



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 08:24 AM BST

PDB ID : 6XT2
Title : EQADH-NADH-HEPTAFLUOROBUTANOL, P21
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Deposited on : 2020-07-16
Resolution : 1.55 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 : 2.13.1
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) : 2.13.1

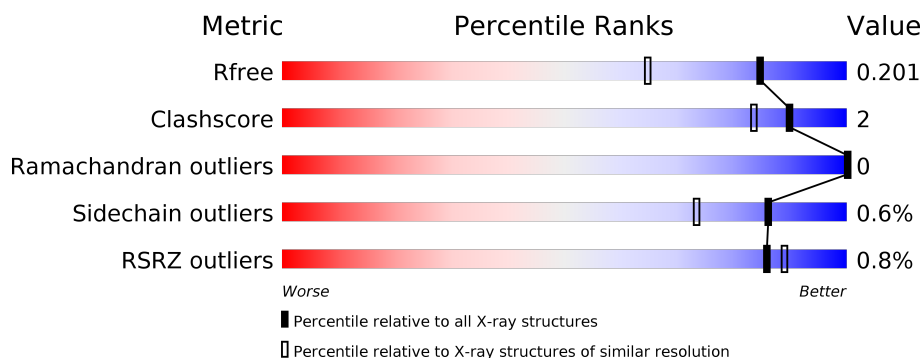
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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	374	<div> <div></div> <div>97%</div> <div></div> </div>
1	B	374	<div> <div>2%</div> <div></div> <div>96%</div> <div></div> </div>
1	C	374	<div> <div></div> <div>96%</div> <div></div> </div>
1	D	374	<div> <div>%</div> <div></div> <div>95%</div> <div>5%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12890 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.

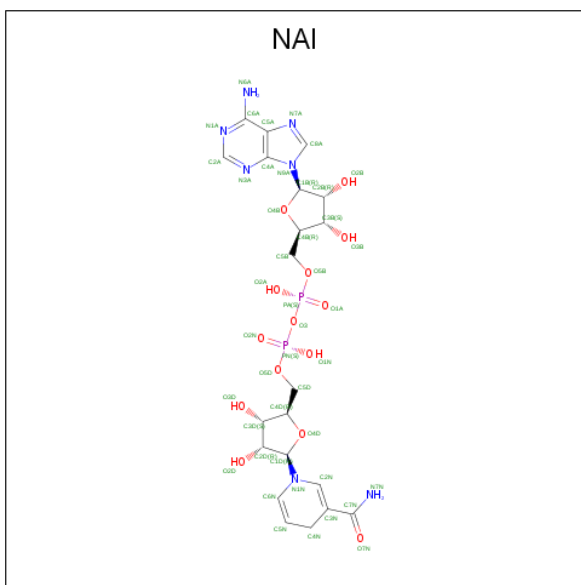
- Molecule 1 is a protein called Alcohol dehydrogenase E chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	0	11	0
			2826	1797	476	528	25			
1	B	374	Total	C	N	O	S	0	19	0
			2855	1813	482	536	24			
1	C	374	Total	C	N	O	S	0	11	0
			2833	1801	479	530	23			
1	D	374	Total	C	N	O	S	0	14	0
			2842	1805	479	533	25			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

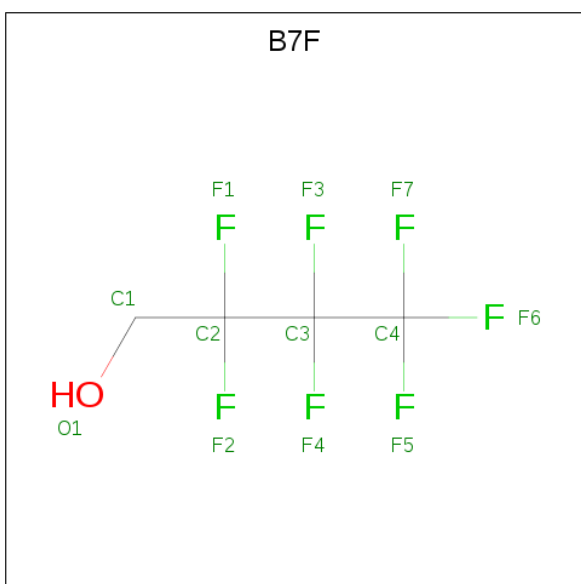
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		

- Molecule 3 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: C₂₁H₂₉N₇O₁₄P₂) (labeled as "Ligand of Interest" by author).



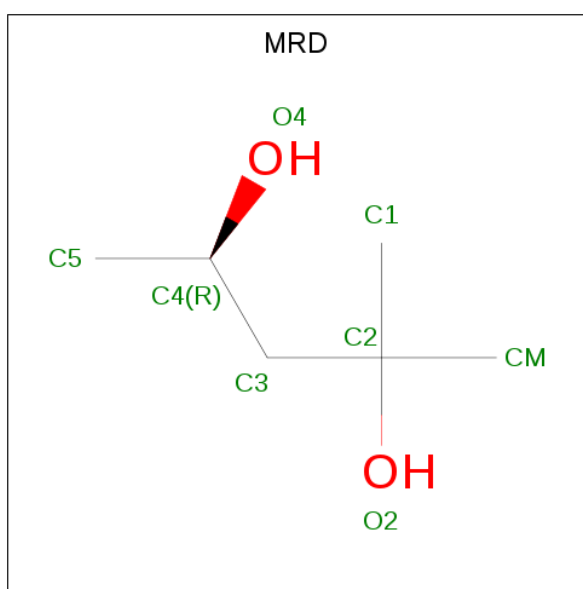
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
3	B	1	Total 44	C 21	N 7	O 14	P 2	0	0
3	C	1	Total 44	C 21	N 7	O 14	P 2	0	0
3	D	1	Total 44	C 21	N 7	O 14	P 2	0	0

- Molecule 4 is 2,2,3,3,4,4,4-heptafluorobutan-1-ol (three-letter code: B7F) (formula: $\text{C}_4\text{H}_3\text{F}_7\text{O}$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	F	O	0	1
			24	8	14	2		
4	B	1	Total	C	F	O	0	1
			24	8	14	2		
4	C	1	Total	C	F	O	0	1
			24	8	14	2		
4	D	1	Total	C	F	O	0	1
			24	8	14	2		

- Molecule 5 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			8	6	2		
5	C	1	Total	C	O	0	1
			8	6	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	278	Total	O	0	8
			285	285		
6	B	298	Total	O	0	7
			300	300		
6	C	326	Total	O	0	10
			328	328		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	317	Total	O	0	14
			325	325		

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: Alcohol dehydrogenase E chain

Chain A:  97%



- Molecule 1: Alcohol dehydrogenase E chain

Chain B:  96%



- Molecule 1: Alcohol dehydrogenase E chain

Chain C:  96%



- Molecule 1: Alcohol dehydrogenase E chain

Chain D:  95% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.15Å 180.27Å 86.90Å 90.00° 105.83° 90.00°	Depositor
Resolution (Å)	19.84 – 1.55 19.84 – 1.55	Depositor EDS
% Data completeness (in resolution range)	88.3 (19.84-1.55) 88.3 (19.84-1.55)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.99 (at 1.55Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.138 , 0.192 0.148 , 0.201	Depositor DCC
R_{free} test set	1769 reflections (0.94%)	wwPDB-VP
Wilson B-factor (Å ²)	17.2	Xtriage
Anisotropy	0.682	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	12890	wwPDB-VP
Average B, all atoms (Å ²)	22.0	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 67.99 % 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 4.7056e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MRD, ZN, NAI, B7F

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	0.86	1/2923 (0.0%)	0.93	2/3946 (0.1%)
1	B	0.89	3/2986 (0.1%)	0.89	0/4029
1	C	0.87	0/2931	0.92	2/3957 (0.1%)
1	D	0.88	2/2944 (0.1%)	0.93	2/3976 (0.1%)
All	All	0.87	6/11784 (0.1%)	0.92	6/15908 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	239	GLU	CD-OE2	8.91	1.35	1.25
1	B	167	GLU	CD-OE2	7.11	1.33	1.25
1	D	25	GLU	CD-OE1	-6.29	1.18	1.25
1	D	265	SER	CA-CB	-5.57	1.44	1.52
1	A	167	GLU	CD-OE1	5.54	1.31	1.25
1	B	239	GLU	CD-OE1	-5.05	1.20	1.25

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	40	MET	CG-SD-CE	6.55	110.68	100.20
1	D	218	ARG	NE-CZ-NH1	-5.68	117.46	120.30
1	D	40	MET	CG-SD-CE	5.53	109.05	100.20
1	C	174	CYS	CA-CB-SG	-5.31	104.45	114.00
1	A	133	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	C	37	ARG	NE-CZ-NH2	-5.11	117.74	120.30

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	2826	0	2897	6	0
1	B	2855	0	2909	11	0
1	C	2833	0	2903	8	0
1	D	2842	0	2905	10	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	44	0	27	2	0
3	B	44	0	27	2	0
3	C	44	0	27	3	0
3	D	44	0	27	2	0
4	A	24	0	0	3	0
4	B	24	0	0	2	0
4	C	24	0	0	4	0
4	D	24	0	0	3	0
5	B	8	0	14	3	0
5	C	8	0	14	2	0
6	A	285	0	0	0	0
6	B	300	0	0	0	0
6	C	328	0	0	0	0
6	D	325	0	0	1	0
All	All	12890	0	11750	42	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 2.

All (42) 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:116:LEU:HD23	4:A:404[B]:B7F:F5	1.83	0.69
1:B:100:CYS:HB2	1:B:112:LEU:HD12	1.78	0.66
5:C:405[A]:MRD:H5C3	5:C:405[A]:MRD:HMC2	1.77	0.65
1:C:116:LEU:HD23	4:C:404[B]:B7F:F5	1.88	0.64
1:A:178:THR:HG21	3:A:403:NAI:H4N	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:403:NAI:H42N	4:D:404[A]:B7F:C1	2.28	0.63
5:C:405[A]:MRD:H5C2	5:C:405[A]:MRD:H1C1	1.80	0.61
1:C:178:THR:HG21	3:C:403:NAI:H4N	1.83	0.59
3:B:403:NAI:H42N	4:B:404[B]:B7F:C1	2.35	0.57
5:B:405:MRD:C1	5:B:405:MRD:O4	2.56	0.54
3:A:403:NAI:H42N	4:A:404[A]:B7F:C1	2.38	0.53
1:B:239:GLU:CG	5:B:405:MRD:HMC1	2.38	0.53
1:B:178:THR:HG21	3:B:403:NAI:H4N	1.91	0.53
1:B:238:THR:C	1:B:239:GLU:HG3	2.29	0.52
1:D:251:GLN:HA	1:D:281[B]:CYS:SG	2.48	0.52
3:C:403:NAI:H42N	4:C:404[B]:B7F:C1	2.40	0.52
1:B:239:GLU:HG2	5:B:405:MRD:HMC1	1.93	0.49
4:D:404[B]:B7F:F1	4:D:404[B]:B7F:F5	2.08	0.49
1:B:116:LEU:HD23	4:B:404[B]:B7F:F7	2.04	0.48
1:B:253:VAL:O	1:B:257:MET:HG3	2.13	0.48
1:B:238:THR:O	1:B:239:GLU:HG3	2.13	0.48
1:D:16:GLU:HG3	1:D:19:LYS:HG3	1.95	0.48
1:D:48:SER:OG	4:D:404[B]:B7F:F2	2.21	0.47
3:C:403:NAI:H42N	4:C:404[A]:B7F:C1	2.45	0.47
1:C:88:LYS:HD3	1:C:166:LEU:HD21	1.96	0.47
1:D:70:ALA:HB1	1:D:166:LEU:HD22	1.98	0.46
1:B:364:SER:OG	1:B:366[B]:GLU:HG3	2.15	0.46
1:A:116:LEU:CD2	4:A:404[B]:B7F:F5	2.54	0.45
1:D:178:THR:HG21	3:D:403:NAI:H4N	1.98	0.45
1:A:286:TYR:OH	1:B:101:ARG:NH2	2.50	0.45
1:A:88:LYS:HD3	1:A:166:LEU:HD21	1.97	0.45
1:D:120:ARG:HB2	6:D:582:HOH:O	2.16	0.45
1:C:220:ILE:HG12	1:C:239:GLU:HG3	1.98	0.43
1:C:350:LEU:O	1:C:372:LEU:HA	2.18	0.43
1:A:230:ALA:O	1:A:234:GLU:HG3	2.18	0.43
1:D:282[B]:CYS:HB3	1:D:287:GLY:HA3	2.00	0.43
1:D:195:CYS:HA	1:D:264:PHE:O	2.19	0.42
1:B:301:LEU:C	1:B:301:LEU:HD12	2.41	0.41
1:D:38:ILE:HG22	1:D:40:MET:HE2	2.02	0.41
1:C:295:PRO:HG3	1:D:305:PRO:HG2	2.03	0.41
1:C:100:CYS:HB2	1:C:112:LEU:HD12	2.03	0.40
1:C:48:SER:OG	4:C:404[B]:B7F:O1	2.35	0.40

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	383/374 (102%)	372 (97%)	11 (3%)	0	100	100
1	B	391/374 (104%)	375 (96%)	16 (4%)	0	100	100
1	C	383/374 (102%)	370 (97%)	13 (3%)	0	100	100
1	D	386/374 (103%)	375 (97%)	11 (3%)	0	100	100
All	All	1543/1496 (103%)	1492 (97%)	51 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	318/308 (103%)	315 (99%)	3 (1%)	78	61
1	B	325/308 (106%)	323 (99%)	2 (1%)	86	73
1	C	319/308 (104%)	317 (99%)	2 (1%)	86	73
1	D	321/308 (104%)	320 (100%)	1 (0%)	92	85
All	All	1283/1232 (104%)	1275 (99%)	8 (1%)	86	73

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	SER
1	A	78	GLU

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Mol	Chain	Res	Type
1	A	164	SER
1	B	118	MET
1	B	256	GLU
1	C	1	SER
1	C	239	GLU
1	D	338	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 22 ligands modelled in this entry, 8 are monoatomic - leaving 14 for Mogul analysis.

