446	66% 25% 5% •
1	B	446	68% 23% 5% •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6557 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.

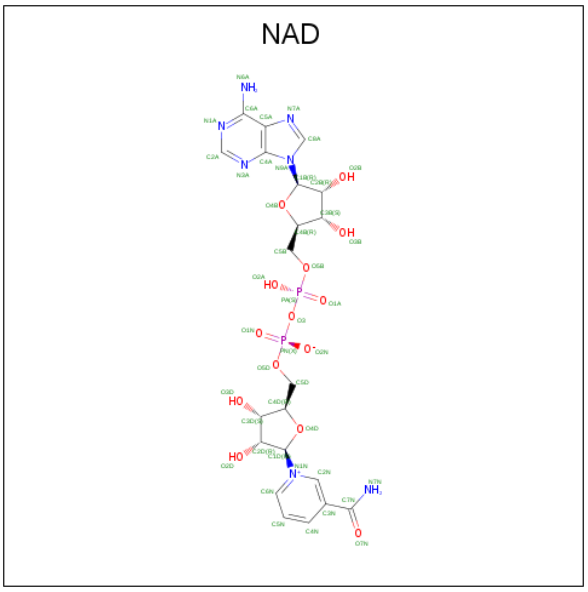
- Molecule 1 is a protein called UDP-GLUCOSE DEHYDROGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	429	Total	C	N	O	S	Se	0	0	0
			3234	2035	563	623	4	9			
1	B	429	Total	C	N	O	S	Se	0	0	0
			3235	2036	563	623	4	9			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	HIS	-	expression tag	UNP A4UTT2
A	-7	HIS	-	expression tag	UNP A4UTT2
A	-6	HIS	-	expression tag	UNP A4UTT2
A	-5	HIS	-	expression tag	UNP A4UTT2
A	-4	HIS	-	expression tag	UNP A4UTT2
A	-3	HIS	-	expression tag	UNP A4UTT2
A	-2	GLY	-	expression tag	UNP A4UTT2
A	-1	SER	-	expression tag	UNP A4UTT2
A	1	VAL	MET	SEE REMARK 999	UNP A4UTT2
B	-8	HIS	-	expression tag	UNP A4UTT2
B	-7	HIS	-	expression tag	UNP A4UTT2
B	-6	HIS	-	expression tag	UNP A4UTT2
B	-5	HIS	-	expression tag	UNP A4UTT2
B	-4	HIS	-	expression tag	UNP A4UTT2
B	-3	HIS	-	expression tag	UNP A4UTT2
B	-2	GLY	-	expression tag	UNP A4UTT2
B	-1	SER	-	expression tag	UNP A4UTT2
B	1	VAL	MET	SEE REMARK 999	UNP A4UTT2

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



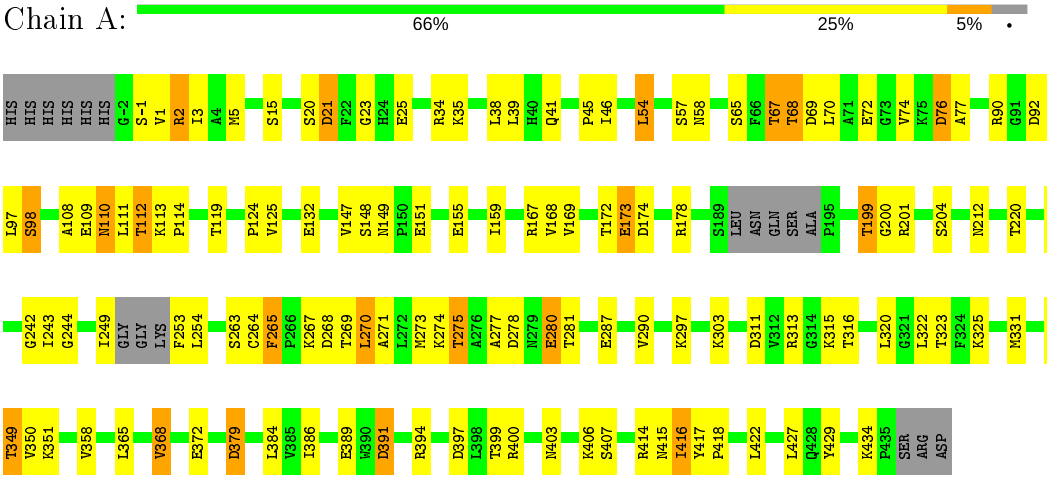
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

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. 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. 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.

