



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 10, 2023 – 10:27 AM EDT

PDB ID : 4J4T  
Title : Crystal Structure of FabI from *F. tularensis* in complex with novel inhibitors based on the benzimidazole scaffold  
Authors : Mehboob, S.; Boci, T.; Brubaker, L.; Santarsiero, B.D.; Johnson, M.E.  
Deposited on : 2013-02-07  
Resolution : 2.34 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](mailto: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>.

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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 : 2.35.1  
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) : 2.35.1

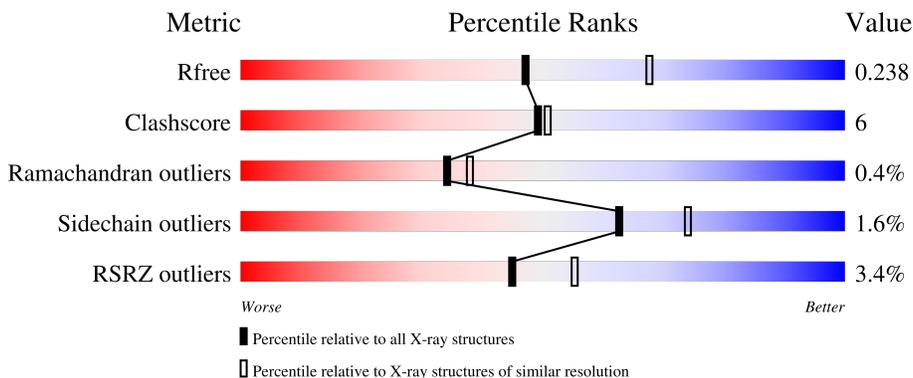
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.34 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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  $\geq 3$ , 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	280	 3% 82% 9% 8%
1	B	280	 3% 81% 11% 8%
1	C	280	 3% 81% 10% 8%
1	D	280	 4% 81% 10% 8%
1	E	280	 3% 83% 9% 8%

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Mol	Chain	Length	Quality of chain
1	F	280	<p>4% 82% 10% 8%</p>
1	G	280	<p>2% 81% 11% 8%</p>
1	H	280	<p>4% 79% 12% 8%</p>

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
4	GOL	D	303	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 16987 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 Enoyl-[acyl-carrier-protein] reductase [NADH].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	259	Total 1942	C 1234	N 324	O 367	S 17	0	1	0
1	B	259	Total 1942	C 1234	N 324	O 367	S 17	0	1	0
1	C	259	Total 1944	C 1235	N 325	O 367	S 17	0	1	0
1	D	259	Total 1948	C 1237	N 325	O 368	S 18	0	2	0
1	E	259	Total 1942	C 1234	N 324	O 367	S 17	0	1	0
1	F	259	Total 1945	C 1235	N 325	O 368	S 17	0	1	0
1	G	259	Total 1936	C 1230	N 324	O 366	S 16	0	1	0
1	H	259	Total 1942	C 1234	N 324	O 367	S 17	0	1	0

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q5NGQ3
A	-18	GLY	-	expression tag	UNP Q5NGQ3
A	-17	SER	-	expression tag	UNP Q5NGQ3
A	-16	SER	-	expression tag	UNP Q5NGQ3
A	-15	HIS	-	expression tag	UNP Q5NGQ3
A	-14	HIS	-	expression tag	UNP Q5NGQ3
A	-13	HIS	-	expression tag	UNP Q5NGQ3
A	-12	HIS	-	expression tag	UNP Q5NGQ3
A	-11	HIS	-	expression tag	UNP Q5NGQ3
A	-10	HIS	-	expression tag	UNP Q5NGQ3
A	-9	SER	-	expression tag	UNP Q5NGQ3
A	-8	SER	-	expression tag	UNP Q5NGQ3
A	-7	GLY	-	expression tag	UNP Q5NGQ3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP Q5NGQ3
A	-5	VAL	-	expression tag	UNP Q5NGQ3
A	-4	PRO	-	expression tag	UNP Q5NGQ3
A	-3	ARG	-	expression tag	UNP Q5NGQ3
A	-2	GLY	-	expression tag	UNP Q5NGQ3
A	-1	SER	-	expression tag	UNP Q5NGQ3
A	0	HIS	-	expression tag	UNP Q5NGQ3
B	-19	MET	-	expression tag	UNP Q5NGQ3
B	-18	GLY	-	expression tag	UNP Q5NGQ3
B	-17	SER	-	expression tag	UNP Q5NGQ3
B	-16	SER	-	expression tag	UNP Q5NGQ3
B	-15	HIS	-	expression tag	UNP Q5NGQ3
B	-14	HIS	-	expression tag	UNP Q5NGQ3
B	-13	HIS	-	expression tag	UNP Q5NGQ3
B	-12	HIS	-	expression tag	UNP Q5NGQ3
B	-11	HIS	-	expression tag	UNP Q5NGQ3
B	-10	HIS	-	expression tag	UNP Q5NGQ3
B	-9	SER	-	expression tag	UNP Q5NGQ3
B	-8	SER	-	expression tag	UNP Q5NGQ3
B	-7	GLY	-	expression tag	UNP Q5NGQ3
B	-6	LEU	-	expression tag	UNP Q5NGQ3
B	-5	VAL	-	expression tag	UNP Q5NGQ3
B	-4	PRO	-	expression tag	UNP Q5NGQ3
B	-3	ARG	-	expression tag	UNP Q5NGQ3
B	-2	GLY	-	expression tag	UNP Q5NGQ3
B	-1	SER	-	expression tag	UNP Q5NGQ3
B	0	HIS	-	expression tag	UNP Q5NGQ3
C	-19	MET	-	expression tag	UNP Q5NGQ3
C	-18	GLY	-	expression tag	UNP Q5NGQ3
C	-17	SER	-	expression tag	UNP Q5NGQ3
C	-16	SER	-	expression tag	UNP Q5NGQ3
C	-15	HIS	-	expression tag	UNP Q5NGQ3
C	-14	HIS	-	expression tag	UNP Q5NGQ3
C	-13	HIS	-	expression tag	UNP Q5NGQ3
C	-12	HIS	-	expression tag	UNP Q5NGQ3
C	-11	HIS	-	expression tag	UNP Q5NGQ3
C	-10	HIS	-	expression tag	UNP Q5NGQ3
C	-9	SER	-	expression tag	UNP Q5NGQ3
C	-8	SER	-	expression tag	UNP Q5NGQ3
C	-7	GLY	-	expression tag	UNP Q5NGQ3
C	-6	LEU	-	expression tag	UNP Q5NGQ3
C	-5	VAL	-	expression tag	UNP Q5NGQ3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	PRO	-	expression tag	UNP Q5NGQ3
C	-3	ARG	-	expression tag	UNP Q5NGQ3
C	-2	GLY	-	expression tag	UNP Q5NGQ3
C	-1	SER	-	expression tag	UNP Q5NGQ3
C	0	HIS	-	expression tag	UNP Q5NGQ3
D	-19	MET	-	expression tag	UNP Q5NGQ3
D	-18	GLY	-	expression tag	UNP Q5NGQ3
D	-17	SER	-	expression tag	UNP Q5NGQ3
D	-16	SER	-	expression tag	UNP Q5NGQ3
D	-15	HIS	-	expression tag	UNP Q5NGQ3
D	-14	HIS	-	expression tag	UNP Q5NGQ3
D	-13	HIS	-	expression tag	UNP Q5NGQ3
D	-12	HIS	-	expression tag	UNP Q5NGQ3
D	-11	HIS	-	expression tag	UNP Q5NGQ3
D	-10	HIS	-	expression tag	UNP Q5NGQ3
D	-9	SER	-	expression tag	UNP Q5NGQ3
D	-8	SER	-	expression tag	UNP Q5NGQ3
D	-7	GLY	-	expression tag	UNP Q5NGQ3
D	-6	LEU	-	expression tag	UNP Q5NGQ3
D	-5	VAL	-	expression tag	UNP Q5NGQ3
D	-4	PRO	-	expression tag	UNP Q5NGQ3
D	-3	ARG	-	expression tag	UNP Q5NGQ3
D	-2	GLY	-	expression tag	UNP Q5NGQ3
D	-1	SER	-	expression tag	UNP Q5NGQ3
D	0	HIS	-	expression tag	UNP Q5NGQ3
E	-19	MET	-	expression tag	UNP Q5NGQ3
E	-18	GLY	-	expression tag	UNP Q5NGQ3
E	-17	SER	-	expression tag	UNP Q5NGQ3
E	-16	SER	-	expression tag	UNP Q5NGQ3
E	-15	HIS	-	expression tag	UNP Q5NGQ3
E	-14	HIS	-	expression tag	UNP Q5NGQ3
E	-13	HIS	-	expression tag	UNP Q5NGQ3
E	-12	HIS	-	expression tag	UNP Q5NGQ3
E	-11	HIS	-	expression tag	UNP Q5NGQ3
E	-10	HIS	-	expression tag	UNP Q5NGQ3
E	-9	SER	-	expression tag	UNP Q5NGQ3
E	-8	SER	-	expression tag	UNP Q5NGQ3
E	-7	GLY	-	expression tag	UNP Q5NGQ3
E	-6	LEU	-	expression tag	UNP Q5NGQ3
E	-5	VAL	-	expression tag	UNP Q5NGQ3
E	-4	PRO	-	expression tag	UNP Q5NGQ3
E	-3	ARG	-	expression tag	UNP Q5NGQ3

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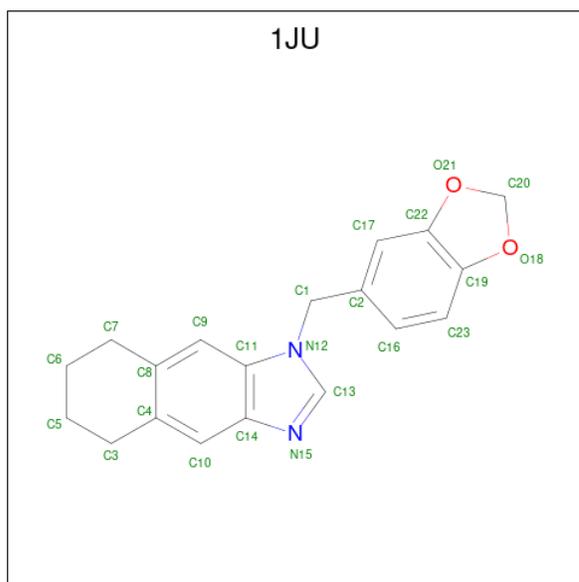
Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP Q5NGQ3
E	-1	SER	-	expression tag	UNP Q5NGQ3
E	0	HIS	-	expression tag	UNP Q5NGQ3
F	-19	MET	-	expression tag	UNP Q5NGQ3
F	-18	GLY	-	expression tag	UNP Q5NGQ3
F	-17	SER	-	expression tag	UNP Q5NGQ3
F	-16	SER	-	expression tag	UNP Q5NGQ3
F	-15	HIS	-	expression tag	UNP Q5NGQ3
F	-14	HIS	-	expression tag	UNP Q5NGQ3
F	-13	HIS	-	expression tag	UNP Q5NGQ3
F	-12	HIS	-	expression tag	UNP Q5NGQ3
F	-11	HIS	-	expression tag	UNP Q5NGQ3
F	-10	HIS	-	expression tag	UNP Q5NGQ3
F	-9	SER	-	expression tag	UNP Q5NGQ3
F	-8	SER	-	expression tag	UNP Q5NGQ3
F	-7	GLY	-	expression tag	UNP Q5NGQ3
F	-6	LEU	-	expression tag	UNP Q5NGQ3
F	-5	VAL	-	expression tag	UNP Q5NGQ3
F	-4	PRO	-	expression tag	UNP Q5NGQ3
F	-3	ARG	-	expression tag	UNP Q5NGQ3
F	-2	GLY	-	expression tag	UNP Q5NGQ3
F	-1	SER	-	expression tag	UNP Q5NGQ3
F	0	HIS	-	expression tag	UNP Q5NGQ3
G	-19	MET	-	expression tag	UNP Q5NGQ3
G	-18	GLY	-	expression tag	UNP Q5NGQ3
G	-17	SER	-	expression tag	UNP Q5NGQ3
G	-16	SER	-	expression tag	UNP Q5NGQ3
G	-15	HIS	-	expression tag	UNP Q5NGQ3
G	-14	HIS	-	expression tag	UNP Q5NGQ3
G	-13	HIS	-	expression tag	UNP Q5NGQ3
G	-12	HIS	-	expression tag	UNP Q5NGQ3
G	-11	HIS	-	expression tag	UNP Q5NGQ3
G	-10	HIS	-	expression tag	UNP Q5NGQ3
G	-9	SER	-	expression tag	UNP Q5NGQ3
G	-8	SER	-	expression tag	UNP Q5NGQ3
G	-7	GLY	-	expression tag	UNP Q5NGQ3
G	-6	LEU	-	expression tag	UNP Q5NGQ3
G	-5	VAL	-	expression tag	UNP Q5NGQ3
G	-4	PRO	-	expression tag	UNP Q5NGQ3
G	-3	ARG	-	expression tag	UNP Q5NGQ3
G	-2	GLY	-	expression tag	UNP Q5NGQ3
G	-1	SER	-	expression tag	UNP Q5NGQ3

