

wwPDB X-ray Structure Validation Summary Report (i)

Dec 10, 2023 – 08:52 am GMT

PDB ID : 2C20

Title : CRYSTAL STRUCTURE OF UDP-GLUCOSE 4-EPIMERASE

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Deposited on : 2005-09-22

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 (i) 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.4, 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)

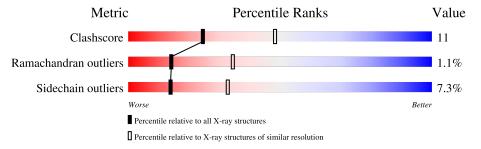
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (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 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain					
1	A	330	70%	28%	•			
1	В	330	71%	25%	•			
1	С	330	77%	21%	••			
1	D	330	70%	26%	-			
1	Е	330	74%	23%	·			
1	F	330	75%	21%				



2 Entry composition (i)

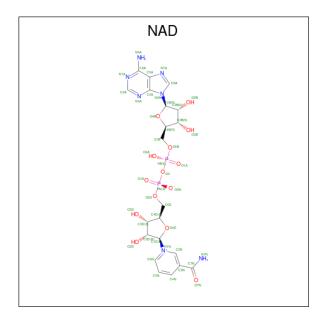
There are 4 unique types of molecules in this entry. The entry contains 16074 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 UDP-GLUCOSE 4-EPIMERASE.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	A	329	Total	С	Ν	О	S	0	1	0
1	Λ	329	2595	1645	440	499	11	U	1	
1	В	329	Total	С	N	О	S	0	1	0
1	Ъ	329	2595	1645	440	499	11	U	1	
1	С	329	Total	С	N	О	S	0	1	0
1		329	2595	1645	440	499	11	U	1	
1	D	329	Total	С	N	О	S	0	1	0
1	D	329	2595	1645	440	499	11	U	1	
1	Е	329	Total	С	N	O	S	0	1	0
1	ш	323	2595	1645	440	499	11	U	1	
1	F	329	Total	С	N	О	S	0	1	0
1	I.	329	2595	1645	440	499	11	U	1	

• Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).





Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
2	Λ	1	Total	С	N	О	Р	0	0
2	A	1	44	21	7	14	2	U	0
2	В	1	Total	С	N	О	Р	0	0
2	Б	1	44	21	7	14	2	U	0
2	С	1	Total	С	N	О	Р	0	0
2		1	44	21	7	14	2	U	
2	D	1	Total	С	N	О	Р	0	0
2	D	1	44	21	7	14	2	U	
2	E	1	Total	С	N	О	Р	0	0
2	<u> </u>	1	44	21	7	14	2	U	
2	F	1	Total	С	N	О	Р	0	0
	Г	1	44	21	7	14	2	U	

• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Zn 1 1	0	0
3	В	1	Total Zn 1 1	0	0
3	С	1	Total Zn 1 1	0	0
3	D	1	Total Zn 1 1	0	0
3	E	1	Total Zn 1 1	0	0
3	F	1	Total Zn 1 1	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	41	Total O 41 41	0	0
4	В	41	Total O 41 41	0	0
4	С	38	Total O 38 38	0	0
4	D	36	Total O 36 36	0	0
4	E	36	Total O 36 36	0	0
4	F	42	Total O 42 42	0	0

