



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2023 – 06:30 AM EDT

PDB ID : 6VV8
Title : Mycobacterium tuberculosis dihydrofolate reductase in complex with JEB285
Authors : Ribeiro, J.A.; Chavez-Pacheco, S.M.; Dias, M.V.B.
Deposited on : 2020-02-17
Resolution : 2.68 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : **FAILED**
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) : 2.35.1

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 2.68 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2681 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 Dihydrofolate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	159	1244	783	228	228	5	0	0	0
1	B	159	1244	783	228	228	5	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP A5U6B6
A	0	THR	-	expression tag	UNP A5U6B6
B	-1	MET	-	initiating methionine	UNP A5U6B6
B	0	THR	-	expression tag	UNP A5U6B6

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Co	0	0
			2	2		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	B	1	28	21	4	3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	14	Total	O	0	0
			14	14		
5	B	25	Total	O	0	0
			25	25		

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics i

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.17Å 71.49Å 72.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.75 – 2.68	Depositor
% Data completeness (in resolution range)	99.8 (35.75-2.68)	Depositor
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.68Å)	Xtrriage
Refinement program	PHENIX 1.14	Depositor
R, R_{free}	0.201 , 0.258	Depositor
Wilson B-factor (Å ²)	37.5	Xtrriage
Anisotropy	0.349	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.259 for -h,l,k	Xtrriage
Reported twinning fraction	0.230 for -h,l,k	Depositor
Outliers	0 of 9276 reflections	Xtrriage
Total number of atoms	2681	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.62% of the height of the origin peak. No significant pseudotranslation is detected.*

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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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
3	NAP	B	201	-	45,52,52	2.51	13 (28%)	56,80,80	1.92	16 (28%)
4	RPV	A	204	-	29,31,31	1.85	5 (17%)	30,43,43	1.63	8 (26%)
4	RPV	B	202	-	29,31,31	1.82	5 (17%)	30,43,43	1.73	8 (26%)
3	NAP	A	203	-	45,52,52	2.44	14 (31%)	56,80,80	2.03	14 (25%)

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	NAP	B	201	-	-	7/31/67/67	0/5/5/5
4	RPV	A	204	-	-	1/12/17/17	0/4/4/4
4	RPV	B	202	-	-	3/12/17/17	0/4/4/4
3	NAP	A	203	-	-	8/31/67/67	0/5/5/5

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	203	NAP	P2B-O2B	10.46	1.79	1.59
3	B	201	NAP	P2B-O2B	10.31	1.78	1.59
4	A	204	RPV	C14-N15	5.46	1.47	1.36
4	B	202	RPV	C14-N15	5.03	1.46	1.36
3	B	201	NAP	PN-O5D	4.95	1.79	1.59
4	A	204	RPV	C16-N15	4.70	1.46	1.35
4	B	202	RPV	C16-N15	4.48	1.45	1.35
3	A	203	NAP	C4N-C3N	4.45	1.46	1.39
3	A	203	NAP	C5N-C4N	4.39	1.48	1.38
3	B	201	NAP	C7N-N7N	4.38	1.41	1.33
3	B	201	NAP	C5N-C4N	3.97	1.47	1.38
3	A	203	NAP	PN-O5D	3.92	1.75	1.59
3	B	201	NAP	C4N-C3N	3.78	1.45	1.39
4	A	204	RPV	C08-N07	-3.71	1.32	1.44
3	B	201	NAP	O2B-C2B	-3.58	1.31	1.44
4	B	202	RPV	C14-N07	-3.55	1.33	1.37
4	B	202	RPV	C08-N07	-3.49	1.33	1.44
3	A	203	NAP	O2B-C2B	-3.47	1.31	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	203	NAP	C3N-C7N	-3.05	1.46	1.50
3	B	201	NAP	C2N-N1N	3.00	1.38	1.35
3	A	203	NAP	O4B-C1B	2.99	1.45	1.41
3	B	201	NAP	C3N-C7N	-2.97	1.46	1.50
4	A	204	RPV	C14-N07	-2.89	1.34	1.37
3	B	201	NAP	C4A-N3A	2.86	1.39	1.35
3	A	203	NAP	C7N-N7N	2.84	1.38	1.33
3	B	201	NAP	C2N-C3N	-2.73	1.34	1.39
3	A	203	NAP	C2A-N1A	2.58	1.38	1.33
3	A	203	NAP	C6N-N1N	2.49	1.41	1.35
4	B	202	RPV	O17-C16	-2.39	1.18	1.23
3	B	201	NAP	C2A-N1A	2.38	1.38	1.33
3	B	201	NAP	C6N-C5N	-2.30	1.33	1.38
3	A	203	NAP	C2N-N1N	2.26	1.37	1.35
4	A	204	RPV	O17-C16	-2.22	1.18	1.23
3	A	203	NAP	O3D-C3D	-2.17	1.37	1.43
3	A	203	NAP	C6N-C5N	-2.14	1.33	1.38
3	A	203	NAP	C2A-N3A	2.12	1.35	1.32
3	B	201	NAP	C3D-C4D	2.04	1.58	1.53

