Full wwPDB X-ray Structure Validation Report (i)

Aug 8, 2022 – 10:34 am BST

PDB ID	:	7QUY
Title	:	Alcohol Dehydrogenase from Thauera aromatica complexed with NADH
Authors	:	Petchey, M.L.; Stark, F.; Ansorge-Schumacher, M.; Grogan, G.
Deposited on	:	2022-01-19
Resolution	:	2.60 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 (i) 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 (i)) were used in the production of this report:

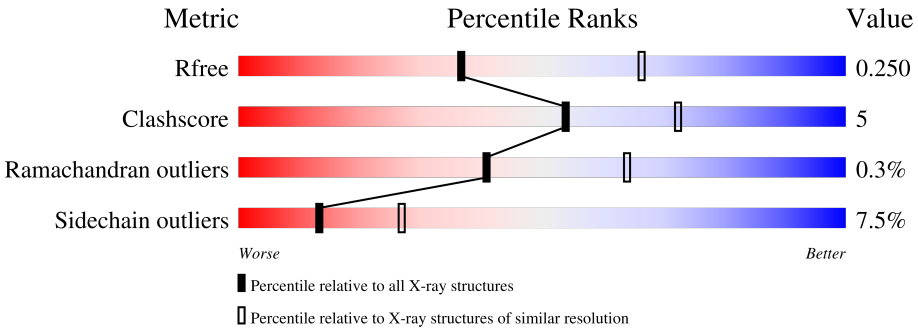
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

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 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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%

Mol	Chain	Length	Quality of chain
1	A	354	85% 13% ••
1	B	354	87% 11% ••
1	C	354	86% 12% ••

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	ZN	B	405	-	-	X	-

2 Entry composition (i)

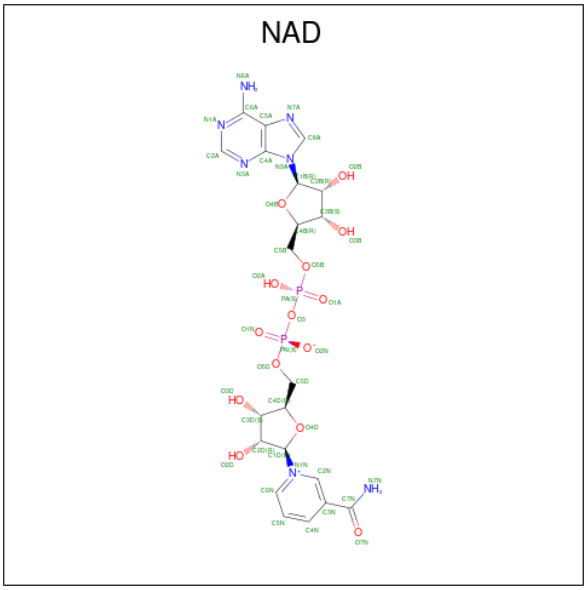
There are 5 unique types of molecules in this entry. The entry contains 7807 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase.

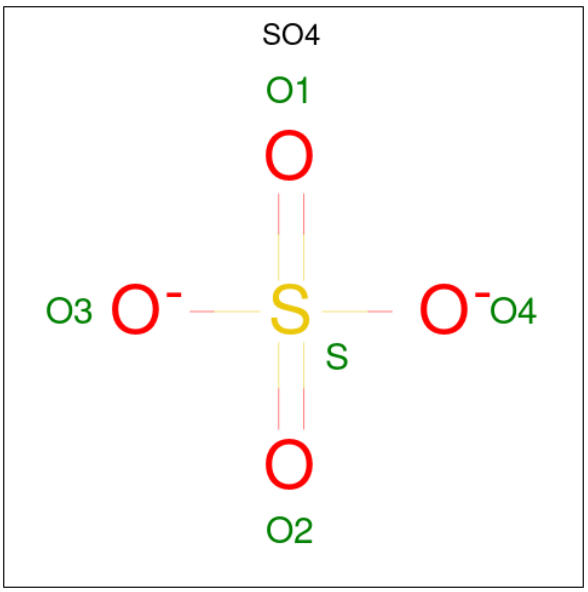
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	0	0
			2532	1596	450	468	18			
1	B	352	Total	C	N	O	S	0	0	0
			2541	1603	451	469	18			
1	C	352	Total	C	N	O	S	0	0	0
			2473	1563	434	458	18			

- Molecule 2 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
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		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Zn 2 2	0	0
4	B	2	Total Zn 2 2	0	0
4	C	2	Total Zn 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	43	Total O 43 43	0	0
5	B	40	Total O 40 40	0	0

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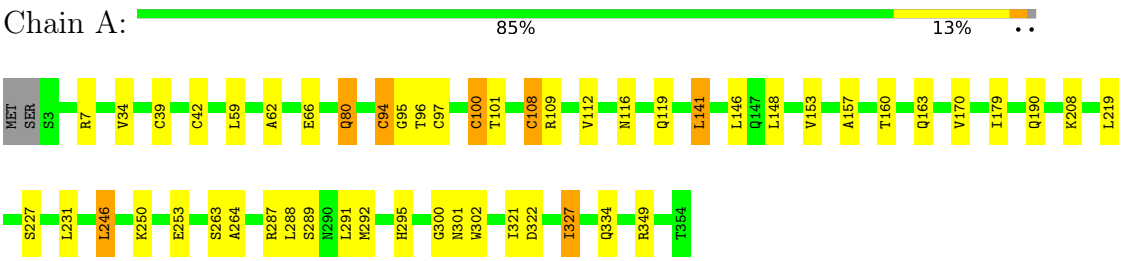
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	20	Total O 20 20	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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.

