



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:26 AM UTC

PDB ID : 2B37 / pdb_00002b37
Title : Crystal structure of Mycobacterium tuberculosis enoyl reductase (InhA) inhibited by 5-octyl-2-phenoxyphenol
Authors : Sullivan, T.J.; Truglio, J.J.; Novichenok, P.; Stratton, C.; Zhang, X.; Kaur, T.; Johnson, F.; Boyne, M.S.; Amin, A.
Deposited on : 2005-09-19
Resolution : 2.60 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 ⓘ 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)
Xtrriage (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

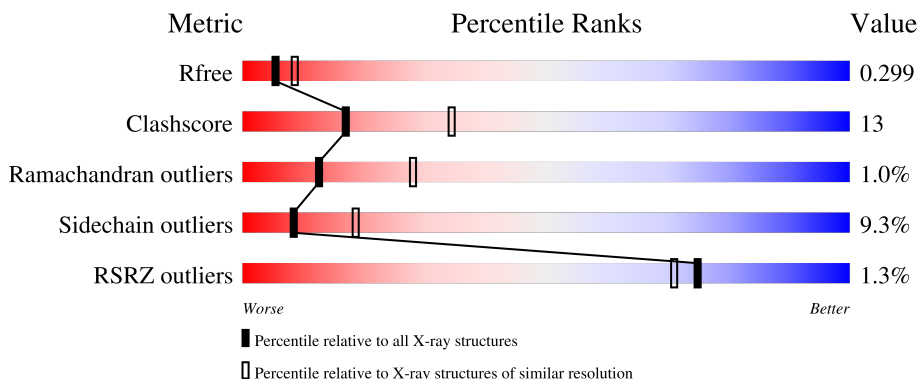
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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.



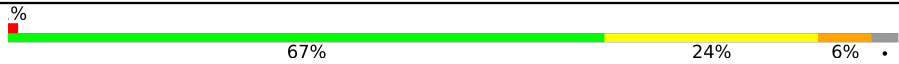

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	269	 62% 27% 8%
1	B	269	 65% 22% 9%
1	C	269	 71% 20% 5%
1	D	269	 73% 19%

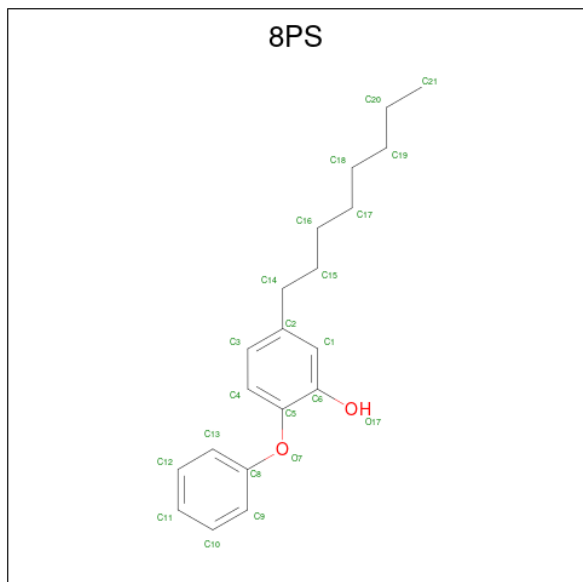
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Mol	Chain	Length	Quality of chain
1	E	269	 <p>% 67% 24% 6%</p>
1	F	269	 <p>% 57% 32% 8%</p>

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		

- Molecule 3 is 5-OCTYL-2-PHENOXYPHENOL (CCD ID: 8PS) (formula: C₂₀H₂₆O₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	C O	0	0
			22	20 2		
3	D	1	Total	C O	0	0
			22	20 2		

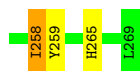
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	7	Total O	0	0
			7 7		
4	B	2	Total O	0	0
			2 2		

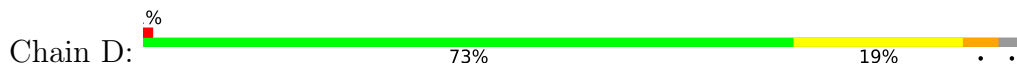
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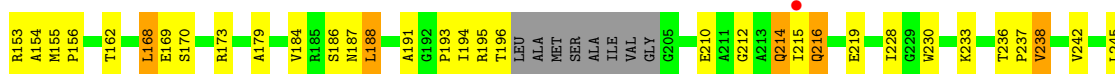
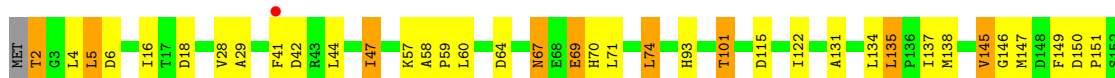
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	7	Total O 7 7	0	0
4	D	6	Total O 6 6	0	0
4	E	3	Total O 3 3	0	0
4	F	5	Total O 5 5	0	0



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



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4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	82.34Å 100.29Å 379.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.60 15.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.4 (15.00-2.60) 95.7 (15.00-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.97 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.225 , 0.294 0.231 , 0.299	Depositor DCC
R_{free} test set	2384 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtrriage
Anisotropy	0.817	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11736	wwPDB-VP
Average B, all atoms (Å ²)	40.0	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 30.88 % 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 1.2140e-03. 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 8PS, 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	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.91	1/1902 (0.1%)	0.87	2/2583 (0.1%)
1	B	0.96	1/1877 (0.1%)	0.87	1/2549 (0.0%)
1	C	1.12	2/1981 (0.1%)	0.96	1/2689 (0.0%)
1	D	1.12	2/1981 (0.1%)	0.94	1/2689 (0.0%)
1	E	1.03	2/1981 (0.1%)	0.91	2/2689 (0.1%)
1	F	0.98	3/1898 (0.2%)	0.89	1/2577 (0.0%)
All	All	1.02	11/11620 (0.1%)	0.91	8/15776 (0.1%)

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	215	ILE	CA-CB	8.00	1.62	1.54
1	F	228	ILE	CA-CB	7.09	1.64	1.54
1	F	16	ILE	CA-C	6.54	1.59	1.52
1	B	120	ILE	CA-CB	6.18	1.61	1.54
1	C	236	THR	CA-CB	6.11	1.61	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	14	GLY	N-CA-C	6.39	122.29	114.69
1	E	250	LEU	CA-C-N	5.43	125.12	119.64
1	E	250	LEU	C-N-CA	5.43	125.12	119.64
1	F	58	ALA	N-CA-C	5.41	115.09	108.11
1	B	36	LEU	N-CA-C	5.22	118.24	110.52

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	1865	0	1880	55	0
1	B	1840	0	1852	49	0
1	C	1944	0	1954	45	0
1	D	1944	0	1954	47	0
1	E	1944	0	1954	59	0
1	F	1861	0	1877	65	0
2	A	44	0	26	1	0
2	B	44	0	26	1	0
2	C	44	0	26	2	0
2	D	44	0	26	4	0
2	E	44	0	26	4	0
2	F	44	0	26	2	0
3	C	22	0	25	3	0
3	D	22	0	25	8	0
4	A	7	0	0	0	0
4	B	2	0	0	0	0
4	C	7	0	0	3	0
4	D	6	0	0	0	0
4	E	3	0	0	1	0
4	F	5	0	0	0	0
All	All	11736	0	11677	296	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 13.

