



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 6, 2023 – 12:44 PM JST

PDB ID : 8JFG
Title : Crystal structure of 3-oxoacyl-ACP reductase FabG in complex with NADP⁺ and 3-keto-octanoyl-ACP from *Helicobacter pylori*
Authors : Zhou, J.S.; Zhang, L.
Deposited on : 2023-05-18
Resolution : 2.83 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 ⓘ 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 ⓘ](#)) 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

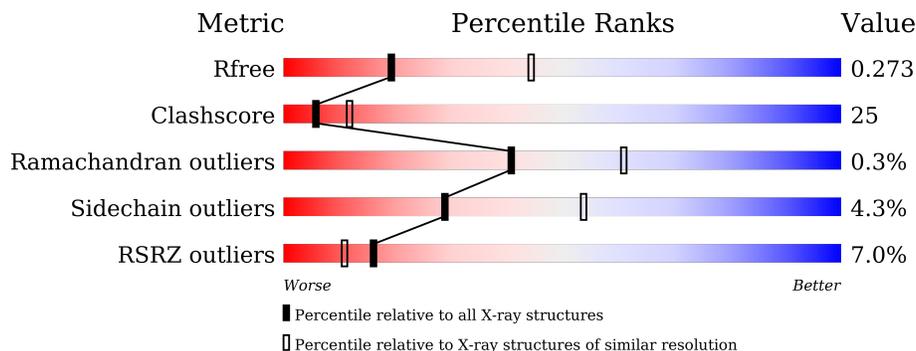
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.83 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.



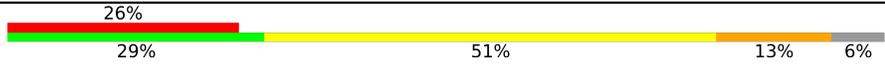
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1031 (2.86-2.82)
Clashscore	141614	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)
RSRZ outliers	127900	1019 (2.86-2.82)

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 $\leq 5\%$. 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	248	2% (Poor fit) 67% (Green) 29% (Yellow)
1	B	248	2% (Poor fit) 65% (Green) 27% (Yellow) 5% (Grey)
1	C	248	6% (Poor fit) 59% (Green) 33% (Yellow) 2% (Grey)
1	D	248	10% (Poor fit) 51% (Green) 40% (Yellow) 5% (Grey)
1	E	248	6% (Poor fit) 57% (Green) 38% (Yellow) 2% (Grey)
1	F	248	8% (Poor fit) 54% (Green) 41% (Yellow) 2% (Grey)

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Mol	Chain	Length	Quality of chain
2	G	78	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into five segments with the following percentages from left to right: 26% (red), 29% (green), 51% (yellow), 13% (orange), and 6% (grey).</p>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11747 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 3-oxoacyl-[acyl-carrier-protein] reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	248	1875	1179	323	363	10	0	0	0
1	B	236	1780	1122	307	342	9	0	0	0
1	C	239	1803	1135	310	348	10	0	0	0
1	D	236	1780	1122	307	342	9	0	0	0
1	E	241	1821	1147	313	352	9	0	0	0
1	F	239	1803	1135	310	348	10	0	0	0

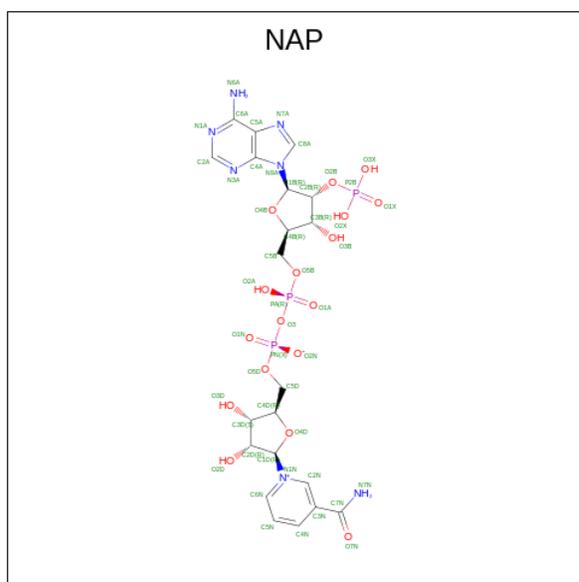
There are 6 discrepancies between the modelled and reference sequences:

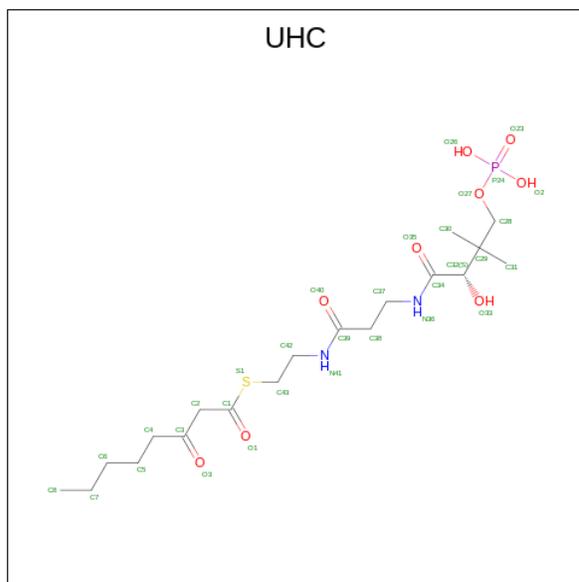
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP G2M827
B	0	SER	-	expression tag	UNP G2M827
C	0	SER	-	expression tag	UNP G2M827
D	0	SER	-	expression tag	UNP G2M827
E	0	SER	-	expression tag	UNP G2M827
F	0	SER	-	expression tag	UNP G2M827

- Molecule 2 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	G	73	566	359	85	121	1	0	0	0

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃) (labeled as "Ligand of Interest" by depositor).