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

- Molecule 3 is 1-(1,3-benzodioxol-5-ylmethyl)-5,6,7,8-tetrahydro-1H-naphtho[2,3-d]imidazole (three-letter code: 1JU) (formula: C<sub>19</sub>H<sub>18</sub>N<sub>2</sub>O<sub>2</sub>).



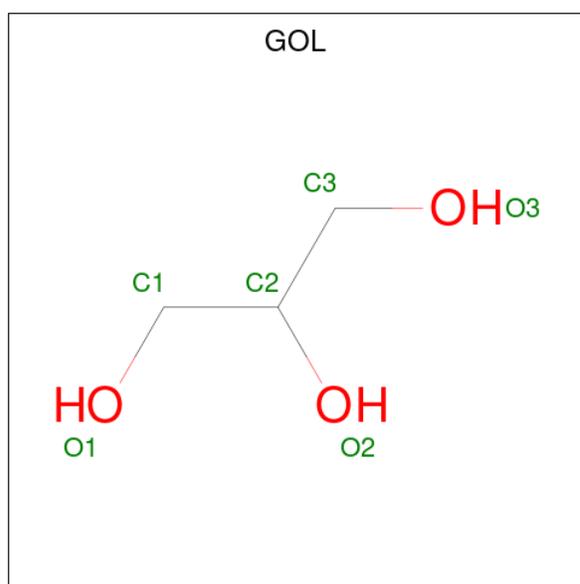
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			23	19	2	2		
3	B	1	Total	C	N	O	0	0
			23	19	2	2		
3	C	1	Total	C	N	O	0	0
			23	19	2	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			23	19	2	2		
3	E	1	Total	C	N	O	0	0
			23	19	2	2		
3	F	1	Total	C	N	O	0	0
			23	19	2	2		
3	G	1	Total	C	N	O	0	0
			23	19	2	2		
3	H	1	Total	C	N	O	0	0
			23	19	2	2		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		

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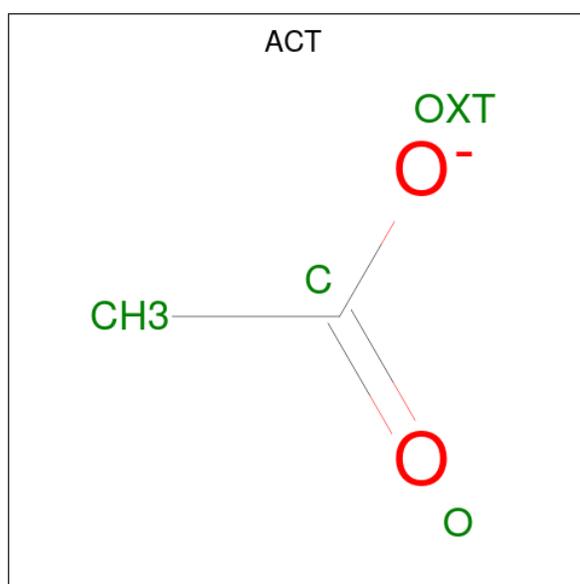
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Na	0	0
			1	1		
5	F	1	Total	Na	0	0
			1	1		
5	H	1	Total	Na	0	0
			1	1		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	120	Total	O	0	0
			120	120		

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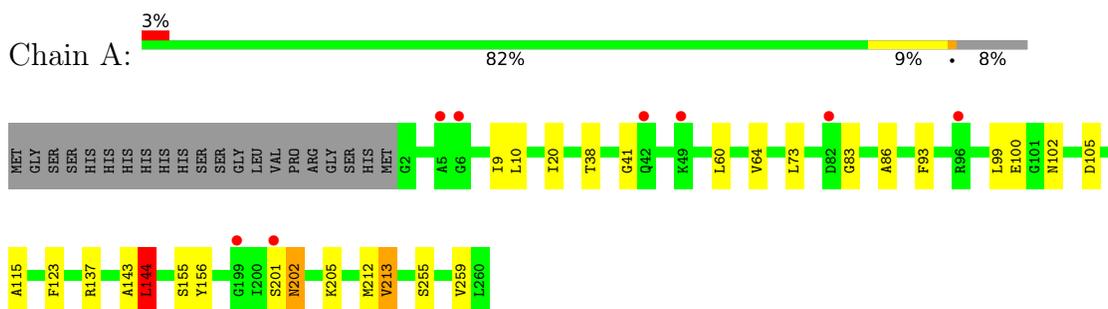
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
7	B	93	Total 93	O 93	0	0
7	C	109	Total 109	O 109	0	0
7	D	119	Total 119	O 119	0	0
7	E	95	Total 95	O 95	0	0
7	F	107	Total 107	O 107	0	0
7	G	119	Total 119	O 119	0	0
7	H	95	Total 95	O 95	0	0

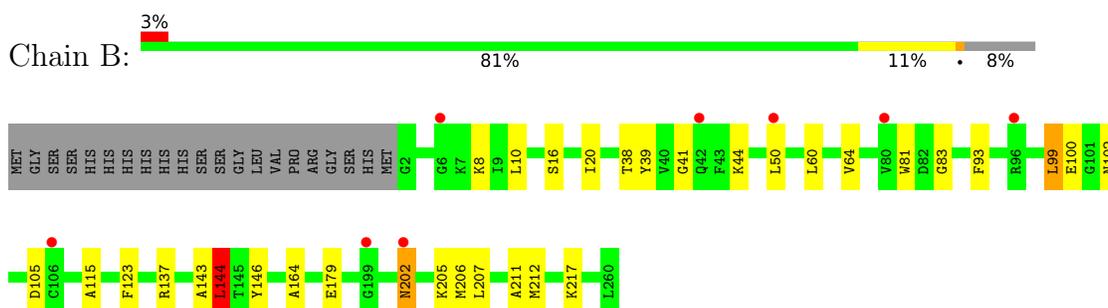
### 3 Residue-property plots [i](#)

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 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.

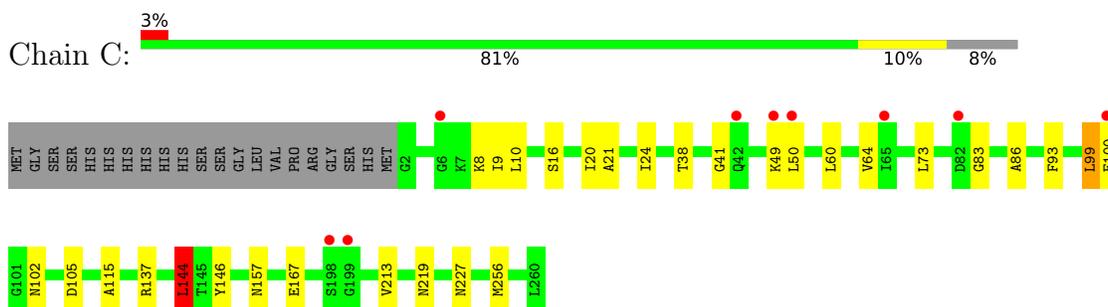
- Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]



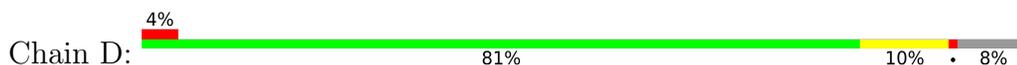
- Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]

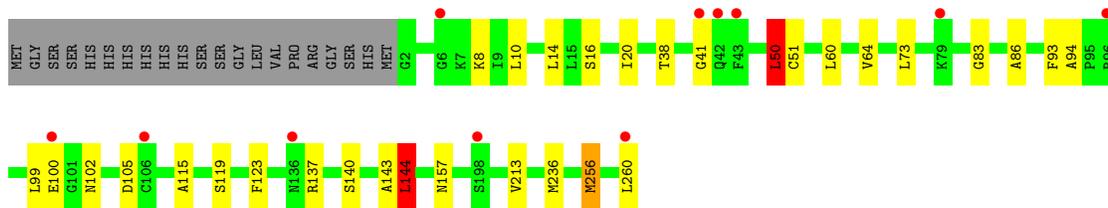


- Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]

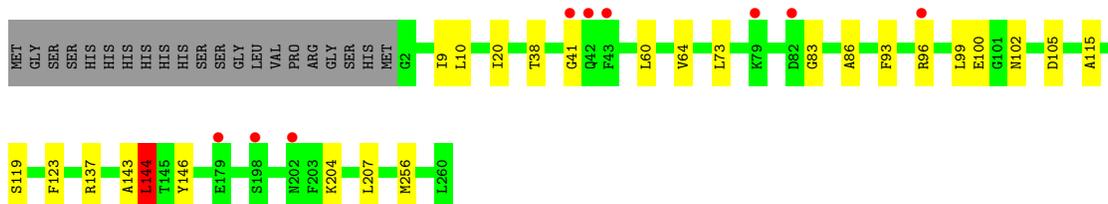
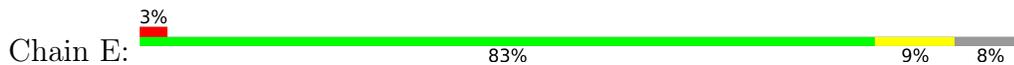


- Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]

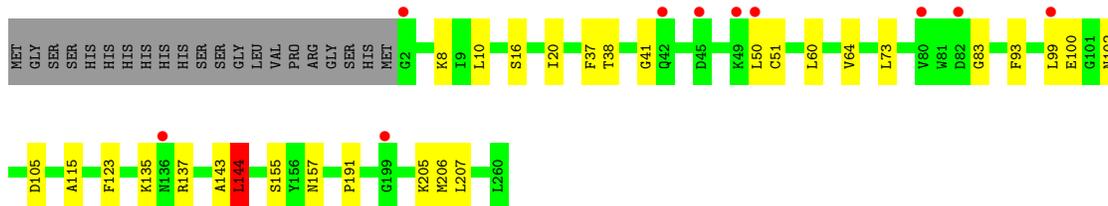
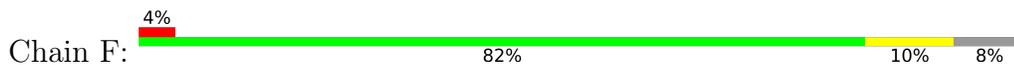