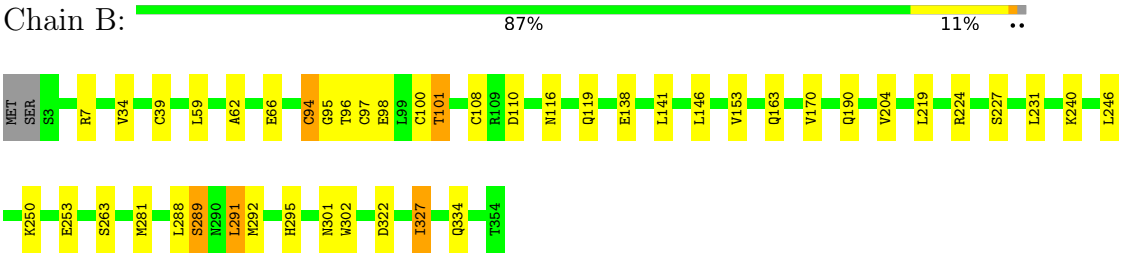
• Molecule 1: 6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase

Chain A:



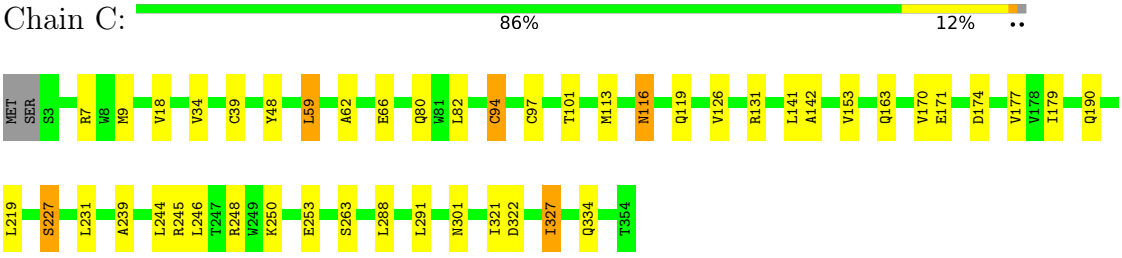
• Molecule 1: 6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase

Chain B:



• Molecule 1: 6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase

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	75.42Å 239.33Å 168.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.37 – 2.60 84.23 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (84.37-2.60) 100.0 (84.23-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.10 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.215 , 0.252 0.219 , 0.250	Depositor DCC
R_{free} test set	2352 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	58.7	Xtriage
Anisotropy	0.739	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7807	wwPDB-VP
Average B, all atoms (Å^2)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.31% 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: SO4, ZN, 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	0.70	0/2583	0.87	3/3527 (0.1%)
1	B	0.69	0/2592	0.82	1/3537 (0.0%)
1	C	0.72	0/2524	0.82	1/3455 (0.0%)
All	All	0.70	0/7699	0.83	5/10519 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	108	CYS	CA-CB-SG	-9.08	97.65	114.00
1	A	100	CYS	CA-CB-SG	7.89	128.19	114.00
1	A	94	CYS	CB-CA-C	-7.13	96.14	110.40
1	C	94	CYS	CA-CB-SG	5.99	124.78	114.00
1	B	94	CYS	CB-CA-C	-5.77	98.86	110.40

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	2532	0	2473	27	0
1	B	2541	0	2494	32	0
1	C	2473	0	2367	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	44	0	26	2	0
2	B	44	0	26	1	0
2	C	44	0	26	0	0
3	A	10	0	0	0	0
3	B	10	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	4	0
4	C	2	0	0	0	0
5	A	43	0	0	0	0
5	B	40	0	0	1	0
5	C	20	0	0	1	0
All	All	7807	0	7412	77	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 5.