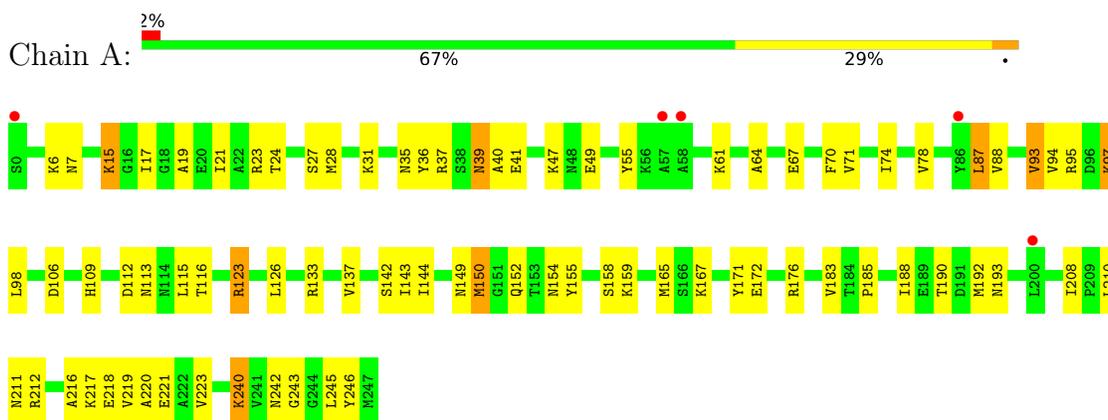


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
4	G	1	31	19	2	8	1	1	0	0

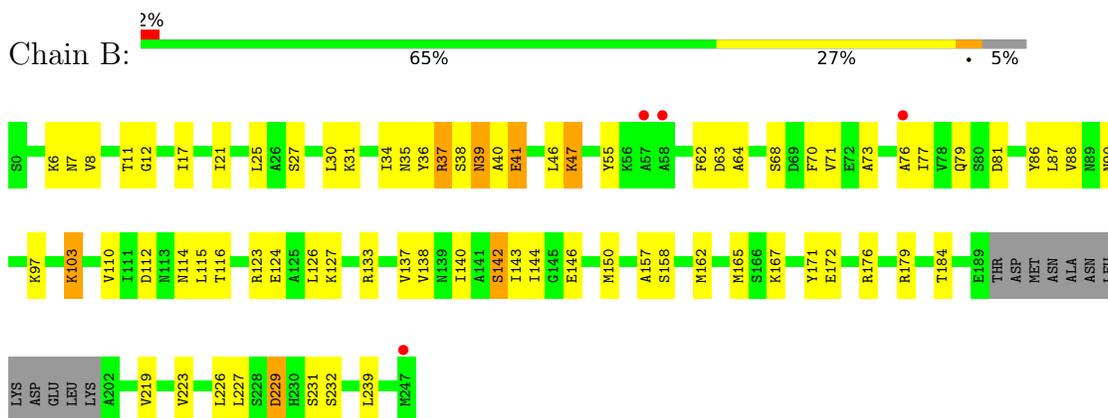
3 Residue-property plots [i](#)

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: 3-oxoacyl-[acyl-carrier-protein] reductase



- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase

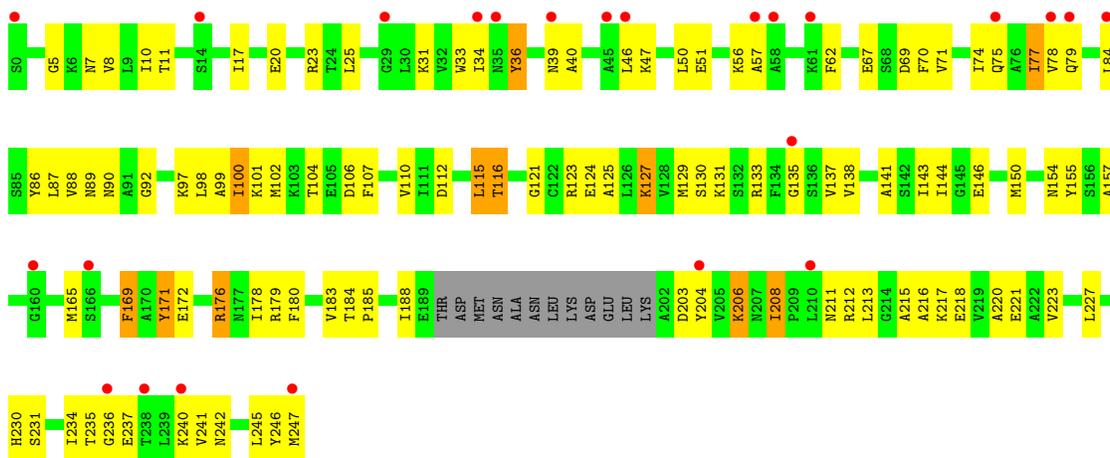


- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase

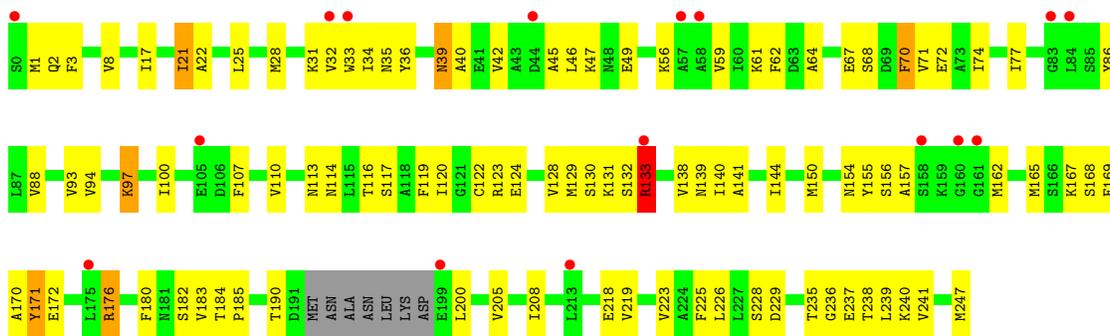




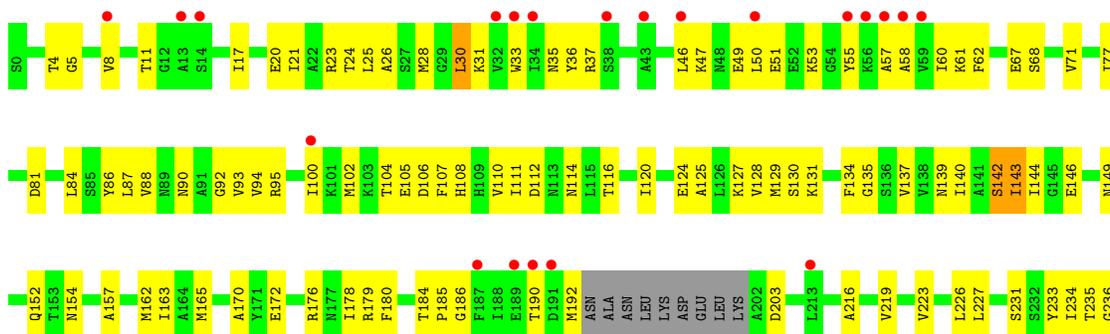
• Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase



• Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase



• Molecule 1: 3-oxoacyl-[acyl-carrier-protein] reductase





- Molecule 2: Acyl carrier protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	85.42Å 246.93Å 166.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.56 – 2.83 41.56 – 2.83	Depositor EDS
% Data completeness (in resolution range)	98.8 (41.56-2.83) 86.7 (41.56-2.83)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.81Å)	Xtrriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.256 , 0.279 0.257 , 0.273	Depositor DCC
R_{free} test set	1973 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	61.6	Xtrriage
Anisotropy	0.765	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11747	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

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

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	0.52	0/1899	0.73	6/2553 (0.2%)
1	B	0.62	1/1803 (0.1%)	0.76	2/2423 (0.1%)
1	C	0.54	2/1826 (0.1%)	0.77	4/2454 (0.2%)
1	D	0.50	0/1803	0.79	5/2423 (0.2%)
1	E	0.50	0/1844	0.80	7/2478 (0.3%)
1	F	0.43	0/1826	0.71	3/2454 (0.1%)
2	G	0.59	0/571	1.00	1/774 (0.1%)
All	All	0.52	3/11572 (0.0%)	0.77	28/15559 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	41	GLU	CD-OE1	-5.82	1.19	1.25
1	B	142	SER	CA-CB	-5.54	1.44	1.52
1	C	68	SER	C-O	-5.05	1.13	1.23

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	176	ARG	NE-CZ-NH1	-13.60	113.50	120.30
1	E	176	ARG	NE-CZ-NH2	8.47	124.53	120.30
1	D	206	LYS	CD-CE-NZ	-8.37	92.45	111.70
1	C	37	ARG	CB-CA-C	-8.02	94.35	110.40
1	B	126	LEU	CB-CG-CD2	-6.86	99.34	111.00

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	1875	0	1894	76	0
1	B	1780	0	1798	75	0
1	C	1803	0	1818	98	0
1	D	1780	0	1798	135	0
1	E	1821	0	1839	115	0
1	F	1803	0	1818	99	0
2	G	566	0	553	55	0
3	A	48	0	24	6	0
3	B	48	0	25	7	0
3	C	48	0	25	3	0
3	D	48	0	25	4	0
3	E	48	0	25	3	0
3	F	48	0	25	7	0
4	G	31	0	0	2	0
All	All	11747	0	11667	593	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 25.