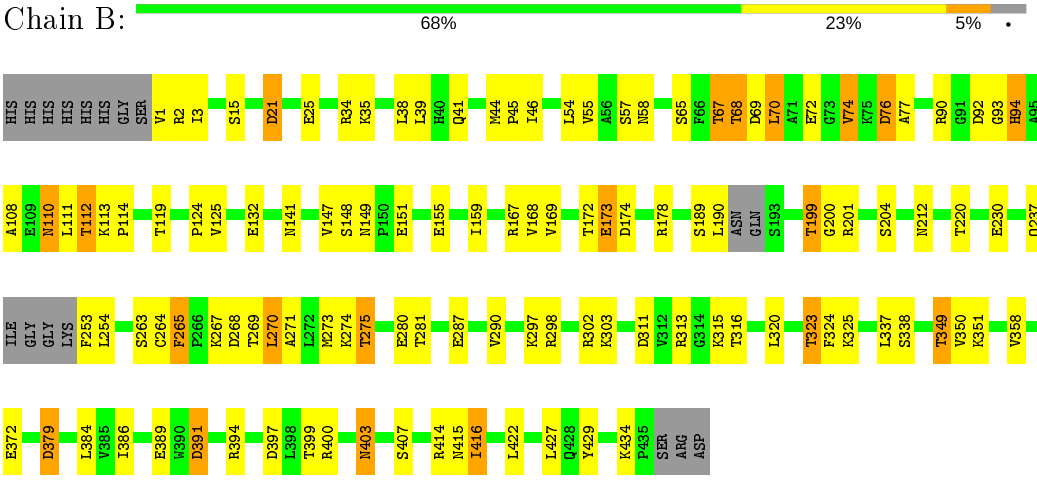
- Molecule 1: UDP-GLUCOSE DEHYDROGENASE

Chain A:



- Molecule 1: UDP-GLUCOSE DEHYDROGENASE

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	109.03Å 109.03Å 175.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.76 – 3.40 48.76 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.76-3.40) 99.2 (48.76-3.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.63 (at 3.40Å)	Xtriage
Refinement program		Depositor
R, R_{free}	0.230 , (Not available) 0.450 , 0.456	Depositor DCC
R_{free} test set	1014 reflections (6.72%)	wwPDB-VP
Wilson B-factor (Å^2)	226.7	Xtriage
Anisotropy	0.205	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 83.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.68$, $< L^2 > = 0.55$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	6557	wwPDB-VP
Average B, all atoms (Å^2)	130.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.65% 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: 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	0.26	0/3275	0.52	0/4422
1	B	0.26	0/3276	0.52	0/4425
All	All	0.26	0/6551	0.52	0/8847