All (77) 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:B:94:CYS:SG	1:B:96:THR:N	2.20	1.14
1:A:94:CYS:SG	1:A:96:THR:N	2.27	1.07
1:B:94:CYS:SG	1:B:95:GLY:N	2.28	1.07
1:A:94:CYS:SG	1:A:95:GLY:N	2.38	0.96
1:B:108:CYS:HG	4:B:405:ZN:ZN	0.81	0.91
1:B:190:GLN:HE22	1:B:322:ASP:H	1.31	0.78
1:C:190:GLN:HE22	1:C:322:ASP:H	1.31	0.76
1:A:190:GLN:HE22	1:A:322:ASP:H	1.32	0.75
1:B:108:CYS:SG	4:B:405:ZN:ZN	1.76	0.74
1:B:100:CYS:HG	4:B:405:ZN:ZN	0.99	0.74
1:B:153:VAL:HG21	1:B:327:ILE:HD11	1.70	0.72
1:C:153:VAL:HG21	1:C:327:ILE:HD11	1.71	0.72
1:C:94:CYS:SG	1:C:97:CYS:N	2.62	0.71
1:A:80:GLN:HE21	1:A:80:GLN:H	1.40	0.68
1:A:153:VAL:HG21	1:A:327:ILE:HD11	1.77	0.66
1:B:100:CYS:SG	4:B:405:ZN:ZN	1.88	0.63
1:C:239:ALA:HA	1:C:244:LEU:HD12	1.82	0.60
1:C:177:VAL:HG12	1:C:179:ILE:CD1	2.31	0.60
1:C:177:VAL:HG12	1:C:179:ILE:HD11	1.83	0.58
1:C:113:MET:HE2	1:C:116:ASN:HB2	1.88	0.56
1:A:190:GLN:NE2	1:A:322:ASP:H	2.03	0.56
1:B:190:GLN:NE2	1:B:322:ASP:H	2.03	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:SER:O	1:A:231:LEU:HB2	2.07	0.54
1:B:227:SER:O	1:B:231:LEU:HB2	2.07	0.54
2:A:401:NAD:H2N	1:B:292:MET:CE	2.39	0.53
1:C:179:ILE:HD12	1:C:179:ILE:N	2.22	0.53
1:C:227:SER:O	1:C:231:LEU:HB2	2.08	0.53
1:C:190:GLN:NE2	1:C:322:ASP:H	2.03	0.52
1:A:94:CYS:SG	1:A:97:CYS:N	2.73	0.52
1:B:289:SER:O	1:B:292:MET:HG3	2.10	0.52
1:A:289:SER:O	1:A:292:MET:HG3	2.10	0.52
1:C:48:TYR:OH	1:C:113:MET:HE2	2.11	0.51
1:B:138:GLU:HB2	1:C:142:ALA:HB1	1.94	0.49
1:B:163:GLN:HG2	1:B:301:ASN:OD1	2.13	0.49
1:A:287:ARG:NH1	1:B:281:MET:O	2.45	0.48
1:C:62:ALA:H	1:C:119:GLN:HE22	1.62	0.48
1:B:100:CYS:HG	1:B:108:CYS:HG	1.60	0.48
1:C:48:TYR:OH	1:C:113:MET:CE	2.61	0.48
1:B:94:CYS:SG	1:B:97:CYS:N	2.75	0.48
1:B:204:VAL:HB	1:B:224:ARG:CZ	2.44	0.48
1:A:94:CYS:SG	1:A:100:CYS:HB2	2.55	0.47
1:A:160:THR:HG21	2:A:401:NAD:C4N	2.45	0.47
1:A:295:HIS:CD2	1:B:302:TRP:H	2.33	0.47
1:C:245:ARG:HG2	1:C:248:ARG:NH1	2.29	0.47
1:C:163:GLN:HG2	1:C:301:ASN:OD1	2.15	0.46
1:B:240:LYS:NZ	5:B:501:HOH:O	2.48	0.46
1:C:62:ALA:H	1:C:119:GLN:NE2	2.14	0.45
1:A:246:LEU:HD13	1:A:246:LEU:HA	1.82	0.45
1:A:163:GLN:HG2	1:A:301:ASN:OD1	2.17	0.45
1:A:292:MET:HE2	2:B:401:NAD:N7N	2.32	0.45
1:A:302:TRP:H	1:B:295:HIS:CD2	2.35	0.45
1:B:94:CYS:HB3	1:B:108:CYS:SG	2.57	0.45
1:A:62:ALA:H	1:A:119:GLN:NE2	2.15	0.45
1:B:62:ALA:H	1:B:119:GLN:NE2	2.15	0.44
1:A:153:VAL:O	1:A:157:ALA:HB3	2.18	0.43
1:A:300:GLY:HA3	1:B:291:LEU:O	2.18	0.43
1:B:94:CYS:SG	1:B:100:CYS:CB	3.07	0.43
1:B:170:VAL:HG22	1:B:250:LYS:HG3	1.99	0.43
1:A:62:ALA:H	1:A:119:GLN:HE22	1.65	0.43
1:B:94:CYS:SG	1:B:95:GLY:C	2.93	0.43
1:B:98:GLU:HA	1:B:101:THR:HG22	2.01	0.43
1:B:39:CYS:HA	1:B:66:GLU:O	2.19	0.42
1:A:42:CYS:HB2	1:A:66:GLU:OE2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:VAL:HG22	1:A:250:LYS:HG3	2.00	0.42
1:C:39:CYS:HA	1:C:66:GLU:O	2.19	0.42
1:A:39:CYS:HA	1:A:66:GLU:O	2.20	0.41
1:B:62:ALA:H	1:B:119:GLN:HE22	1.67	0.41
1:A:190:GLN:HB3	1:A:321:ILE:HG22	2.02	0.41
1:C:126:VAL:HA	5:C:507:HOH:O	2.21	0.41
1:C:170:VAL:HG22	1:C:250:LYS:HG3	2.03	0.41
1:C:171:GLU:O	1:C:174:ASP:HB2	2.21	0.41
1:C:190:GLN:HB3	1:C:321:ILE:HG22	2.02	0.41
1:B:291:LEU:HD12	1:B:291:LEU:HA	1.88	0.41
1:C:59:LEU:H	1:C:59:LEU:HD22	1.86	0.41
1:A:141:LEU:HD11	1:A:148:LEU:HA	2.03	0.41
1:B:94:CYS:SG	1:B:95:GLY:CA	3.07	0.40
1:A:179:ILE:CD1	1:A:264:ALA:HB2	2.51	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	350/354 (99%)	341 (97%)	8 (2%)	1 (0%)	41	64
1	B	350/354 (99%)	341 (97%)	8 (2%)	1 (0%)	41	64
1	C	350/354 (99%)	339 (97%)	10 (3%)	1 (0%)	41	64
All	All	1050/1062 (99%)	1021 (97%)	26 (2%)	3 (0%)	41	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	116	ASN
1	C	116	ASN
1	A	116	ASN