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	203	NAP	C5N-C4N-C3N	-6.39	112.78	120.34
3	B	201	NAP	PN-O3-PA	-6.09	111.92	132.83
3	A	203	NAP	PN-O3-PA	-5.41	114.27	132.83
3	B	201	NAP	C5N-C4N-C3N	-5.28	114.09	120.34
3	A	203	NAP	O7N-C7N-C3N	4.73	125.30	119.63
4	B	202	RPV	C05-N06-N07	4.20	109.43	103.93
4	A	204	RPV	C05-N06-N07	3.83	108.95	103.93
3	A	203	NAP	C2N-C3N-C4N	3.66	122.41	118.26
3	B	201	NAP	O7N-C7N-C3N	3.39	123.69	119.63
3	B	201	NAP	O2B-P2B-O1X	-3.35	96.46	109.39
3	A	203	NAP	O4D-C1D-C2D	-3.32	102.08	106.93
4	A	204	RPV	C18-C16-N15	3.26	120.33	114.59
3	B	201	NAP	C3D-C2D-C1D	-3.20	96.15	100.98
4	B	202	RPV	C18-C16-N15	3.19	120.22	114.59
3	B	201	NAP	C2N-C3N-C4N	3.08	121.75	118.26
4	B	202	RPV	C27-C28-C23	3.05	122.21	118.17
3	B	201	NAP	PA-O5B-C5B	-2.96	104.32	121.68
4	B	202	RPV	C18-C19-C20	-2.95	104.68	112.48
3	A	203	NAP	C6N-N1N-C2N	-2.87	119.35	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	203	NAP	O7N-C7N-N7N	-2.83	118.55	122.58
3	A	203	NAP	PA-O5B-C5B	-2.83	105.07	121.68
4	B	202	RPV	C14-N15-C16	-2.81	121.07	126.52
4	A	204	RPV	C14-N15-C16	-2.79	121.11	126.52
3	A	203	NAP	O3X-P2B-O2X	2.77	118.22	107.64
3	A	203	NAP	O2B-P2B-O1X	-2.65	99.18	109.39
3	B	201	NAP	O3X-P2B-O2X	2.64	117.73	107.64
4	A	204	RPV	C19-C18-C16	2.49	118.44	112.72
4	A	204	RPV	C27-C28-C23	2.49	121.47	118.17
3	A	203	NAP	O3X-P2B-O2B	-2.46	94.95	105.99
3	B	201	NAP	PN-O5D-C5D	-2.46	107.25	121.68
3	B	201	NAP	O5D-PN-O1N	-2.38	99.76	109.07
4	A	204	RPV	O17-C16-N15	-2.36	119.32	123.63
3	B	201	NAP	O7N-C7N-N7N	-2.34	119.25	122.58
3	B	201	NAP	C2A-N1A-C6A	-2.31	114.80	118.75
3	A	203	NAP	C2A-N1A-C6A	-2.31	114.81	118.75
3	A	203	NAP	O3D-C3D-C4D	-2.27	104.49	111.05
3	A	203	NAP	PN-O5D-C5D	-2.18	108.89	121.68
3	B	201	NAP	C2B-C3B-C4B	-2.18	97.26	101.99
4	A	204	RPV	O03-C02-C04	-2.14	116.73	121.94
4	B	202	RPV	C26-C27-C28	-2.12	117.96	120.89
4	B	202	RPV	O01-C02-C04	2.11	121.39	115.31
4	A	204	RPV	C18-C19-C20	-2.08	106.97	112.48
3	B	201	NAP	O4D-C1D-C2D	-2.08	103.89	106.93
3	B	201	NAP	O3X-P2B-O2B	-2.03	96.90	105.99
4	B	202	RPV	C08-N07-C14	-2.03	126.65	129.12
3	B	201	NAP	O2N-PN-O1N	2.00	122.13	112.24

