



wwPDB X-ray Structure Validation Summary Report ⓘ

May 23, 2020 – 08:45 pm BST

PDB ID : 3ASV
Title : The Closed form of serine dehydrogenase complexed with NADP+
Authors : Yamazawa, R.; Nakajima, Y.; Yoshimoto, T.; Ito, K.
Deposited on : 2010-12-21
Resolution : 2.70 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 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 : 2.11
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

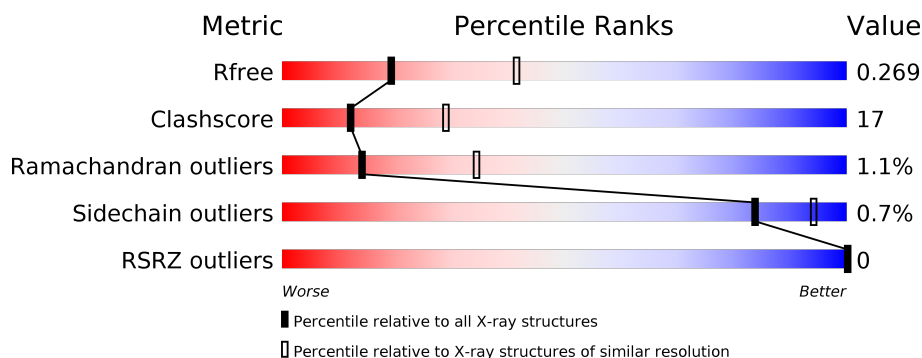
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 $\leq 5\%$. 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	<div> <div>76%</div> <div>23%</div> <div>.</div> </div>
1	B	248	<div> <div>77%</div> <div>22%</div> <div>.</div> </div>
1	C	248	<div> <div>71%</div> <div>28%</div> <div>.</div> </div>
1	D	248	<div> <div>64%</div> <div>35%</div> <div>.</div> </div>
1	E	248	<div> <div>58%</div> <div>40%</div> <div>.</div> </div>
1	F	248	<div> <div>58%</div> <div>41%</div> <div>.</div> </div>

2 Entry composition ⓘ

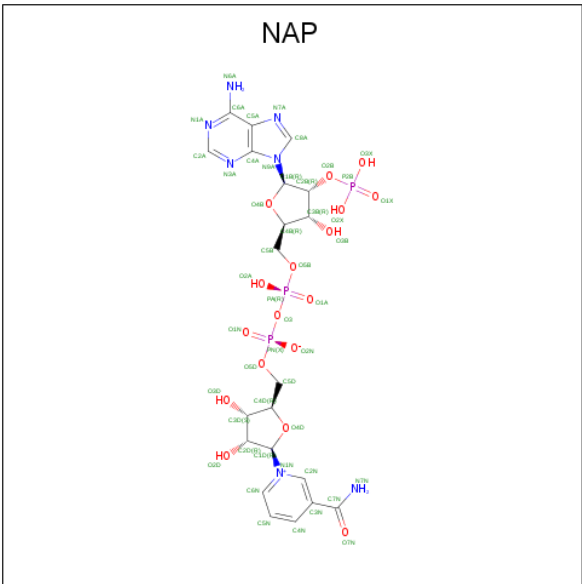
There are 4 unique types of molecules in this entry. The entry contains 12045 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Short-chain dehydrogenase/reductase SDR.

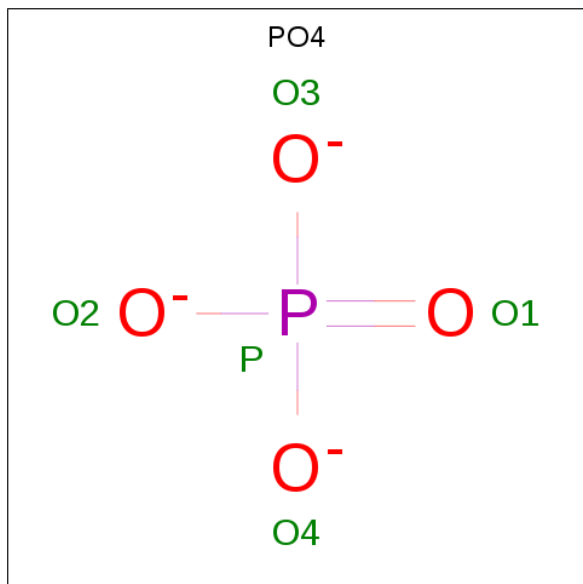
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	0	0
			1891	1186	341	354	10			
1	B	248	Total	C	N	O	S	0	0	0
			1911	1196	341	364	10			
1	C	248	Total	C	N	O	S	0	0	0
			1900	1191	340	359	10			
1	D	248	Total	C	N	O	S	0	0	0
			1907	1194	341	362	10			
1	E	248	Total	C	N	O	S	0	0	0
			1891	1185	338	358	10			
1	F	248	Total	C	N	O	S	0	0	0
			1880	1177	334	359	10			

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



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

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		

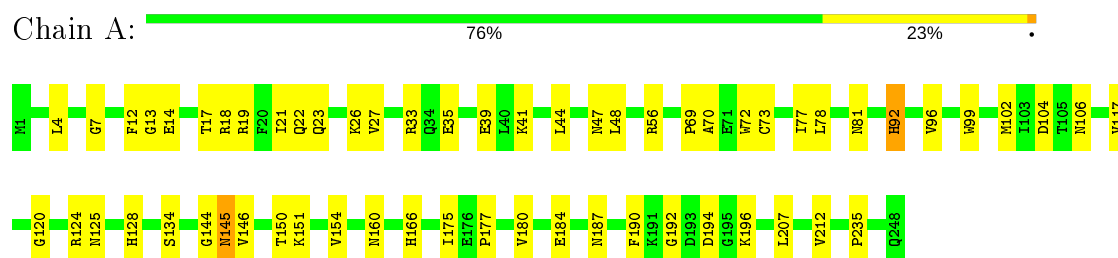
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	72	Total 72	O 72	0	0
4	B	66	Total 66	O 66	0	0
4	C	65	Total 65	O 65	0	0
4	D	52	Total 52	O 52	0	0
4	E	47	Total 47	O 47	0	0
4	F	45	Total 45	O 45	0	0

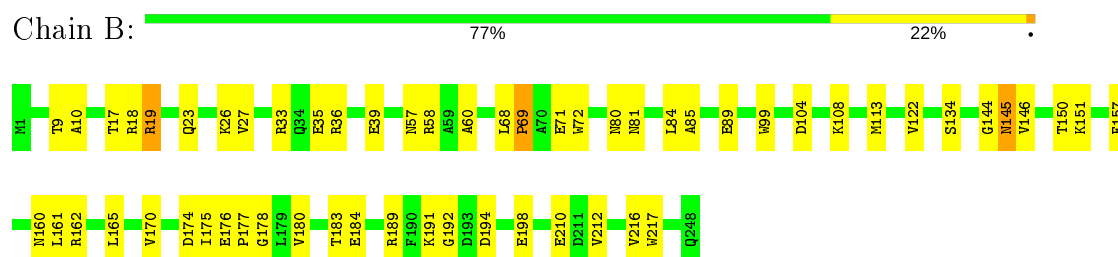
3 Residue-property plots [i](#)

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 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.