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	3234	0	3264	61	1
1	B	3235	0	3265	56	1
2	A	44	0	26	0	0
2	B	44	0	26	0	0
All	All	6557	0	6581	112	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (112) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:THR:OG1	1:A:113:LYS:N	2.25	0.70
1:B:112:THR:OG1	1:B:113:LYS:N	2.24	0.68
1:B:351:LYS:NZ	1:B:379:ASP:O	2.29	0.65
1:A:2:ARG:HG2	1:A:77:ALA:HA	1.80	0.64
1:A:351:LYS:NZ	1:A:379:ASP:O	2.30	0.62
1:A:391:ASP:OD1	1:A:391:ASP:N	2.32	0.62
1:A:269:THR:OG1	1:A:270:LEU:N	2.34	0.61
1:B:2:ARG:HG2	1:B:77:ALA:HA	1.81	0.61
1:B:92:ASP:OD1	1:B:93:GLY:N	2.34	0.60
1:B:365:LEU:HB3	1:B:368:VAL:HG21	1.83	0.60
1:A:365:LEU:HB3	1:A:368:VAL:HG21	1.83	0.59
1:A:92:ASP:OD1	1:A:93:GLY:N	2.34	0.59
1:B:149:ASN:ND2	1:B:169:VAL:O	2.30	0.59
1:B:269:THR:OG1	1:B:270:LEU:N	2.34	0.59
1:B:311:ASP:OD2	1:B:313:ARG:NH1	2.36	0.59
1:A:149:ASN:ND2	1:A:169:VAL:O	2.30	0.57
1:B:391:ASP:OD1	1:B:391:ASP:N	2.32	0.57
1:B:271:ALA:O	1:B:275:THR:OG1	2.23	0.57
1:B:96:ASP:OD1	1:B:98:SER:OG	2.22	0.56
1:A:96:ASP:OD1	1:A:98:SER:OG	2.24	0.56
1:A:311:ASP:OD2	1:A:313:ARG:NH1	2.39	0.55
1:A:108:ALA:HA	1:A:111:LEU:HD22	1.90	0.54
1:A:94:HIS:HB2	1:A:274:LYS:HZ2	1.72	0.54
1:A:2:ARG:HA	1:A:25:GLU:HB2	1.90	0.54
1:A:271:ALA:O	1:A:275:THR:OG1	2.24	0.54
1:B:108:ALA:HA	1:B:111:LEU:HD22	1.89	0.54
1:B:1:VAL:O	1:B:25:GLU:N	2.39	0.53
1:A:57:SER:OG	1:A:58:ASN:N	2.42	0.53
1:B:2:ARG:HA	1:B:25:GLU:HB2	1.90	0.53
1:B:57:SER:OG	1:B:58:ASN:N	2.41	0.53
1:A:69:ASP:OD1	1:A:72:GLU:N	2.38	0.53
1:A:-1:SER:HB2	1:A:23:GLY:O	2.08	0.53
1:A:273:MSE:SE	1:A:287:GLU:HA	2.59	0.53
1:A:3:ILE:N	1:A:25:GLU:O	2.39	0.52
1:B:273:MSE:SE	1:B:287:GLU:HA	2.59	0.52
1:A:67:THR:OG1	1:A:68:THR:N	2.43	0.52
1:A:278:ASP:OD2	1:B:298:ARG:NH2	2.42	0.52
1:B:237:GLN:NE2	1:B:415:ASN:HB3	2.25	0.52
1:B:67:THR:OG1	1:B:68:THR:N	2.43	0.52
1:A:267:LYS:NZ	1:A:268:ASP:OD1	2.40	0.52
1:A:237:GLN:NE2	1:A:415:ASN:HB3	2.25	0.52
1:A:94:HIS:CG	1:A:274:LYS:HG2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:GLU:OE1	1:A:201:ARG:NH2	2.43	0.51
1:B:94:HIS:HB2	1:B:274:LYS:HZ2	1.75	0.51
1:A:244:GLY:HA2	1:A:249:ILE:HG21	1.92	0.51
1:B:132:GLU:OE1	1:B:201:ARG:NH2	2.42	0.51
1:B:391:ASP:HA	1:B:394:ARG:HG3	1.93	0.51
1:A:1:VAL:O	1:A:25:GLU:N	2.39	0.51
1:B:397:ASP:OD1	1:B:400:ARG:N	2.43	0.51
1:A:397:ASP:OD1	1:A:400:ARG:N	2.43	0.50
1:B:94:HIS:CG	1:B:274:LYS:HG2	2.47	0.50
1:A:39:LEU:HD21	1:A:45:PRO:HD3	1.94	0.49
1:A:391:ASP:HA	1:A:394:ARG:HG3	1.94	0.49
1:B:3:ILE:N	1:B:25:GLU:O	2.39	0.49
1:A:422:LEU:HD12	1:A:427:LEU:HD12	1.95	0.49
1:B:39:LEU:HD21	1:B:45:PRO:HD3	1.94	0.49
1:B:422:LEU:HD12	1:B:427:LEU:HD12	1.95	0.49
1:A:278:ASP:OD1	1:B:298:ARG:NE	2.44	0.48
1:B:267:LYS:NZ	1:B:268:ASP:OD1	2.40	0.48
1:A:237:GLN:HE21	1:A:415:ASN:HB3	1.79	0.48
1:A:21:ASP:OD1	1:A:58:ASN:ND2	2.46	0.47
1:A:34:ARG:HD2	1:A:34:ARG:HA	1.64	0.46
1:A:20:SER:OG	1:A:58:ASN:ND2	2.36	0.46
1:B:237:GLN:HE21	1:B:415:ASN:HB3	1.80	0.46
1:A:199:THR:OG1	1:A:200:GLY:O	2.34	0.45
1:B:199:THR:OG1	1:B:200:GLY:O	2.34	0.45
1:B:21:ASP:OD1	1:B:58:ASN:ND2	2.45	0.45
1:A:97:LEU:HD11	1:A:124:PRO:HG2	1.99	0.45
1:A:422:LEU:O	1:A:427:LEU:N	2.46	0.45
1:B:155:GLU:O	1:B:325:LYS:NZ	2.44	0.45
1:B:386:ILE:HG21	1:B:416:ILE:HD11	1.97	0.45
1:A:320:LEU:HG	1:A:384:LEU:HD11	1.99	0.44
1:A:386:ILE:HG21	1:A:416:ILE:HD11	1.98	0.44
1:B:69:ASP:OD1	1:B:72:GLU:N	2.37	0.44
1:B:320:LEU:HG	1:B:384:LEU:HD11	1.98	0.44
1:A:-1:SER:OG	1:A:-1:SER:O	2.34	0.44
1:A:97:LEU:HD21	1:A:124:PRO:HD2	1.98	0.44
1:B:172:THR:OG1	1:B:173:GLU:N	2.51	0.44
1:B:97:LEU:HD11	1:B:124:PRO:HG2	1.99	0.44
1:A:172:THR:OG1	1:A:173:GLU:N	2.51	0.44
1:B:97:LEU:HD21	1:B:124:PRO:HD2	1.98	0.43
1:B:422:LEU:O	1:B:427:LEU:N	2.45	0.43
1:A:172:THR:O	1:A:178:ARG:NH2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:LEU:HD22	1:A:54:LEU:HA	1.77	0.43
1:A:277:ALA:O	1:B:302:ARG:NH1	2.51	0.43
1:A:331:MSE:HB3	1:A:331:MSE:HE3	1.89	0.43
1:B:172:THR:O	1:B:178:ARG:NH2	2.52	0.43
1:B:315:LYS:HD3	1:B:315:LYS:HA	1.79	0.43
1:B:110:ASN:N	1:B:110:ASN:OD1	2.51	0.43
1:B:34:ARG:HA	1:B:34:ARG:HD2	1.65	0.43
1:B:434:LYS:HA	1:B:434:LYS:HD3	1.83	0.43
1:B:389:GLU:HG2	1:B:414:ARG:HD2	2.00	0.42
1:A:315:LYS:O	1:A:349:THR:OG1	2.37	0.42
1:A:389:GLU:HG2	1:A:414:ARG:HD2	2.01	0.42
1:A:278:ASP:HA	1:B:302:ARG:HD3	2.00	0.42
1:A:155:GLU:O	1:A:325:LYS:NZ	2.44	0.42
1:A:417:TYR:HA	1:A:418:PRO:HD2	1.93	0.42
1:A:230:GLU:CD	1:A:303:LYS:HZ1	2.23	0.42
1:A:280:GLU:OE2	1:B:302:ARG:NH2	2.44	0.41
1:A:110:ASN:OD1	1:A:110:ASN:N	2.53	0.41
1:A:76:ASP:HA	1:A:113:LYS:HG2	2.02	0.41
1:B:403:ASN:OD1	1:B:403:ASN:N	2.52	0.41
1:B:230:GLU:CD	1:B:303:LYS:HZ3	2.23	0.41
1:B:44:MSE:HE1	1:B:55:VAL:HG11	2.03	0.41
1:B:70:LEU:HD23	1:B:74:VAL:HG21	2.03	0.41
1:B:76:ASP:HA	1:B:113:LYS:HG2	2.02	0.41
1:A:434:LYS:HD3	1:A:434:LYS:HA	1.82	0.40
1:B:315:LYS:O	1:B:349:THR:OG1	2.37	0.40
1:A:322:LEU:O	1:A:336:SER:OG	2.28	0.40
1:B:323:THR:OG1	1:B:324:PHE:N	2.54	0.40
1:A:5:MSE:HB2	1:A:5:MSE:HE2	1.94	0.40
1:A:238:GLU:O	1:A:242:GLY:N	2.51	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:LYS:NZ	1:B:141:ASN:OD1[7_467]	2.13	0.07

