



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 01:10 AM UTC

PDB ID : 5VN1 / pdb_00005vn1
Title : horse liver alcohol dehydrogenase complexed with NADH (R,S)-N-1-methylhexylformamide
Authors : Plapp, B.V.; Ramaswamy, S.; Ferraro, D.J.; Baskar Raj, S.
Deposited on : 2017-04-28
Resolution : 1.25 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 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

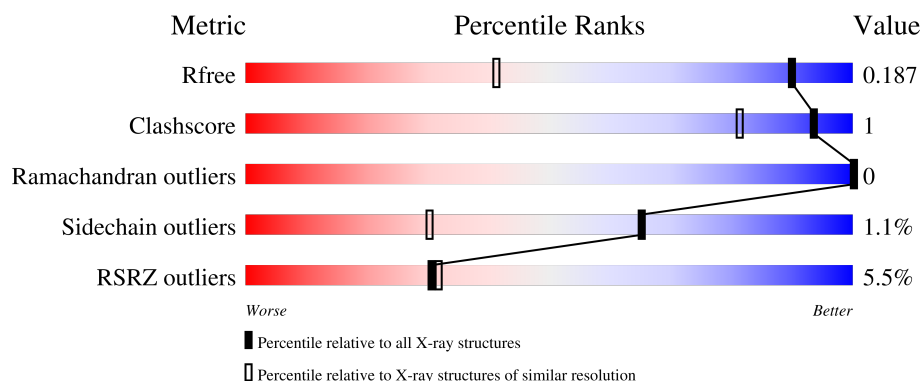
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.25 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1693 (1.28-1.24)
Clashscore	190562	1730 (1.28-1.24)
Ramachandran outliers	187476	1695 (1.28-1.24)
Sidechain outliers	187428	1694 (1.28-1.24)
RSRZ outliers	180081	1693 (1.28-1.24)

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	374	4% 97% ..
1	B	374	6% 98% .
1	C	374	6% 96% .
1	D	374	6% 95% 5%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12774 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	4	0
			2799	1778	473	522	26			
1	B	374	Total	C	N	O	S	0	1	0
			2788	1772	472	521	23			
1	C	374	Total	C	N	O	S	0	7	0
			2808	1784	472	527	25			
1	D	374	Total	C	N	O	S	0	5	0
			2800	1779	474	523	24			

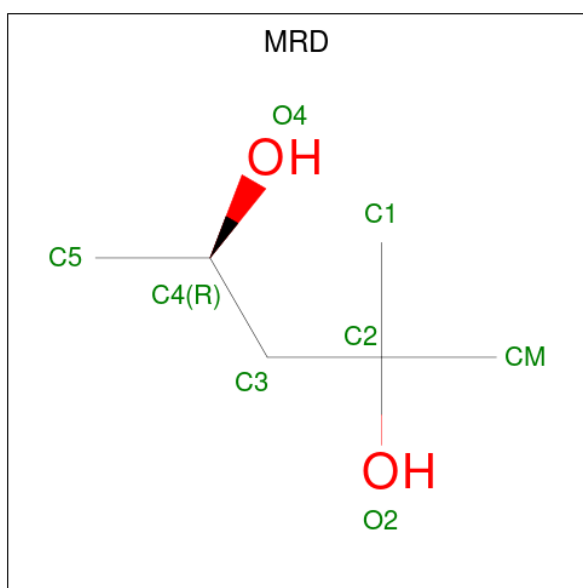
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: C₂₁H₂₉N₇O₁₄P₂).

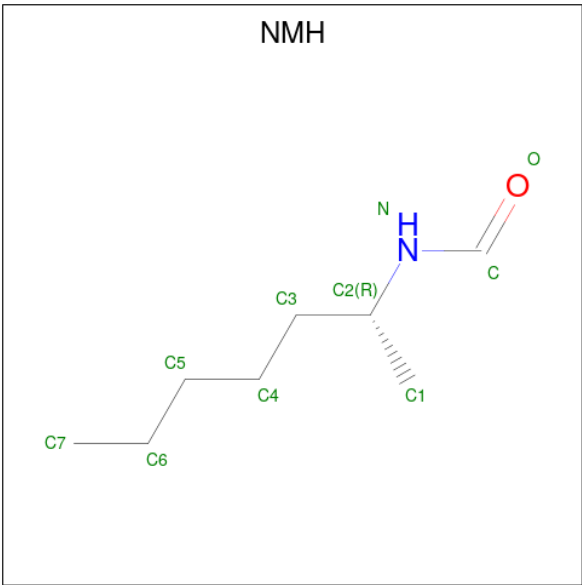
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			10	8	1	1		
4	B	1	Total	C	N	O	0	0
			10	8	1	1		
4	C	1	Total	C	N	O	0	1
			10	8	1	1		
4	D	1	Total	C	N	O	0	0
			10	8	1	1		

- Molecule 5 is (4R)-2-METHYLPENTANE-2,4-DIOL (CCD ID: 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	0
			8	6	2		

- Molecule 6 is (R)-N-(1-METHYL-HEXYL)-FORMAMIDE (CCD ID: NMH) (formula: C₈H₁₇NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	N	O	0	1
			10	8	1	1		

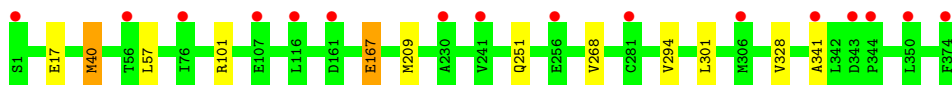
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	319	Total	O	0	1
			320	320		
7	B	314	Total	O	0	0
			314	314		
7	C	358	Total	O	0	7
			361	361		
7	D	330	Total	O	0	4
			334	334		

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.

