



# wwPDB X-ray Structure Validation Summary Report

Mar 5, 2026 – 05:06 PM UTC

PDB ID : 6SLE / pdb\_00006sle  
Title : Structure of Reductive Aminase from Neosartorya fumigata in complex with NADP+  
Authors : Sharma, M.; Mangas-Sanchez, J.; Turner, N.J.; Grogan, G.  
Deposited on : 2019-08-19  
Resolution : 2.77 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](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references](#) ) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

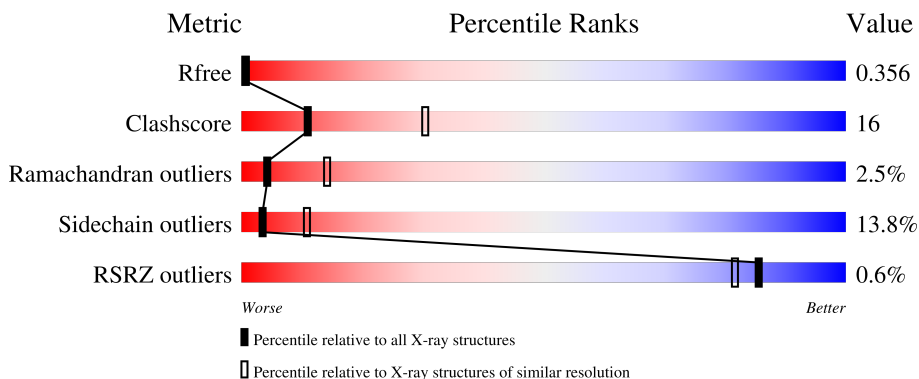
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.77 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))
$R_{free}$	180053	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	285	 62% 31% 5% •
1	B	285	 2% 69% 18% • 8%
1	C	285	 % 72% 21% • •
1	D	285	 % 62% 30% 5% •
1	E	285	 68% 22% • 6%

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Mol	Chain	Length	Quality of chain
1	F	285	 63% 32% . .
1	G	285	%  71% 24% . .
1	H	285	 66% 28% . .

## 2 Entry composition

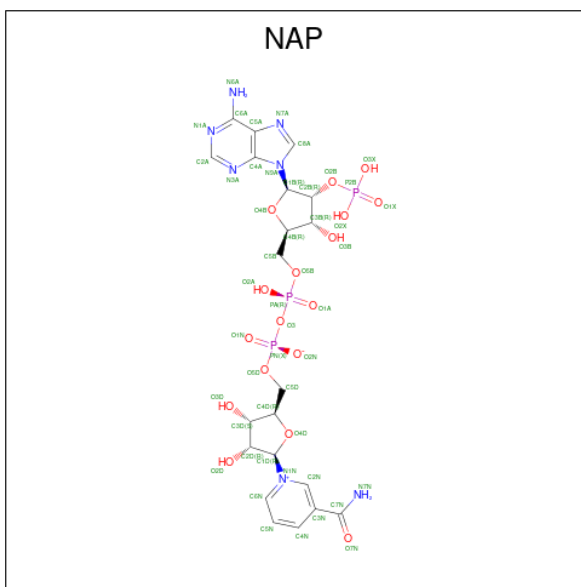
There are 3 unique types of molecules in this entry. The entry contains 15201 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Oxidoreductase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	281	Total 1951	C 1234	N 332	O 374	S 11	0	1	0
1	B	261	Total 1648	C 1032	N 286	O 320	S 10	0	1	0
1	C	273	Total 1820	C 1152	N 315	O 340	S 13	0	0	0
1	D	278	Total 1920	C 1222	N 320	O 367	S 11	0	0	0
1	E	268	Total 1708	C 1070	N 300	O 328	S 10	0	0	0
1	F	280	Total 1930	C 1221	N 326	O 372	S 11	0	0	0
1	G	279	Total 1820	C 1137	N 317	O 353	S 13	0	0	0
1	H	278	Total 1915	C 1210	N 322	O 372	S 11	0	0	0

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	C	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	D	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	E	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	F	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	G	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	H	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 3 is water.

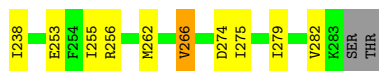
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total 15	O 15	0	0
3	B	15	Total 15	O 15	0	0
3	C	8	Total 8	O 8	0	0
3	D	11	Total 11	O 11	0	0

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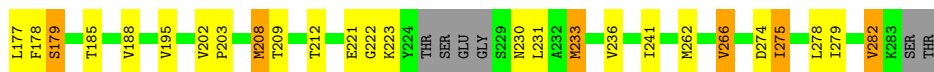
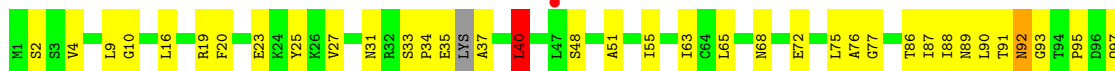
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	E	15	Total 15	O 15	0	0
3	F	14	Total 14	O 14	0	0
3	G	13	Total 13	O 13	0	0
3	H	14	Total 14	O 14	0	0

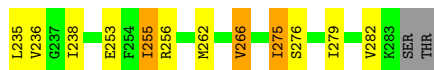
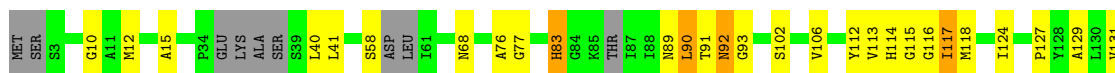




