



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 06:20 am BST

PDB ID : 1FMC
Title : 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE COMPLEX WITH
NADH AND 7-OXO GLYCOCHENODEOXYCHOLIC ACID
Authors : Tanaka, N.; Nonaka, T.; Mitsui, Y.
Deposited on : 1996-04-26
Resolution : 1.80 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

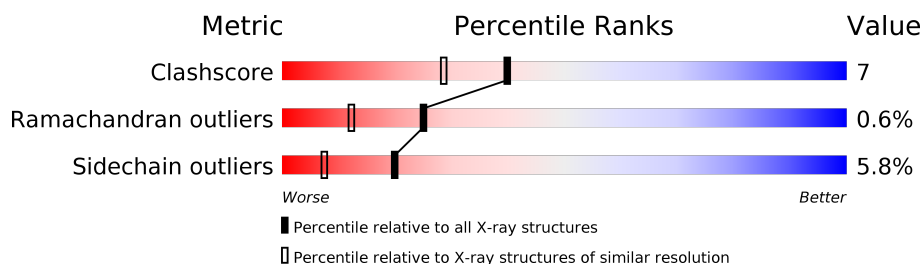
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	255	
1	B	255	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CHO	A	301	X	-	-	-
2	CHO	B	301	X	-	-	-

2 Entry composition [i](#)

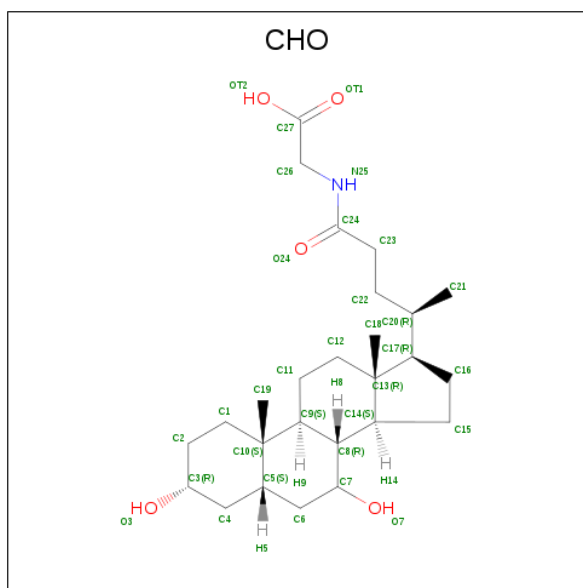
There are 4 unique types of molecules in this entry. The entry contains 4138 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 7 ALPHA-HYDROXYSTEROID DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	0	0
			1876	1174	326	364	12			
1	B	255	Total	C	N	O	S	0	0	0
			1876	1174	326	364	12			

- Molecule 2 is GLYCOCHENODEOXYCHOLIC ACID (three-letter code: CHO) (formula: $C_{26}H_{43}NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			28	24	1	3		
2	B	1	Total	C	N	O	0	0
			28	24	1	3		

- Molecule 3 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$).



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

- Molecule 4 is water.

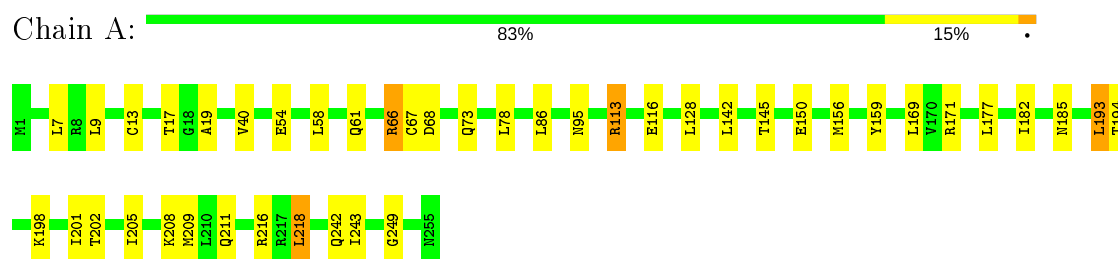
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	112	Total	O	0	0
			112	112		
4	B	130	Total	O	0	0
			130	130		