The worst 5 of 296 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:F:101:THR:HG21	1:F:112:PRO:HD2	1.57	0.85
1:F:195:ARG:HG2	1:F:195:ARG:HH11	1.47	0.79
1:E:168:LEU:HD22	1:E:188:LEU:HD21	1.65	0.78
1:A:35:GLN:HE22	1:A:82:ILE:HG22	1.51	0.76
1:E:4:LEU:HD13	1:E:5:LEU:HD13	1.67	0.75

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	244/269 (91%)	224 (92%)	18 (7%)	2 (1%)	16	34
1	B	241/269 (90%)	220 (91%)	19 (8%)	2 (1%)	16	34
1	C	256/269 (95%)	237 (93%)	18 (7%)	1 (0%)	30	51
1	D	256/269 (95%)	234 (91%)	18 (7%)	4 (2%)	7	16
1	E	256/269 (95%)	237 (93%)	17 (7%)	2 (1%)	16	34
1	F	244/269 (91%)	217 (89%)	23 (9%)	4 (2%)	7	16
All	All	1497/1614 (93%)	1369 (91%)	113 (8%)	15 (1%)	12	28

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	195	ARG
1	D	207	LEU
1	D	209	GLU
1	E	195	ARG
1	F	108	PHE

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	193/205 (94%)	178 (92%)	15 (8%)	11	26
1	B	190/205 (93%)	175 (92%)	15 (8%)	11	26
1	C	199/205 (97%)	176 (88%)	23 (12%)	5	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	199/205 (97%)	185 (93%)	14 (7%)	14	31
1	E	199/205 (97%)	176 (88%)	23 (12%)	5	11
1	F	192/205 (94%)	173 (90%)	19 (10%)	7	16
All	All	1172/1230 (95%)	1063 (91%)	109 (9%)	8	18

5 of 109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	71	LEU
1	E	47	ILE
1	F	170	SER
1	D	135	LEU
1	D	245	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	24	HIS
1	F	67	ASN
1	D	70	HIS
1	F	139	ASN
1	E	216	GLN

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

8 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
2	NAD	C	403	-	46,48,48	1.93	8 (17%)	64,73,73	1.89	13 (20%)
3	8PS	C	300	-	23,23,23	1.25	1 (4%)	28,28,28	1.13	4 (14%)
3	8PS	D	301	-	23,23,23	1.31	1 (4%)	28,28,28	1.30	3 (10%)
2	NAD	B	402	-	46,48,48	1.80	7 (15%)	64,73,73	1.70	12 (18%)
2	NAD	F	406	-	46,48,48	1.65	4 (8%)	64,73,73	1.80	9 (14%)
2	NAD	D	404	-	46,48,48	1.88	7 (15%)	64,73,73	1.76	13 (20%)
2	NAD	E	405	-	46,48,48	1.88	7 (15%)	64,73,73	1.87	16 (25%)
2	NAD	A	401	-	46,48,48	1.62	5 (10%)	64,73,73	1.68	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	C	403	-	-	7/30/62/62	0/5/5/5
3	8PS	C	300	-	-	1/12/12/12	0/2/2/2
3	8PS	D	301	-	-	2/12/12/12	0/2/2/2
2	NAD	B	402	-	-	6/30/62/62	0/5/5/5
2	NAD	F	406	-	-	9/30/62/62	0/5/5/5
2	NAD	D	404	-	-	10/30/62/62	0/5/5/5
2	NAD	E	405	-	-	5/30/62/62	0/5/5/5
2	NAD	A	401	-	-	6/30/62/62	0/5/5/5

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	405	NAD	O7N-C7N	9.26	1.41	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	404	NAD	O7N-C7N	9.14	1.41	1.24
2	C	403	NAD	O7N-C7N	9.08	1.41	1.24
2	F	406	NAD	O7N-C7N	9.04	1.41	1.24
2	B	402	NAD	O7N-C7N	8.70	1.40	1.24

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	406	NAD	O4B-C1B-N9A	6.35	120.29	108.09
2	F	406	NAD	N3A-C2A-N1A	-6.33	119.00	128.58
2	A	401	NAD	N3A-C2A-N1A	-6.06	119.42	128.58
2	C	403	NAD	N3A-C2A-N1A	-6.05	119.43	128.58
2	E	405	NAD	N3A-C2A-N1A	-6.03	119.45	128.58

There are no chirality outliers.

5 of 46 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	NAD	C5D-O5D-PN-O3
2	A	401	NAD	O4D-C1D-N1N-C2N
2	A	401	NAD	O4D-C1D-N1N-C6N
2	B	402	NAD	C5D-O5D-PN-O3
2	B	402	NAD	C5D-O5D-PN-O1N