- Molecule 1: Oxidoreductase, putative



- Molecule 1: Oxidoreductase, putative

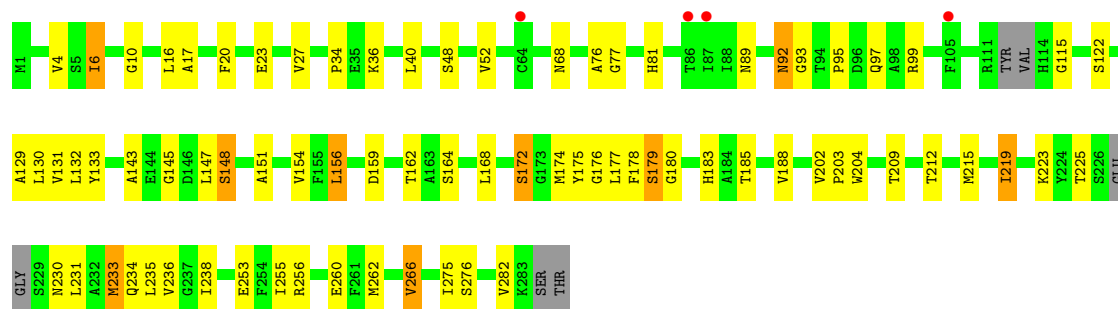


- Molecule 1: Oxidoreductase, putative



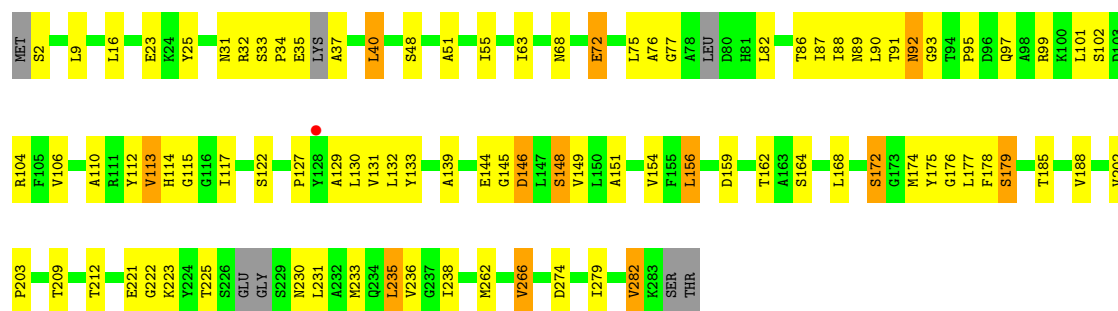
- Molecule 1: Oxidoreductase, putative





- Molecule 1: Oxidoreductase, putative

Chain H: 66% 28%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.39Å 89.31Å 97.93Å 105.56° 90.00° 93.99°	Depositor
Resolution (Å)	48.28 – 2.77 48.28 – 2.77	Depositor EDS
% Data completeness (in resolution range)	79.0 (48.28-2.77) 79.1 (48.28-2.77)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.83 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, $R_{free}$	0.286 , 0.357 0.287 , 0.356	Depositor DCC
$R_{free}$ test set	2666 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	45.9	Xtriage
Anisotropy	0.812	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 68.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Reported twinning fraction	0.866 for H, K, L 0.134 for h,-k,-l	Depositor
Outliers	0 of 53895 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	15201	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.99 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.5207e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  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: 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	1.15	0/1986	1.60	2/2701 (0.1%)
1	B	1.20	0/1671	1.65	4/2281 (0.2%)
1	C	1.15	0/1846	1.57	0/2510
1	D	1.16	0/1952	1.58	3/2658 (0.1%)
1	E	1.17	0/1729	1.63	4/2359 (0.2%)
1	F	1.16	1/1962 (0.1%)	1.59	1/2673 (0.0%)
1	G	1.18	0/1848	1.62	0/2521
1	H	1.16	0/1945	1.60	3/2647 (0.1%)
All	All	1.16	1/14939 (0.0%)	1.60	17/20350 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	166	HIS	CE1-NE2	5.45	1.38	1.32

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	96	ASP	CA-CB-CG	7.30	119.90	112.60
1	B	81	HIS	CA-CB-CG	6.44	120.24	113.80
1	H	221	GLU	CB-CG-CD	5.94	122.70	112.60
1	A	41	LEU	CA-C-N	5.73	126.45	120.03
1	A	41	LEU	C-N-CA	5.73	126.45	120.03

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	1951	0	1816	79	0
1	B	1648	0	1353	48	0
1	C	1820	0	1620	40	0
1	D	1920	0	1801	67	0
1	E	1708	0	1434	70	0
1	F	1930	0	1782	74	0
1	G	1820	0	1555	59	0
1	H	1915	0	1779	57	0
2	A	48	0	25	4	0
2	B	48	0	25	3	0
2	C	48	0	25	1	0
2	D	48	0	25	5	0
2	E	48	0	25	4	0
2	F	48	0	25	5	0
2	G	48	0	25	4	0
2	H	48	0	25	2	0
3	A	15	0	0	3	0
3	B	15	0	0	2	0
3	C	8	0	0	3	0
3	D	11	0	0	2	0
3	E	15	0	0	5	0
3	F	14	0	0	6	0
3	G	13	0	0	3	0
3	H	14	0	0	0	0
All	All	15201	0	13340	468	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 16.

The worst 5 of 468 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:D:127:PRO:HA	1:F:127:PRO:HA	1.20	1.16
1:A:127:PRO:HA	1:H:127:PRO:HA	1.26	1.09
1:A:40:LEU:HD23	1:A:40:LEU:O	1.58	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:ARG:CD	1:A:139:ALA:HB2	1.92	1.00
1:E:12:MET:SD	1:E:124:ILE:HD11	2.04	0.98

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	278/285 (98%)	244 (88%)	26 (9%)	8 (3%)	3	11
1	B	248/285 (87%)	220 (89%)	22 (9%)	6 (2%)	4	15
1	C	261/285 (92%)	233 (89%)	23 (9%)	5 (2%)	6	19
1	D	272/285 (95%)	245 (90%)	20 (7%)	7 (3%)	4	13
1	E	256/285 (90%)	229 (90%)	22 (9%)	5 (2%)	6	18
1	F	276/285 (97%)	243 (88%)	24 (9%)	9 (3%)	3	9
1	G	273/285 (96%)	243 (89%)	23 (8%)	7 (3%)	4	13
1	H	270/285 (95%)	244 (90%)	19 (7%)	7 (3%)	4	13
All	All	2134/2280 (94%)	1901 (89%)	179 (8%)	54 (2%)	4	14

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	35	GLU
1	E	40	LEU
1	F	80	ASP
1	G	40	LEU
1	H	40	LEU

### 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	177/221 (80%)	151 (85%)	26 (15%)	3	9
1	B	116/221 (52%)	98 (84%)	18 (16%)	2	8
1	C	147/221 (66%)	129 (88%)	18 (12%)	5	14
1	D	176/221 (80%)	150 (85%)	26 (15%)	3	9
1	E	125/221 (57%)	107 (86%)	18 (14%)	3	10
1	F	173/221 (78%)	151 (87%)	22 (13%)	4	13
1	G	142/221 (64%)	123 (87%)	19 (13%)	4	12
1	H	176/221 (80%)	152 (86%)	24 (14%)	3	11
All	All	1232/1768 (70%)	1061 (86%)	171 (14%)	3	11

5 of 171 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	113	VAL
1	G	236	VAL
1	F	156	LEU
1	G	23	GLU
1	H	35	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	68	ASN
1	G	68	ASN
1	F	81	HIS
1	F	230	ASN
1	G	114	HIS

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

8 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	301	-	50,52,52	1.22	4 (8%)	71,80,80	1.75	15 (21%)
2	NAP	H	1001	-	50,52,52	1.75	7 (14%)	71,80,80	2.12	19 (26%)
2	NAP	B	301	-	50,52,52	1.49	7 (14%)	71,80,80	1.74	16 (22%)
2	NAP	G	301	-	50,52,52	1.37	6 (12%)	71,80,80	1.78	15 (21%)
2	NAP	F	301	-	50,52,52	1.47	11 (22%)	71,80,80	2.19	23 (32%)
2	NAP	A	1000	-	50,52,52	1.64	9 (18%)	71,80,80	2.06	24 (33%)
2	NAP	D	301	-	50,52,52	1.57	9 (18%)	71,80,80	2.25	22 (30%)
2	NAP	E	301	-	50,52,52	1.30	5 (10%)	71,80,80	1.61	11 (15%)

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	301	-	-	12/35/67/67	0/5/5/5
2	NAP	H	1001	-	-	11/35/67/67	0/5/5/5
2	NAP	B	301	-	-	11/35/67/67	0/5/5/5
2	NAP	G	301	-	-	7/35/67/67	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAP	F	301	-	-	14/35/67/67	0/5/5/5
2	NAP	A	1000	-	-	7/35/67/67	0/5/5/5
2	NAP	D	301	-	-	2/35/67/67	0/5/5/5
2	NAP	E	301	-	-	14/35/67/67	0/5/5/5

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	NAP	C5A-C4A	5.81	1.49	1.39
2	H	1001	NAP	C5A-C4A	5.75	1.49	1.39
2	E	301	NAP	C5A-C4A	5.17	1.48	1.39
2	C	301	NAP	C5A-C4A	5.00	1.48	1.39
2	D	301	NAP	C5A-C4A	4.83	1.47	1.39

The worst 5 of 145 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1001	NAP	O4B-C1B-N9A	6.74	121.03	108.09
2	D	301	NAP	O3B-C3B-C4B	-6.43	92.60	111.08
2	E	301	NAP	C5A-C4A-N3A	-6.35	117.98	126.72
2	G	301	NAP	C5A-C4A-N3A	-6.03	118.42	126.72
2	H	1001	NAP	C4D-O4D-C1D	-6.00	104.43	109.92

There are no chirality outliers.

5 of 78 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1000	NAP	C5B-O5B-PA-O1A
2	A	1000	NAP	C5B-O5B-PA-O2A
2	A	1000	NAP	C5B-O5B-PA-O3
2	A	1000	NAP	O4D-C1D-N1N-C2N
2	A	1000	NAP	O4D-C1D-N1N-C6N

There are no ring outliers.