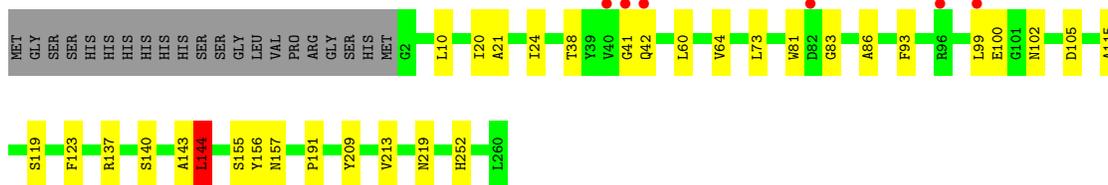
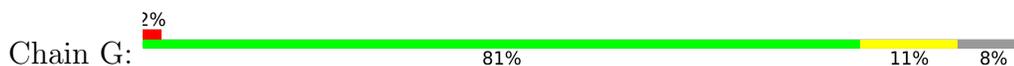
• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]



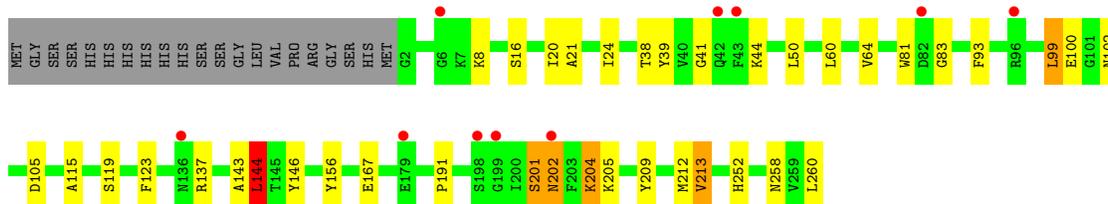
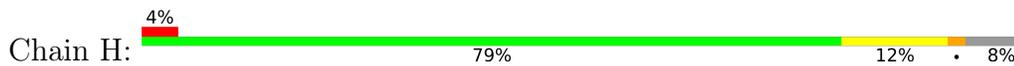
• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]



• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]



• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.40Å 123.35Å 202.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 2.34 19.89 – 2.34	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.89-2.34) 99.1 (19.89-2.34)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.45 (at 2.33Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.199 , 0.241 0.197 , 0.238	Depositor DCC
$R_{free}$ test set	4518 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.5	Xtrriage
Anisotropy	0.238	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 35.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16987	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 64.72 % 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 7.9258e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAD, NA, 1JU, GOL, ACT

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	0.63	0/1976	0.71	1/2665 (0.0%)
1	B	0.62	1/1976 (0.1%)	0.71	1/2665 (0.0%)
1	C	0.60	0/1975	0.71	1/2665 (0.0%)
1	D	0.60	0/1982	0.74	2/2673 (0.1%)
1	E	0.63	0/1976	0.88	4/2665 (0.2%)
1	F	0.59	0/1976	0.70	2/2665 (0.1%)
1	G	0.61	1/1967 (0.1%)	0.70	1/2655 (0.0%)
1	H	0.60	1/1976 (0.1%)	0.70	1/2665 (0.0%)
All	All	0.61	3/15804 (0.0%)	0.73	13/21318 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	81	TRP	CD2-CE2	5.86	1.48	1.41
1	H	81	TRP	CD2-CE2	5.12	1.47	1.41
1	B	81	TRP	CD2-CE2	5.05	1.47	1.41

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	96	ARG	NE-CZ-NH2	19.09	129.85	120.30
1	E	96	ARG	NE-CZ-NH1	-18.28	111.16	120.30
1	E	96	ARG	CD-NE-CZ	9.72	137.20	123.60
1	D	144	LEU	CA-CB-CG	-6.42	100.52	115.30
1	F	144	LEU	CA-CB-CG	-6.12	101.23	115.30

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	1942	0	1965	26	0
1	B	1942	0	1965	25	0
1	C	1944	0	1964	22	1
1	D	1948	0	1969	26	0
1	E	1942	0	1965	17	0
1	F	1945	0	1964	22	0
1	G	1936	0	1956	25	0
1	H	1942	0	1965	38	0
2	A	44	0	26	1	0
2	B	44	0	26	1	0
2	C	44	0	26	1	0
2	D	44	0	26	1	0
2	E	44	0	26	1	0
2	F	44	0	26	2	0
2	G	44	0	26	2	0
2	H	44	0	26	2	0
3	A	23	0	18	3	0
3	B	23	0	18	5	0
3	C	23	0	18	3	0
3	D	23	0	18	3	0
3	E	23	0	18	3	0
3	F	23	0	18	2	0
3	G	23	0	18	5	0
3	H	23	0	18	5	0
4	A	12	0	16	1	0
4	B	6	0	8	0	0
4	C	6	0	8	1	0
4	D	6	0	8	0	0
4	H	12	0	16	1	0
5	B	1	0	0	0	0
5	F	1	0	0	0	0
5	H	1	0	0	0	0
6	B	4	0	3	1	0
6	D	4	0	3	0	0
7	A	120	0	0	0	0
7	B	93	0	0	1	0
7	C	109	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	119	0	0	4	0
7	E	95	0	0	0	0
7	F	107	0	0	3	0
7	G	119	0	0	4	1
7	H	95	0	0	4	0
All	All	16987	0	16127	190	1

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 6.

The worst 5 of 190 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:B:179:GLU:OE2	1:H:204:LYS:HD3	1.40	1.21
1:A:212[A]:MET:SD	1:H:212[A]:MET:SD	2.54	1.05
1:H:204:LYS:HG2	7:H:484:HOH:O	1.58	1.02
1:D:256[A]:MET:HG3	1:D:256[A]:MET:O	1.63	0.97
1:C:93:PHE:HA	3:C:302:1JU:H5	1.52	0.92

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:LYS:NZ	7:G:508:HOH:O[4_555]	2.02	0.18

## 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	258/280 (92%)	243 (94%)	14 (5%)	1 (0%)	34 38
1	B	258/280 (92%)	245 (95%)	12 (5%)	1 (0%)	34 38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	258/280 (92%)	249 (96%)	8 (3%)	1 (0%)	34	38
1	D	259/280 (92%)	246 (95%)	12 (5%)	1 (0%)	34	38
1	E	258/280 (92%)	247 (96%)	10 (4%)	1 (0%)	34	38
1	F	258/280 (92%)	246 (95%)	11 (4%)	1 (0%)	34	38
1	G	257/280 (92%)	244 (95%)	12 (5%)	1 (0%)	34	38
1	H	258/280 (92%)	245 (95%)	12 (5%)	1 (0%)	34	38
All	All	2064/2240 (92%)	1965 (95%)	91 (4%)	8 (0%)	34	38

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	GLY
1	B	41	GLY
1	C	41	GLY
1	D	41	GLY
1	E	41	GLY

### 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	204/221 (92%)	201 (98%)	3 (2%)	65	76
1	B	204/221 (92%)	200 (98%)	4 (2%)	55	66
1	C	204/221 (92%)	201 (98%)	3 (2%)	65	76
1	D	205/221 (93%)	200 (98%)	5 (2%)	49	59
1	E	204/221 (92%)	201 (98%)	3 (2%)	65	76
1	F	204/221 (92%)	203 (100%)	1 (0%)	88	93
1	G	203/221 (92%)	201 (99%)	2 (1%)	76	85
1	H	204/221 (92%)	198 (97%)	6 (3%)	42	52
All	All	1632/1768 (92%)	1605 (98%)	27 (2%)	62	72

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	256[B]	MET
1	E	207	LEU
1	H	202	ASN
1	E	204	LYS
1	F	144	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	138	ASN
1	G	157	ASN
1	F	157	ASN
1	F	252	HIS
1	G	252	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 3 are monoatomic - leaving 25 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
2	NAD	H	301	-	42,48,48	2.15	11 (26%)	50,73,73	1.57	7 (14%)
3	1JU	G	302	-	26,27,27	0.88	1 (3%)	34,39,39	0.93	0
4	GOL	A	304	-	5,5,5	0.46	0	5,5,5	0.69	0
3	1JU	A	302	-	26,27,27	0.86	2 (7%)	34,39,39	0.80	0
2	NAD	D	301	-	42,48,48	2.26	9 (21%)	50,73,73	1.66	8 (16%)
3	1JU	H	302	-	26,27,27	0.82	0	34,39,39	0.77	0
2	NAD	A	301	-	42,48,48	2.41	11 (26%)	50,73,73	1.89	10 (20%)
3	1JU	D	302	-	26,27,27	0.78	0	34,39,39	0.73	0
4	GOL	A	303	-	5,5,5	0.39	0	5,5,5	0.44	0
6	ACT	D	304	-	3,3,3	0.78	0	3,3,3	0.86	0
4	GOL	H	304	-	5,5,5	0.72	0	5,5,5	1.33	1 (20%)
2	NAD	E	301	-	42,48,48	2.19	10 (23%)	50,73,73	1.52	5 (10%)
2	NAD	G	301	-	42,48,48	2.29	11 (26%)	50,73,73	1.74	5 (10%)
4	GOL	H	305	-	5,5,5	0.32	0	5,5,5	0.82	0
3	1JU	C	302	-	26,27,27	0.81	0	34,39,39	0.77	0
2	NAD	C	301	-	42,48,48	2.22	10 (23%)	50,73,73	1.84	15 (30%)
4	GOL	C	303	-	5,5,5	0.64	0	5,5,5	0.82	0
2	NAD	F	301	-	42,48,48	2.34	12 (28%)	50,73,73	1.60	8 (16%)
4	GOL	B	304	-	5,5,5	0.57	0	5,5,5	0.97	0
2	NAD	B	301	-	42,48,48	2.27	11 (26%)	50,73,73	1.69	8 (16%)
3	1JU	E	302	-	26,27,27	0.80	0	34,39,39	0.79	0
3	1JU	F	302	-	26,27,27	0.84	0	34,39,39	0.82	0
3	1JU	B	302	-	26,27,27	0.79	0	34,39,39	0.80	0
4	GOL	D	303	-	5,5,5	0.44	0	5,5,5	0.23	0
6	ACT	B	305	-	3,3,3	0.72	0	3,3,3	0.95	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	H	301	-	-	8/26/62/62	0/5/5/5
3	1JU	G	302	-	-	0/4/17/17	0/5/5/5
4	GOL	A	304	-	-	0/4/4/4	-
3	1JU	A	302	-	-	0/4/17/17	0/5/5/5
2	NAD	D	301	-	-	8/26/62/62	0/5/5/5
3	1JU	H	302	-	-	0/4/17/17	0/5/5/5
2	NAD	A	301	-	-	6/26/62/62	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	1JU	D	302	-	-	0/4/17/17	0/5/5/5
4	GOL	A	303	-	-	2/4/4/4	-
4	GOL	H	304	-	-	2/4/4/4	-
2	NAD	E	301	-	-	8/26/62/62	0/5/5/5
2	NAD	G	301	-	-	6/26/62/62	0/5/5/5
4	GOL	H	305	-	-	4/4/4/4	-
3	1JU	C	302	-	-	0/4/17/17	0/5/5/5
2	NAD	C	301	-	-	4/26/62/62	0/5/5/5
4	GOL	C	303	-	-	3/4/4/4	-
2	NAD	F	301	-	-	9/26/62/62	0/5/5/5
4	GOL	B	304	-	-	2/4/4/4	-
2	NAD	B	301	-	-	7/26/62/62	0/5/5/5
3	1JU	E	302	-	-	0/4/17/17	0/5/5/5
3	1JU	F	302	-	-	0/4/17/17	0/5/5/5
3	1JU	B	302	-	-	0/4/17/17	0/5/5/5
4	GOL	D	303	-	-	0/4/4/4	-

The worst 5 of 88 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	301	NAD	C2N-N1N	10.97	1.48	1.35
2	A	301	NAD	C2N-N1N	10.41	1.47	1.35
2	G	301	NAD	C2N-N1N	10.08	1.47	1.35
2	C	301	NAD	C2N-N1N	9.98	1.47	1.35
2	B	301	NAD	C2N-N1N	9.95	1.47	1.35

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	NAD	C1B-N9A-C4A	-5.75	116.53	126.64
2	A	301	NAD	N3A-C2A-N1A	-5.64	119.86	128.68
2	D	301	NAD	C1B-N9A-C4A	-5.53	116.93	126.64
2	H	301	NAD	C1B-N9A-C4A	-5.48	117.01	126.64
2	G	301	NAD	C1B-N9A-C4A	-5.45	117.06	126.64

There are no chirality outliers.