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	423/446 (95%)	381 (90%)	38 (9%)	4 (1%)	17 49
1	B	423/446 (95%)	382 (90%)	36 (8%)	5 (1%)	13 41
All	All	846/892 (95%)	763 (90%)	74 (9%)	9 (1%)	14 44

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	379	ASP
1	B	379	ASP
1	B	189	SER
1	A	114	PRO
1	B	114	PRO
1	B	358	VAL
1	A	265	PHE
1	A	358	VAL
1	B	265	PHE

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	341/346 (99%)	281 (82%)	60 (18%)	2 6
1	B	341/346 (99%)	282 (83%)	59 (17%)	2 7
All	All	682/692 (99%)	563 (83%)	119 (17%)	2 7

All (119) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	15	SER
1	A	21	ASP
1	A	35	LYS
1	A	38	LEU
1	A	41	GLN
1	A	46	ILE
1	A	54	LEU
1	A	65	SER
1	A	67	THR
1	A	68	THR
1	A	70	LEU
1	A	74	VAL
1	A	76	ASP
1	A	90	ARG
1	A	94	HIS
1	A	98	SER
1	A	109	GLU
1	A	110	ASN
1	A	112	THR
1	A	119	THR
1	A	125	VAL
1	A	147	VAL
1	A	148	SER
1	A	151	GLU
1	A	159	ILE
1	A	167	ARG
1	A	168	VAL
1	A	173	GLU
1	A	174	ASP
1	A	199	THR
1	A	204	SER
1	A	212	ASN
1	A	220	THR
1	A	243	ILE
1	A	253	PHE
1	A	254	LEU
1	A	263	SER
1	A	264	CYS
1	A	265	PHE
1	A	270	LEU
1	A	275	THR

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Mol	Chain	Res	Type
1	A	280	GLU
1	A	281	THR
1	A	290	VAL
1	A	297	LYS
1	A	316	THR
1	A	323	THR
1	A	337	LEU
1	A	338	SER
1	A	349	THR
1	A	350	VAL
1	A	368	VAL
1	A	372	GLU
1	A	391	ASP
1	A	399	THR
1	A	403	ASN
1	A	407	SER
1	A	416	ILE
1	A	429	TYR
1	B	15	SER
1	B	21	ASP
1	B	35	LYS
1	B	38	LEU
1	B	41	GLN
1	B	46	ILE
1	B	54	LEU
1	B	65	SER
1	B	67	THR
1	B	68	THR
1	B	70	LEU
1	B	74	VAL
1	B	76	ASP
1	B	90	ARG
1	B	94	HIS
1	B	98	SER
1	B	110	ASN
1	B	112	THR
1	B	119	THR
1	B	125	VAL
1	B	147	VAL
1	B	148	SER
1	B	151	GLU
1	B	159	ILE

