Full wwPDB X-ray Structure Validation Report (i)

May 21, 2020 – 07:26 pm BST

PDB ID	:	2GWL
Title	:	Crystal structure of the Salmonella SpvB ATR Domain in complex with NADH
Authors	:	Stebbins, C.E.; Margarit, S.M.
Deposited on	:	2006-05-04
Resolution	:	1.90 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 following versions of software and data (see references (i)) were used in the production of this report:

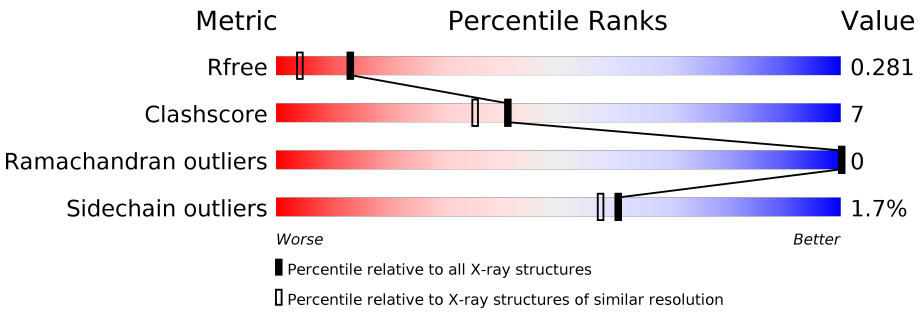
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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	200	84% 16% •

2 Entry composition (i)

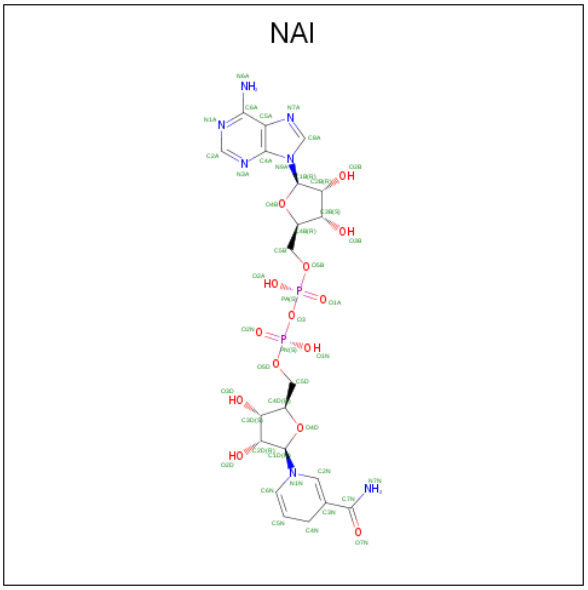
There are 3 unique types of molecules in this entry. The entry contains 1777 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 65 kDa virulence protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	200	1589	999	271	314	5	0	0	0

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	144	144	144	0	0

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: 65 kDa virulence protein

Chain A:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	55.59Å 55.59Å 143.58Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.90 24.66 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (30.00-1.90) 99.3 (24.66-1.90)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.56 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.194 , 0.235 0.241 , 0.281	Depositor DCC
R_{free} test set	1079 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å^2)	29.9	Xtriage
Anisotropy	0.476	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 47.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.035 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	1777	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.86% 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: NAI

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	0.98	2/1615 (0.1%)	0.94	6/2179 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	579	ARG	CZ-NH1	8.46	1.44	1.33
1	A	570	SER	CB-OG	6.56	1.50	1.42

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	579	ARG	NE-CZ-NH1	11.20	125.90	120.30
1	A	559	ASP	CB-CG-OD1	8.37	125.83	118.30
1	A	579	ARG	NE-CZ-NH2	-7.67	116.47	120.30
1	A	559	ASP	CB-CG-OD2	-6.93	112.06	118.30
1	A	496	ASP	CB-CG-OD1	5.33	123.09	118.30
1	A	399	ARG	NE-CZ-NH1	5.28	122.94	120.30

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	1589	0	1590	23	3
2	A	44	0	27	0	0
3	A	144	0	0	13	1
All	All	1777	0	1617	23	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 7.