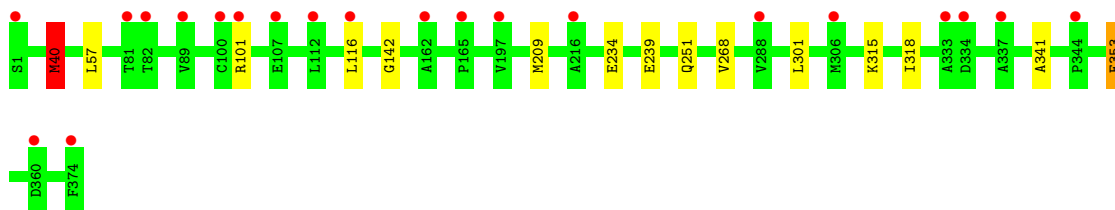
- Molecule 1: Alcohol dehydrogenase E chain



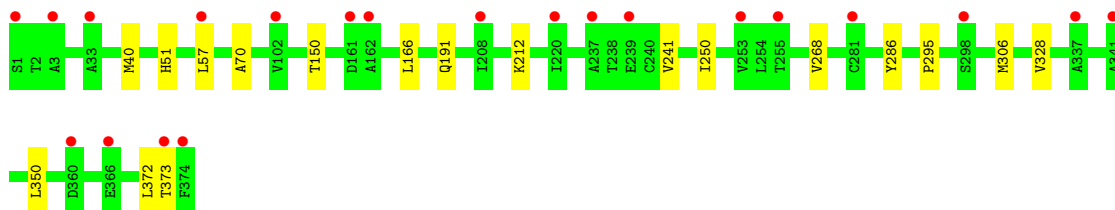
- Molecule 1: Alcohol dehydrogenase E chain



- Molecule 1: Alcohol dehydrogenase E chain



- Molecule 1: Alcohol dehydrogenase E chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.21Å 180.81Å 86.84Å 90.00° 106.12° 90.00°	Depositor
Resolution (Å)	20.00 – 1.25 20.00 – 1.25	Depositor EDS
% Data completeness (in resolution range)	80.0 (20.00-1.25) 80.0 (20.00-1.25)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 1.22Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.151 , 0.187 0.152 , 0.187	Depositor DCC
R_{free} test set	1750 reflections (0.40%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	0.489	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 33.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12774	wwPDB-VP
Average B, all atoms (Å ²)	26.0	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 61.29 % 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 1.3397e-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: NAI, NMH, ZN, MRD, NWH

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.04	1/2868 (0.0%)	0.97	3/3874 (0.1%)
1	B	1.07	1/2844 (0.0%)	0.98	2/3844 (0.1%)
1	C	1.11	2/2890 (0.1%)	1.02	2/3904 (0.1%)
1	D	1.05	1/2877 (0.0%)	1.01	1/3886 (0.0%)
All	All	1.07	5/11479 (0.0%)	1.00	8/15508 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	40	MET	SD-CE	-7.96	1.59	1.79
1	D	295	PRO	CA-C	-5.72	1.46	1.52
1	A	294	VAL	CA-C	5.48	1.57	1.53
1	C	315	LYS	CA-CB	-5.35	1.44	1.53
1	B	239	GLU	CD-OE2	5.33	1.35	1.25

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	40	MET	CG-SD-CE	8.09	118.71	100.90
1	B	40	MET	CG-SD-CE	7.79	118.03	100.90
1	C	353	GLU	CA-CB-CG	6.96	128.02	114.10
1	D	328	VAL	O-C-N	5.70	124.12	120.07
1	C	40	MET	CG-SD-CE	5.44	112.87	100.90
1	A	101	ARG	NE-CZ-NH2	5.40	124.06	119.20
1	B	282	CYS	CA-CB-SG	5.06	126.03	114.40
1	A	328	VAL	O-C-N	5.05	123.65	120.42

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	2799	0	2863	6	0
1	B	2788	0	2853	3	0
1	C	2808	0	2865	10	0
1	D	2800	0	2862	13	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	0	0
3	B	44	0	27	0	0
3	C	44	0	27	0	0
3	D	44	0	27	0	0
4	A	10	0	0	2	0
4	B	10	0	0	1	0
4	C	10	0	0	1	0
4	D	10	0	0	0	0
5	B	8	0	14	0	0
5	C	8	0	14	1	0
6	C	10	0	17	1	0
7	A	320	0	0	1	0
7	B	314	0	0	0	0
7	C	361	0	0	4	0
7	D	334	0	0	3	0
All	All	12774	0	11596	32	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 1.

All (32) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:241[B]:VAL:HG21	1:D:250:ILE:HD11	1.57	0.85
1:D:373:THR:HG23	7:D:596:HOH:O	1.78	0.83
1:D:241[B]:VAL:CG2	1:D:250:ILE:HD11	2.15	0.76
5:C:406:MRD:H5C2	5:C:406:MRD:H1C1	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:209[B]:MET:HE1	1:C:341:ALA:H	1.56	0.70
1:A:209[B]:MET:HE1	1:A:341:ALA:H	1.59	0.67
1:A:57:LEU:HD21	4:A:404:NWH:C5	2.25	0.65
1:B:220:ILE:HG12	1:B:239:GLU:HG3	1.78	0.64
1:C:234:GLU:OE2	7:C:501:HOH:O	2.15	0.64
1:D:51:HIS:HB3	1:D:57:LEU:HB2	1.89	0.54
1:A:167:GLU:H	1:A:167:GLU:CD	2.15	0.54
1:C:116:LEU:HD22	1:C:318[B]:ILE:HD12	1.89	0.53
1:C:101:ARG:NH1	7:C:502:HOH:O	2.33	0.53
1:D:40:MET:HE1	1:D:150:THR:HG22	1.92	0.52
1:C:40:MET:HA	1:C:40:MET:HE2	1.94	0.50
1:D:191:GLN:HG2	7:D:738:HOH:O	2.12	0.49
1:C:318[B]:ILE:HG22	7:C:621:HOH:O	2.14	0.48
1:D:212:LYS:NZ	7:D:502:HOH:O	2.46	0.47
1:A:17:GLU:OE1	7:A:501:HOH:O	2.20	0.47
1:C:57:LEU:HD11	4:C:404[A]:NWH:C6	2.45	0.47
1:C:101:ARG:NH1	1:D:286:TYR:OH	2.48	0.47
1:B:57:LEU:HD21	4:B:404:NWH:C5	2.46	0.46
6:C:405[B]:NMH:HC71	1:D:306:MET:HE1	1.98	0.45
1:D:40:MET:HE2	1:D:40:MET:HB2	1.82	0.44
1:B:51:HIS:HB3	1:B:57:LEU:HB2	2.00	0.43
1:D:40:MET:HE1	1:D:150:THR:CG2	2.48	0.43
1:A:301:LEU:HD12	1:A:301:LEU:C	2.43	0.43
1:A:57:LEU:HD11	4:A:404:NWH:C5	2.50	0.42
1:C:301:LEU:C	1:C:301:LEU:HD12	2.45	0.41
1:D:70:ALA:HB1	1:D:166:LEU:HD22	2.03	0.40
1:D:350:LEU:O	1:D:372:LEU:HA	2.21	0.40
1:C:142:GLY:HA2	7:C:775:HOH:O	2.20	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	376/374 (100%)	365 (97%)	11 (3%)	0	100	100
1	B	373/374 (100%)	364 (98%)	9 (2%)	0	100	100
1	C	379/374 (101%)	369 (97%)	10 (3%)	0	100	100
1	D	377/374 (101%)	365 (97%)	12 (3%)	0	100	100
All	All	1505/1496 (101%)	1463 (97%)	42 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	312/308 (101%)	307 (98%)	5 (2%)	55	19
1	B	309/308 (100%)	306 (99%)	3 (1%)	68	34
1	C	315/308 (102%)	310 (98%)	5 (2%)	55	19
1	D	313/308 (102%)	312 (100%)	1 (0%)	86	65
All	All	1249/1232 (101%)	1235 (99%)	14 (1%)	65	30

