wwPDB X-ray Structure Validation Summary Report (i)

Nov 20, 2023 – 11:16 AM JST

PDB ID	:	7CGQ
Title	:	Crystal structure of Azospirillum brasilense L-arabinose 1-dehydrogenase E147A mutant (NADP and L-arabinose bound form)
Authors	:	Yoshiwara, K.; Watanabe, Y.; Watanabe, S.
Deposited on	:	2020-07-02
Resolution	:	2.21 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

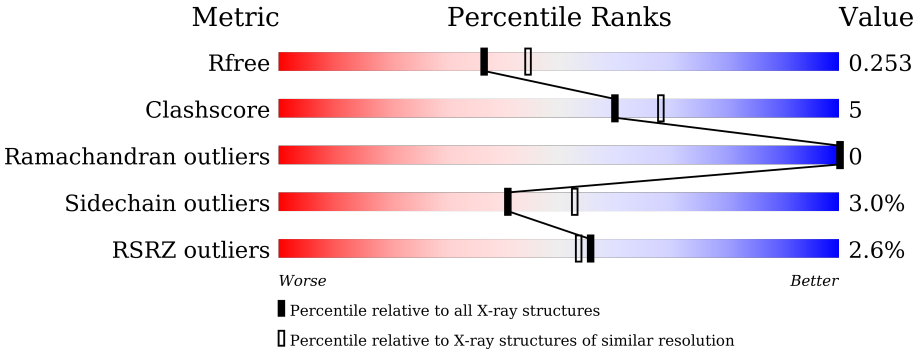
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.21 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	319	.% 87% 7% • •
1	B	319	5% 84% 9% • 6%
1	C	319	3% 86% 8% • •
1	D	319	.% 86% 9% • •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9868 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 L-arabinose 1-dehydrogenase (NAD(P)(+)).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	306	2356	1489	438	424	5	0	0	0
1	B	300	2309	1459	426	419	5	0	0	0
1	C	306	2353	1488	435	425	5	0	0	0
1	D	305	2348	1485	434	424	5	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	initiating methionine	UNP Q53TZ2
A	-8	ARG	-	expression tag	UNP Q53TZ2
A	-7	GLY	-	expression tag	UNP Q53TZ2
A	-6	SER	-	expression tag	UNP Q53TZ2
A	-5	HIS	-	expression tag	UNP Q53TZ2
A	-4	HIS	-	expression tag	UNP Q53TZ2
A	-3	HIS	-	expression tag	UNP Q53TZ2
A	-2	HIS	-	expression tag	UNP Q53TZ2
A	-1	HIS	-	expression tag	UNP Q53TZ2
A	0	HIS	-	expression tag	UNP Q53TZ2
A	1	GLY	-	expression tag	UNP Q53TZ2
A	147	ALA	GLU	engineered mutation	UNP Q53TZ2
B	-9	MET	-	initiating methionine	UNP Q53TZ2
B	-8	ARG	-	expression tag	UNP Q53TZ2
B	-7	GLY	-	expression tag	UNP Q53TZ2
B	-6	SER	-	expression tag	UNP Q53TZ2
B	-5	HIS	-	expression tag	UNP Q53TZ2
B	-4	HIS	-	expression tag	UNP Q53TZ2
B	-3	HIS	-	expression tag	UNP Q53TZ2
B	-2	HIS	-	expression tag	UNP Q53TZ2
B	-1	HIS	-	expression tag	UNP Q53TZ2

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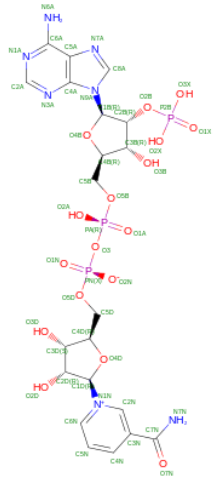
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	HIS	-	expression tag	UNP Q53TZ2
B	1	GLY	-	expression tag	UNP Q53TZ2
B	147	ALA	GLU	engineered mutation	UNP Q53TZ2
C	-9	MET	-	initiating methionine	UNP Q53TZ2
C	-8	ARG	-	expression tag	UNP Q53TZ2
C	-7	GLY	-	expression tag	UNP Q53TZ2
C	-6	SER	-	expression tag	UNP Q53TZ2
C	-5	HIS	-	expression tag	UNP Q53TZ2
C	-4	HIS	-	expression tag	UNP Q53TZ2
C	-3	HIS	-	expression tag	UNP Q53TZ2
C	-2	HIS	-	expression tag	UNP Q53TZ2
C	-1	HIS	-	expression tag	UNP Q53TZ2
C	0	HIS	-	expression tag	UNP Q53TZ2
C	1	GLY	-	expression tag	UNP Q53TZ2
C	147	ALA	GLU	engineered mutation	UNP Q53TZ2
D	-9	MET	-	initiating methionine	UNP Q53TZ2
D	-8	ARG	-	expression tag	UNP Q53TZ2
D	-7	GLY	-	expression tag	UNP Q53TZ2
D	-6	SER	-	expression tag	UNP Q53TZ2
D	-5	HIS	-	expression tag	UNP Q53TZ2
D	-4	HIS	-	expression tag	UNP Q53TZ2
D	-3	HIS	-	expression tag	UNP Q53TZ2
D	-2	HIS	-	expression tag	UNP Q53TZ2
D	-1	HIS	-	expression tag	UNP Q53TZ2
D	0	HIS	-	expression tag	UNP Q53TZ2
D	1	GLY	-	expression tag	UNP Q53TZ2
D	147	ALA	GLU	engineered mutation	UNP Q53TZ2