All (23) 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:444:LYS:CE	3:A:45:HOH:O	2.03	1.05
1:A:444:LYS:NZ	3:A:45:HOH:O	1.93	0.97
1:A:404:GLN:OE1	3:A:140:HOH:O	1.92	0.88
1:A:482:ASP:HB3	3:A:102:HOH:O	1.80	0.79
1:A:393:LYS:HG3	3:A:47:HOH:O	1.86	0.76
1:A:392:SER:N	3:A:67:HOH:O	2.18	0.76
1:A:444:LYS:HE2	3:A:45:HOH:O	1.76	0.75
1:A:566:LYS:CE	3:A:41:HOH:O	2.40	0.68
1:A:566:LYS:HE3	3:A:41:HOH:O	2.01	0.59
1:A:590:ASN:O	1:A:591:SER:HB3	2.07	0.55
1:A:409:ILE:HD12	1:A:451:ILE:HG12	1.91	0.53
1:A:487:TYR:CE2	1:A:586:MET:HE1	2.46	0.51
1:A:564:LEU:HD12	1:A:567:LEU:HD12	1.96	0.47
1:A:532:HIS:HE1	3:A:103:HOH:O	1.98	0.47
1:A:590:ASN:O	1:A:591:SER:CB	2.63	0.46
1:A:399:ARG:NH2	1:A:529:ASP:O	2.49	0.45
1:A:490:ILE:HG22	3:A:131:HOH:O	2.17	0.45
1:A:409:ILE:HD12	1:A:451:ILE:CG1	2.48	0.44
1:A:419:PRO:HB2	1:A:422:GLN:HB2	2.01	0.42
1:A:474:LYS:HD3	1:A:477:LYS:HE2	2.01	0.42
1:A:566:LYS:HE2	3:A:41:HOH:O	2.13	0.42
1:A:566:LYS:HG3	3:A:41:HOH:O	2.19	0.41
1:A:494:ILE:HD12	1:A:549:ILE:HD11	2.04	0.40

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)
3:A:142:HOH:O	3:A:143:HOH:O[5_665]	1.44	0.76
1:A:393:LYS:NZ	1:A:566:LYS:NZ[3_665]	1.54	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:ARG:O	1:A:566:LYS:NZ[3_665]	2.16	0.04
1:A:393:LYS:NZ	1:A:566:LYS:CE[3_665]	2.16	0.04

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	198/200 (99%)	195 (98%)	3 (2%)	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	177/177 (100%)	174 (98%)	3 (2%)	60 57

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	435	THR
1	A	436	ASN
1	A	441	GLU

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

Mol	Chain	Res	Type
1	A	436	ASN
1	A	558	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	NAI	A	592	-	42,48,48	1.77	8 (19%)	47,73,73	1.89	10 (21%)

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	NAI	A	592	-	-	6/25/72/72	0/5/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	592	NAI	O7N-C7N	6.33	1.39	1.24
2	A	592	NAI	C4N-C3N	-4.47	1.41	1.49
2	A	592	NAI	C4N-C5N	-3.47	1.39	1.48
2	A	592	NAI	C2A-N3A	3.36	1.37	1.32
2	A	592	NAI	C6N-C5N	2.86	1.38	1.33
2	A	592	NAI	C2A-N1A	2.38	1.38	1.33
2	A	592	NAI	C7N-C3N	2.26	1.53	1.48
2	A	592	NAI	O4B-C4B	-2.06	1.40	1.45

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	592	NAI	N3A-C2A-N1A	-6.00	119.30	128.68
2	A	592	NAI	O4B-C4B-C5B	-5.37	91.71	109.37
2	A	592	NAI	C3N-C7N-N7N	3.78	124.37	117.67
2	A	592	NAI	C3B-C2B-C1B	3.37	106.06	100.98
2	A	592	NAI	N6A-C6A-N1A	3.15	125.11	118.57
2	A	592	NAI	C5A-C6A-N6A	-2.78	116.12	120.35
2	A	592	NAI	O7N-C7N-C3N	-2.24	116.68	120.90
2	A	592	NAI	O2A-PA-O5B	2.19	117.93	107.75
2	A	592	NAI	C3N-C2N-N1N	-2.14	120.04	123.10
2	A	592	NAI	PN-O3-PA	-2.10	125.61	132.83

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	592	NAI	C5B-O5B-PA-O1A
2	A	592	NAI	C5B-O5B-PA-O2A
2	A	592	NAI	O4D-C1D-N1N-C6N
2	A	592	NAI	O4B-C4B-C5B-O5B
2	A	592	NAI	C5B-O5B-PA-O3
2	A	592	NAI	PA-O3-PN-O2N