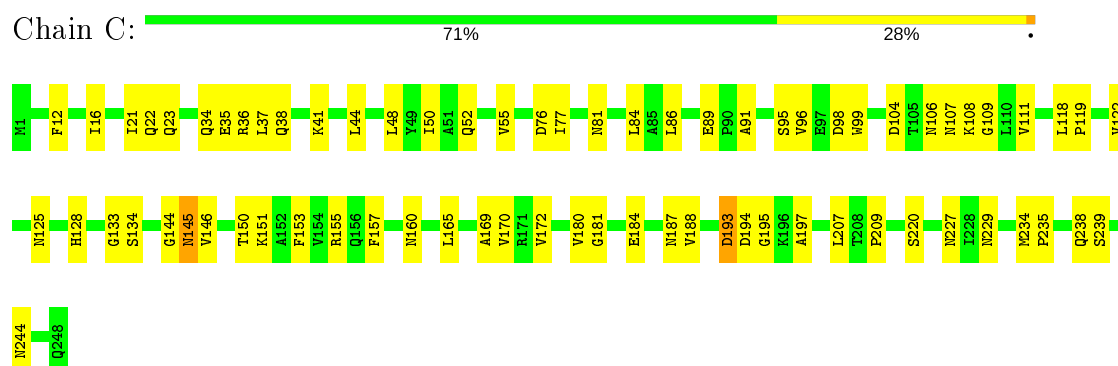
- Molecule 1: Short-chain dehydrogenase/reductase SDR



- Molecule 1: Short-chain dehydrogenase/reductase SDR



- Molecule 1: Short-chain dehydrogenase/reductase SDR



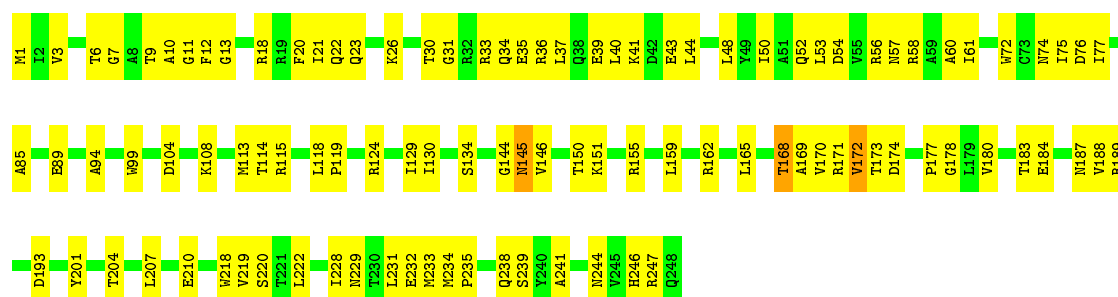
- Molecule 1: Short-chain dehydrogenase/reductase SDR





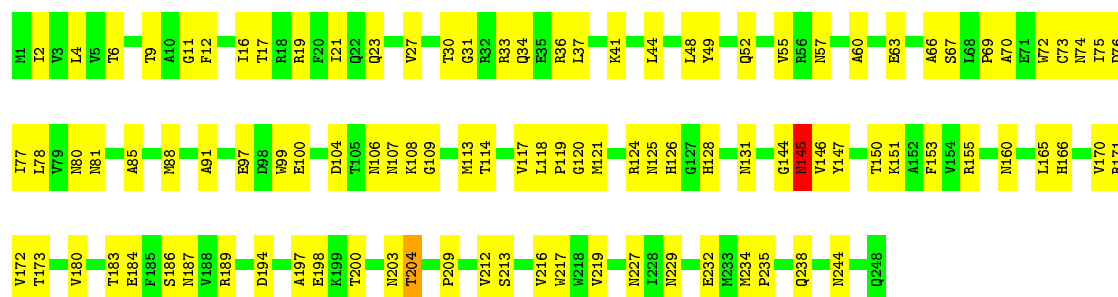
- Molecule 1: Short-chain dehydrogenase/reductase SDR

Chain E: 58% 40%



- Molecule 1: Short-chain dehydrogenase/reductase SDR

Chain F: 58% 41%



4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	113.86Å 113.86Å 197.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.70 21.53 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-2.70) 99.8 (21.53-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 2.71Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.192 , 0.273 0.187 , 0.269	Depositor DCC
R_{free} test set	1991 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 17.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.326 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12045	wwPDB-VP
Average B, all atoms (Å ²)	34.0	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 27.47 % 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 2.1867e-03. 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, 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	0.35	0/1927	0.62	0/2620
1	B	0.36	0/1947	0.61	0/2645
1	C	0.35	0/1936	0.62	0/2631
1	D	0.35	0/1943	0.60	0/2640
1	E	0.34	0/1927	0.60	0/2621
1	F	0.36	0/1916	0.62	0/2609
All	All	0.35	0/11596	0.61	0/15766

There are no bond length outliers.

There are no bond angle outliers.

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	1891	0	1861	53	0
1	B	1911	0	1881	43	0
1	C	1900	0	1869	60	0
1	D	1907	0	1877	87	0
1	E	1891	0	1850	100	0
1	F	1880	0	1818	82	0
2	A	48	0	25	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	48	0	25	2	0
2	C	48	0	25	3	0
2	D	48	0	25	2	0
2	E	48	0	25	3	0
2	F	48	0	25	2	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
4	A	72	0	0	5	0
4	B	66	0	0	3	0
4	C	65	0	0	6	0
4	D	52	0	0	0	0
4	E	47	0	0	2	0
4	F	45	0	0	4	0
All	All	12045	0	11306	393	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 17.

The worst 5 of 393 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:E:168:THR:HG23	1:E:170:VAL:H	1.12	1.08
1:D:168:THR:HG23	1:D:170:VAL:H	1.30	0.96
1:E:184:GLU:HA	1:E:187:ASN:HD22	1.31	0.93
1:F:41:LYS:HA	1:F:48:LEU:HD23	1.60	0.84
1:F:17:THR:HG23	1:F:27:VAL:HG11	1.59	0.83

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%)	222 (90%)	21 (8%)	3 (1%)	13	32
1	B	246/248 (99%)	230 (94%)	13 (5%)	3 (1%)	13	32
1	C	246/248 (99%)	229 (93%)	15 (6%)	2 (1%)	19	43
1	D	246/248 (99%)	226 (92%)	18 (7%)	2 (1%)	19	43
1	E	246/248 (99%)	229 (93%)	15 (6%)	2 (1%)	19	43
1	F	246/248 (99%)	222 (90%)	20 (8%)	4 (2%)	9	24
All	All	1476/1488 (99%)	1358 (92%)	102 (7%)	16 (1%)	14	34

