



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:37 PM UTC

PDB ID : 1W0C / pdb_00001w0c
Title : Inhibition of Leishmania major pteridine reductase (PTR1) by 2,4,6-triamino quinazoline; structure of the NADP ternary complex.
Authors : Mcluskey, K.; Gibellini, F.; Carvalho, P.; Avery, M.; Hunter, W.
Deposited on : 2004-06-02
Resolution : 2.60 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 : 4-5-2 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

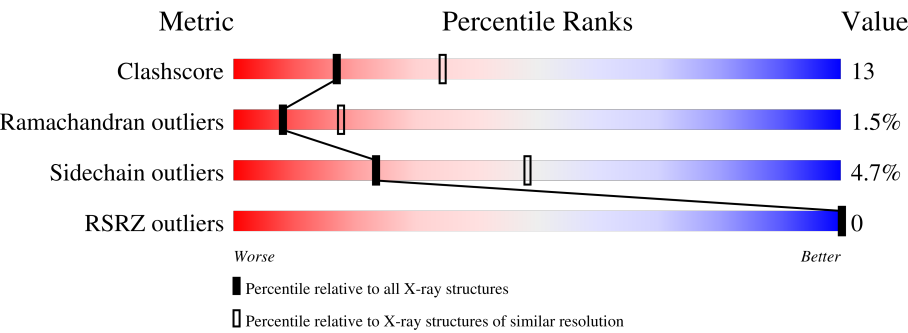
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	307	68%20%10%
1	B	307	68%18%11%
1	C	307	71%14%14%
1	D	307	66%16%17%
1	E	307	66%18%13%
1	F	307	65%20%12%

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Mol	Chain	Length	Quality of chain
1	G	307	59% 23% • • 14%
1	H	307	64% 20% • 15%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17458 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.

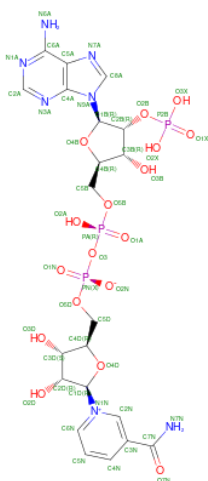
- Molecule 1 is a protein called PTERIDINE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	3	0	0
			2041	1282	361	387	11			
1	B	274	Total	C	N	O	S	3	0	0
			2031	1276	361	383	11			
1	C	264	Total	C	N	O	S	22	0	0
			1954	1227	351	366	10			
1	D	256	Total	C	N	O	S	10	0	0
			1906	1201	342	353	10			
1	E	267	Total	C	N	O	S	0	0	0
			1992	1254	355	372	11			
1	F	270	Total	C	N	O	S	3	0	0
			2013	1265	358	379	11			
1	G	263	Total	C	N	O	S	22	0	0
			1962	1233	350	368	11			
1	H	260	Total	C	N	O	S	10	0	0
			1941	1225	347	359	10			

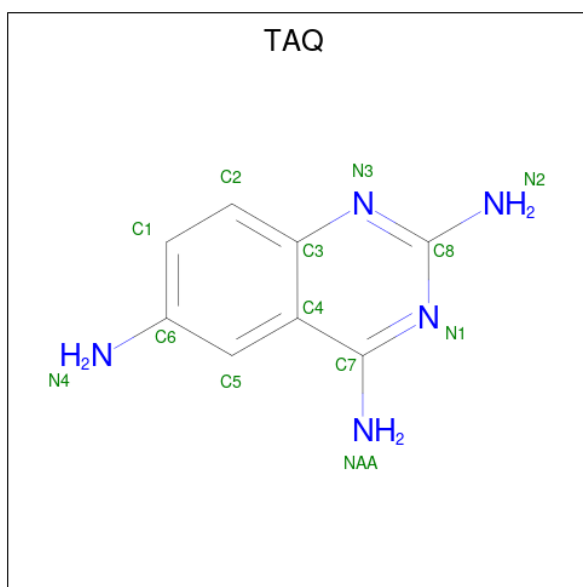
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	162	VAL	PHE	conflict	UNP Q01782
B	162	VAL	PHE	conflict	UNP Q01782
C	162	VAL	PHE	conflict	UNP Q01782
D	162	VAL	PHE	conflict	UNP Q01782
E	162	VAL	PHE	conflict	UNP Q01782
F	162	VAL	PHE	conflict	UNP Q01782
G	162	VAL	PHE	conflict	UNP Q01782
H	162	VAL	PHE	conflict	UNP Q01782

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



- Molecule 3 is 2,4,6-TRIAMINOQUINAZOLINE (CCD ID: TAQ) (formula: $\text{C}_8\text{H}_9\text{N}_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			13	8	5		
3	A	1	Total	C	N	0	0
			13	8	5		
3	B	1	Total	C	N	0	0
			13	8	5		
3	C	1	Total	C	N	0	0
			13	8	5		
3	D	1	Total	C	N	0	0
			13	8	5		
3	E	1	Total	C	N	0	0
			13	8	5		
3	F	1	Total	C	N	0	0
			13	8	5		
3	G	1	Total	C	N	0	0
			13	8	5		
3	H	1	Total	C	N	0	0
			13	8	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	214	Total	O	0	0
			214	214		
4	B	216	Total	O	0	0
			216	216		
4	C	117	Total	O	0	0
			117	117		

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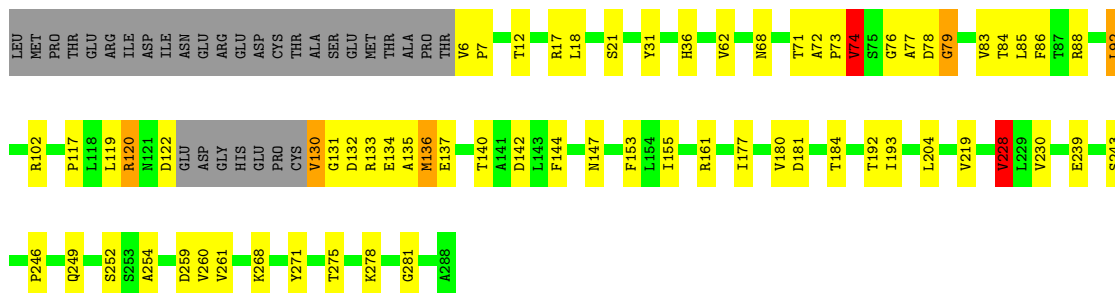
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	97	Total 97	O 97	0	0
4	E	127	Total 127	O 127	0	0
4	F	104	Total 104	O 104	0	0
4	G	143	Total 143	O 143	0	0
4	H	99	Total 99	O 99	0	0

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.

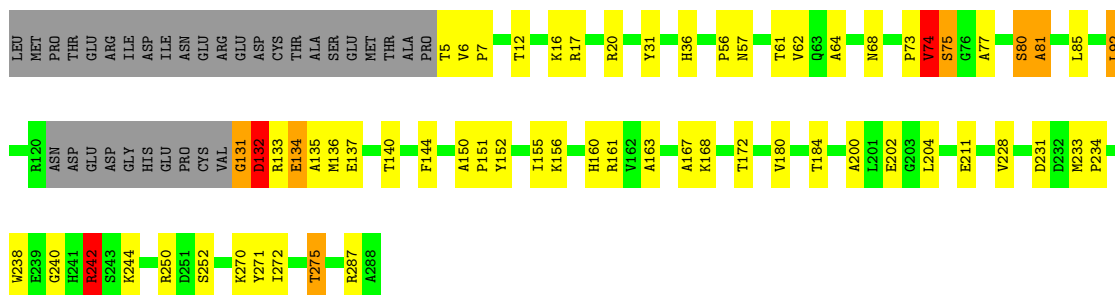
- Molecule 1: PTERIDINE REDUCTASE

Chain A: 



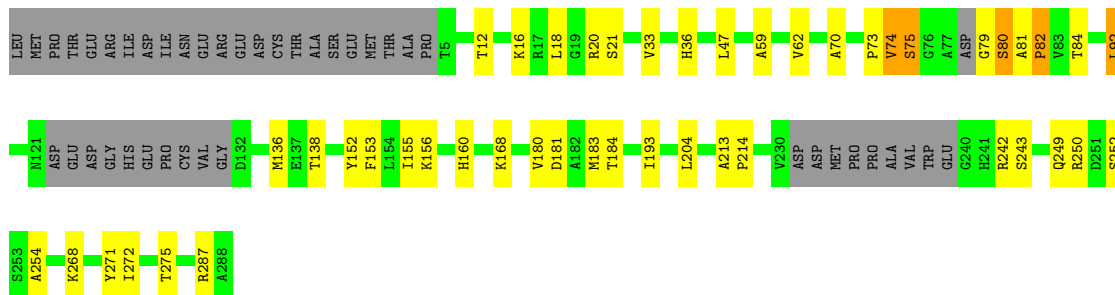
- Molecule 1: PTERIDINE REDUCTASE

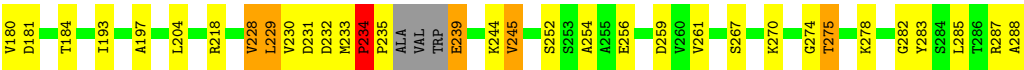
Chain B: 