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	NAI	D	403	-	42,48,48	1.73	5 (11%)	47,73,73	1.70	7 (14%)
3	NAI	B	403	-	42,48,48	1.80	7 (16%)	47,73,73	1.63	11 (23%)
4	B7F	A	404[B]	2	10,11,11	0.56	0	17,19,19	3.96	3 (17%)
3	NAI	C	403	-	42,48,48	1.89	8 (19%)	47,73,73	1.86	10 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	MRD	C	405[A]	-	7,7,7	0.44	0	9,10,10	1.20	1 (11%)
3	NAI	A	403	-	42,48,48	1.64	7 (16%)	47,73,73	1.56	7 (14%)
4	B7F	D	404[A]	2	10,11,11	0.87	1 (10%)	17,19,19	3.29	4 (23%)
4	B7F	B	404[B]	2	10,11,11	0.62	0	17,19,19	1.89	3 (17%)
5	MRD	B	405	-	7,7,7	0.65	0	9,10,10	0.52	0
4	B7F	D	404[B]	2	10,11,11	0.87	0	17,19,19	1.58	2 (11%)
4	B7F	C	404[B]	2	10,11,11	0.81	0	17,19,19	3.35	4 (23%)
4	B7F	C	404[A]	2	10,11,11	0.71	0	17,19,19	1.32	3 (17%)
4	B7F	A	404[A]	2	10,11,11	0.70	0	17,19,19	1.93	4 (23%)
4	B7F	B	404[A]	2	10,11,11	0.77	0	17,19,19	1.97	6 (35%)

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
3	NAI	D	403	-	-	3/25/72/72	0/5/5/5
3	NAI	B	403	-	-	4/25/72/72	0/5/5/5
4	B7F	A	404[B]	2	-	2/21/21/21	-
3	NAI	C	403	-	-	3/25/72/72	0/5/5/5
5	MRD	C	405[A]	-	-	2/5/5/5	-
3	NAI	A	403	-	-	4/25/72/72	0/5/5/5
4	B7F	D	404[A]	2	-	5/21/21/21	-
4	B7F	B	404[B]	2	-	12/21/21/21	-
5	MRD	B	405	-	-	0/5/5/5	-
4	B7F	D	404[B]	2	-	11/21/21/21	-
4	B7F	C	404[B]	2	-	12/21/21/21	-
4	B7F	C	404[A]	2	-	3/21/21/21	-
4	B7F	A	404[A]	2	-	3/21/21/21	-
4	B7F	B	404[A]	2	-	3/21/21/21	-

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	403	NAI	C2A-N3A	6.65	1.42	1.32
3	C	403	NAI	C2A-N3A	6.42	1.42	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	403	NAI	C2A-N3A	5.79	1.41	1.32
3	B	403	NAI	C4A-N3A	-5.71	1.27	1.35
3	D	403	NAI	C6N-N1N	5.50	1.51	1.37
3	A	403	NAI	C2A-N3A	5.01	1.40	1.32
3	A	403	NAI	C4A-N3A	4.73	1.42	1.35
3	C	403	NAI	C2A-N1A	4.64	1.42	1.33
3	C	403	NAI	C4N-C3N	-4.11	1.41	1.49
3	C	403	NAI	C6N-N1N	3.94	1.47	1.37
3	A	403	NAI	C4N-C5N	-3.87	1.38	1.48
3	C	403	NAI	C4N-C5N	-3.47	1.39	1.48
3	D	403	NAI	O4B-C1B	3.44	1.45	1.41
3	D	403	NAI	C5A-C4A	-3.36	1.32	1.40
3	B	403	NAI	C4N-C5N	-3.27	1.40	1.48
3	D	403	NAI	C8A-N7A	-3.17	1.29	1.34
3	B	403	NAI	C7N-C3N	-2.93	1.42	1.48
3	A	403	NAI	C5A-C4A	-2.87	1.33	1.40
3	B	403	NAI	C6N-N1N	2.81	1.44	1.37
3	C	403	NAI	C6A-N1A	-2.70	1.25	1.37
3	A	403	NAI	C6N-N1N	2.65	1.43	1.37
3	B	403	NAI	C8A-N7A	-2.33	1.30	1.34
3	A	403	NAI	C2A-N1A	2.33	1.38	1.33
3	A	403	NAI	C6A-N1A	-2.30	1.27	1.37
3	C	403	NAI	C4A-N3A	-2.27	1.32	1.35
3	C	403	NAI	C6N-C5N	-2.17	1.29	1.33
3	B	403	NAI	C4N-C3N	2.15	1.54	1.49
4	D	404[A]	B7F	O1-C1	2.07	1.49	1.42

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	404[B]	B7F	F1-C2-C1	-14.64	97.27	110.01
4	C	404[B]	B7F	F1-C2-C1	-12.44	99.19	110.01
4	D	404[A]	B7F	F2-C2-C1	12.24	120.65	110.01
3	C	403	NAI	N3A-C2A-N1A	-7.85	116.41	128.68
3	D	403	NAI	N3A-C2A-N1A	-7.21	117.41	128.68
4	B	404[B]	B7F	F2-C2-C1	-5.81	104.95	110.01
3	A	403	NAI	N3A-C2A-N1A	-5.06	120.78	128.68
3	B	403	NAI	N3A-C2A-N1A	-5.02	120.83	128.68
4	B	404[A]	B7F	F1-C2-C1	-4.99	105.66	110.01
4	A	404[A]	B7F	F2-C2-C1	4.42	113.85	110.01
4	A	404[B]	B7F	F2-C2-F1	4.18	117.16	105.94
4	D	404[B]	B7F	F1-C2-C1	-4.10	106.44	110.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	403	NAI	O7N-C7N-N7N	-3.99	113.55	122.88
4	A	404[B]	B7F	F2-C2-C1	-3.97	106.56	110.01
4	A	404[A]	B7F	F5-C4-F7	3.84	119.27	107.53
4	B	404[A]	B7F	F5-C4-C3	-3.59	93.74	110.34
3	D	403	NAI	O4D-C4D-C3D	3.53	112.09	105.11
3	A	403	NAI	C1B-N9A-C4A	-3.46	120.57	126.64
3	A	403	NAI	O4B-C1B-C2B	-3.44	101.90	106.93
3	B	403	NAI	C3N-C7N-N7N	3.38	123.66	117.67
3	A	403	NAI	C2A-N1A-C6A	3.31	124.41	118.75
4	C	404[B]	B7F	F4-C3-C2	3.22	115.86	107.73
4	C	404[B]	B7F	F2-C2-C1	3.21	112.80	110.01
3	A	403	NAI	C3N-C2N-N1N	3.16	127.61	123.10
3	C	403	NAI	C2A-N1A-C6A	3.14	124.12	118.75
3	D	403	NAI	C2D-C3D-C4D	-3.07	96.68	102.64
3	B	403	NAI	O2A-PA-O1A	3.06	127.34	112.24
3	A	403	NAI	O2A-PA-O1A	3.02	127.19	112.24
4	A	404[A]	B7F	C4-C3-C2	-2.91	105.82	117.60
3	D	403	NAI	C2A-N1A-C6A	2.87	123.67	118.75
3	B	403	NAI	C1B-N9A-C4A	-2.85	121.64	126.64
4	B	404[B]	B7F	F2-C2-F1	2.76	113.35	105.94
4	A	404[A]	B7F	F1-C2-C1	2.75	112.40	110.01
4	D	404[B]	B7F	F3-C3-C2	2.73	114.63	107.73
3	B	403	NAI	C2D-C1D-N1N	2.61	119.85	113.30
3	B	403	NAI	C2A-N1A-C6A	2.58	123.17	118.75
3	D	403	NAI	O2A-PA-O1A	2.51	124.64	112.24
4	B	404[A]	B7F	F6-C4-F7	2.48	115.10	107.53
3	C	403	NAI	C3N-C2N-N1N	-2.46	119.59	123.10
3	A	403	NAI	C2D-C1D-N1N	2.46	119.46	113.30
3	C	403	NAI	C2D-C1D-N1N	2.43	119.39	113.30
4	B	404[A]	B7F	F2-C2-C1	2.43	112.12	110.01
3	B	403	NAI	C3B-C2B-C1B	2.42	104.63	100.98
3	C	403	NAI	C1B-N9A-C4A	-2.42	122.39	126.64
3	B	403	NAI	O7N-C7N-N7N	-2.41	117.24	122.88
3	C	403	NAI	O7N-C7N-C3N	2.33	125.28	120.90
3	C	403	NAI	C1D-N1N-C6N	-2.31	115.85	120.83
3	B	403	NAI	O4B-C1B-C2B	-2.29	103.58	106.93
3	D	403	NAI	C5A-C6A-N6A	2.26	123.79	120.35
5	C	405[A]	MRD	C5-C4-C3	2.26	122.32	111.69
4	C	404[A]	B7F	F4-C3-C4	2.25	116.44	106.63
4	D	404[A]	B7F	F4-C3-C4	2.25	116.39	106.63
3	C	403	NAI	O2A-PA-O1A	2.24	123.32	112.24
3	B	403	NAI	O4D-C4D-C5D	2.21	116.65	109.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	404[B]	B7F	F6-C4-F7	2.21	114.27	107.53
4	C	404[A]	B7F	F1-C2-C1	2.20	111.92	110.01
4	B	404[A]	B7F	F6-C4-F5	2.17	114.17	107.53
4	C	404[A]	B7F	F3-C3-C2	-2.15	102.30	107.73
4	B	404[B]	B7F	F4-C3-C2	2.11	113.07	107.73
4	D	404[A]	B7F	F4-C3-C2	-2.11	102.42	107.73
4	D	404[A]	B7F	F1-C2-C1	2.10	111.83	110.01
3	B	403	NAI	O4D-C1D-N1N	-2.06	104.03	108.06
3	C	403	NAI	O2B-C2B-C3B	2.04	118.44	111.82
3	D	403	NAI	O1N-PN-O2N	2.04	122.32	112.24
4	B	404[A]	B7F	F1-C2-C3	2.01	113.77	107.21

There are no chirality outliers.