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	248/264 (94%)	228 (92%)	20 (8%)	11 23
1	B	250/264 (95%)	234 (94%)	16 (6%)	17 35
1	C	234/264 (89%)	215 (92%)	19 (8%)	11 23
All	All	732/792 (92%)	677 (92%)	55 (8%)	13 27

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ARG
1	A	34	VAL
1	A	59	LEU
1	A	80	GLN
1	A	101	THR
1	A	108	CYS
1	A	109	ARG
1	A	112	VAL
1	A	141	LEU
1	A	146	LEU
1	A	208	LYS
1	A	219	LEU
1	A	246	LEU
1	A	253	GLU
1	A	263	SER
1	A	288	LEU
1	A	291	LEU
1	A	327	ILE
1	A	334	GLN
1	A	349	ARG
1	B	7	ARG
1	B	34	VAL
1	B	59	LEU
1	B	101	THR
1	B	110	ASP
1	B	141	LEU

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Mol	Chain	Res	Type
1	B	146	LEU
1	B	219	LEU
1	B	246	LEU
1	B	253	GLU
1	B	263	SER
1	B	288	LEU
1	B	289	SER
1	B	291	LEU
1	B	327	ILE
1	B	334	GLN
1	C	7	ARG
1	C	9	MET
1	C	18	VAL
1	C	34	VAL
1	C	59	LEU
1	C	80	GLN
1	C	82	LEU
1	C	101	THR
1	C	131	ARG
1	C	141	LEU
1	C	219	LEU
1	C	227	SER
1	C	246	LEU
1	C	253	GLU
1	C	263	SER
1	C	288	LEU
1	C	291	LEU
1	C	327	ILE
1	C	334	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	ASN
1	A	80	GLN
1	A	119	GLN
1	A	167	GLN
1	A	190	GLN
1	A	242	ASN
1	B	56	ASN
1	B	119	GLN
1	B	190	GLN

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Mol	Chain	Res	Type
1	B	242	ASN
1	B	295	HIS
1	C	56	ASN
1	C	119	GLN
1	C	190	GLN
1	C	242	ASN

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 13 ligands modelled in this entry, 6 are monoatomic - leaving 7 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	SO4	A	402	-	4,4,4	0.54	0	6,6,6	0.06	0
2	NAD	A	401	-	42,48,48	0.65	0	50,73,73	0.99	3 (6%)
3	SO4	B	402	-	4,4,4	0.36	0	6,6,6	0.12	0
2	NAD	B	401	-	42,48,48	0.57	0	50,73,73	1.02	4 (8%)
3	SO4	A	403	-	4,4,4	0.31	0	6,6,6	0.08	0
3	SO4	B	403	-	4,4,4	0.33	0	6,6,6	0.08	0
2	NAD	C	401	-	42,48,48	0.58	0	50,73,73	0.90	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
2	NAD	C	401	-	-	11/26/62/62	0/5/5/5
2	NAD	A	401	-	-	2/26/62/62	0/5/5/5
2	NAD	B	401	-	-	7/26/62/62	0/5/5/5