The worst 5 of 593 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:36:TYR:CE2	1:A:40:ALA:HB2	1.57	1.39
1:E:34:ILE:HD13	1:E:46:LEU:HD23	1.24	1.18
1:E:167:LYS:HG2	1:F:247:MET:CE	1.77	1.12
1:E:236:GLY:HA3	1:F:247:MET:SD	1.88	1.12
1:D:138:VAL:HG11	1:D:223:VAL:HG13	1.12	1.09

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	246/248 (99%)	237 (96%)	9 (4%)	0	100	100
1	B	232/248 (94%)	219 (94%)	13 (6%)	0	100	100
1	C	235/248 (95%)	218 (93%)	17 (7%)	0	100	100
1	D	232/248 (94%)	210 (90%)	19 (8%)	3 (1%)	12	26
1	E	237/248 (96%)	221 (93%)	16 (7%)	0	100	100
1	F	235/248 (95%)	219 (93%)	15 (6%)	1 (0%)	34	56
2	G	71/78 (91%)	58 (82%)	12 (17%)	1 (1%)	11	24
All	All	1488/1566 (95%)	1382 (93%)	101 (7%)	5 (0%)	41	61

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	100	ILE
1	D	77	ILE
1	D	99	ALA
1	F	68	SER
2	G	35	ASP

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	197/197 (100%)	190 (96%)	7 (4%)	35	60
1	B	186/197 (94%)	177 (95%)	9 (5%)	25	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	189/197 (96%)	179 (95%)	10 (5%)	22	43
1	D	186/197 (94%)	181 (97%)	5 (3%)	44	69
1	E	191/197 (97%)	184 (96%)	7 (4%)	34	59
1	F	189/197 (96%)	185 (98%)	4 (2%)	53	75
2	G	62/65 (95%)	52 (84%)	10 (16%)	2	4
All	All	1200/1247 (96%)	1148 (96%)	52 (4%)	29	54

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	116	THR
1	E	133	ARG
2	G	54	ILE
1	D	127	LYS
1	E	70	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	154	ASN
2	G	14	GLN
1	D	79	GLN
2	G	16	ASN
1	E	139	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

7 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
3	NAP	D	301	-	45,52,52	0.70	1 (2%)	56,80,80	0.71	2 (3%)
4	UHC	G	101	-	23,30,31	0.67	0	29,38,41	2.25	8 (27%)
3	NAP	C	301	-	45,52,52	1.15	5 (11%)	56,80,80	2.26	14 (25%)
3	NAP	B	301	-	45,52,52	1.31	6 (13%)	56,80,80	1.60	7 (12%)
3	NAP	E	301	-	45,52,52	0.69	1 (2%)	56,80,80	0.72	1 (1%)
3	NAP	F	301	-	45,52,52	0.69	1 (2%)	56,80,80	0.68	1 (1%)
3	NAP	A	301	-	45,52,52	1.16	3 (6%)	56,80,80	1.94	12 (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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAP	D	301	-	-	11/31/67/67	0/5/5/5
4	UHC	G	101	-	-	18/35/38/39	-
3	NAP	C	301	-	-	4/31/67/67	0/5/5/5
3	NAP	B	301	-	-	7/31/67/67	0/5/5/5
3	NAP	E	301	-	-	8/31/67/67	0/5/5/5
3	NAP	F	301	-	-	11/31/67/67	0/5/5/5
3	NAP	A	301	-	-	11/31/67/67	0/5/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	NAP	P2B-O2B	-4.87	1.50	1.59
3	C	301	NAP	C6N-N1N	-3.94	1.25	1.35
3	A	301	NAP	C6N-N1N	-3.50	1.26	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	NAP	C2N-N1N	3.02	1.38	1.35
3	B	301	NAP	C4N-C3N	-2.65	1.34	1.39

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	301	NAP	C3N-C2N-N1N	-7.50	113.10	120.43
3	C	301	NAP	C3D-C2D-C1D	-7.24	90.08	100.98
3	A	301	NAP	O2B-C2B-C3B	6.35	134.69	111.68
3	B	301	NAP	PN-O3-PA	-6.13	111.81	132.83
3	C	301	NAP	C6N-N1N-C2N	-5.56	116.90	121.97

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	NAP	C3B-C2B-O2B-P2B
3	A	301	NAP	C5D-O5D-PN-O3
3	A	301	NAP	O4D-C4D-C5D-O5D
3	A	301	NAP	C3D-C4D-C5D-O5D
3	B	301	NAP	C2B-O2B-P2B-O1X

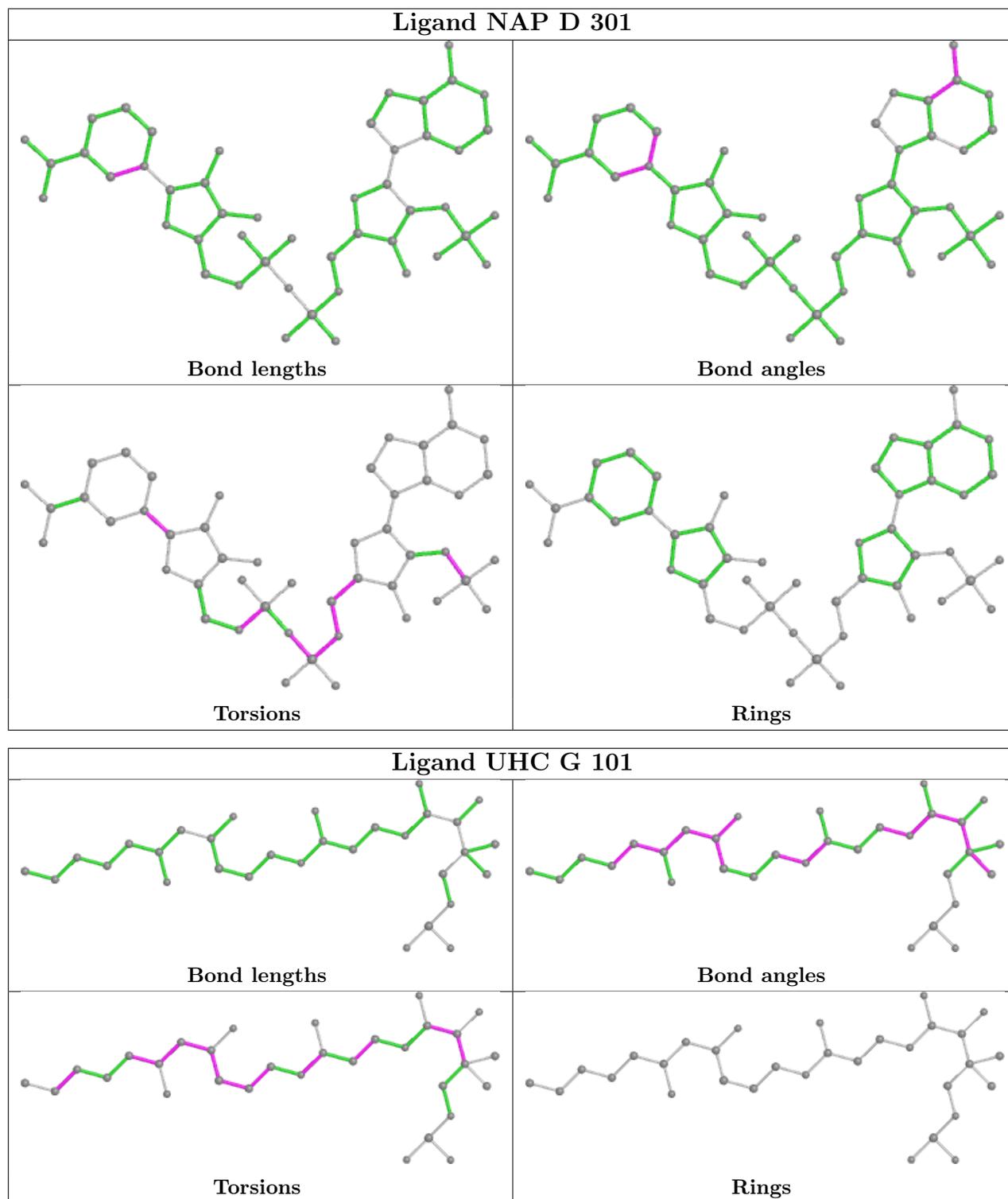
There are no ring outliers.