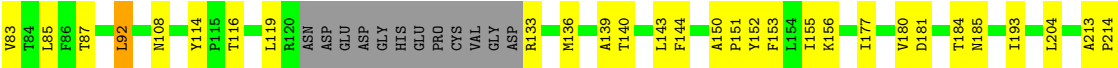
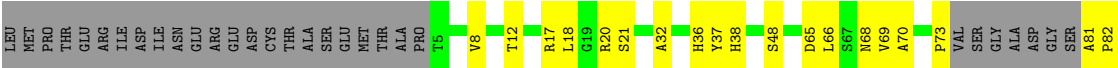
- Molecule 1: PTERIDINE REDUCTASE

Chain C: 





● Molecule 1: PTERIDINE REDUCTASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.85Å 102.94Å 146.71Å 90.00° 108.32° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 30.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	91.0 (30.00-2.60) 87.3 (30.00-2.60)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 2.61Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.267 , 0.337 0.273 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	18.8	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 22.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.166 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	17458	wwPDB-VP
Average B, all atoms (Å ²)	20.0	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 55.25 % 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 3.2472e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: TAQ, 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	0.77	0/2081	1.01	6/2837 (0.2%)
1	B	0.77	0/2071	0.99	2/2822 (0.1%)
1	C	0.66	0/1988	0.94	1/2703 (0.0%)
1	D	0.66	0/1940	0.93	3/2638 (0.1%)
1	E	0.76	0/2031	0.97	0/2766
1	F	0.82	2/2052 (0.1%)	1.06	7/2795 (0.3%)
1	G	0.73	0/1998	1.01	5/2718 (0.2%)
1	H	0.74	0/1977	0.96	1/2690 (0.0%)
All	All	0.74	2/16138 (0.0%)	0.99	25/21969 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2
1	D	0	1
1	G	0	1
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	192	THR	CB-CG2	-11.56	1.14	1.52
1	F	120	ARG	N-CA	6.45	1.50	1.46

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	192	THR	OG1-CB-CG2	-14.24	80.81	109.30
1	G	231	ASP	N-CA-C	7.93	122.39	109.94
1	F	133	ARG	N-CA-C	-7.51	103.58	112.89
1	A	74	VAL	N-CA-C	7.50	119.74	108.80
1	F	192	THR	N-CA-CB	7.01	120.53	110.16

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	131	GLY	Peptide
1	B	132	ASP	Peptide
1	D	81	ALA	Peptide
1	G	234	PRO	Peptide

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	2041	0	2033	56	0
1	B	2031	0	2032	68	0
1	C	1954	0	1968	41	0
1	D	1906	0	1928	41	0
1	E	1992	0	1996	52	0
1	F	2013	0	2011	66	0
1	G	1962	0	1968	70	0
1	H	1941	0	1958	60	0
2	A	48	0	25	1	0
2	B	48	0	25	0	0
2	C	48	0	25	1	0
2	D	48	0	25	1	0
2	E	48	0	25	1	0
2	F	48	0	25	0	0
2	G	48	0	25	3	0
2	H	48	0	25	1	0
3	A	26	0	18	2	0
3	B	13	0	9	0	0
3	C	13	0	9	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	13	0	9	0	0
3	E	13	0	9	1	0
3	F	13	0	9	1	0
3	G	13	0	9	3	0
3	H	13	0	9	1	0
4	A	214	0	0	19	2
4	B	216	0	0	29	1
4	C	117	0	0	6	1
4	D	97	0	0	8	0
4	E	127	0	0	8	1
4	F	104	0	0	22	1
4	G	143	0	0	27	0
4	H	99	0	0	23	0
All	All	17458	0	16175	411	3

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 13.

The worst 5 of 411 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:242:ARG:HG2	1:B:242:ARG:HH11	1.09	1.13
1:G:234:PRO:HB2	1:G:235:PRO:CD	1.78	1.11
1:C:81:ALA:HB1	1:C:82:PRO:HD2	1.22	1.10
1:F:180:VAL:HG13	4:F:2058:HOH:O	1.55	1.04
1:G:234:PRO:CB	1:G:235:PRO:HD3	1.88	1.03

All (3) 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)
4:B:2016:HOH:O	4:E:2018:HOH:O[2_646]	1.95	0.25
4:A:2174:HOH:O	4:F:2018:HOH:O[2_546]	2.11	0.09
4:A:2051:HOH:O	4:C:2023:HOH:O[2_545]	2.13	0.07

5.3 Torsion angles

5.3.1 Protein backbone

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	272/307 (89%)	253 (93%)	15 (6%)	4 (2%)	8	18
1	B	270/307 (88%)	240 (89%)	24 (9%)	6 (2%)	5	10
1	C	256/307 (83%)	234 (91%)	17 (7%)	5 (2%)	6	12
1	D	248/307 (81%)	231 (93%)	16 (6%)	1 (0%)	30	51
1	E	261/307 (85%)	239 (92%)	20 (8%)	2 (1%)	16	34
1	F	264/307 (86%)	243 (92%)	17 (6%)	4 (2%)	8	18
1	G	255/307 (83%)	235 (92%)	15 (6%)	5 (2%)	6	12
1	H	252/307 (82%)	233 (92%)	15 (6%)	4 (2%)	7	16
All	All	2078/2456 (85%)	1908 (92%)	139 (7%)	31 (2%)	8	18

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	77	ALA
1	B	74	VAL
1	B	75	SER
1	B	80	SER
1	B	81	ALA

5.3.2 Protein sidechains

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	212/241 (88%)	199 (94%)	13 (6%)	17	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	211/241 (88%)	201 (95%)	10 (5%)	23	48
1	C	203/241 (84%)	197 (97%)	6 (3%)	36	64
1	D	198/241 (82%)	189 (96%)	9 (4%)	24	50
1	E	207/241 (86%)	195 (94%)	12 (6%)	18	39
1	F	210/241 (87%)	200 (95%)	10 (5%)	23	47
1	G	205/241 (85%)	193 (94%)	12 (6%)	18	38
1	H	201/241 (83%)	196 (98%)	5 (2%)	42	69
All	All	1647/1928 (85%)	1570 (95%)	77 (5%)	23	48

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	230	VAL
1	G	275	THR
1	F	275	THR
1	G	136	MET
1	H	241	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	216	GLN
1	G	108	ASN
1	G	45	ASN
1	G	169	HIS
1	C	160	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

17 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	D	300	-	50,52,52	1.72	7 (14%)	71,80,80	1.63	12 (16%)
3	TAQ	F	301	-	14,14,14	1.39	2 (14%)	18,20,20	1.92	5 (27%)
3	TAQ	A	301	-	14,14,14	1.68	2 (14%)	18,20,20	1.76	3 (16%)
3	TAQ	E	301	-	14,14,14	1.46	1 (7%)	18,20,20	1.99	4 (22%)
2	NAP	A	300	-	50,52,52	1.67	7 (14%)	71,80,80	1.57	9 (12%)
3	TAQ	A	302	-	14,14,14	1.72	1 (7%)	18,20,20	2.10	5 (27%)
2	NAP	G	300	-	50,52,52	1.77	7 (14%)	71,80,80	1.61	11 (15%)
3	TAQ	G	301	-	14,14,14	1.21	2 (14%)	18,20,20	1.72	3 (16%)
2	NAP	E	300	-	50,52,52	1.73	6 (12%)	71,80,80	1.61	13 (18%)
3	TAQ	B	301	-	14,14,14	1.51	2 (14%)	18,20,20	2.09	5 (27%)
3	TAQ	D	301	-	14,14,14	1.24	1 (7%)	18,20,20	1.95	3 (16%)
2	NAP	H	300	-	50,52,52	1.90	7 (14%)	71,80,80	1.71	10 (14%)
2	NAP	C	300	-	50,52,52	1.55	5 (10%)	71,80,80	1.57	11 (15%)
3	TAQ	C	301	-	14,14,14	1.75	1 (7%)	18,20,20	1.98	4 (22%)
2	NAP	B	300	-	50,52,52	1.56	4 (8%)	71,80,80	1.57	11 (15%)
3	TAQ	H	301	-	14,14,14	1.49	1 (7%)	18,20,20	1.77	3 (16%)
2	NAP	F	300	-	50,52,52	1.70	4 (8%)	71,80,80	1.49	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	D	300	-	-	6/35/67/67	0/5/5/5
3	TAQ	F	301	-	-	-	0/2/2/2
3	TAQ	A	301	-	-	-	0/2/2/2
3	TAQ	E	301	-	-	-	0/2/2/2
2	NAP	A	300	-	-	6/35/67/67	0/5/5/5
3	TAQ	A	302	-	-	-	0/2/2/2
2	NAP	G	300	-	-	5/35/67/67	0/5/5/5
3	TAQ	G	301	-	-	-	0/2/2/2
2	NAP	E	300	-	-	5/35/67/67	0/5/5/5
3	TAQ	B	301	-	-	-	0/2/2/2
3	TAQ	D	301	-	-	-	0/2/2/2
2	NAP	H	300	-	-	6/35/67/67	0/5/5/5
2	NAP	C	300	-	-	5/35/67/67	0/5/5/5
3	TAQ	C	301	-	-	-	0/2/2/2
2	NAP	B	300	-	-	6/35/67/67	0/5/5/5
3	TAQ	H	301	-	-	-	0/2/2/2
2	NAP	F	300	-	-	5/35/67/67	0/5/5/5

