



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 10, 2023 – 07:45 pm BST

PDB ID : 8C31  
Title : Dark state 1.8 Angstrom crystal structure of cobalamin binding domain belonging to a light-dependent transcription regulator TtCarH obtained under aerobic condition  
Authors : Poddar, H.; Leys, D.  
Deposited on : 2022-12-23  
Resolution : 1.80 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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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

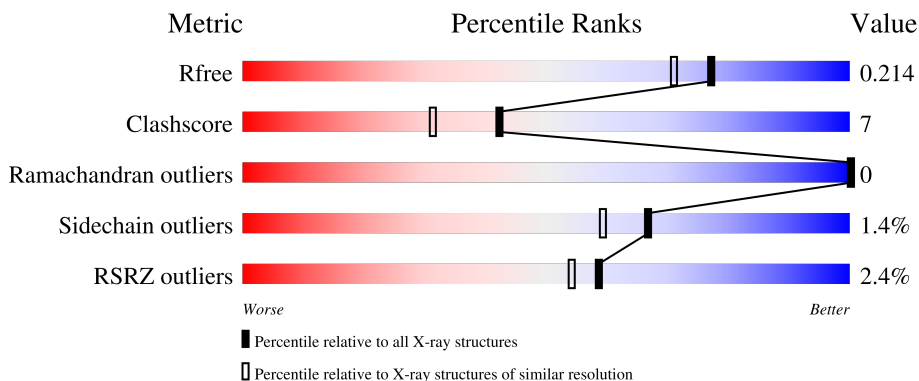
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	215	 5% 79% 11% 10%
1	B	215	 2% 83% 7% 8%
1	C	215	 87% 5% 8%
1	D	215	 82% 7% 10%

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:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
2	BR	B	301	-	-	X	-
3	B12	B	302	X	-	-	-

## 2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 6897 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 Probable transcriptional regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	194	1475	946	266	261	2	0	1	0
1	B	198	1498	960	273	263	2	0	0	0
1	C	197	1488	951	271	264	2	0	0	0
1	D	194	1467	938	268	259	2	0	1	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	286	GLY	-	expression tag	UNP Q746J7
A	287	HIS	-	expression tag	UNP Q746J7
A	288	HIS	-	expression tag	UNP Q746J7
A	289	HIS	-	expression tag	UNP Q746J7
A	290	HIS	-	expression tag	UNP Q746J7
A	291	HIS	-	expression tag	UNP Q746J7
A	292	HIS	-	expression tag	UNP Q746J7
B	286	GLY	-	expression tag	UNP Q746J7
B	287	HIS	-	expression tag	UNP Q746J7
B	288	HIS	-	expression tag	UNP Q746J7
B	289	HIS	-	expression tag	UNP Q746J7
B	290	HIS	-	expression tag	UNP Q746J7
B	291	HIS	-	expression tag	UNP Q746J7
B	292	HIS	-	expression tag	UNP Q746J7
C	286	GLY	-	expression tag	UNP Q746J7
C	287	HIS	-	expression tag	UNP Q746J7
C	288	HIS	-	expression tag	UNP Q746J7
C	289	HIS	-	expression tag	UNP Q746J7
C	290	HIS	-	expression tag	UNP Q746J7
C	291	HIS	-	expression tag	UNP Q746J7
C	292	HIS	-	expression tag	UNP Q746J7