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	145	ASN
1	B	145	ASN
1	C	145	ASN
1	C	193	ASP
1	D	145	ASN

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	196/202 (97%)	195 (100%)	1 (0%)	88	96
1	B	201/202 (100%)	200 (100%)	1 (0%)	88	96
1	C	198/202 (98%)	197 (100%)	1 (0%)	88	96
1	D	200/202 (99%)	199 (100%)	1 (0%)	88	96
1	E	196/202 (97%)	193 (98%)	3 (2%)	65	86
1	F	193/202 (96%)	192 (100%)	1 (0%)	88	96
All	All	1184/1212 (98%)	1176 (99%)	8 (1%)	84	94

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	168	THR
1	F	145	ASN
1	E	172	VAL
1	C	84	LEU
1	E	168	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	107	ASN
1	D	229	ASN
1	F	227	ASN
1	D	131	ASN
1	D	166	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

12 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	304	-	45,52,52	2.13	8 (17%)	56,80,80	1.34	1 (1%)
2	NAP	F	306	-	45,52,52	2.21	8 (17%)	56,80,80	1.34	3 (5%)
3	PO4	A	311	-	4,4,4	1.58	0	6,6,6	0.44	0
2	NAP	C	303	-	45,52,52	2.21	9 (20%)	56,80,80	1.31	2 (3%)
3	PO4	B	312	-	4,4,4	1.60	0	6,6,6	0.45	0
3	PO4	F	316	-	4,4,4	1.60	0	6,6,6	0.44	0
2	NAP	B	302	-	45,52,52	2.25	10 (22%)	56,80,80	1.28	2 (3%)
2	NAP	E	305	-	45,52,52	2.14	7 (15%)	56,80,80	1.25	1 (1%)
3	PO4	C	313	-	4,4,4	1.57	0	6,6,6	0.43	0
2	NAP	A	301	-	45,52,52	2.17	8 (17%)	56,80,80	1.28	1 (1%)
3	PO4	D	314	-	4,4,4	1.60	0	6,6,6	0.43	0
3	PO4	E	315	-	4,4,4	1.63	0	6,6,6	0.44	0

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	304	-	-	12/31/67/67	0/5/5/5
2	NAP	F	306	-	-	12/31/67/67	0/5/5/5
2	NAP	C	303	-	-	12/31/67/67	0/5/5/5
2	NAP	B	302	-	-	12/31/67/67	0/5/5/5
2	NAP	A	301	-	-	10/31/67/67	0/5/5/5
2	NAP	E	305	-	-	12/31/67/67	0/5/5/5

The worst 5 of 50 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	NAP	O7N-C7N	9.00	1.41	1.24
2	F	306	NAP	O7N-C7N	8.79	1.41	1.24
2	E	305	NAP	O7N-C7N	8.72	1.40	1.24
2	B	302	NAP	O7N-C7N	8.69	1.40	1.24
2	D	304	NAP	O7N-C7N	8.59	1.40	1.24

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	304	NAP	N3A-C2A-N1A	-6.78	118.08	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	NAP	N3A-C2A-N1A	-6.65	118.28	128.68
2	E	305	NAP	N3A-C2A-N1A	-6.61	118.34	128.68
2	C	303	NAP	N3A-C2A-N1A	-6.57	118.41	128.68
2	F	306	NAP	N3A-C2A-N1A	-6.54	118.45	128.68

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

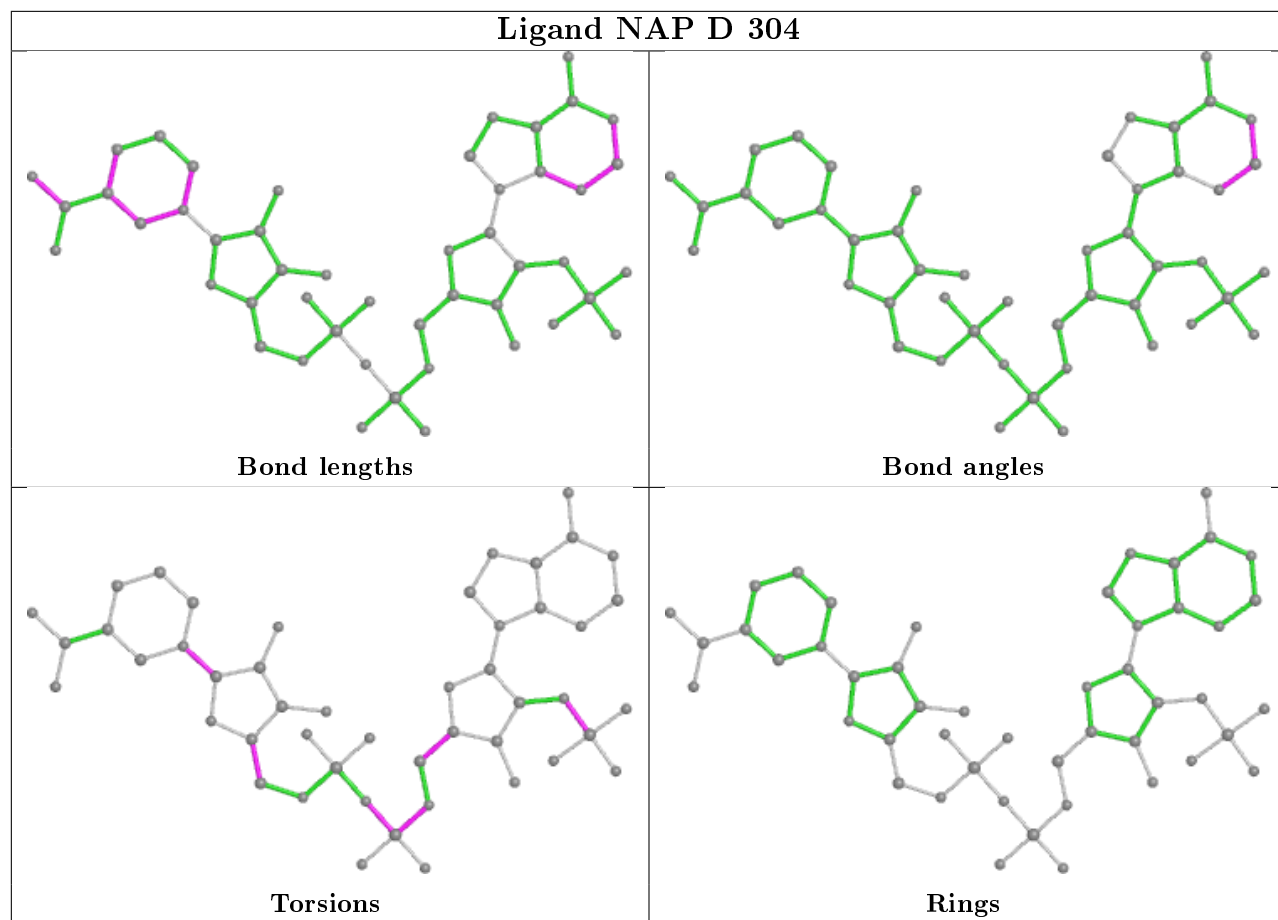
Mol	Chain	Res	Type	Atoms
2	D	304	NAP	C5B-O5B-PA-O1A
2	D	304	NAP	C5B-O5B-PA-O2A
2	D	304	NAP	C5B-O5B-PA-O3
2	D	304	NAP	O4B-C4B-C5B-O5B
2	D	304	NAP	C2B-O2B-P2B-O1X