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).

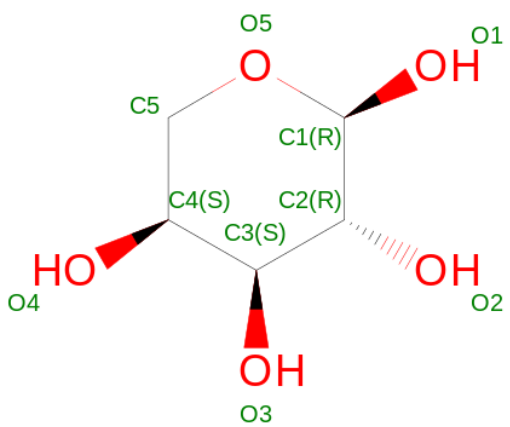
NAP



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	48	21	7	17	3	0	0
			Total	C	N	O	P		
2	B	1	27	10	5	10	2	0	0
			Total	C	N	O	P		
2	C	1	27	10	5	10	2	0	0
			Total	C	N	O	P		
2	D	1	48	21	7	17	3	0	0

- Molecule 3 is alpha-L-arabinopyranose (three-letter code: ARA) (formula: $C_5H_{10}O_5$).

ARA



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	10	5	5	0	0

- Molecule 4 is water.

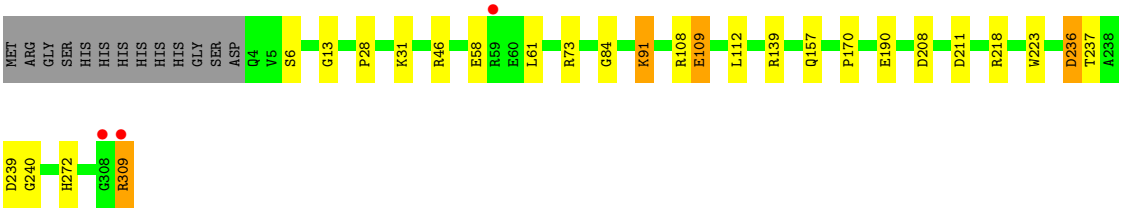
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	86	86	86	0	0
			Total	O		
4	B	69	69	69	0	0
			Total	O		
4	C	95	95	95	0	0
			Total	O		
4	D	92	92	92	0	0

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 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.

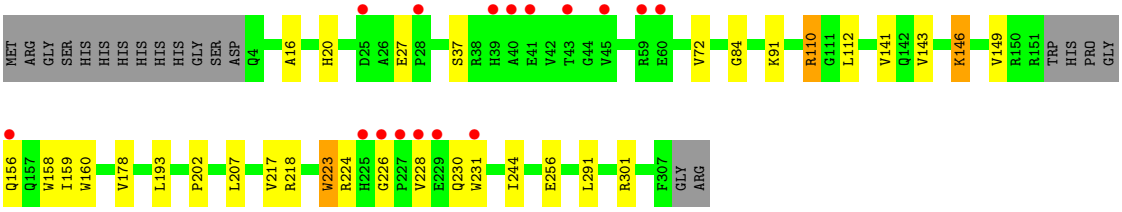
• Molecule 1: L-arabinose 1-dehydrogenase (NAD(P)(+))

Chain A:



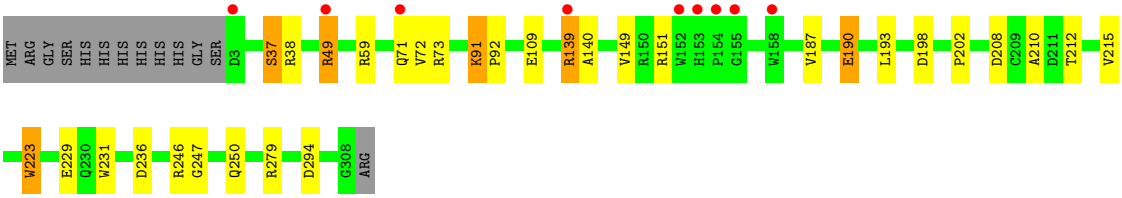
• Molecule 1: L-arabinose 1-dehydrogenase (NAD(P)(+))