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	MET
1	A	167	GLU
1	A	251[A]	GLN
1	A	251[B]	GLN
1	A	268	VAL
1	B	40	MET
1	B	239	GLU
1	B	268	VAL
1	C	40	MET
1	C	239	GLU
1	C	251	GLN
1	C	268	VAL
1	C	353	GLU

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Mol	Chain	Res	Type
1	D	268	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	124	GLN
1	A	300	ASN
1	B	300	ASN
1	C	251	GLN
1	C	300	ASN
1	D	34	HIS
1	D	138	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 8 are monoatomic - leaving 11 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	$\# Z > 2$
4	NWH	A	404	2	9,9,9	0.57	0	8,9,9	1.39	3 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NWH	D	404	2	9,9,9	0.46	0	8,9,9	1.11	1 (12%)
3	NAI	B	403	-	47,48,48	1.43	6 (12%)	64,73,73	1.40	8 (12%)
5	MRD	B	405	-	7,7,7	0.60	0	9,10,10	1.40	1 (11%)
3	NAI	C	403	-	47,48,48	1.61	6 (12%)	64,73,73	1.75	10 (15%)
5	MRD	C	406	-	7,7,7	0.48	0	9,10,10	1.09	0
3	NAI	A	403	-	47,48,48	1.17	3 (6%)	64,73,73	1.36	8 (12%)
4	NWH	B	404	2	9,9,9	0.66	0	8,9,9	0.65	0
4	NWH	C	404[A]	2	9,9,9	0.81	0	8,9,9	1.56	2 (25%)
6	NMH	C	405[B]	2	9,9,9	0.34	0	8,9,9	1.01	0
3	NAI	D	403	-	47,48,48	1.59	11 (23%)	64,73,73	1.70	10 (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
4	NWH	A	404	2	-	2/8/8/8	-
4	NWH	D	404	2	-	2/8/8/8	-
3	NAI	B	403	-	-	3/29/72/72	0/5/5/5
5	MRD	B	405	-	-	5/5/5/5	-
3	NAI	C	403	-	-	3/29/72/72	0/5/5/5
5	MRD	C	406	-	-	3/5/5/5	-
3	NAI	A	403	-	-	3/29/72/72	0/5/5/5
4	NWH	B	404	2	-	2/8/8/8	-
4	NWH	C	404[A]	2	-	4/8/8/8	-
6	NMH	C	405[B]	2	-	3/8/8/8	-
3	NAI	D	403	-	-	3/29/72/72	0/5/5/5

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	403	NAI	C2A-N1A	5.47	1.43	1.33
3	C	403	NAI	C5A-C4A	4.73	1.47	1.39
3	C	403	NAI	C2A-N3A	4.30	1.41	1.33
3	A	403	NAI	C8A-N7A	3.98	1.39	1.31
3	D	403	NAI	C6N-N1N	3.75	1.46	1.37
3	B	403	NAI	C6A-N1A	-3.74	1.25	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	403	NAI	C4N-C3N	-3.62	1.43	1.50
3	B	403	NAI	C4A-N9A	-3.58	1.30	1.37
3	B	403	NAI	C5A-C4A	3.44	1.45	1.39
3	B	403	NAI	C2A-N3A	3.41	1.40	1.33
3	A	403	NAI	C2A-N3A	3.36	1.39	1.33
3	D	403	NAI	C2A-N3A	3.34	1.39	1.33
3	D	403	NAI	C4A-N9A	-3.23	1.31	1.37
3	A	403	NAI	C4N-C3N	-3.10	1.44	1.50
3	D	403	NAI	C6A-N6A	2.77	1.41	1.34
3	D	403	NAI	C4A-N3A	2.70	1.39	1.34
3	D	403	NAI	C8A-N7A	2.67	1.36	1.31
3	B	403	NAI	C6A-N6A	2.47	1.40	1.34
3	D	403	NAI	C6A-N1A	-2.42	1.29	1.35
3	C	403	NAI	C6A-N1A	-2.41	1.29	1.35
3	B	403	NAI	C2A-N1A	2.40	1.38	1.33
3	D	403	NAI	PN-O3	2.37	1.62	1.59
3	D	403	NAI	C1D-N1N	-2.35	1.39	1.46
3	C	403	NAI	C2N-C3N	2.33	1.41	1.35
3	C	403	NAI	C4N-C3N	-2.17	1.45	1.50
3	D	403	NAI	C8A-N9A	-2.16	1.33	1.37

