



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 10:05 AM UTC

PDB ID : 4BB5 / pdb\_00004bb5  
Title : Free-Wilson and Structural Approaches to Co-optimising Human and Rodent Isoform Potency for 11b-Hydroxysteroid Dehydrogenase Type 1 11b-HSD1 Inhibitors  
Authors : Goldberg, F.W.; Leach, A.G.; Scott, J.S.; Snelson, W.L.; Groombridge, S.D.; Donald, C.S.; Bennett, S.N.L.; Bodin, C.; Morentin Gutierrez, P.; Gyte, A.C.  
Deposited on : 2012-09-20  
Resolution : 2.20 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](#) ①) 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

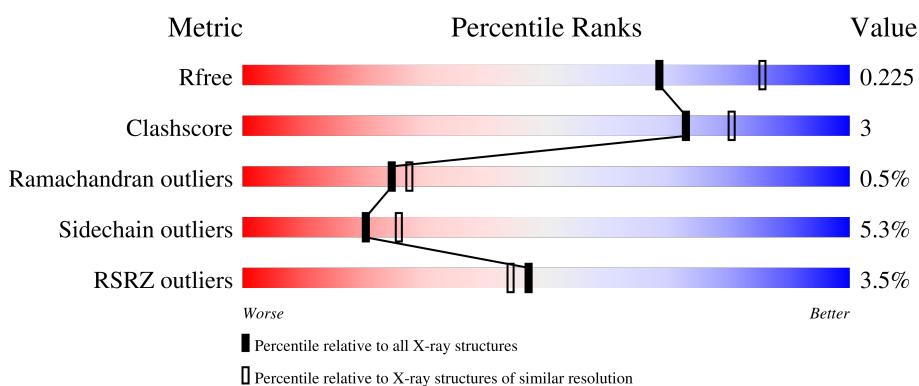
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	292	 5% 80% 9% • 10%
1	B	292	 3% 81% 8% • 10%
1	C	292	 % 77% 9% • 13%
1	D	292	 4% 80% 8% • 10%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8641 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 CORTICOSTEROID 11-BETA-DEHYDROGENASE ISOZYME 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	263	2023	1288	346	374	15	0	0	0
1	B	264	2032	1293	347	377	15	0	0	0
1	C	254	1943	1237	333	359	14	0	0	0
1	D	262	2015	1282	343	375	15	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	179	LEU	MET	conflict	UNP P28845
A	262	ARG	LEU	conflict	UNP P28845
A	272	SER	CYS	conflict	UNP P28845
A	278	GLU	PHE	conflict	UNP P28845
B	179	LEU	MET	conflict	UNP P28845
B	262	ARG	LEU	conflict	UNP P28845
B	272	SER	CYS	conflict	UNP P28845
B	278	GLU	PHE	conflict	UNP P28845
C	179	LEU	MET	conflict	UNP P28845
C	262	ARG	LEU	conflict	UNP P28845
C	272	SER	CYS	conflict	UNP P28845
C	278	GLU	PHE	conflict	UNP P28845
D	179	LEU	MET	conflict	UNP P28845
D	262	ARG	LEU	conflict	UNP P28845
D	272	SER	CYS	conflict	UNP P28845
D	278	GLU	PHE	conflict	UNP P28845

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			31	24	4	3		
3	B	1	Total	C	N	O	0	0
			31	24	4	3		
3	C	1	Total	C	N	O	0	0
			31	24	4	3		
3	D	1	Total	C	N	O	0	0
			31	24	4	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	98	Total	O	0	0
			98	98		
4	B	89	Total	O	0	0
			89	89		
4	C	90	Total	O	0	0
			90	90		
4	D	35	Total	O	0	0
			35	35		





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.78Å 132.48Å 154.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 2.20 35.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (35.00-2.20) 99.6 (35.00-2.20)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.22 (at 2.20Å)	Xtrriage
Refinement program	BUSTER 2.11.1	Depositor
R, $R_{free}$	0.182 , 0.220 0.184 , 0.225	Depositor DCC
$R_{free}$ test set	2607 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.0	Xtrriage
Anisotropy	0.367	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 38.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8641	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.09% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: NAP, HD2

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	0.82	0/2057	1.27	3/2776 (0.1%)
1	B	0.83	0/2066	1.28	3/2788 (0.1%)
1	C	0.83	0/1974	1.25	3/2664 (0.1%)
1	D	0.79	0/2047	1.25	3/2760 (0.1%)
All	All	0.82	0/8144	1.26	12/10988 (0.1%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	127	ASN	CA-CB-CG	7.47	120.07	112.60
1	A	264	THR	N-CA-C	-6.77	103.97	111.82
1	C	94	GLU	N-CA-C	-5.50	106.07	112.89
1	B	94	GLU	N-CA-C	-5.49	106.08	112.89
1	D	285	ASN	CA-CB-CG	5.31	117.91	112.60

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	2023	0	2070	20	0
1	B	2032	0	2076	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1943	0	2000	20	0
1	D	2015	0	2059	17	0
2	A	48	0	25	2	0
2	B	48	0	25	0	0
2	C	48	0	25	1	0
2	D	48	0	25	0	0
3	A	31	0	34	2	0
3	B	31	0	34	1	0
3	C	31	0	34	1	0
3	D	31	0	34	2	0
4	A	98	0	0	1	0
4	B	89	0	0	1	0
4	C	90	0	0	1	0
4	D	35	0	0	1	0
All	All	8641	0	8441	54	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 3.

The worst 5 of 54 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:MET:HE2	1:B:140:MET:HE2	1.72	0.70
1:A:87:HIS:HD2	4:A:2007:HOH:O	1.79	0.66
1:C:129:PHE:HB3	1:D:197:ILE:HD11	1.79	0.64
1:D:216:GLY:HA3	1:D:259:ASP:OD1	1.97	0.64
1:C:197:ILE:HD11	1:D:129:PHE:HB3	1.79	0.63

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	261/292 (89%)	250 (96%)	11 (4%)	0	100	100
1	B	262/292 (90%)	251 (96%)	8 (3%)	3 (1%)	11	10
1	C	252/292 (86%)	243 (96%)	8 (3%)	1 (0%)	30	34
1	D	258/292 (88%)	247 (96%)	10 (4%)	1 (0%)	30	34
All	All	1033/1168 (88%)	991 (96%)	37 (4%)	5 (0%)	24	27

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	233	MET
1	D	283	SER
1	B	219	ASP
1	B	283	SER
1	C	219	ASP

### 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	220/245 (90%)	207 (94%)	13 (6%)	18	22
1	B	221/245 (90%)	210 (95%)	11 (5%)	22	28
1	C	211/245 (86%)	200 (95%)	11 (5%)	21	26
1	D	219/245 (89%)	208 (95%)	11 (5%)	22	28
All	All	871/980 (89%)	825 (95%)	46 (5%)	20	26

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	205	ARG
1	D	145	LEU
1	C	207	ASN
1	C	266	LEU
1	D	175	VAL

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	D	130	HIS
1	D	160	GLN
1	B	135	HIS
1	B	130	HIS
1	D	207	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