3 Residue-property plots [i](#)

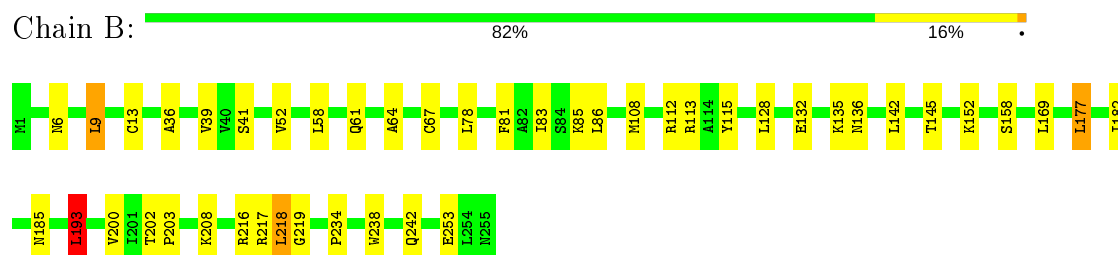
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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.

Note EDS was not executed.

• Molecule 1: 7 ALPHA-HYDROXYSTEROID DEHYDROGENASE



• Molecule 1: 7 ALPHA-HYDROXYSTEROID DEHYDROGENASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	81.65Å 81.65Å 214.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 1.80	Depositor
% Data completeness (in resolution range)	83.8 (8.00-1.80)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.207 , 0.252	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4138	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

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: NAI, CHO

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	0.53	1/1903 (0.1%)	0.68	0/2574
1	B	0.53	0/1903	0.68	0/2574
All	All	0.53	1/3806 (0.0%)	0.68	0/5148

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	150	GLU	CG-CD	5.39	1.60	1.51

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	1876	0	1882	30	0
1	B	1876	0	1882	26	0
2	A	28	0	37	1	0
2	B	28	0	37	1	0
3	A	44	0	27	2	0
3	B	44	0	27	3	0
4	A	112	0	0	4	0
4	B	130	0	0	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4138	0	3892	57	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 7.