5 of 69 torsion outliers are listed below:

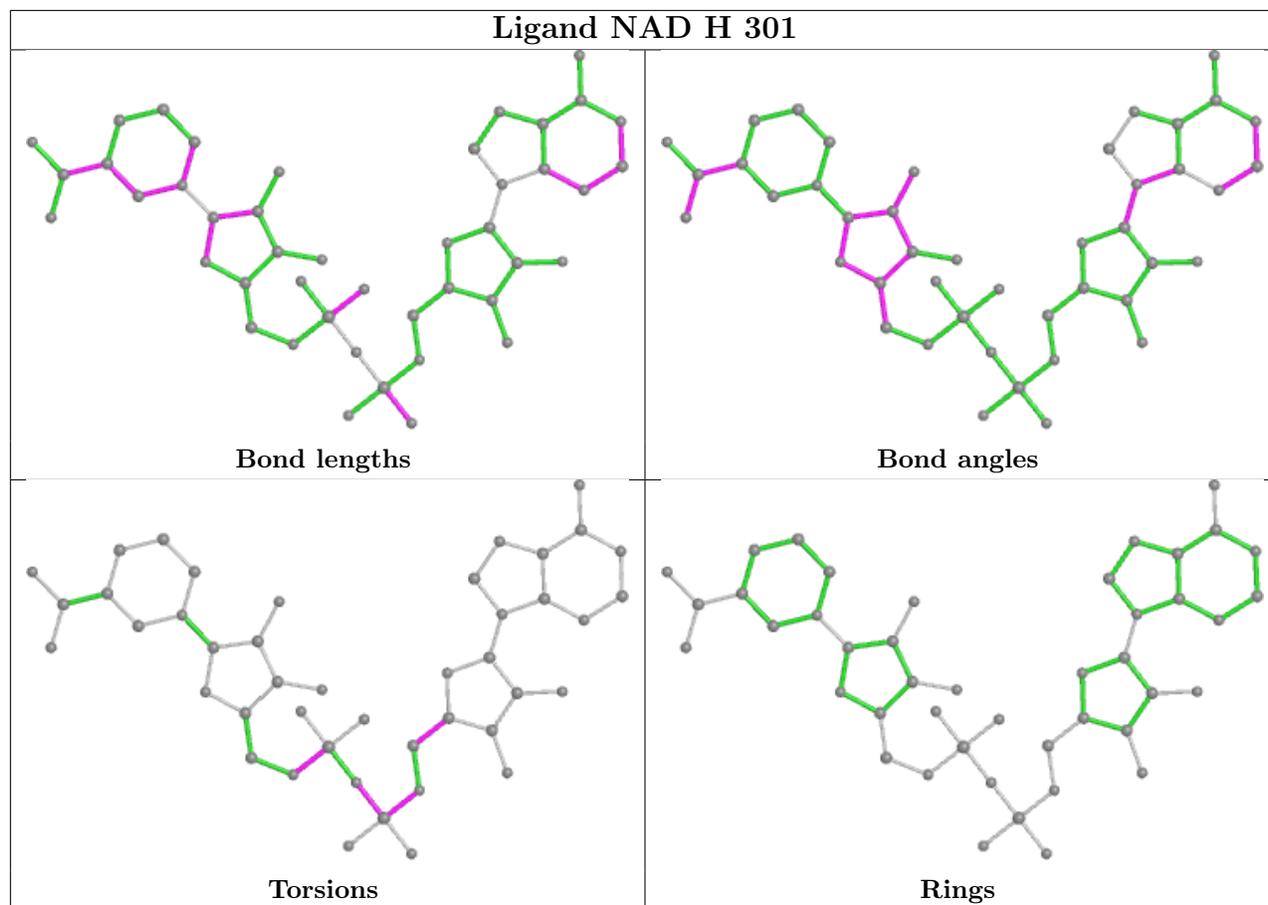
Mol	Chain	Res	Type	Atoms
2	A	301	NAD	PN-O3-PA-O5B
2	A	301	NAD	C5D-O5D-PN-O3
2	A	301	NAD	C5D-O5D-PN-O1N
2	A	301	NAD	C5D-O5D-PN-O2N
2	A	301	NAD	O4D-C1D-N1N-C2N

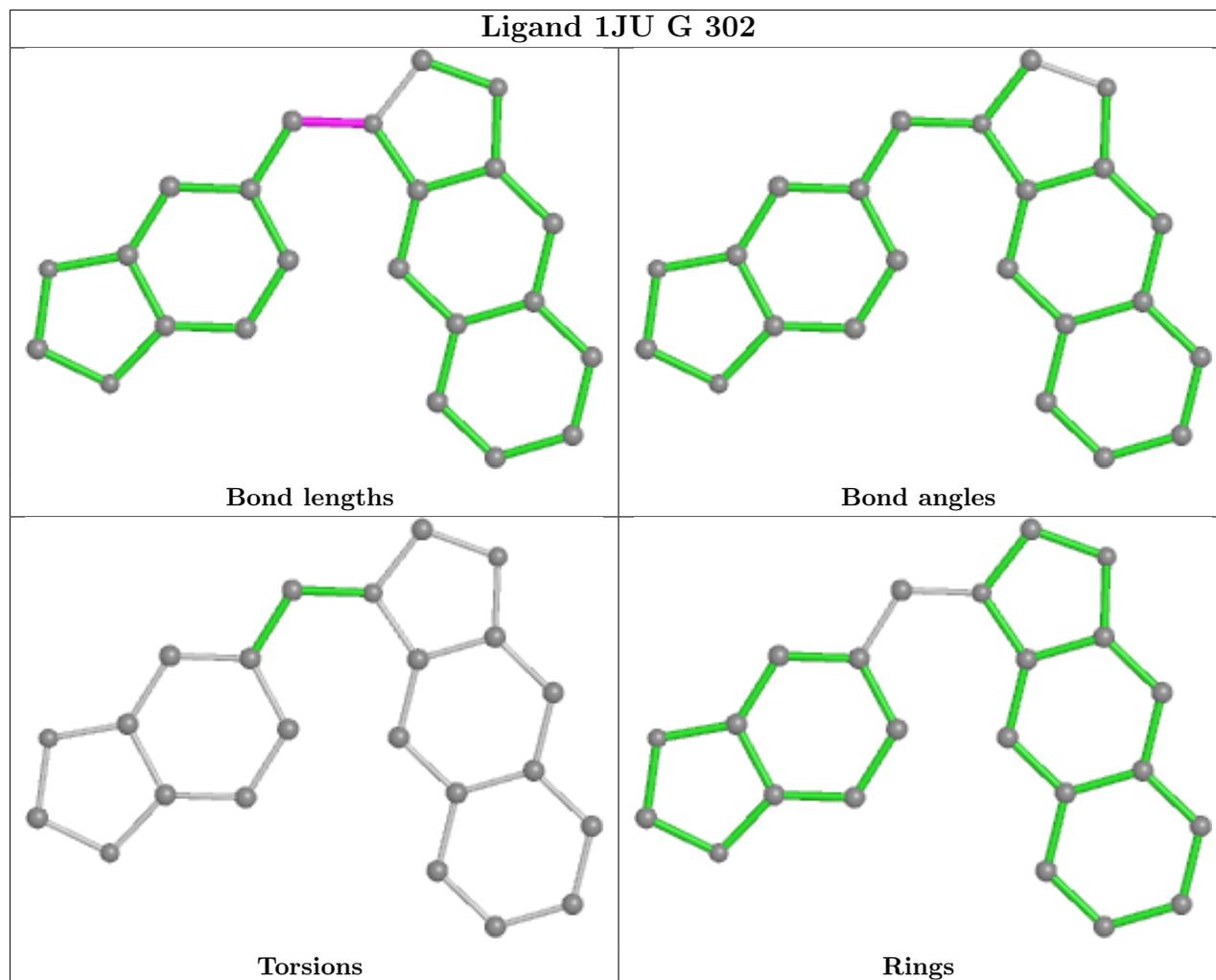
There are no ring outliers.

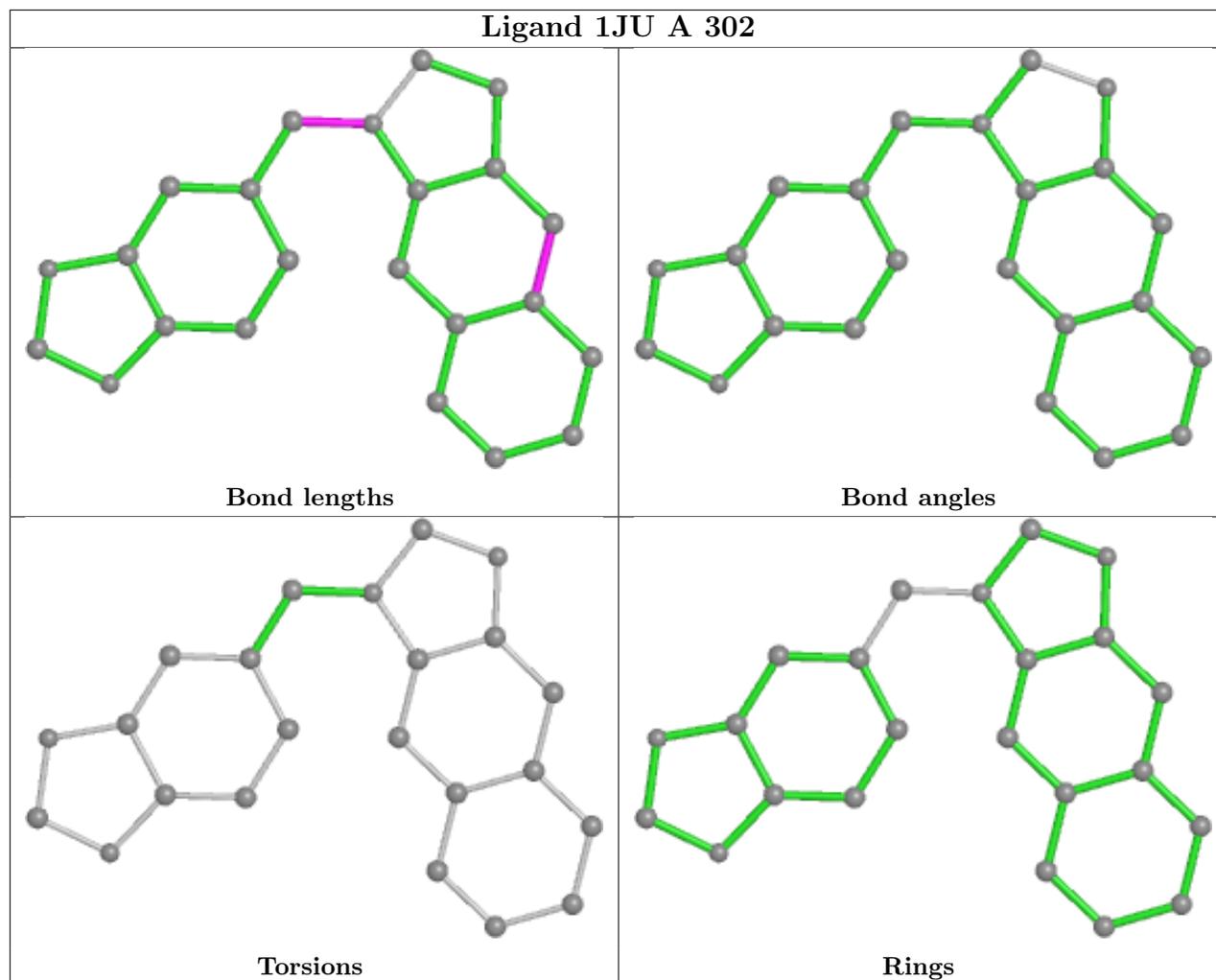
20 monomers are involved in 44 short contacts:

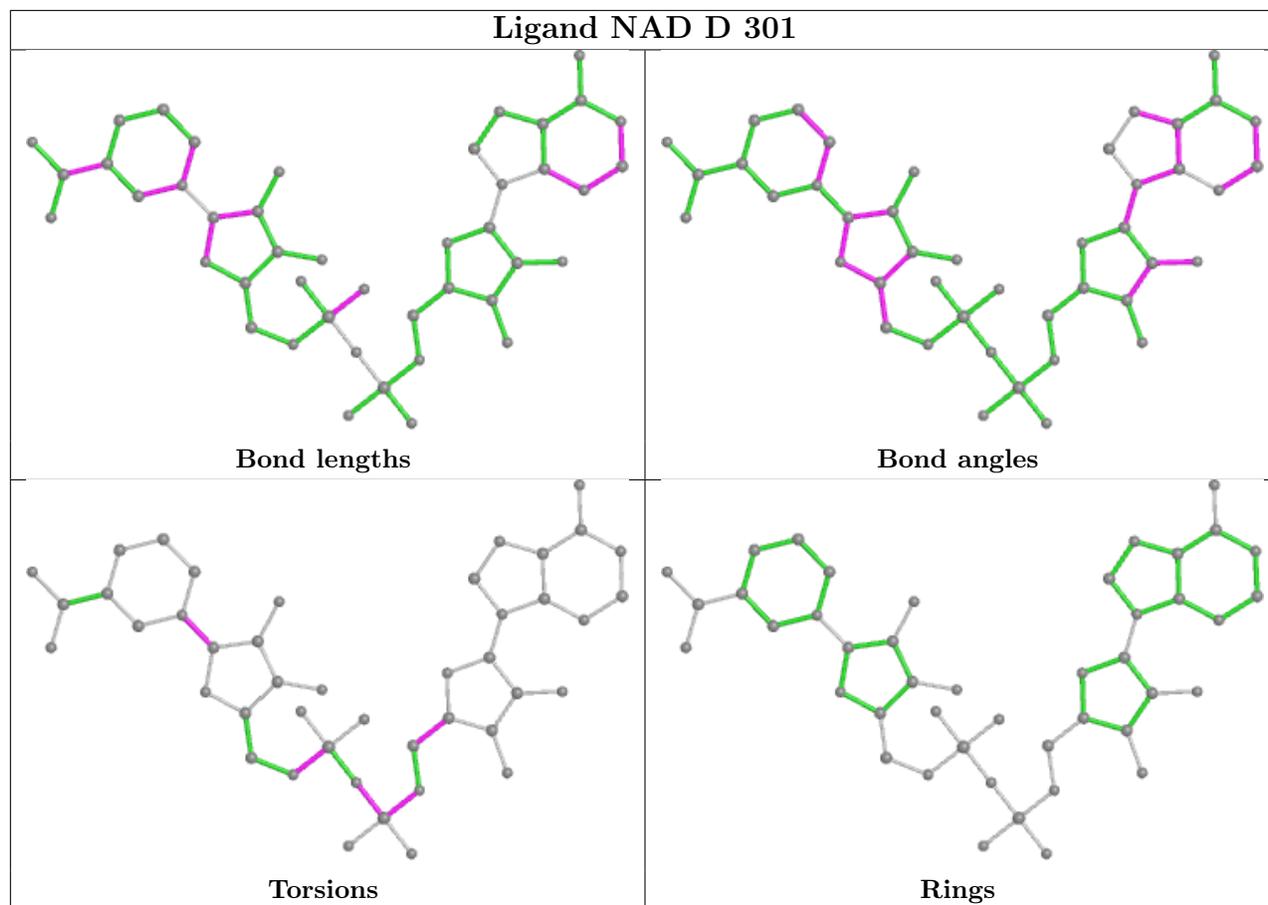
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	301	NAD	2	0
3	G	302	1JU	5	0
3	A	302	1JU	3	0
2	D	301	NAD	1	0
3	H	302	1JU	5	0
2	A	301	NAD	1	0
3	D	302	1JU	3	0
4	A	303	GOL	1	0
2	E	301	NAD	1	0
2	G	301	NAD	2	0
4	H	305	GOL	1	0
3	C	302	1JU	3	0
2	C	301	NAD	1	0
4	C	303	GOL	1	0
2	F	301	NAD	2	0
2	B	301	NAD	1	0
3	E	302	1JU	3	0
3	F	302	1JU	2	0
3	B	302	1JU	5	0
6	B	305	ACT	1	0

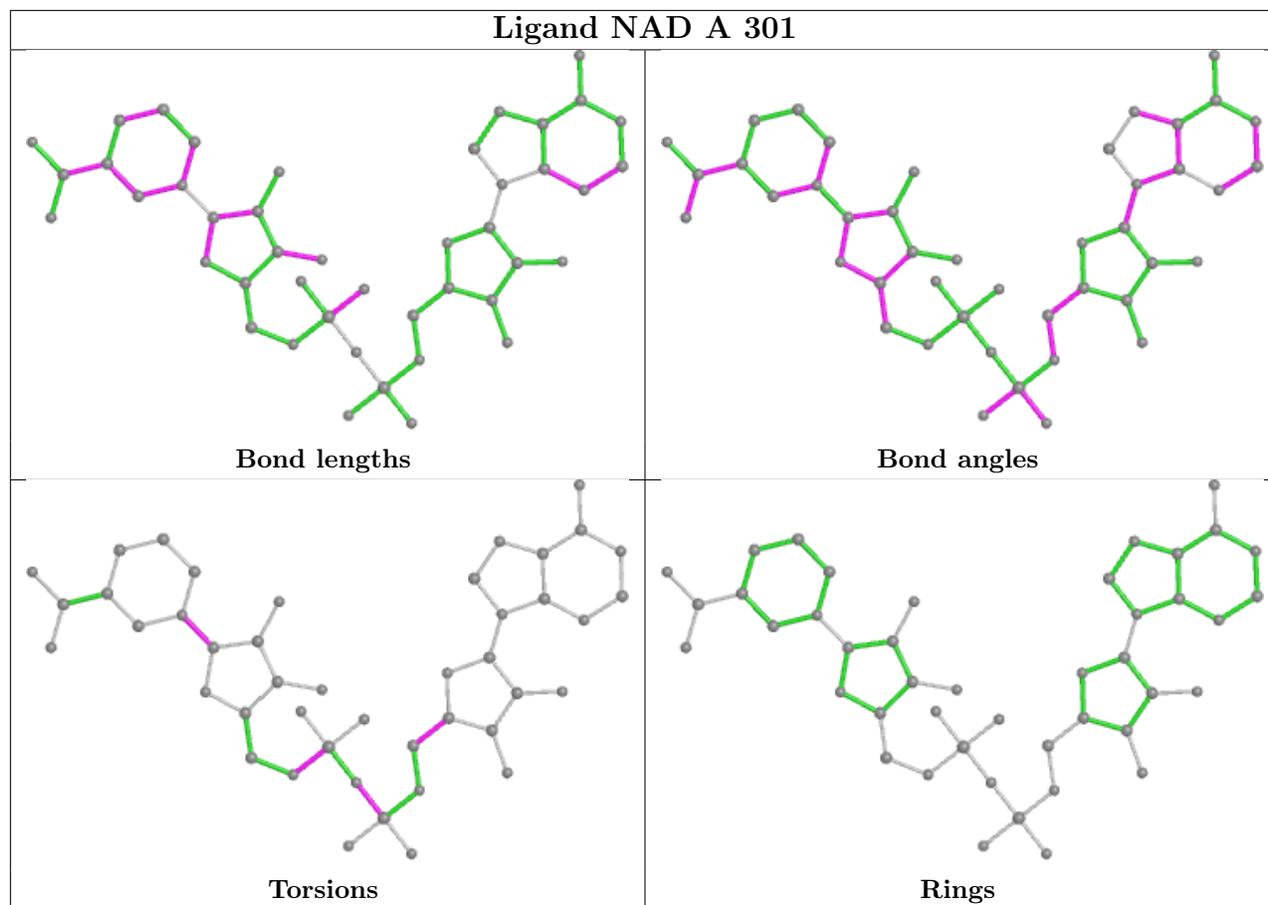
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