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	203	NAP	C5B-O5B-PA-O1A
3	A	203	NAP	C5B-O5B-PA-O2A
3	A	203	NAP	C5B-O5B-PA-O3
3	A	203	NAP	O4D-C1D-N1N-C6N
3	B	201	NAP	O4D-C1D-N1N-C2N
3	B	201	NAP	O4D-C1D-N1N-C6N
3	B	201	NAP	C2D-C1D-N1N-C2N
4	A	204	RPV	C16-C18-C19-C20
4	B	202	RPV	C18-C19-C20-C28
3	B	201	NAP	C3D-C4D-C5D-O5D

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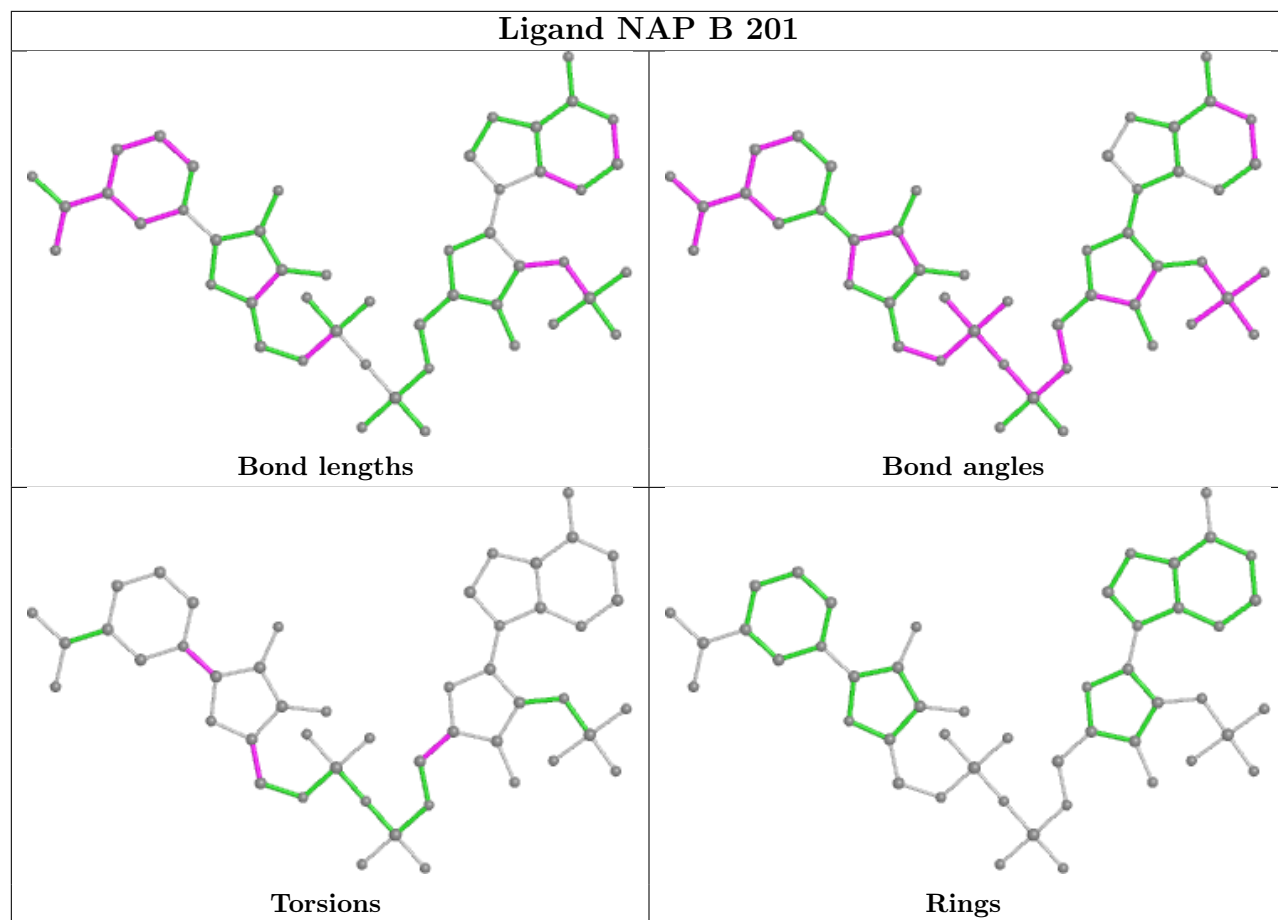