8 monomers are involved in 28 short contacts:

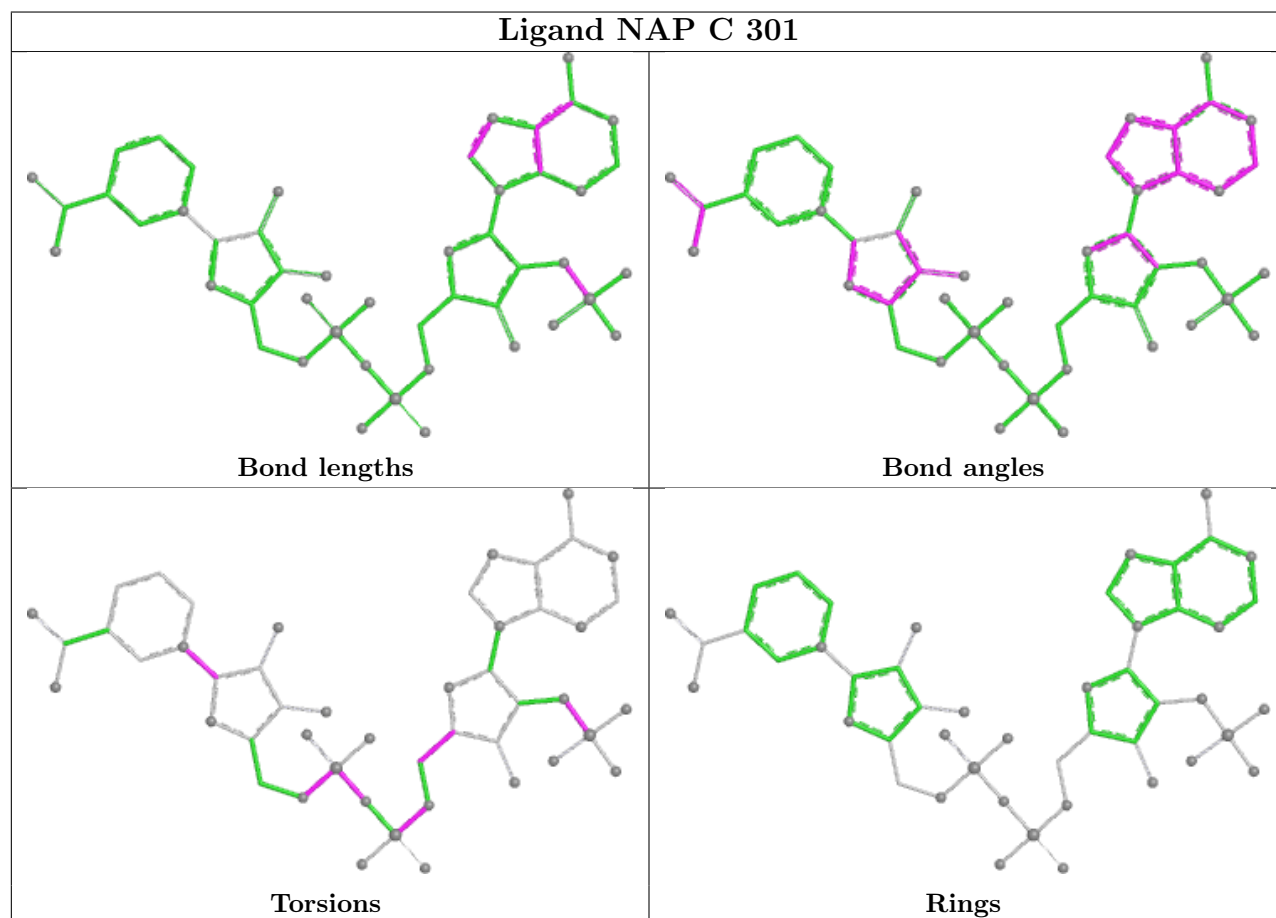
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	NAP	1	0
2	H	1001	NAP	2	0
2	B	301	NAP	3	0