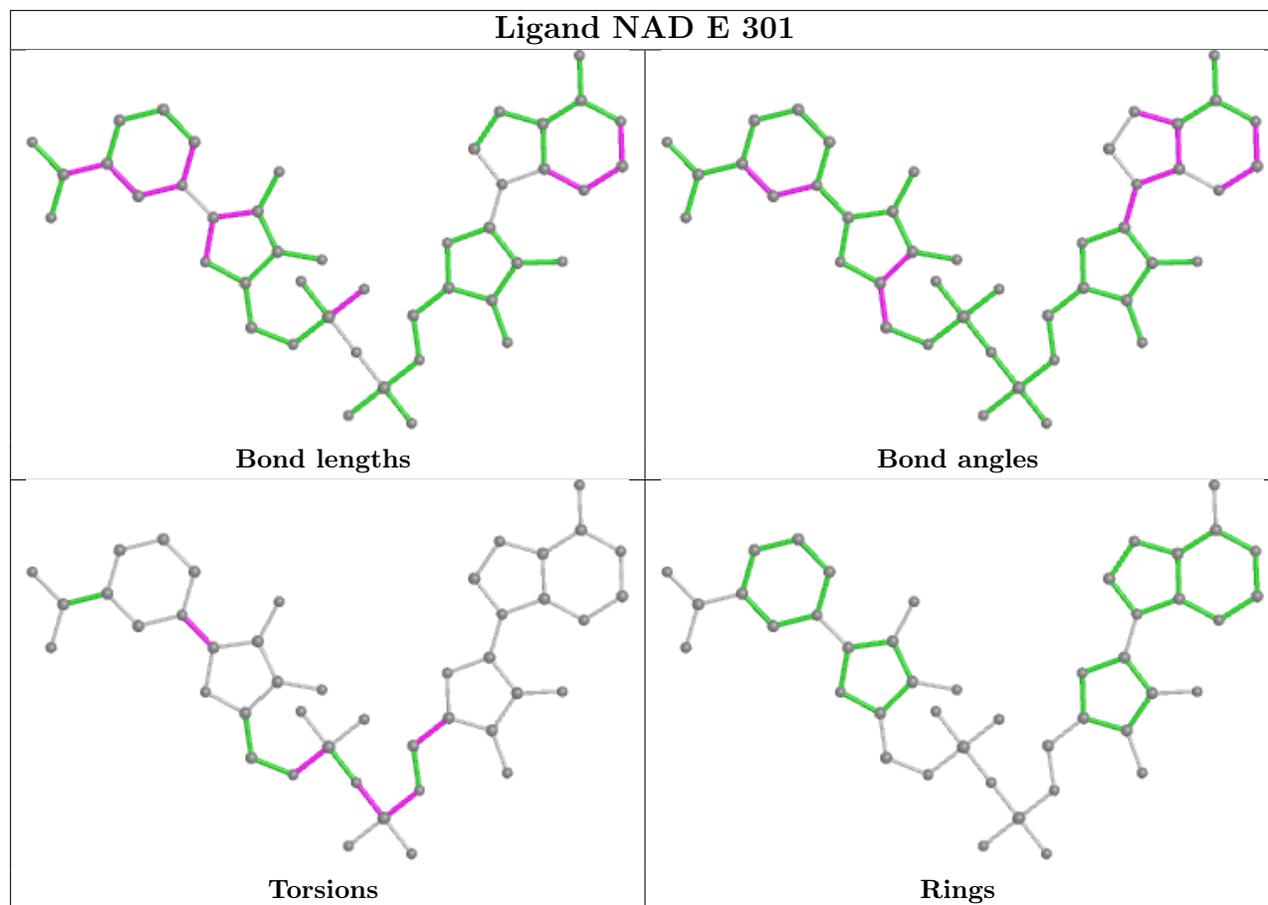


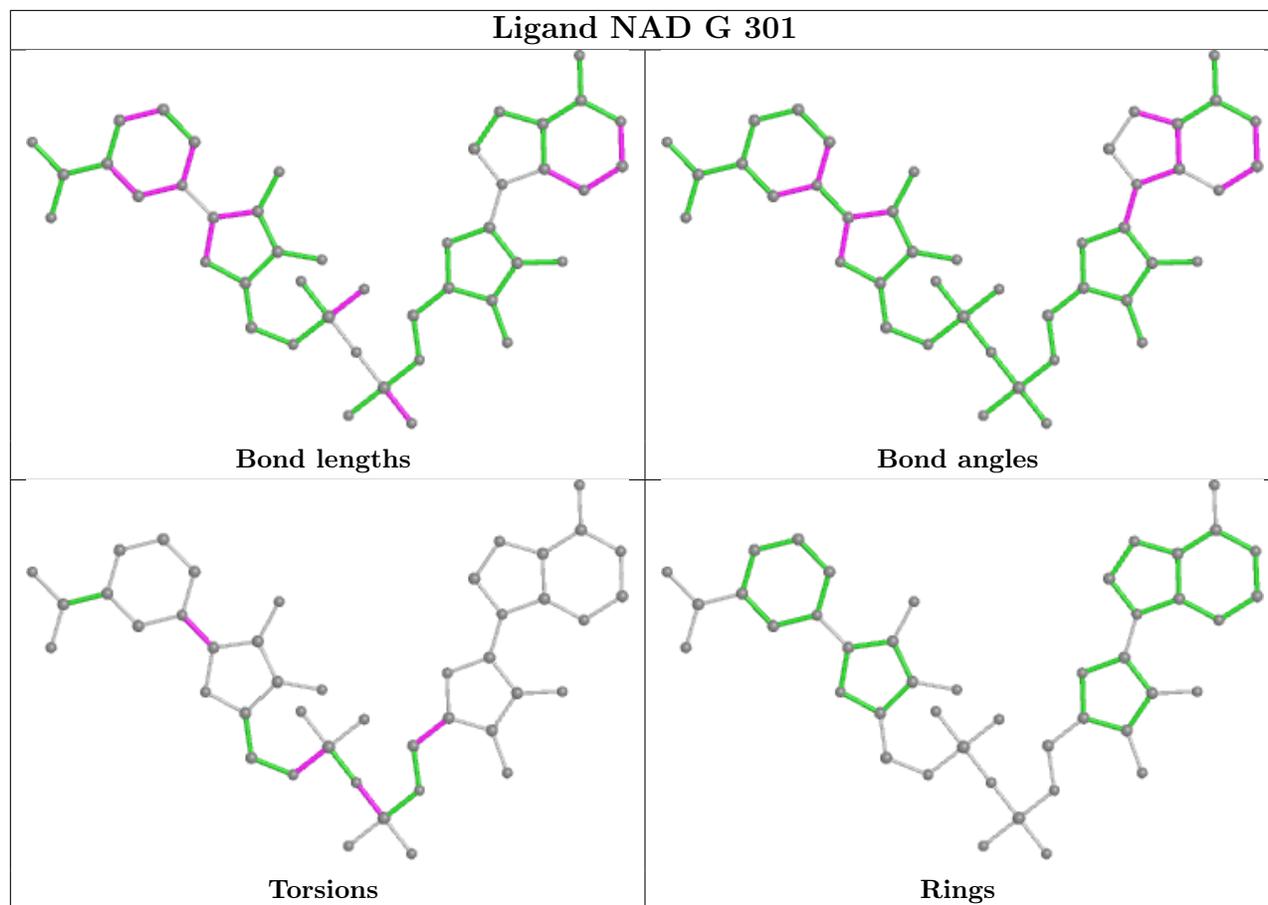


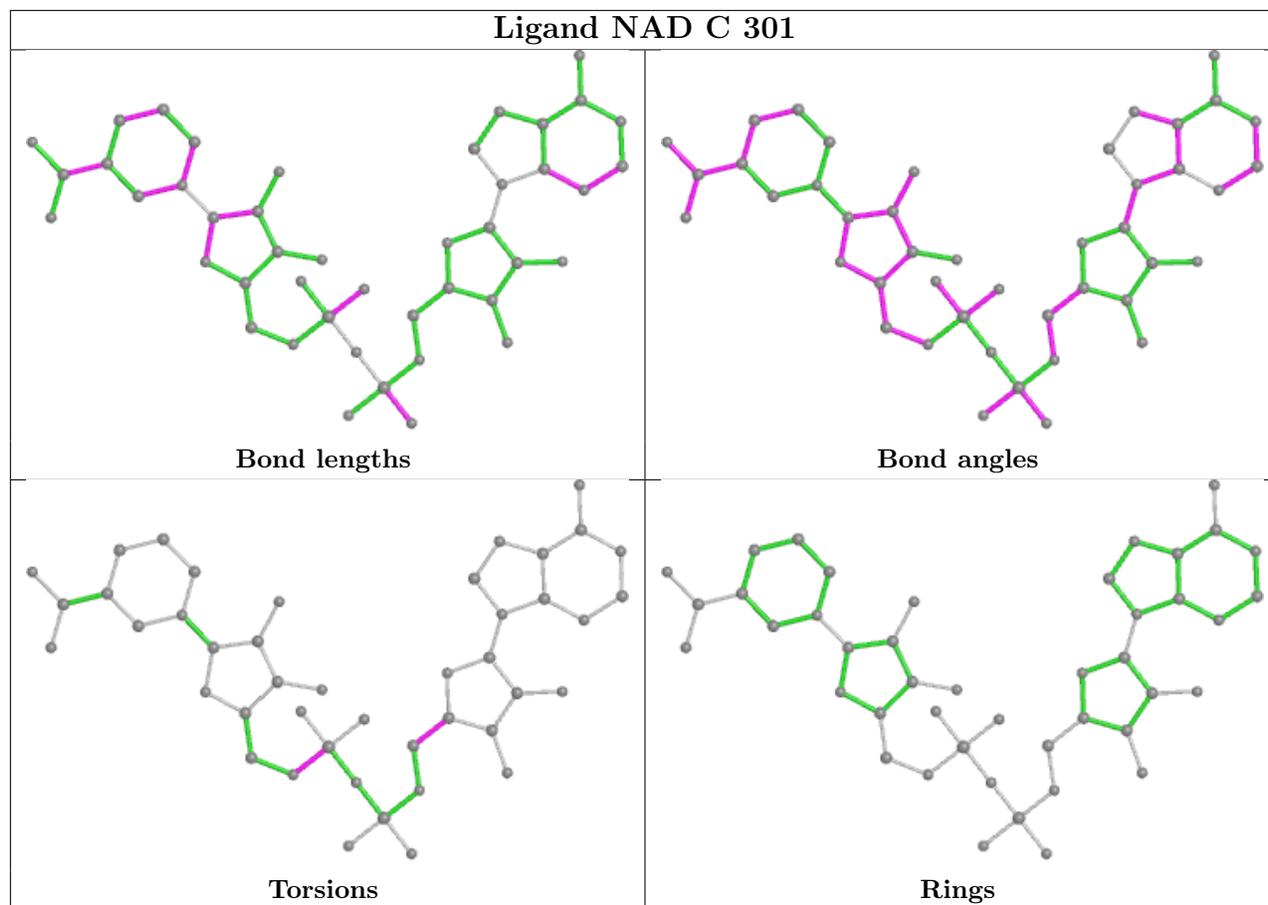


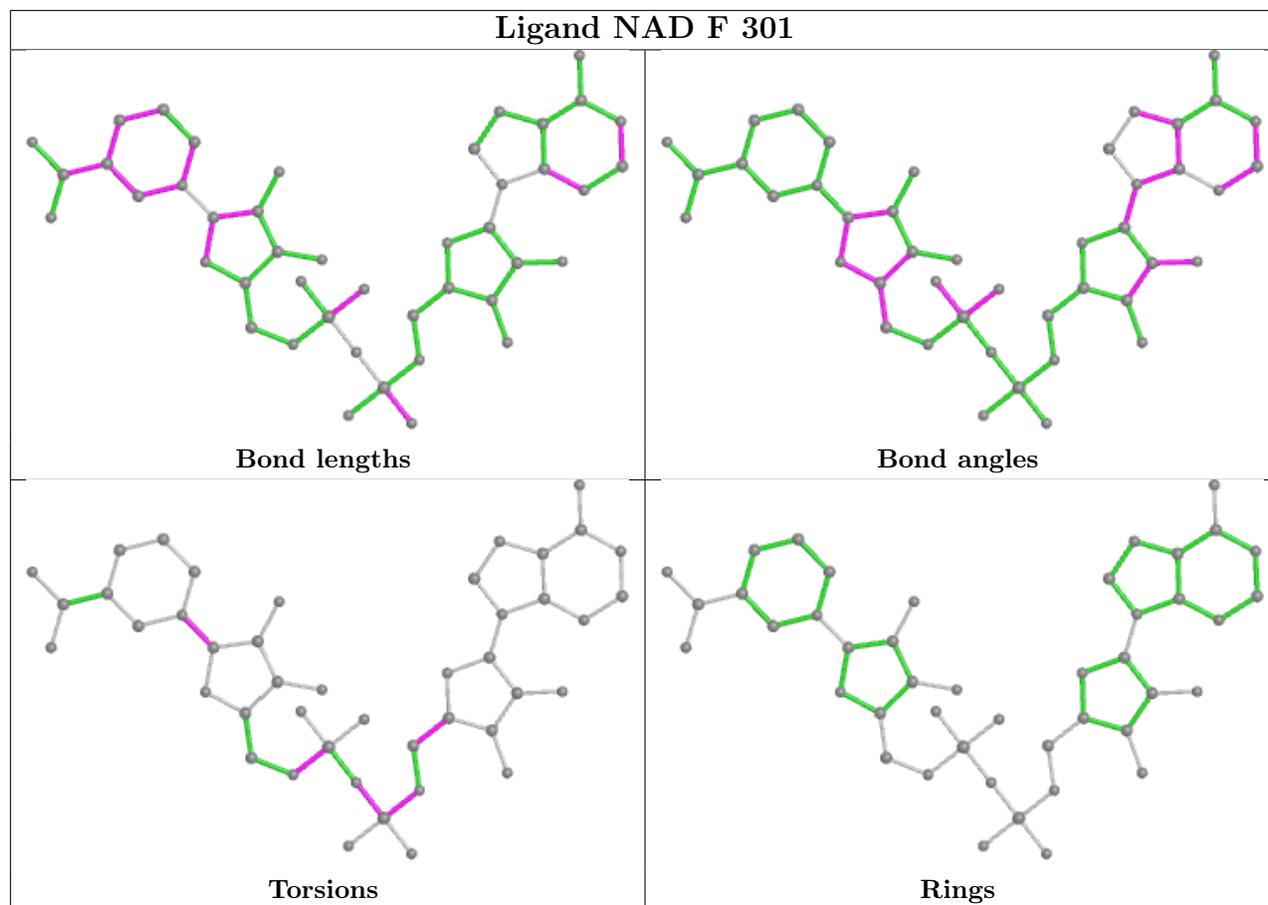


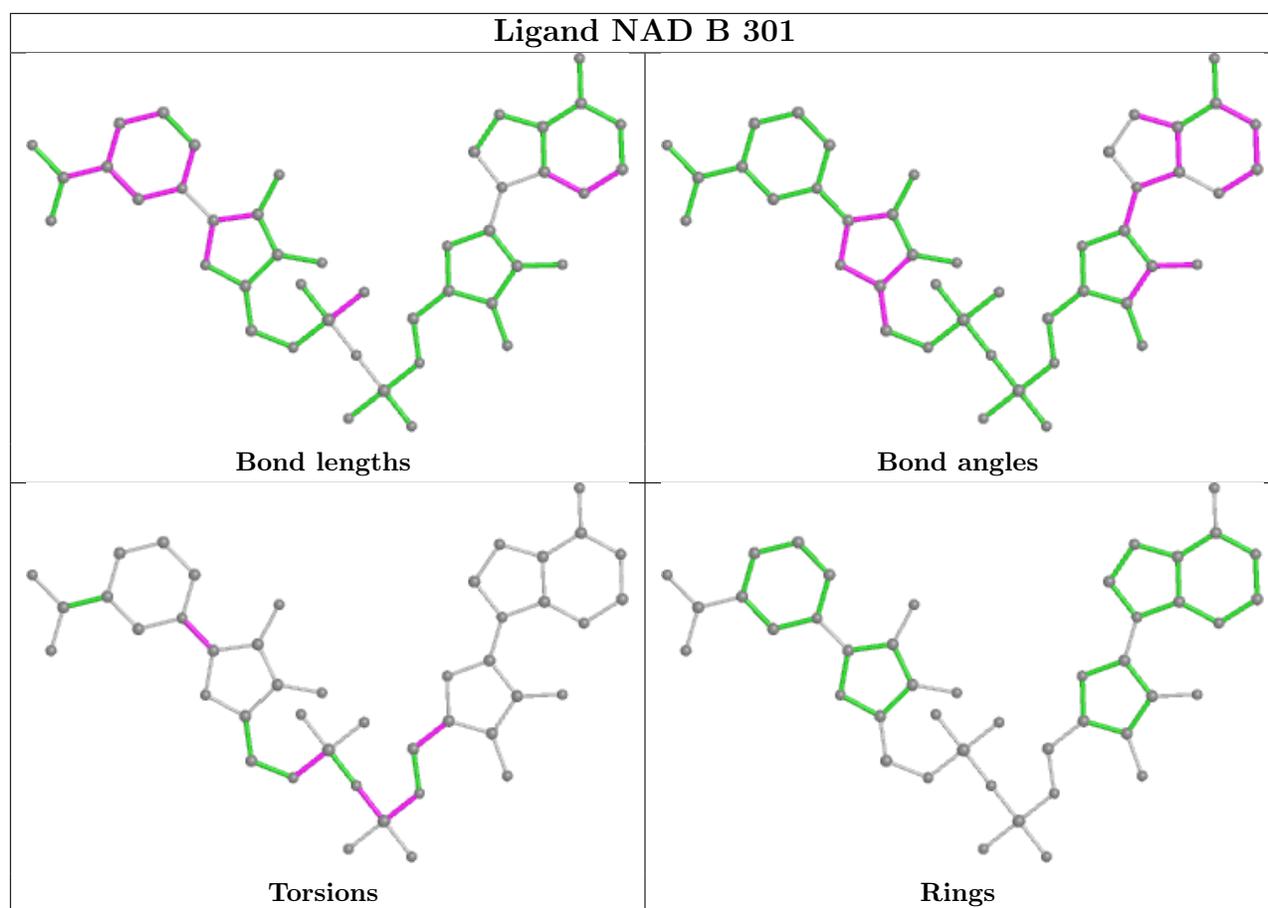












## 5.7 Other polymers [i](#)

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	259/280 (92%)	0.19	8 (3%) 49 59	12, 20, 40, 62	0
1	B	259/280 (92%)	0.21	8 (3%) 49 59	14, 21, 45, 70	1 (0%)
1	C	259/280 (92%)	0.10	9 (3%) 44 54	12, 20, 38, 73	0
1	D	259/280 (92%)	0.18	11 (4%) 36 47	13, 20, 39, 71	1 (0%)
1	E	259/280 (92%)	0.17	9 (3%) 44 54	13, 21, 44, 72	0
1	F	259/280 (92%)	0.15	10 (3%) 39 50	12, 20, 39, 60	0
1	G	259/280 (92%)	0.09	6 (2%) 60 69	13, 20, 35, 70	0
1	H	259/280 (92%)	0.24	10 (3%) 39 50	14, 22, 41, 68	1 (0%)
All	All	2072/2240 (92%)	0.17	71 (3%) 45 55	12, 21, 40, 73	3 (0%)

The worst 5 of 71 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	106	CYS	5.3
1	B	42	GLN	5.1
1	H	202	ASN	4.9
1	C	42	GLN	4.6
1	D	41	GLY	4.5

### 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 monosaccharides in this entry.

## 6.4 Ligands

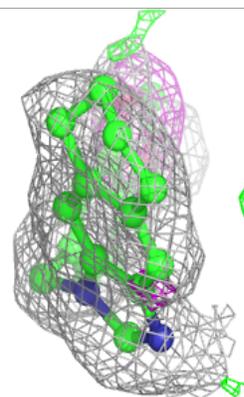
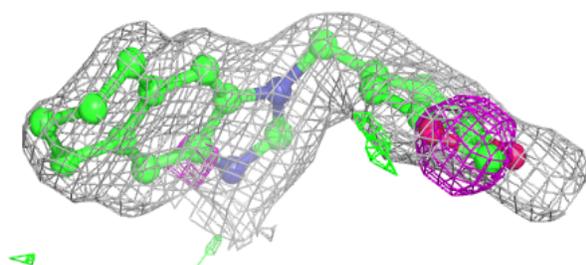
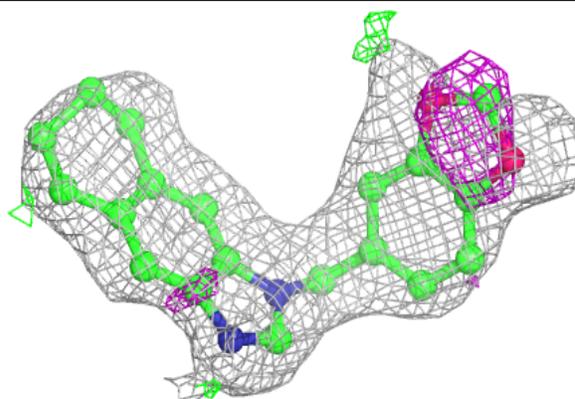
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	GOL	D	303	6/6	0.73	0.41	55,58,61,61	0
6	ACT	D	304	4/4	0.79	0.22	28,30,32,34	0
4	GOL	C	303	6/6	0.80	0.22	21,28,33,38	0
4	GOL	H	304	6/6	0.81	0.23	28,32,32,33	0