All (57) 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:243:ILE:HG12	4:A:507:HOH:O	1.76	0.85
1:B:158:SER:HA	4:B:509:HOH:O	1.78	0.82
1:B:132:GLU:O	1:B:135:LYS:HG2	1.93	0.68
1:A:202:THR:HG22	1:A:205:ILE:HG13	1.74	0.68
1:B:217:ARG:NH1	4:B:519:HOH:O	2.24	0.68
1:A:13:CYS:HB3	1:A:86:LEU:HD13	1.77	0.66
1:B:115:TYR:HE1	4:B:509:HOH:O	1.77	0.66
1:A:113:ARG:HG2	1:A:113:ARG:HH11	1.61	0.65
1:B:108:MET:O	1:B:112:ARG:HG3	1.98	0.64
1:B:13:CYS:HB3	1:B:86:LEU:HD13	1.80	0.63
1:B:136:ASN:HB2	4:B:525:HOH:O	2.01	0.60
1:B:67:CYS:HB2	4:B:429:HOH:O	2.00	0.60
1:A:202:THR:HG22	1:A:205:ILE:CG1	2.33	0.58
1:A:171:ARG:HB3	1:B:152:LYS:HG2	1.87	0.57
1:B:41:SER:OG	1:B:67:CYS:HB3	2.05	0.57
1:A:156:MET:HE1	1:A:159:TYR:HD2	1.69	0.57
1:B:145:THR:O	3:B:302:NAI:H6N	2.06	0.56
1:A:194:THR:O	1:A:198:LYS:HD3	2.06	0.56
1:A:198:LYS:HA	1:A:201:ILE:HG22	1.89	0.55
1:A:156:MET:HE1	1:A:159:TYR:CD2	2.41	0.55
1:A:185:ASN:HD22	1:A:242:GLN:H	1.54	0.55
1:A:66:ARG:HH12	1:A:68:ASP:HB2	1.72	0.55
1:A:116:GLU:OE2	1:B:112:ARG:NH2	2.40	0.54
1:B:52:VAL:HG21	1:B:64:ALA:HB2	1.88	0.54
1:A:193:LEU:HD21	1:A:218:LEU:HD23	1.89	0.54
1:B:202:THR:HB	1:B:203:PRO:HD2	1.90	0.54
1:B:83:ILE:HD11	1:B:132:GLU:HG3	1.90	0.52
1:A:193:LEU:CD2	1:A:218:LEU:HD23	2.40	0.51
1:B:193:LEU:HD23	1:B:218:LEU:HB3	1.93	0.51
1:A:177:LEU:HB3	1:A:182:ILE:HB	1.93	0.50
1:B:208:LYS:HE3	1:B:253:GLU:O	2.11	0.50
1:A:67:CYS:HB2	4:A:441:HOH:O	2.13	0.48
1:B:132:GLU:HG2	4:B:517:HOH:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:VAL:HG23	1:B:86:LEU:HD11	1.95	0.47
1:A:185:ASN:ND2	1:A:242:GLN:H	2.12	0.47
1:A:205:ILE:O	1:A:209:MET:HG3	2.16	0.46
1:B:81:PHE:CE1	1:B:85:LYS:HE3	2.51	0.46
1:A:7:LEU:HD22	4:A:443:HOH:O	2.16	0.46
1:B:6:ASN:O	1:B:234:PRO:HD2	2.15	0.45
1:A:66:ARG:HD3	1:A:66:ARG:O	2.17	0.45
1:A:54:GLU:O	1:A:58:LEU:HD13	2.17	0.45
1:A:156:MET:HE3	1:A:159:TYR:HB3	1.99	0.45
1:B:177:LEU:HB3	1:B:182:ILE:HB	1.99	0.44
1:A:113:ARG:HH11	1:A:113:ARG:CG	2.26	0.44
1:A:249:GLY:N	4:A:508:HOH:O	2.50	0.43
1:A:208:LYS:HA	1:A:211:GLN:HG2	2.00	0.43
1:B:219:GLY:HA2	4:B:519:HOH:O	2.18	0.42
1:B:185:ASN:HD22	1:B:242:GLN:H	1.67	0.42
1:B:52:VAL:CG2	1:B:64:ALA:HB2	2.49	0.42
1:A:145:THR:O	3:A:302:NAI:H6N	2.20	0.42
1:A:17:THR:O	1:A:95:ASN:HB3	2.19	0.42
1:A:19:ALA:HB3	1:A:40:VAL:HG13	2.01	0.41
3:B:302:NAI:H2A	4:B:436:HOH:O	2.20	0.41
1:A:73:GLN:H	1:A:73:GLN:CD	2.24	0.41
2:B:301:CHO:C7	3:B:302:NAI:H4N	2.51	0.41
1:B:9:LEU:HB3	1:B:36:ALA:HB2	2.03	0.40
2:A:301:CHO:C7	3:A:302:NAI:H4N	2.51	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	253/255 (99%)	245 (97%)	7 (3%)	1 (0%)	34 21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	253/255 (99%)	248 (98%)	3 (1%)	2 (1%)	19	7
All	All	506/510 (99%)	493 (97%)	10 (2%)	3 (1%)	25	12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	216	ARG
1	B	216	ARG
1	B	193	LEU

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	197/197 (100%)	187 (95%)	10 (5%)	24	10
1	B	197/197 (100%)	184 (93%)	13 (7%)	16	5
All	All	394/394 (100%)	371 (94%)	23 (6%)	20	7

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	61	GLN
1	A	66	ARG
1	A	78	LEU
1	A	113	ARG
1	A	128	LEU
1	A	142	LEU
1	A	169	LEU
1	A	193	LEU
1	A	218	LEU
1	B	9	LEU
1	B	58	LEU
1	B	61	GLN

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Mol	Chain	Res	Type
1	B	78	LEU
1	B	113	ARG
1	B	128	LEU
1	B	142	LEU
1	B	169	LEU
1	B	177	LEU
1	B	193	LEU
1	B	200	VAL
1	B	218	LEU
1	B	238	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	56	GLN
1	A	61	GLN
1	A	181	ASN
1	A	185	ASN
1	A	211	GLN
1	A	212	HIS
1	B	56	GLN
1	B	185	ASN
1	B	212	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAI	A	302	-	42,48,48	1.47	6 (14%)	47,73,73	1.14	3 (6%)
3	NAI	B	302	-	42,48,48	1.50	6 (14%)	47,73,73	1.20	4 (8%)
2	CHO	B	301	-	31,31,35	2.06	5 (16%)	49,49,54	1.75	5 (10%)
2	CHO	A	301	-	31,31,35	1.89	4 (12%)	49,49,54	1.62	4 (8%)