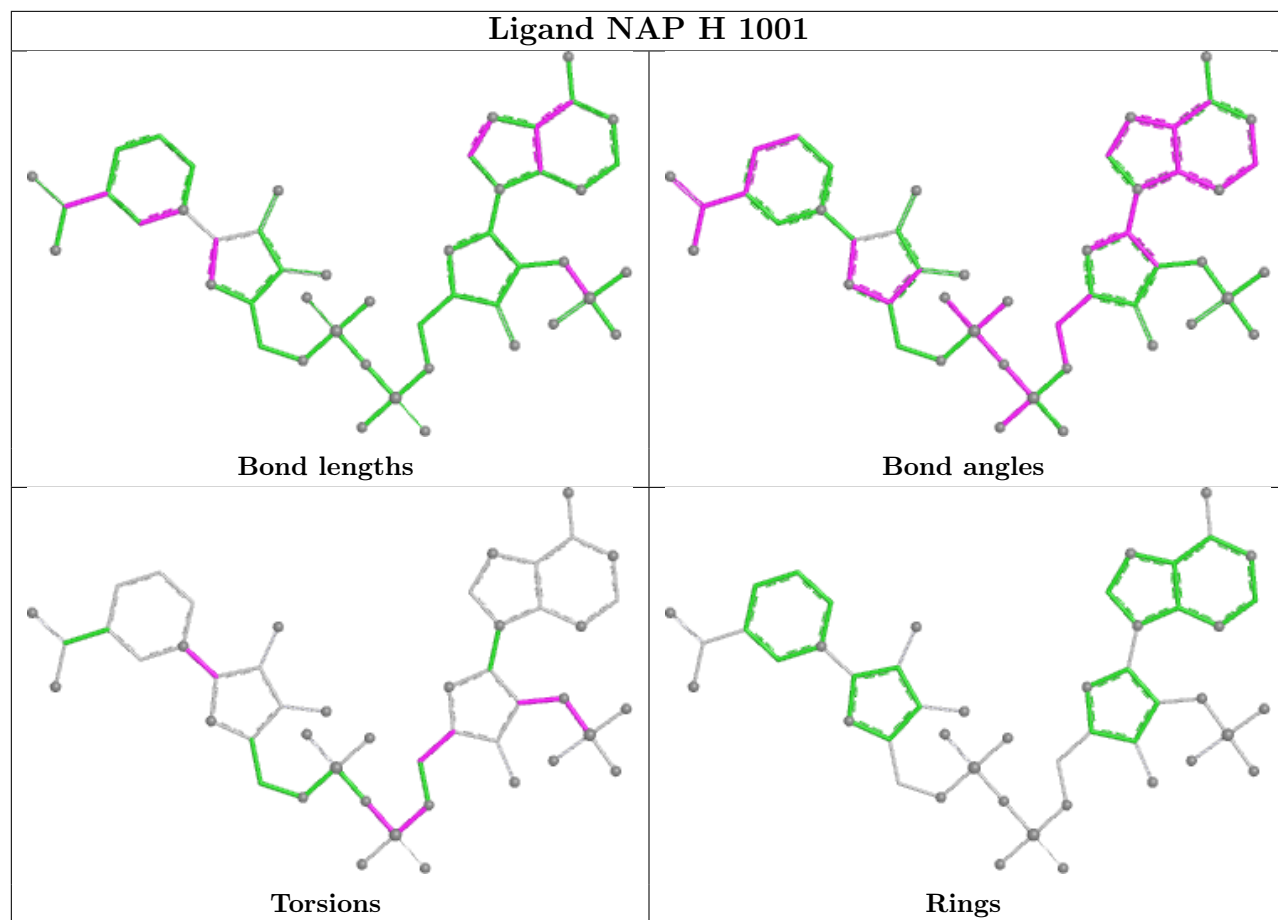
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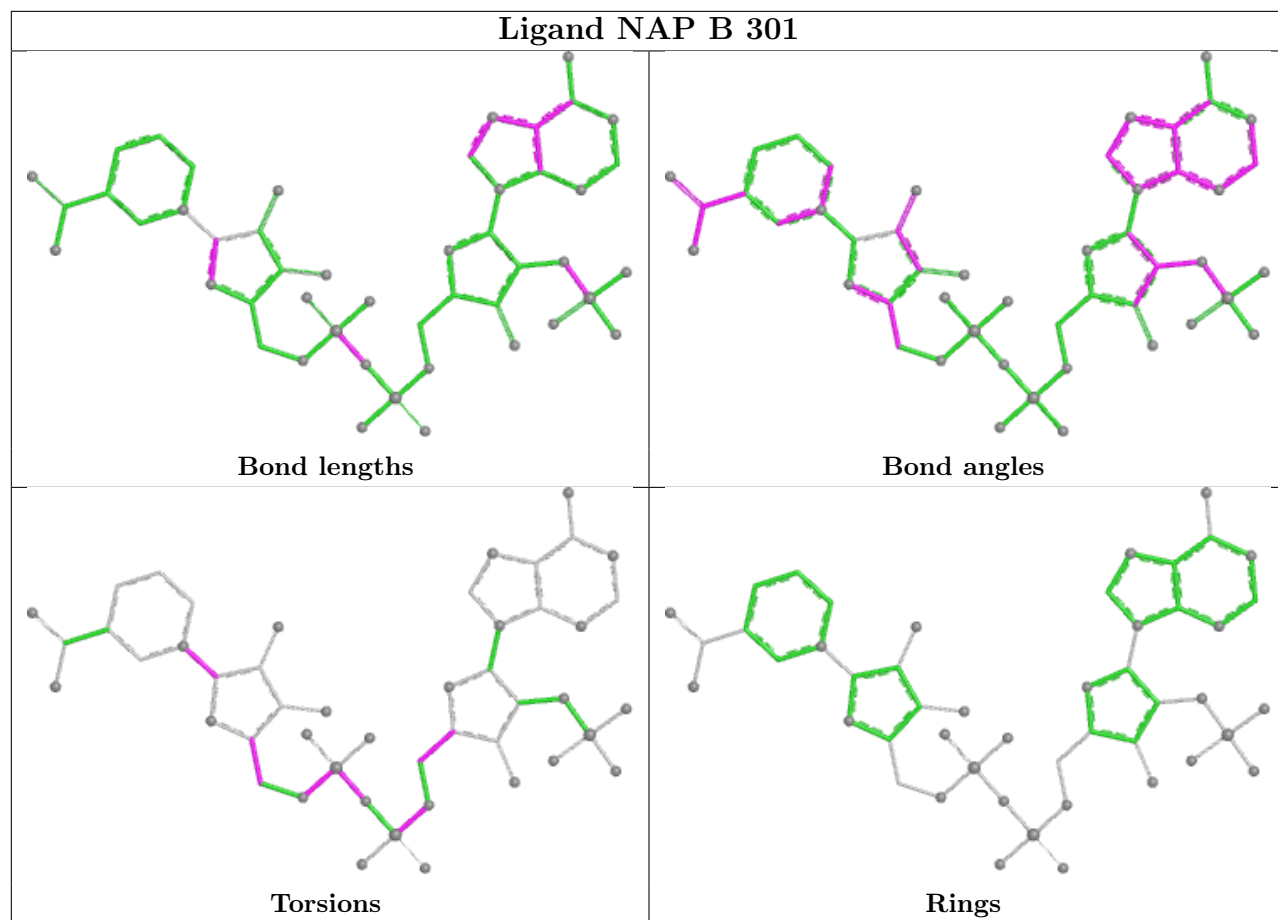
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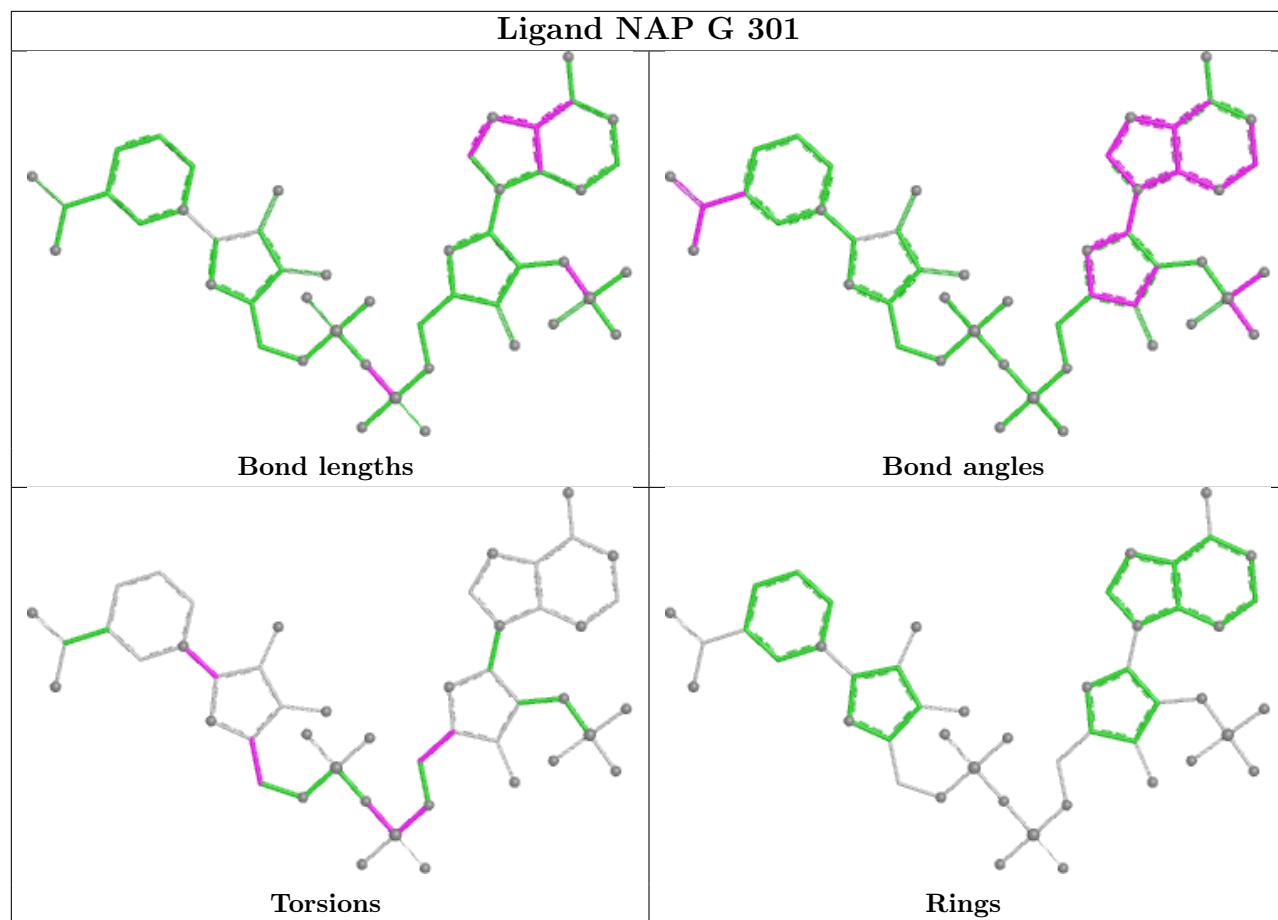
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	301	NAP	4	0
2	F	301	NAP	5	0
2	A	1000	NAP	4	0
2	D	301	NAP	5	0
2	E	301	NAP	4	0