3	1JU	H	302	23/23	0.84	0.21	21,25,34,36	0
3	1JU	G	302	23/23	0.85	0.18	17,18,19,20	0
3	1JU	F	302	23/23	0.85	0.18	19,20,21,24	0
4	GOL	A	303	6/6	0.85	0.21	22,24,27,30	0
4	GOL	A	304	6/6	0.85	0.29	22,27,33,36	0
4	GOL	H	305	6/6	0.86	0.27	23,26,30,33	0
6	ACT	B	305	4/4	0.87	0.16	20,23,25,26	0
3	1JU	A	302	23/23	0.87	0.19	18,22,28,29	0
3	1JU	E	302	23/23	0.88	0.17	23,26,30,32	0
3	1JU	B	302	23/23	0.88	0.17	22,24,28,29	0
4	GOL	B	304	6/6	0.88	0.17	22,26,30,33	0
3	1JU	D	302	23/23	0.89	0.17	18,19,29,30	0
5	NA	F	303	1/1	0.90	0.06	29,29,29,29	0
3	1JU	C	302	23/23	0.91	0.16	19,20,23,24	0
5	NA	H	303	1/1	0.93	0.12	29,29,29,29	0
5	NA	B	303	1/1	0.93	0.09	28,28,28,28	0
2	NAD	B	301	44/44	0.93	0.13	15,21,26,27	0
2	NAD	H	301	44/44	0.94	0.12	18,25,28,30	0
2	NAD	C	301	44/44	0.94	0.13	13,17,23,24	0
2	NAD	F	301	44/44	0.94	0.11	11,17,23,24	0
2	NAD	E	301	44/44	0.95	0.11	11,16,25,26	0
2	NAD	A	301	44/44	0.95	0.11	11,16,22,25	0
2	NAD	G	301	44/44	0.95	0.11	12,17,20,21	0
2	NAD	D	301	44/44	0.95	0.10	13,15,22,23	0

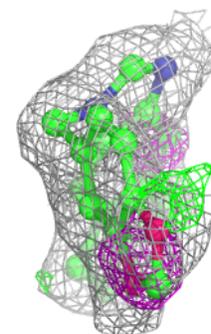
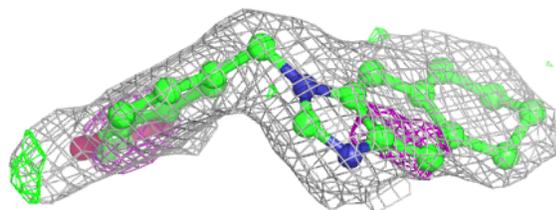
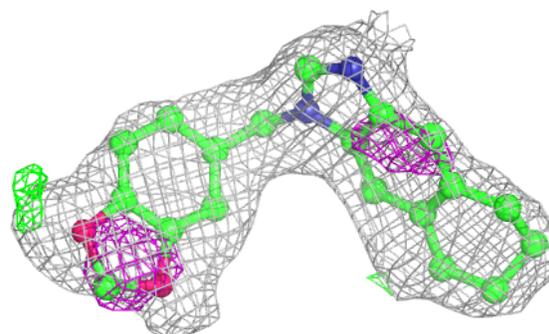
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around 1JU G 302:**

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

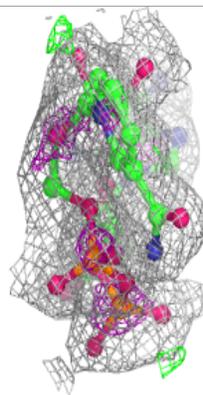
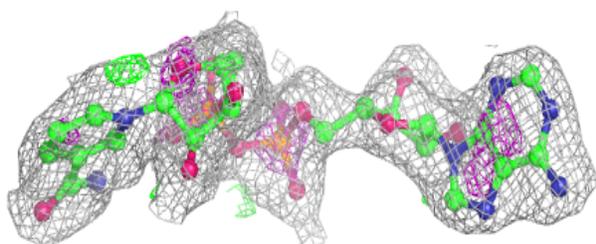
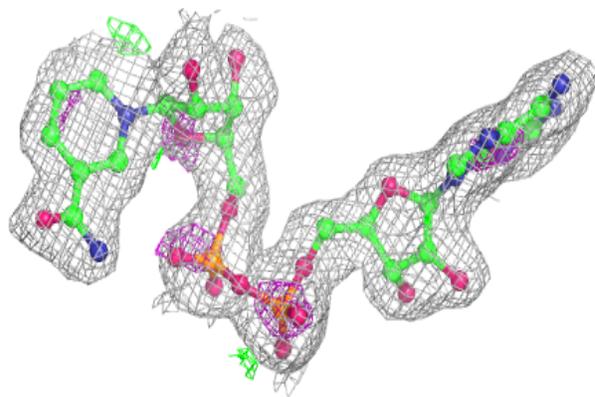
**Electron density around 1JU A 302:**