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$
3	HD2	B	1291	-	36,36,36	1.24	2 (5%)	45,54,54	1.21	5 (11%)
3	HD2	A	1291	-	36,36,36	1.11	2 (5%)	45,54,54	1.65	7 (15%)
2	NAP	A	1290	-	50,52,52	3.49	23 (46%)	71,80,80	2.58	30 (42%)
3	HD2	D	1292	-	36,36,36	1.11	3 (8%)	45,54,54	1.53	7 (15%)
2	NAP	B	1290	-	50,52,52	3.83	29 (58%)	71,80,80	2.90	33 (46%)
3	HD2	C	1281	-	36,36,36	1.17	2 (5%)	45,54,54	1.56	9 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAP	D	1291	-	50,52,52	3.45	27 (54%)	71,80,80	2.94	36 (50%)
2	NAP	C	1280	-	50,52,52	3.40	25 (50%)	71,80,80	2.72	33 (46%)

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	HD2	B	1291	-	-	3/16/61/61	0/7/6/6
3	HD2	A	1291	-	-	4/16/61/61	0/7/6/6
2	NAP	A	1290	-	-	6/35/67/67	0/5/5/5
3	HD2	D	1292	-	-	3/16/61/61	0/7/6/6
2	NAP	B	1290	-	-	4/35/67/67	0/5/5/5
3	HD2	C	1281	-	-	3/16/61/61	0/7/6/6
2	NAP	D	1291	-	-	5/35/67/67	0/5/5/5
2	NAP	C	1280	-	-	6/35/67/67	0/5/5/5

The worst 5 of 113 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1290	NAP	C4N-C3N	9.96	1.54	1.39
2	C	1280	NAP	C4N-C3N	9.29	1.53	1.39
2	A	1290	NAP	C4N-C3N	9.09	1.53	1.39
2	A	1290	NAP	PA-O3	8.46	1.68	1.59
2	D	1291	NAP	C4N-C3N	8.28	1.52	1.39

The worst 5 of 160 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1291	NAP	N3A-C2A-N1A	-7.58	117.11	128.58
2	B	1290	NAP	C2B-C1B-N9A	-7.28	101.77	113.75
2	A	1290	NAP	C2B-C1B-N9A	-7.17	101.95	113.75
2	C	1280	NAP	O3X-P2B-O2X	6.92	133.76	107.80
2	D	1291	NAP	C2B-C1B-N9A	-6.82	102.53	113.75

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

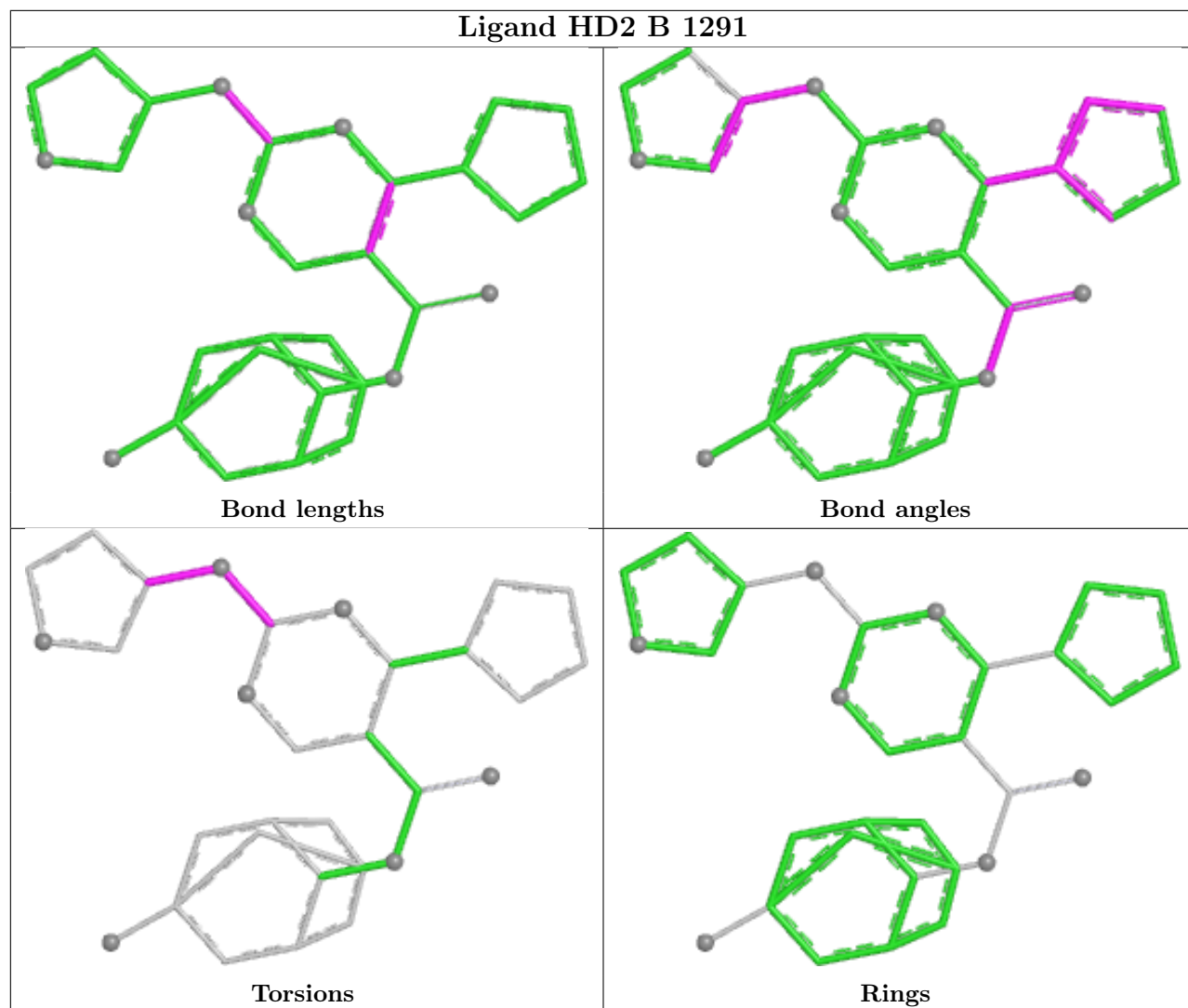
Mol	Chain	Res	Type	Atoms
2	A	1290	NAP	C5D-O5D-PN-O3
2	A	1290	NAP	C5D-O5D-PN-O1N
2	B	1290	NAP	C5D-O5D-PN-O3
2	B	1290	NAP	C5D-O5D-PN-O1N
2	C	1280	NAP	C5D-O5D-PN-O3