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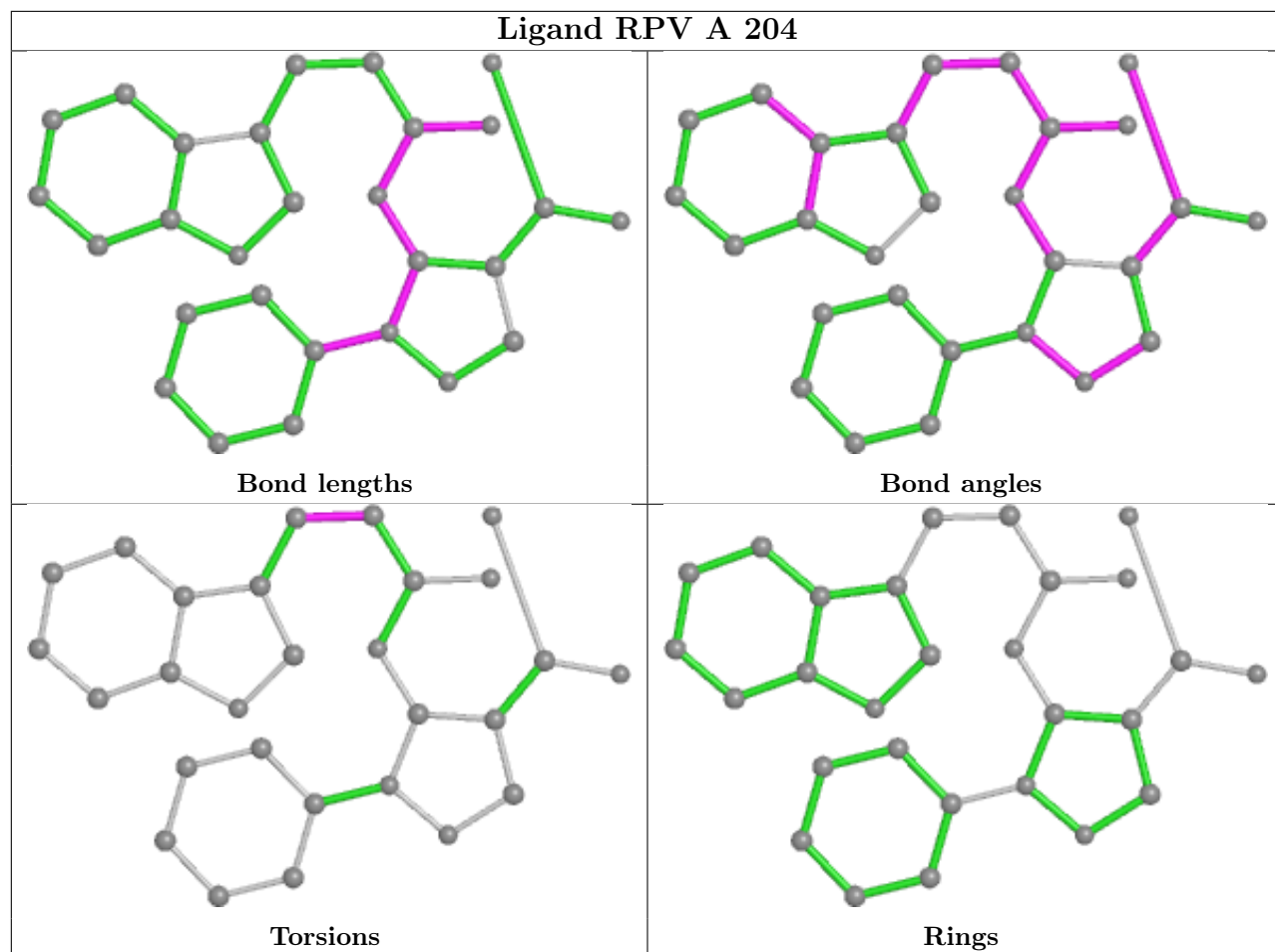
Mol	Chain	Res	Type	Atoms
3	B	201	NAP	O4D-C4D-C5D-O5D
3	A	203	NAP	C3D-C4D-C5D-O5D
3	B	201	NAP	C3B-C4B-C5B-O5B
3	A	203	NAP	PA-O3-PN-O5D
3	A	203	NAP	O4D-C4D-C5D-O5D
4	B	202	RPV	O17-C16-C18-C19
4	B	202	RPV	N15-C16-C18-C19
3	A	203	NAP	C2D-C1D-N1N-C2N
3	B	201	NAP	C2D-C1D-N1N-C6N