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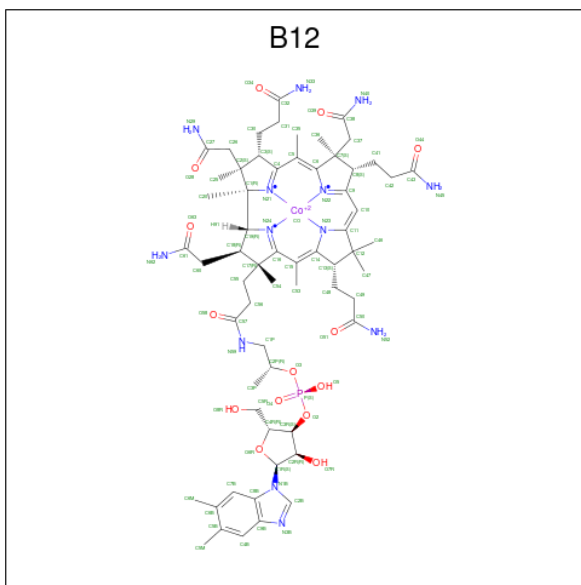
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Chain	Residue	Modelled	Actual	Comment	Reference
D	286	GLY	-	expression tag	UNP Q746J7
D	287	HIS	-	expression tag	UNP Q746J7
D	288	HIS	-	expression tag	UNP Q746J7
D	289	HIS	-	expression tag	UNP Q746J7
D	290	HIS	-	expression tag	UNP Q746J7
D	291	HIS	-	expression tag	UNP Q746J7
D	292	HIS	-	expression tag	UNP Q746J7

- Molecule 2 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Br 1 1	0	0
2	B	1	Total Br 1 1	0	0
2	C	1	Total Br 1 1	0	0

- Molecule 3 is COBALAMIN (three-letter code: B12) (formula: C<sub>62</sub>H<sub>89</sub>CoN<sub>13</sub>O<sub>14</sub>P) (labeled as "Ligand of Interest" by depositor).



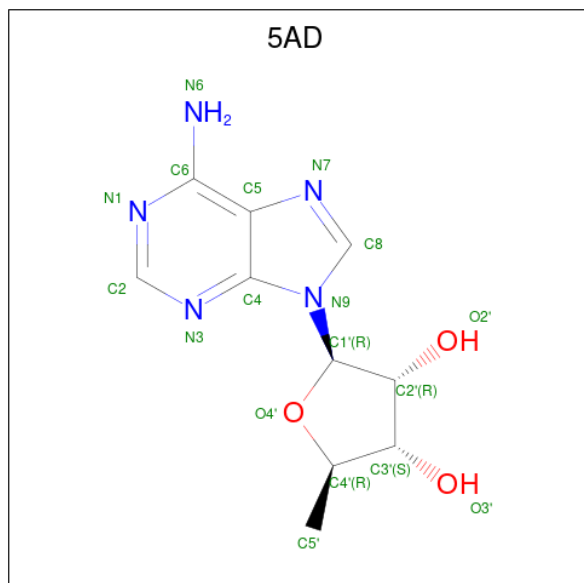
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C Co N O P 91 62 1 13 14 1	0	0
3	B	1	Total C Co N O P 91 62 1 13 14 1	0	0

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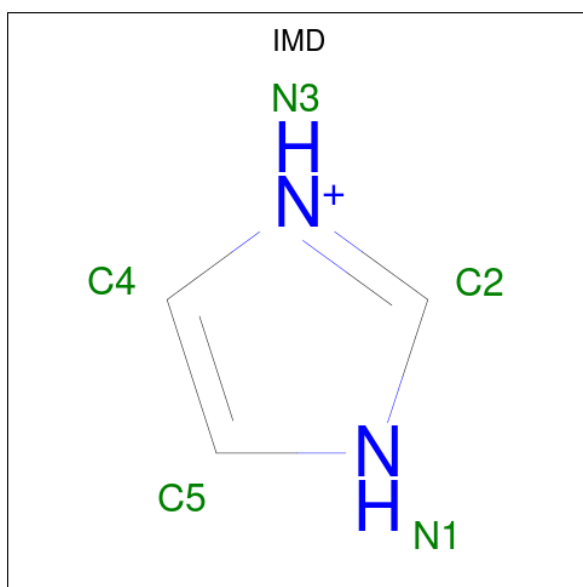
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	C	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		
3	D	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		