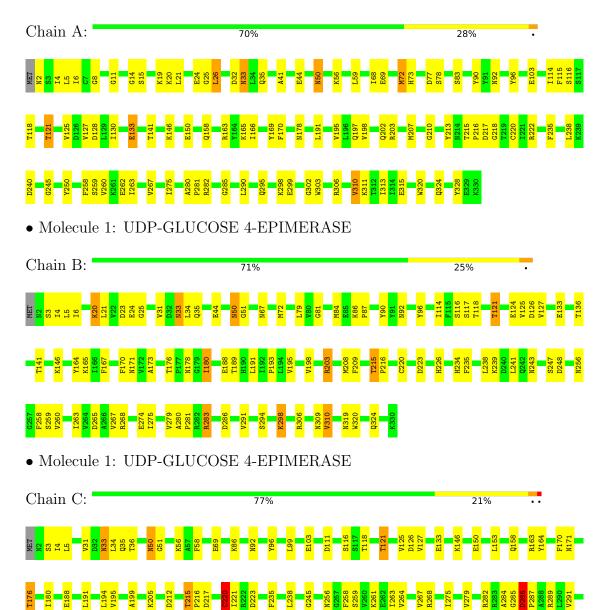


3 Residue-property plots (i)

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

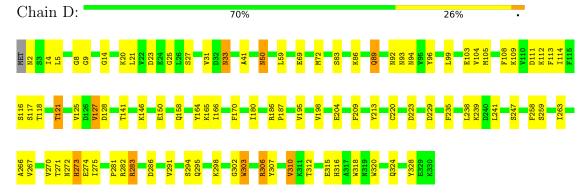
• Molecule 1: UDP-GLUCOSE 4-EPIMERASE



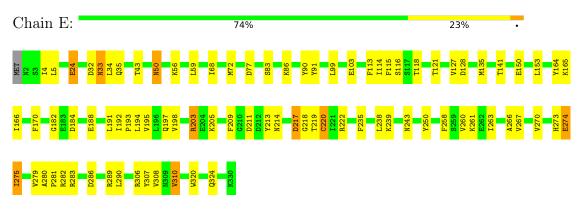




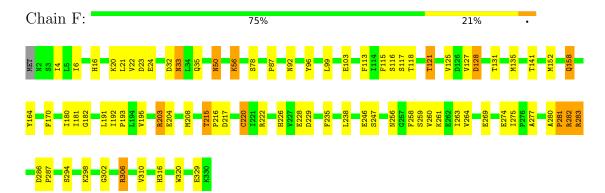
• Molecule 1: UDP-GLUCOSE 4-EPIMERASE



• Molecule 1: UDP-GLUCOSE 4-EPIMERASE



• Molecule 1: UDP-GLUCOSE 4-EPIMERASE





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 32 1 2	Depositor	
Cell constants	136.16Å 136.16Å 248.65Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	25.02 - 2.70	Depositor	
% Data completeness	73.1 (25.02-2.70)	Depositor	
(in resolution range)	10.1 (20.02 2.10)	Depositor	
R_{merge}	0.08	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	REFMAC 5.2.0005	Depositor	
R, R_{free}	0.205 , 0.276	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	16074	wwPDB-VP	
Average B, all atoms (Å ²)	16.0	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: ZN, NAD

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	Bo	nd lengths	Bo	Bond angles		
MIOI	Moi Chain		# Z > 5	RMSZ	# Z > 5		
1	A	0.67	1/2656~(0.0%)	0.72	0/3600		
1	В	0.71	$1/2656 \ (0.0\%)$	0.73	0/3600		
1	С	0.69	1/2656~(0.0%)	0.72	0/3600		
1	D	0.63	0/2656	0.71	0/3600		
1	Е	1.15	$2/2656 \ (0.1\%)$	0.73	2/3600 (0.1%)		
1	F	0.68	$1/2656 \ (0.0\%)$	0.71	0/3600		
All	All	0.78	$6/15936 \ (0.0\%)$	0.72	$2/21600 \ (0.0\%)$		

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
1	Е	274	GLU	CD-OE2	36.08	1.65	1.25
1	Е	274	GLU	CD-OE1	30.32	1.59	1.25
1	В	44	GLU	CD-OE2	6.86	1.33	1.25
1	F	220	CYS	CB-SG	-6.49	1.71	1.82
1	С	220	CYS	CB-SG	-6.08	1.72	1.82