Chain B:



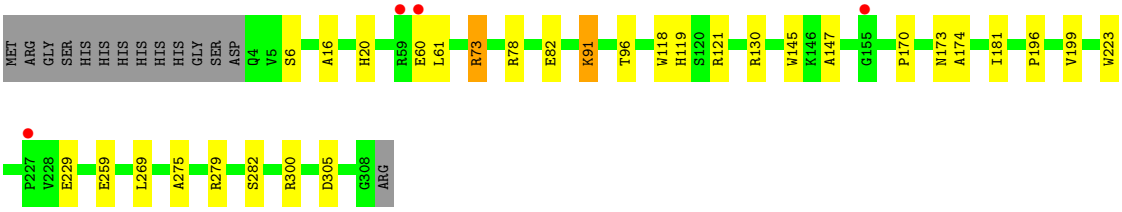
• Molecule 1: L-arabinose 1-dehydrogenase (NAD(P)(+))

Chain C:



• Molecule 1: L-arabinose 1-dehydrogenase (NAD(P)(+))

Chain D:


MET
ARG
GLY
SER
HIS
HIS
HIS
HIS
HIS
GLY
SER
ASP
Q4
V5
S6
A16
H20
R59
E60
L61
R73
R78
E82
K91
T96
W118
H119
S120
R121
R130
W145
K146
A147
G155
P170
N173
A174
I181
P196
V199
W223
P227
V228
E229
E259
L269
A275
R279
S282
R300
D305
G308
ARG

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	60.08Å 92.10Å 135.13Å 90.00° 102.25° 90.00°	Depositor
Resolution (Å)	49.38 – 2.21 49.39 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.38-2.21) 99.2 (49.39-2.21)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.53 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.185 , 0.222 0.209 , 0.253	Depositor DCC
R_{free} test set	3629 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	34.6	Xtriage
Anisotropy	0.935	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 41.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9868	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.14% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ARA, NAP

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	0.25	0/2410	0.47	0/3285
1	B	0.26	0/2358	0.48	0/3213
1	C	0.37	2/2407 (0.1%)	0.59	3/3283 (0.1%)
1	D	0.25	0/2402	0.46	0/3276
All	All	0.29	2/9577 (0.0%)	0.51	3/13057 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	139	ARG	CG-CD	-6.42	1.35	1.51
1	C	139	ARG	CD-NE	-6.01	1.36	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	49	ARG	NE-CZ-NH2	-14.74	112.93	120.30
1	C	49	ARG	NE-CZ-NH1	8.16	124.38	120.30
1	C	139	ARG	CA-CB-CG	-6.91	98.20	113.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	2356	0	2354	14	1
1	B	2309	0	2314	27	1
1	C	2353	0	2347	27	0
1	D	2348	0	2345	22	0
2	A	48	0	24	2	0
2	B	27	0	11	2	0
2	C	27	0	11	2	0
2	D	48	0	24	1	0
3	A	10	0	9	0	0
4	A	86	0	0	1	0
4	B	69	0	0	3	0
4	C	95	0	0	1	0
4	D	92	0	0	1	0
All	All	9868	0	9439	87	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 5.

The worst 5 of 87 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:146:LYS:HD2	1:B:228:VAL:O	1.59	1.01
1:A:237:THR:HG22	1:A:239:ASP:H	1.29	0.95
1:B:146:LYS:CD	1:B:228:VAL:O	2.18	0.91
1:C:49:ARG:NH1	4:C:501:HOH:O	2.06	0.84
1:B:207:LEU:HD23	1:B:291:LEU:HD21	1.65	0.78

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:108:ARG:NH1	1:B:226:GLY:O[2_545]	2.10	0.10

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	304/319 (95%)	295 (97%)	9 (3%)	0	100	100
1	B	296/319 (93%)	289 (98%)	7 (2%)	0	100	100
1	C	304/319 (95%)	297 (98%)	7 (2%)	0	100	100
1	D	303/319 (95%)	293 (97%)	10 (3%)	0	100	100
All	All	1207/1276 (95%)	1174 (97%)	33 (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	235/247 (95%)	227 (97%)	8 (3%)	37	47
1	B	232/247 (94%)	224 (97%)	8 (3%)	37	47
1	C	235/247 (95%)	228 (97%)	7 (3%)	41	53
1	D	235/247 (95%)	230 (98%)	5 (2%)	53	67
All	All	937/988 (95%)	909 (97%)	28 (3%)	41	53

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	223	TRP
1	D	282	SER
1	C	59	ARG
1	D	73	ARG
1	C	37	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	153	HIS
1	D	156	GLN

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)