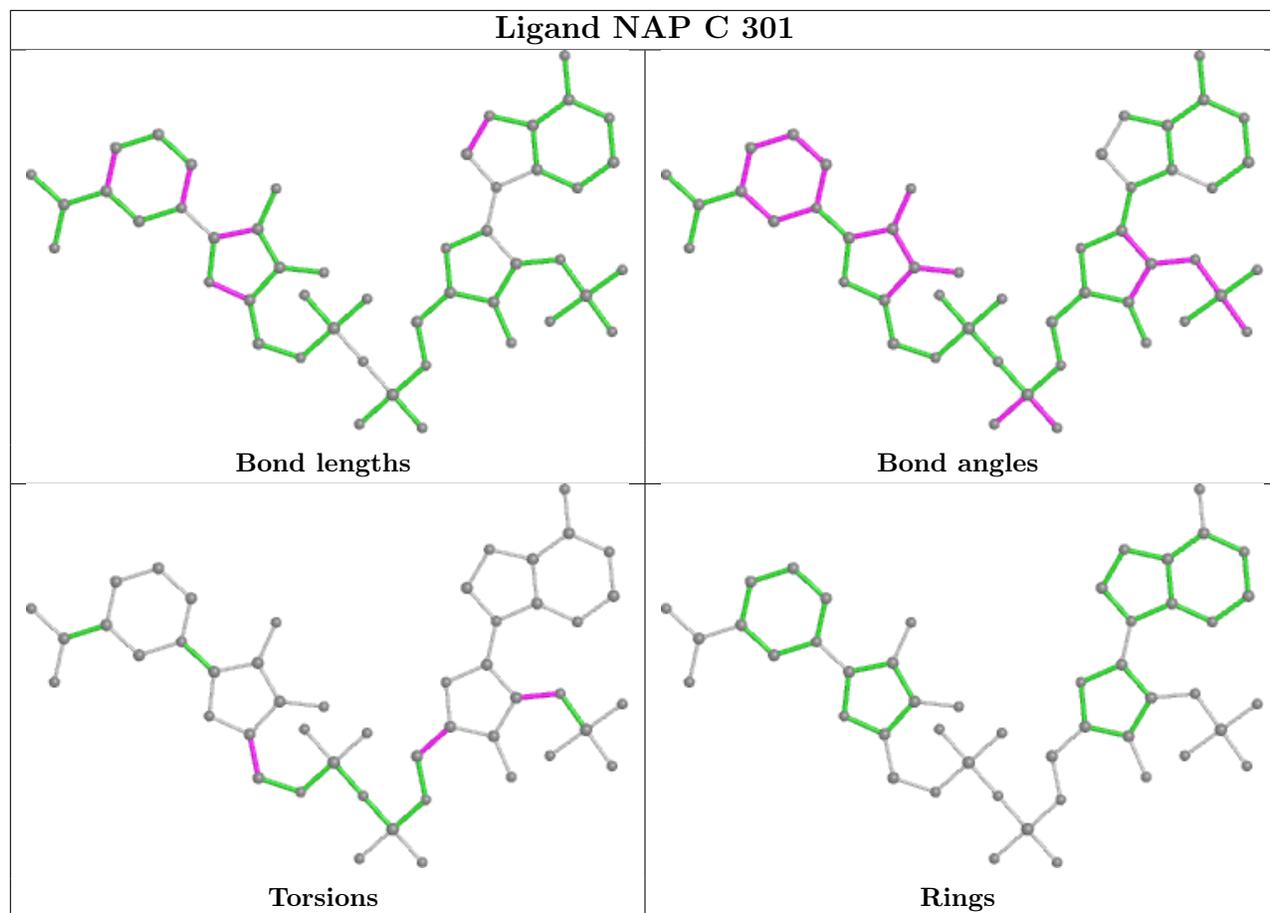
7 monomers are involved in 32 short contacts:

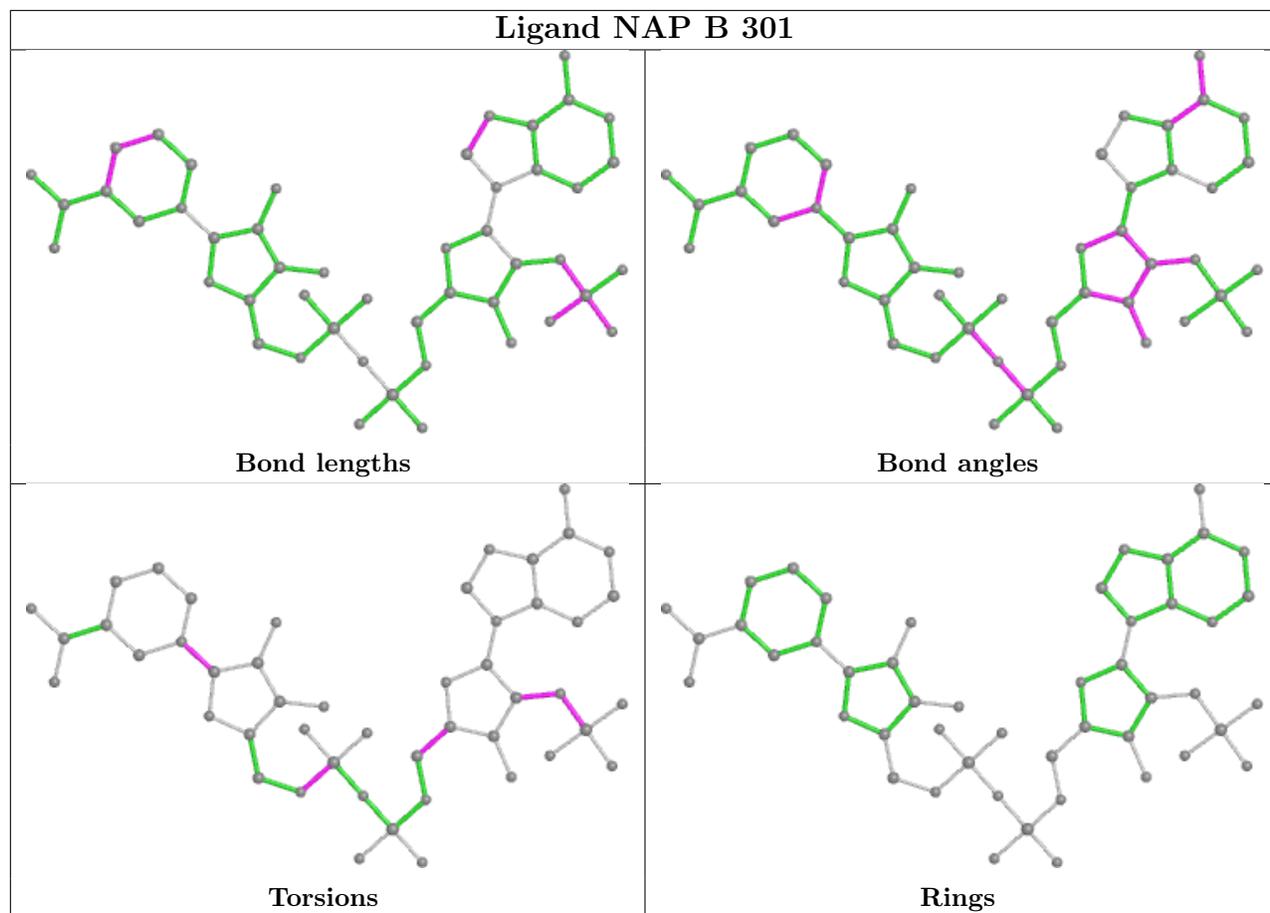
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	301	NAP	4	0
4	G	101	UHC	2	0
3	C	301	NAP	3	0
3	B	301	NAP	7	0
3	E	301	NAP	3	0
3	F	301	NAP	7	0
3	A	301	NAP	6	0