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	Е	274	GLU	OE1-CD-OE2	9.22	134.37	123.30
1	Е	184	ASP	CB-CG-OD1	5.31	123.08	118.30

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	2595	0	2513	62	0
1	В	2595	0	2513	57	0
1	С	2595	0	2513	52	0
1	D	2595	0	2513	59	0
1	Е	2595	0	2513	48	0
1	F	2595	0	2513	57	0
2	A	44	0	26	4	0
2	В	44	0	26	1	0
2	С	44	0	26	2	0
2	D	44	0	26	1	0
2	Е	44	0	26	2	0
2	F	44	0	26	3	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
3	С	1	0	0	0	0
3	D	1	0	0	0	0
3	Е	1	0	0	0	0
3	F	1	0	0	0	0
4	A	41	0	0	0	0
4	В	41	0	0	0	0
4	С	38	0	0	1	0
4	D	36	0	0	0	0
4	Е	36	0	0	1	0
4	F	42	0	0	1	0
All	All	16074	0	15234	337	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 11.

The worst 5 of 337 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:E:274:GLU:CD	1:E:274:GLU:OE2	1.65	1.35
1:C:212:ASP:C	1:C:282:ARG:HH22	1.59	1.03
1:F:158:GLN:HE21	1:F:158:GLN:HA	1.35	0.92

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Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:E:280:ALA:HB1	1:E:281:PRO:HD2	1.53	0.91
1:F:158:GLN:HE21	1:F:158:GLN:CA	1.84	0.90

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	328/330~(99%)	297 (90%)	27 (8%)	4 (1%)	13 32
1	В	328/330 (99%)	307 (94%)	19 (6%)	2 (1%)	25 50
1	С	328/330 (99%)	309 (94%)	17 (5%)	2 (1%)	25 50
1	D	328/330 (99%)	302 (92%)	22 (7%)	4 (1%)	13 32
1	Е	328/330 (99%)	291 (89%)	33 (10%)	4 (1%)	13 32
1	F	328/330 (99%)	301 (92%)	22 (7%)	5 (2%)	10 26
All	All	1968/1980 (99%)	1807 (92%)	140 (7%)	21 (1%)	14 34

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	С	286	ASP
1	A	25	GLY
1	D	272	ASN
1	F	281	PRO
1	F	282	ARG

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	Perce	entiles
1	A	$276/277\ (100\%)$	258 (94%)	18 (6%)	17	38
1	В	276/277 (100%)	250 (91%)	26 (9%)	8	20
1	С	276/277 (100%)	256 (93%)	20 (7%)	14	34
1	D	276/277 (100%)	258 (94%)	18 (6%)	17	38
1	E	276/277 (100%)	259 (94%)	17 (6%)	18	40
1	F	276/277 (100%)	254 (92%)	22 (8%)	12	27
All	All	1656/1662 (100%)	1535 (93%)	121 (7%)	14	33

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	235	PHE
1	F	180	ILE
1	D	121	THR
1	F	158	GLN
1	F	306	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	89	GLN
1	F	158	GLN
1	С	33	ASN
1	В	319	ASN
1	F	171	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAD	A	401	1	42,48,48	1.92	4 (9%)	50,73,73	1.35	6 (12%)
2	NAD	В	401	-	42,48,48	1.86	4 (9%)	50,73,73	1.48	7 (14%)
2	NAD	D	401	-	42,48,48	1.92	5 (11%)	50,73,73	1.44	4 (8%)
2	NAD	С	401	-	42,48,48	1.88	4 (9%)	50,73,73	1.48	6 (12%)
2	NAD	E	401	-	42,48,48	1.92	4 (9%)	50,73,73	1.56	8 (16%)
2	NAD	F	401	-	42,48,48	1.81	4 (9%)	50,73,73	1.39	7 (14%)