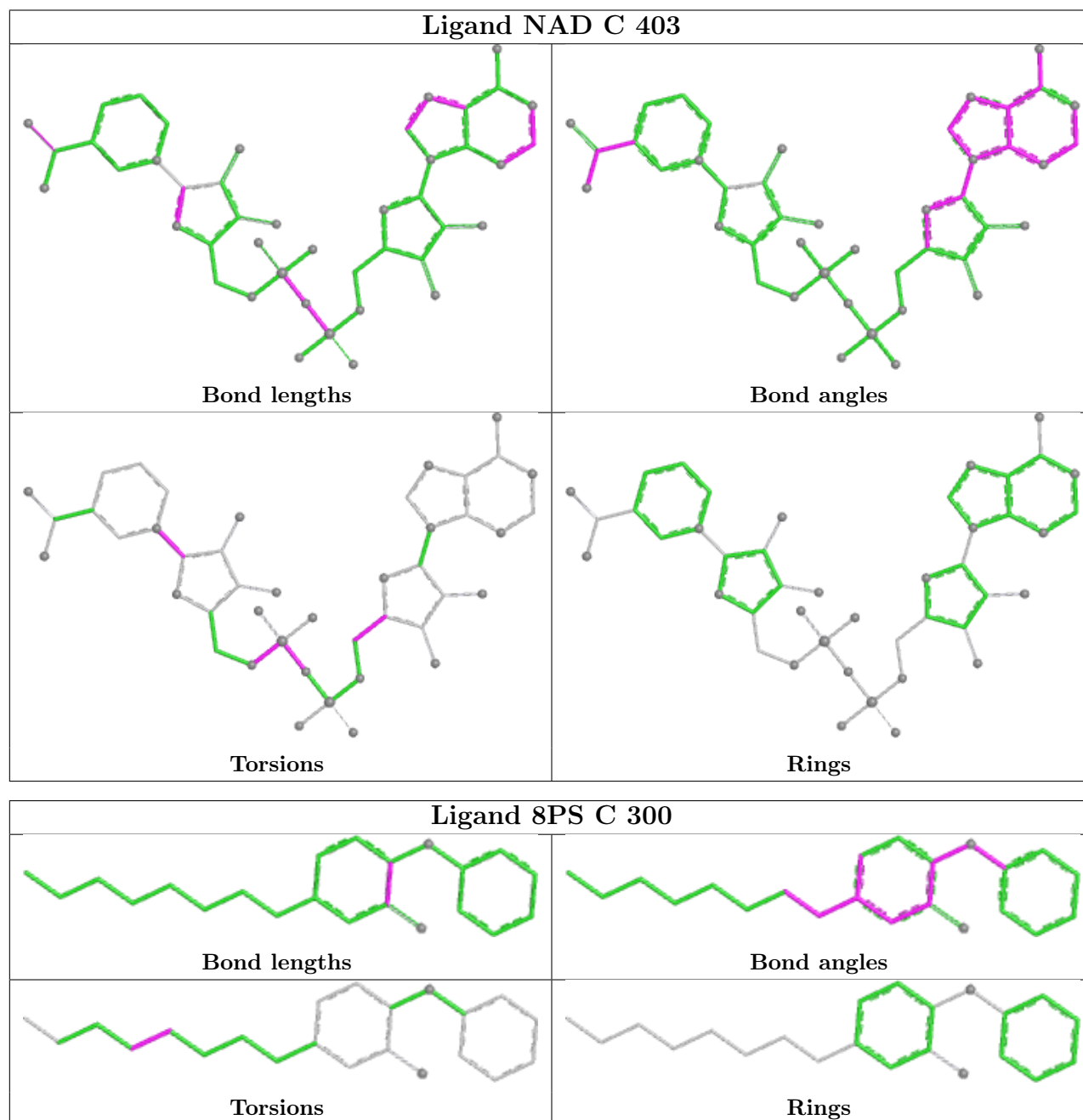
There are no ring outliers.

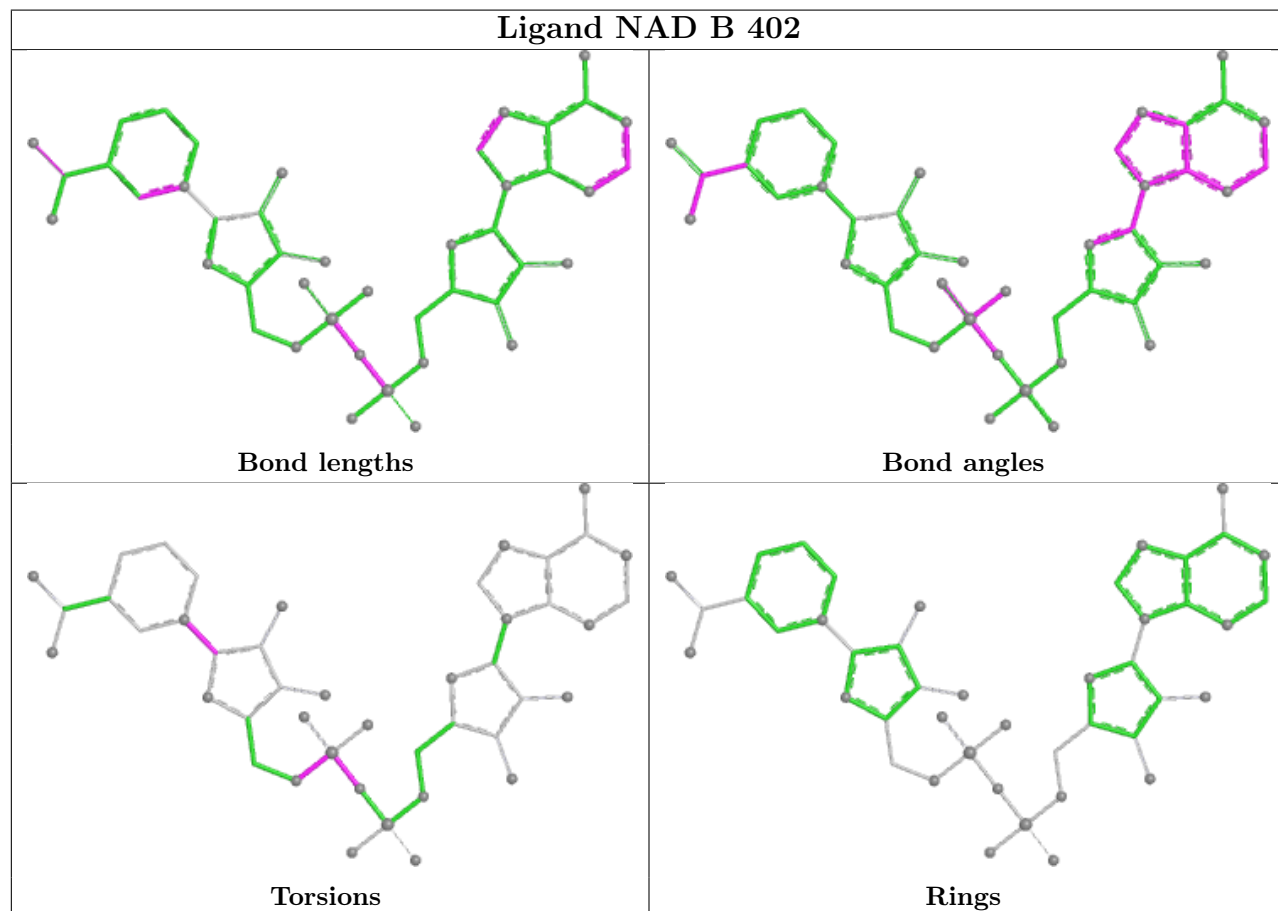
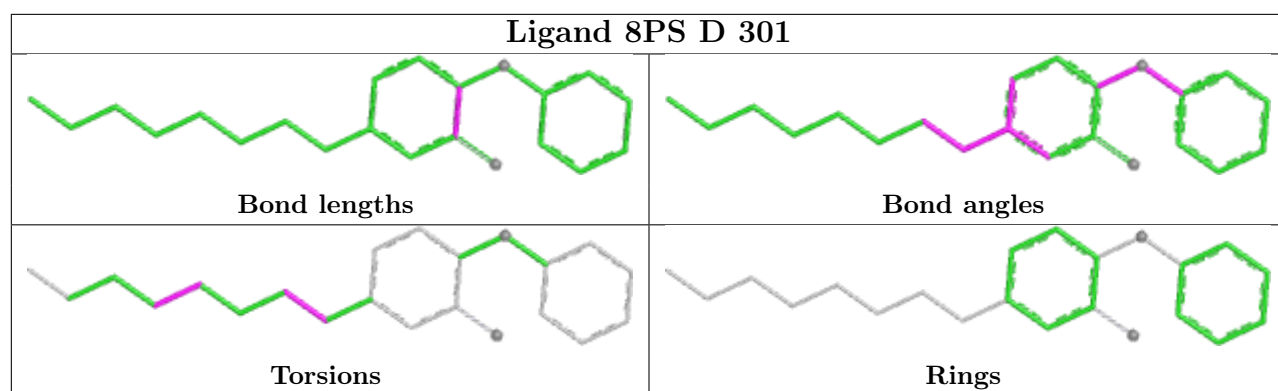
8 monomers are involved in 25 short contacts:

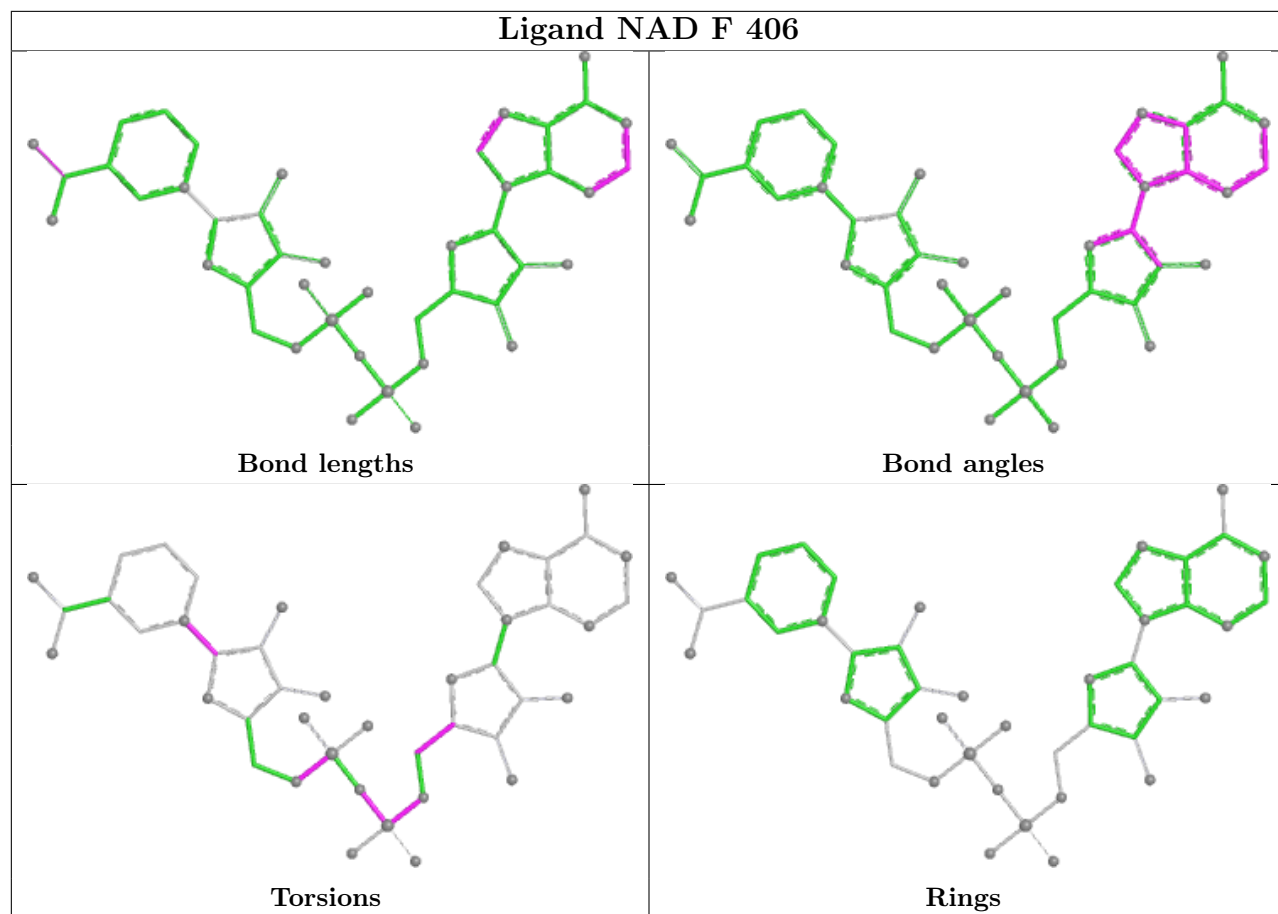
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	403	NAD	2	0
3	C	300	8PS	3	0
3	D	301	8PS	8	0
2	B	402	NAD	1	0
2	F	406	NAD	2	0
2	D	404	NAD	4	0
2	E	405	NAD	4	0
2	A	401	NAD	1	0