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	A	302	-	-	2/25/72/72	0/5/5/5
3	NAI	B	302	-	-	5/25/72/72	0/5/5/5
2	CHO	B	301	-	1/1/11/13	0/9/70/75	0/4/4/4
2	CHO	A	301	-	1/1/11/13	0/9/70/75	0/4/4/4

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	CHO	O7-C7	-9.14	1.24	1.43
2	A	301	CHO	O7-C7	-8.65	1.25	1.43
3	A	302	NAI	C4N-C3N	-5.01	1.40	1.49
3	B	302	NAI	C4N-C3N	-4.87	1.40	1.49
3	B	302	NAI	C6N-C5N	3.98	1.40	1.33
3	B	302	NAI	C4N-C5N	-3.72	1.39	1.48
3	A	302	NAI	C4N-C5N	-3.33	1.40	1.48
3	A	302	NAI	C7N-C3N	3.26	1.55	1.48
3	A	302	NAI	C6N-C5N	3.10	1.38	1.33
3	B	302	NAI	C7N-C3N	2.75	1.54	1.48
2	A	301	CHO	C24-N25	-2.64	1.24	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	CHO	C13-C17	2.61	1.60	1.55
2	B	301	CHO	C24-N25	-2.52	1.24	1.32
2	B	301	CHO	C10-C5	2.42	1.59	1.55
2	B	301	CHO	C10-C9	2.38	1.60	1.56
2	A	301	CHO	C10-C5	2.38	1.59	1.55
3	B	302	NAI	O4B-C1B	2.23	1.44	1.41
3	B	302	NAI	C2N-C3N	2.20	1.41	1.34
2	A	301	CHO	C10-C9	2.14	1.60	1.56
3	A	302	NAI	C2N-C3N	2.06	1.40	1.34
3	A	302	NAI	C5A-N7A	-2.00	1.32	1.39

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	CHO	O7-C7-C8	6.58	124.12	109.43
2	B	301	CHO	O7-C7-C8	6.16	123.18	109.43
2	A	301	CHO	O7-C7-C6	5.68	124.02	109.94
2	B	301	CHO	O7-C7-C6	5.63	123.91	109.94
2	B	301	CHO	C5-C6-C7	-4.82	109.15	114.46
2	B	301	CHO	C9-C8-C7	-3.82	107.30	111.88
3	B	302	NAI	N3A-C2A-N1A	-3.70	122.89	128.68
3	A	302	NAI	N3A-C2A-N1A	-3.69	122.92	128.68
2	A	301	CHO	C9-C8-C7	-3.66	107.49	111.88
3	A	302	NAI	C4A-C5A-N7A	3.43	112.97	109.40
2	A	301	CHO	C19-C10-C1	-2.52	104.19	108.26
3	B	302	NAI	C5A-C6A-N1A	-2.43	114.85	120.35
3	A	302	NAI	C3N-C2N-N1N	-2.32	119.79	123.10
2	B	301	CHO	C22-C20-C17	-2.27	105.59	110.28
3	B	302	NAI	C4A-C5A-N7A	2.26	111.75	109.40
3	B	302	NAI	C3N-C2N-N1N	-2.07	120.14	123.10

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	301	CHO	C7
2	A	301	CHO	C7

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	302	NAI	C5D-O5D-PN-O2N
3	A	302	NAI	O4D-C1D-N1N-C6N