All (67) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	405[A]	MRD	C2-C3-C4-C5
4	C	404[B]	B7F	F3-C3-C4-F7
4	C	404[B]	B7F	F4-C3-C4-F5
4	B	404[B]	B7F	F4-C3-C4-F7
4	B	404[B]	B7F	F3-C3-C4-F6
4	B	404[B]	B7F	C2-C3-C4-F5
4	B	404[B]	B7F	F3-C3-C4-F7
4	B	404[B]	B7F	F4-C3-C4-F5
4	C	404[B]	B7F	F4-C3-C4-F7
4	C	404[B]	B7F	F3-C3-C4-F5
4	C	404[B]	B7F	F4-C3-C4-F6
4	B	404[B]	B7F	F3-C3-C4-F5
4	B	404[B]	B7F	F4-C3-C4-F6
4	C	404[B]	B7F	F3-C3-C4-F6
4	B	404[B]	B7F	O1-C1-C2-F2
4	C	404[B]	B7F	C2-C3-C4-F5
4	B	404[B]	B7F	C2-C3-C4-F7
4	C	404[B]	B7F	C2-C3-C4-F7
4	B	404[B]	B7F	C2-C3-C4-F6
4	C	404[B]	B7F	C2-C3-C4-F6
4	B	404[B]	B7F	O1-C1-C2-F1
4	B	404[A]	B7F	O1-C1-C2-F1
4	B	404[A]	B7F	O1-C1-C2-F2
4	D	404[B]	B7F	F1-C2-C3-F3
4	D	404[B]	B7F	F1-C2-C3-C4
4	D	404[B]	B7F	F2-C2-C3-C4

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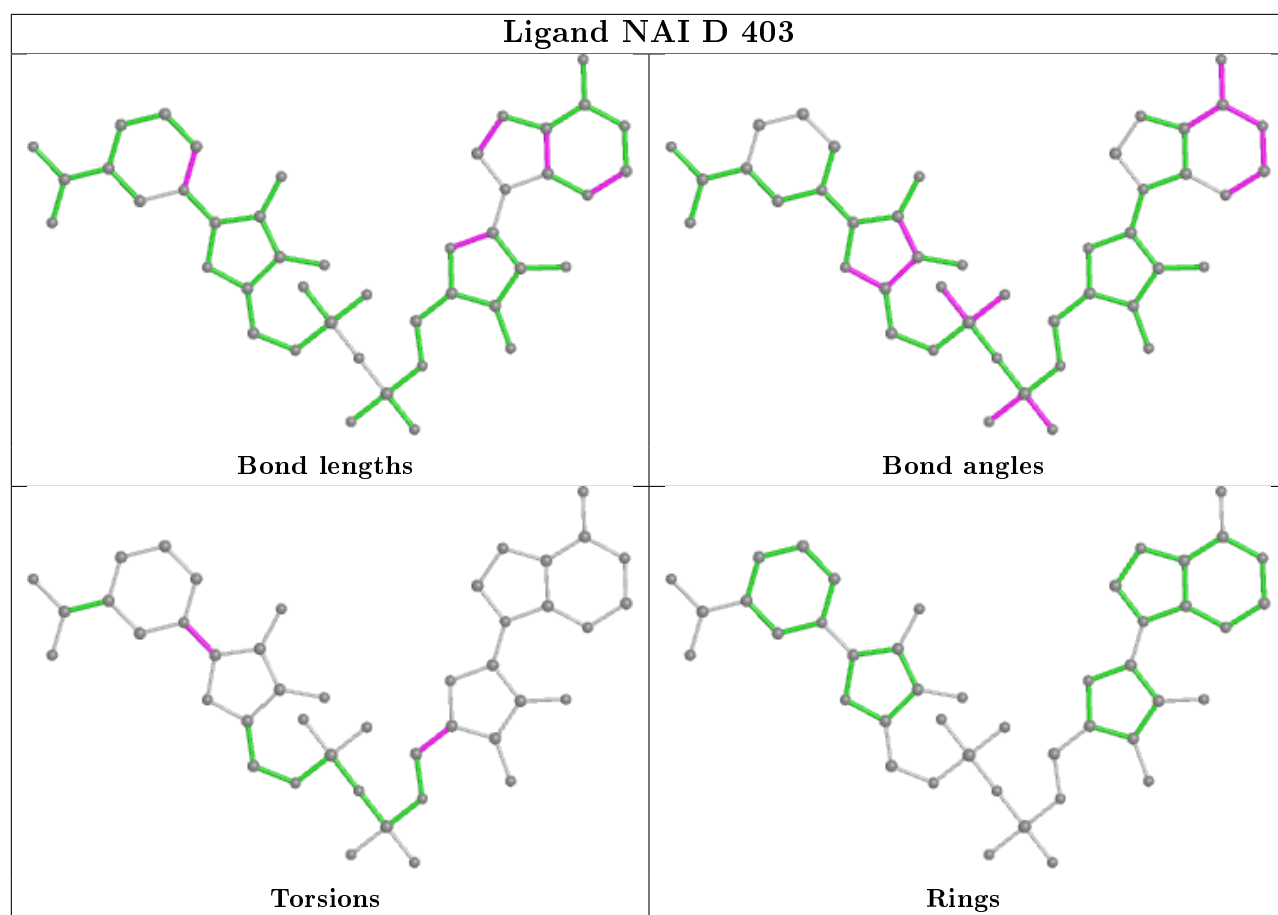
Mol	Chain	Res	Type	Atoms
4	C	404[A]	B7F	O1-C1-C2-F2
4	A	404[A]	B7F	O1-C1-C2-F1
4	D	404[B]	B7F	F2-C2-C3-F3
4	D	404[A]	B7F	O1-C1-C2-F1
4	D	404[A]	B7F	O1-C1-C2-F2
4	C	404[B]	B7F	O1-C1-C2-F1
4	C	404[B]	B7F	O1-C1-C2-F2
4	A	404[A]	B7F	O1-C1-C2-F2
4	B	404[B]	B7F	O1-C1-C2-C3
4	D	404[B]	B7F	F2-C2-C3-F4
4	C	404[A]	B7F	O1-C1-C2-F1
4	D	404[B]	B7F	F1-C2-C3-F4
4	D	404[B]	B7F	C1-C2-C3-F3
4	D	404[B]	B7F	O1-C1-C2-C3
4	B	404[A]	B7F	O1-C1-C2-C3
4	D	404[B]	B7F	O1-C1-C2-F2
3	C	403	NAI	O4D-C1D-N1N-C2N
3	A	403	NAI	O4D-C1D-N1N-C2N
4	D	404[A]	B7F	O1-C1-C2-C3
4	C	404[B]	B7F	O1-C1-C2-C3
4	C	404[A]	B7F	O1-C1-C2-C3
4	A	404[A]	B7F	O1-C1-C2-C3
3	B	403	NAI	O4D-C1D-N1N-C2N
3	B	403	NAI	C2D-C1D-N1N-C2N
3	A	403	NAI	C2D-C1D-N1N-C2N
4	A	404[B]	B7F	O1-C1-C2-F2
3	D	403	NAI	O4D-C1D-N1N-C2N
3	D	403	NAI	C2D-C1D-N1N-C2N
4	D	404[B]	B7F	C1-C2-C3-C4
4	D	404[B]	B7F	C1-C2-C3-F4
3	C	403	NAI	C2D-C1D-N1N-C2N
4	D	404[A]	B7F	F4-C3-C4-F6
4	A	404[B]	B7F	O1-C1-C2-F1
3	A	403	NAI	O4D-C1D-N1N-C6N
3	B	403	NAI	C2D-C1D-N1N-C6N
3	B	403	NAI	O4B-C4B-C5B-O5B
3	C	403	NAI	O4B-C4B-C5B-O5B
3	D	403	NAI	O4B-C4B-C5B-O5B
3	A	403	NAI	O4B-C4B-C5B-O5B
4	D	404[A]	B7F	F1-C2-C3-F3
5	C	405[A]	MRD	C2-C3-C4-O4

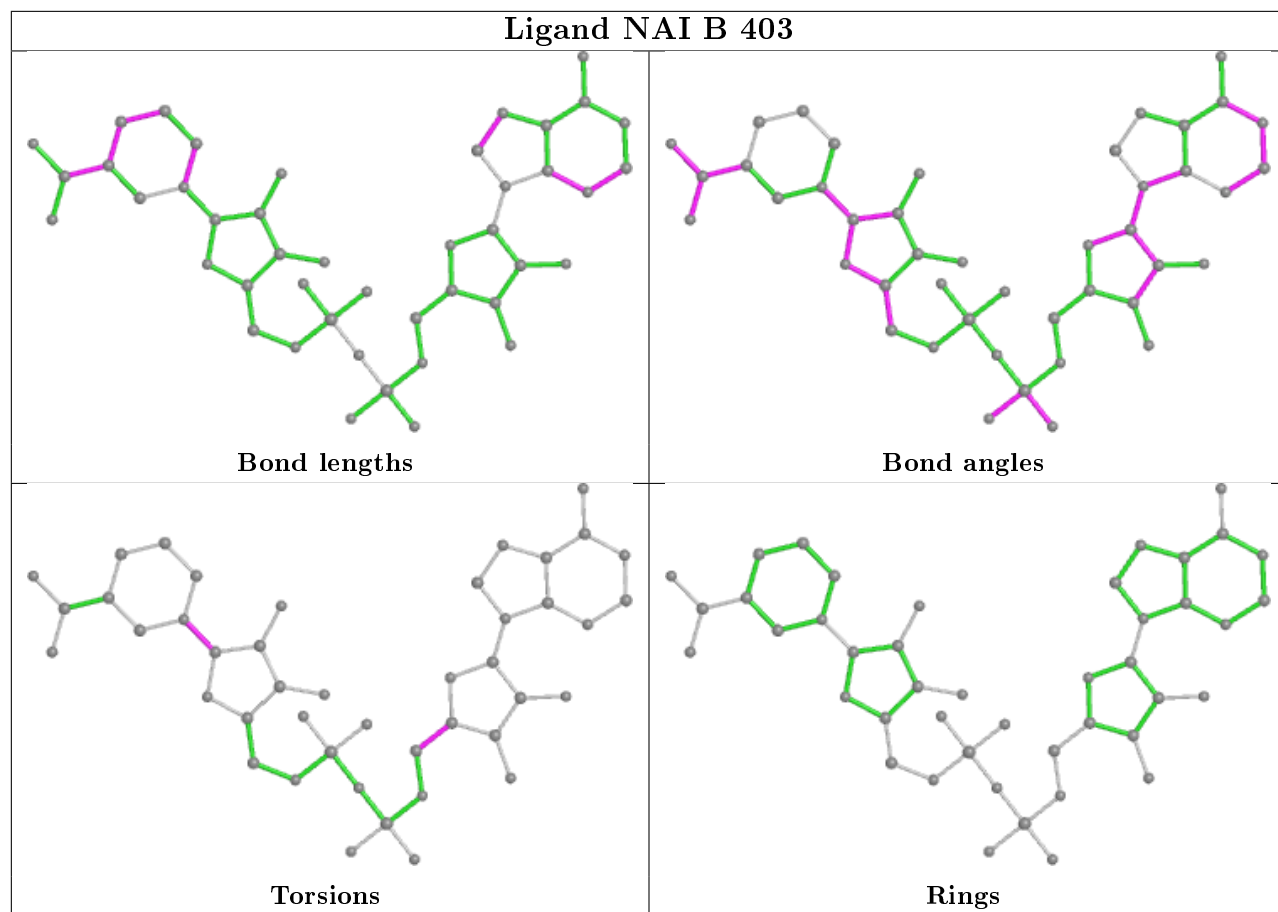
There are no ring outliers.

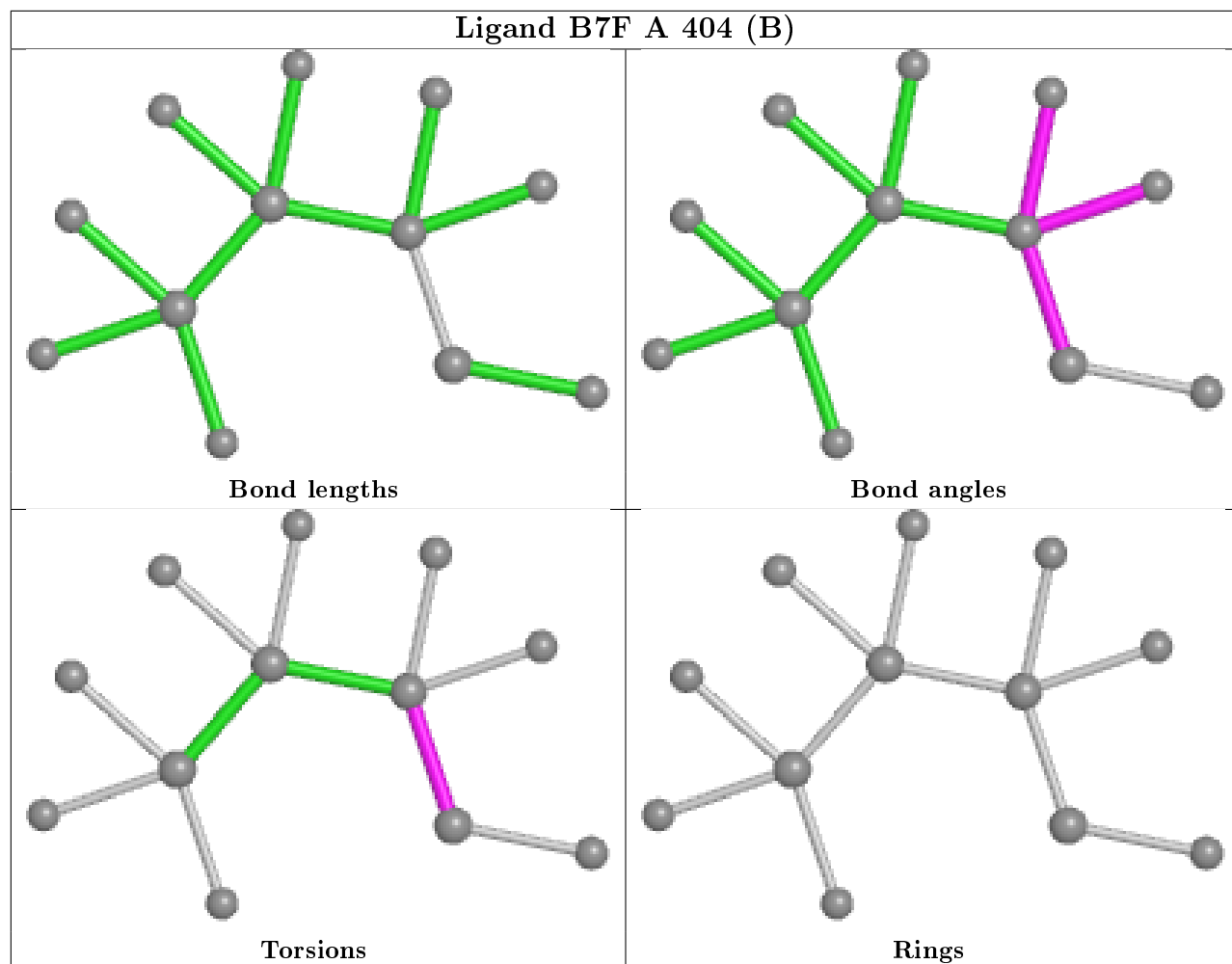
13 monomers are involved in 21 short contacts:

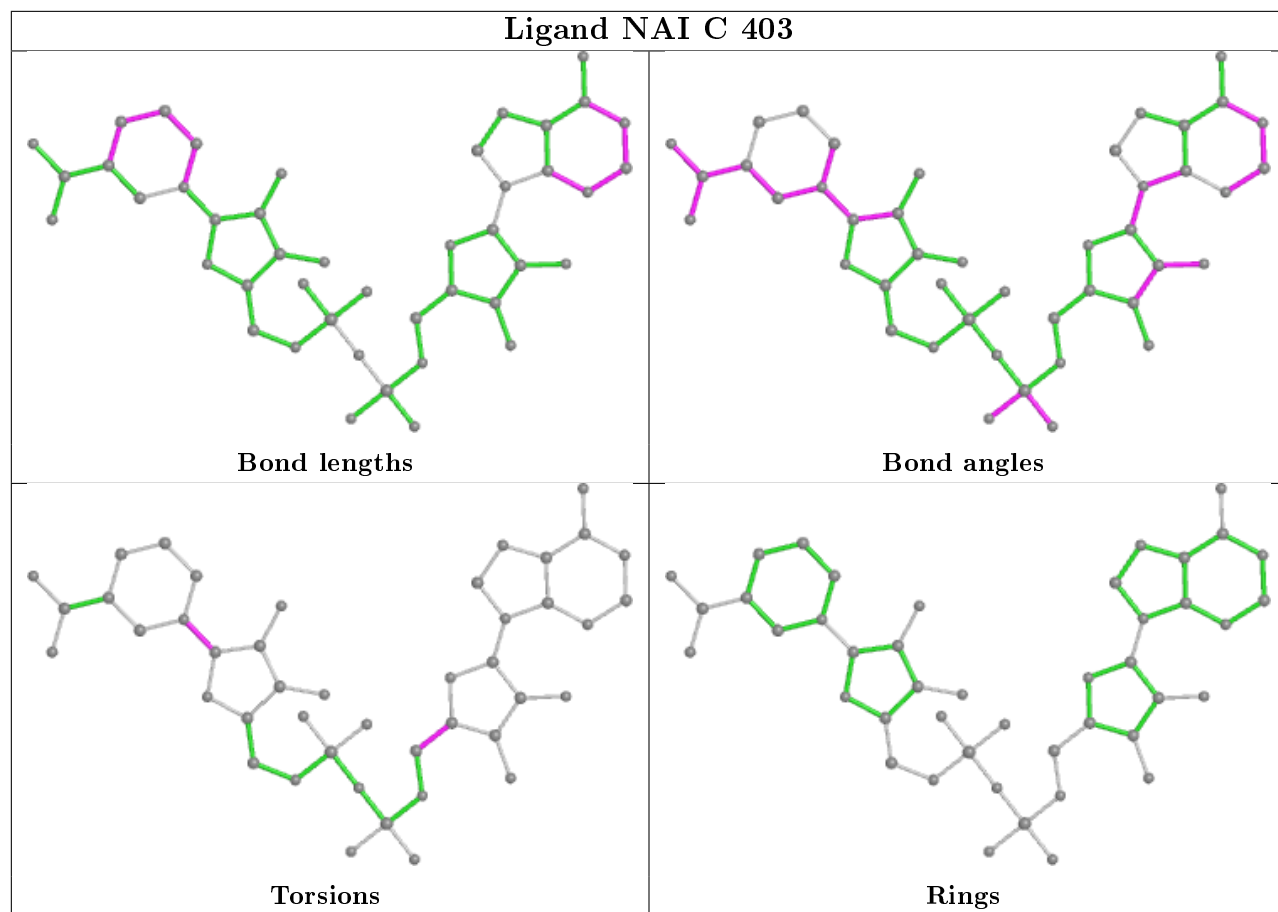
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	403	NAI	2	0
3	B	403	NAI	2	0
4	A	404[B]	B7F	2	0
3	C	403	NAI	3	0
5	C	405[A]	MRD	2	0
3	A	403	NAI	2	0
4	D	404[A]	B7F	1	0
4	B	404[B]	B7F	2	0
5	B	405	MRD	3	0
4	D	404[B]	B7F	2	0
4	C	404[B]	B7F	3	0
4	C	404[A]	B7F	1	0
4	A	404[A]	B7F	1	0

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.