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	300	NAP	O7N-C7N	9.24	1.41	1.24
2	H	300	NAP	O7N-C7N	9.15	1.41	1.24
2	G	300	NAP	O7N-C7N	9.12	1.41	1.24
2	D	300	NAP	O7N-C7N	8.85	1.40	1.24
2	E	300	NAP	O7N-C7N	8.76	1.40	1.24

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	300	NAP	N3A-C2A-N1A	-6.39	118.91	128.58
2	D	300	NAP	N3A-C2A-N1A	-6.00	119.50	128.58
2	G	300	NAP	N3A-C2A-N1A	-5.92	119.63	128.58
2	A	300	NAP	N3A-C2A-N1A	-5.90	119.66	128.58
2	B	300	NAP	N3A-C2A-N1A	-5.66	120.02	128.58

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	300	NAP	C5B-O5B-PA-O1A

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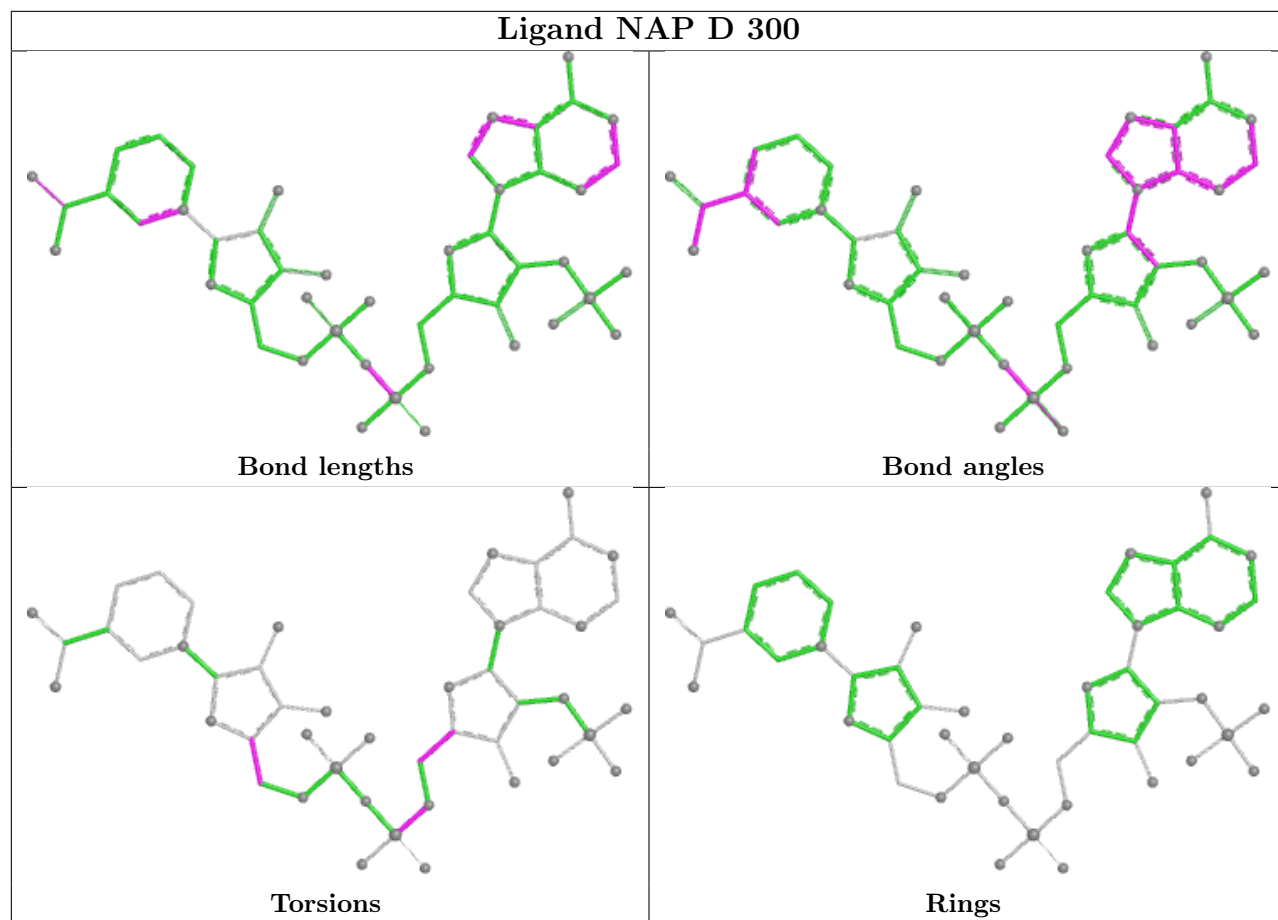
Mol	Chain	Res	Type	Atoms
2	A	300	NAP	C5B-O5B-PA-O2A
2	B	300	NAP	C5B-O5B-PA-O1A
2	B	300	NAP	C5B-O5B-PA-O2A
2	B	300	NAP	C5B-O5B-PA-O3

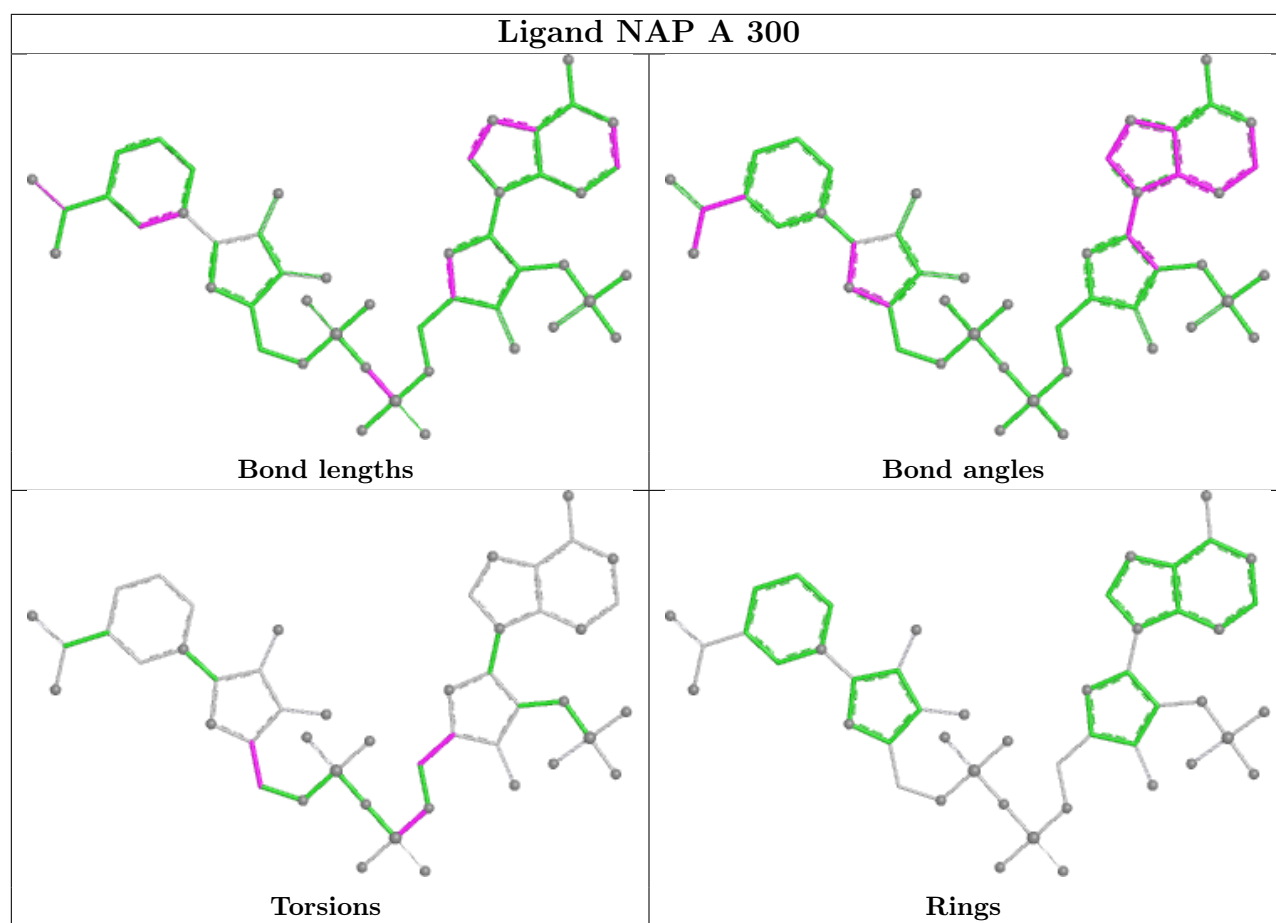
There are no ring outliers.