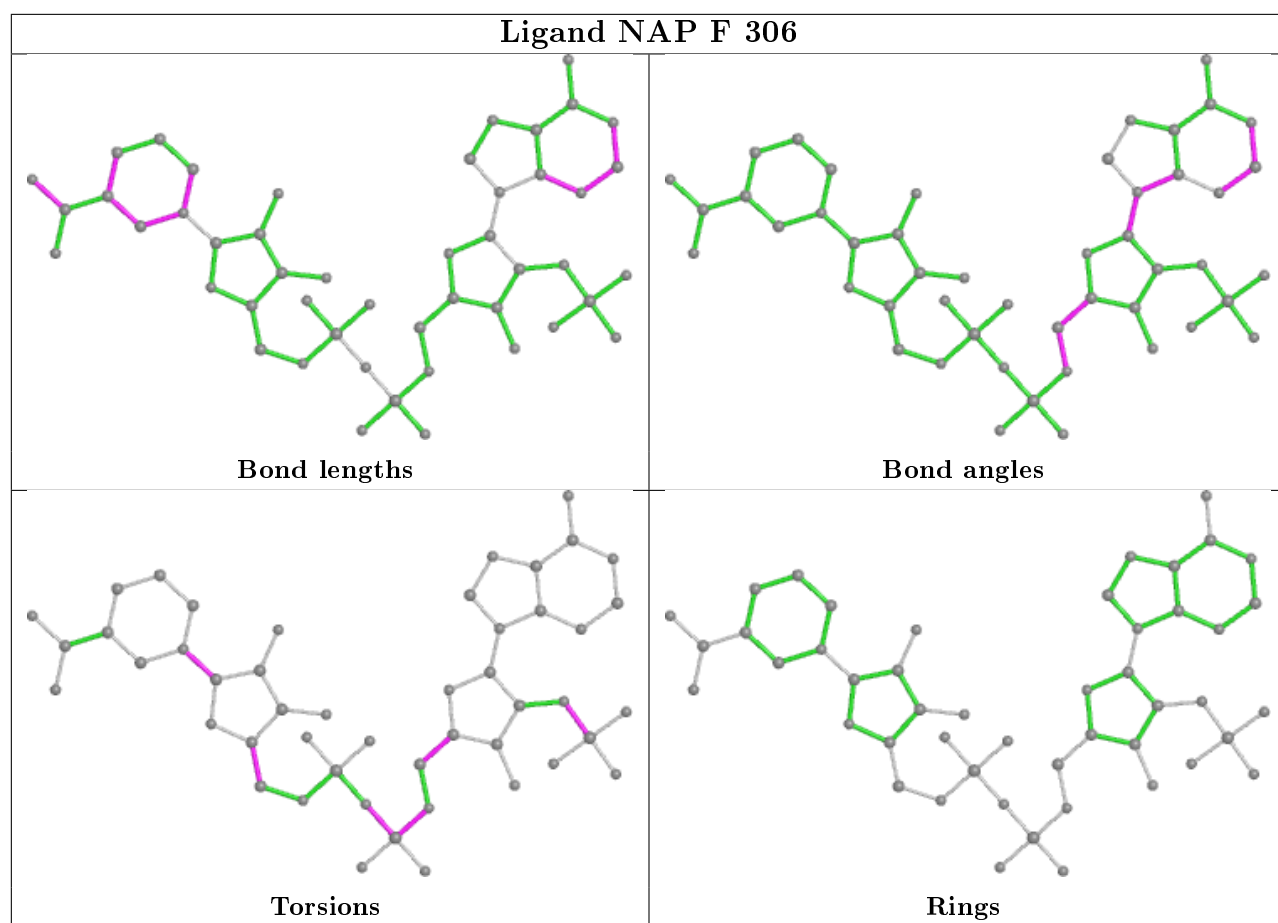
There are no ring outliers.

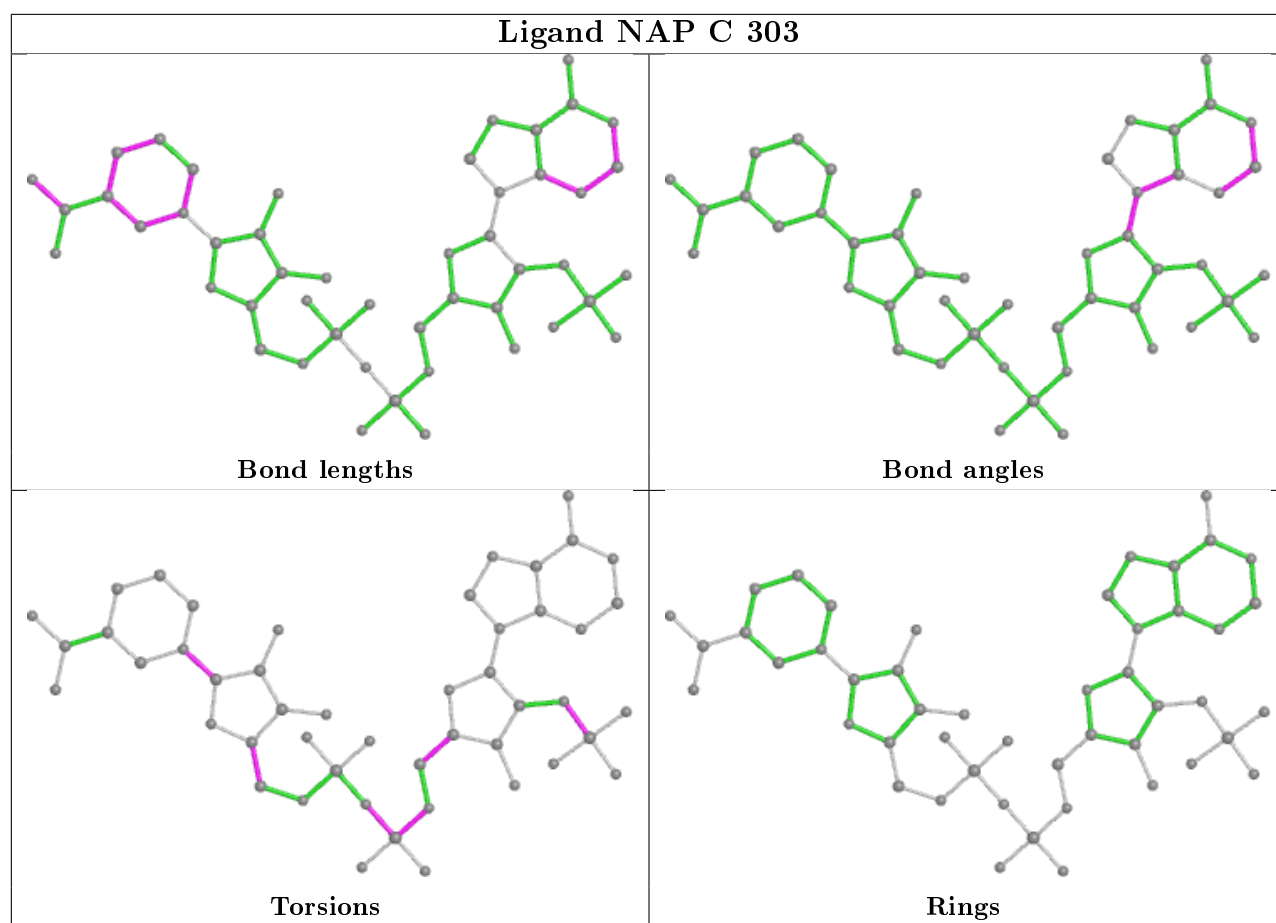
6 monomers are involved in 14 short contacts:

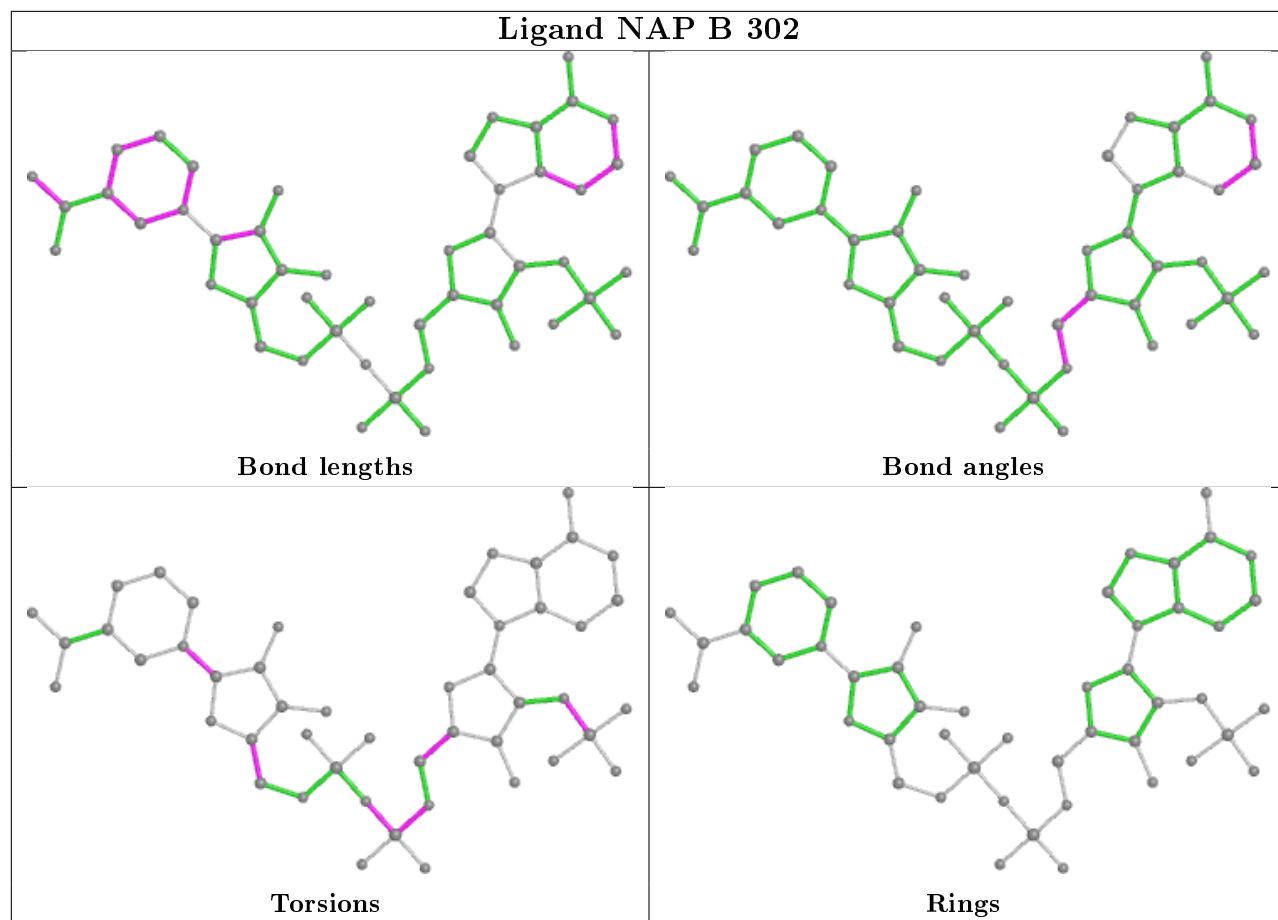
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	304	NAP	2	0
2	F	306	NAP	2	0
2	C	303	NAP	3	0
2	B	302	NAP	2	0
2	E	305	NAP	3	0
2	A	301	NAP	2	0

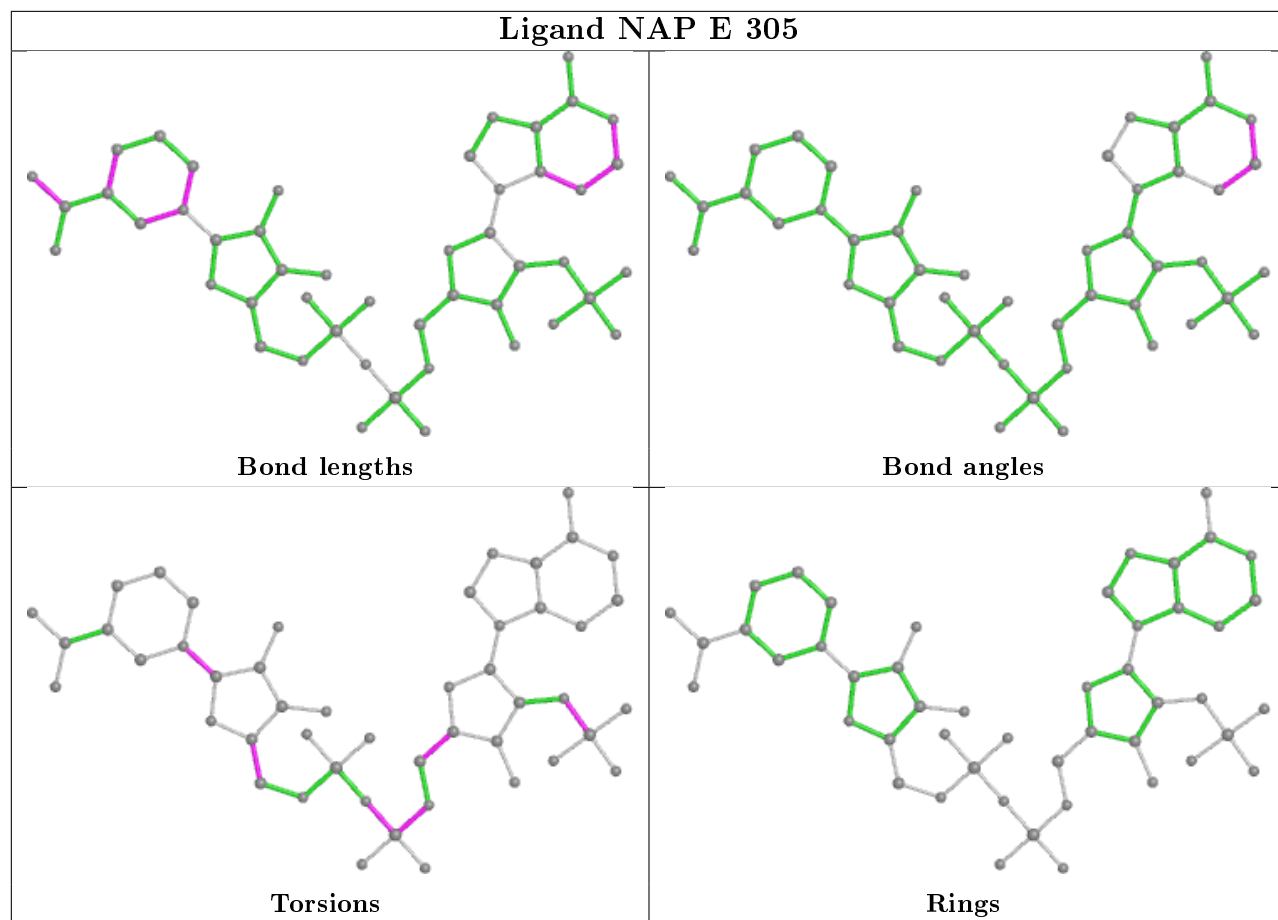
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