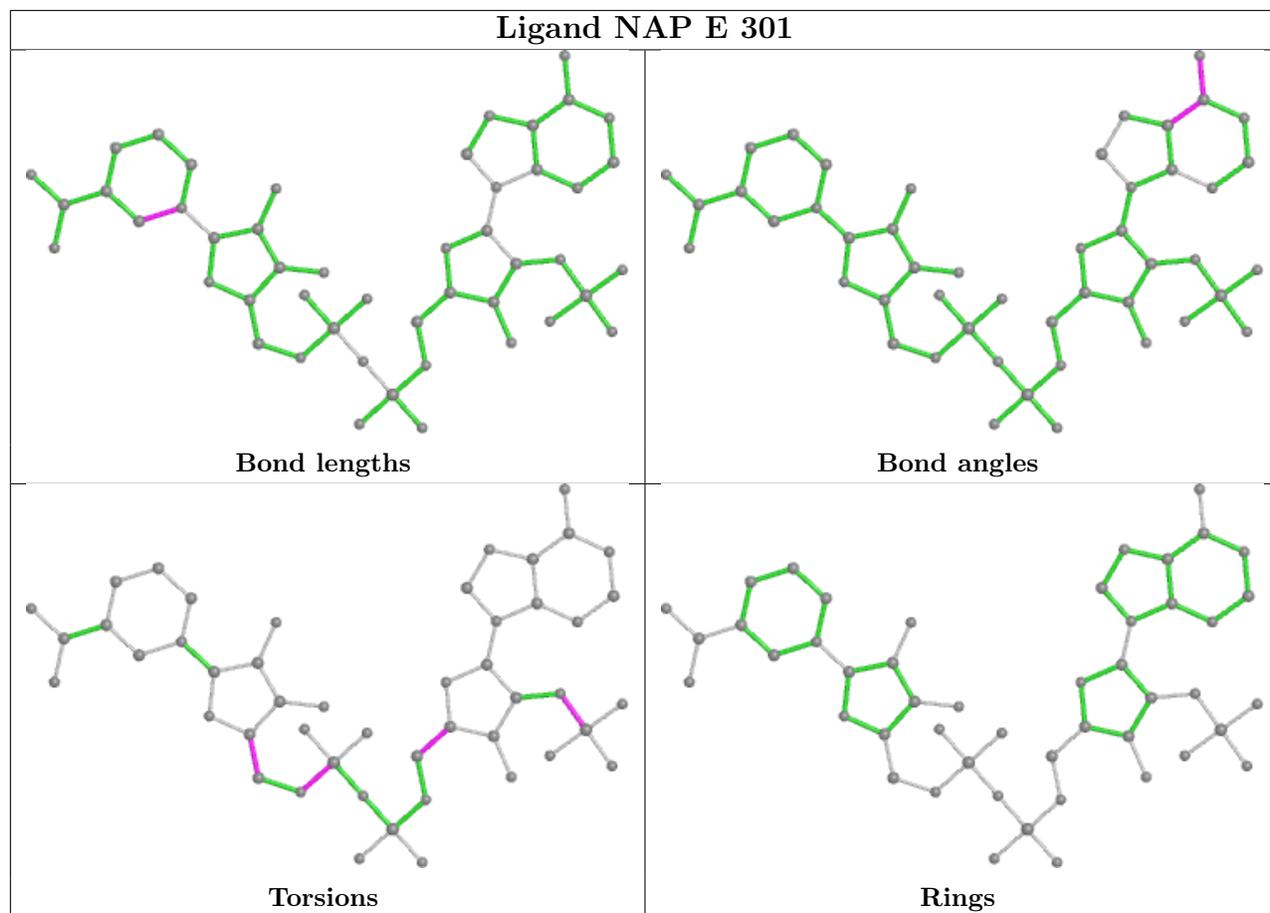
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