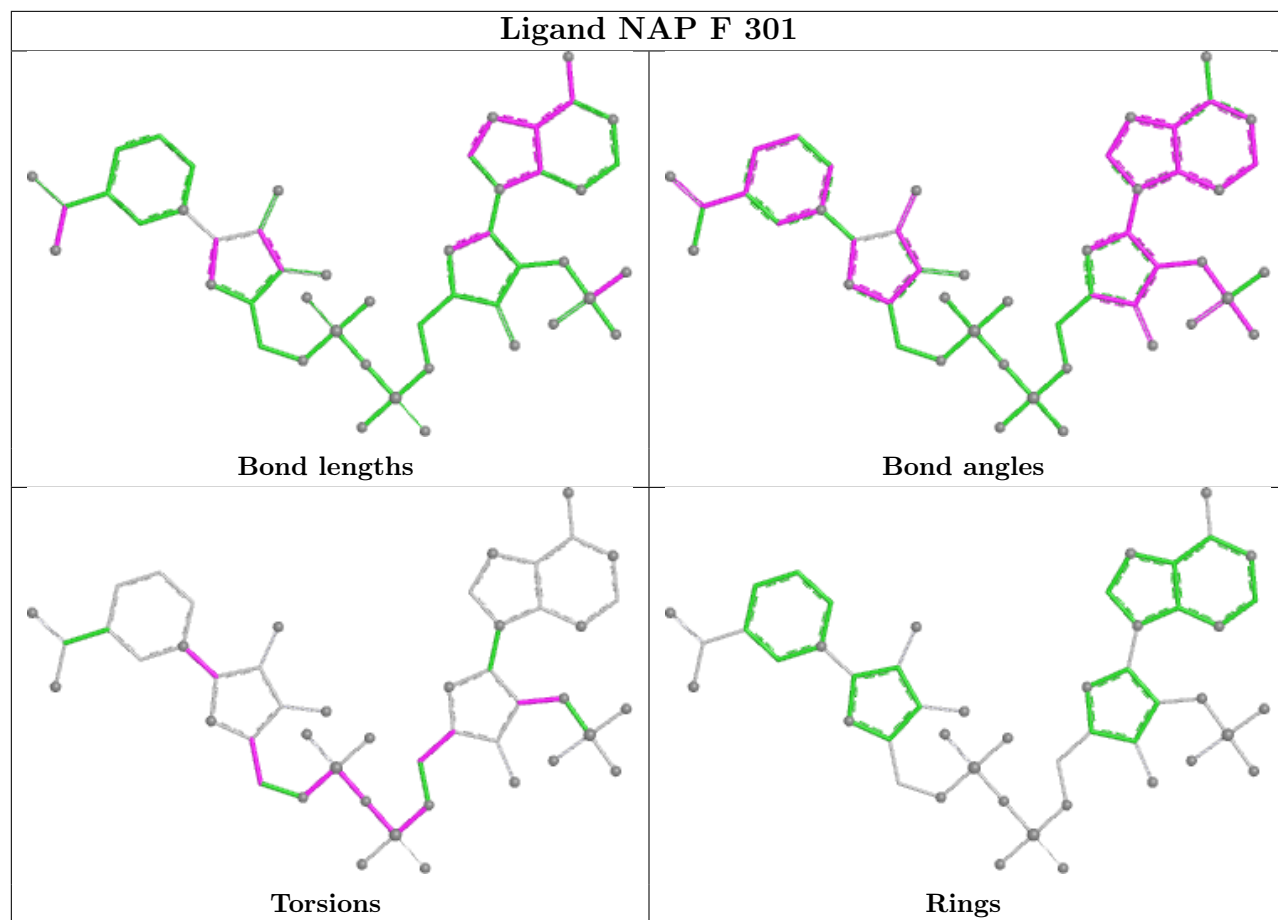
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