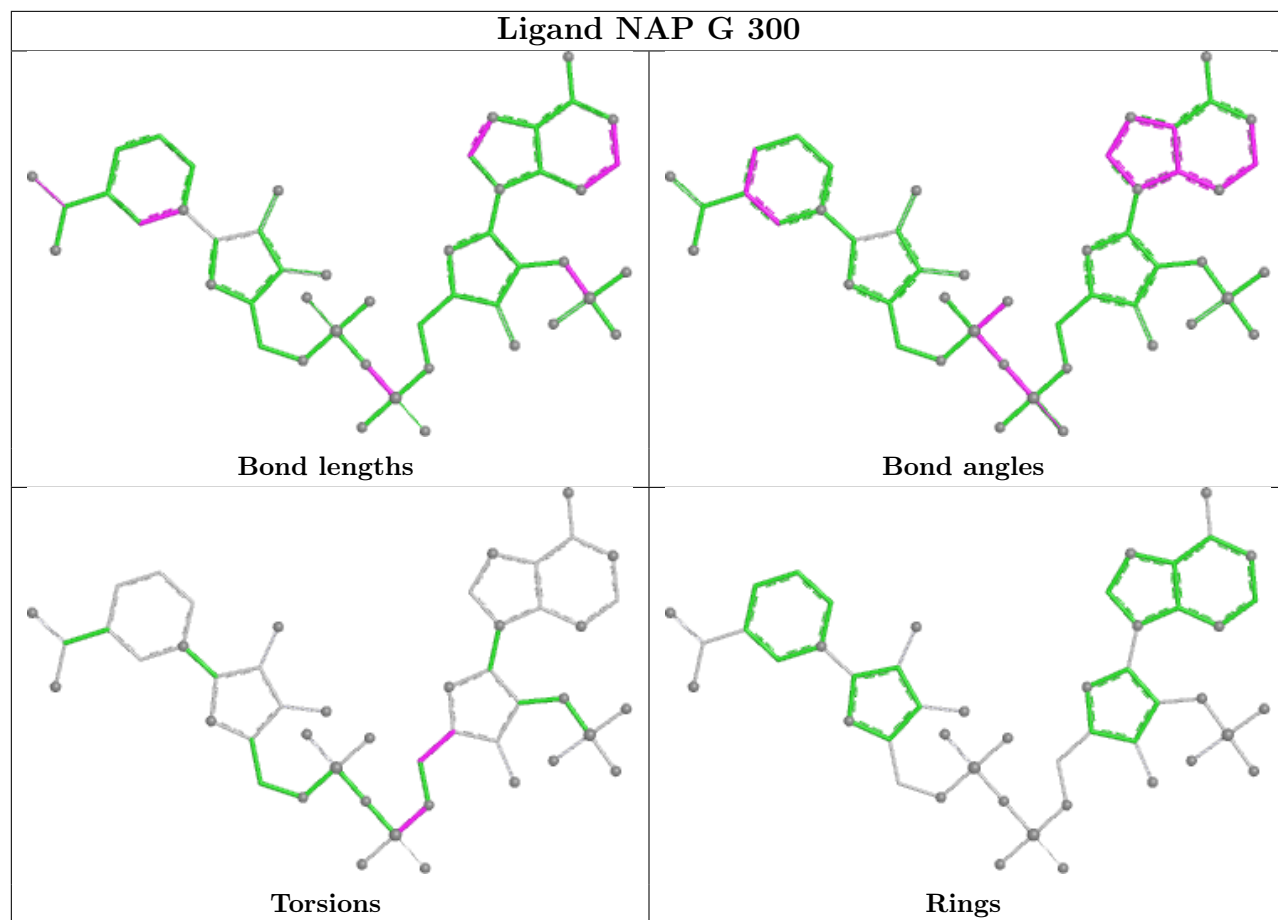
12 monomers are involved in 16 short contacts:

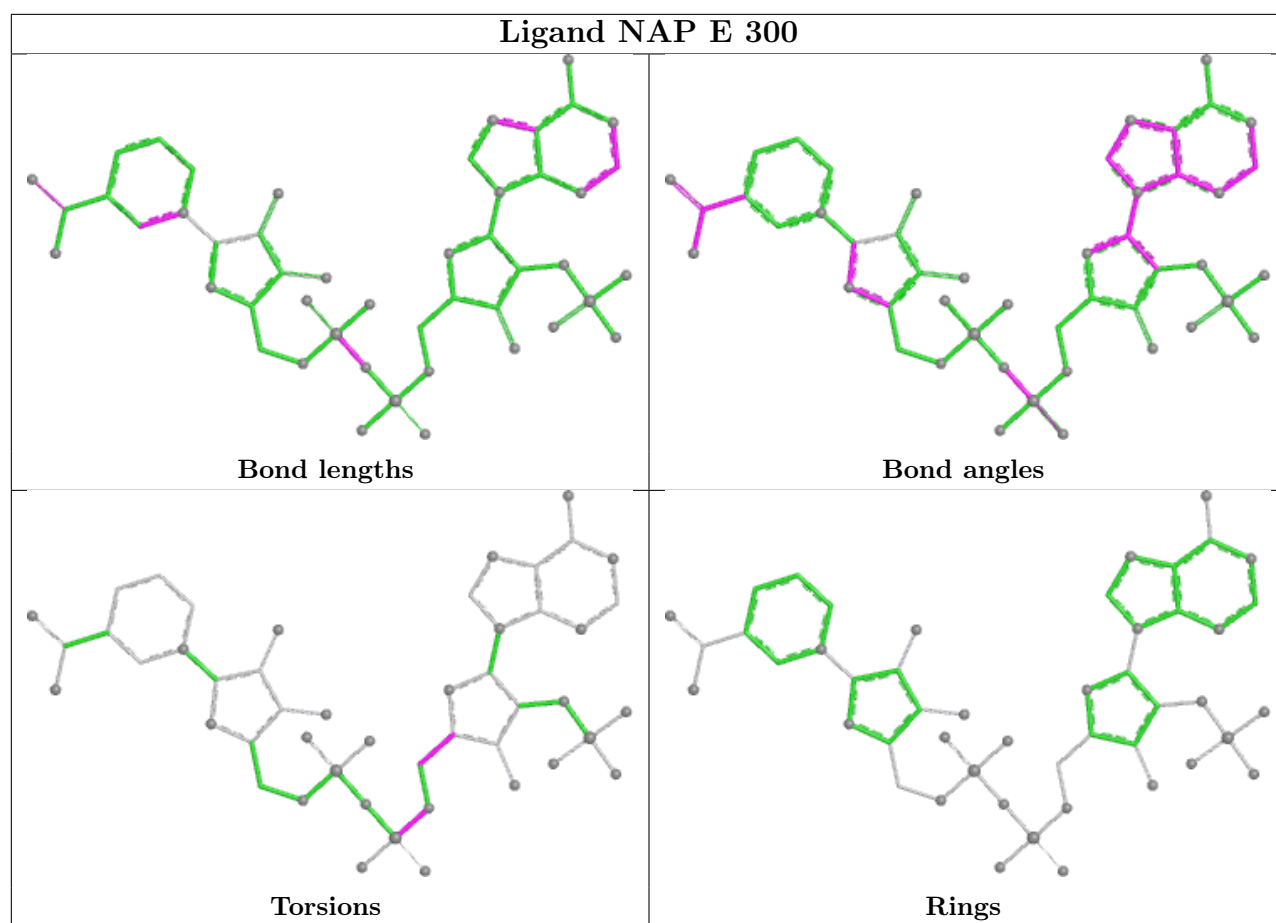
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	300	NAP	1	0
3	F	301	TAQ	1	0
3	A	301	TAQ	1	0
3	E	301	TAQ	1	0
2	A	300	NAP	1	0
3	A	302	TAQ	1	0
2	G	300	NAP	3	0
3	G	301	TAQ	3	0
2	E	300	NAP	1	0
2	H	300	NAP	1	0
2	C	300	NAP	1	0
3	H	301	TAQ	1	0