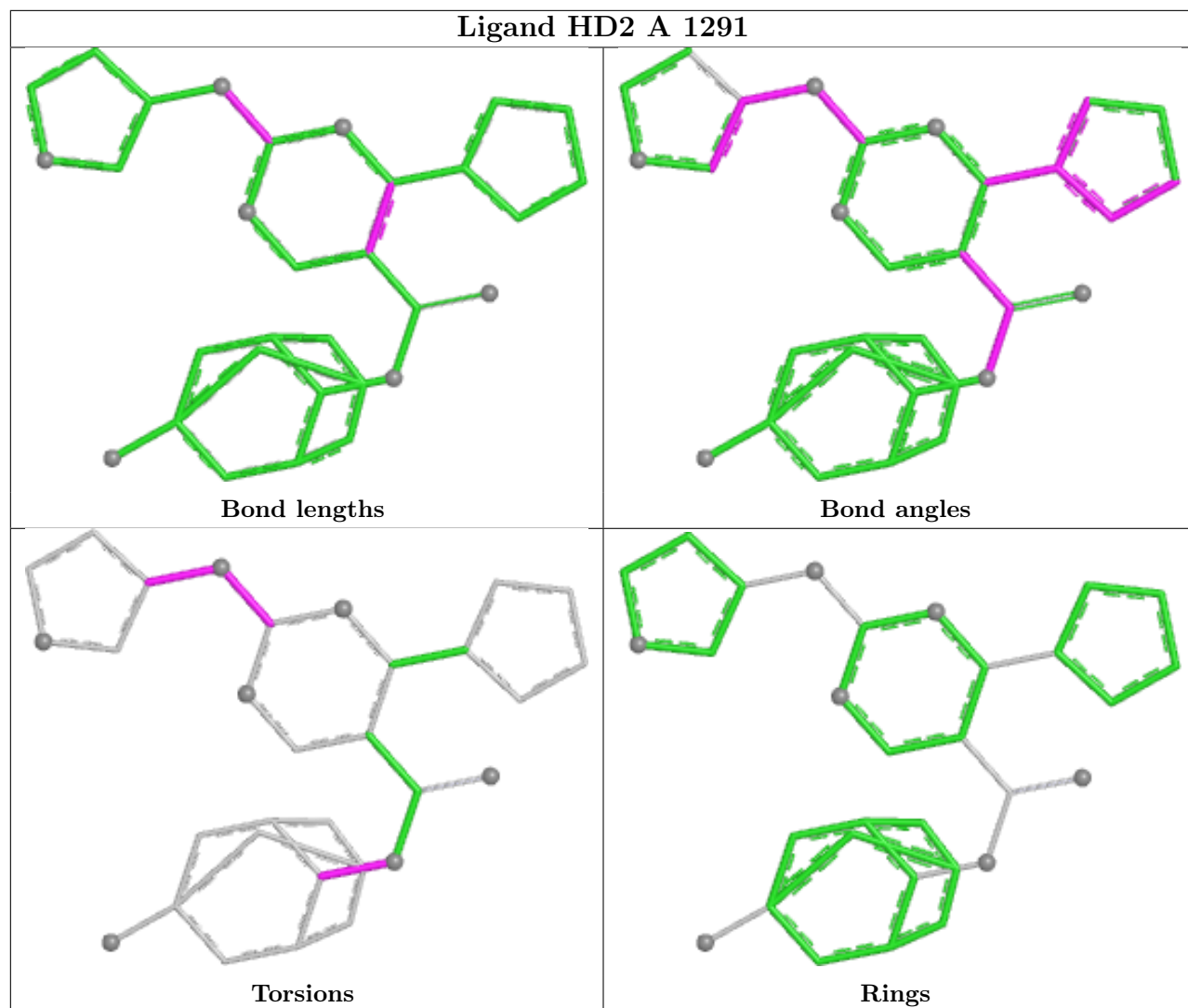
There are no ring outliers.

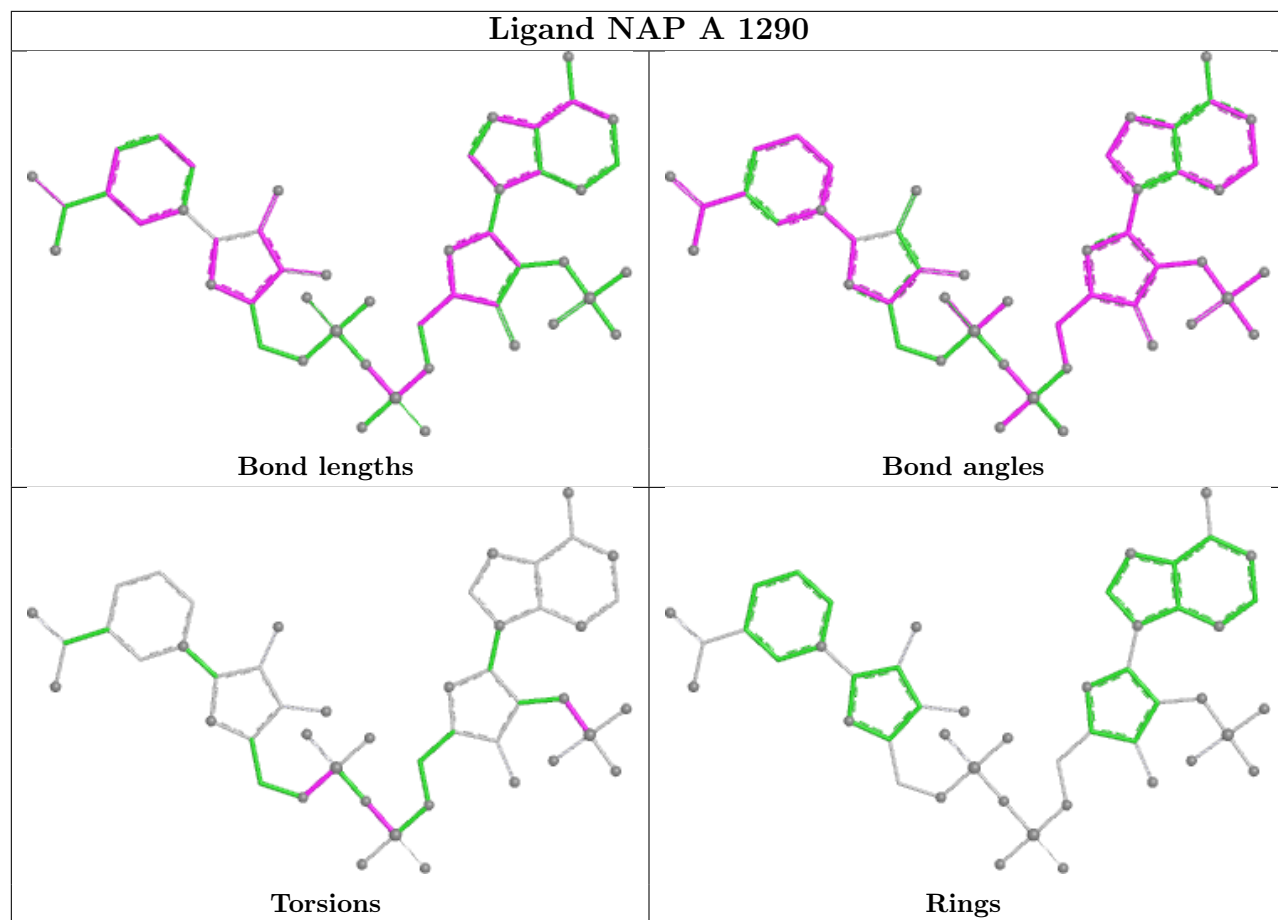
6 monomers are involved in 9 short contacts:

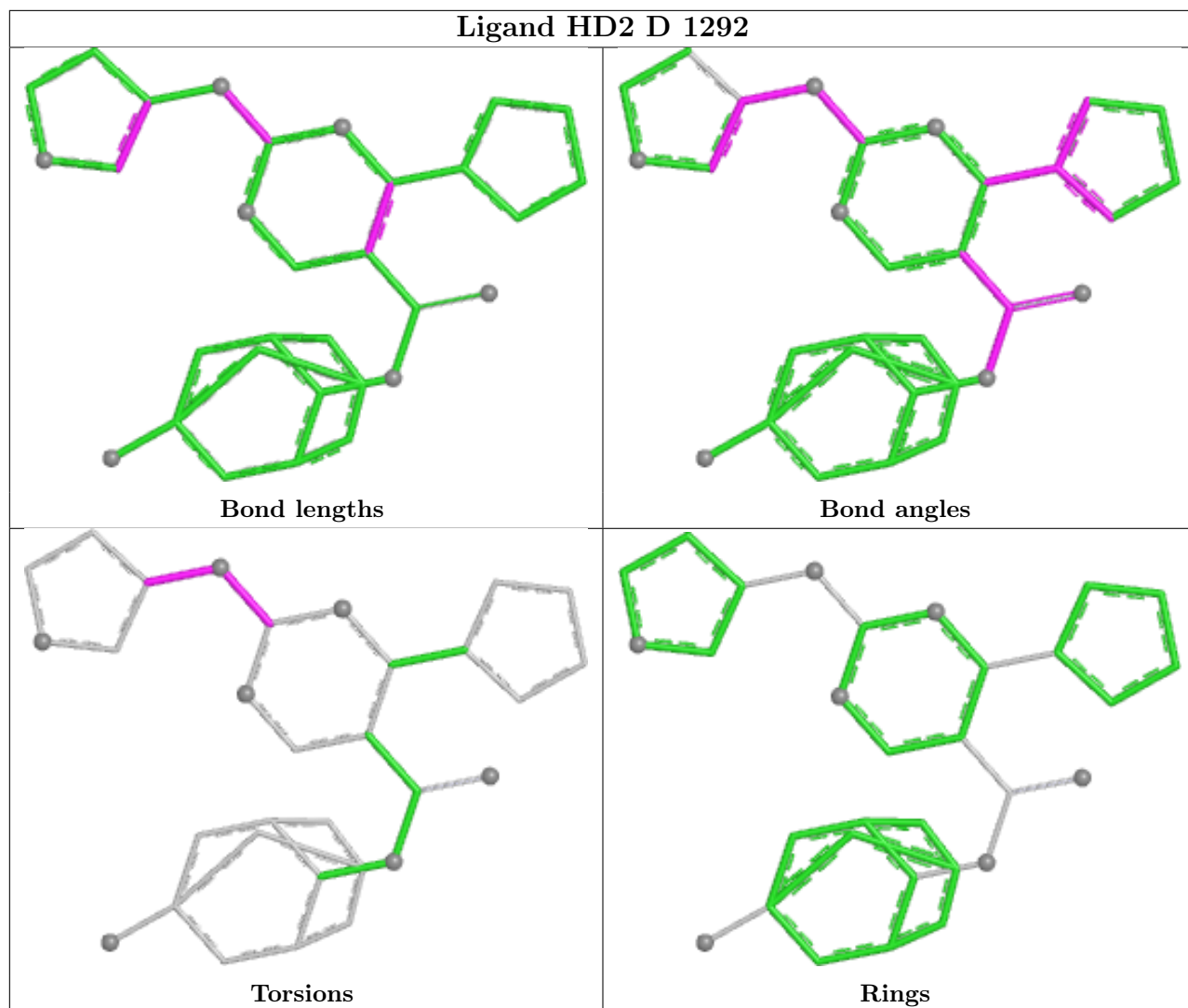
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1291	HD2	1	0
3	A	1291	HD2	2	0
2	A	1290	NAP	2	0
3	D	1292	HD2	2	0
3	C	1281	HD2	1	0
2	C	1280	NAP	1	0

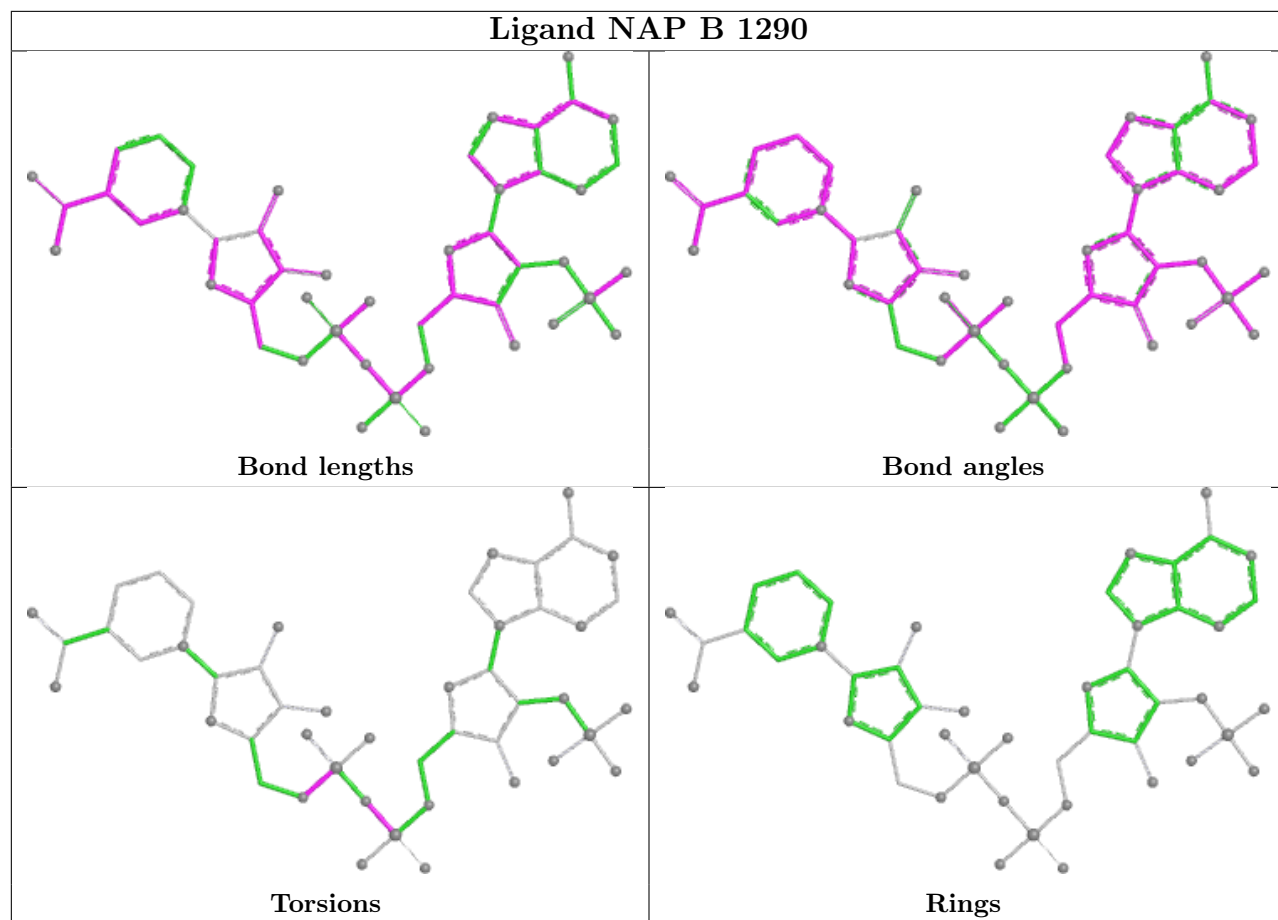
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