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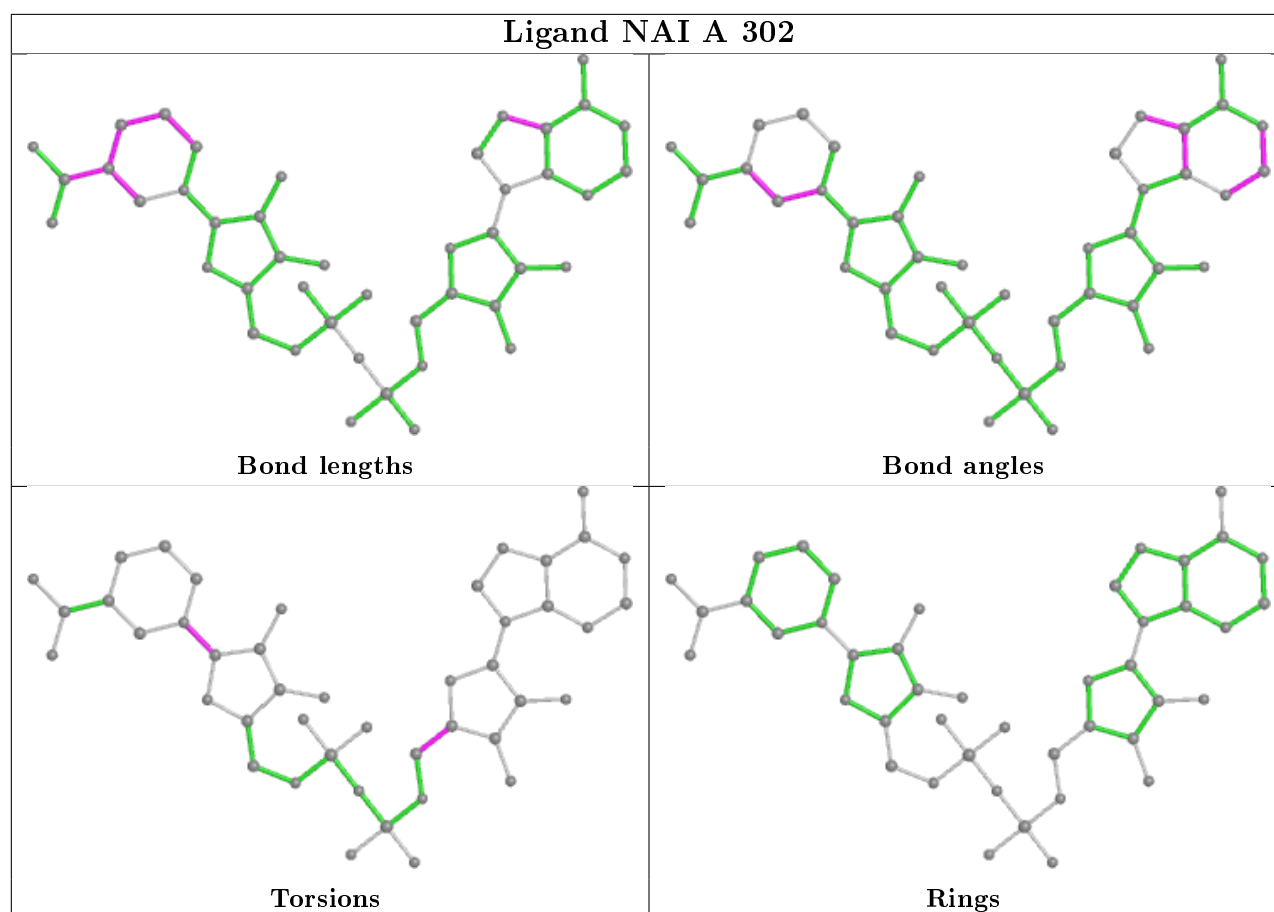
Mol	Chain	Res	Type	Atoms
3	B	302	NAI	O4D-C1D-N1N-C6N
3	B	302	NAI	C5D-O5D-PN-O1N
3	B	302	NAI	O4B-C4B-C5B-O5B
3	B	302	NAI	C5D-O5D-PN-O3
3	A	302	NAI	O4B-C4B-C5B-O5B