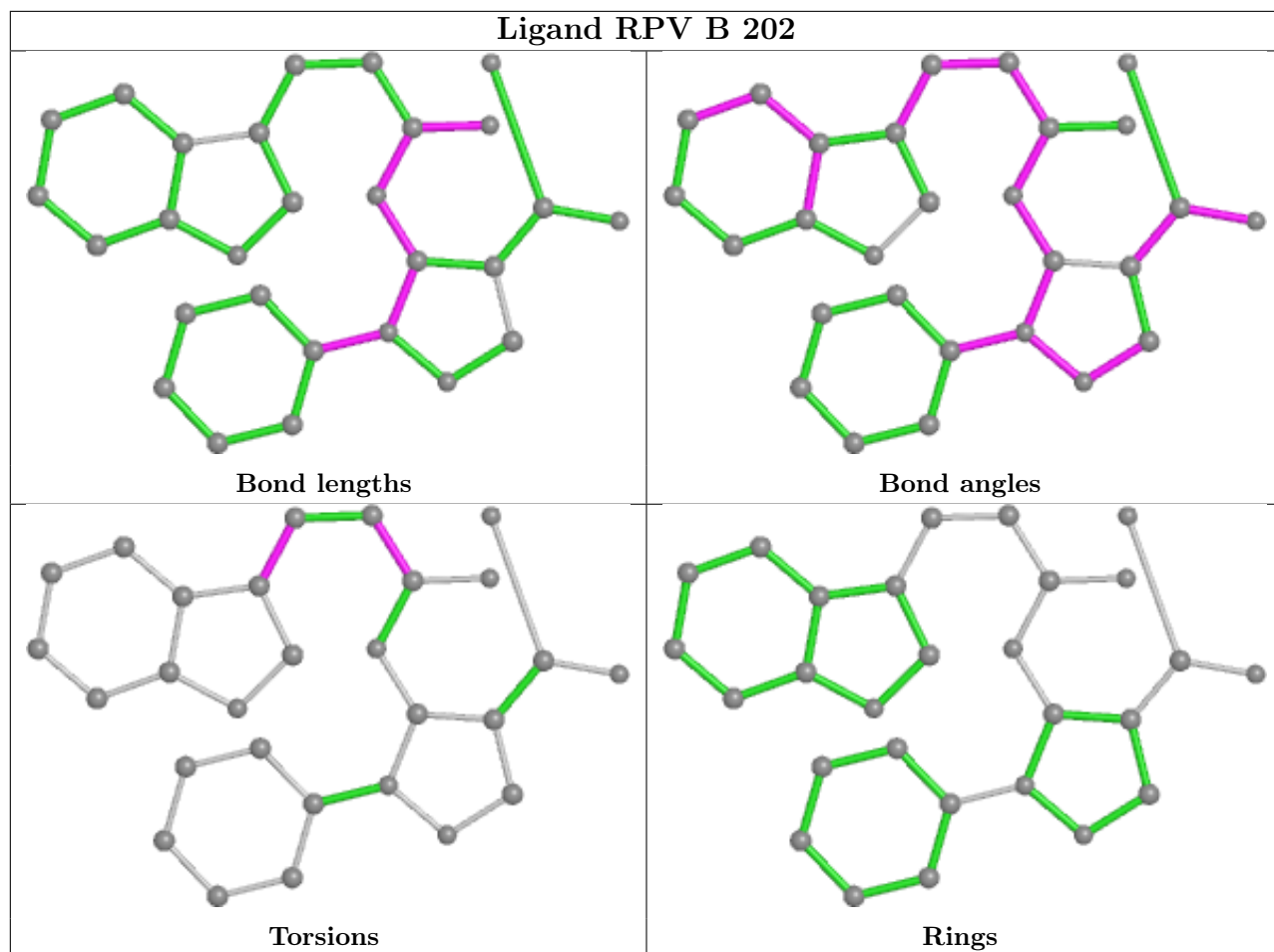
There are no ring outliers.