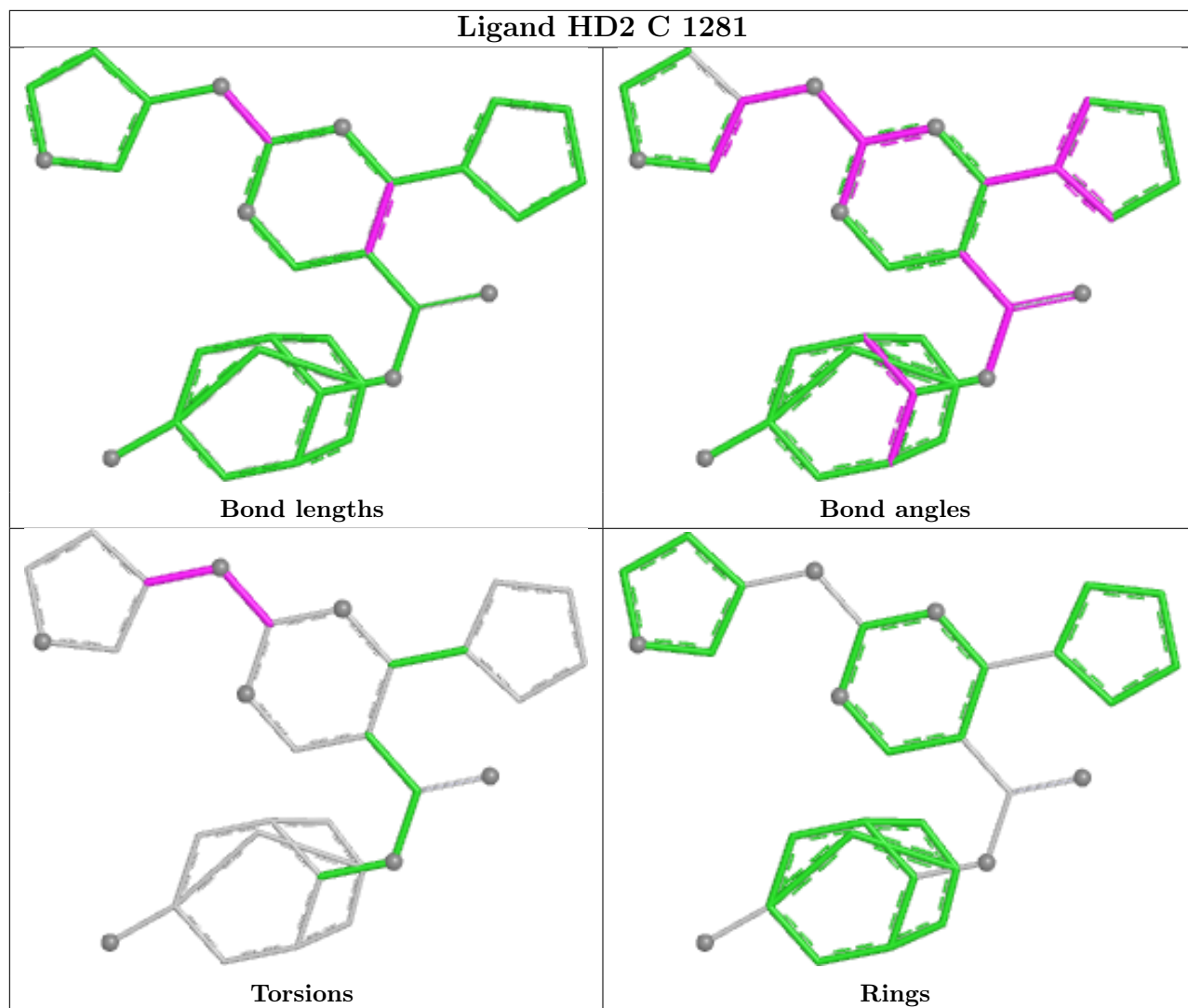


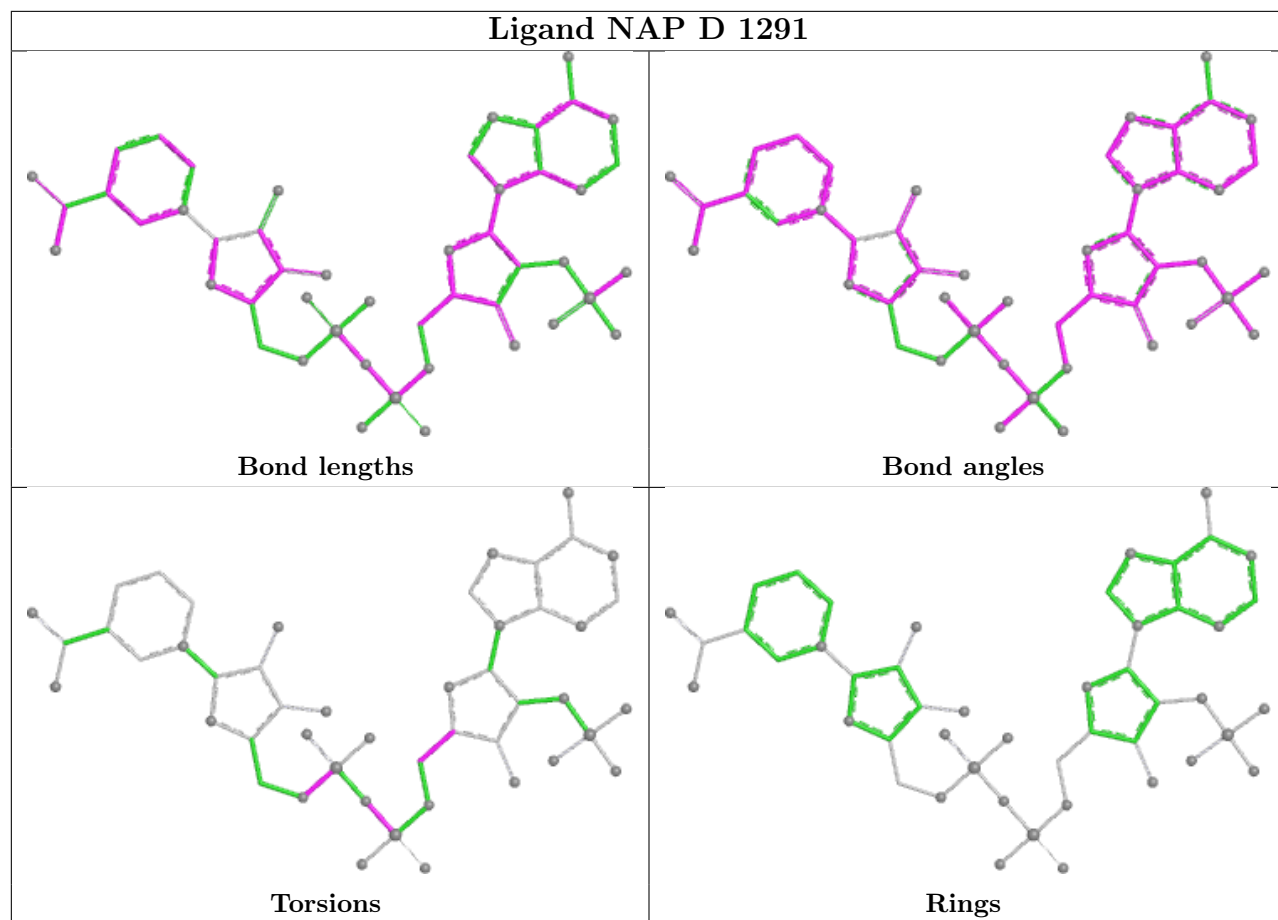


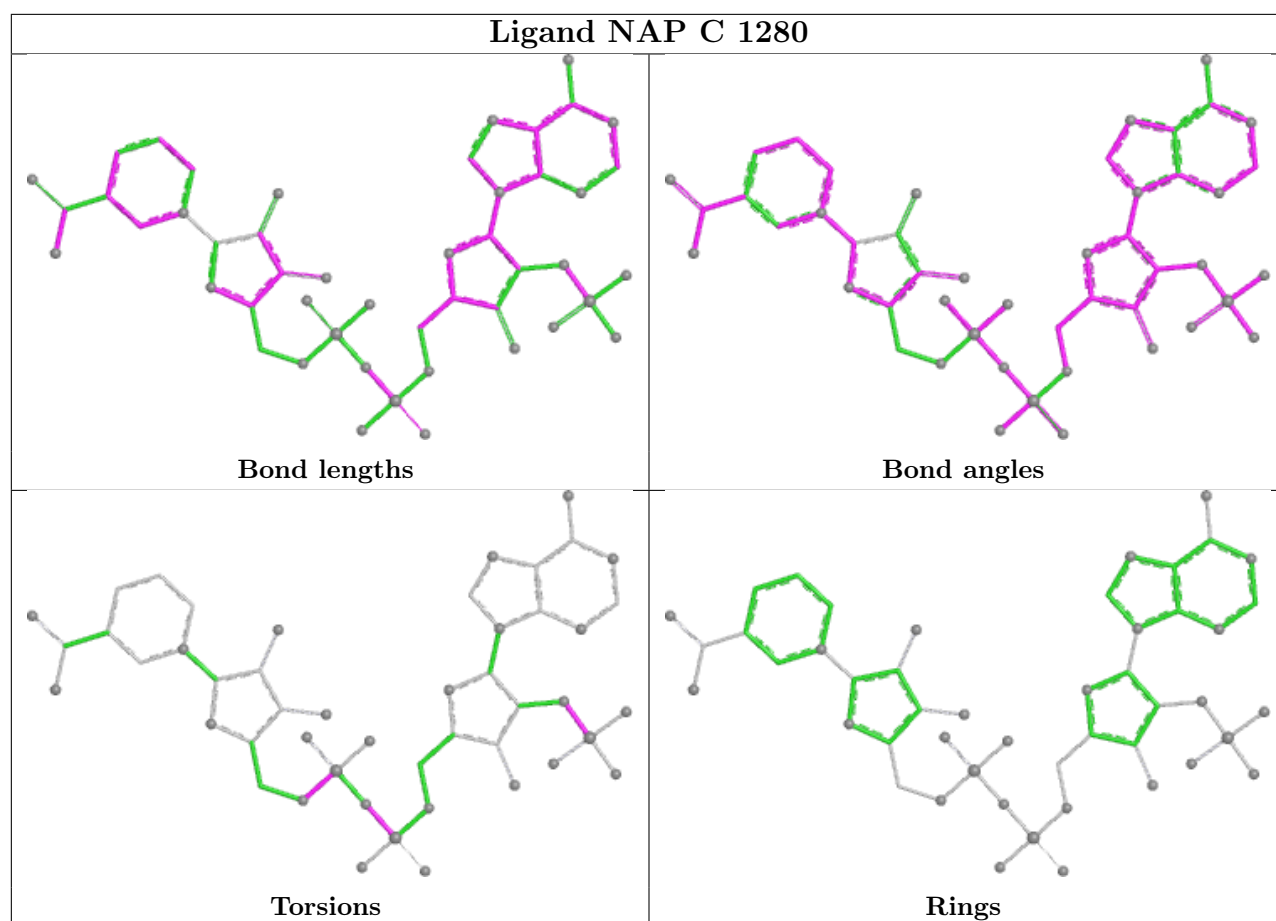












## 5.7 Other polymers [\(i\)](#)

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	263/292 (90%)	0.04	14 (5%) 32 29	5, 21, 49, 69	0
1	B	264/292 (90%)	-0.18	9 (3%) 48 45	6, 18, 52, 68	0
1	C	254/292 (86%)	-0.27	3 (1%) 76 74	9, 17, 42, 74	0