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Mol	Chain	Res	Type
1	B	167	ARG
1	B	168	VAL
1	B	173	GLU
1	B	174	ASP
1	B	190	LEU
1	B	199	THR
1	B	204	SER
1	B	212	ASN
1	B	220	THR
1	B	243	ILE
1	B	253	PHE
1	B	254	LEU
1	B	263	SER
1	B	264	CYS
1	B	265	PHE
1	B	270	LEU
1	B	275	THR
1	B	280	GLU
1	B	281	THR
1	B	290	VAL
1	B	297	LYS
1	B	316	THR
1	B	323	THR
1	B	337	LEU
1	B	338	SER
1	B	349	THR
1	B	350	VAL
1	B	368	VAL
1	B	372	GLU
1	B	391	ASP
1	B	399	THR
1	B	403	ASN
1	B	407	SER
1	B	416	ILE
1	B	429	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA

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)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAD	B	501	-	42,48,48	1.93	10 (23%)	50,73,73	1.44	8 (16%)
2	NAD	A	501	-	42,48,48	1.93	10 (23%)	50,73,73	1.44	8 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	B	501	-	-	8/26/62/62	0/5/5/5
2	NAD	A	501	-	-	8/26/62/62	0/5/5/5

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NAD	C2N-N1N	5.99	1.42	1.35
2	B	501	NAD	C7N-N7N	5.94	1.44	1.33
2	B	501	NAD	C2N-N1N	5.90	1.42	1.35
2	A	501	NAD	C7N-N7N	5.89	1.44	1.33
2	A	501	NAD	C2A-N3A	3.25	1.37	1.32
2	B	501	NAD	C2A-N3A	3.24	1.37	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	NAD	C2D-C1D	-3.23	1.48	1.53
2	A	501	NAD	C2D-C1D	-3.16	1.49	1.53
2	A	501	NAD	C6A-N6A	2.85	1.44	1.34
2	B	501	NAD	C6A-N6A	2.85	1.44	1.34
2	B	501	NAD	C2B-C1B	-2.59	1.49	1.53
2	A	501	NAD	C2B-C1B	-2.59	1.49	1.53
2	A	501	NAD	C6N-N1N	2.56	1.41	1.35
2	B	501	NAD	C6N-N1N	2.54	1.41	1.35
2	B	501	NAD	O3D-C3D	-2.20	1.37	1.43
2	A	501	NAD	O3D-C3D	-2.15	1.37	1.43
2	A	501	NAD	C2B-C3B	-2.12	1.47	1.53
2	A	501	NAD	O2B-C2B	-2.09	1.38	1.43
2	B	501	NAD	C2B-C3B	-2.09	1.47	1.53
2	B	501	NAD	O2B-C2B	-2.09	1.38	1.43

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	501	NAD	N3A-C2A-N1A	-5.61	119.91	128.68
2	A	501	NAD	N3A-C2A-N1A	-5.55	120.00	128.68
2	A	501	NAD	PN-O3-PA	-3.90	119.43	132.83
2	B	501	NAD	PN-O3-PA	-3.88	119.50	132.83
2	B	501	NAD	C3N-C7N-N7N	3.37	121.79	117.75
2	A	501	NAD	C3N-C7N-N7N	3.33	121.74	117.75
2	B	501	NAD	O7N-C7N-N7N	-2.35	119.24	122.58
2	A	501	NAD	O4B-C4B-C3B	2.32	109.71	105.11
2	A	501	NAD	C6N-N1N-C2N	-2.32	119.86	121.97
2	B	501	NAD	O4B-C4B-C3B	2.29	109.64	105.11
2	A	501	NAD	O7N-C7N-N7N	-2.27	119.35	122.58
2	B	501	NAD	C6N-N1N-C2N	-2.26	119.91	121.97
2	B	501	NAD	O2N-PN-O1N	-2.22	101.28	112.24
2	A	501	NAD	O2N-PN-O1N	-2.21	101.31	112.24
2	B	501	NAD	C4A-C5A-N7A	-2.19	107.11	109.40
2	A	501	NAD	C4A-C5A-N7A	-2.09	107.22	109.40

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	NAD	O4D-C1D-N1N-C2N
2	B	501	NAD	O4D-C1D-N1N-C6N
2	B	501	NAD	C2D-C1D-N1N-C2N