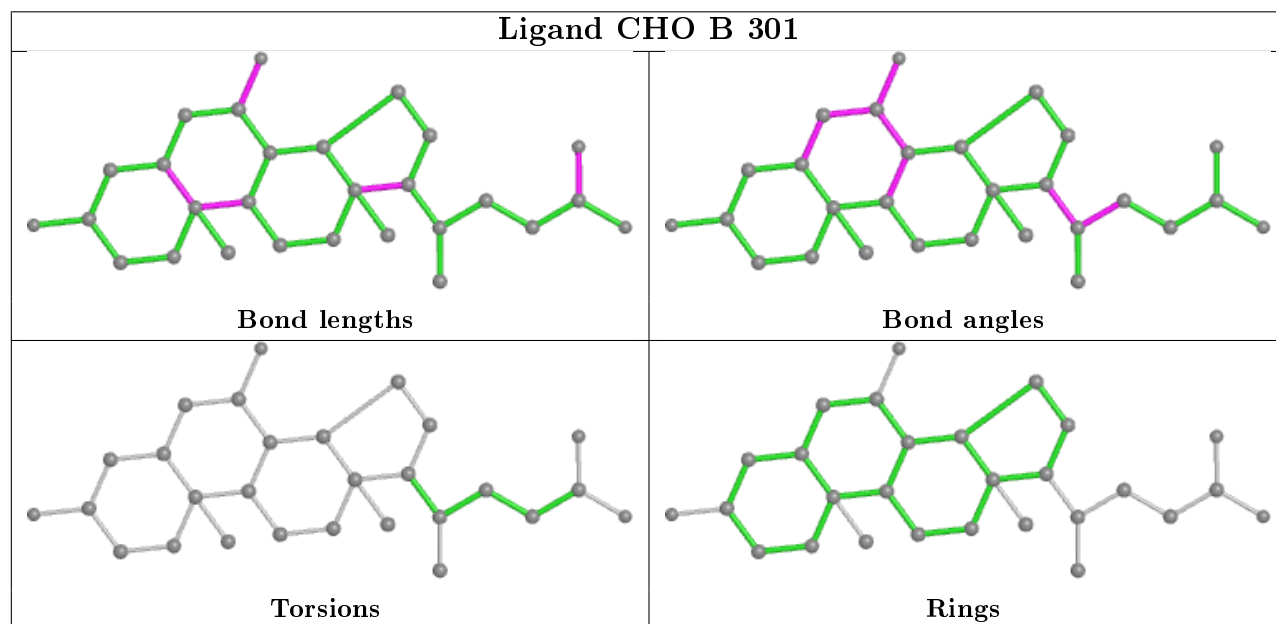
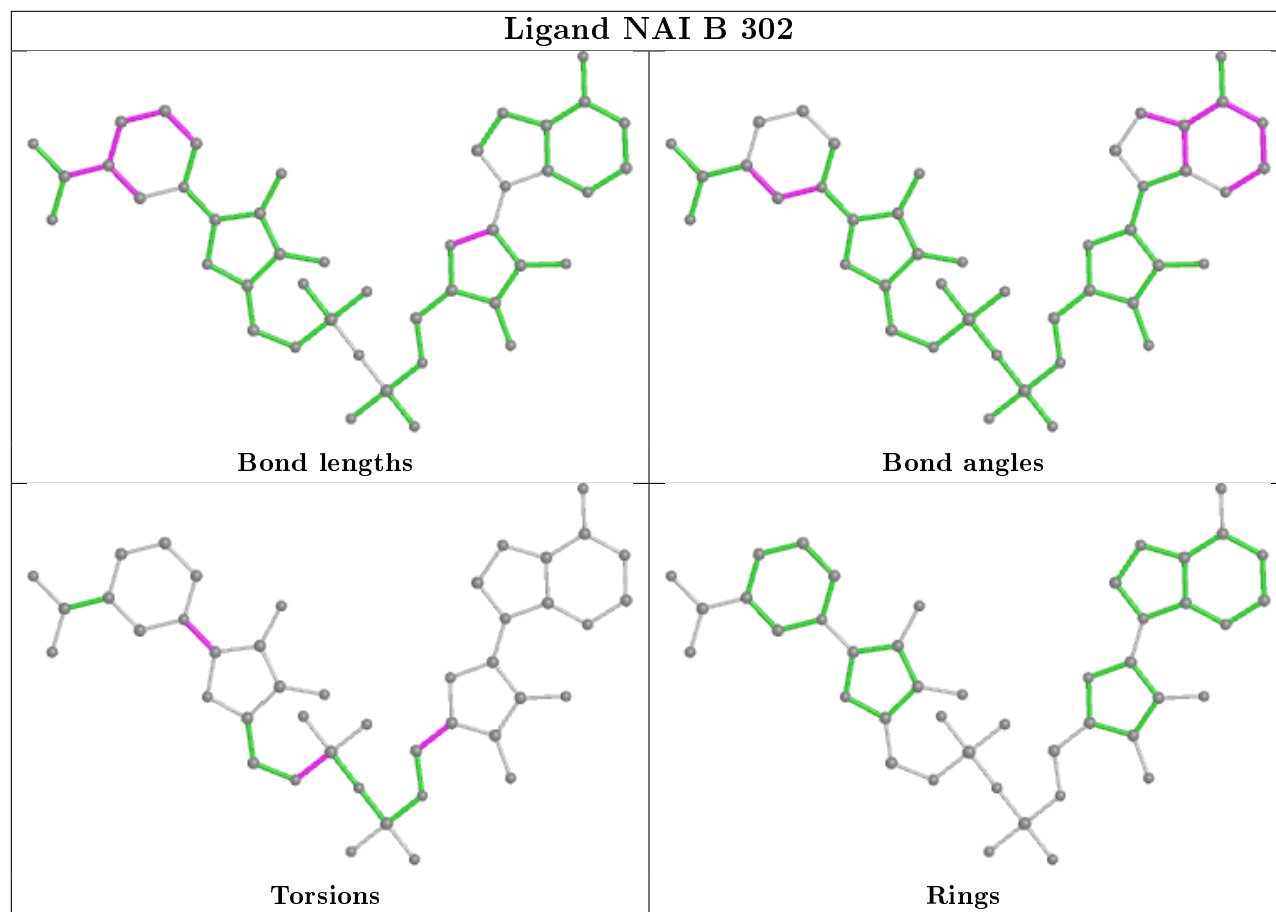
There are no ring outliers.