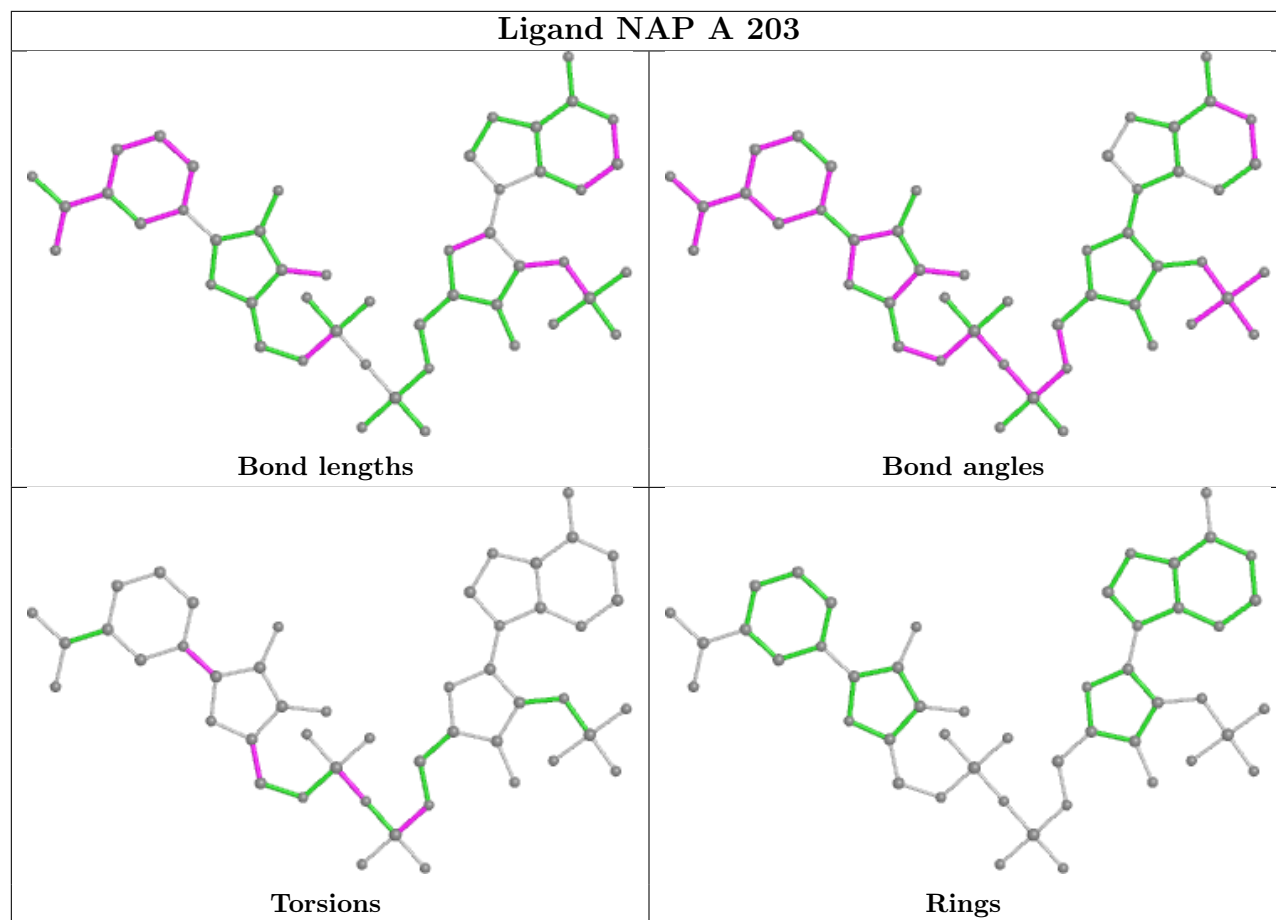
No monomer is involved in short contacts.

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.









4.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.