1	D	262/292 (89%)	0.34	11 (4%) 40 37	10, 30, 58, 71	0
All	All	1043/1168 (89%)	-0.02	37 (3%) 47 44	5, 22, 52, 74	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	279	LEU	5.9
1	A	263	TRP	5.4
1	D	233	MET	4.9
1	D	229	GLY	4.2
1	A	280	TYR	3.9

### 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](#)

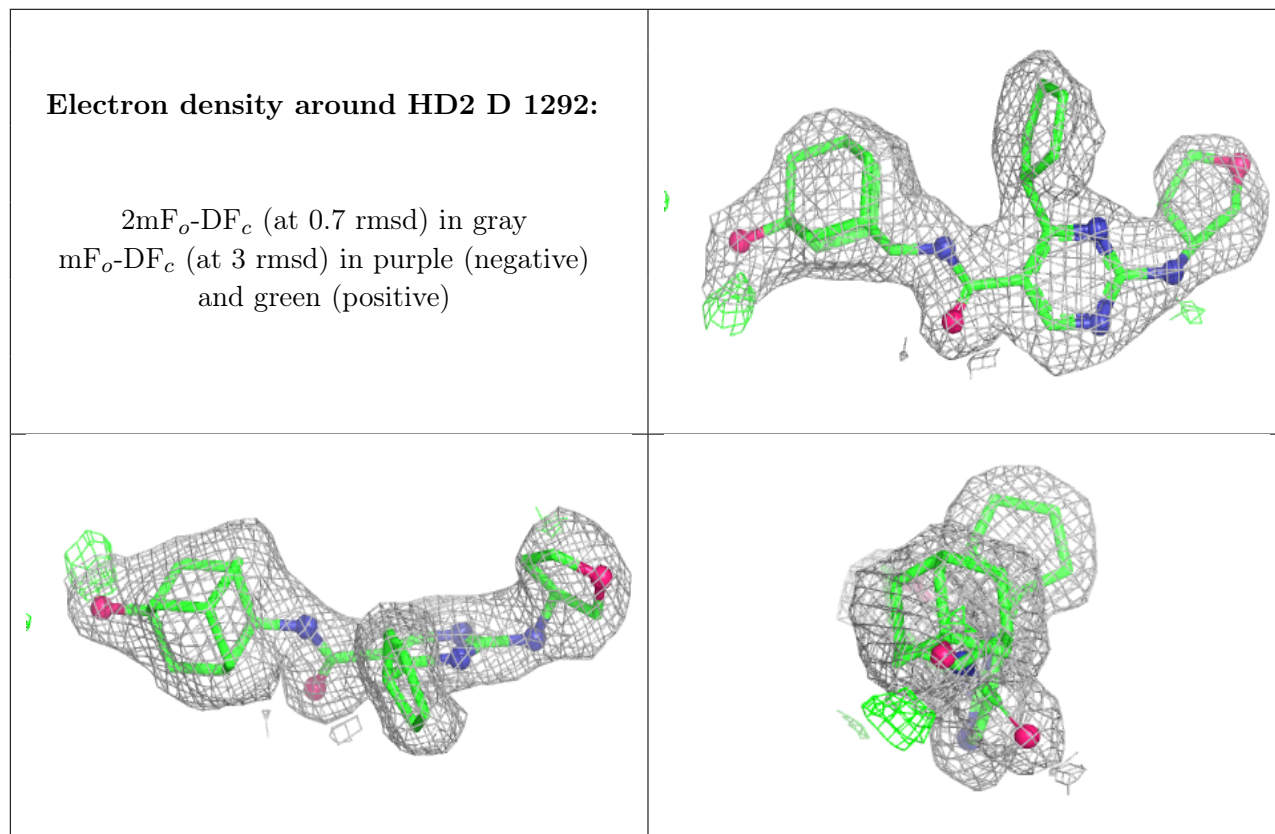
There are no oligosaccharides in this entry.