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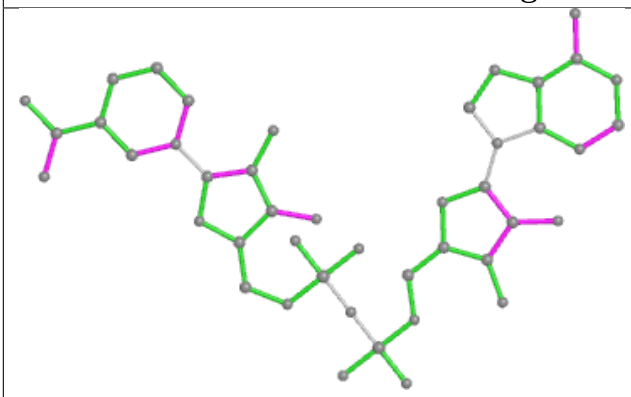
Mol	Chain	Res	Type	Atoms
2	B	501	NAD	C2D-C1D-N1N-C6N
2	A	501	NAD	O4D-C1D-N1N-C2N
2	A	501	NAD	O4D-C1D-N1N-C6N
2	A	501	NAD	C2D-C1D-N1N-C2N
2	A	501	NAD	C2D-C1D-N1N-C6N
2	A	501	NAD	O4B-C4B-C5B-O5B
2	B	501	NAD	O4B-C4B-C5B-O5B
2	B	501	NAD	C5D-O5D-PN-O3
2	A	501	NAD	C5D-O5D-PN-O3
2	B	501	NAD	C5D-O5D-PN-O2N
2	A	501	NAD	C5D-O5D-PN-O2N
2	B	501	NAD	C3D-C4D-C5D-O5D
2	A	501	NAD	C3D-C4D-C5D-O5D

There are no ring outliers.

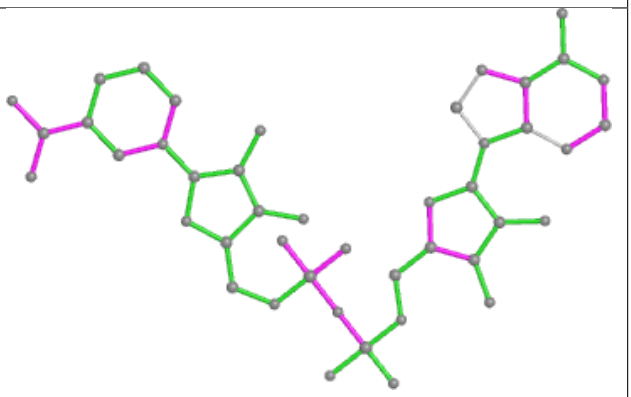
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