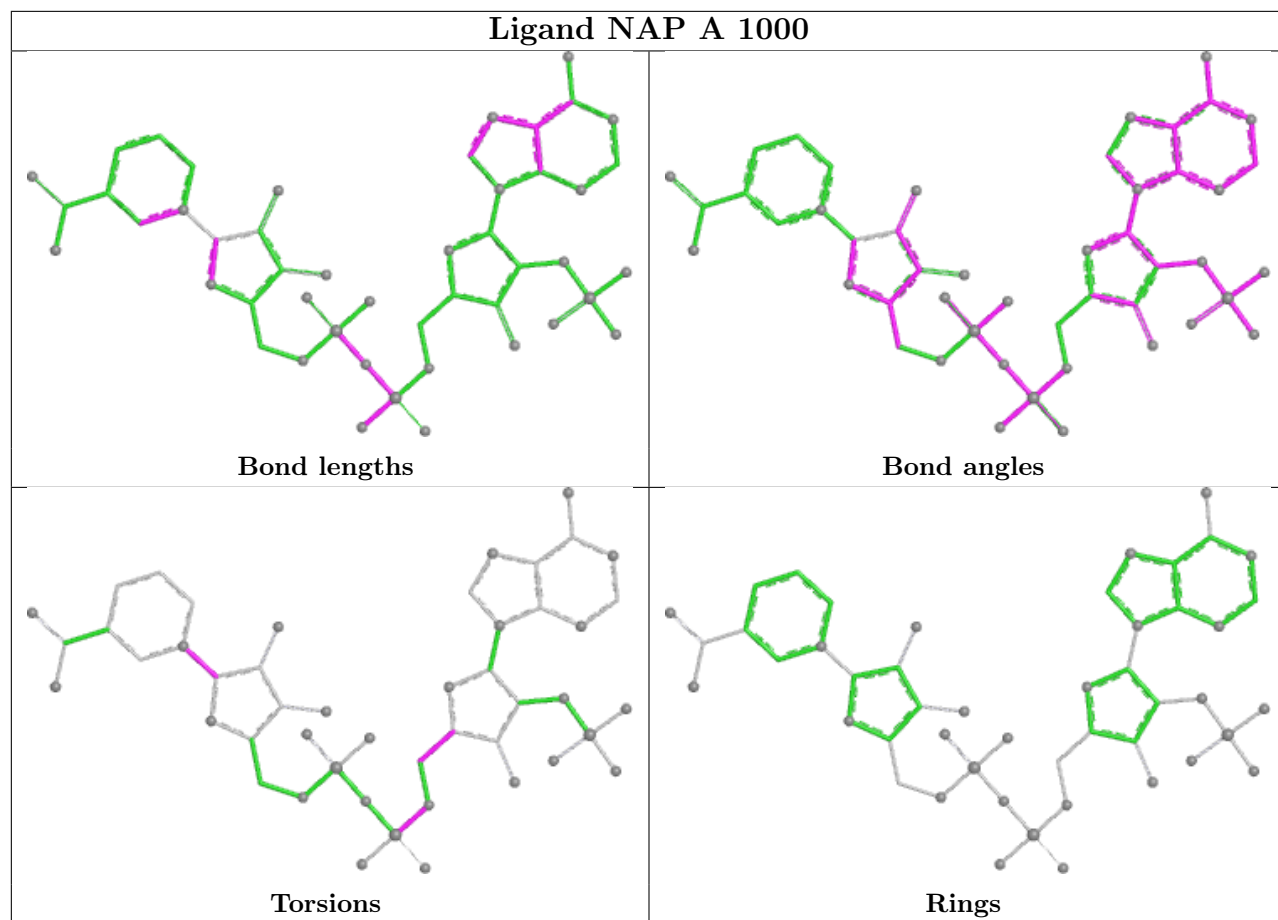


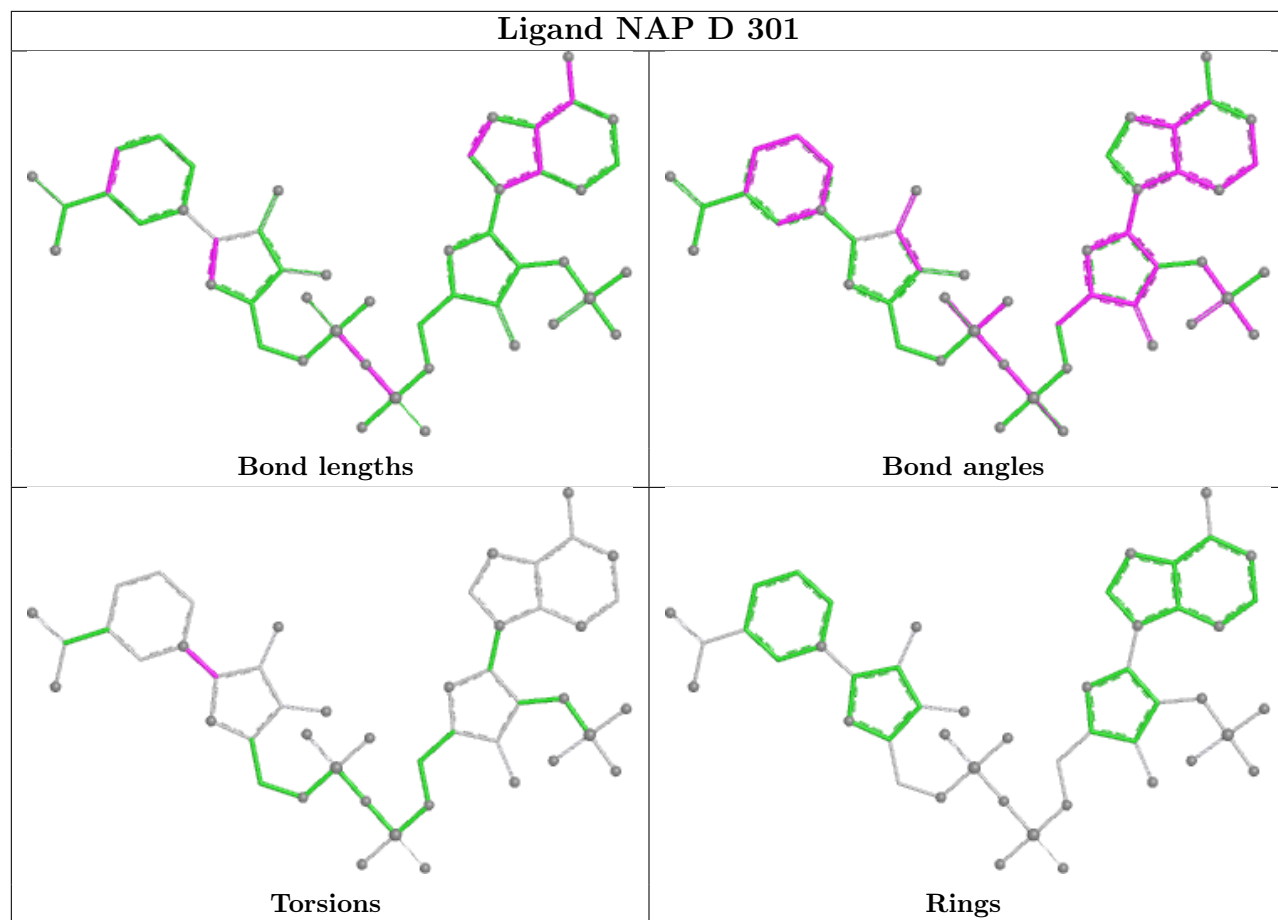


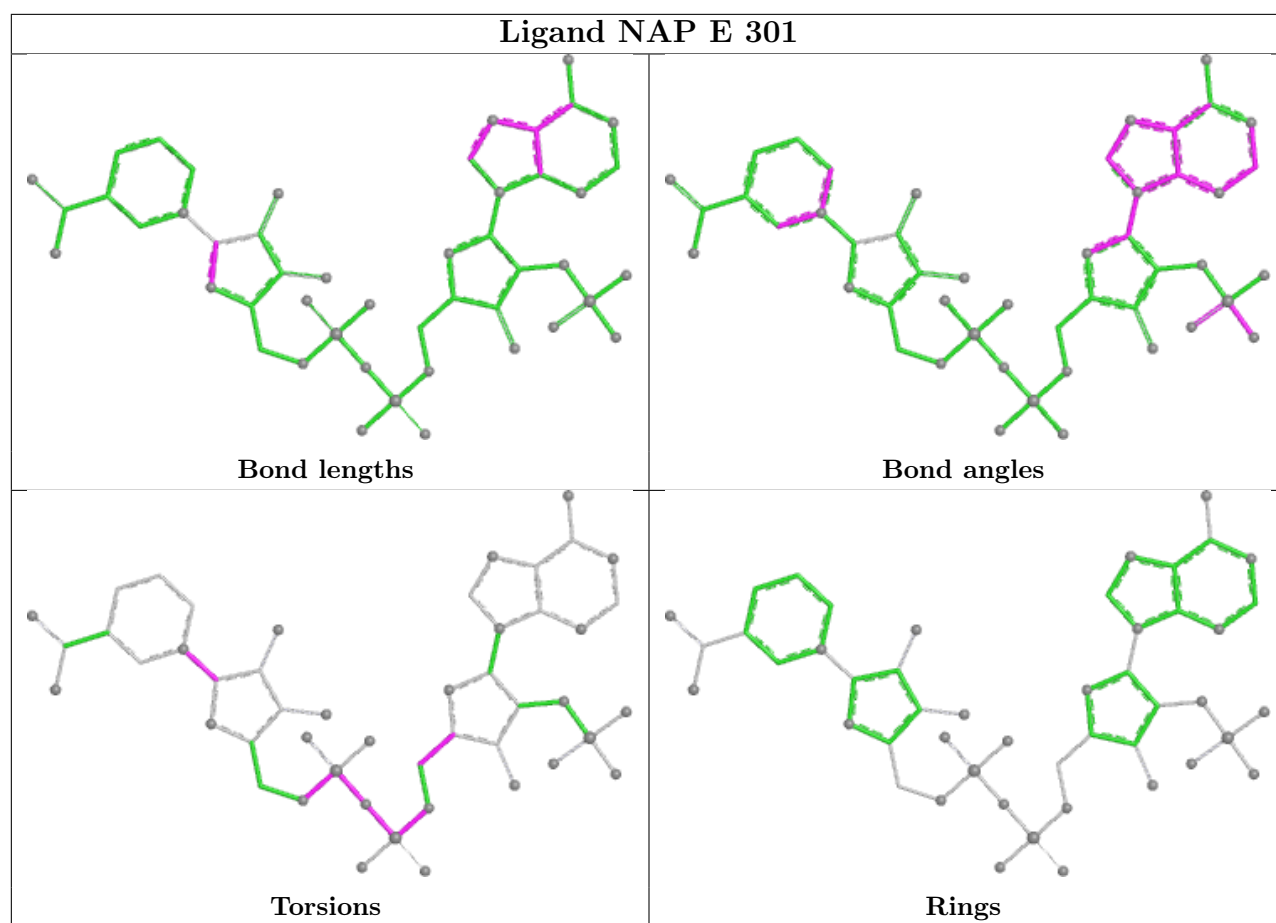












## 5.7 Other polymers [\(i\)](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	281/285 (98%)	-0.92	0 <b>100</b> <b>100</b>	13, 46, 76, 100	1 (0%)
1	B	261/285 (91%)	-0.67	5 (1%) 66 59	17, 74, 118, 152	1 (0%)
1	C	273/285 (95%)	-0.73	2 (0%) 84 79	23, 71, 107, 126	0
1	D	278/285 (97%)	-0.85	2 (0%) 84 79	17, 45, 70, 99	0
1	E	268/285 (94%)	-0.75	0 <b>100</b> <b>100</b>	22, 69, 111, 134	0
1	F	280/285 (98%)	-0.90	0 <b>100</b> <b>100</b>	16, 47, 79, 101	0
1	G	279/285 (97%)	-0.71	4 (1%) 73 67	23, 68, 106, 127	0
1	H	278/285 (97%)	-0.86	1 (0%) 88 85	18, 46, 76, 100	0
All	All	2198/2280 (96%)	-0.80	14 (0%) 85 81	13, 53, 104, 152	2 (0%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	87	ILE	8.0
1	G	86	THR	4.5
1	B	87	ILE	4.0
1	D	47	LEU	3.6
1	B	88	ILE	3.2