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	NAD	C6N-N1N-C2N	-3.43	118.85	121.97
2	C	401	NAD	C6N-N1N-C2N	-3.31	118.96	121.97
2	A	401	NAD	O4D-C1D-C2D	-3.29	102.11	106.93
2	B	401	NAD	O4D-C1D-C2D	-2.84	102.77	106.93
2	B	401	NAD	C6N-N1N-C2N	-2.73	119.48	121.97
2	B	401	NAD	C5A-C6A-N6A	2.69	124.44	120.35
2	B	401	NAD	O4B-C1B-C2B	-2.57	103.17	106.93
2	A	401	NAD	O4B-C1B-C2B	-2.06	103.92	106.93

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	NAD	O4D-C1D-N1N-C6N
2	B	401	NAD	C5D-O5D-PN-O3
2	B	401	NAD	O4D-C1D-N1N-C6N
2	C	401	NAD	C5B-O5B-PA-O1A
2	C	401	NAD	C5B-O5B-PA-O2A
2	C	401	NAD	O4D-C1D-N1N-C2N
2	C	401	NAD	O4D-C1D-N1N-C6N
2	C	401	NAD	C2D-C1D-N1N-C2N
2	C	401	NAD	C2D-C1D-N1N-C6N
2	C	401	NAD	O4B-C4B-C5B-O5B
2	C	401	NAD	C3B-C4B-C5B-O5B
2	B	401	NAD	O4D-C4D-C5D-O5D
2	B	401	NAD	C3D-C4D-C5D-O5D
2	B	401	NAD	C5D-O5D-PN-O1N
2	B	401	NAD	C5D-O5D-PN-O2N
2	C	401	NAD	C5B-O5B-PA-O3

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Mol	Chain	Res	Type	Atoms
2	A	401	NAD	O4B-C4B-C5B-O5B
2	C	401	NAD	PA-O3-PN-O1N
2	C	401	NAD	PA-O3-PN-O2N
2	B	401	NAD	O4B-C4B-C5B-O5B

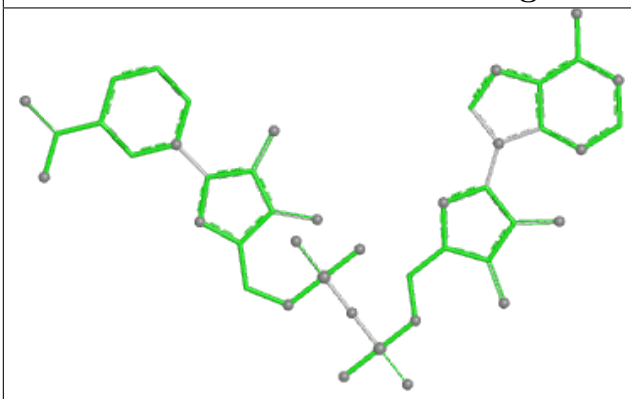
There are no ring outliers.

2 monomers are involved in 3 short contacts:

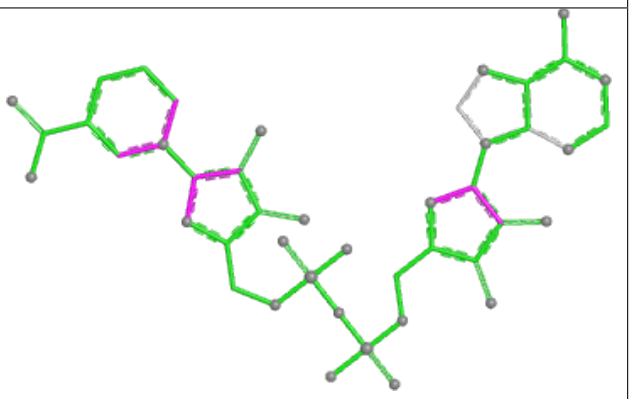
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	NAD	2	0
2	B	401	NAD	1	0