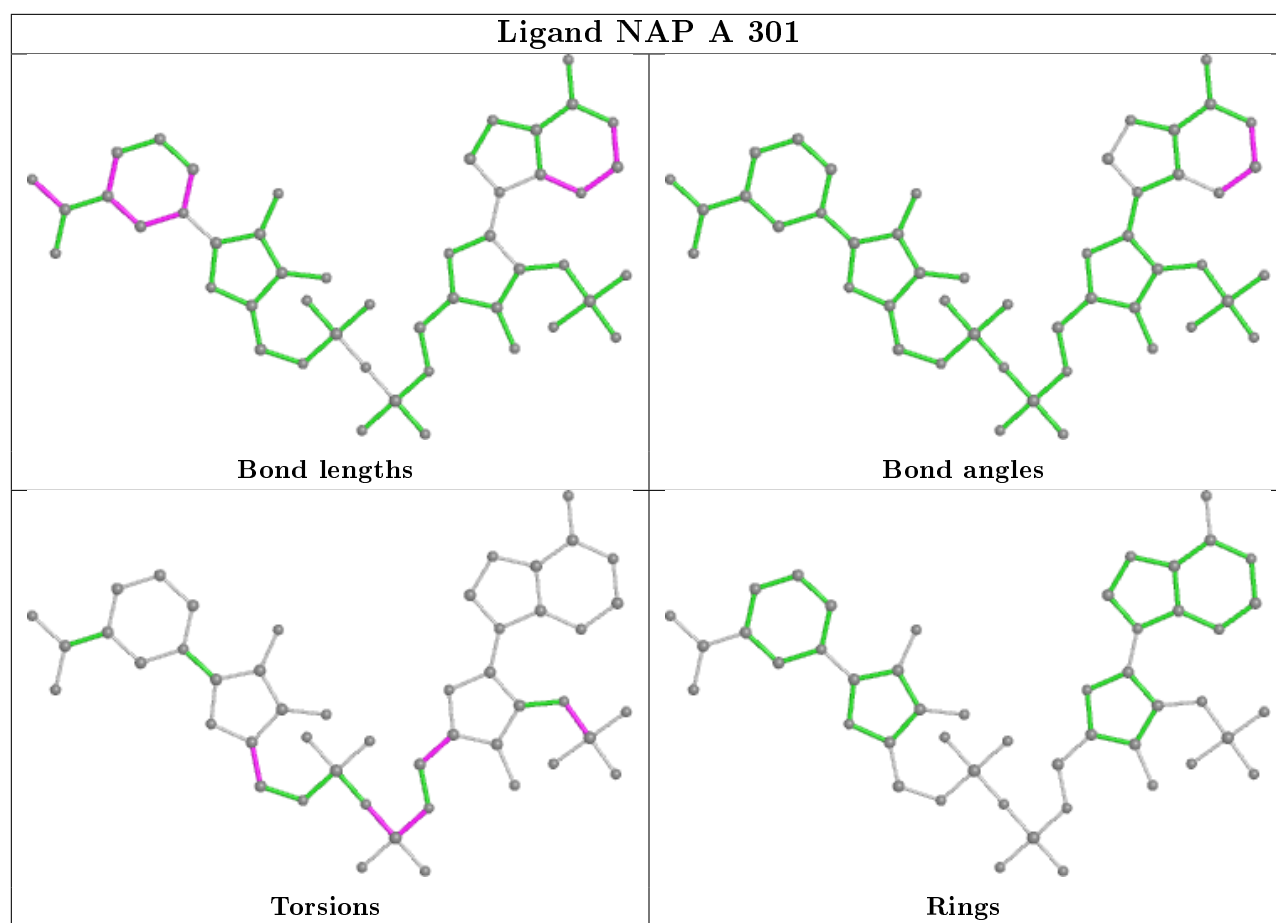












5.7 Other polymers [i](#)

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%)	-0.51	0 100 100	18, 30, 48, 55	0
1	B	248/248 (100%)	-0.53	0 100 100	18, 30, 44, 52	0
1	C	248/248 (100%)	-0.46	0 100 100	20, 32, 46, 55	0
1	D	248/248 (100%)	-0.38	0 100 100	21, 32, 50, 58	0
1	E	248/248 (100%)	-0.36	0 100 100	23, 36, 52, 60	0
1	F	248/248 (100%)	-0.34	0 100 100	26, 36, 53, 61	0
All	All	1488/1488 (100%)	-0.43	0 100 100	18, 32, 50, 61	0

There are no RSRZ outliers to report.

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 carbohydrates 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.