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	$\#\|Z\| > 2$
2	NAP	C	401	-	25,29,52	3.79	9 (36%)	31,45,80	3.69	6 (19%)
2	NAP	A	401	-	45,52,52	3.68	16 (35%)	56,80,80	2.79	8 (14%)
3	ARA	A	402	-	10,10,10	2.04	2 (20%)	14,14,14	2.51	3 (21%)
2	NAP	B	401	-	25,29,52	3.96	9 (36%)	31,45,80	3.55	6 (19%)
2	NAP	D	401	-	45,52,52	3.70	16 (35%)	56,80,80	2.82	9 (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	NAP	C	401	-	-	7/11/31/67	0/3/3/5
2	NAP	A	401	-	-	10/31/67/67	0/5/5/5
3	ARA	A	402	-	-	-	0/1/1/1
2	NAP	B	401	-	-	8/11/31/67	0/3/3/5
2	NAP	D	401	-	-	8/31/67/67	0/5/5/5

The worst 5 of 52 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	NAP	O4B-C1B	10.98	1.56	1.41
2	B	401	NAP	O4B-C1B	10.94	1.56	1.41
2	A	401	NAP	O4B-C1B	10.79	1.56	1.41
2	C	401	NAP	O4B-C1B	10.55	1.55	1.41
2	A	401	NAP	C3B-C4B	-9.82	1.27	1.53

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	401	NAP	C5A-C6A-N6A	13.39	140.70	120.35
2	C	401	NAP	C5A-C6A-N6A	13.37	140.67	120.35
2	A	401	NAP	C5A-C6A-N6A	13.31	140.59	120.35
2	B	401	NAP	C5A-C6A-N6A	13.13	140.31	120.35
2	C	401	NAP	C1B-N9A-C4A	-10.21	108.70	126.64

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	NAP	C5B-O5B-PA-O1A
2	A	401	NAP	O4D-C1D-N1N-C2N
2	A	401	NAP	O4D-C1D-N1N-C6N
2	A	401	NAP	C2D-C1D-N1N-C2N
2	A	401	NAP	C2D-C1D-N1N-C6N

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	NAP	2	0
2	A	401	NAP	2	0
2	B	401	NAP	2	0

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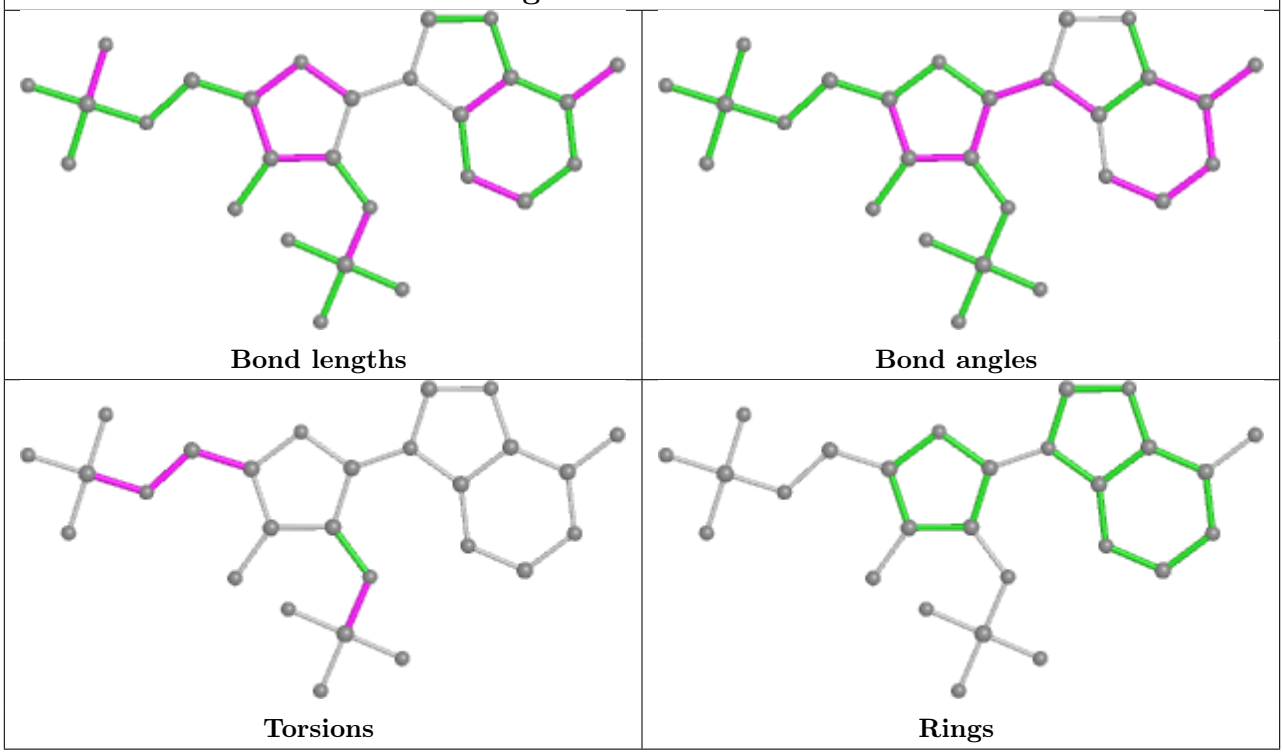
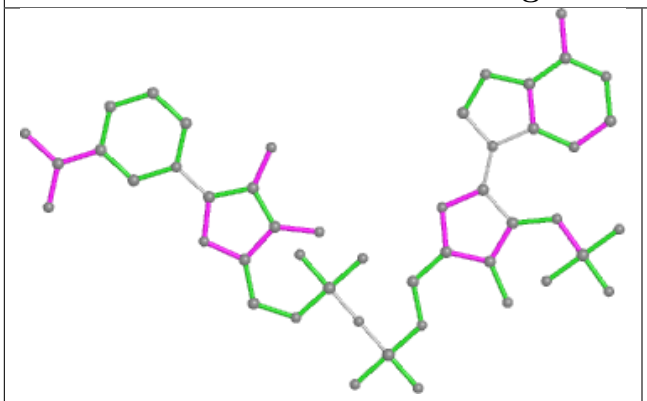
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	NAP	1	0