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	403	NAI	N3A-C2A-N1A	-8.14	116.26	128.58
3	D	403	NAI	N3A-C2A-N1A	-6.16	119.25	128.58
3	D	403	NAI	C4A-N9A-C8A	4.90	110.89	105.74
3	C	403	NAI	C2A-N1A-C6A	4.82	126.64	118.73
3	A	403	NAI	N3A-C2A-N1A	-4.50	121.78	128.58
3	D	403	NAI	C2A-N1A-C6A	4.32	125.83	118.73
3	C	403	NAI	C4A-N9A-C8A	4.32	110.27	105.74
3	B	403	NAI	C4A-N9A-C8A	4.21	110.16	105.74
3	D	403	NAI	C5A-C4A-N3A	-3.91	121.33	126.72
3	B	403	NAI	N3A-C2A-N1A	-3.61	123.11	128.58
3	B	403	NAI	C2A-N1A-C6A	3.49	124.47	118.73
3	A	403	NAI	C2A-N1A-C6A	3.47	124.44	118.73
3	D	403	NAI	N9A-C8A-N7A	-3.29	109.27	113.94
3	D	403	NAI	N3A-C4A-N9A	3.13	132.50	127.17
3	D	403	NAI	C6N-N1N-C2N	-3.07	116.04	119.32
4	C	404[A]	NWH	C4-C3-C2	2.93	120.79	114.07
5	B	405	MRD	C5-C4-C3	2.91	125.21	111.67
3	B	403	NAI	C4A-C5A-N7A	-2.83	107.34	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	403	NAI	N9A-C8A-N7A	-2.69	110.12	113.94
3	B	403	NAI	N9A-C8A-N7A	-2.66	110.16	113.94
3	A	403	NAI	C5A-C4A-N3A	-2.66	123.06	126.72
3	A	403	NAI	O2B-C2B-C3B	2.64	120.26	111.82
3	C	403	NAI	C5A-C4A-N9A	-2.61	102.97	105.81
3	B	403	NAI	C5A-N7A-C8A	2.57	107.50	103.45
3	C	403	NAI	N3A-C4A-N9A	2.48	131.38	127.17
3	A	403	NAI	N9A-C8A-N7A	-2.44	110.47	113.94
4	A	404	NWH	C1-C2-C3	2.38	115.82	111.48
4	C	404[A]	NWH	C3-C2-N	-2.34	106.39	110.42
3	B	403	NAI	N3A-C4A-N9A	2.32	131.12	127.17
3	A	403	NAI	C4A-N9A-C1B	-2.28	121.30	126.63
3	A	403	NAI	O7N-C7N-C3N	-2.26	116.63	120.90
3	C	403	NAI	O7N-C7N-C3N	-2.25	116.67	120.90
3	D	403	NAI	C2A-N3A-C4A	2.20	117.21	111.83
4	A	404	NWH	C4-C3-C2	2.20	119.11	114.07
4	A	404	NWH	C3-C2-N	-2.13	106.75	110.42
3	C	403	NAI	O2B-C2B-C3B	2.11	118.59	111.82
3	A	403	NAI	N6A-C6A-N1A	2.09	123.03	118.38
3	D	403	NAI	C4A-C5A-N7A	-2.08	108.20	110.58
4	D	404	NWH	C1-C2-C3	2.07	115.27	111.48
3	B	403	NAI	O4D-C1D-N1N	2.07	112.04	108.08
3	D	403	NAI	O2A-PA-O1A	2.06	122.01	112.44
3	C	403	NAI	C4A-N9A-C1B	-2.06	121.82	126.63
3	C	403	NAI	C1D-N1N-C2N	-2.05	117.76	121.14

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	404	NWH	C1-C2-C3-C4
4	A	404	NWH	N-C2-C3-C4
4	B	404	NWH	C1-C2-C3-C4
4	C	404[A]	NWH	C1-C2-C3-C4
4	C	404[A]	NWH	N-C2-C3-C4
4	D	404	NWH	C1-C2-C3-C4
4	D	404	NWH	N-C2-C3-C4
5	B	405	MRD	C1-C2-C3-C4
5	B	405	MRD	O2-C2-C3-C4
5	B	405	MRD	C2-C3-C4-C5
5	C	406	MRD	C2-C3-C4-C5
3	B	403	NAI	C2D-C1D-N1N-C2N

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Mol	Chain	Res	Type	Atoms
6	C	405[B]	NMH	C3-C4-C5-C6
3	A	403	NAI	C2D-C1D-N1N-C2N
3	C	403	NAI	C2D-C1D-N1N-C2N
6	C	405[B]	NMH	C1-C2-C3-C4
3	D	403	NAI	C2D-C1D-N1N-C2N
4	C	404[A]	NWH	C4-C5-C6-C7
3	B	403	NAI	O4D-C1D-N1N-C2N
3	D	403	NAI	O4D-C1D-N1N-C2N
3	A	403	NAI	O4D-C1D-N1N-C2N
3	C	403	NAI	O4D-C1D-N1N-C2N
4	C	404[A]	NWH	C2-C3-C4-C5
4	B	404	NWH	N-C2-C3-C4
6	C	405[B]	NMH	N-C2-C3-C4
3	A	403	NAI	O4B-C4B-C5B-O5B
3	D	403	NAI	O4B-C4B-C5B-O5B
5	B	405	MRD	C2-C3-C4-O4
5	C	406	MRD	C2-C3-C4-O4
5	B	405	MRD	CM-C2-C3-C4
5	C	406	MRD	CM-C2-C3-C4
3	C	403	NAI	O4B-C4B-C5B-O5B
3	B	403	NAI	O4B-C4B-C5B-O5B

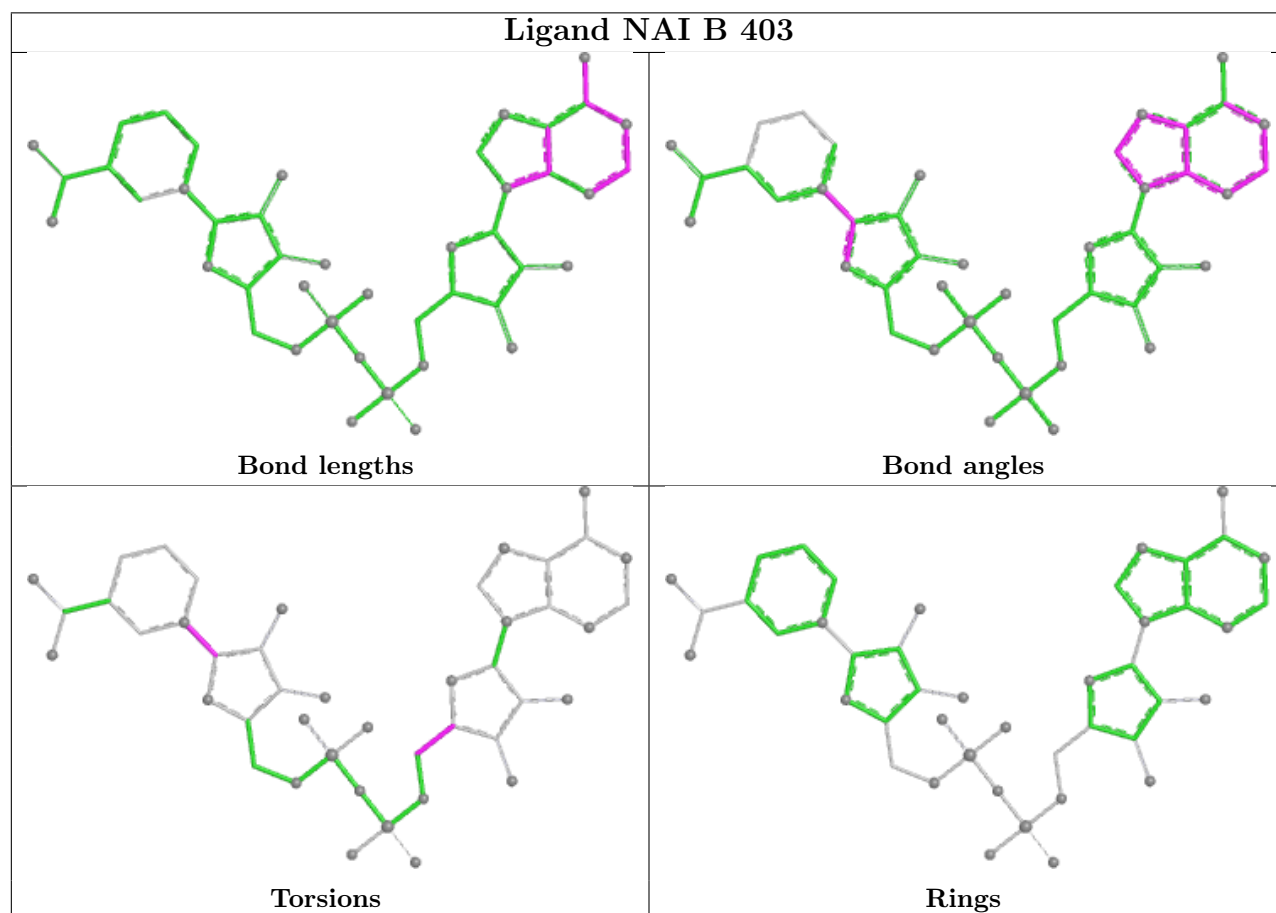
There are no ring outliers.