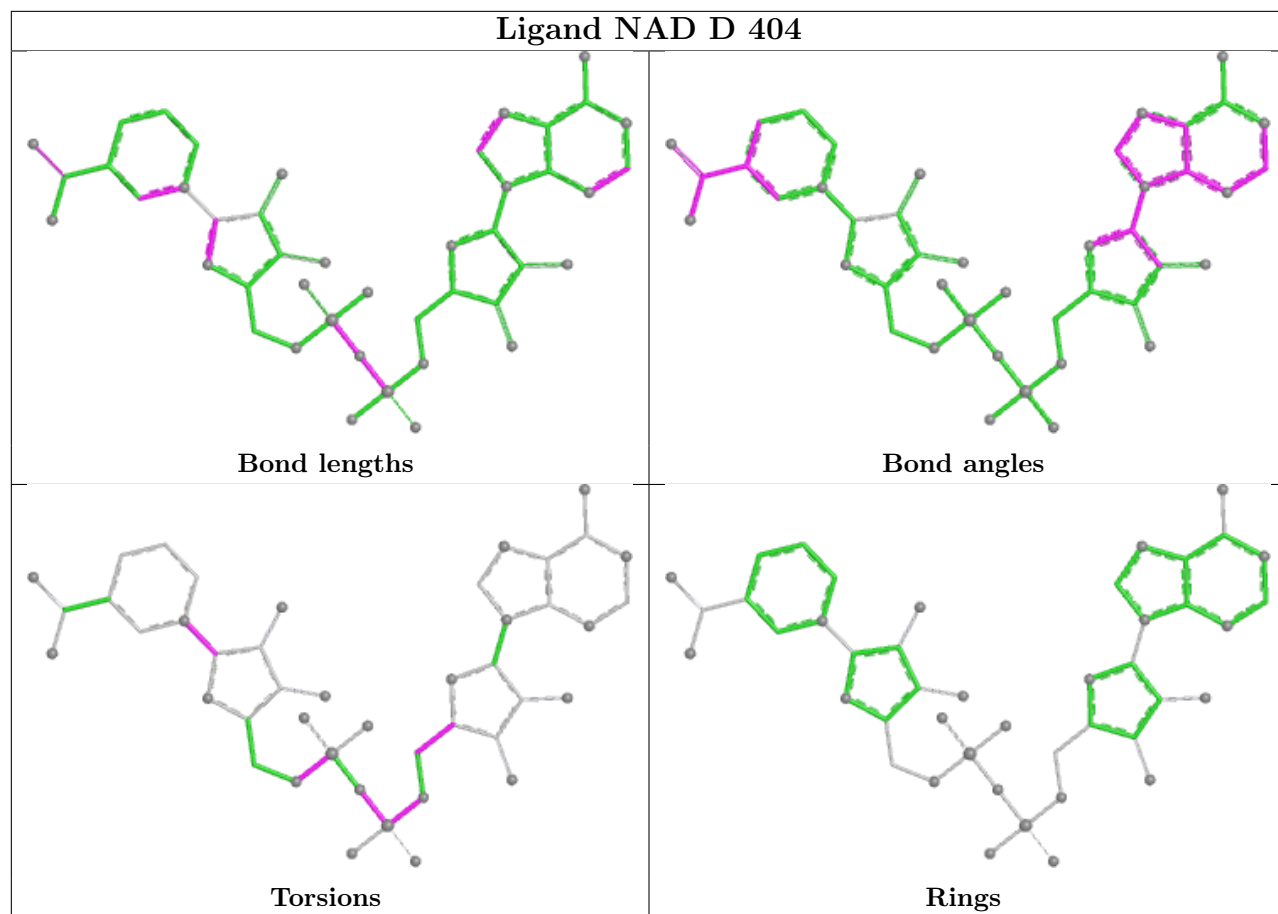
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

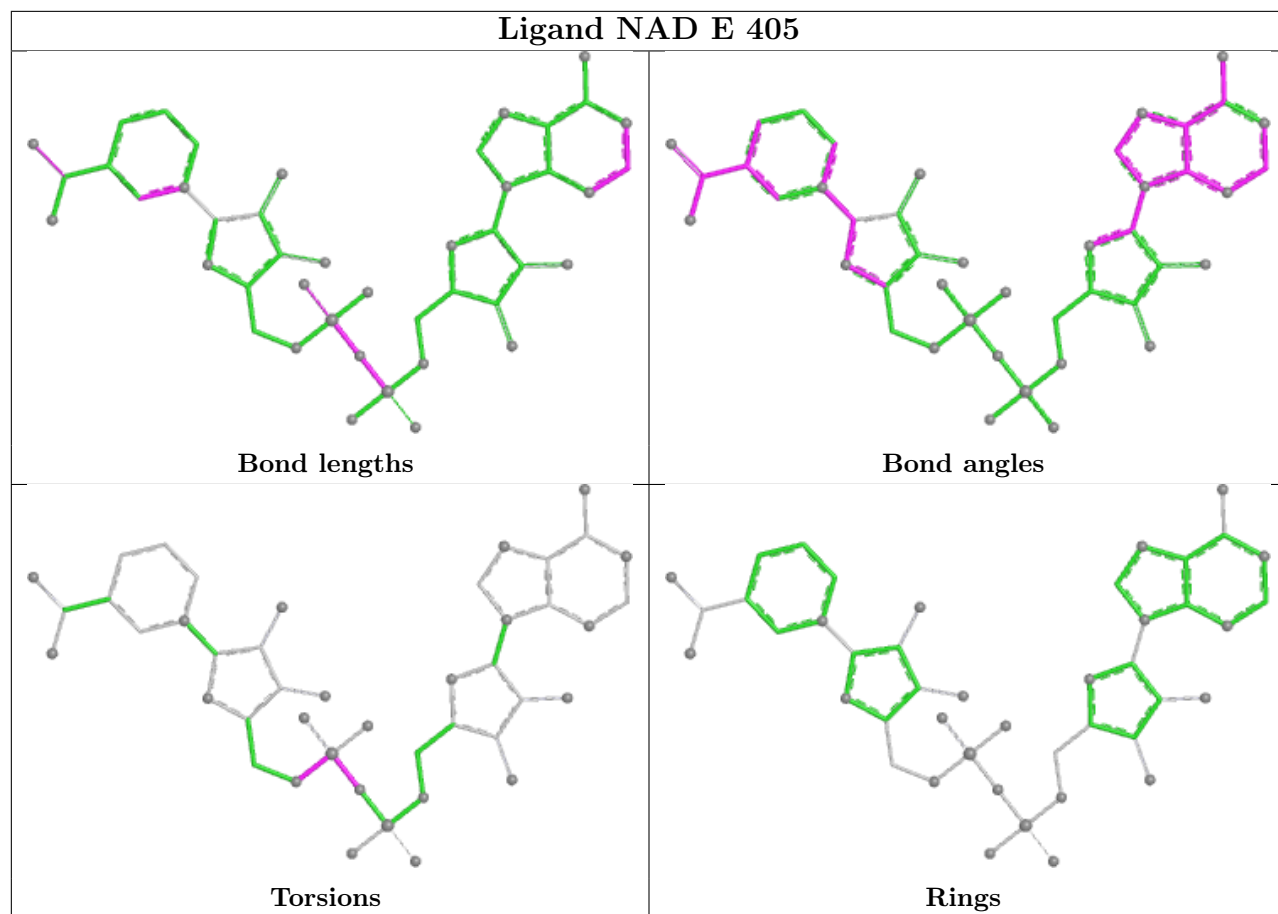
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.