- Molecule 4 is 5'-DEOXYADENOSINE (three-letter code: 5AD) (formula: C<sub>10</sub>H<sub>13</sub>N<sub>5</sub>O<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



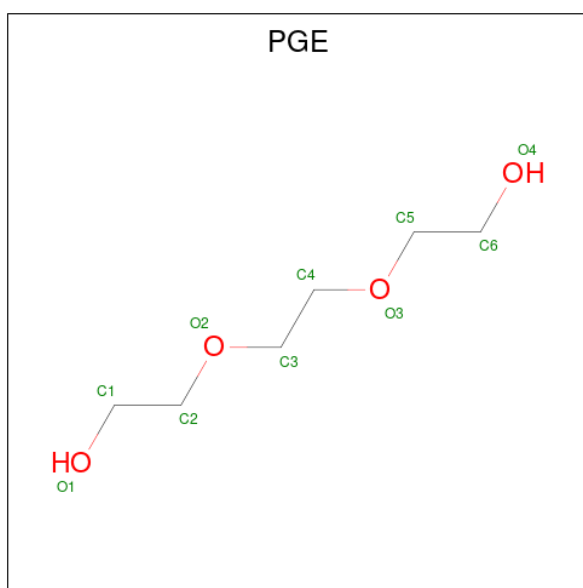
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
4	A	1	Total	C	N	O	0	0
			18	10	5	3		
4	B	1	Total	C	N	O	0	0
			18	10	5	3		
4	C	1	Total	C	N	O	0	0
			18	10	5	3		
4	D	1	Total	C	N	O	0	0
			18	10	5	3		

- Molecule 5 is IMIDAZOLE (three-letter code: IMD) (formula: C<sub>3</sub>H<sub>5</sub>N<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	N	0	0
			5	3	2		
5	C	1	Total	C	N	0	0
			5	3	2		

- Molecule 6 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	94	Total O 94 94	0	0
8	B	112	Total O 112 112	0	0
8	C	150	Total O 150 150	0	0
8	D	134	Total O 134 134	0	0





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.11Å 69.70Å 204.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.18 – 1.80 61.18 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.3 (61.18-1.80) 98.3 (61.18-1.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.59 (at 1.80Å)	Xtrriage
Refinement program	REFMAC 5.8.0352	Depositor
R, $R_{free}$	0.170 , 0.209 0.181 , 0.214	Depositor DCC
$R_{free}$ test set	4386 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.7	Xtrriage
Anisotropy	0.500	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 45.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6897	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.04% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PGE, EDO, BR, IMD, B12, 5AD

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	0.48	0/1512	0.69	0/2055
1	B	0.46	0/1533	0.69	0/2084
1	C	0.45	0/1521	0.67	0/2067
1	D	0.50	0/1502	0.73	0/2040
All	All	0.47	0/6068	0.70	0/8246

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	4
1	C	0	2
1	D	0	2
All	All	0	10

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	213	ARG	Sidechain
1	A	93	ARG	Sidechain
1	B	105	ARG	Sidechain
1	B	176	ARG	Sidechain
1	B	190	ARG	Sidechain

## 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	1475	0	1505	24	0
1	B	1498	0	1534	15	0
1	C	1488	0	1525	10	0
1	D	1467	0	1505	12	0
2	A	1	0	0	0	0
2	B	1	0	0	2	0
2	C	1	0	0	0	0
3	A	91	0	87	14	0
3	B	91	0	87	12	0
3	C	91	0	87	10	0
3	D	91	0	86	6	0
4	A	18	0	12	2	0
4	B	18	0	12	1	0
4	C	18	0	12	0	0
4	D	18	0	12	1	0
5	A	5	0	5	2	0
5	C	5	0	5	0	0
6	C	10	0	14	0	0
7	C	4	0	6	0	0
7	D	16	0	24	0	0
8	A	94	0	0	2	0
8	B	112	0	0	1	0
8	C	150	0	0	1	0
8	D	134	0	0	1	0
All	All	6897	0	6518	89	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 7.