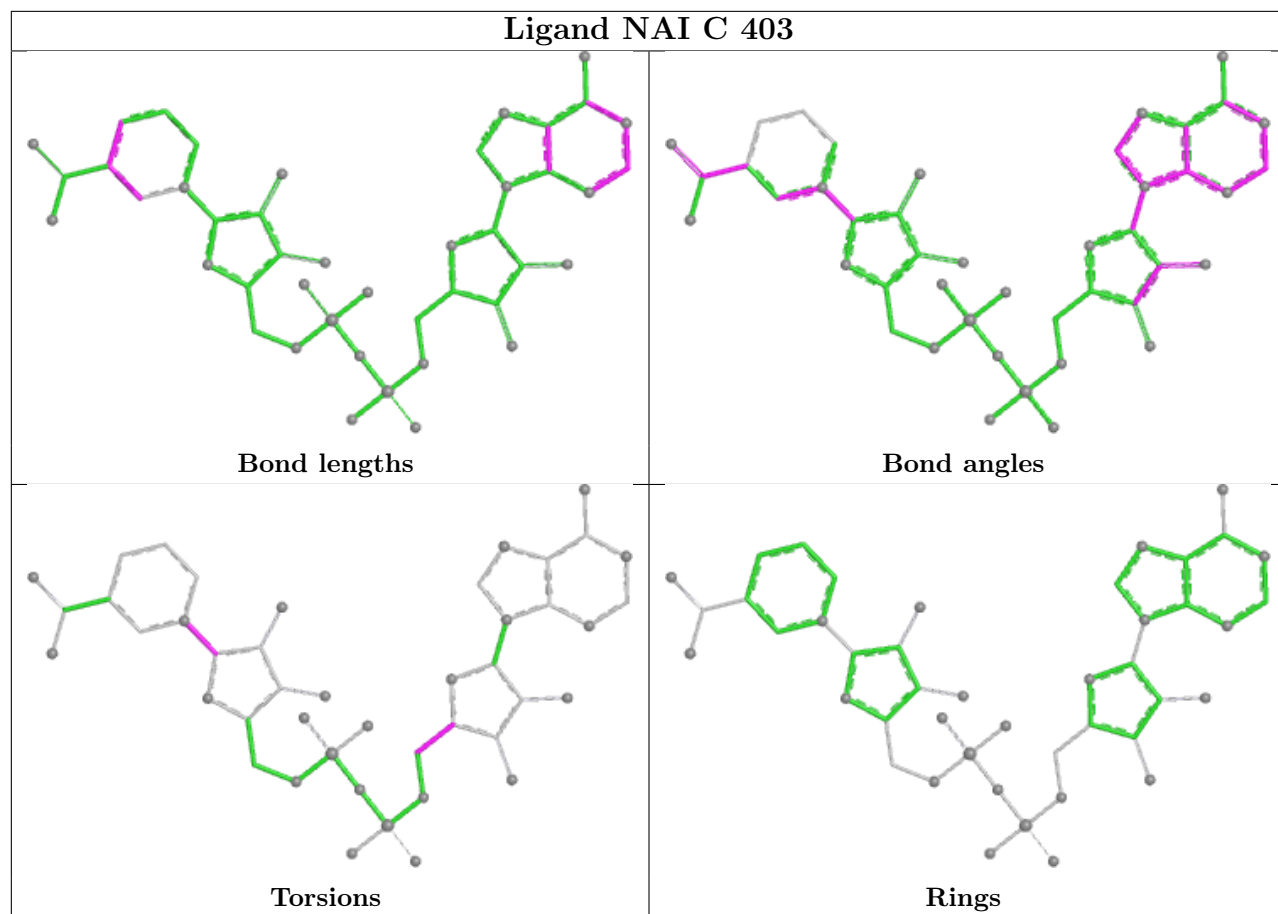
5 monomers are involved in 6 short contacts:

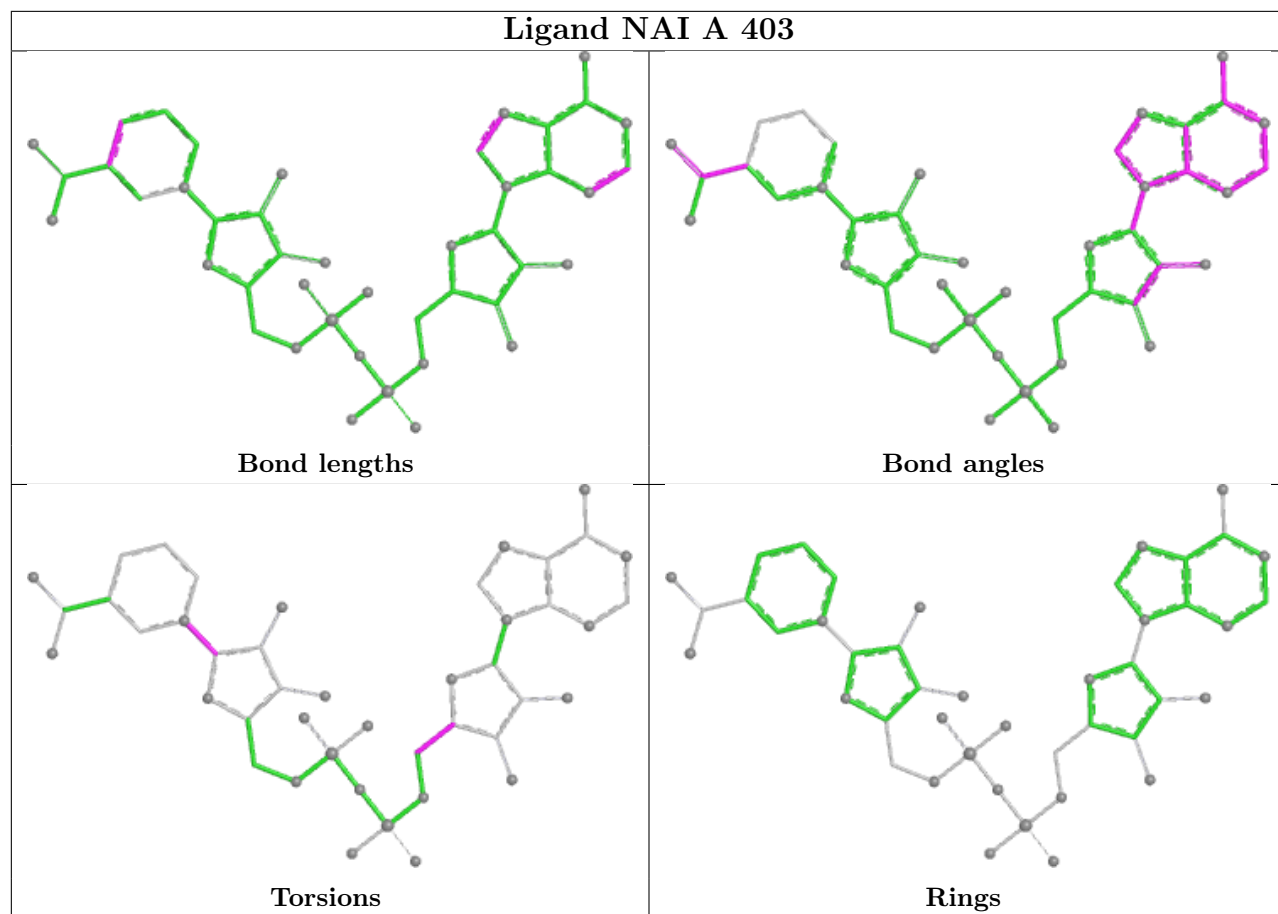
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	404	NWH	2	0
5	C	406	MRD	1	0
4	B	404	NWH	1	0
4	C	404[A]	NWH	1	0
6	C	405[B]	NMH	1	0

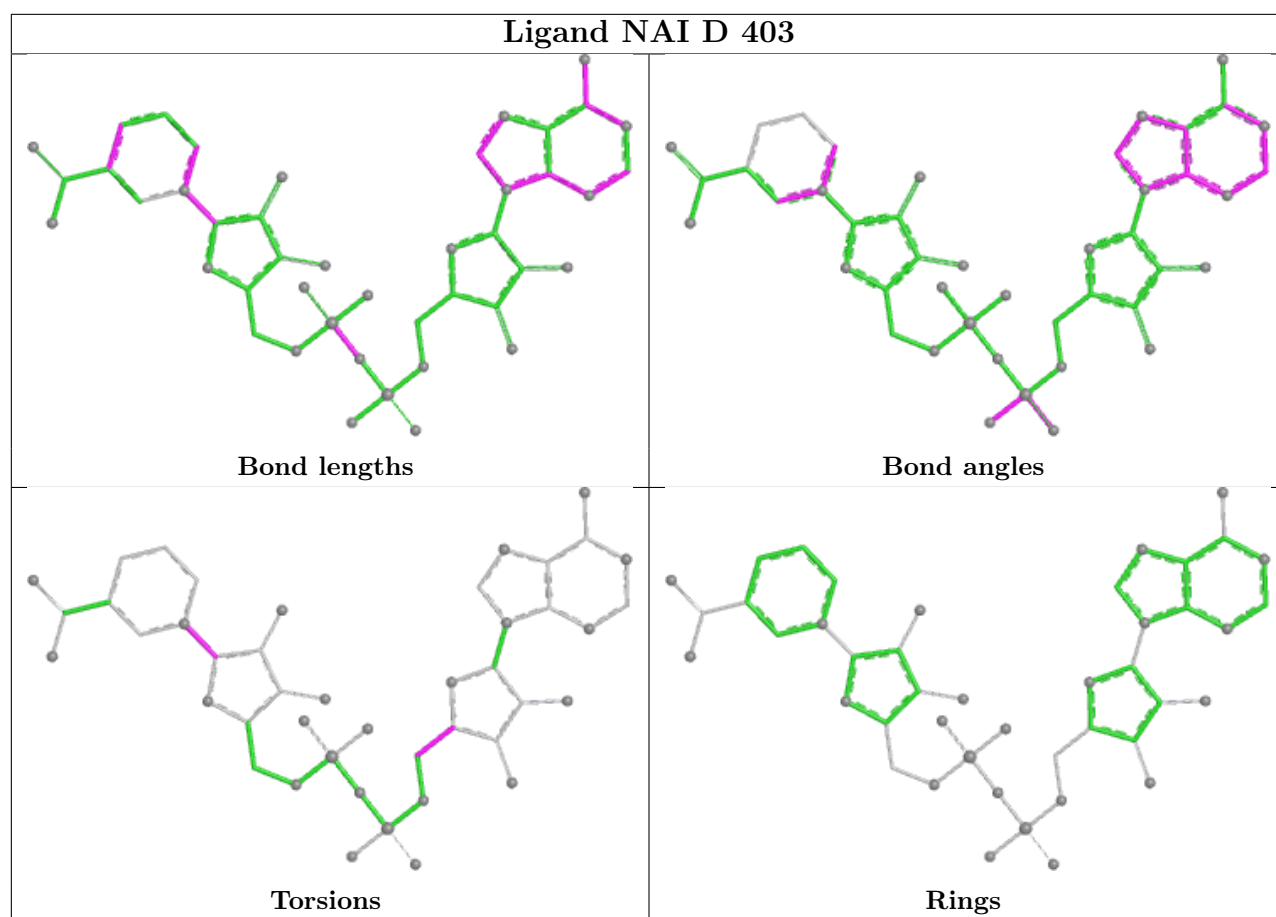
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	374/374 (100%)	0.72	16 (4%)	40	41	15, 23, 35, 44	4 (1%)
1	B	374/374 (100%)	0.78	24 (6%)	25	27	17, 24, 36, 46	1 (0%)
1	C	374/374 (100%)	0.76	21 (5%)	30	31	13, 22, 33, 50	7 (1%)
1	D	374/374 (100%)	0.75	21 (5%)	30	31	14, 23, 35, 43	5 (1%)
All	All	1496/1496 (100%)	0.75	82 (5%)	30	32	13, 23, 35, 50	17 (1%)