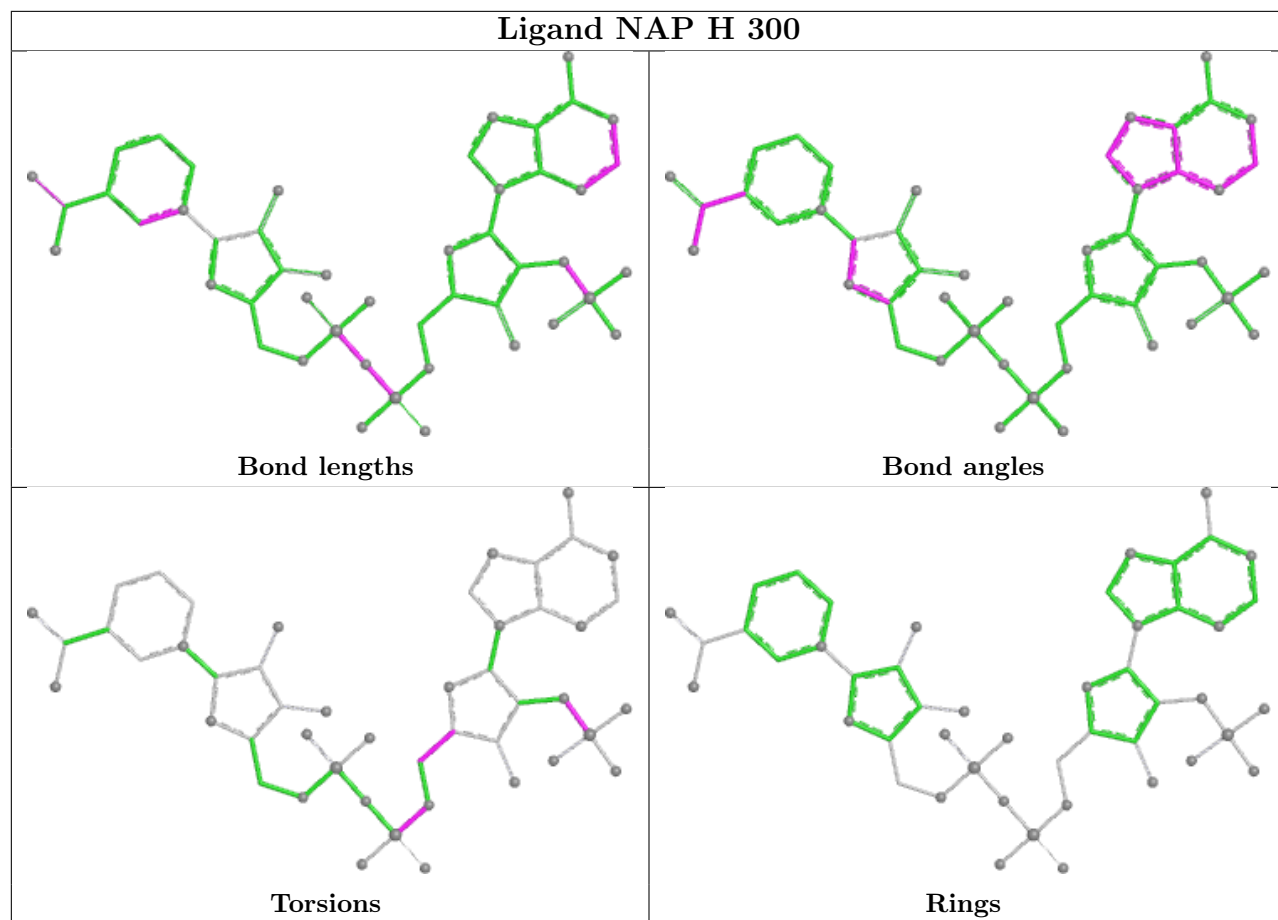
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