The worst 5 of 89 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)
3:A:302:B12:H351	3:A:302:B12:H362	1.31	1.07
3:D:702:B12:H362	3:D:702:B12:H351	1.49	0.95
3:C:302:B12:H362	3:C:302:B12:H351	1.60	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:302:B12:H552	3:A:302:B12:H531	1.61	0.81
3:A:302:B12:H351	3:A:302:B12:C36	2.10	0.80

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	191/215 (89%)	185 (97%)	6 (3%)	0	100	100
1	B	196/215 (91%)	191 (97%)	5 (3%)	0	100	100
1	C	195/215 (91%)	191 (98%)	4 (2%)	0	100	100
1	D	193/215 (90%)	189 (98%)	4 (2%)	0	100	100
All	All	775/860 (90%)	756 (98%)	19 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	145/161 (90%)	142 (98%)	3 (2%)	53	42
1	B	146/161 (91%)	143 (98%)	3 (2%)	53	42
1	C	146/161 (91%)	145 (99%)	1 (1%)	84	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	143/161 (89%)	142 (99%)	1 (1%)	84	81
All	All	580/644 (90%)	572 (99%)	8 (1%)	67	59

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	142	HIS
1	C	142	HIS
1	B	142	HIS
1	B	105	ARG
1	B	206	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	GLN
1	C	153	GLN
1	C	187	HIS
1	D	187	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 19 ligands modelled in this entry, 3 are monoatomic - leaving 16 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
4	5AD	B	303	-	17,20,20	0.64	0	15,30,30	1.06	1 (6%)
4	5AD	D	703	-	17,20,20	0.63	0	15,30,30	0.93	0
3	B12	D	702	1	90,101,101	1.29	11 (12%)	137,166,166	1.81	19 (13%)
7	EDO	C	306	-	3,3,3	0.11	0	2,2,2	0.19	0
7	EDO	D	701	-	3,3,3	0.27	0	2,2,2	0.33	0
5	IMD	A	304	-	3,5,5	0.19	0	4,5,5	0.68	0
6	PGE	C	305	-	9,9,9	0.21	0	8,8,8	0.13	0
3	B12	B	302	1	90,101,101	1.38	9 (10%)	137,166,166	1.80	25 (18%)
5	IMD	C	304	-	3,5,5	0.40	0	4,5,5	0.55	0
3	B12	A	302	1	90,101,101	1.25	6 (6%)	137,166,166	1.77	20 (14%)
7	EDO	D	704	-	3,3,3	0.19	0	2,2,2	0.22	0
7	EDO	D	706	-	3,3,3	0.19	0	2,2,2	0.18	0
4	5AD	A	303	-	17,20,20	0.83	1 (5%)	15,30,30	1.10	1 (6%)
3	B12	C	302	1	90,101,101	1.27	9 (10%)	137,166,166	1.89	28 (20%)
7	EDO	D	705	-	3,3,3	1.02	0	2,2,2	0.94	0
4	5AD	C	303	-	17,20,20	0.57	0	15,30,30	0.98	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
4	5AD	B	303	-	-	0/0/20/20	0/3/3/3
4	5AD	D	703	-	-	0/0/20/20	0/3/3/3
3	B12	D	702	1	-	7/52/223/223	0/3/11/11
7	EDO	C	306	-	-	0/1/1/1	-
7	EDO	D	701	-	-	1/1/1/1	-
6	PGE	C	305	-	-	6/7/7/7	-
5	IMD	A	304	-	-	-	0/1/1/1
3	B12	B	302	1	1/1/36/38	12/52/223/223	0/3/11/11
5	IMD	C	304	-	-	-	0/1/1/1
3	B12	A	302	1	-	11/52/223/223	0/3/11/11
7	EDO	D	704	-	-	1/1/1/1	-
7	EDO	D	706	-	-	0/1/1/1	-
4	5AD	A	303	-	-	0/0/20/20	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	B12	C	302	1	-	14/52/223/223	0/3/11/11
7	EDO	D	705	-	-	1/1/1/1	-
4	5AD	C	303	-	-	0/0/20/20	0/3/3/3