### 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](#)

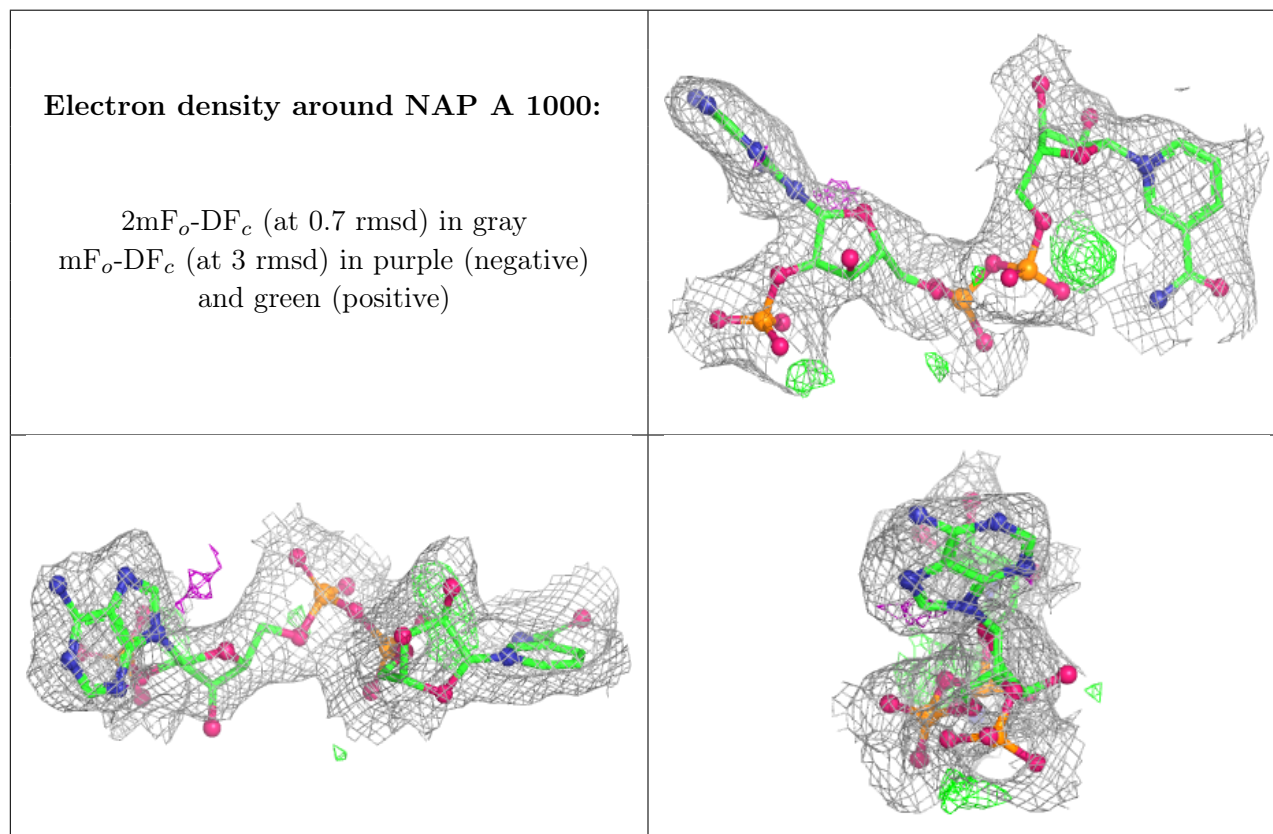
There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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.

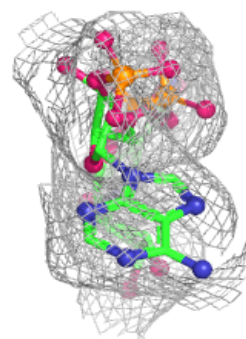
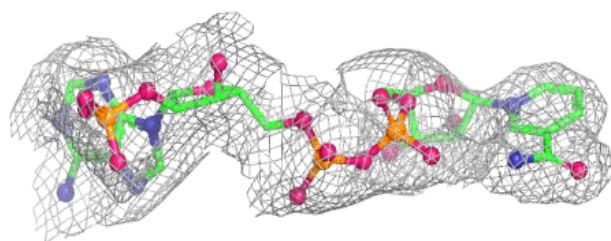
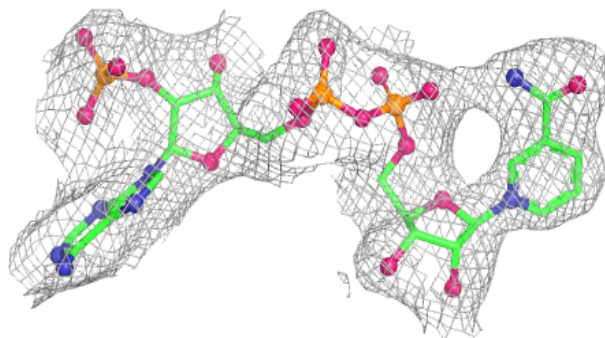
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAP	A	1000	48/48	0.98	0.05	19,25,35,45	0
2	NAP	B	301	48/48	0.98	0.04	26,51,66,68	0
2	NAP	C	301	48/48	0.98	0.04	26,51,81,93	0
2	NAP	D	301	48/48	0.98	0.04	12,19,29,33	0
2	NAP	E	301	48/48	0.98	0.04	35,66,93,100	0
2	NAP	F	301	48/48	0.98	0.05	17,32,36,46	0
2	NAP	G	301	48/48	0.98	0.04	31,47,56,67	0
2	NAP	H	1001	48/48	0.99	0.04	16,21,37,40	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.

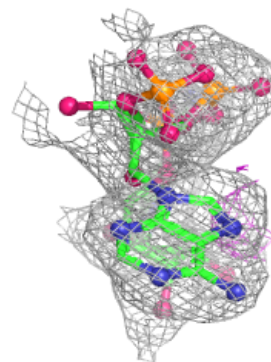
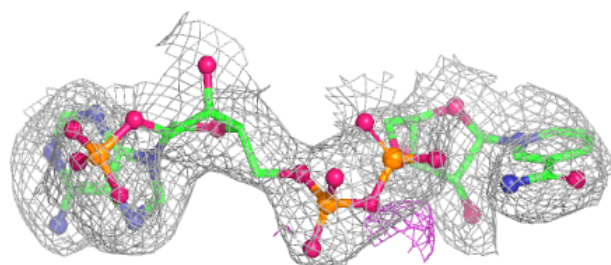
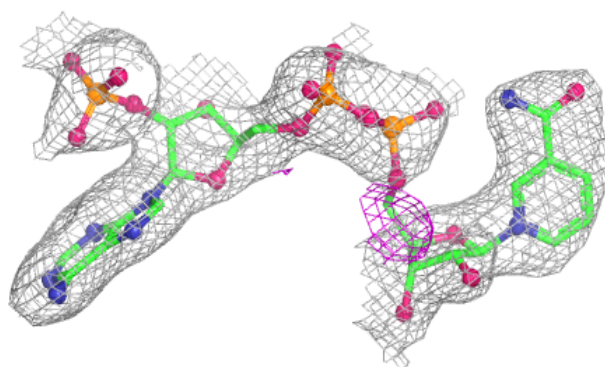


**Electron density around NAP B 301:**

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

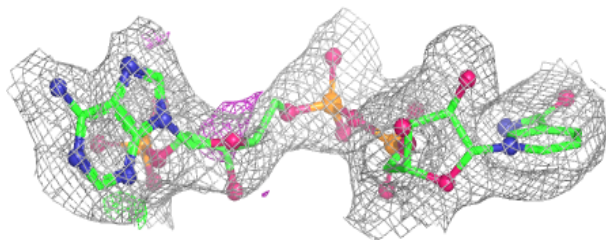
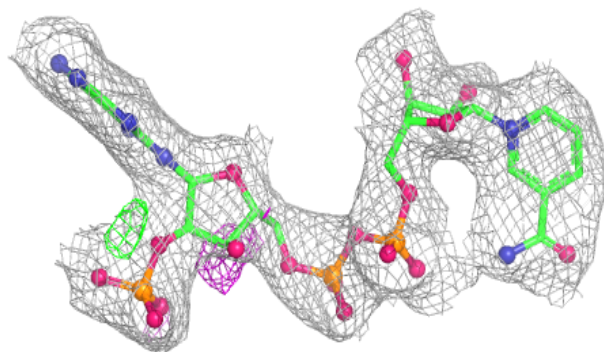
**Electron density around NAP C 301:**