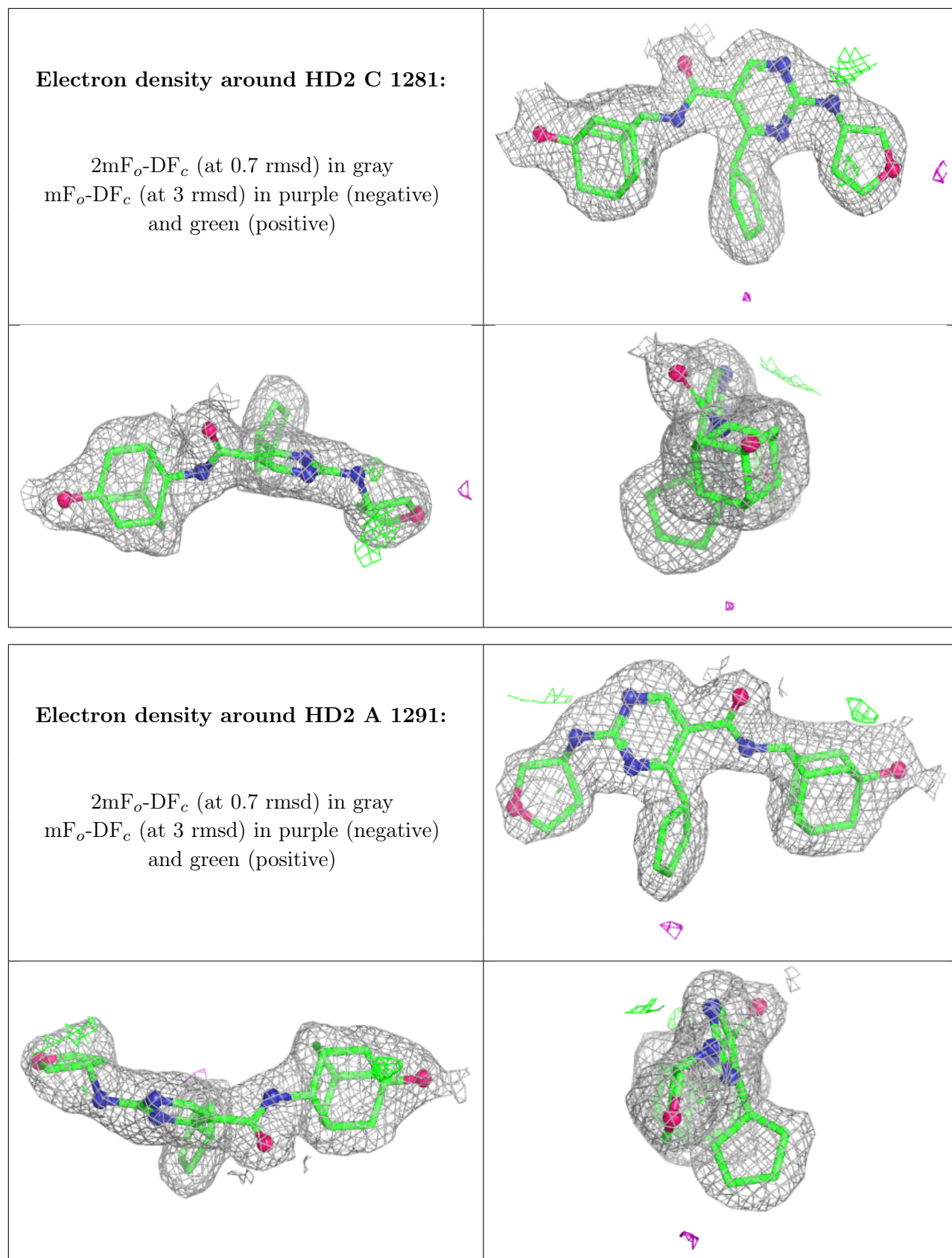
### 6.4 Ligands [i](#)

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, 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( $\text{\AA}^2$ )	Q<0.9
3	HD2	D	1292	31/31	0.91	0.09	21,28,41,45	0
3	HD2	C	1281	31/31	0.93	0.08	10,16,36,40	0
3	HD2	A	1291	31/31	0.93	0.08	15,21,42,44	0
3	HD2	B	1291	31/31	0.94	0.07	12,15,39,43	0
2	NAP	D	1291	48/48	0.96	0.06	15,21,31,33	0
2	NAP	C	1280	48/48	0.98	0.05	7,12,16,21	0
2	NAP	A	1290	48/48	0.98	0.04	5,14,19,22	0
2	NAP	B	1290	48/48	0.99	0.04	5,10,14,22	0

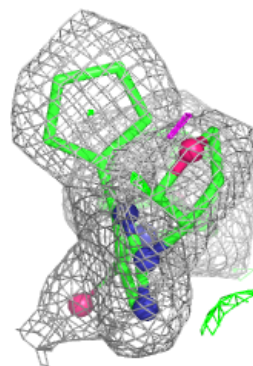
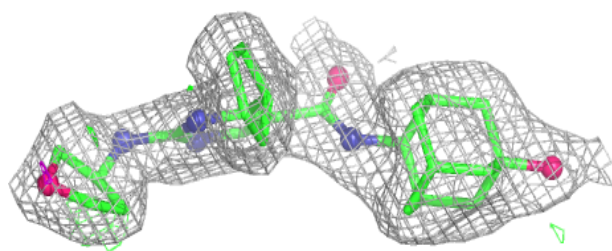
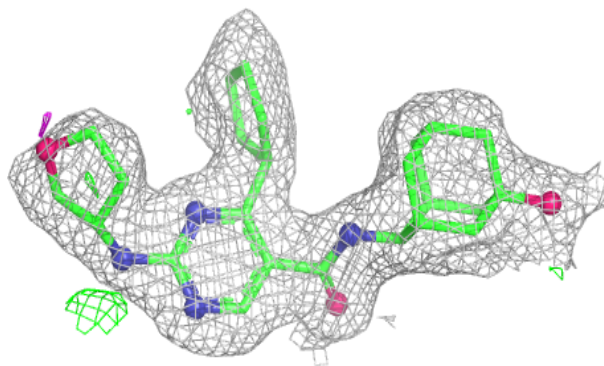
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



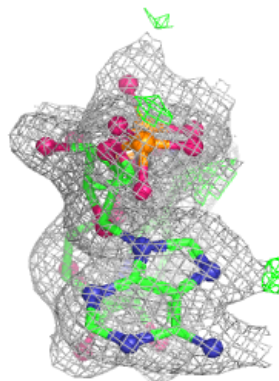
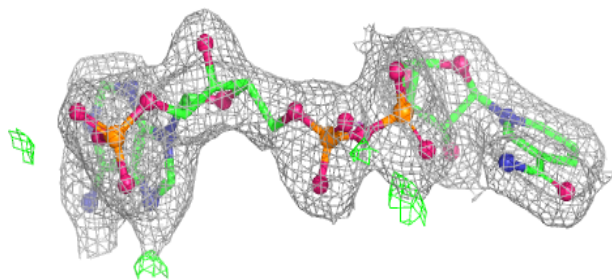
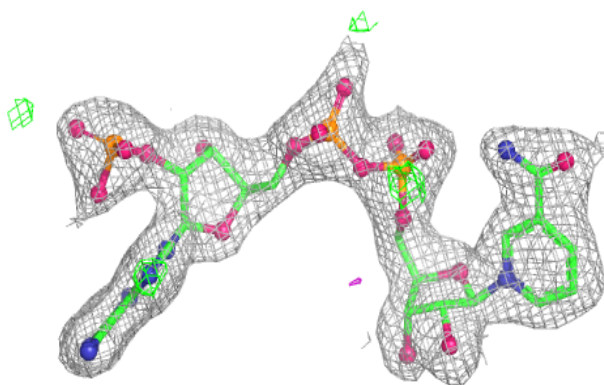