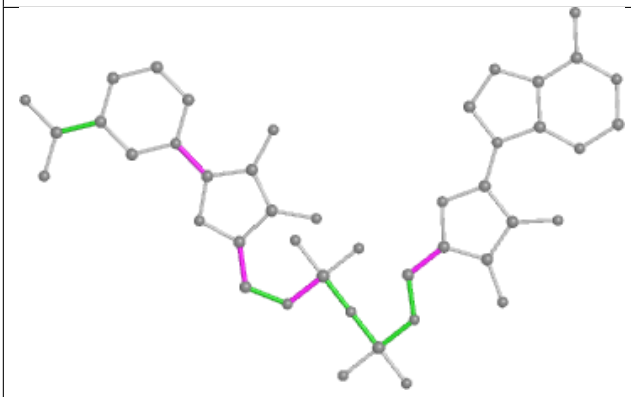
Ligand NAD B 501



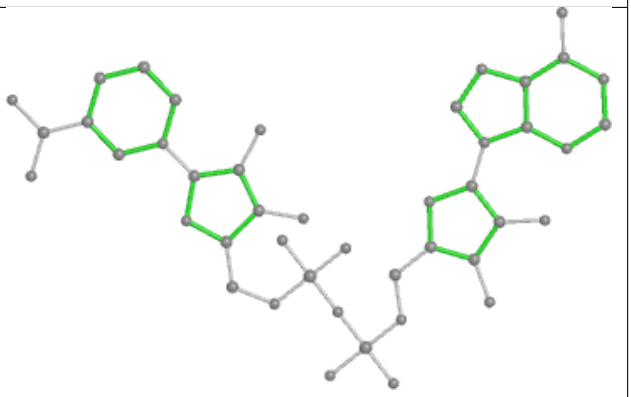
Bond lengths



Bond angles

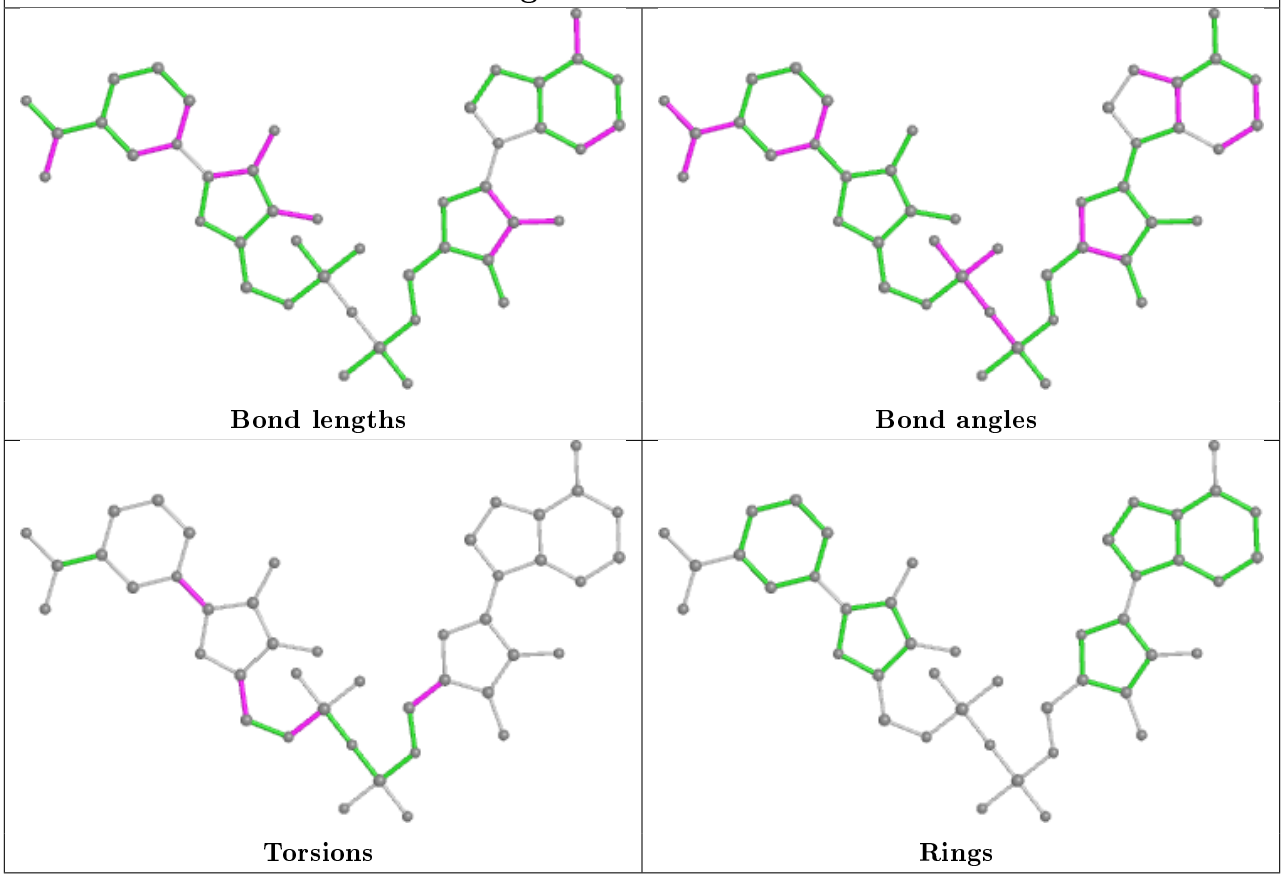


Torsions



Rings

Ligand NAD A 501



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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

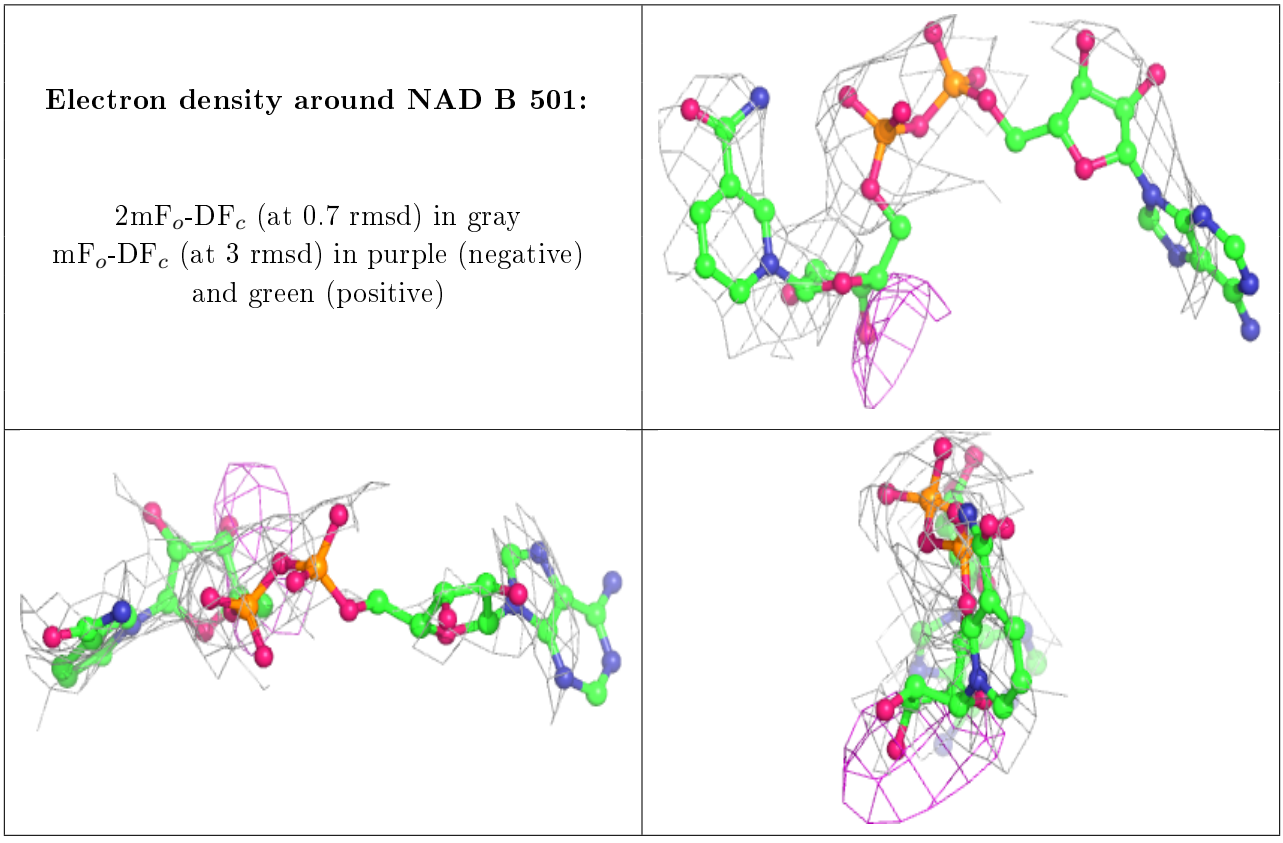
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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