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

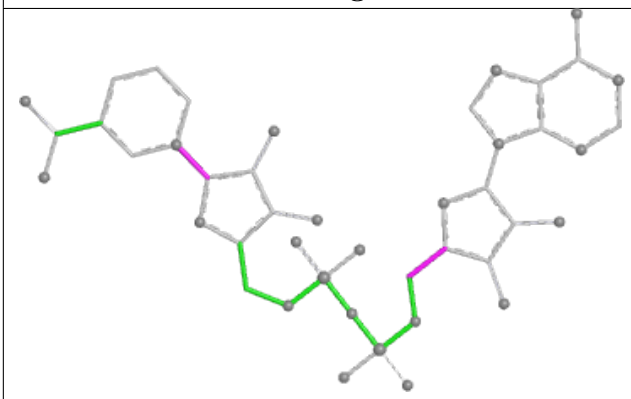
Ligand NAD A 401



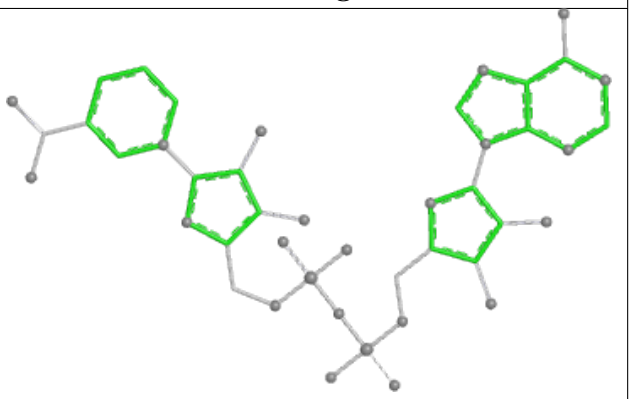
Bond lengths



Bond angles

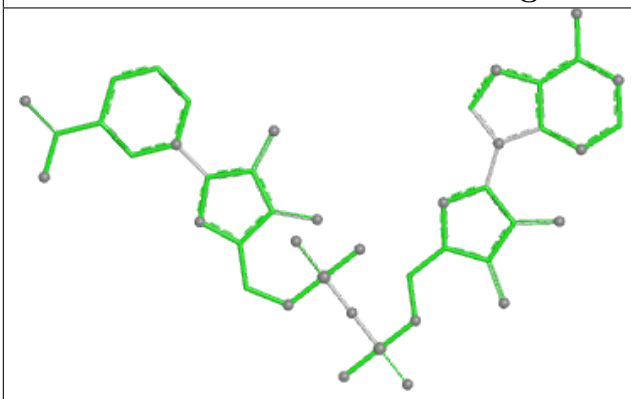


Torsions

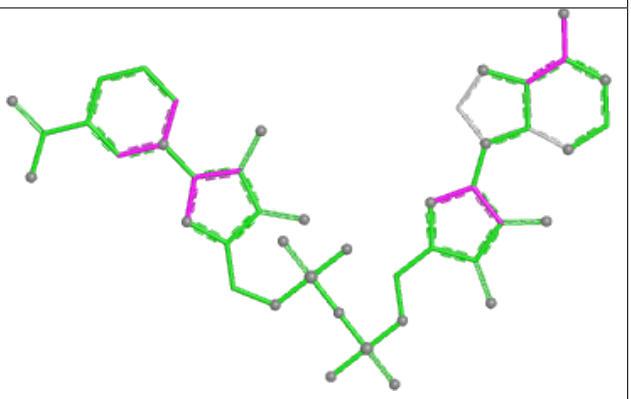


Rings

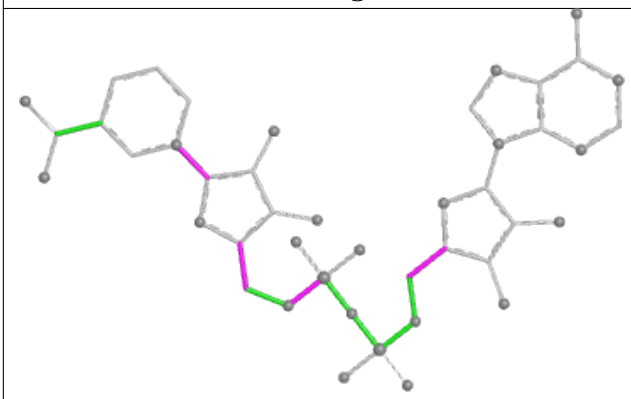
Ligand NAD B 401



Bond lengths



Bond angles



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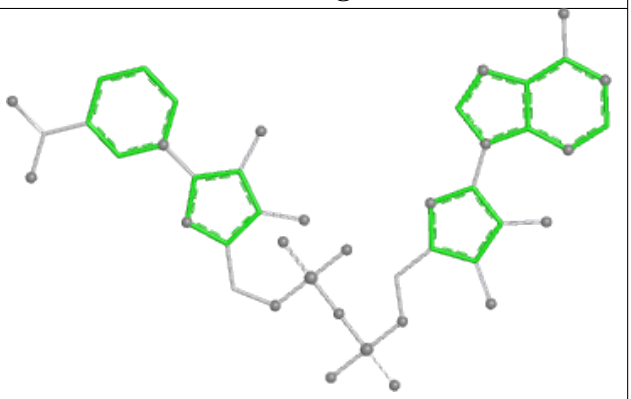
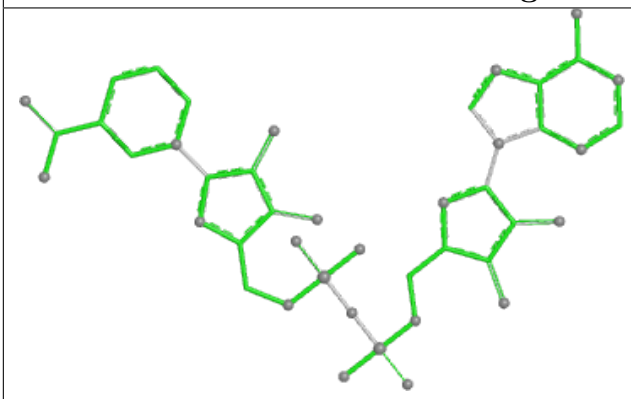
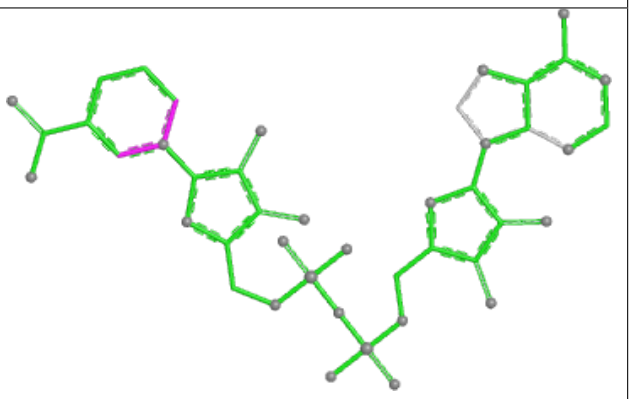