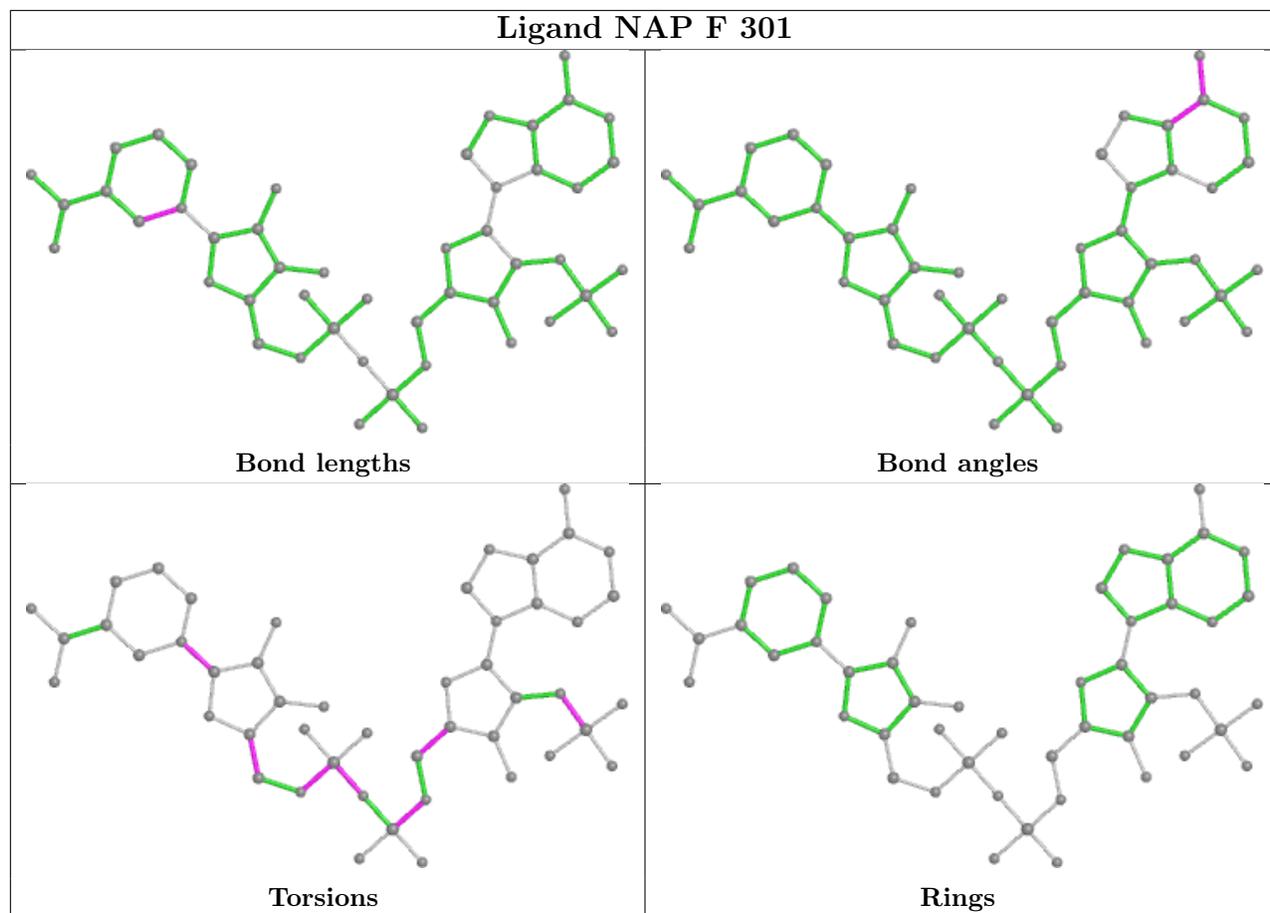
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

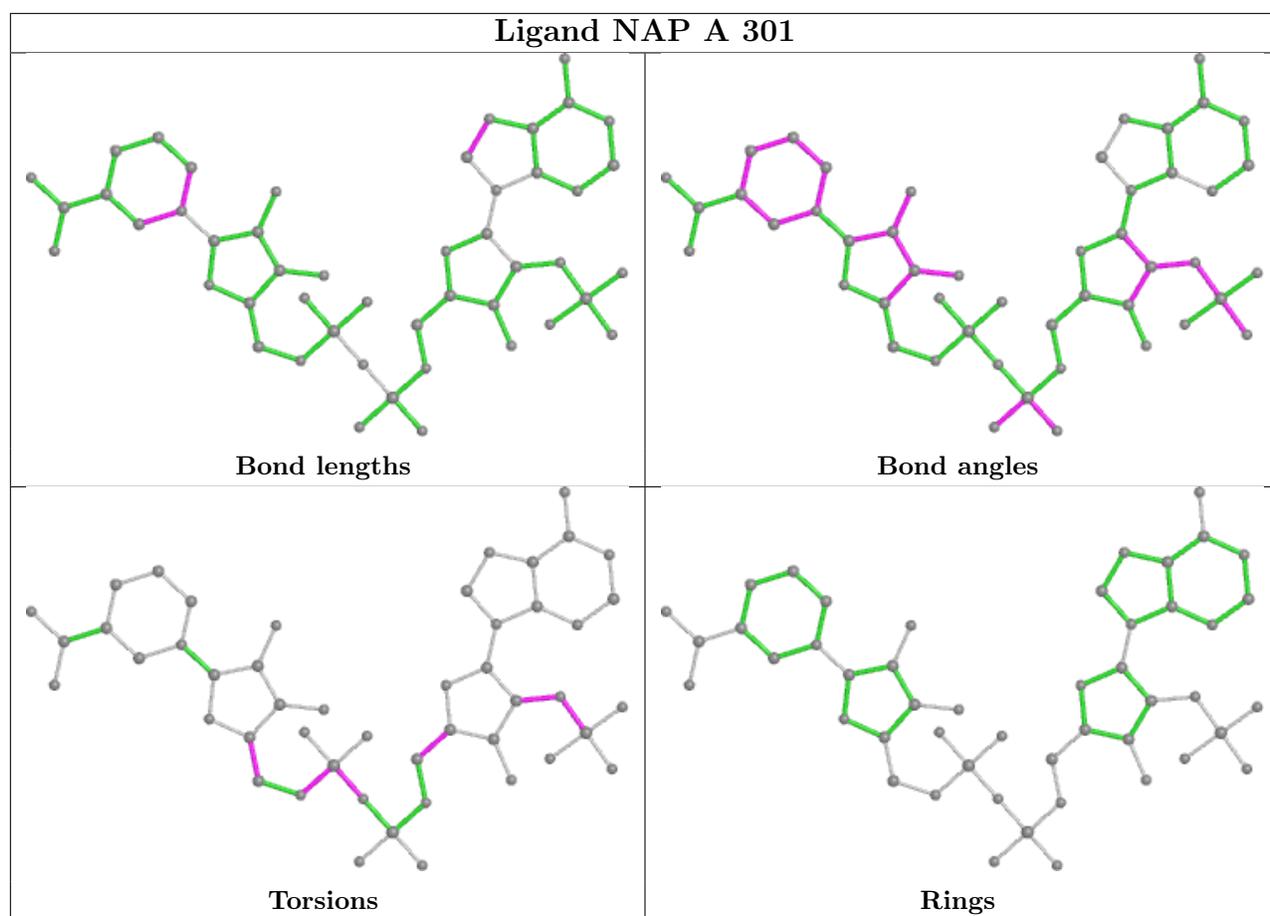












5.7 Other polymers [\(i\)](#)

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, 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	248/248 (100%)	0.23	5 (2%) 65 60	48, 64, 87, 116	0
1	B	236/248 (95%)	0.30	4 (1%) 70 66	50, 67, 88, 109	0
1	C	239/248 (96%)	0.66	16 (6%) 17 12	64, 83, 102, 121	0
1	D	236/248 (95%)	0.78	24 (10%) 6 4	62, 86, 112, 127	0
1	E	241/248 (97%)	0.63	16 (6%) 18 12	59, 80, 107, 131	0
1	F	239/248 (96%)	0.64	21 (8%) 10 5	66, 89, 107, 125	0
2	G	73/78 (93%)	1.22	20 (27%) 0 0	75, 114, 122, 128	0
All	All	1512/1566 (96%)	0.57	106 (7%) 16 11	48, 80, 111, 131	0

The worst 5 of 106 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	0	SER	7.3
1	D	57	ALA	5.9
1	F	57	ALA	5.9
1	B	57	ALA	5.7
1	E	175	LEU	4.9

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](#)