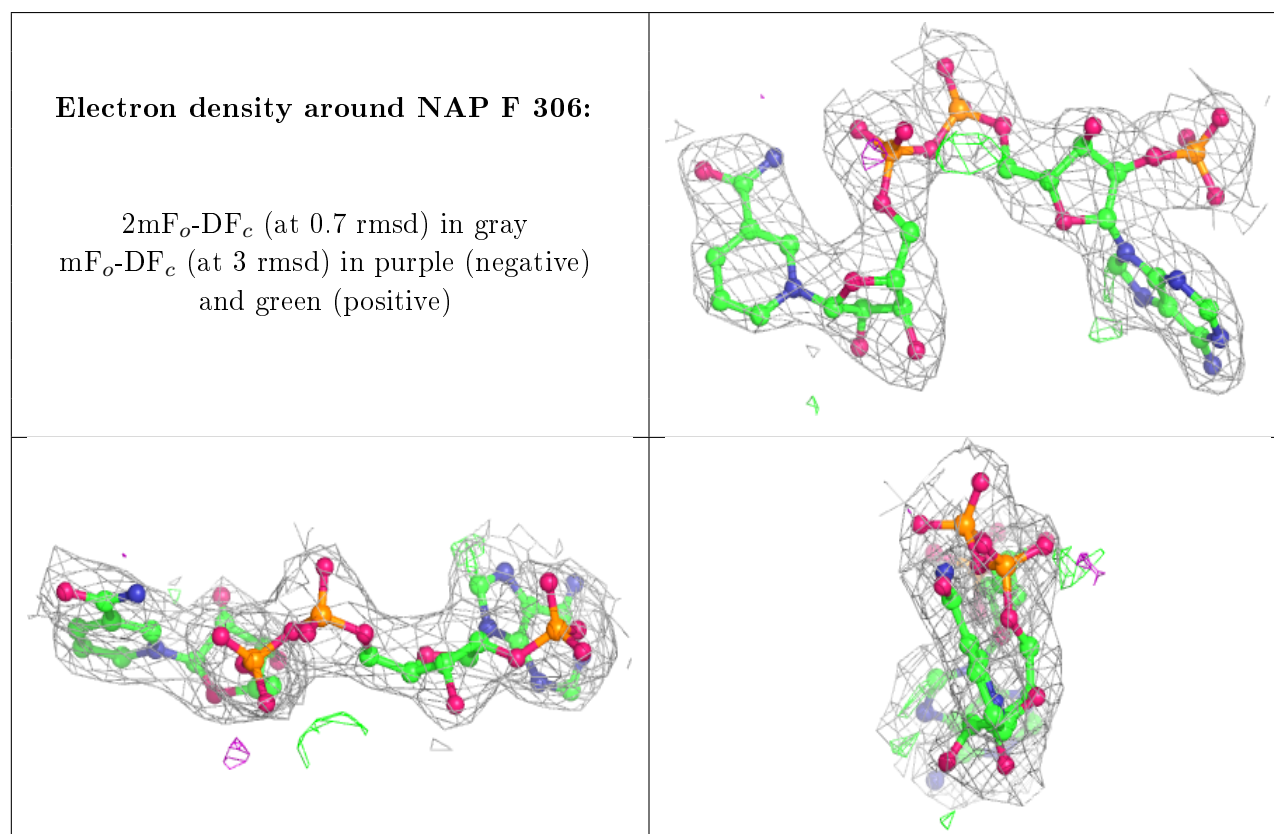
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PO4	E	315	5/5	0.93	0.19	71,71,72,73	0

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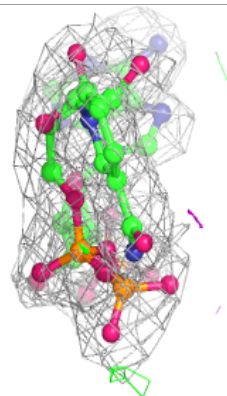
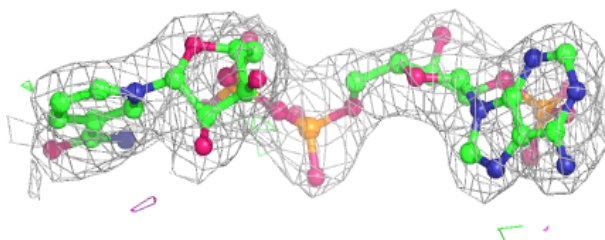
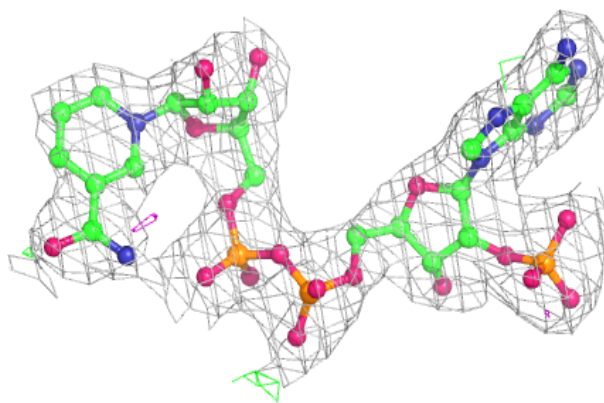
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PO4	C	313	5/5	0.95	0.19	72,73,73,74	0
3	PO4	B	312	5/5	0.95	0.21	61,62,63,64	0
3	PO4	F	316	5/5	0.97	0.18	60,61,62,62	0
3	PO4	A	311	5/5	0.97	0.14	43,43,45,45	0
3	PO4	D	314	5/5	0.97	0.14	66,66,67,67	0
2	NAP	F	306	48/48	0.97	0.15	29,40,45,46	0
2	NAP	E	305	48/48	0.98	0.12	31,37,42,43	0
2	NAP	D	304	48/48	0.98	0.14	26,32,36,38	0
2	NAP	A	301	48/48	0.98	0.12	21,26,33,34	0
2	NAP	C	303	48/48	0.98	0.13	22,29,36,38	0
2	NAP	B	302	48/48	0.98	0.13	19,28,33,34	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.

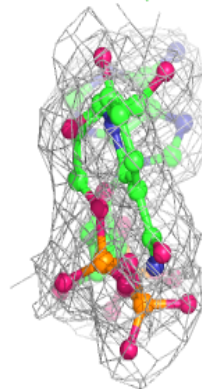
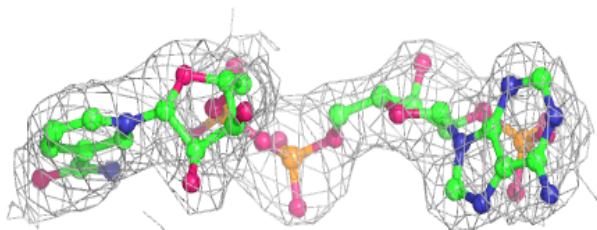
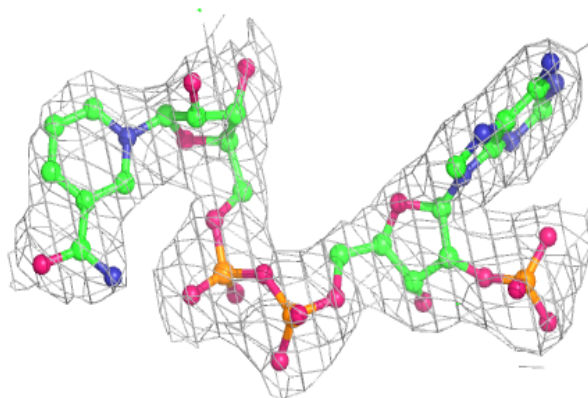