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.

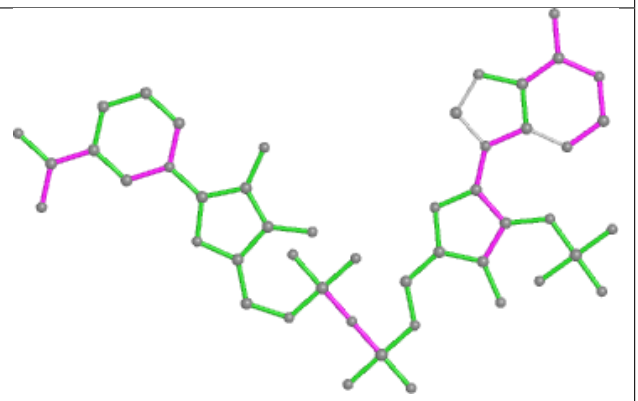
Ligand NAP C 401



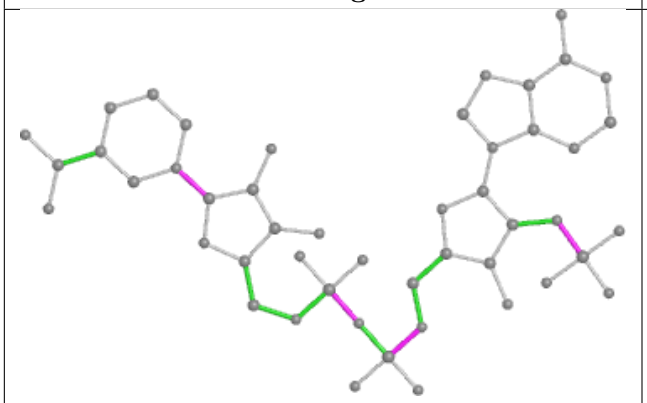
Ligand NAP A 401



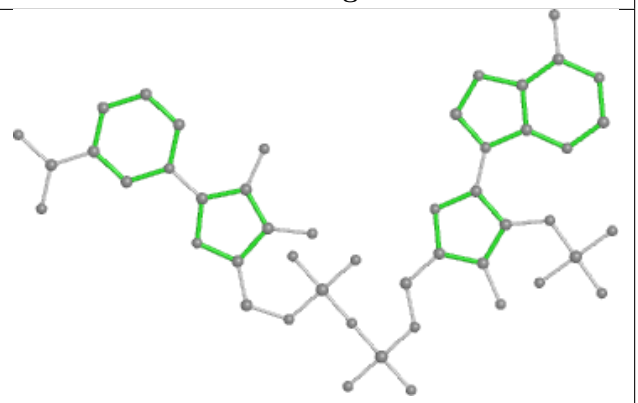
Bond lengths



Bond angles

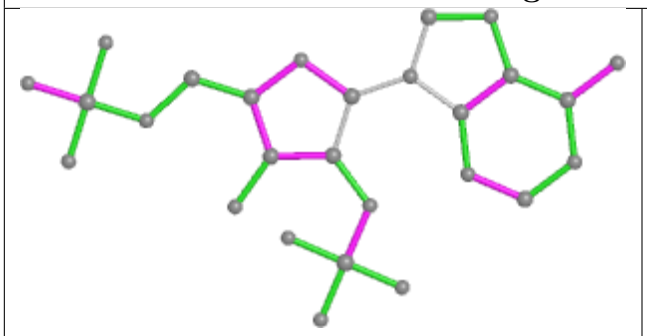


Torsions

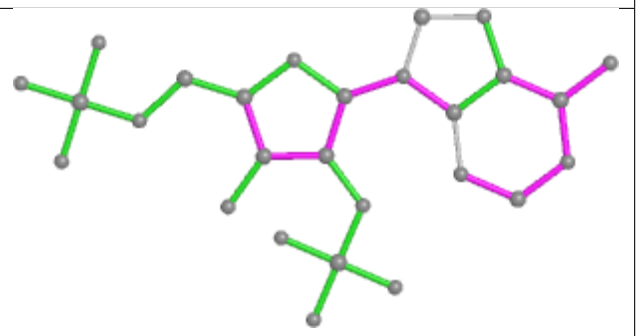


Rings

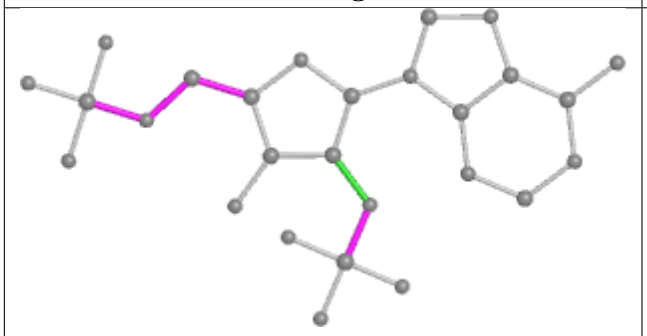
Ligand NAP B 401



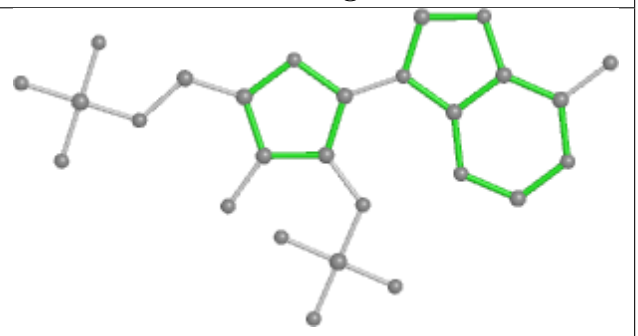
Bond lengths



Bond angles

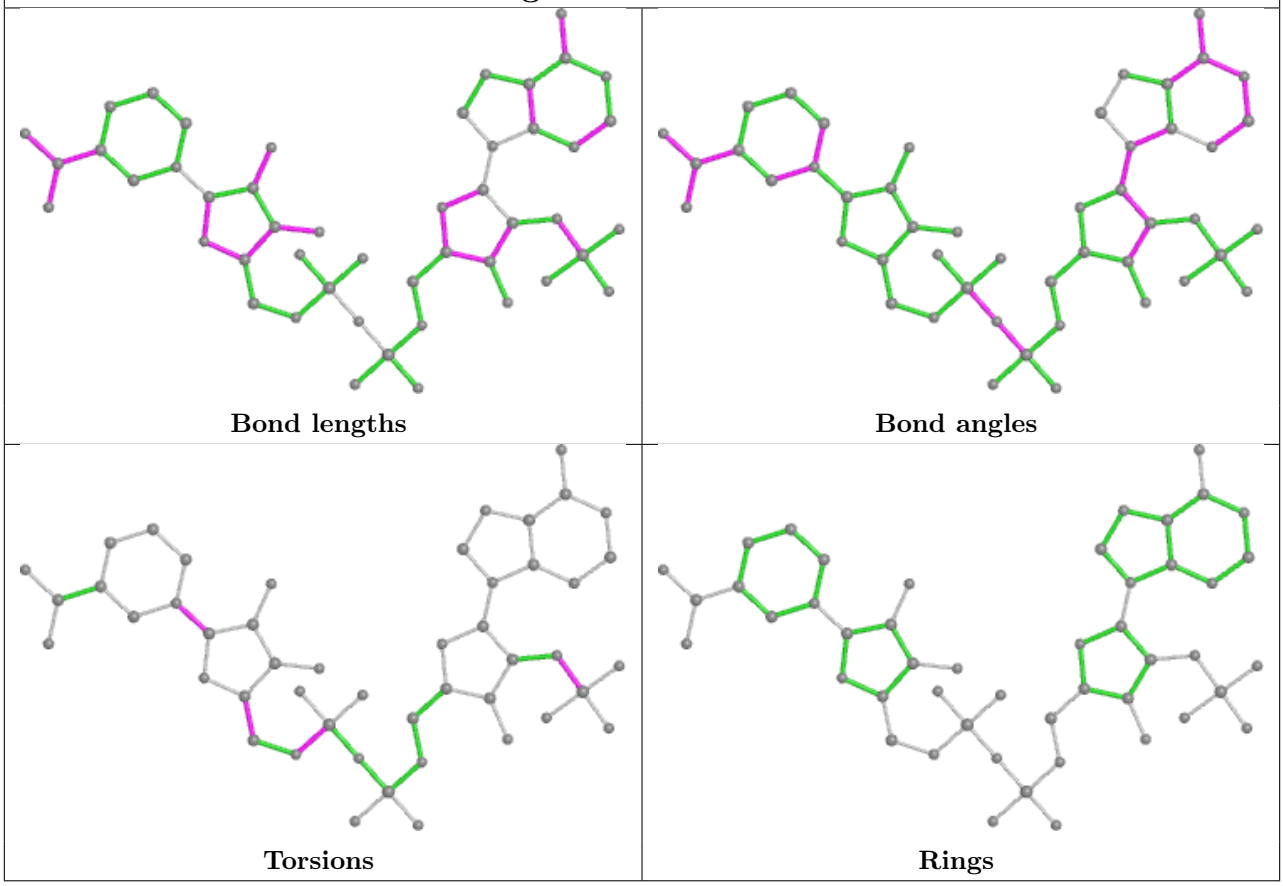


Torsions