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

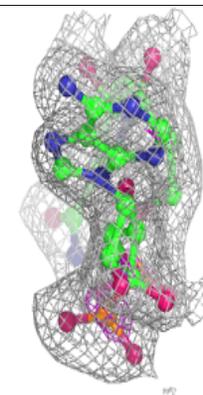
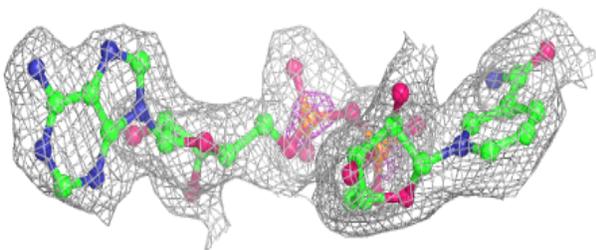
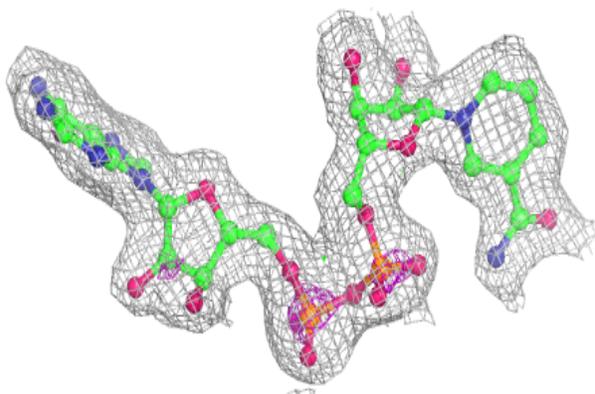


**Electron density around NAD B 301:**

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

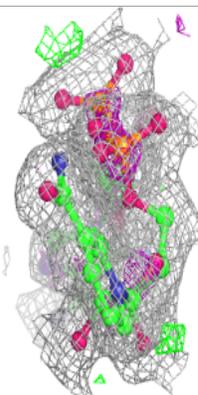
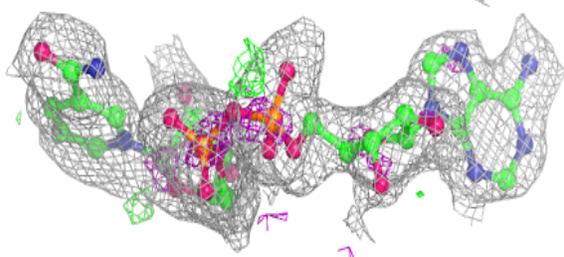
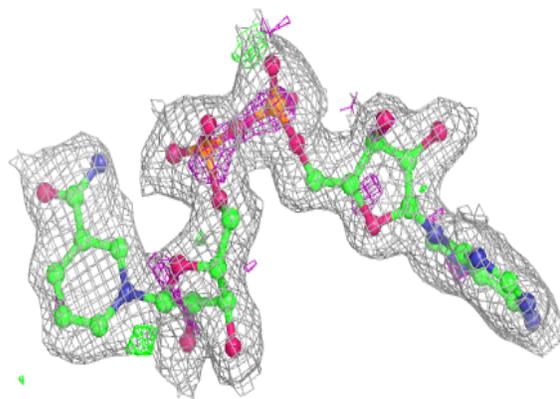
**Electron density around NAD H 301:**

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

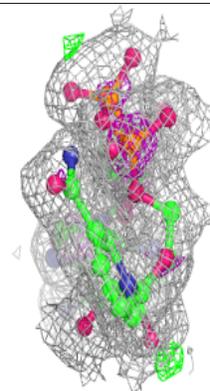
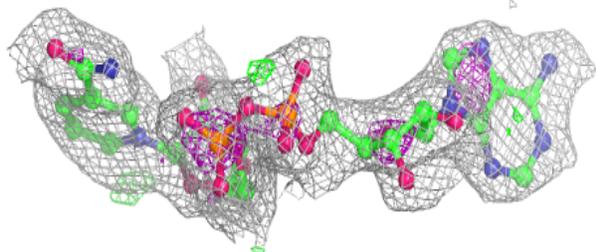
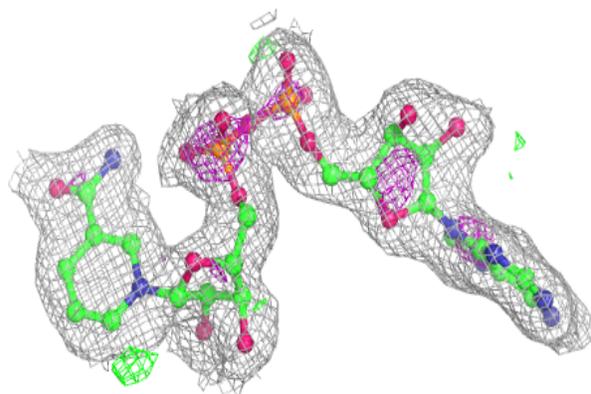


**Electron density around NAD C 301:**

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

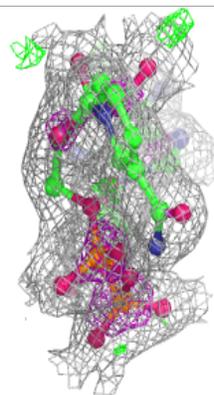
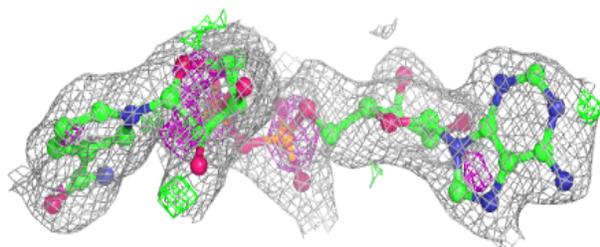
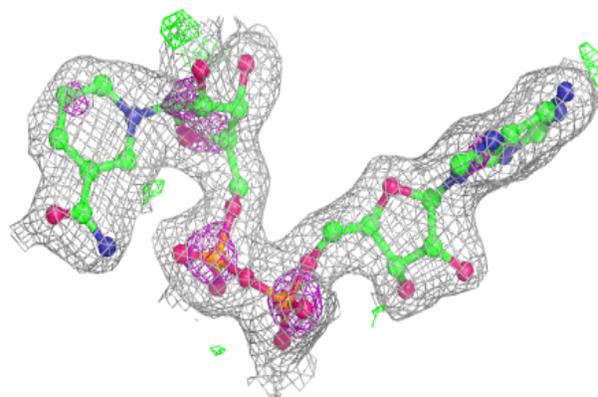
**Electron density around NAD F 301:**

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

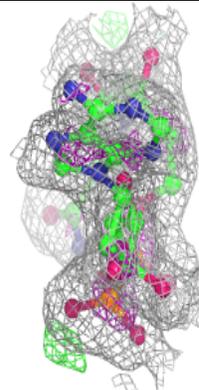
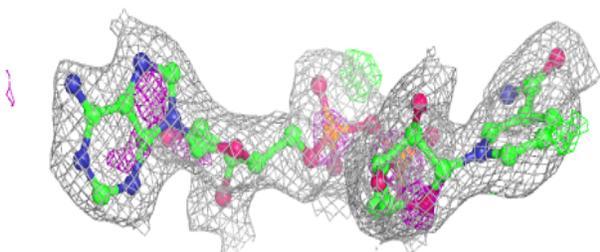
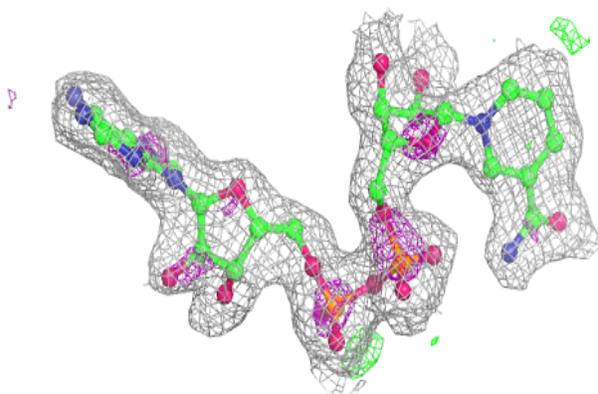


**Electron density around NAD E 301:**

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

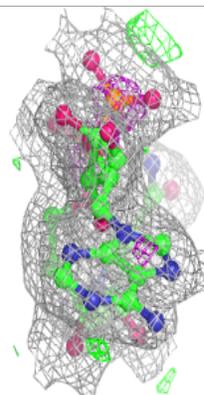
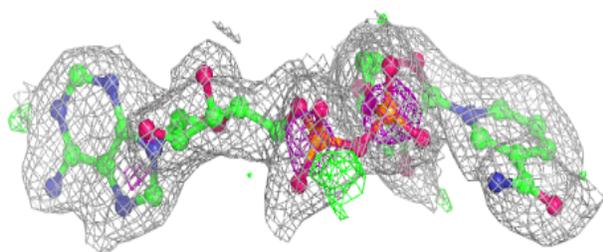
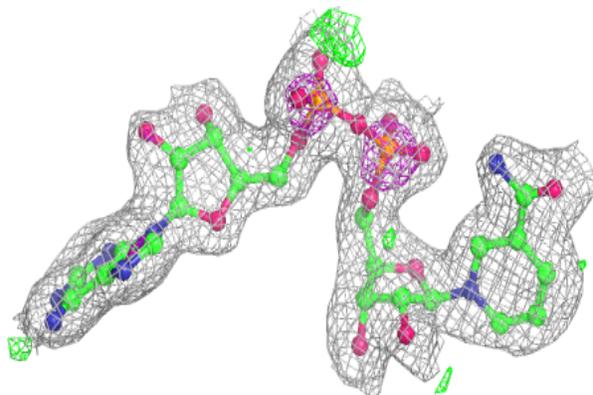
**Electron density around NAD A 301:**

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

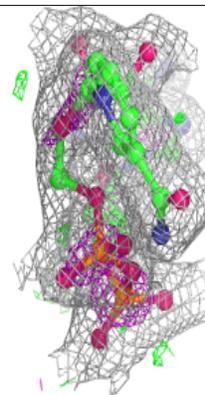
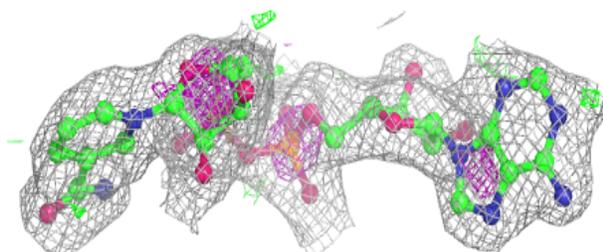
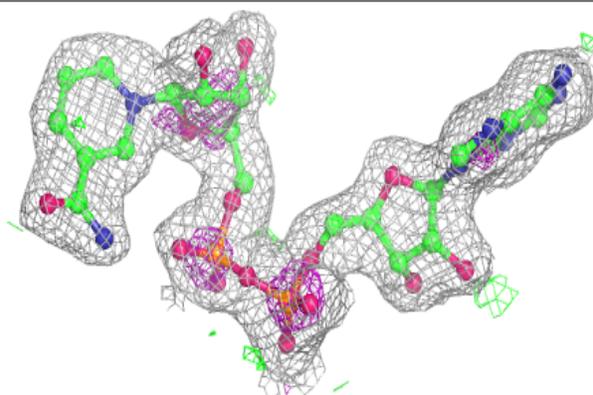


**Electron density around NAD G 301:**

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

**Electron density around NAD D 301:**

$2mF_o-DF_c$  (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.