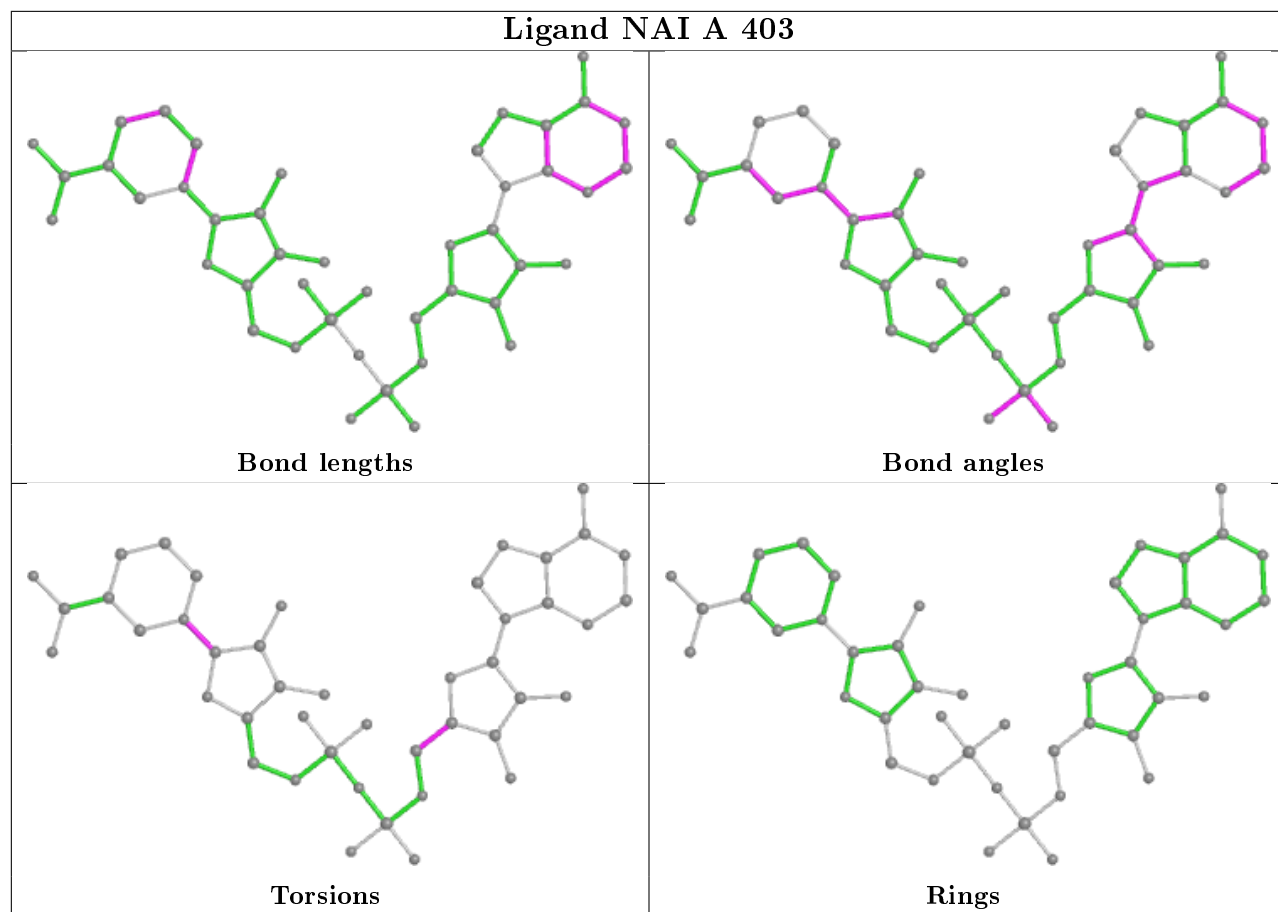


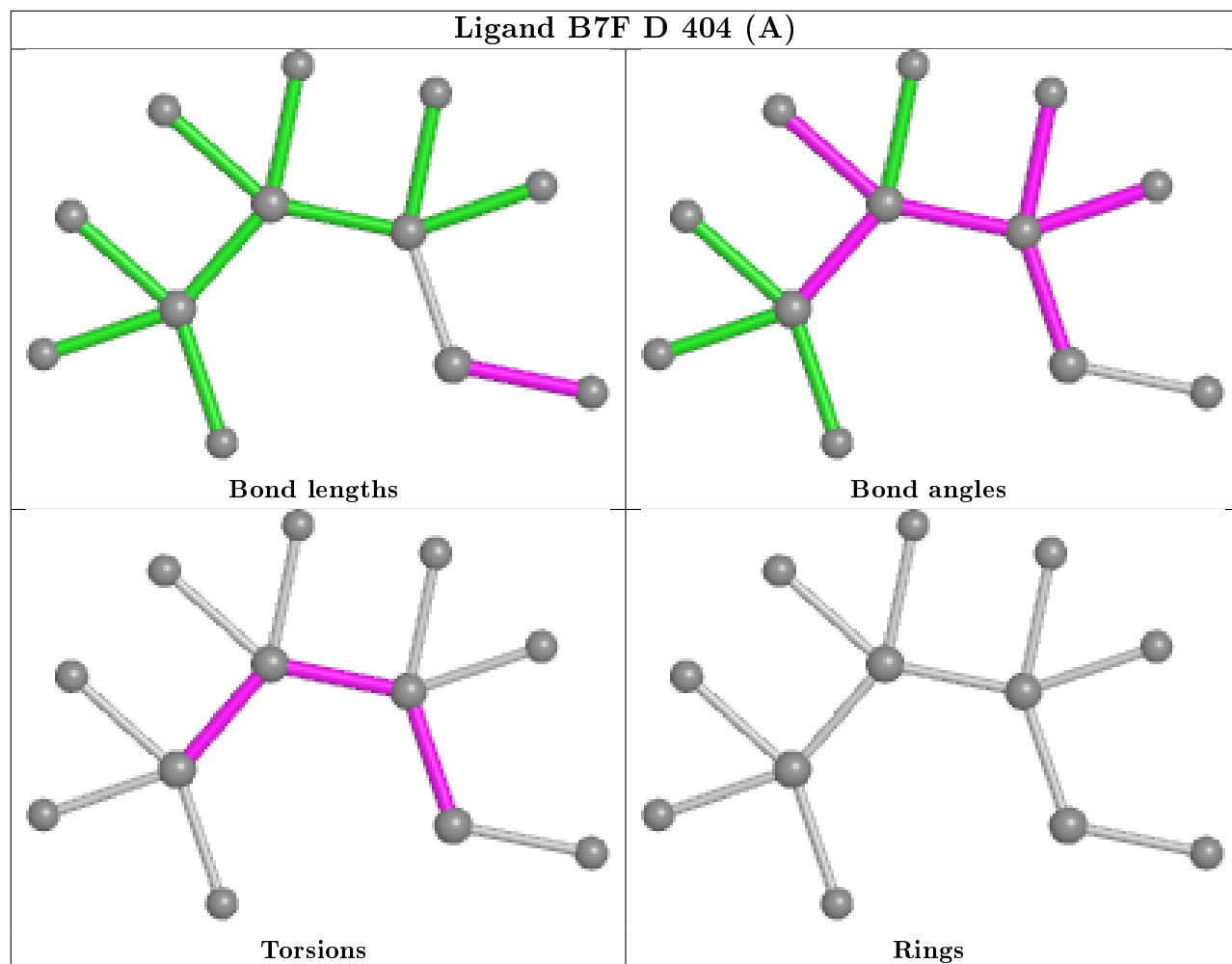


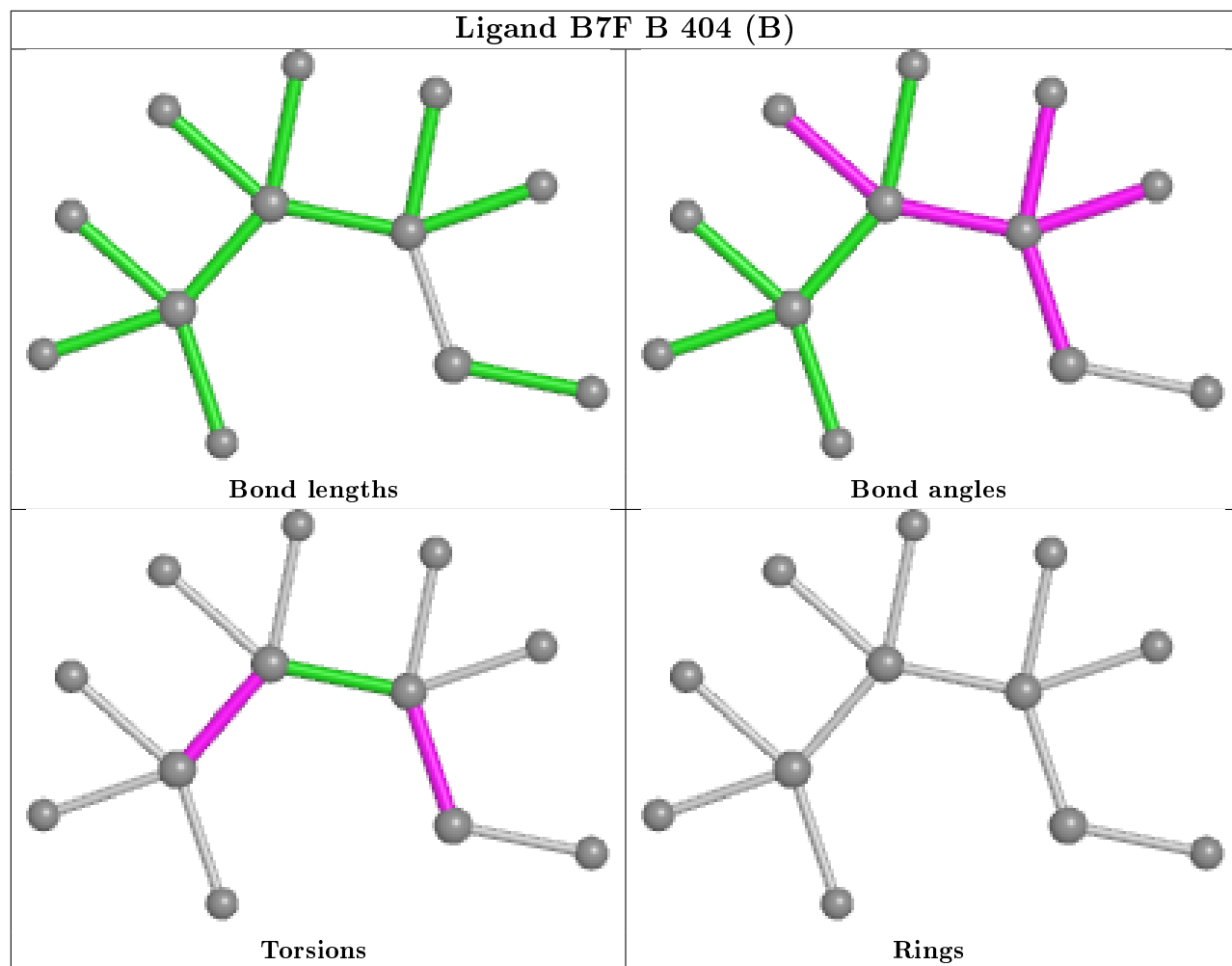


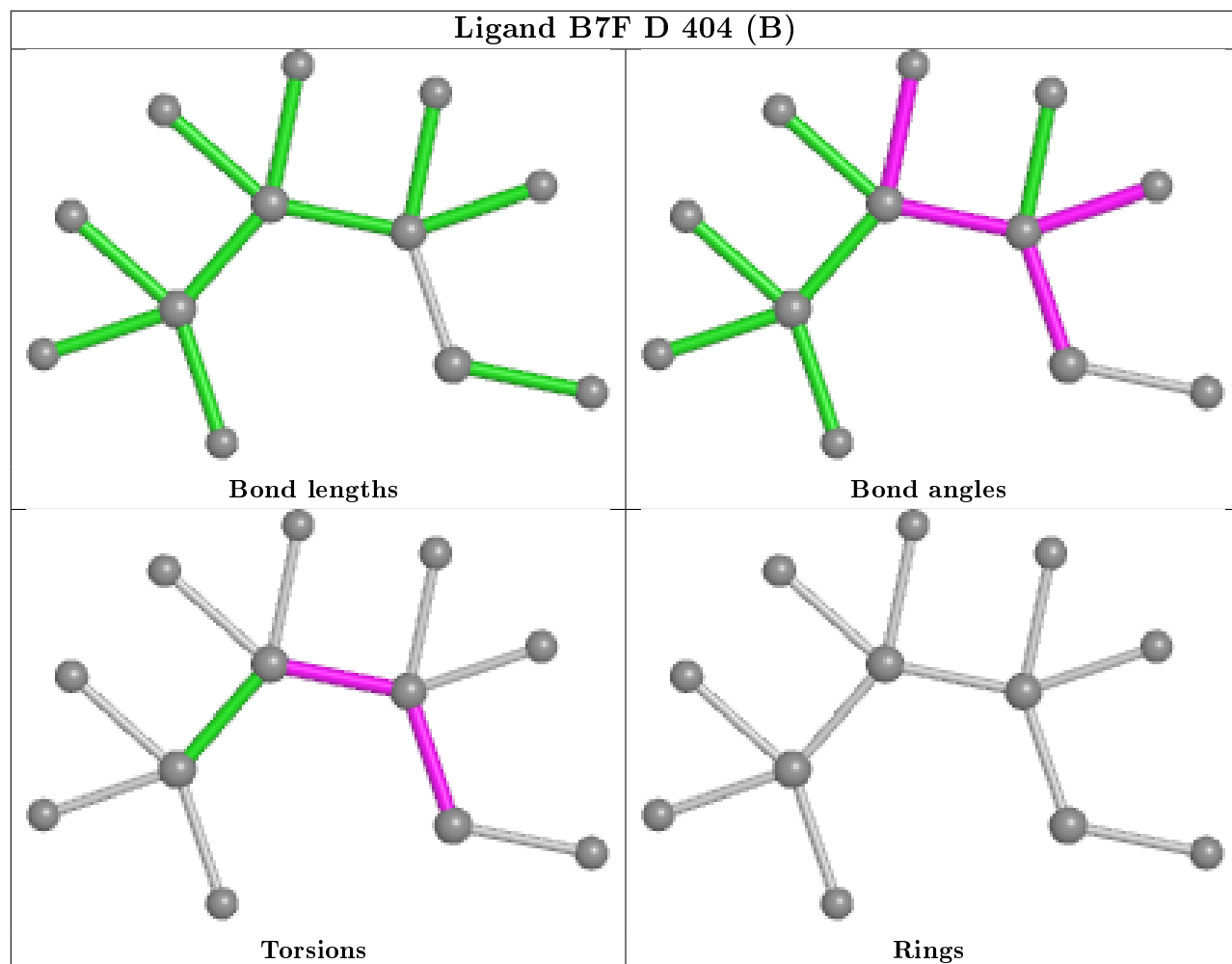


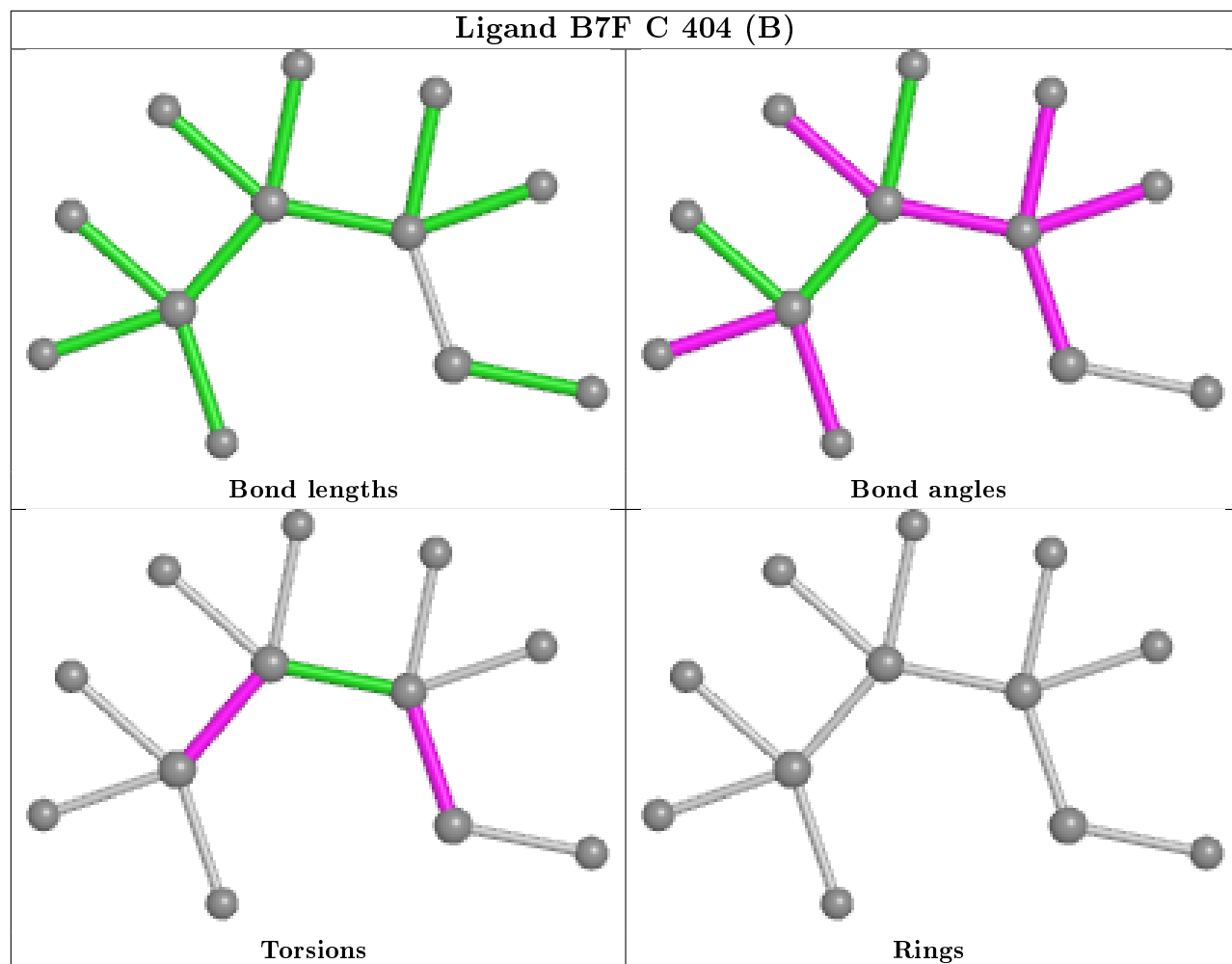
Ligand NAI A 403

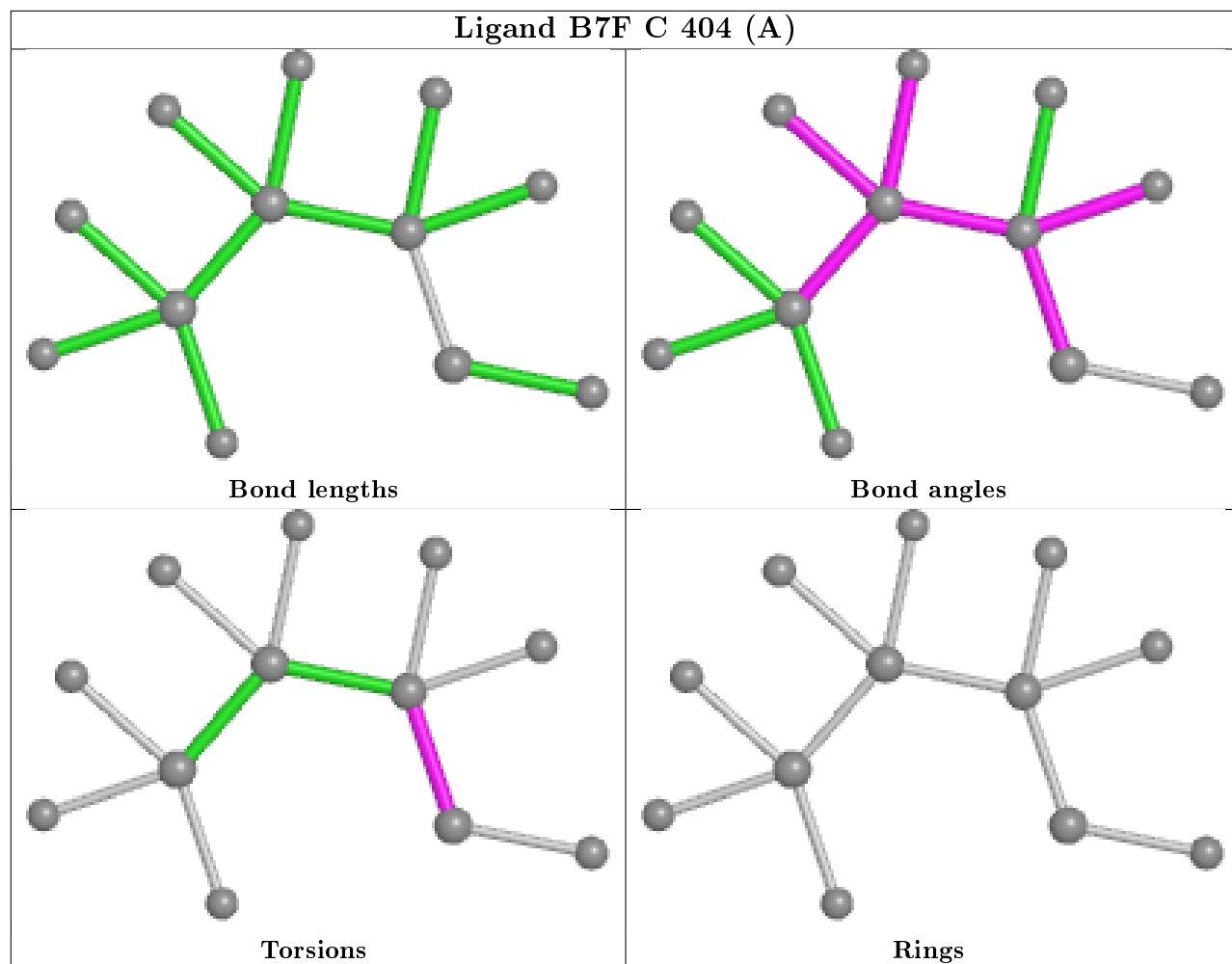


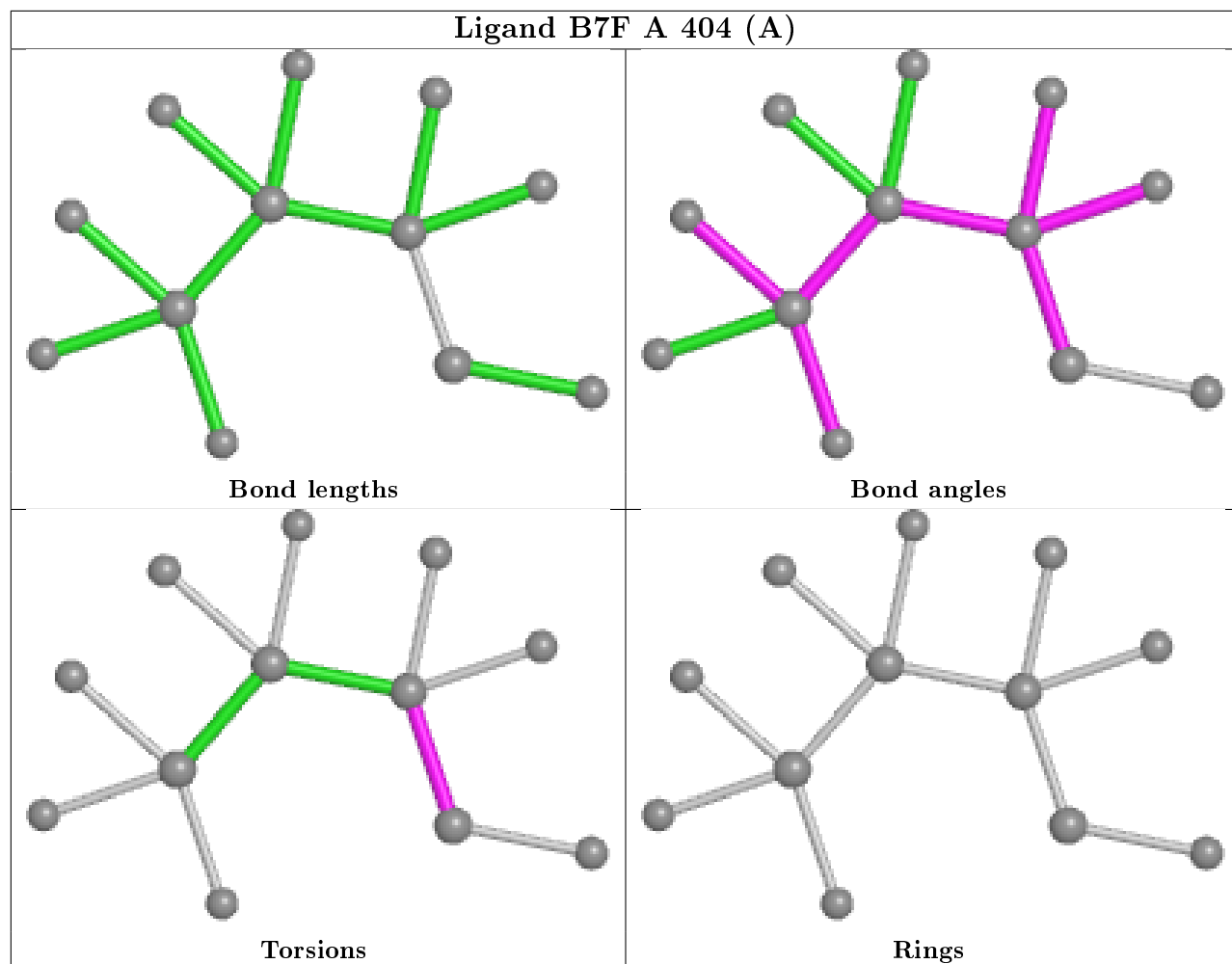


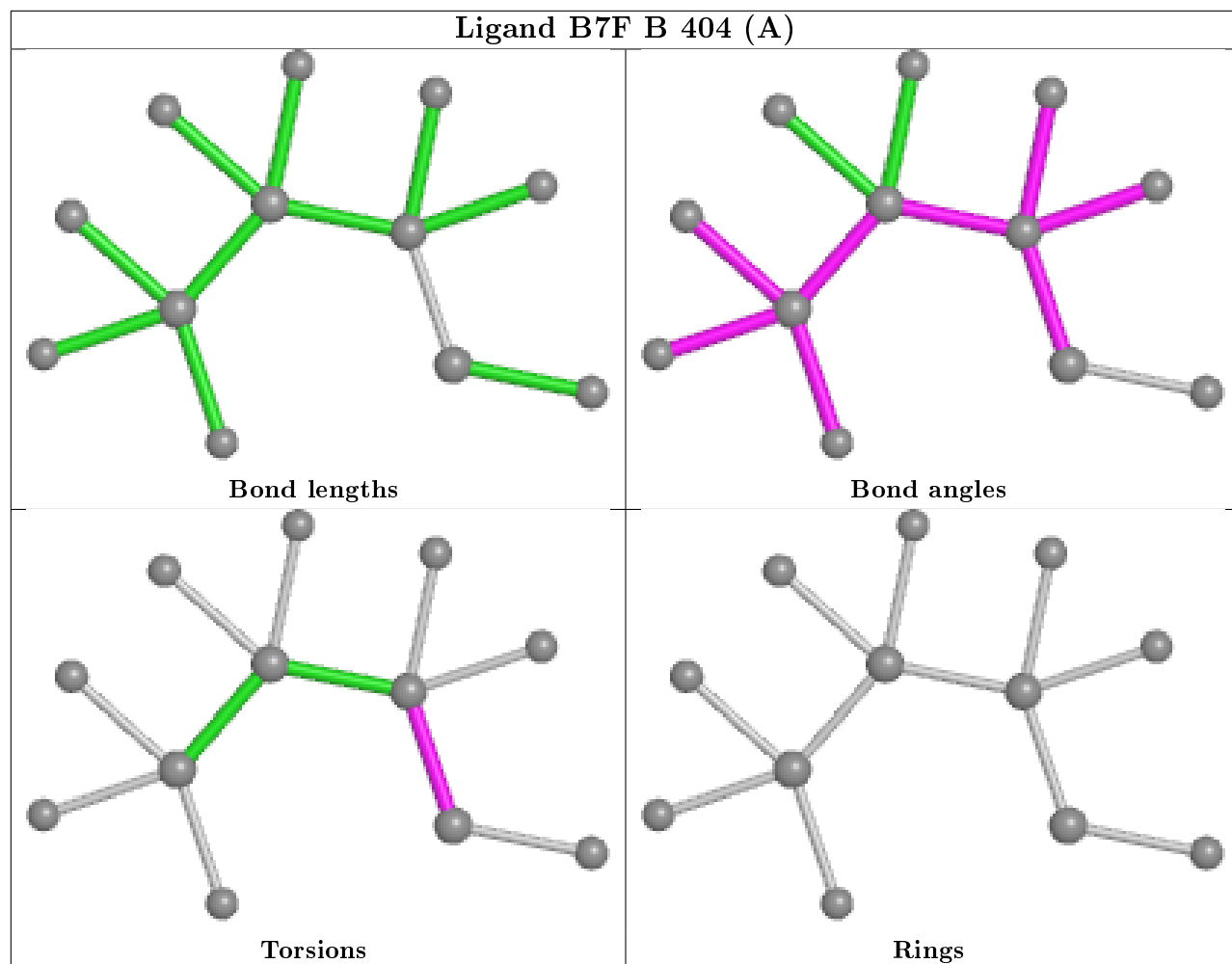












5.7 Other polymers [i](#)

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	374/374 (100%)	0.03	1 (0%) 94 95	13, 20, 33, 44	0
1	B	374/374 (100%)	0.09	6 (1%) 72 77	14, 21, 34, 52	0
1	C	374/374 (100%)	0.01	1 (0%) 94 95	12, 19, 31, 45	0
1	D	374/374 (100%)	0.09	4 (1%) 80 84	13, 20, 34, 45	0
All	All	1496/1496 (100%)	0.05	12 (0%) 86 89	12, 20, 33, 52	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	337	ALA	3.4
1	B	118	MET	2.9
1	B	1	SER	2.9
1	B	249	PRO	2.5
1	B	163	ALA	2.5
1	B	134	GLY	2.4
1	A	118	MET	2.4
1	D	84	ARG	2.3
1	D	118	MET	2.2
1	D	259	ASN	2.2
1	C	197	VAL	2.2
1	B	248	LYS	2.1

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 monosaccharides in this entry.