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	374	PHE	4.9
1	C	162	ALA	4.2
1	C	374	PHE	4.1
1	D	281	CYS	3.8
1	D	255	THR	3.7
1	C	333	ALA	3.6
1	D	341	ALA	3.5
1	D	162	ALA	3.3
1	C	89	VAL	3.1
1	A	281	CYS	3.0
1	D	360	ASP	3.0
1	B	29	ALA	3.0
1	A	1	SER	2.9
1	D	253	VAL	2.9
1	B	374	PHE	2.9
1	D	374	PHE	2.8
1	C	337	ALA	2.8
1	C	344	PRO	2.8
1	B	337	ALA	2.8
1	C	82	THR	2.7
1	D	161	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	116	LEU	2.7
1	C	360	ASP	2.7
1	B	268	VAL	2.7
1	A	230	ALA	2.6
1	B	333	ALA	2.6
1	B	6	VAL	2.6
1	C	306	MET	2.6
1	D	33	ALA	2.6
1	C	112	LEU	2.6
1	D	3	ALA	2.5
1	B	127	THR	2.5
1	B	306	MET	2.5
1	B	76	ILE	2.5
1	D	366	GLU	2.5
1	C	1	SER	2.4
1	A	306	MET	2.4
1	D	57	LEU	2.4
1	D	1	SER	2.4
1	A	341	ALA	2.4
1	C	81	THR	2.4
1	D	102	VAL	2.3
1	A	343	ASP	2.3
1	C	334	ASP	2.3
1	B	282	CYS	2.3
1	B	252	GLU	2.3
1	B	298	SER	2.3
1	C	288	VAL	2.3
1	D	239	GLU	2.3
1	B	281	CYS	2.3
1	B	360	ASP	2.3
1	A	107	GLU	2.3
1	A	56	THR	2.2
1	A	161	ASP	2.2
1	A	256	GLU	2.2
1	C	107	GLU	2.2
1	C	216	ALA	2.2
1	D	337	ALA	2.2
1	B	57	LEU	2.1
1	C	101	ARG	2.1
1	A	241	VAL	2.1
1	A	344	PRO	2.1
1	C	165	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	227	ASP	2.1
1	A	76	ILE	2.1
1	B	162	ALA	2.1
1	D	208	ILE	2.1
1	D	237	ALA	2.1
1	B	117	SER	2.1
1	B	131	THR	2.1
1	B	341	ALA	2.1
1	D	220	ILE	2.1
1	B	165	PRO	2.1
1	B	253	VAL	2.1
1	C	197	VAL	2.1
1	B	94	THR	2.0
1	B	118	MET	2.0
1	A	116	LEU	2.0
1	A	350	LEU	2.0
1	C	100	CYS	2.0
1	D	298	SER	2.0
1	D	373	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B	405	8/8	0.67	0.18	36,43,45,47	0
5	MRD	C	406	8/8	0.76	0.15	63,69,73,79	0
4	NWH	A	404	10/10	0.82	0.15	23,27,56,63	0
6	NMH	C	405[B]	10/10	0.83	0.18	19,24,36,39	10

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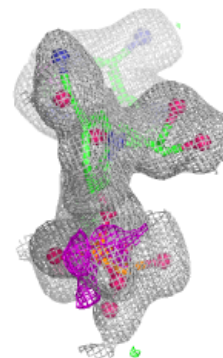
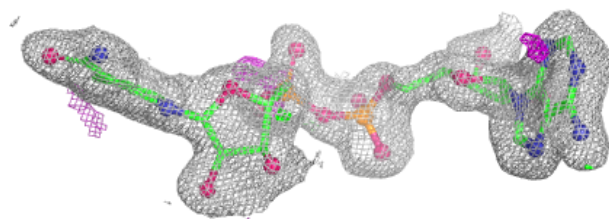
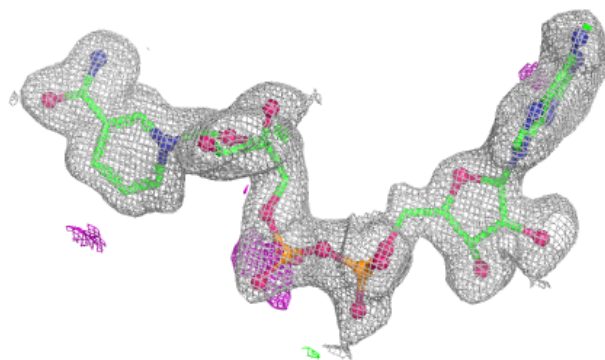
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NWH	C	404[A]	10/10	0.84	0.14	20,24,62,65	10
4	NWH	D	404	10/10	0.89	0.12	21,26,46,51	0
4	NWH	B	404	10/10	0.90	0.12	23,26,43,46	0
3	NAI	D	403	44/44	0.97	0.06	17,20,28,35	0
3	NAI	A	403	44/44	0.97	0.07	17,21,28,34	0
2	ZN	D	401	1/1	0.98	0.08	21,21,21,21	0
2	ZN	A	401	1/1	0.98	0.08	21,21,21,21	0
3	NAI	B	403	44/44	0.98	0.05	17,20,25,28	0
3	NAI	C	403	44/44	0.98	0.05	16,19,25,31	0
2	ZN	B	401	1/1	0.98	0.08	21,21,21,21	0
2	ZN	C	401	1/1	0.98	0.07	20,20,20,20	0
2	ZN	D	402	1/1	0.99	0.04	20,20,20,20	0
2	ZN	A	402	1/1	0.99	0.04	20,20,20,20	0
2	ZN	C	402	1/1	0.99	0.04	21,21,21,21	0
2	ZN	B	402	1/1	0.99	0.04	21,21,21,21	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.