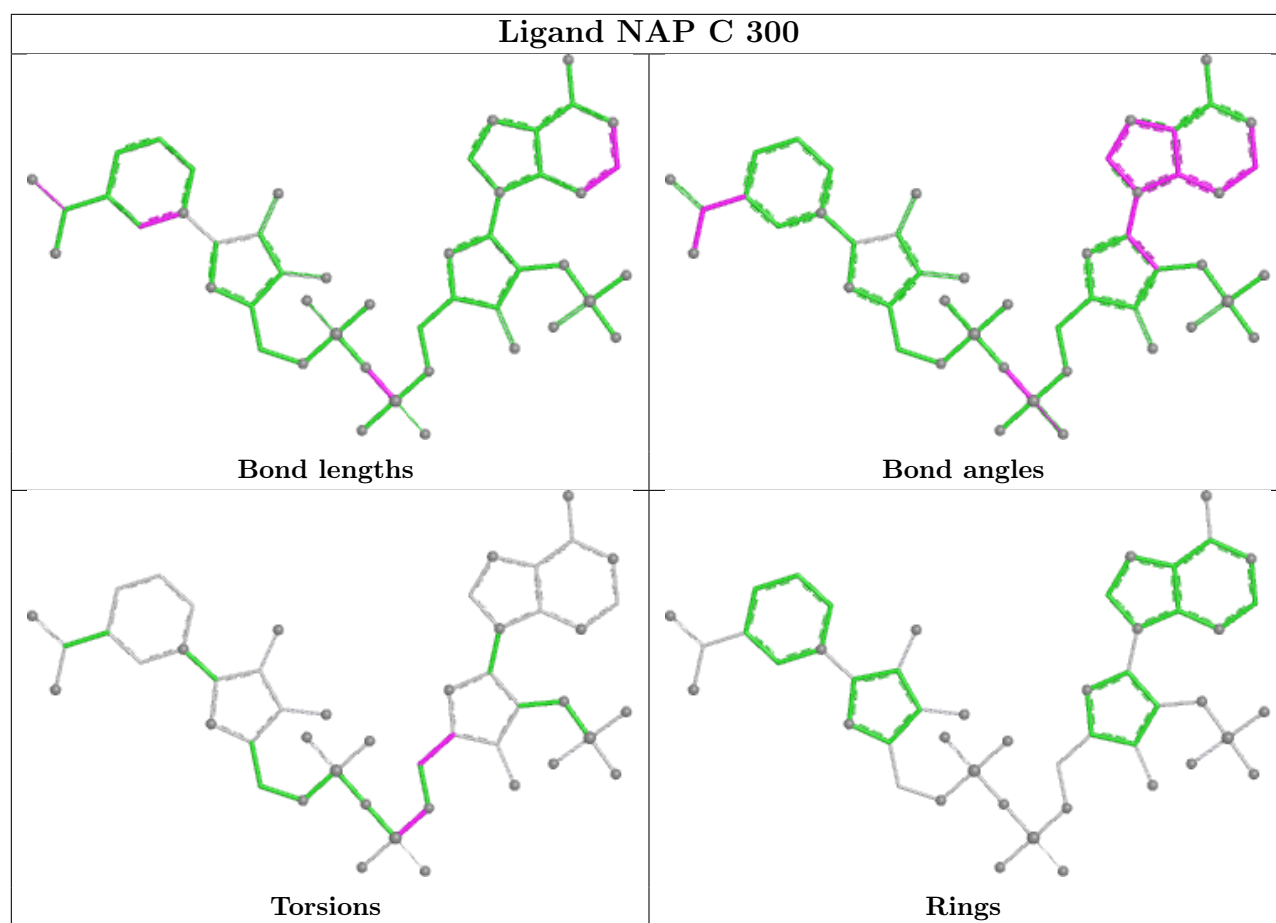


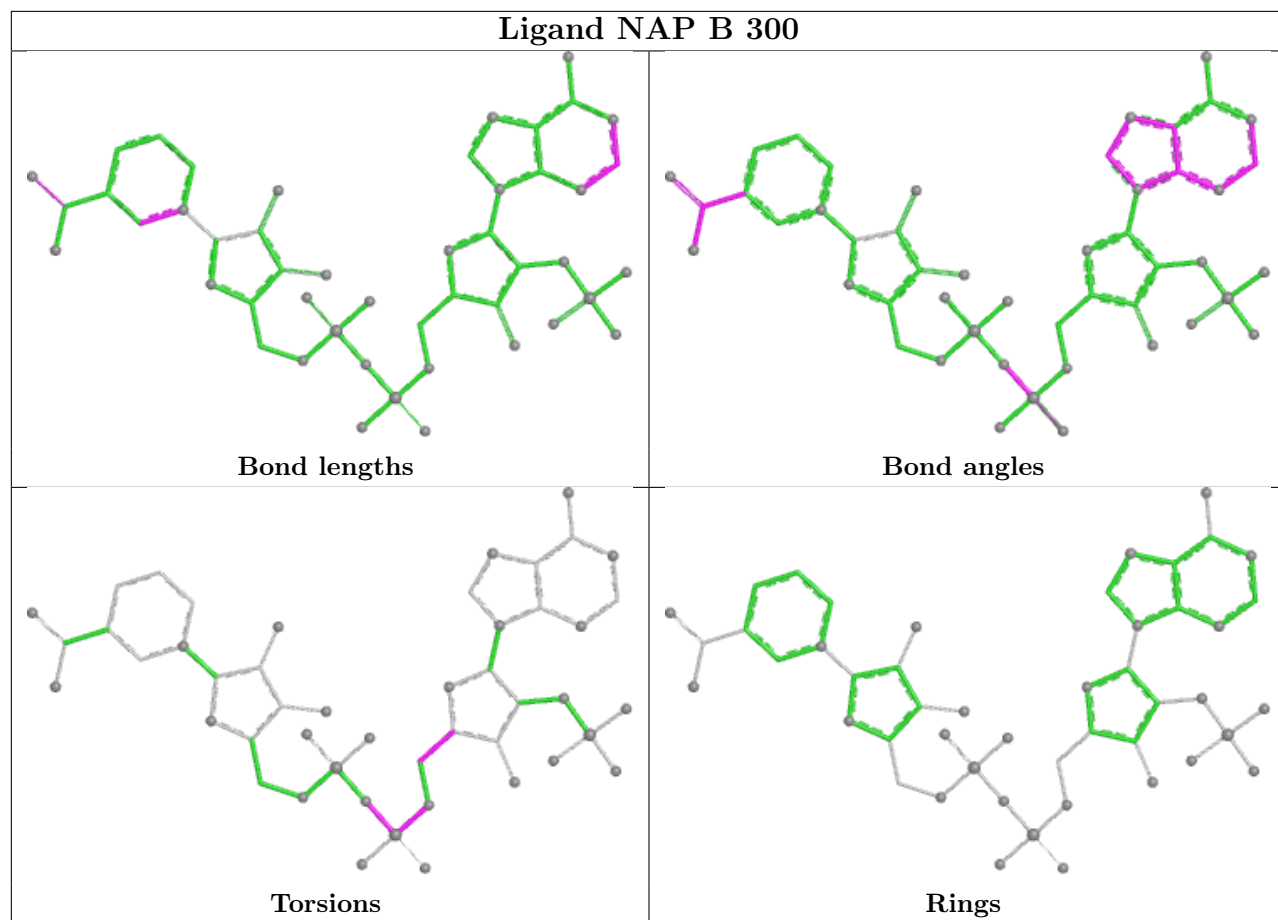


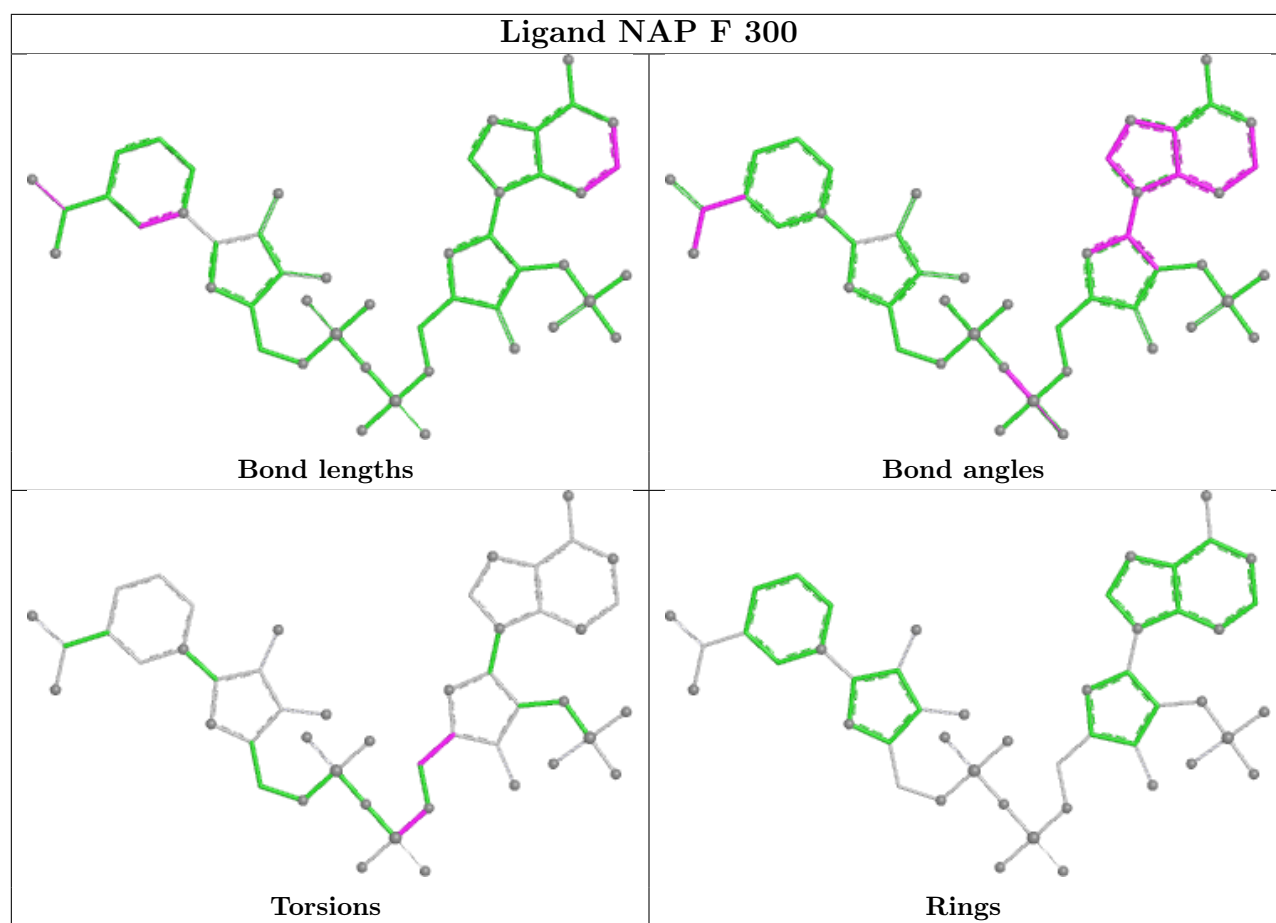












5.7 Other polymers [i](#)

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

6.1 Protein, DNA and RNA chains

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	276/307 (89%)	-1.44	0 100 100	4, 18, 32, 46	1 (0%)
1	B	274/307 (89%)	-1.39	0 100 100	6, 18, 33, 46	1 (0%)
1	C	264/307 (85%)	-1.49	0 100 100	5, 19, 39, 55	5 (1%)
1	D	256/307 (83%)	-1.49	0 100 100	9, 18, 34, 56	2 (0%)
1	E	267/307 (86%)	-1.35	0 100 100	9, 19, 31, 42	0
1	F	270/307 (87%)	-1.41	0 100 100	9, 19, 31, 50	1 (0%)
1	G	263/307 (85%)	-1.22	0 100 100	9, 19, 43, 64	5 (1%)
1	H	260/307 (84%)	-1.28	0 100 100	10, 19, 41, 72	2 (0%)
All	All	2130/2456 (86%)	-1.38	0 100 100	4, 19, 37, 72	17 (0%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