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	NAD	A	401	1	-	8/26/62/62	0/5/5/5
2	NAD	В	401	-	-	5/26/62/62	0/5/5/5
2	NAD	D	401	-	-	11/26/62/62	0/5/5/5
2	NAD	С	401	-	-	12/26/62/62	0/5/5/5
2	NAD	Е	401	-	-	3/26/62/62	0/5/5/5
2	NAD	F	401	-	-	9/26/62/62	0/5/5/5

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

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	Ideal(A)
2	A	401	NAD	O7N-C7N	9.67	1.42	1.24

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Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	D	401	NAD	O7N-C7N	9.61	1.42	1.24
2	F	401	NAD	O7N-C7N	9.29	1.41	1.24
2	С	401	NAD	O7N-C7N	9.28	1.41	1.24
2	В	401	NAD	O7N-C7N	9.27	1.41	1.24

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	D	401	NAD	N3A-C2A-N1A	-6.66	118.27	128.68
2	В	401	NAD	N3A-C2A-N1A	-5.91	119.44	128.68
2	Е	401	NAD	N3A-C2A-N1A	-5.61	119.91	128.68
2	F	401	NAD	N3A-C2A-N1A	-5.47	120.13	128.68
2	A	401	NAD	N3A-C2A-N1A	-5.38	120.26	128.68

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	NAD	C5D-O5D-PN-O2N
2	В	401	NAD	C5D-O5D-PN-O2N
2	С	401	NAD	C5B-O5B-PA-O1A
2	С	401	NAD	PN-O3-PA-O5B
2	С	401	NAD	C5D-O5D-PN-O2N

There are no ring outliers.

6 monomers are involved in 13 short contacts:

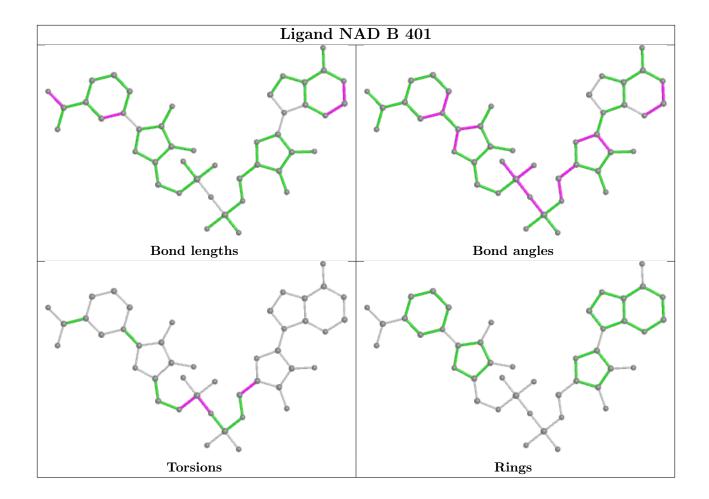
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	NAD	4	0
2	В	401	NAD	1	0
2	D	401	NAD	1	0
2	С	401	NAD	2	0
2	Е	401	NAD	2	0
2	F	401	NAD	3	0

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 then 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