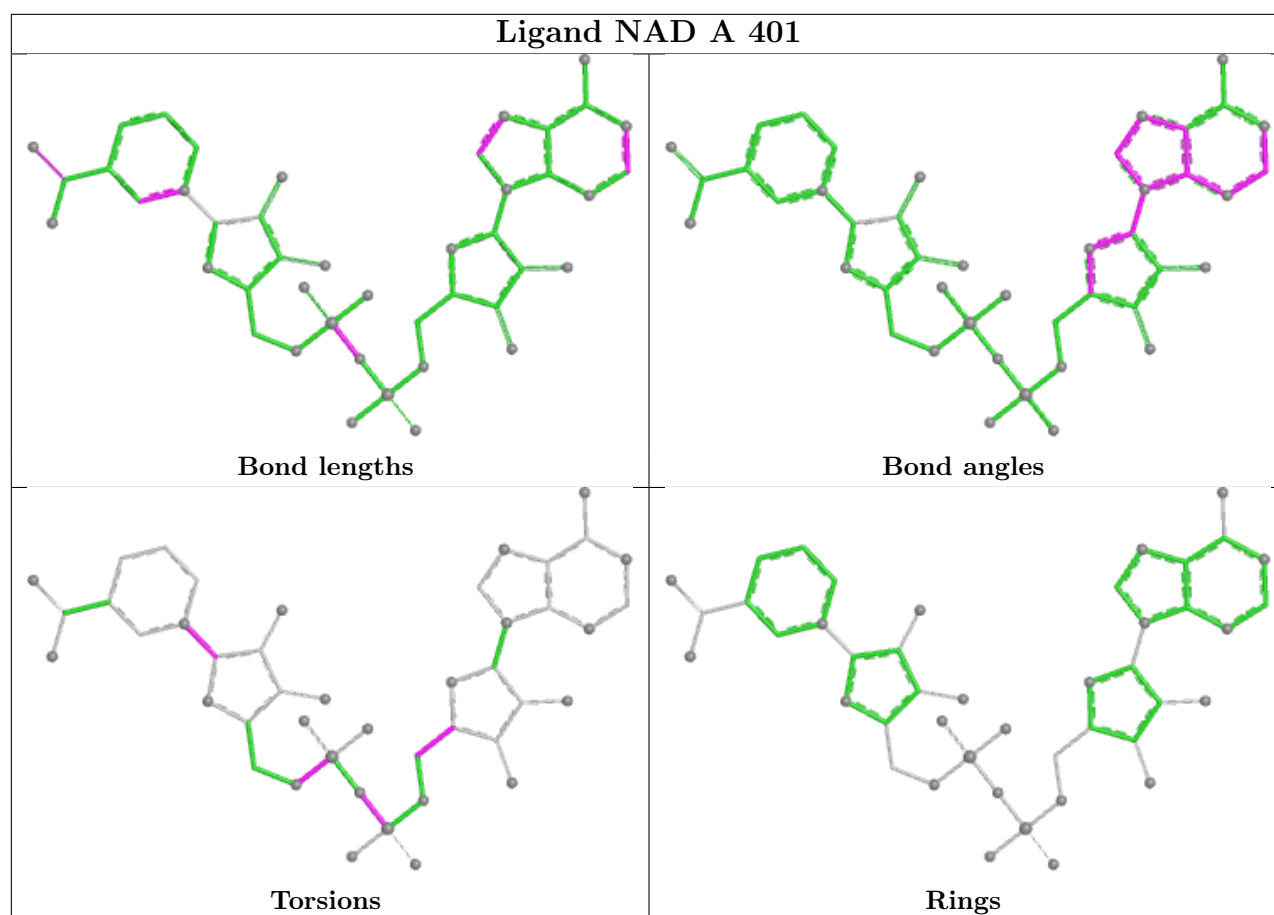












5.7 Other polymers [i](#)

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, 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	248/269 (92%)	0.16	3 (1%) 76 73	28, 44, 66, 77	0
1	B	245/269 (91%)	0.39	5 (2%) 65 60	32, 51, 78, 91	0
1	C	260/269 (96%)	-0.40	3 (1%) 76 73	9, 25, 54, 66	0
1	D	260/269 (96%)	-0.32	4 (1%) 72 68	9, 24, 58, 70	0
1	E	260/269 (96%)	0.03	2 (0%) 82 80	25, 39, 63, 73	0
1	F	248/269 (92%)	0.09	3 (1%) 76 73	25, 44, 64, 76	0
All	All	1521/1614 (94%)	-0.01	20 (1%) 75 71	9, 39, 65, 91	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	215	ILE	4.2
1	C	219	GLU	3.1
1	C	2	THR	3.0
1	E	215	ILE	2.9
1	B	196	THR	2.8

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](#)

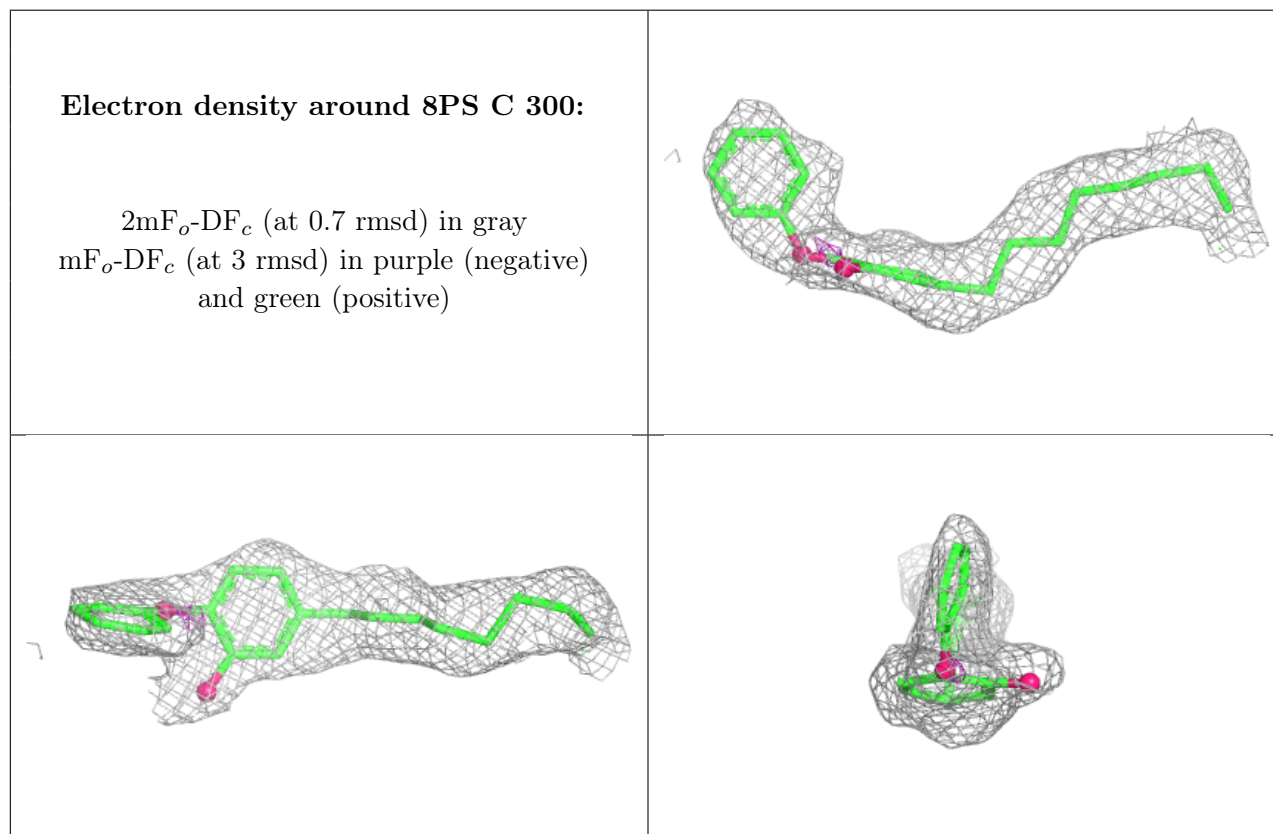
There are no oligosaccharides in this entry.