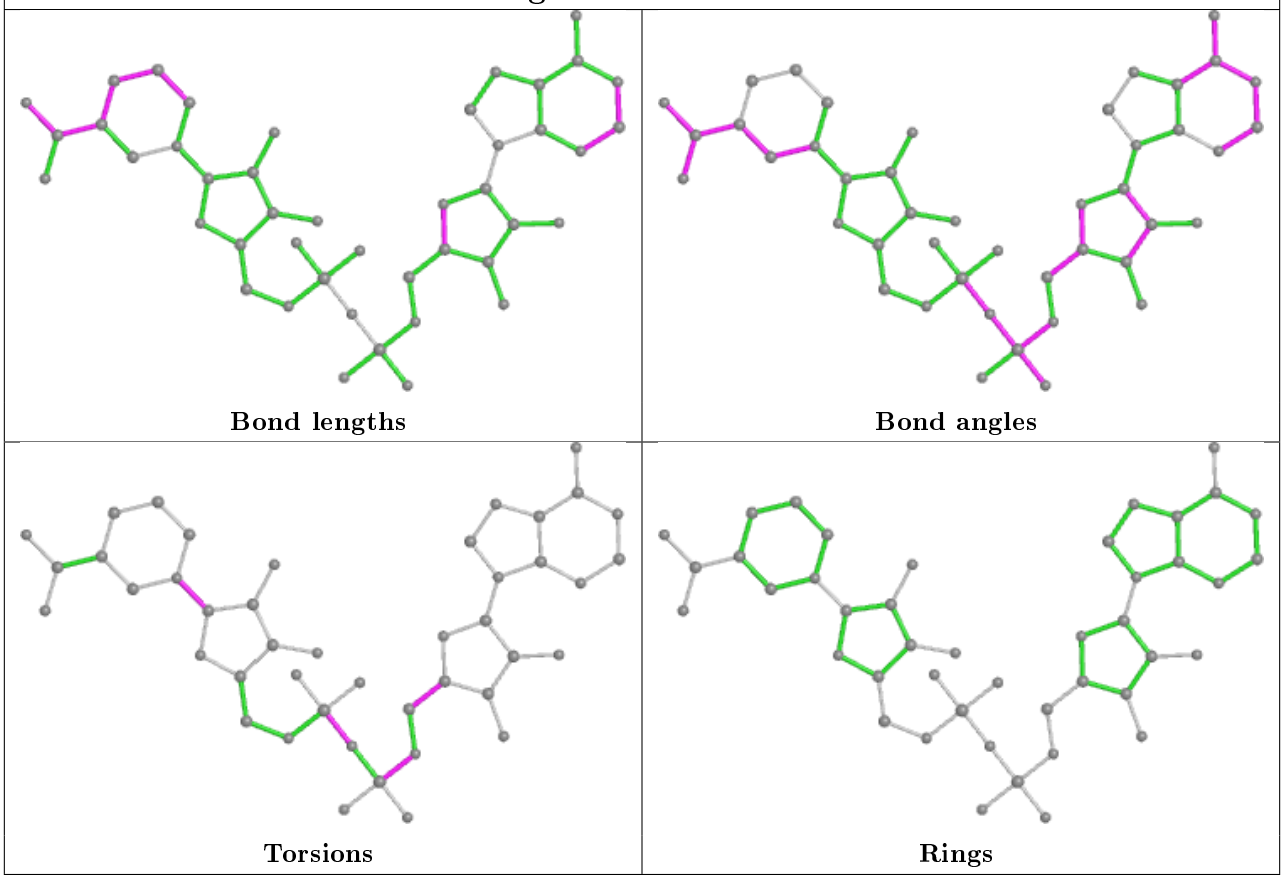
There are no ring outliers.

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 NAI A 592



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)

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

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

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

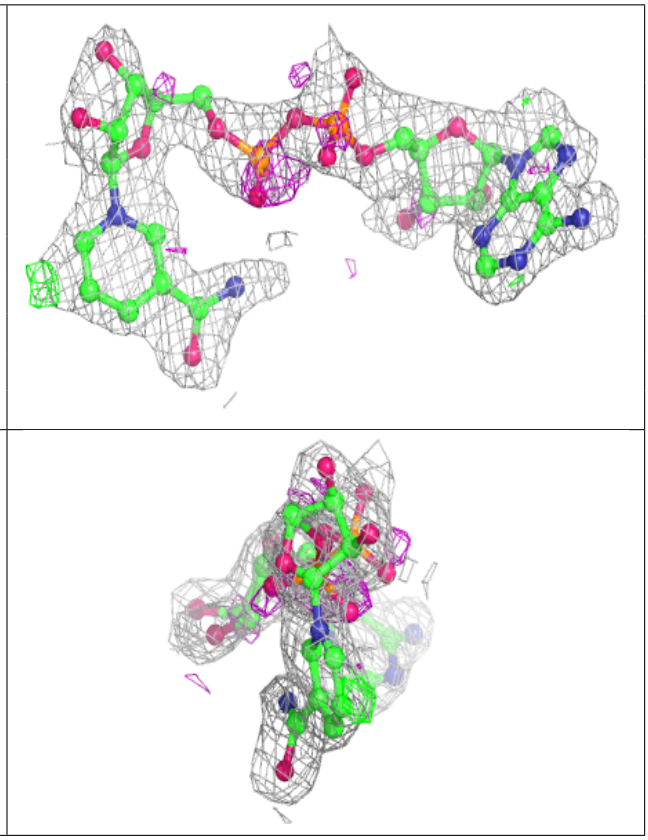
6.4 Ligands (i)

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 NAI A 592:

$2mF_o$-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.