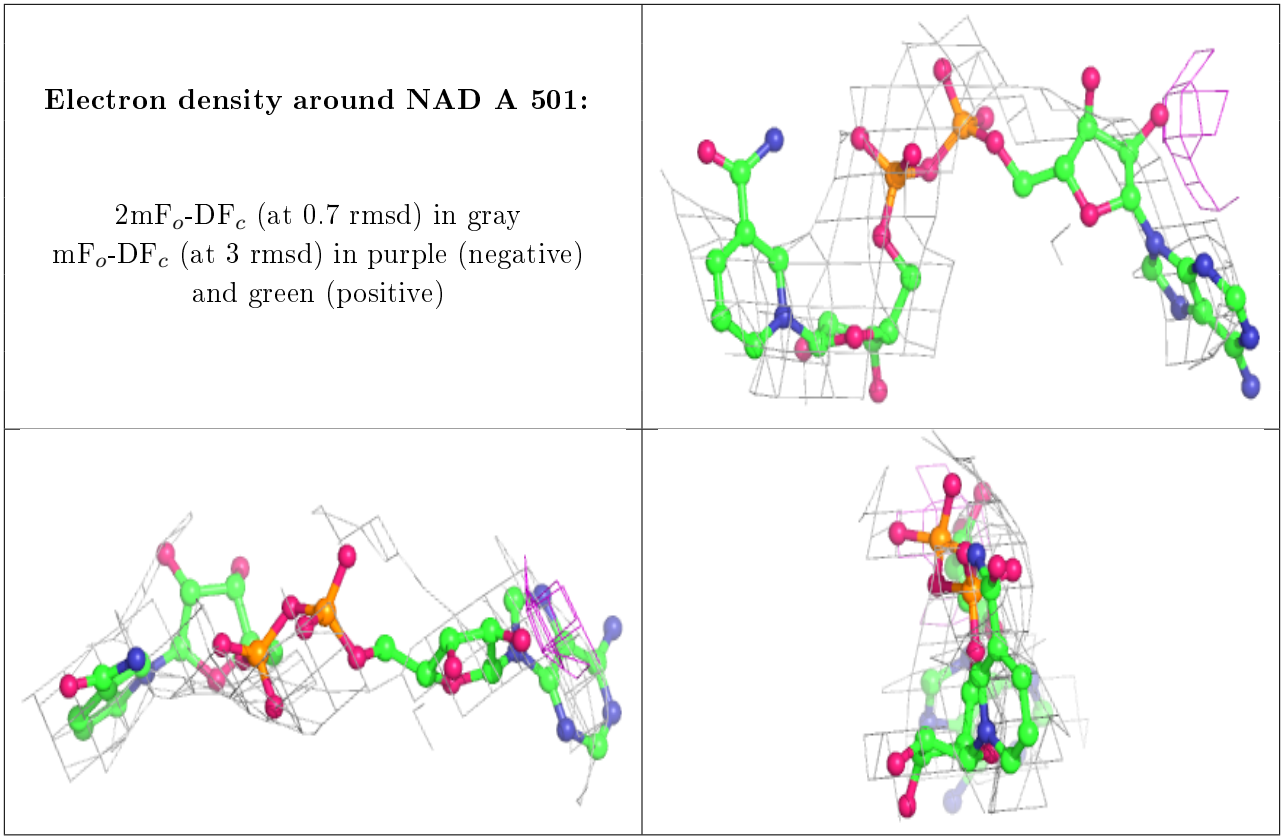
Electron density around NAD B 501:

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



Electron density around NAD A 501:

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



6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.