Rings

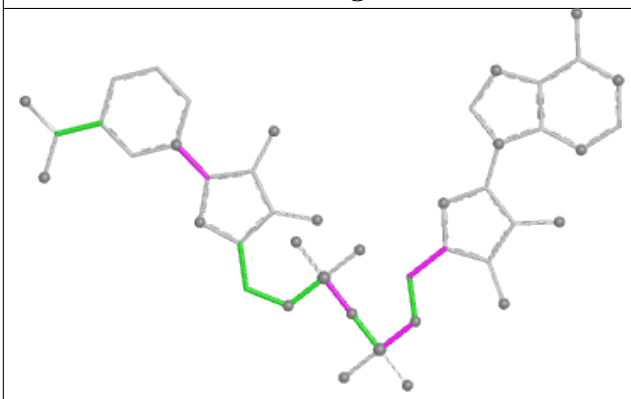
Ligand NAD C 401



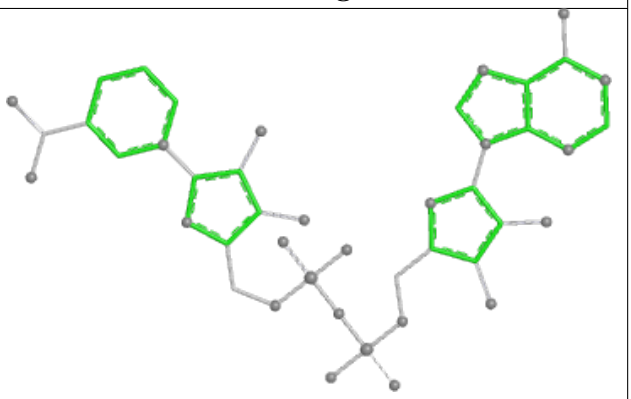
Bond lengths



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

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.