**Electron density around HD2 B 1291:**

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

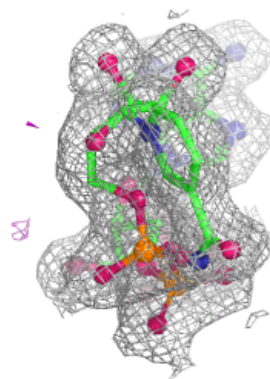
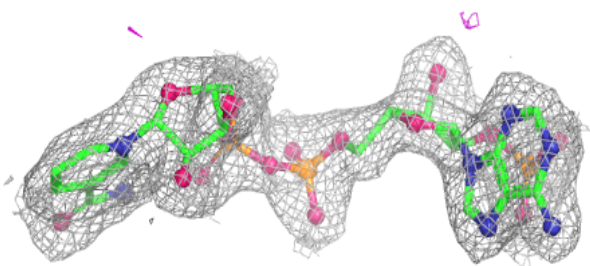
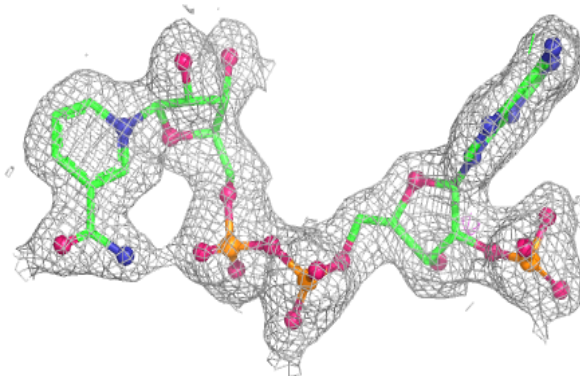
**Electron density around NAP D 1291:**

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

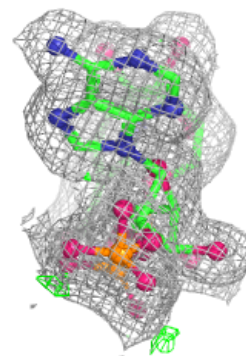
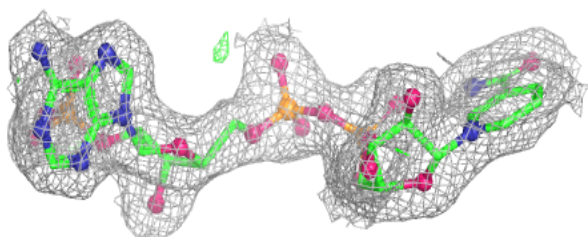
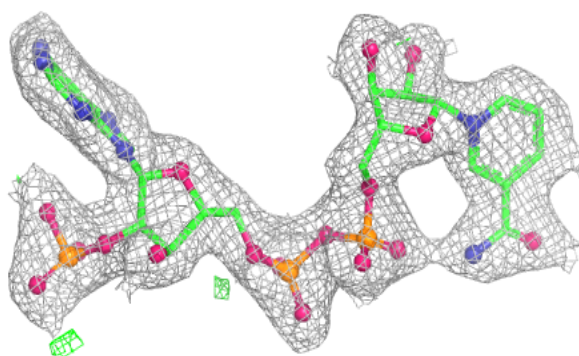


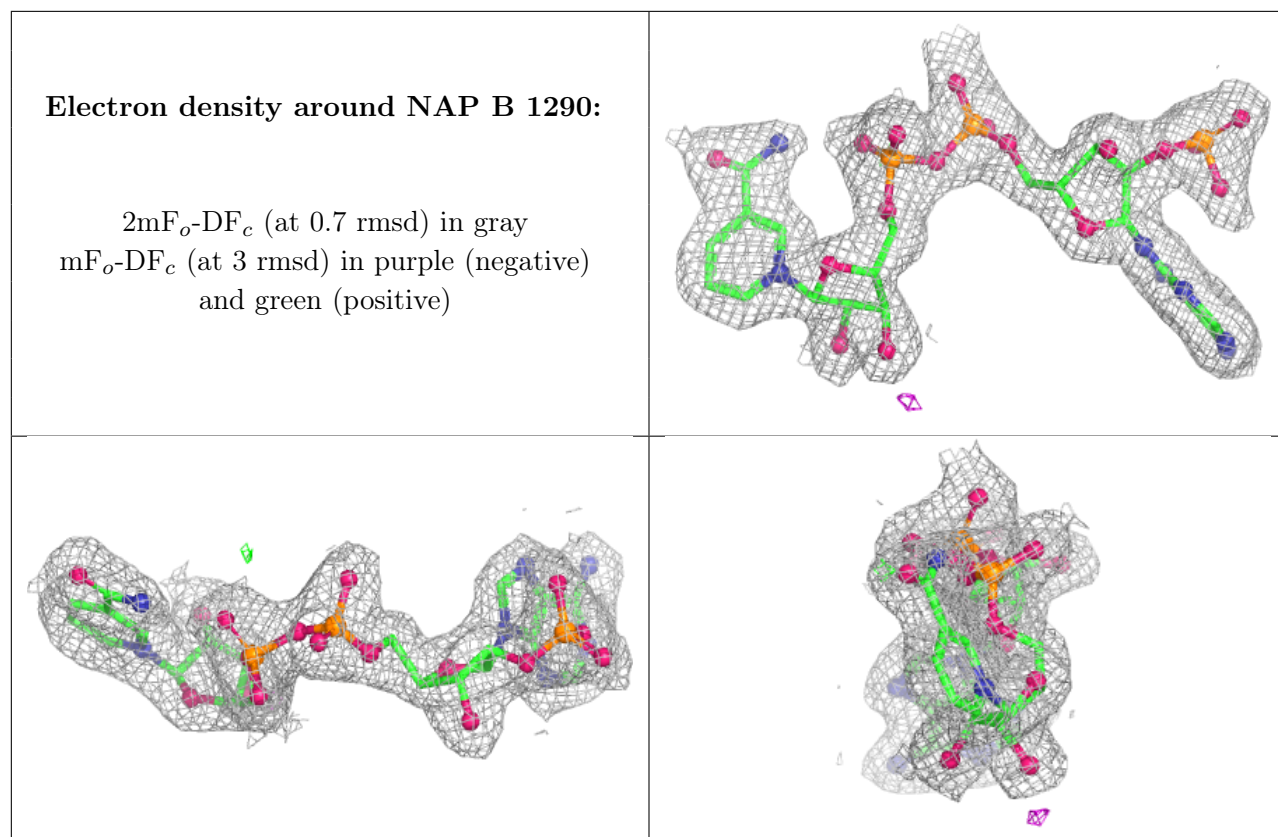
**Electron density around NAP C 1280:**

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

**Electron density around NAP A 1290:**

$2mF_o-DF_c$  (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.