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

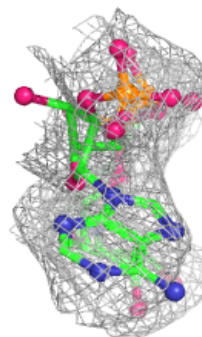
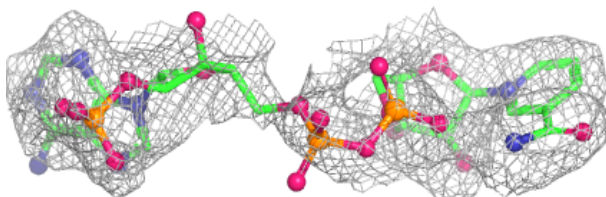
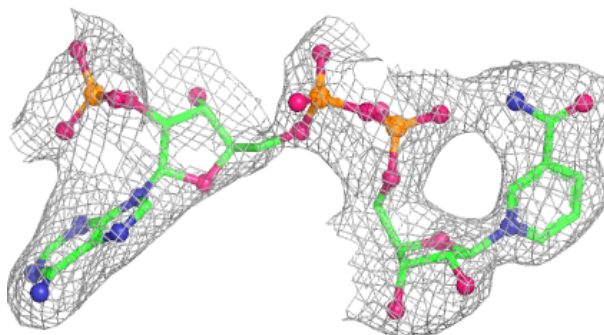


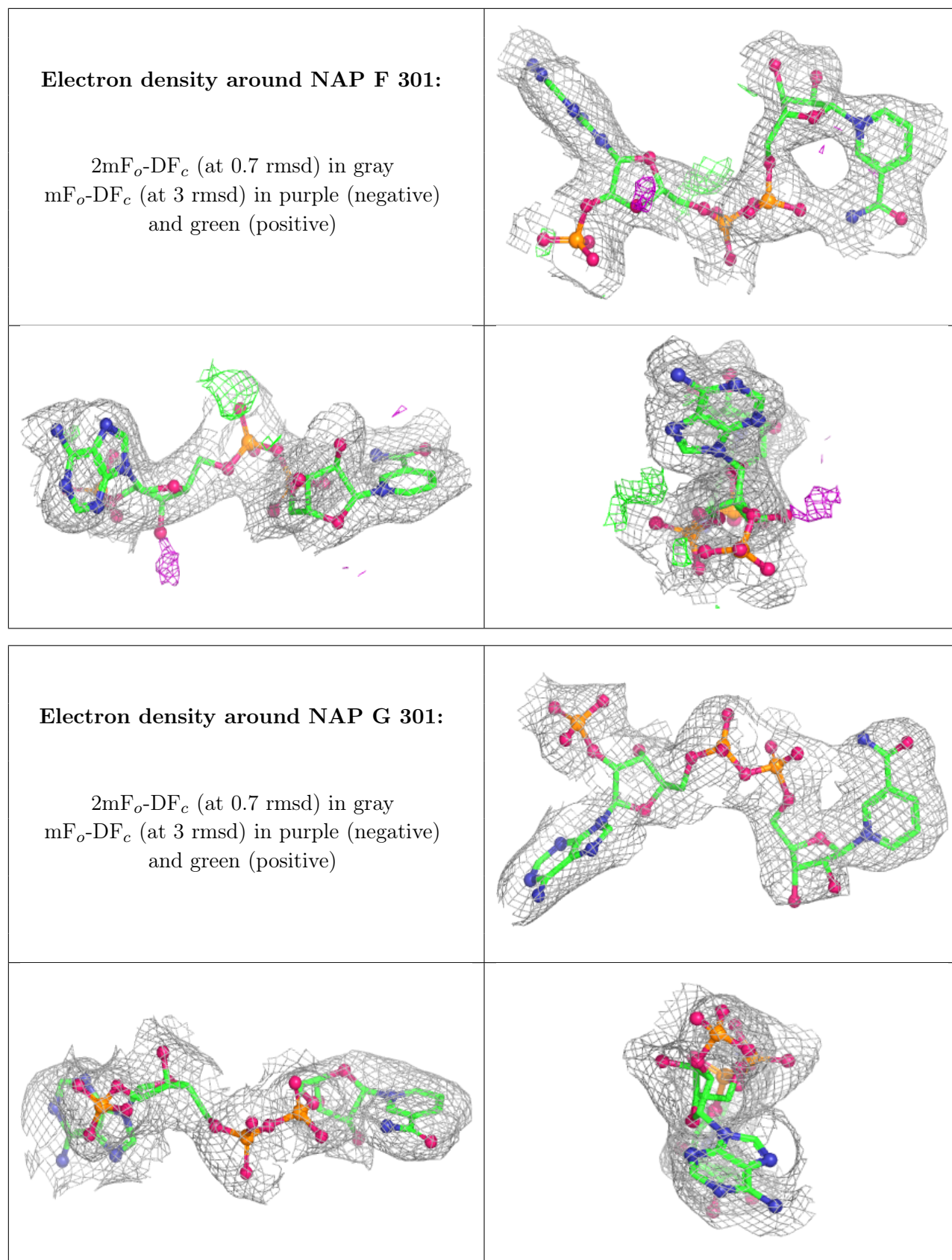
**Electron density around NAP D 301:**

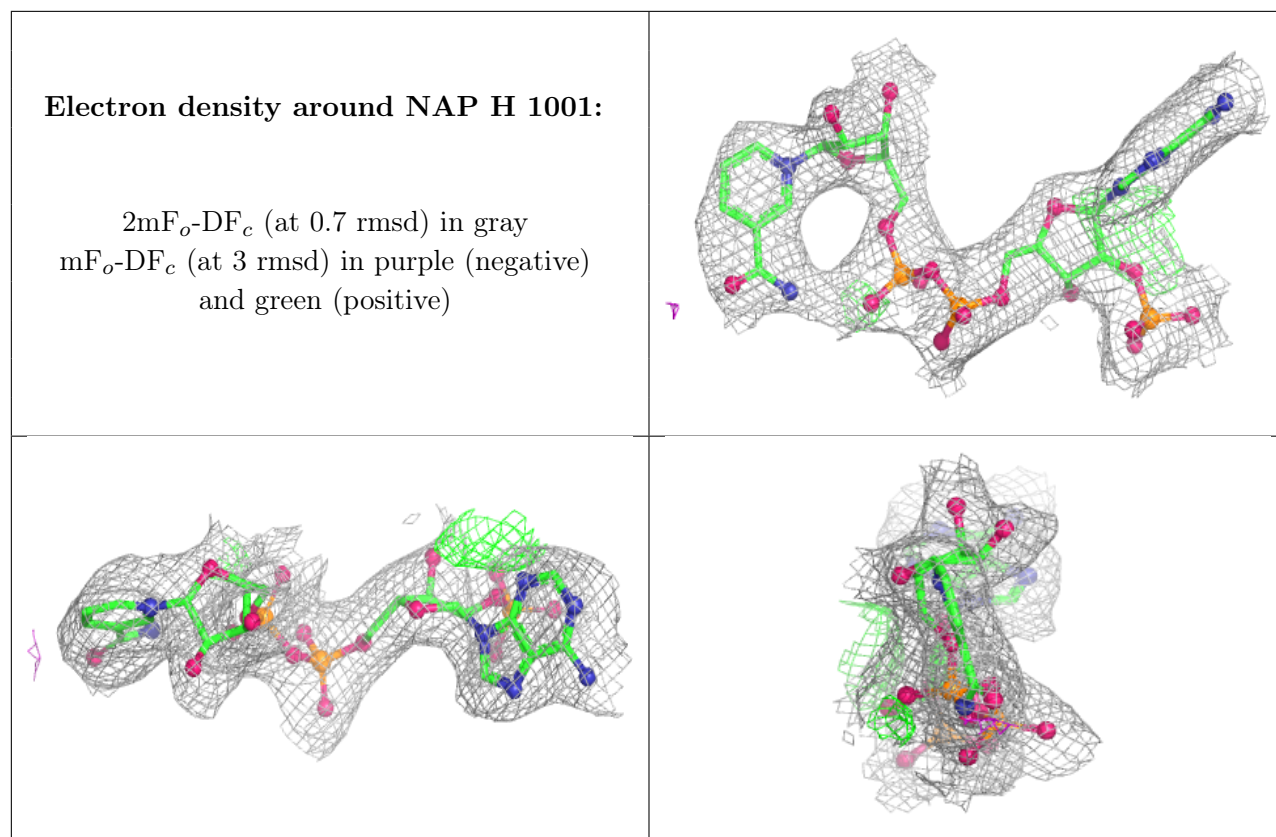
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around NAP E 301:**

$2mF_o-DF_c$  (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.