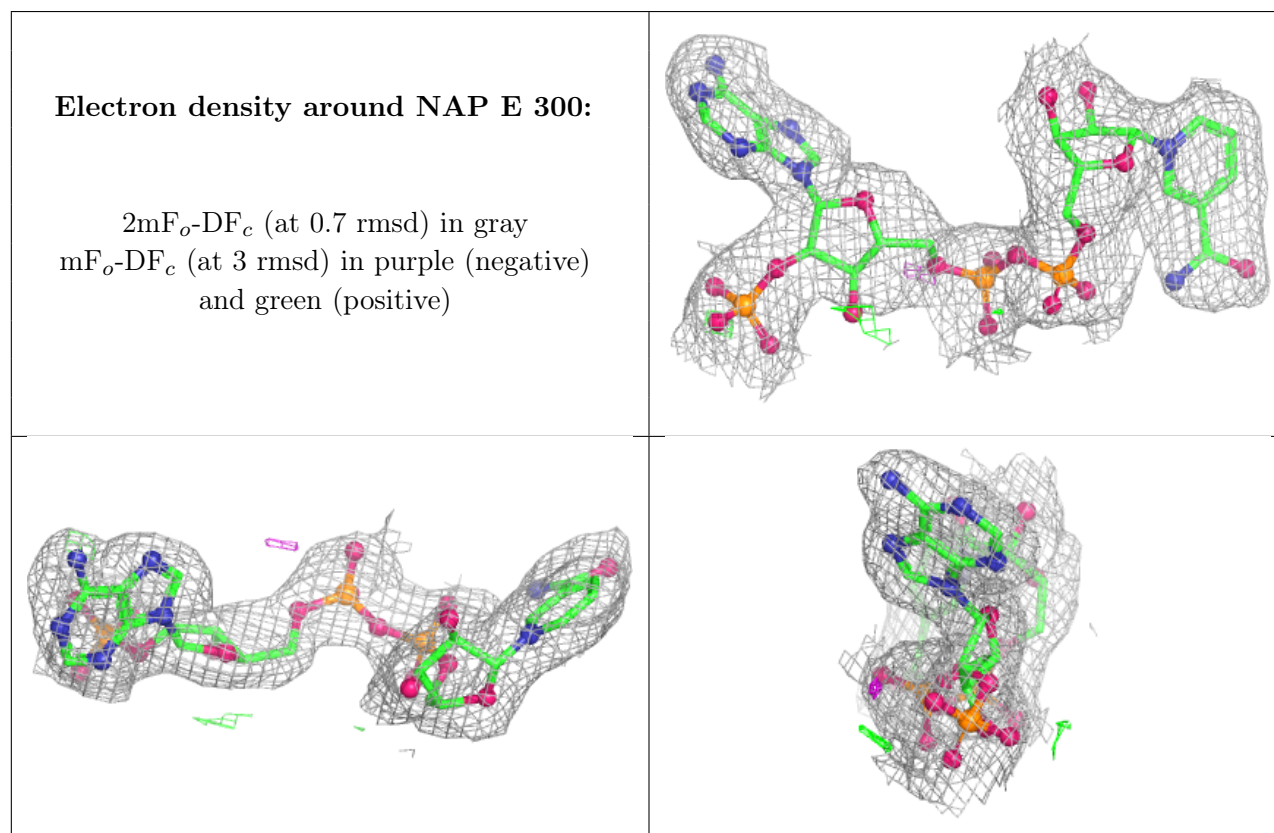
There are no oligosaccharides in this entry.

6.4 Ligands

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.

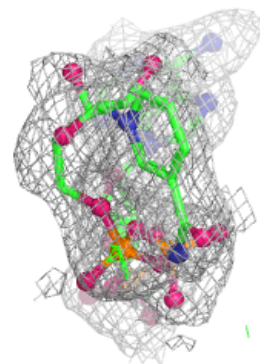
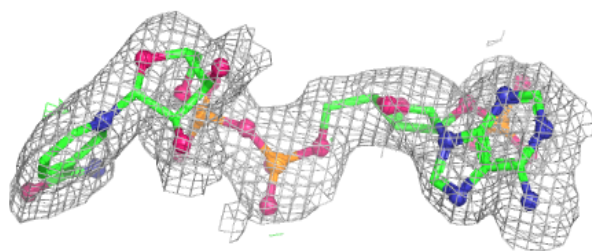
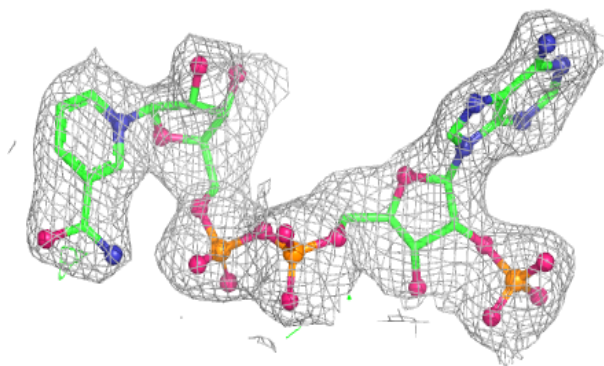
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	TAQ	A	302	13/13	0.98	0.05	25,28,31,31	0
3	TAQ	G	301	13/13	0.98	0.06	13,14,15,16	0
3	TAQ	H	301	13/13	0.98	0.04	13,14,15,15	0
2	NAP	E	300	48/48	0.99	0.03	9,15,19,22	0
2	NAP	F	300	48/48	0.99	0.03	9,15,18,21	0
2	NAP	G	300	48/48	0.99	0.04	9,15,19,21	0
2	NAP	H	300	48/48	0.99	0.04	9,15,19,21	0
3	TAQ	A	301	13/13	0.99	0.04	13,14,15,15	0
2	NAP	A	300	48/48	0.99	0.04	8,15,18,21	0
3	TAQ	B	301	13/13	0.99	0.03	13,14,15,15	0
3	TAQ	C	301	13/13	0.99	0.03	12,14,15,16	0
3	TAQ	D	301	13/13	0.99	0.03	13,14,15,16	0
3	TAQ	E	301	13/13	0.99	0.03	12,14,15,15	0
3	TAQ	F	301	13/13	0.99	0.04	13,14,15,15	0
2	NAP	B	300	48/48	0.99	0.03	9,15,18,21	0
2	NAP	D	300	48/48	0.99	0.03	9,15,19,21	0
2	NAP	C	300	48/48	1.00	0.03	9,15,19,21	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.

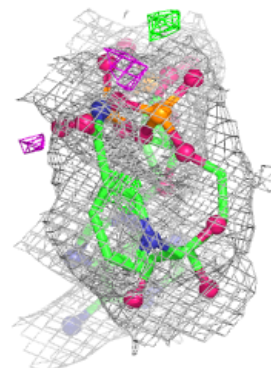
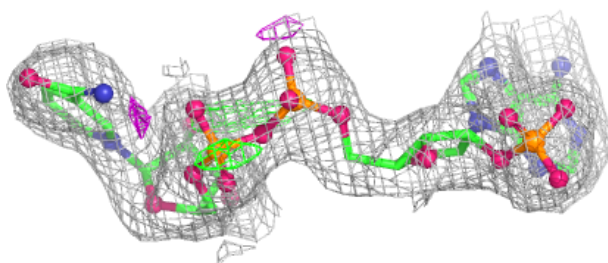
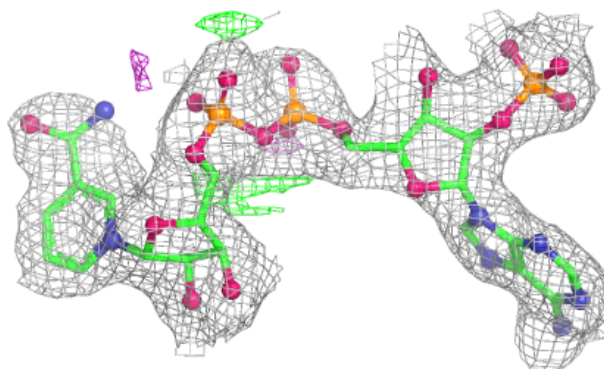


Electron density around NAP F 300:

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

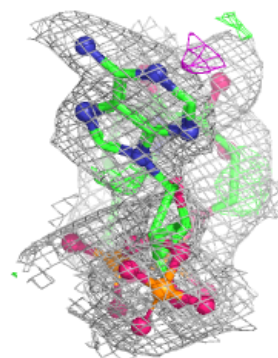
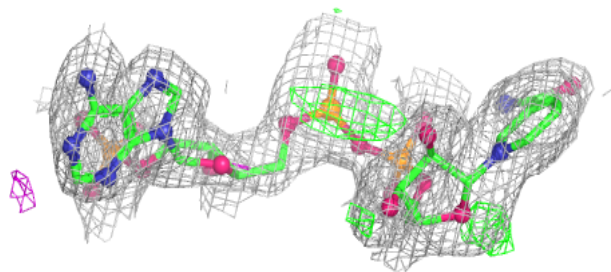
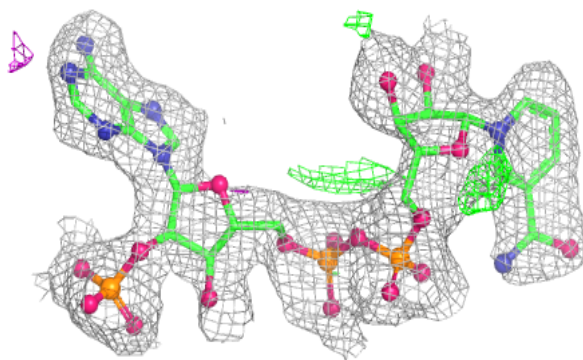
**Electron density around NAP G 300:**