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.

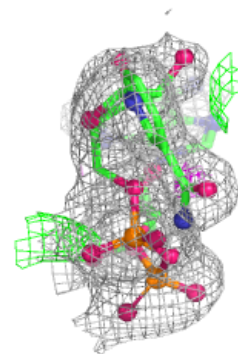
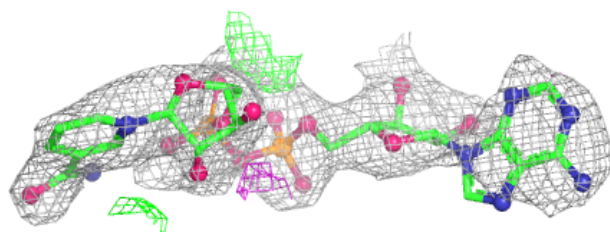
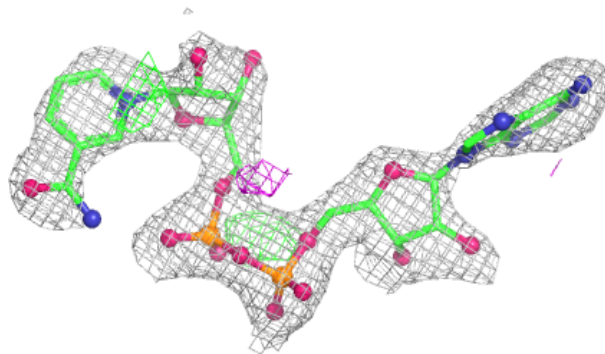
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	8PS	C	300	22/22	0.87	0.10	34,35,37,38	0
2	NAD	B	402	44/44	0.88	0.10	45,53,55,56	0
3	8PS	D	301	22/22	0.89	0.12	36,39,43,44	0
2	NAD	A	401	44/44	0.91	0.09	38,42,44,44	0
2	NAD	F	406	44/44	0.91	0.09	24,46,55,55	0
2	NAD	E	405	44/44	0.93	0.08	29,36,40,41	0
2	NAD	C	403	44/44	0.95	0.07	22,27,33,34	0
2	NAD	D	404	44/44	0.95	0.06	15,26,31,35	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.

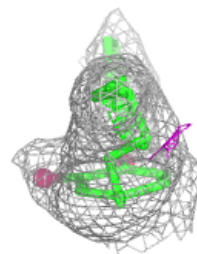
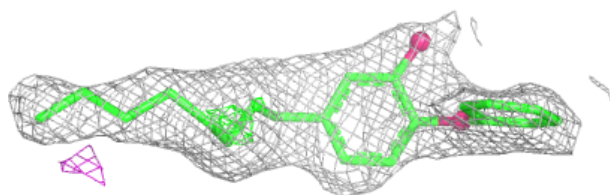
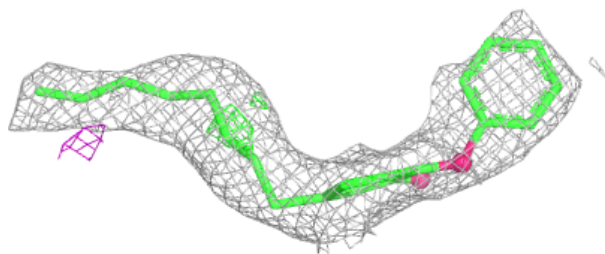


Electron density around NAD B 402:

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

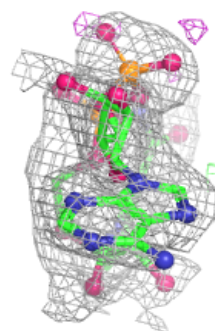
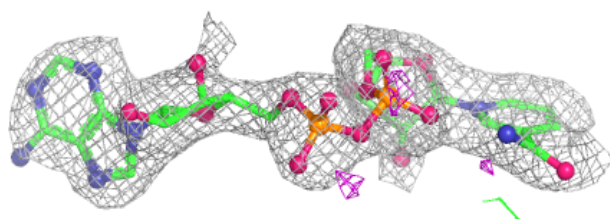
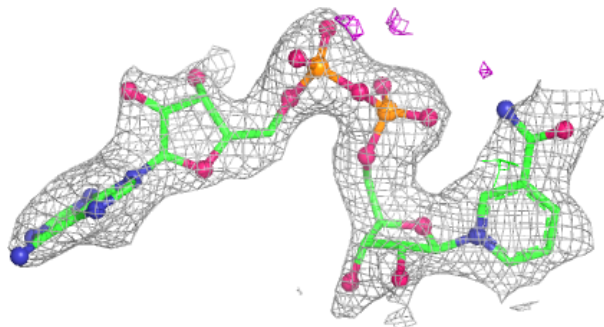
**Electron density around 8PS D 301:**

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

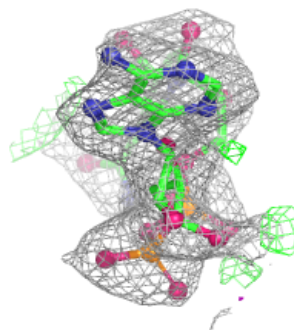
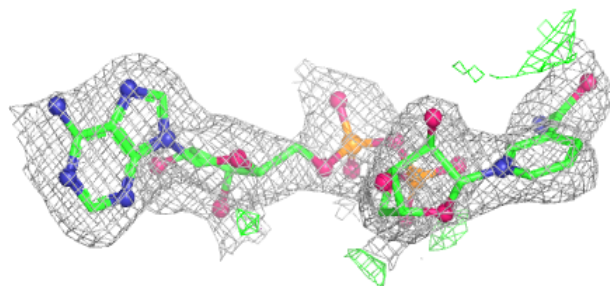
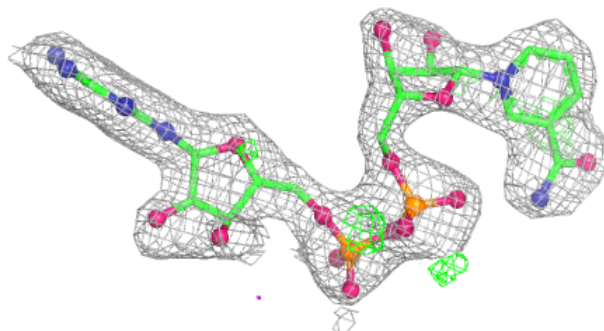