Electron density around NAP E 305:

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

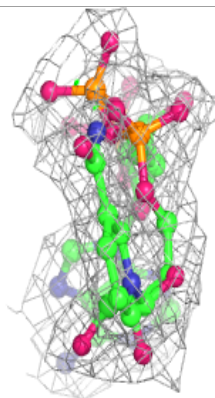
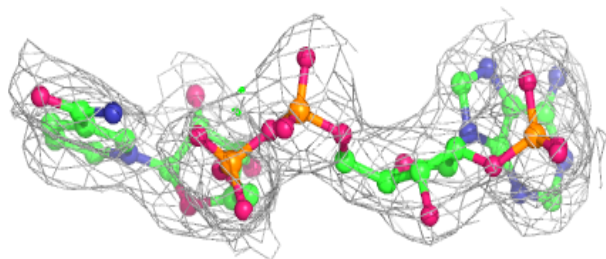
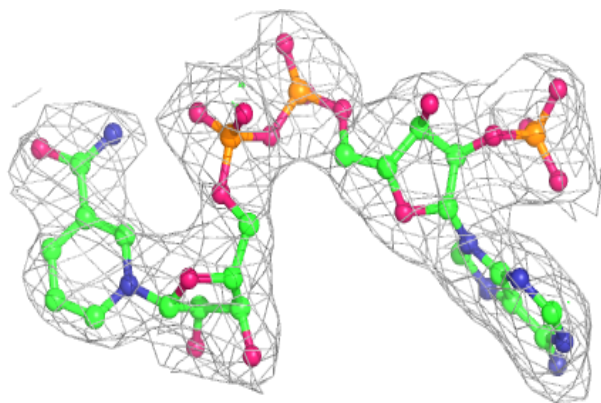
**Electron density around NAP D 304:**

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

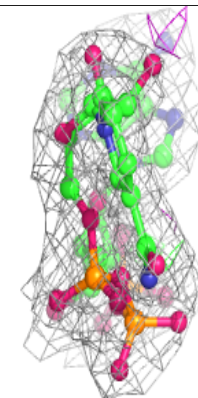
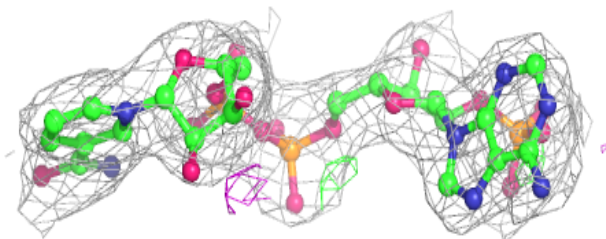
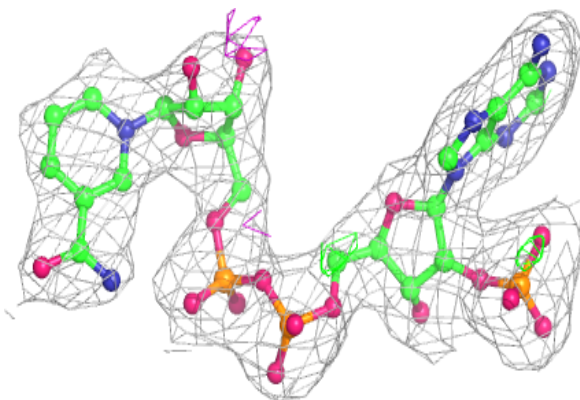


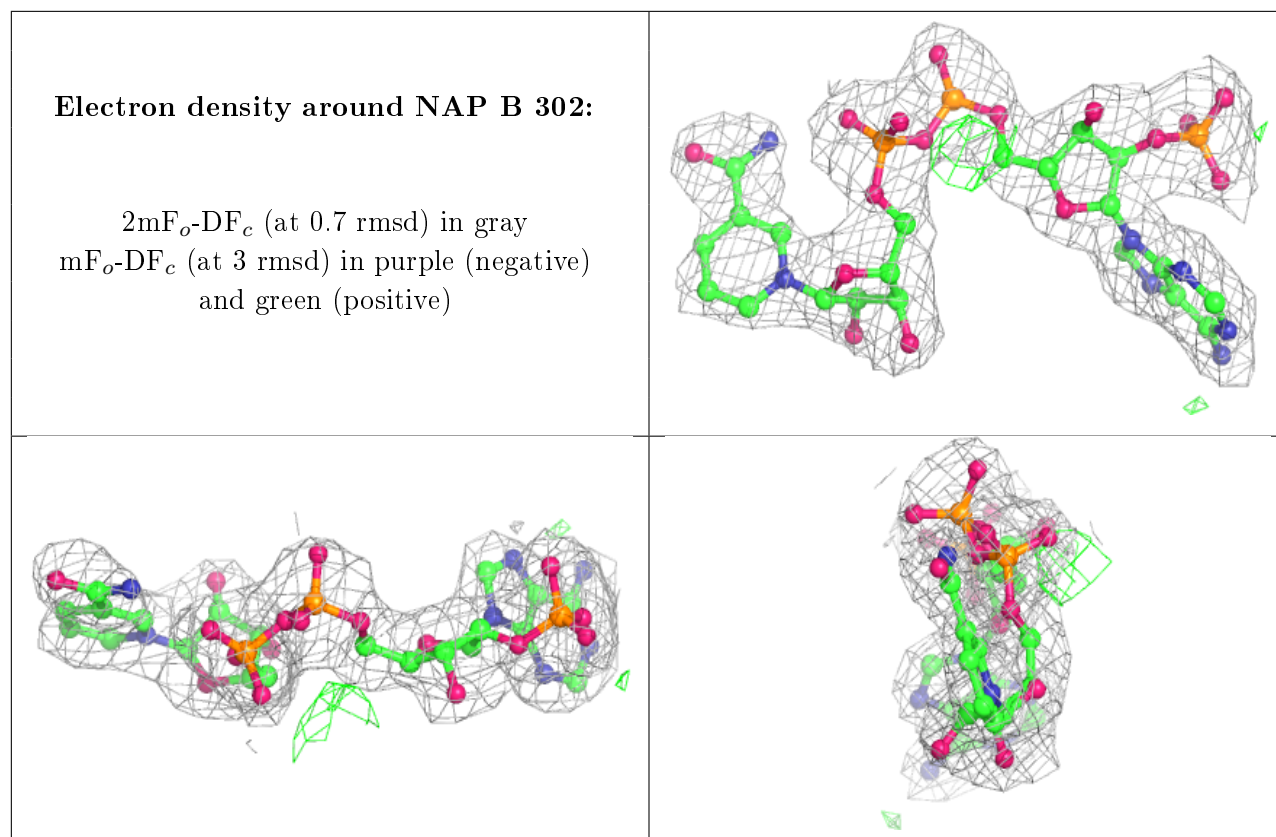
Electron density around NAP A 301:

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

**Electron density around NAP C 303:**

$2mF_o-DF_c$ (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.