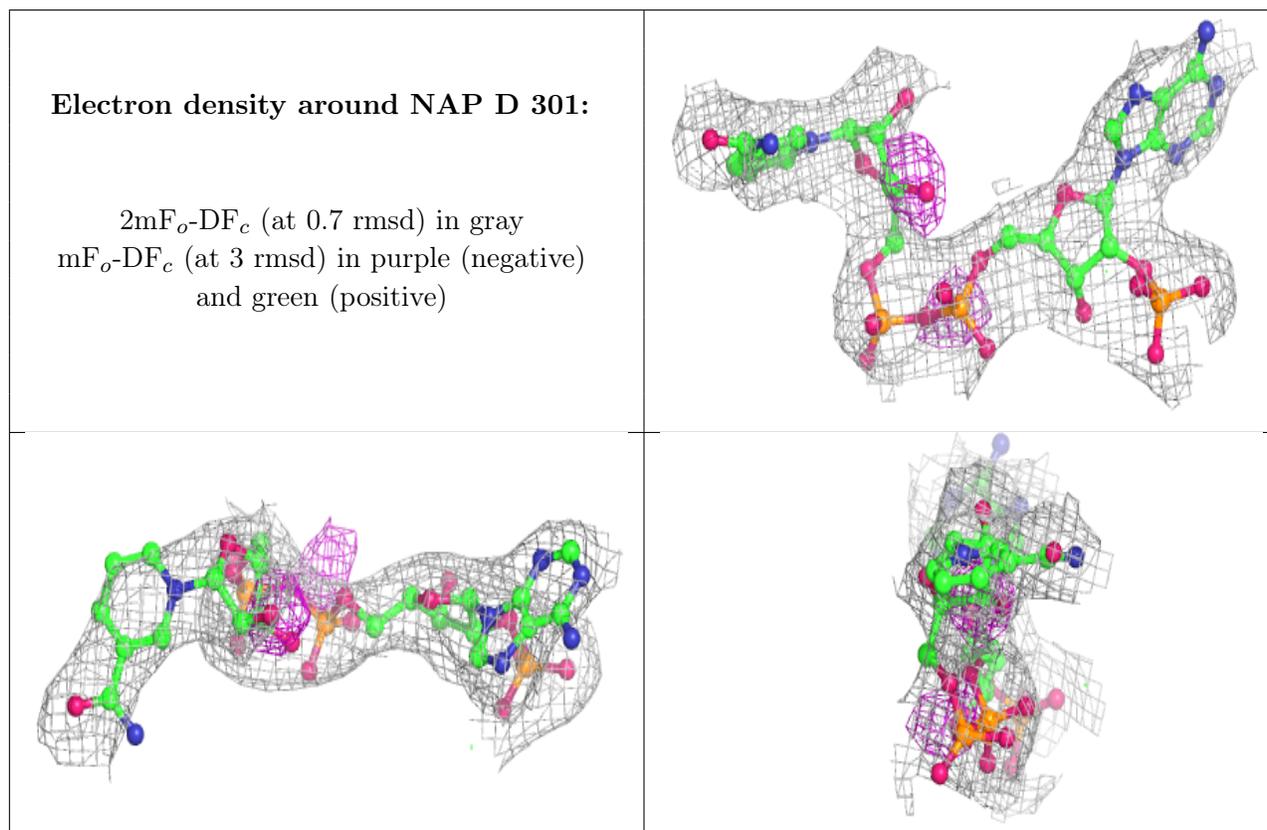
There are no monosaccharides in this entry.

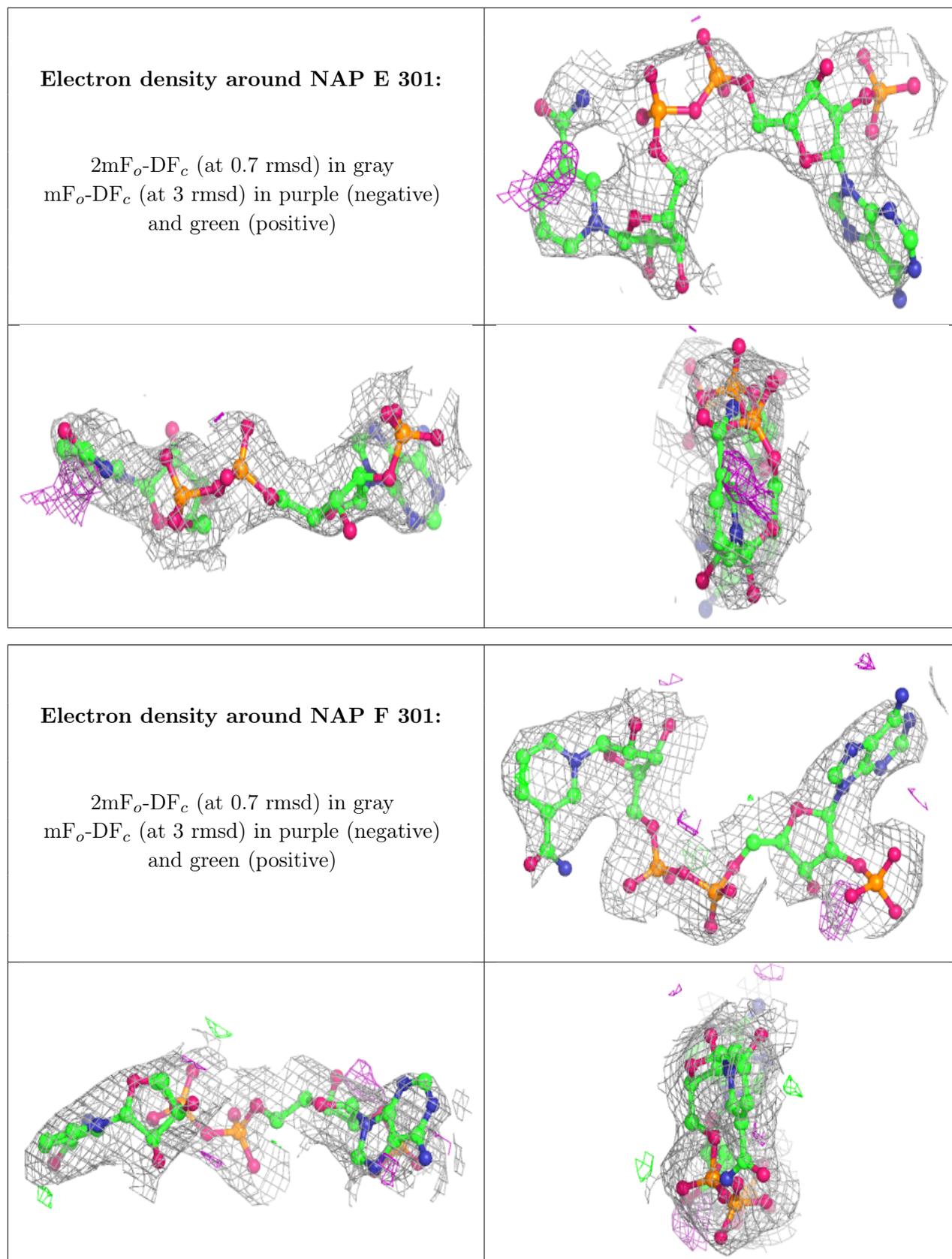
6.4 Ligands [i](#)

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
3	NAP	D	301	48/48	0.82	0.23	85,98,120,125	0
3	NAP	E	301	48/48	0.83	0.28	80,102,119,130	0
3	NAP	F	301	48/48	0.85	0.24	77,96,109,113	0
4	UHC	G	101	31/32	0.88	0.24	58,77,103,120	0
3	NAP	B	301	48/48	0.91	0.17	67,81,97,99	0
3	NAP	C	301	48/48	0.91	0.17	76,83,97,99	0
3	NAP	A	301	48/48	0.93	0.17	51,66,79,87	0