Electron density around NAD A 401:

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

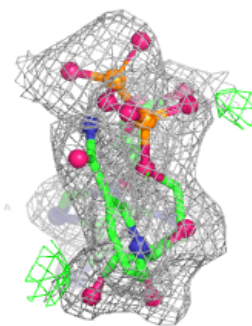
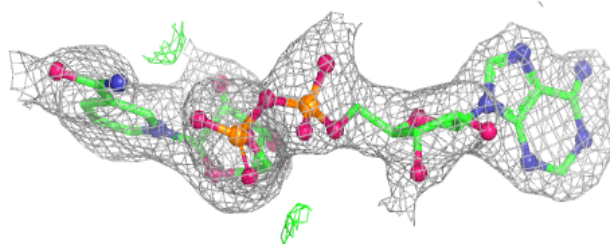
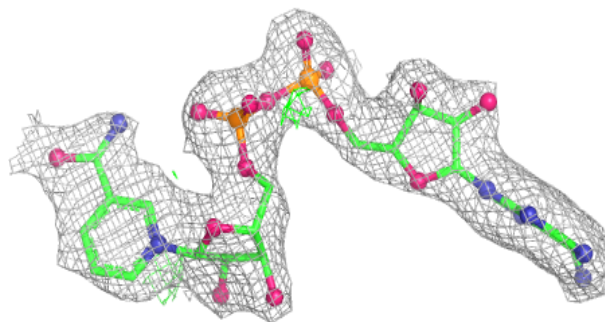
**Electron density around NAD F 406:**

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

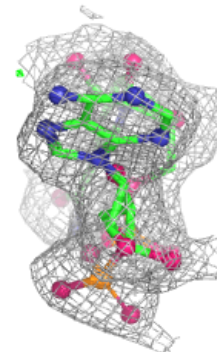
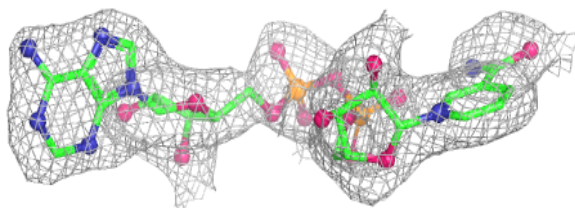
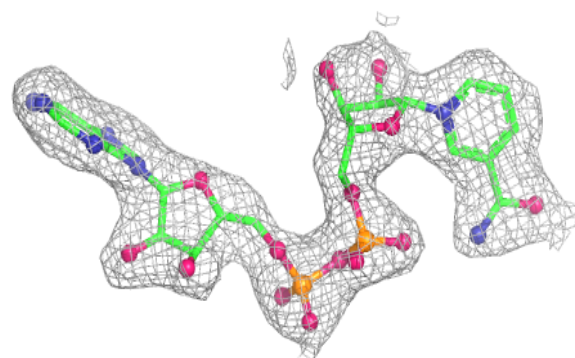


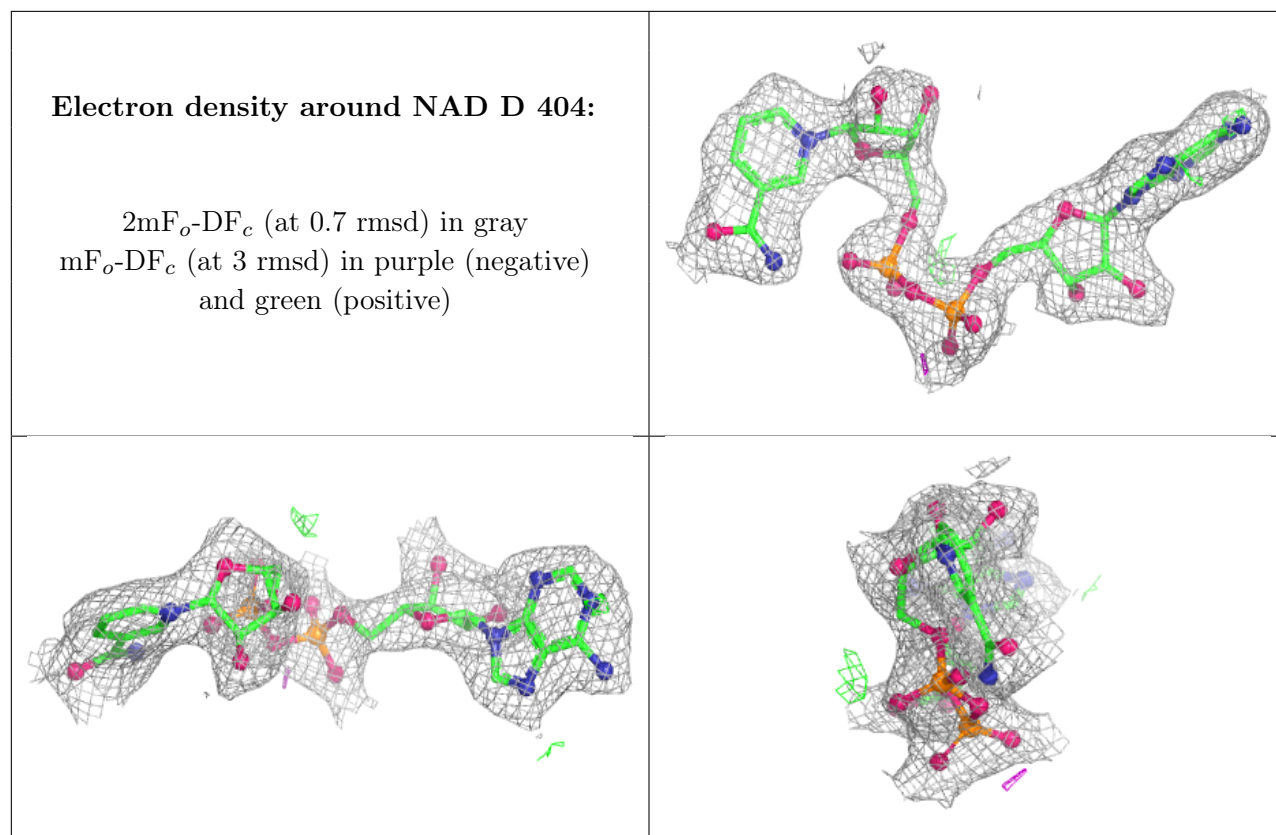
Electron density around NAD E 405:

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

**Electron density around NAD C 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.