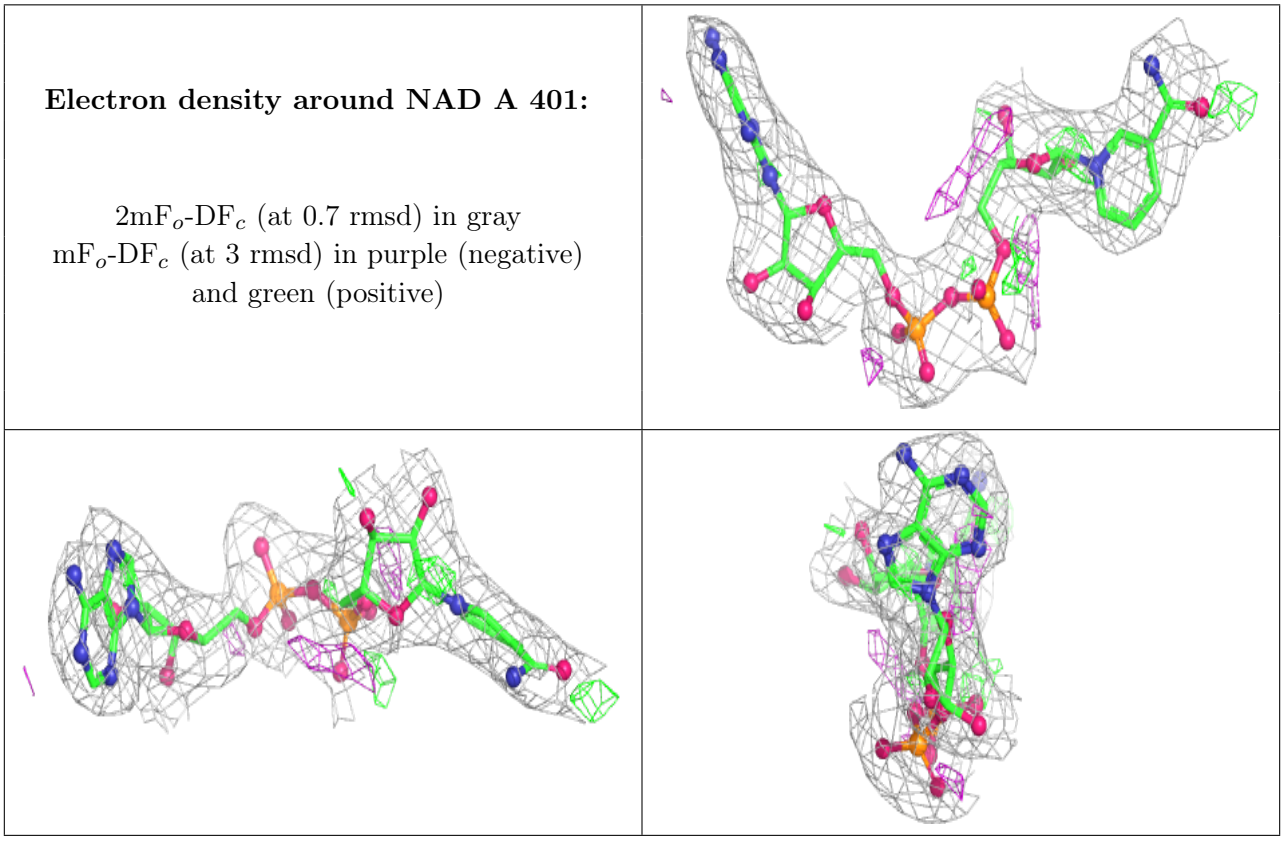
6.4 Ligands

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.

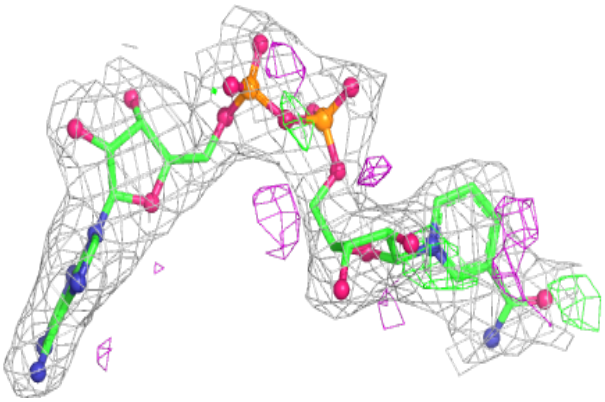
Electron density around NAD A 401:

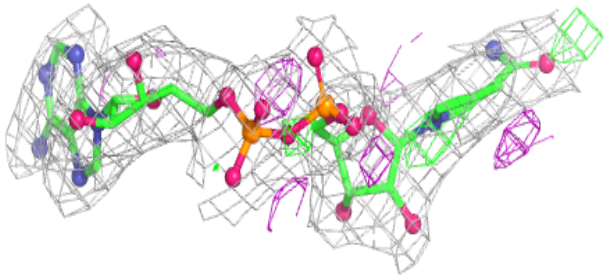
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

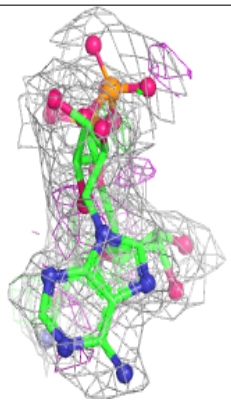


Electron density around NAD B 401:

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

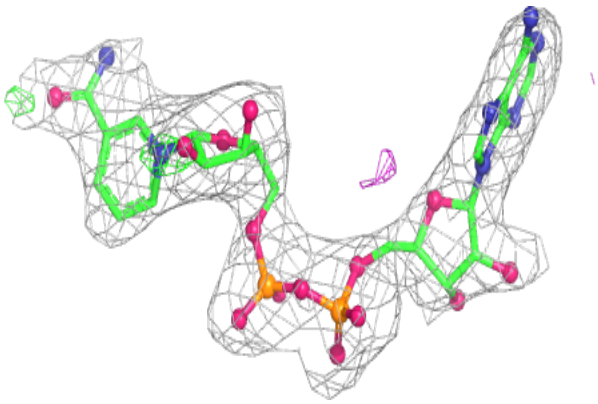


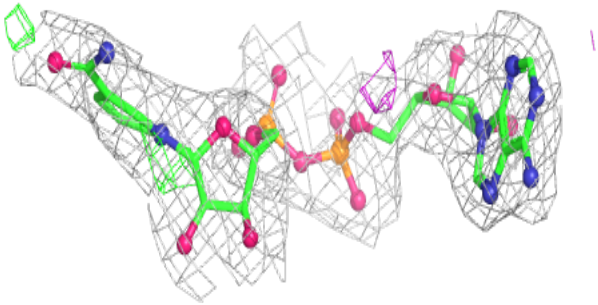


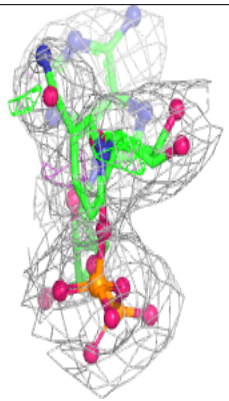


Electron density around NAD C 401:

$2mF_o$-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.