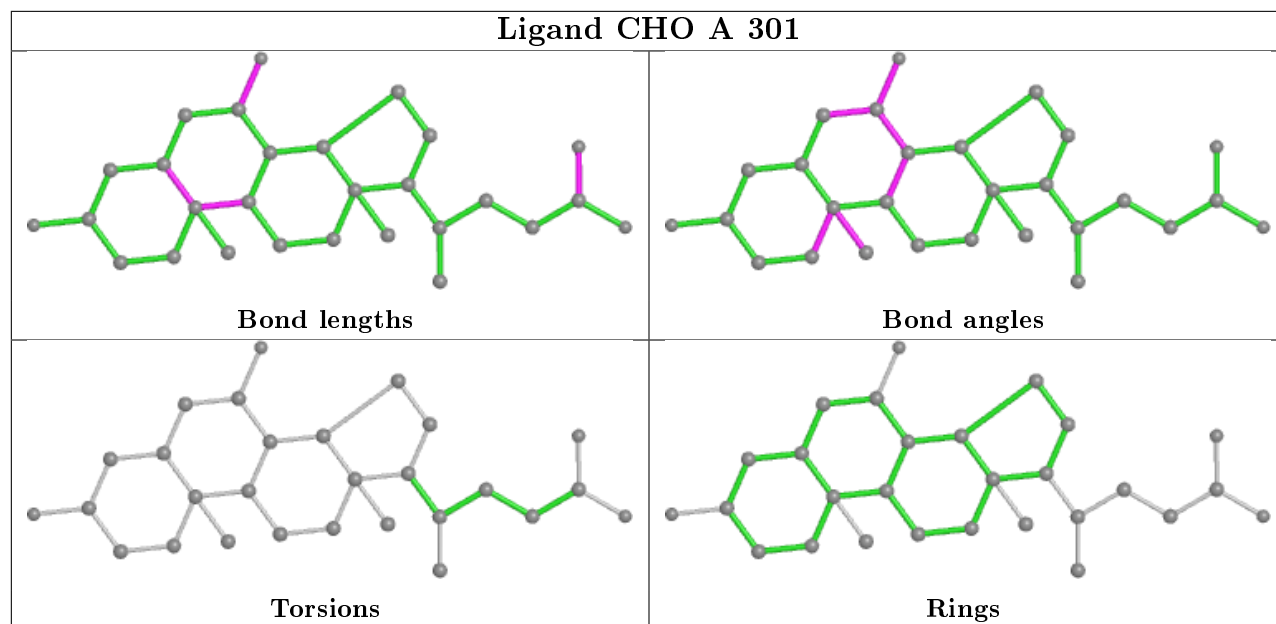
4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302	NAI	2	0
3	B	302	NAI	3	0
2	B	301	CHO	1	0
2	A	301	CHO	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 ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.