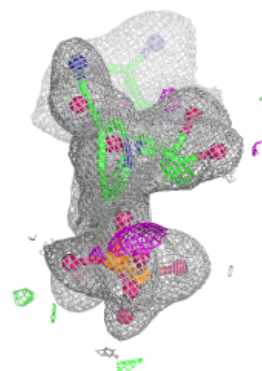
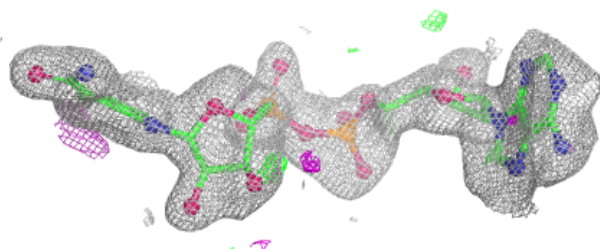
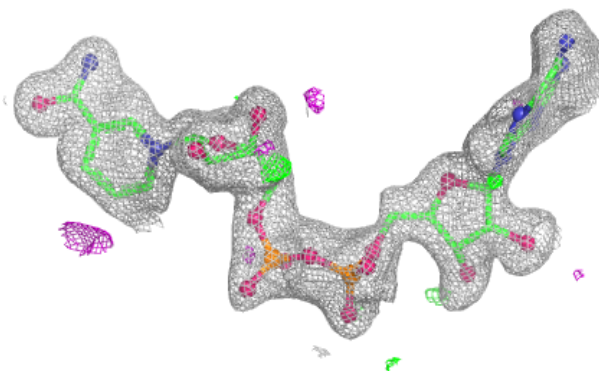
Electron density around NAI D 403:

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

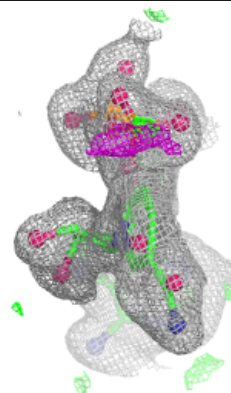
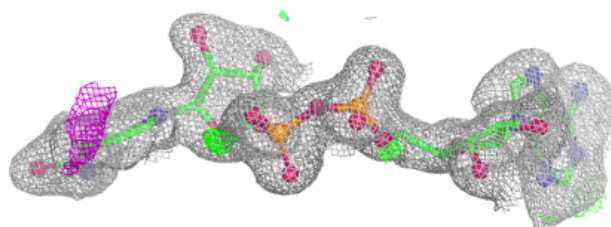
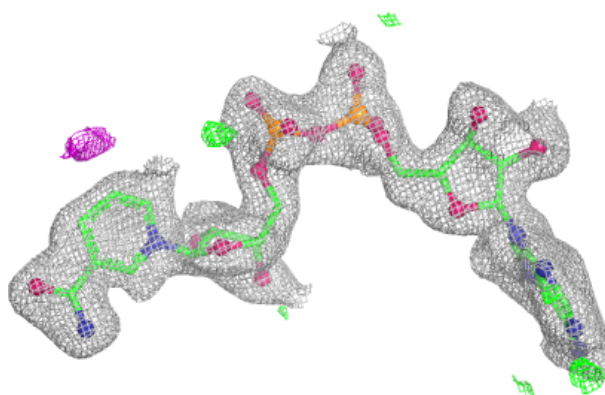


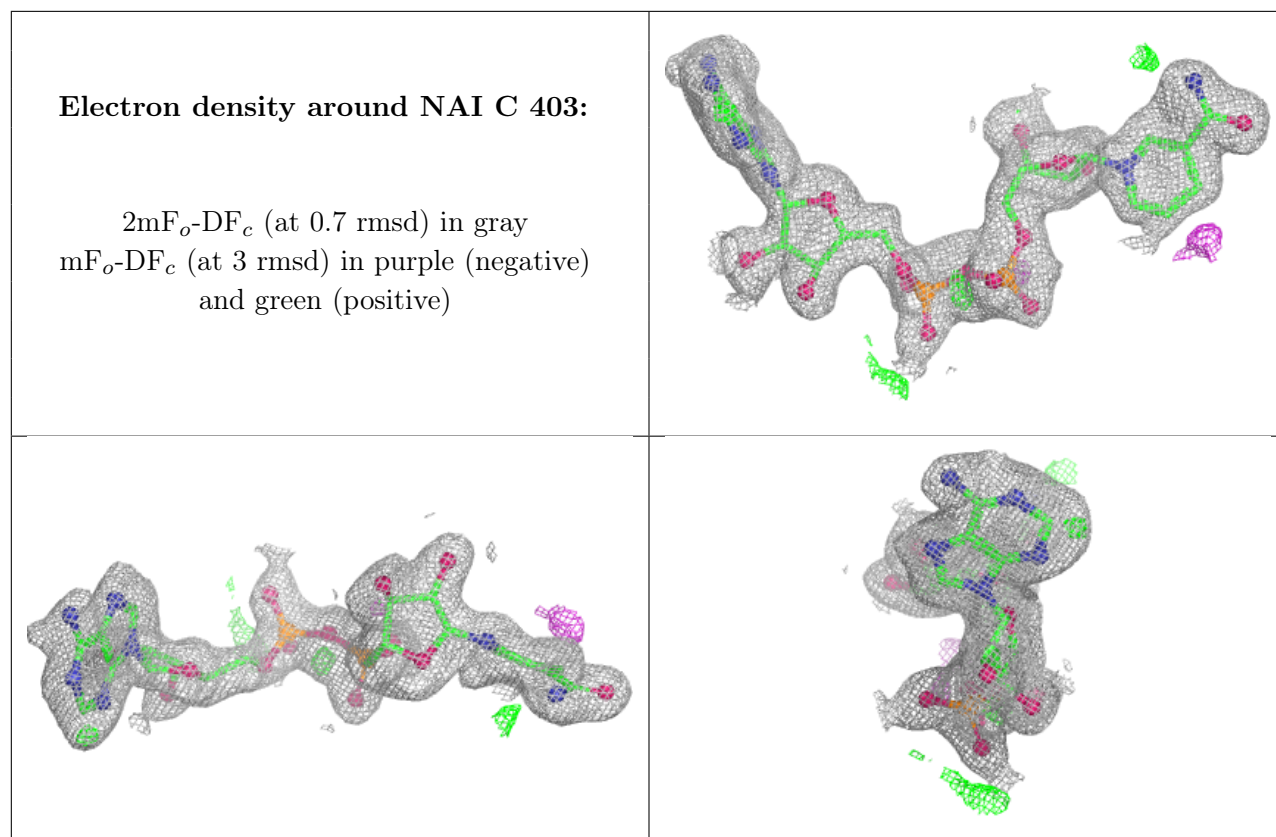
Electron density around NAI A 403:

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

**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)





6.5 Other polymers [i](#)

There are no such residues in this entry.