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

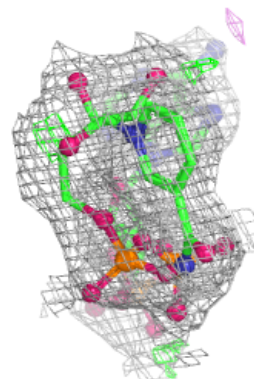
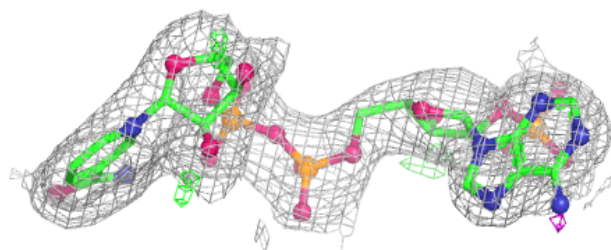
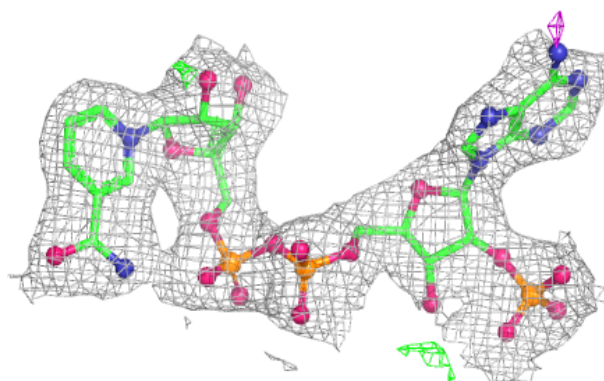


Electron density around NAP H 300:

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

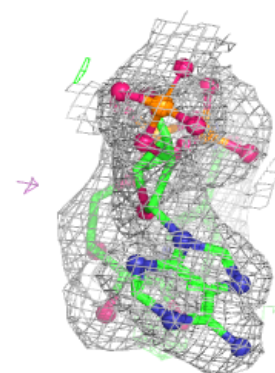
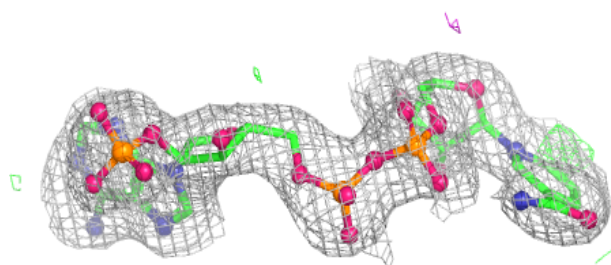
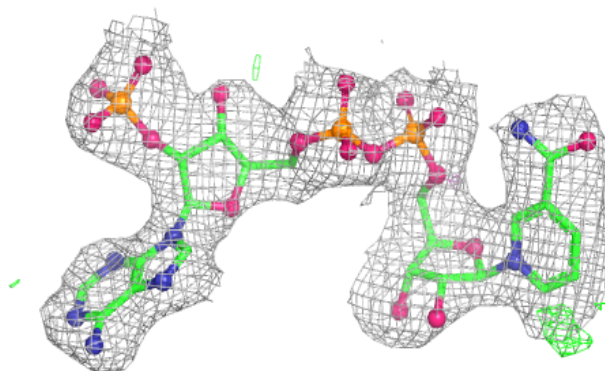
**Electron density around NAP A 300:**

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

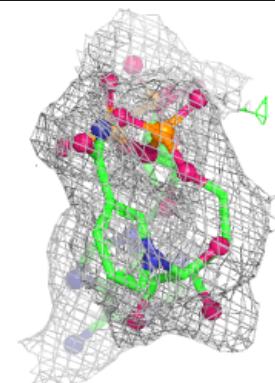
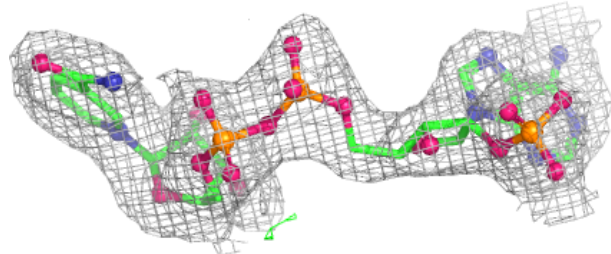
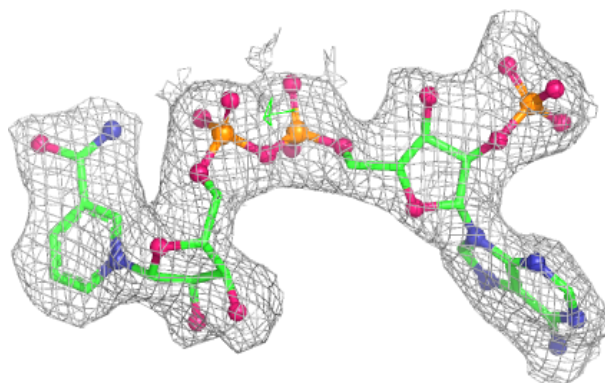


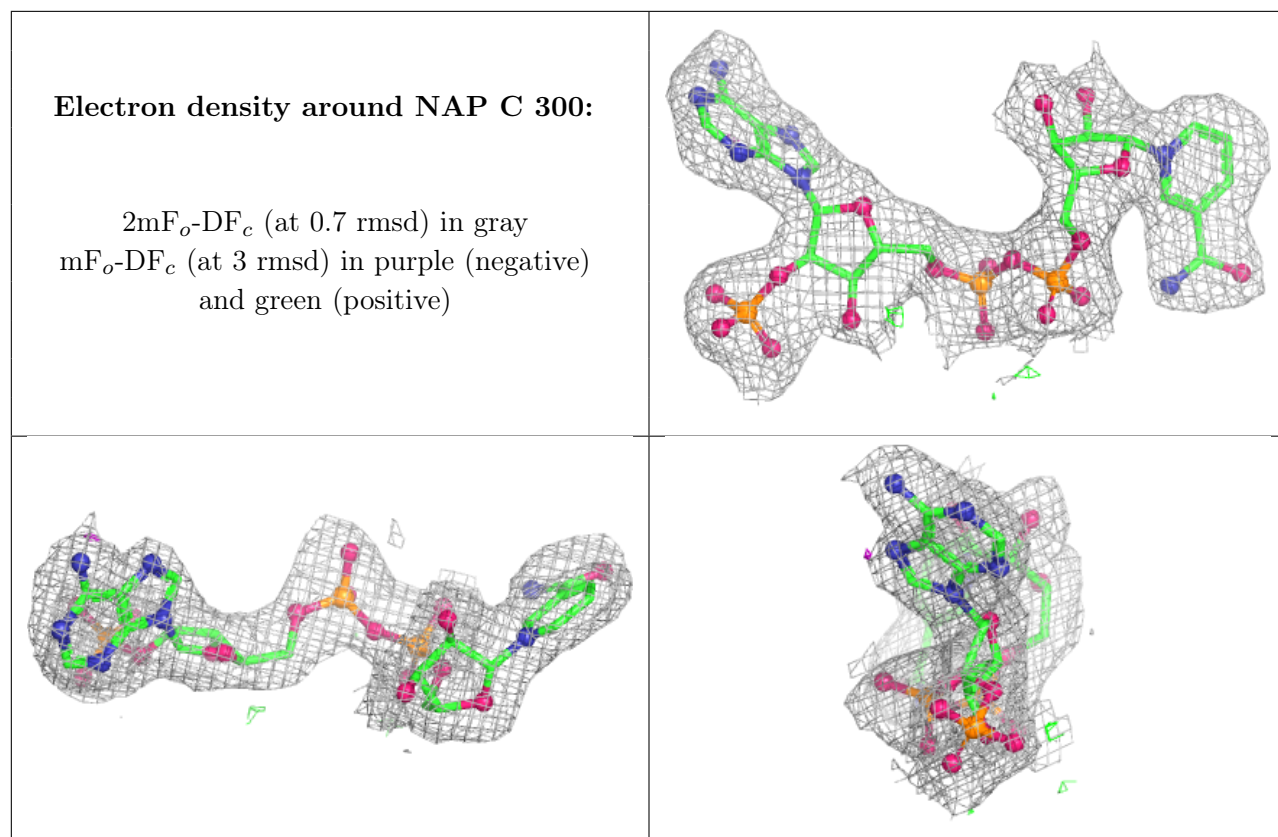
Electron density around NAP B 300:

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

**Electron density around NAP D 300:**

$2mF_o-DF_c$ (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.