6.4 Ligands ⓘ

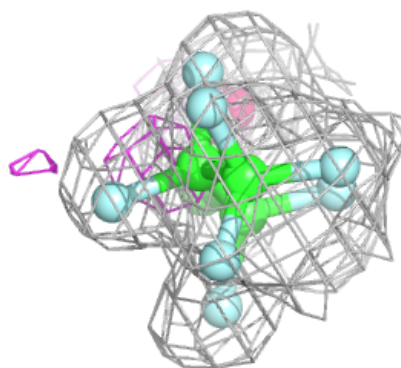
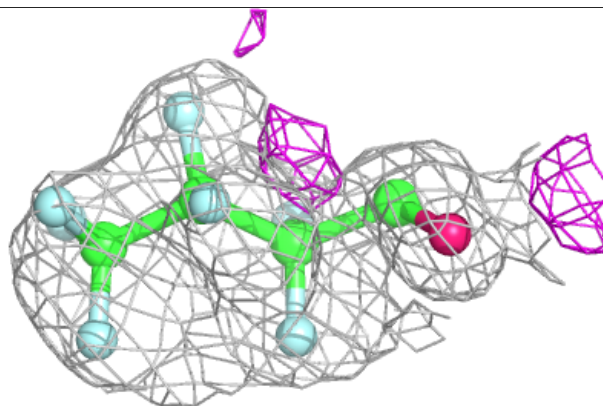
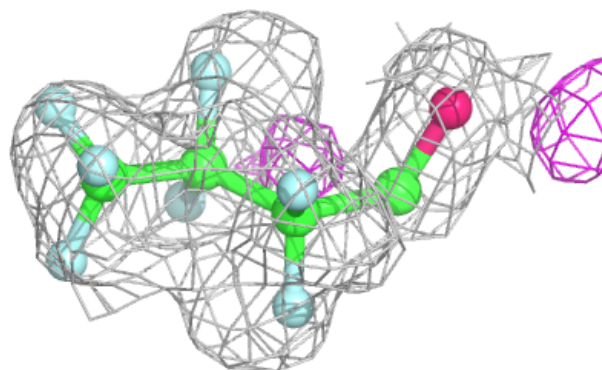
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MRD	C	405[A]	8/8	0.88	0.15	34,39,46,52	8
4	B7F	A	404[B]	12/12	0.93	0.18	17,24,28,28	12
4	B7F	A	404[A]	12/12	0.93	0.18	16,26,28,29	12
4	B7F	C	404[A]	12/12	0.94	0.17	17,31,38,43	12
5	MRD	B	405	8/8	0.94	0.26	19,23,26,27	8
4	B7F	B	404[B]	12/12	0.94	0.13	19,24,30,36	12
4	B7F	B	404[A]	12/12	0.94	0.13	20,27,35,38	12
4	B7F	C	404[B]	12/12	0.94	0.17	18,25,30,34	12
4	B7F	D	404[A]	12/12	0.96	0.15	20,28,31,48	12
4	B7F	D	404[B]	12/12	0.96	0.15	17,23,27,28	12
3	NAI	B	403	44/44	0.97	0.06	12,17,20,27	0
3	NAI	C	403	44/44	0.97	0.07	10,16,20,25	0
3	NAI	D	403	44/44	0.97	0.06	13,17,25,30	0
3	NAI	A	403	44/44	0.98	0.06	11,16,23,26	0
2	ZN	A	401	1/1	1.00	0.03	16,16,16,16	0
2	ZN	D	401	1/1	1.00	0.03	19,19,19,19	0
2	ZN	D	402	1/1	1.00	0.03	18,18,18,18	0
2	ZN	A	402	1/1	1.00	0.03	17,17,17,17	0
2	ZN	B	402	1/1	1.00	0.04	20,20,20,20	0
2	ZN	C	402	1/1	1.00	0.03	19,19,19,19	0
2	ZN	C	401	1/1	1.00	0.03	17,17,17,17	0
2	ZN	B	401	1/1	1.00	0.04	18,18,18,18	0

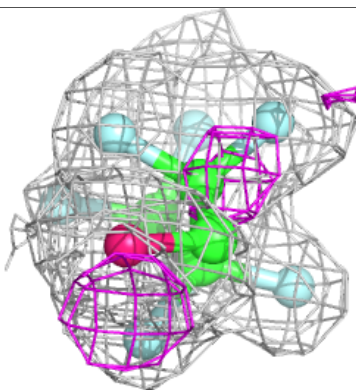
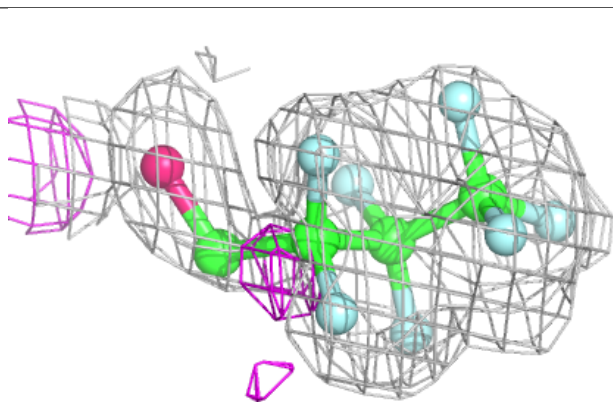
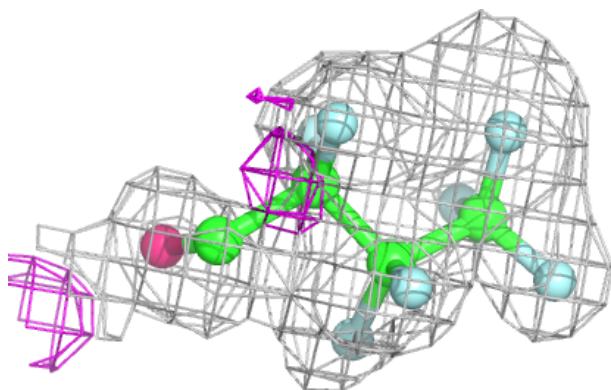
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around B7F A 404 (B):

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

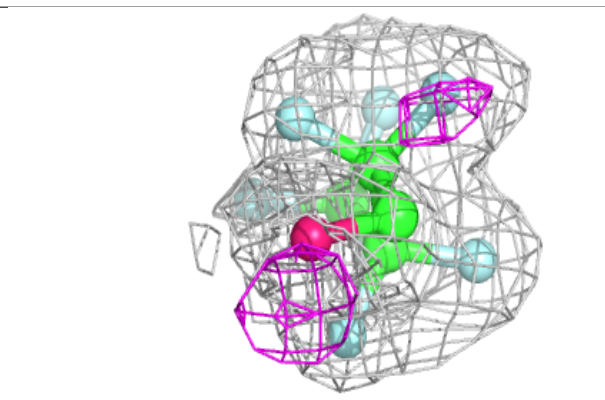
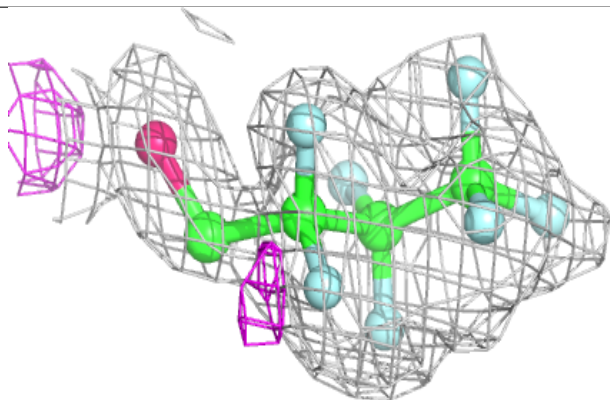
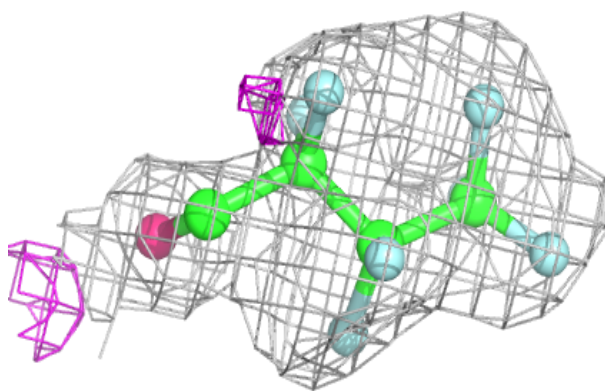
**Electron density around B7F A 404 (A):**

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

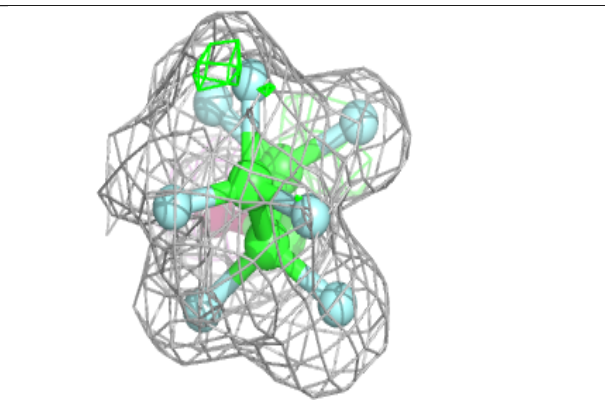
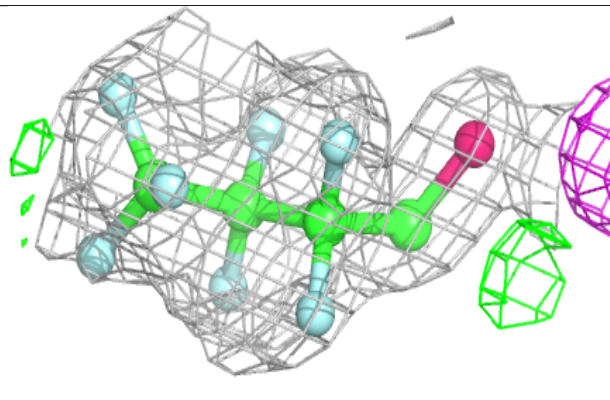
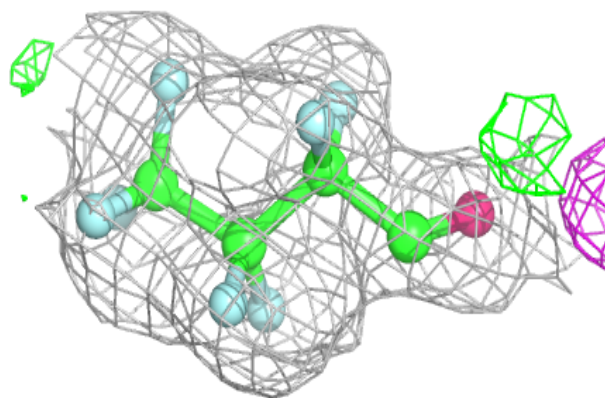


Electron density around B7F C 404 (A):

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

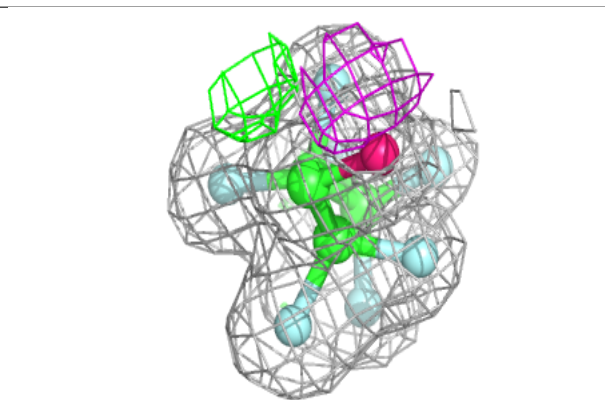
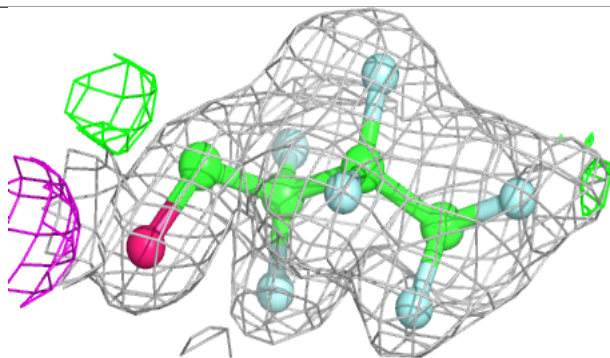
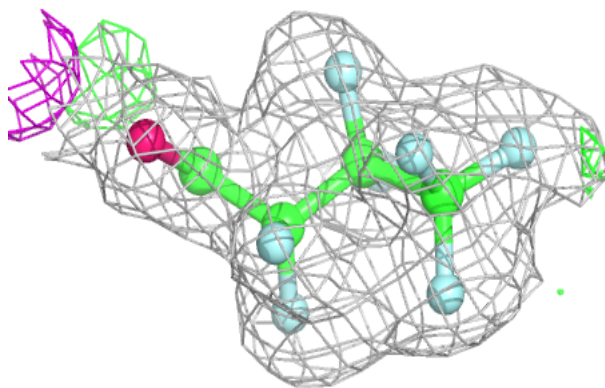
**Electron density around B7F B 404 (B):**