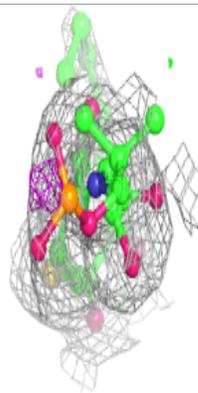
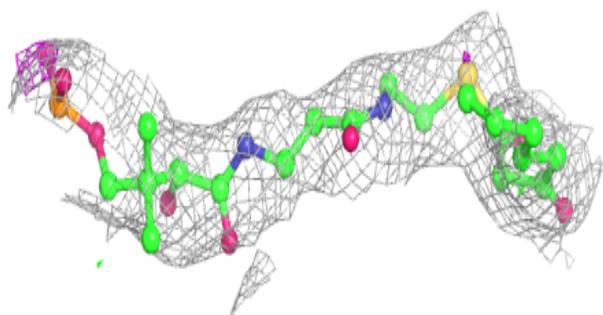
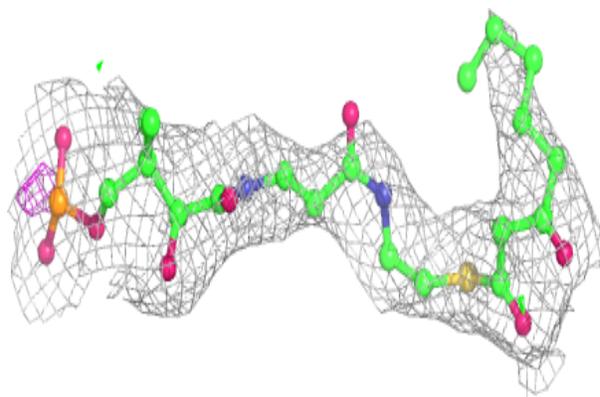
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



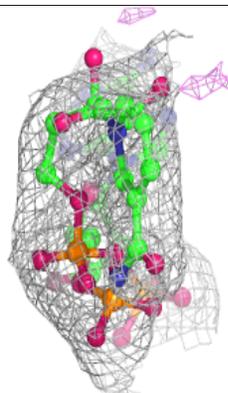
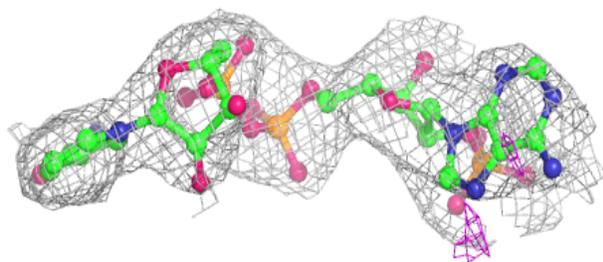
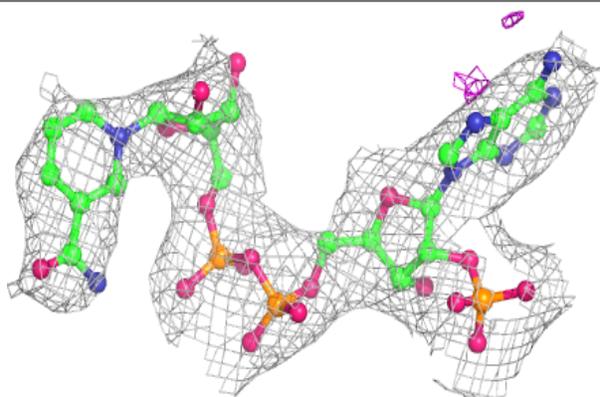


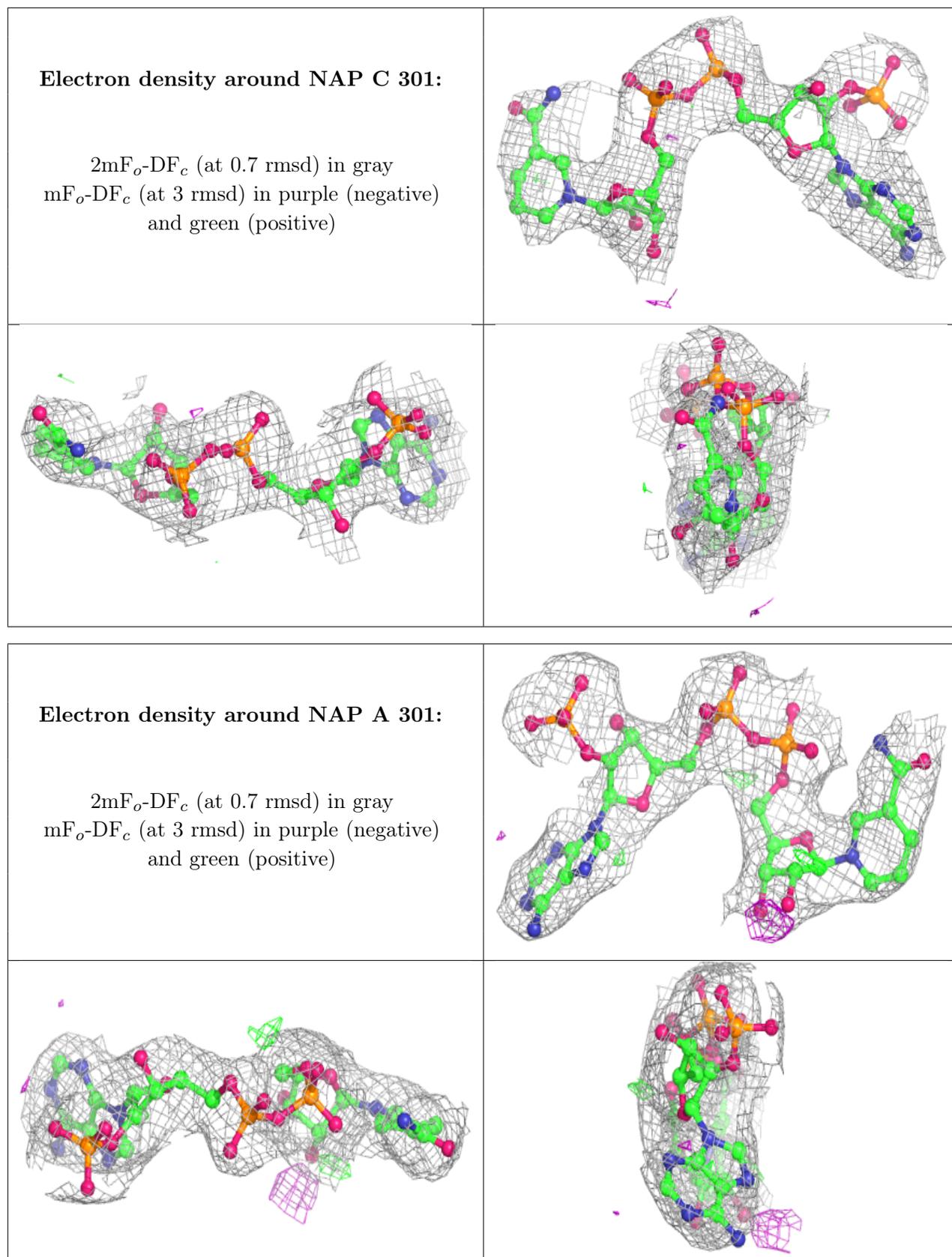
Electron density around UHC G 101:

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

**Electron density around NAP 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.