Rings

Ligand NAP D 401



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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95th 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	306/319 (95%)	0.13	3 (0%)	82	81	29, 40, 55, 76	0
1	B	300/319 (94%)	0.36	16 (5%)	26	25	30, 43, 75, 111	0
1	C	306/319 (95%)	0.29	9 (2%)	51	49	29, 39, 63, 121	0
1	D	305/319 (95%)	0.16	4 (1%)	77	75	28, 39, 53, 69	0
All	All	1217/1276 (95%)	0.24	32 (2%)	56	53	28, 40, 61, 121	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	155	GLY	10.8
1	C	152	TRP	7.6
1	B	226	GLY	6.1
1	B	228	VAL	5.7
1	C	153	HIS	5.1

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)

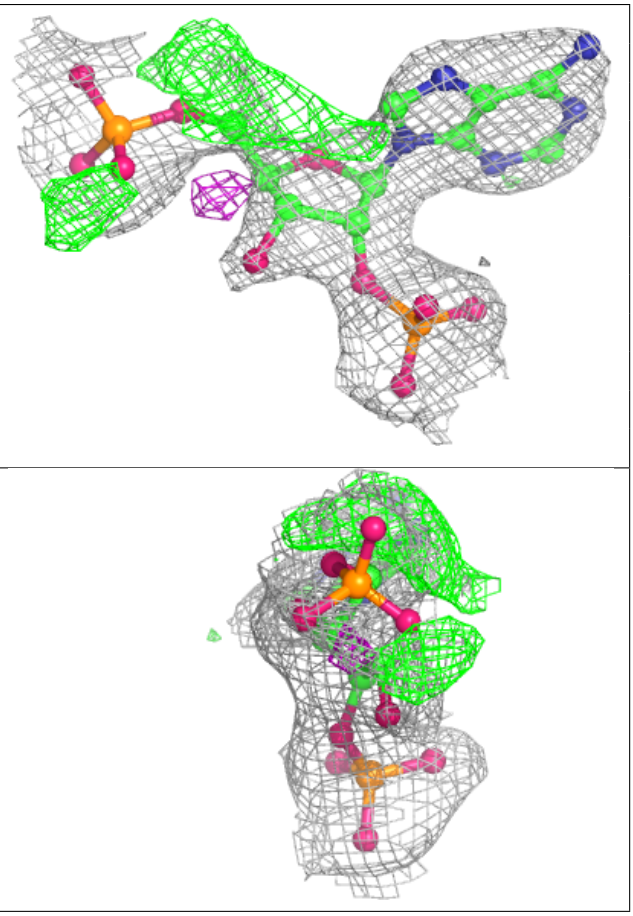
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAP	B	401	27/48	0.80	0.21	59,65,88,93	0
2	NAP	C	401	27/48	0.88	0.20	54,64,85,91	0
3	ARA	A	402	10/10	0.88	0.13	51,57,60,60	0
2	NAP	D	401	48/48	0.93	0.15	39,47,67,72	0
2	NAP	A	401	48/48	0.95	0.14	36,49,59,64	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.

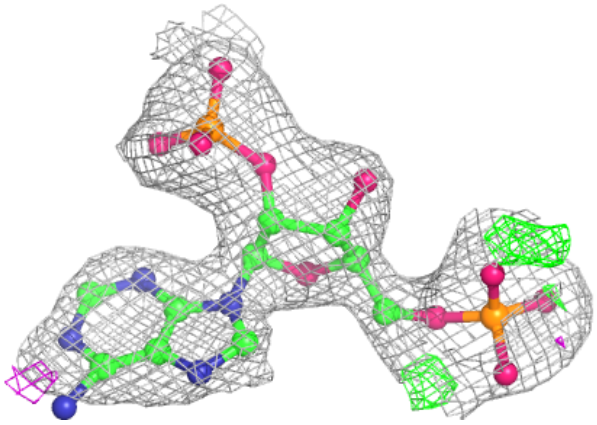
Electron density around NAP B 401:

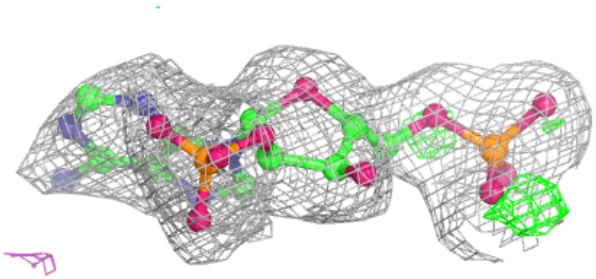
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

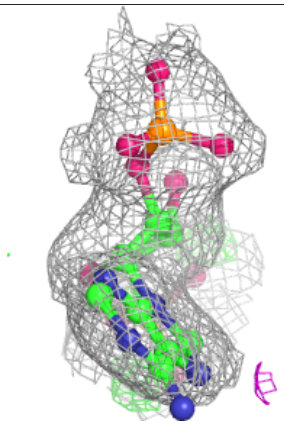


Electron density around NAP C 401:

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

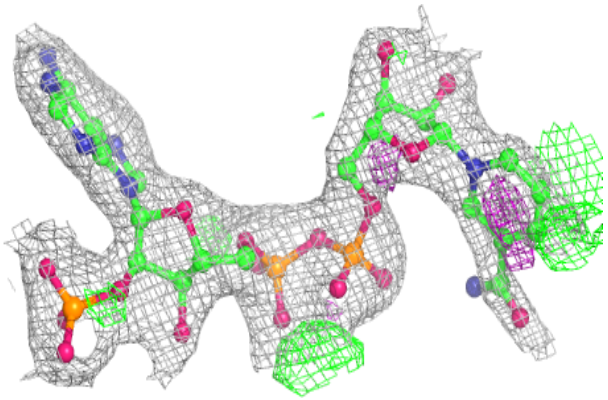


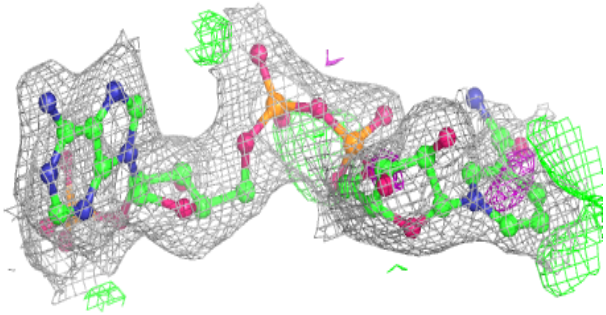


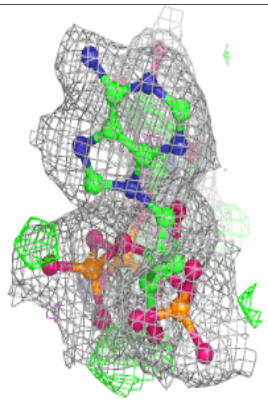


Electron density around NAP D 401:

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

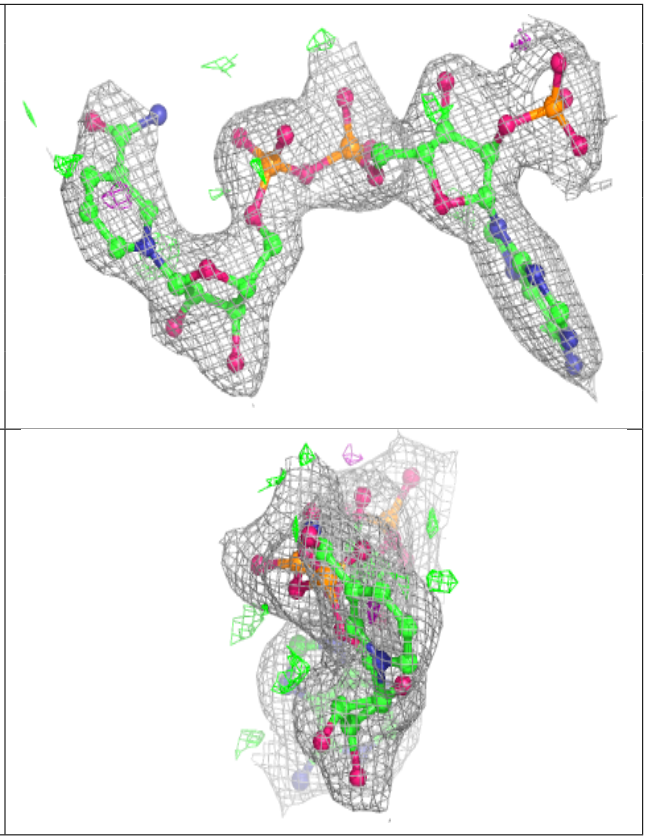






Electron density around NAP A 401:

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



6.5 Other polymers (i)

There are no such residues in this entry.