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

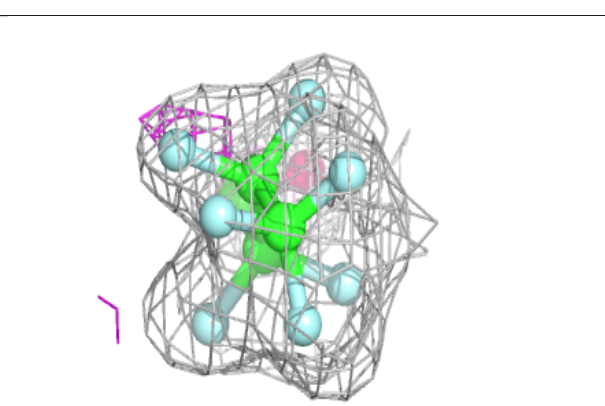
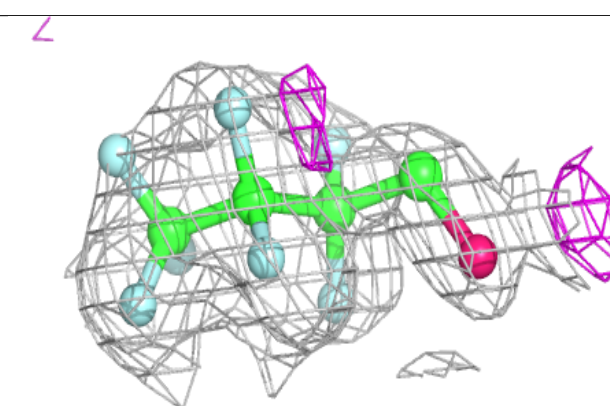
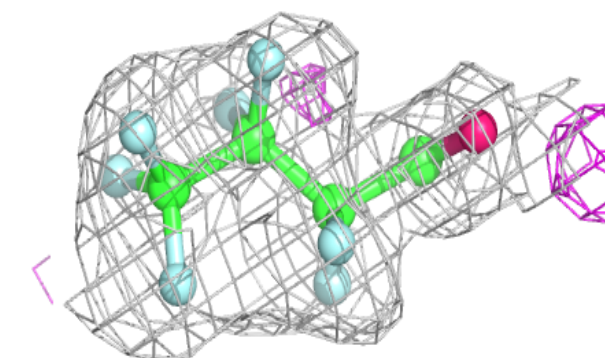


Electron density around B7F B 404 (A):

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

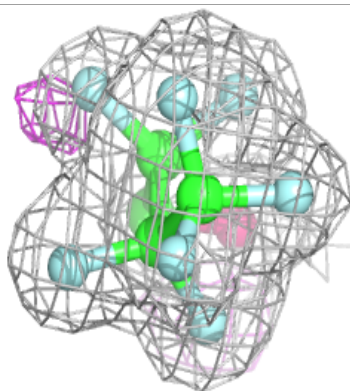
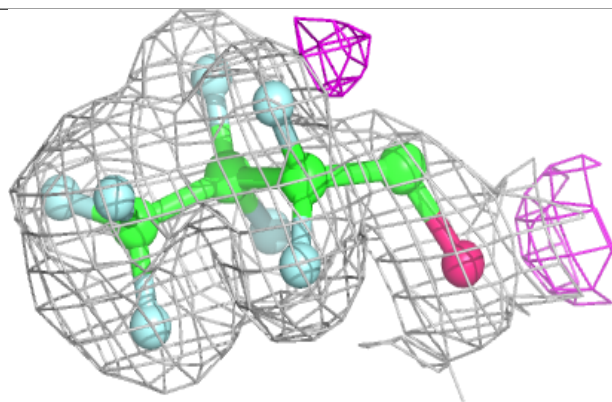
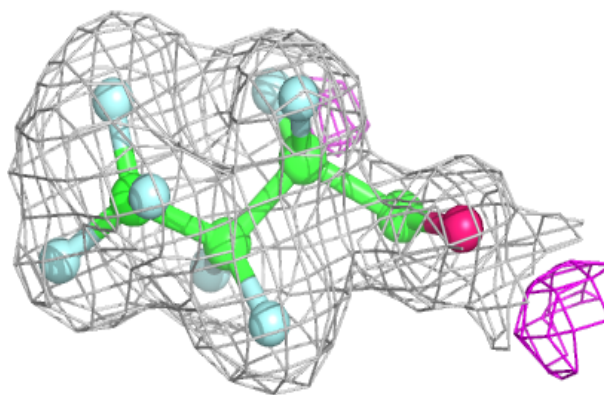
**Electron density around B7F C 404 (B):**

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

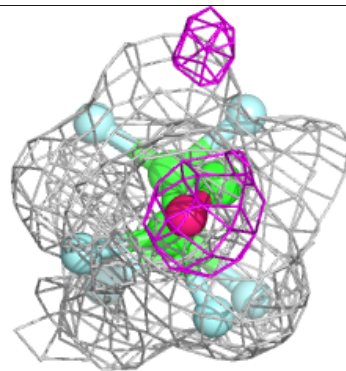
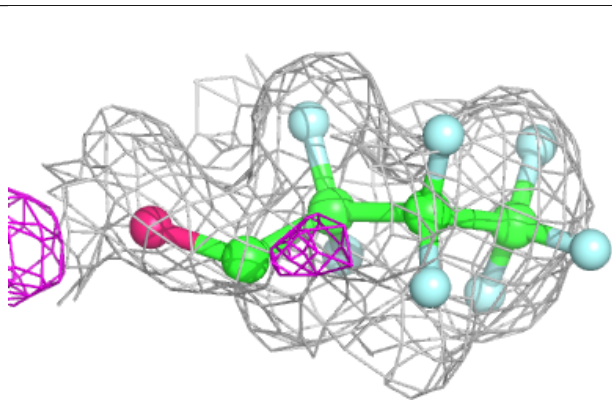
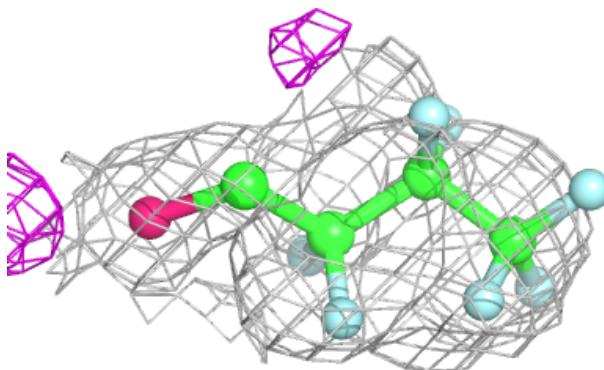


Electron density around B7F D 404 (A):

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

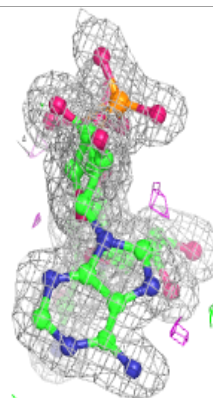
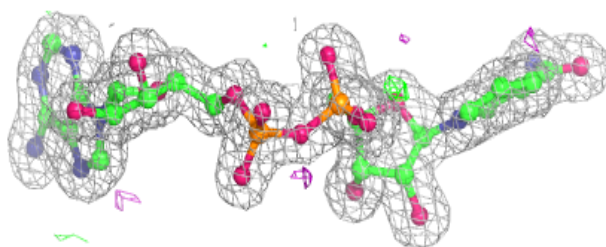
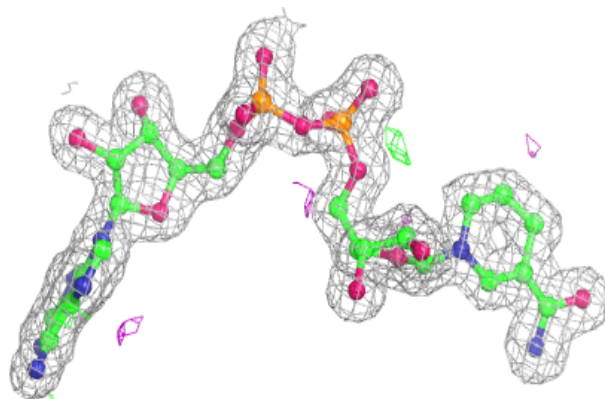
**Electron density around B7F D 404 (B):**

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

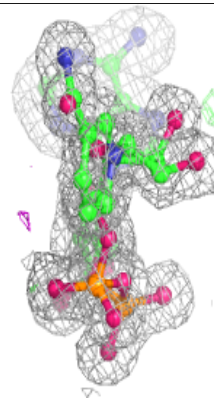
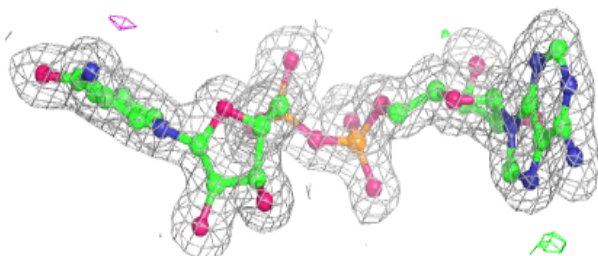
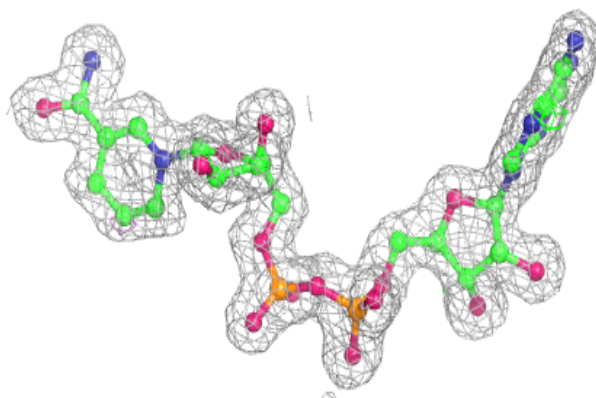


Electron density around NAI B 403:

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

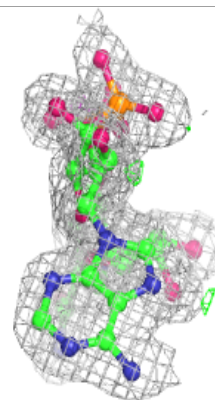
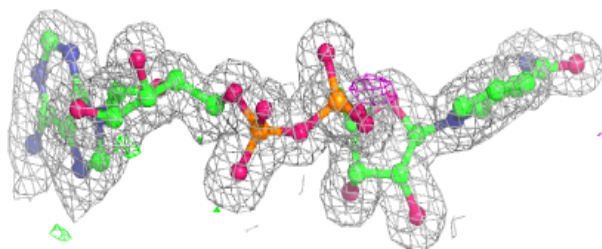
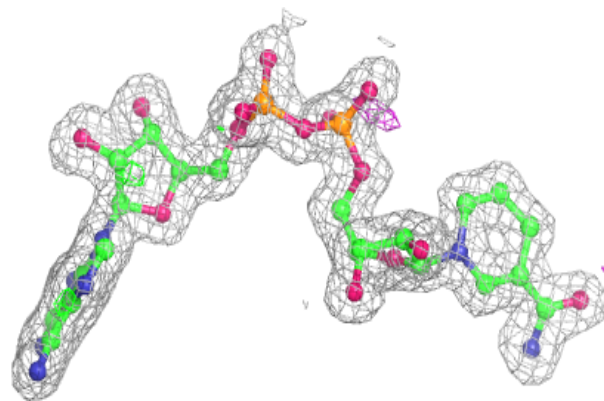
**Electron density around NAI C 403:**

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

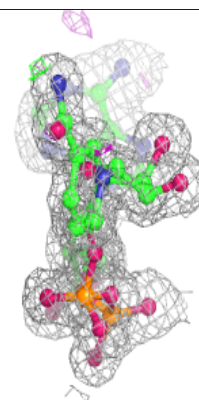
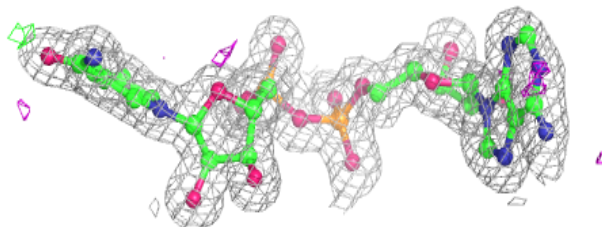
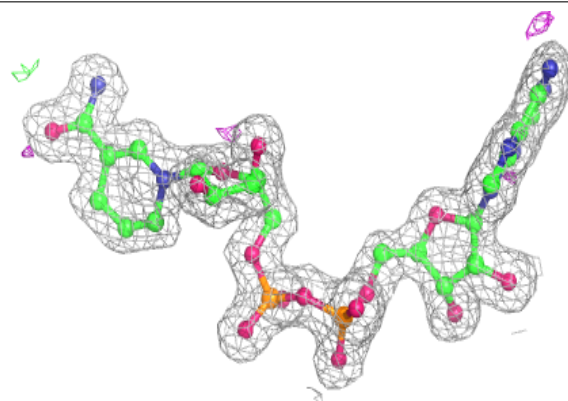


Electron density around NAI D 403:

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

**Electron density around NAI A 403:**

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



6.5 Other polymers

There are no such residues in this entry.