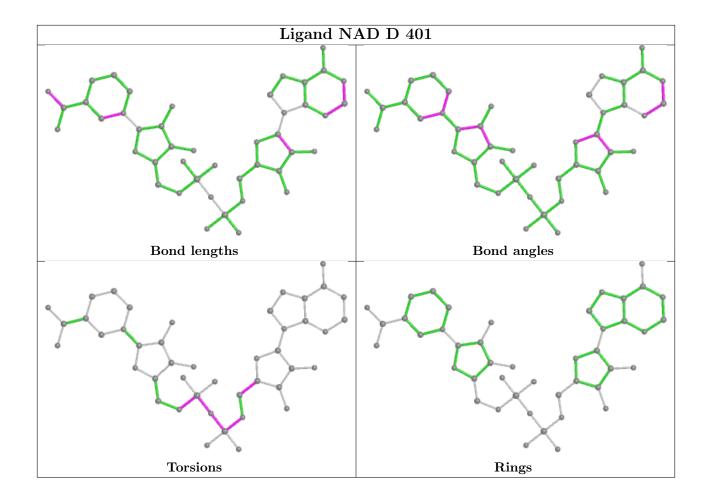


highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

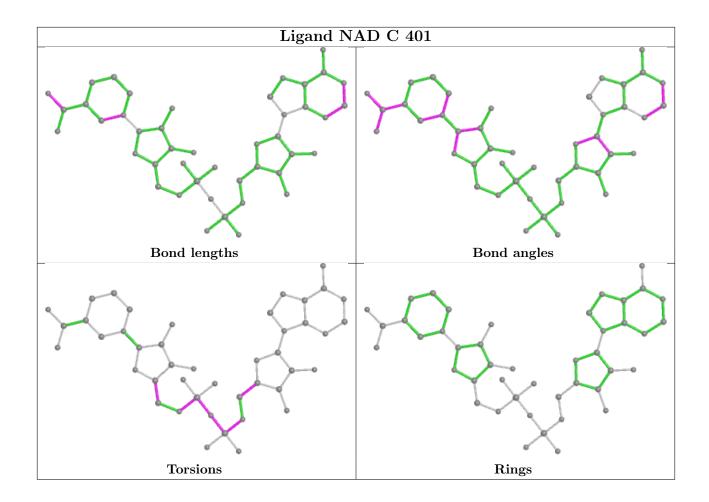




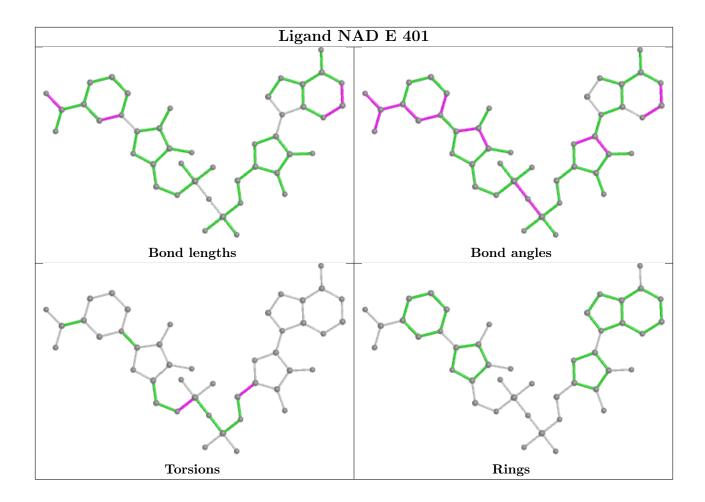




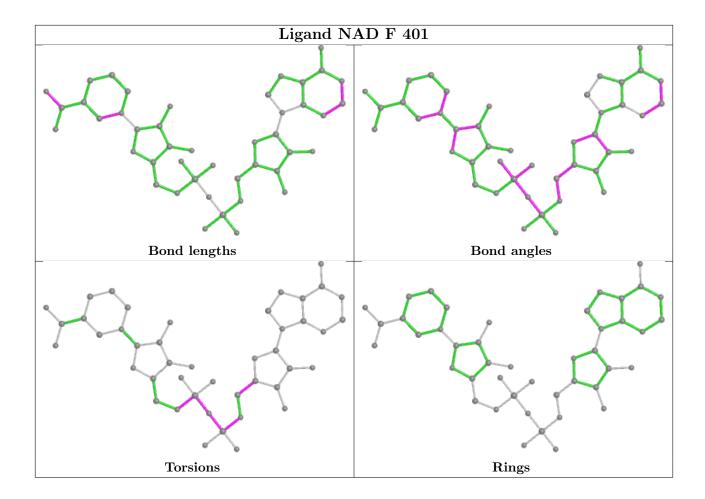












5.7 Other polymers (i)

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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