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	B12	C19-N24	-6.13	1.37	1.48
3	B	302	B12	C14-N23	-5.05	1.28	1.35
3	D	702	B12	O6R-C1R	4.68	1.47	1.41
3	A	302	B12	C8B-C9B	4.58	1.49	1.40
3	D	702	B12	C9-N22	4.42	1.42	1.30

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	702	B12	C1-C19-N24	9.70	117.16	106.24
3	C	302	B12	C20-C1-C19	-9.50	100.20	109.36
3	D	702	B12	C20-C1-C19	-9.08	100.60	109.36
3	B	302	B12	C1-C19-N24	8.76	116.09	106.24
3	C	302	B12	C1-C19-N24	8.06	115.31	106.24

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	302	B12	C19

5 of 53 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	B12	C3R-O2-P-O5
3	B	302	B12	C18-C60-C61-O63
3	B	302	B12	C18-C60-C61-N62
3	C	302	B12	N59-C1P-C2P-C3P
3	C	302	B12	N59-C1P-C2P-O3

There are no ring outliers.

8 monomers are involved in 48 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	303	5AD	1	0

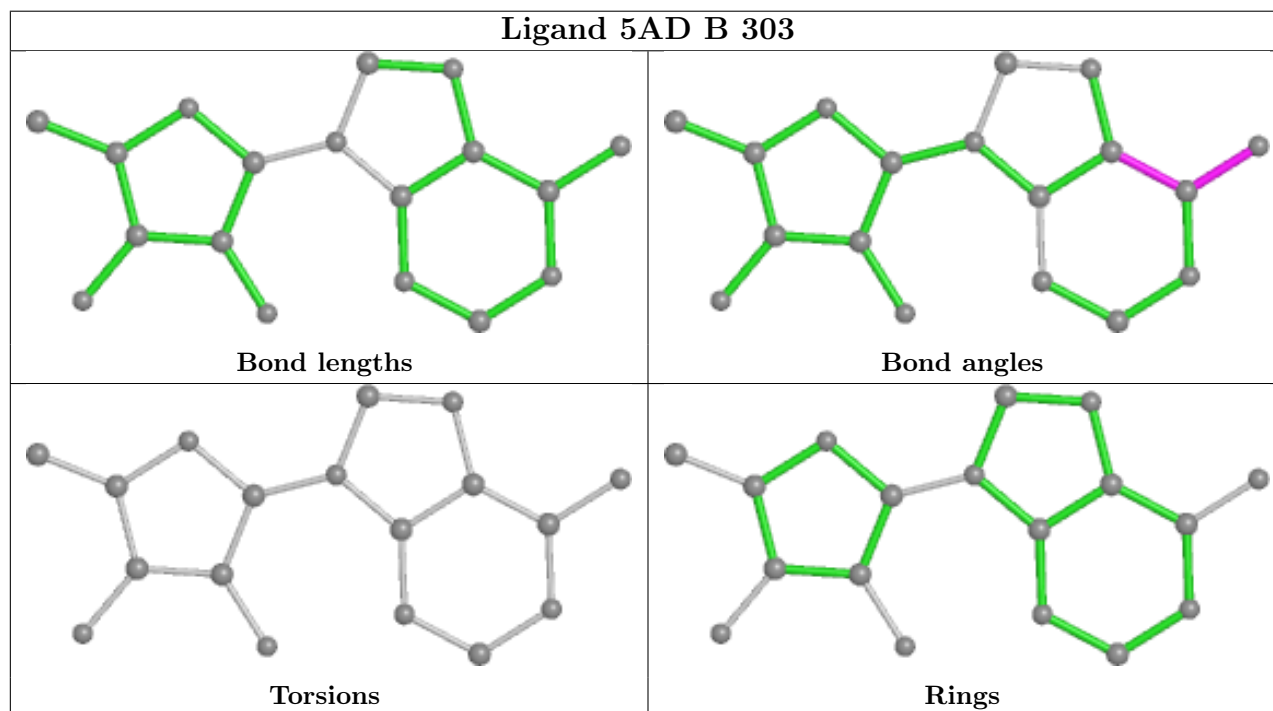
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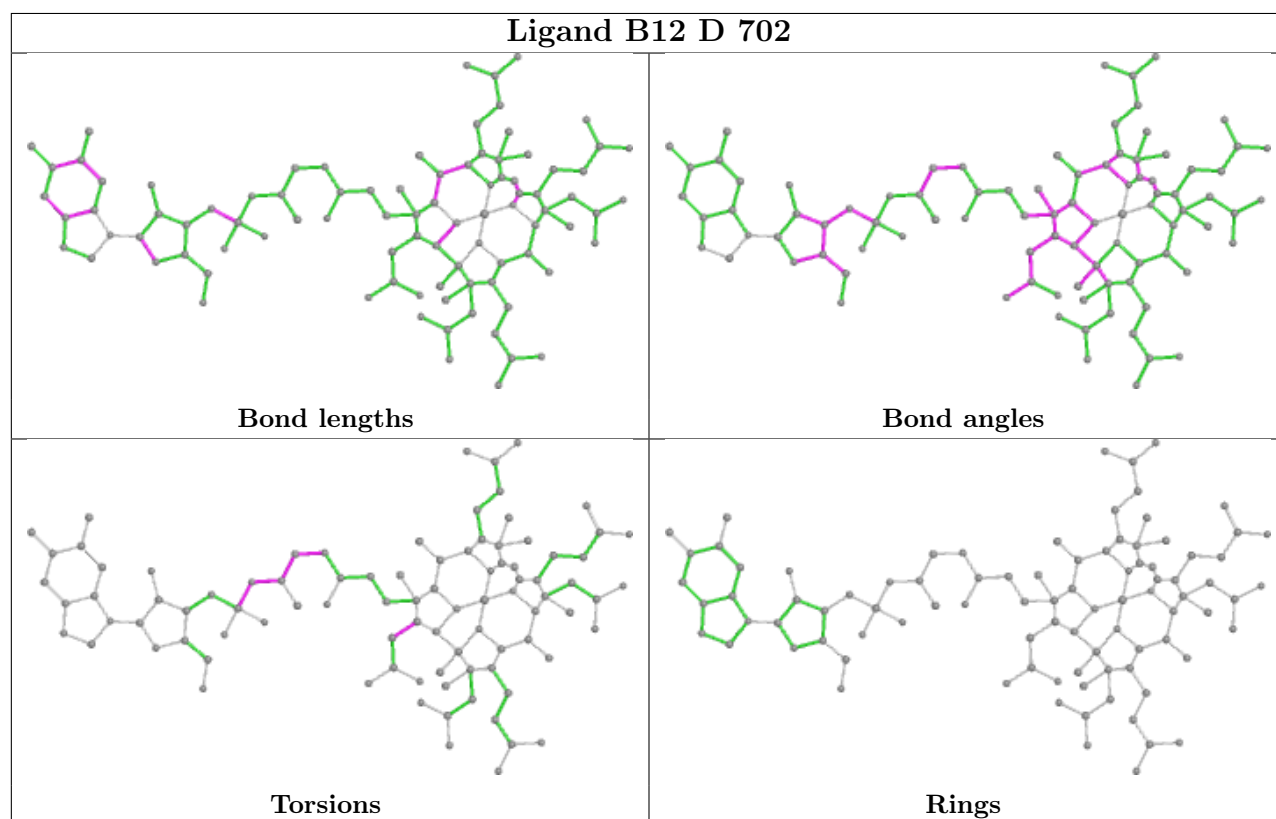
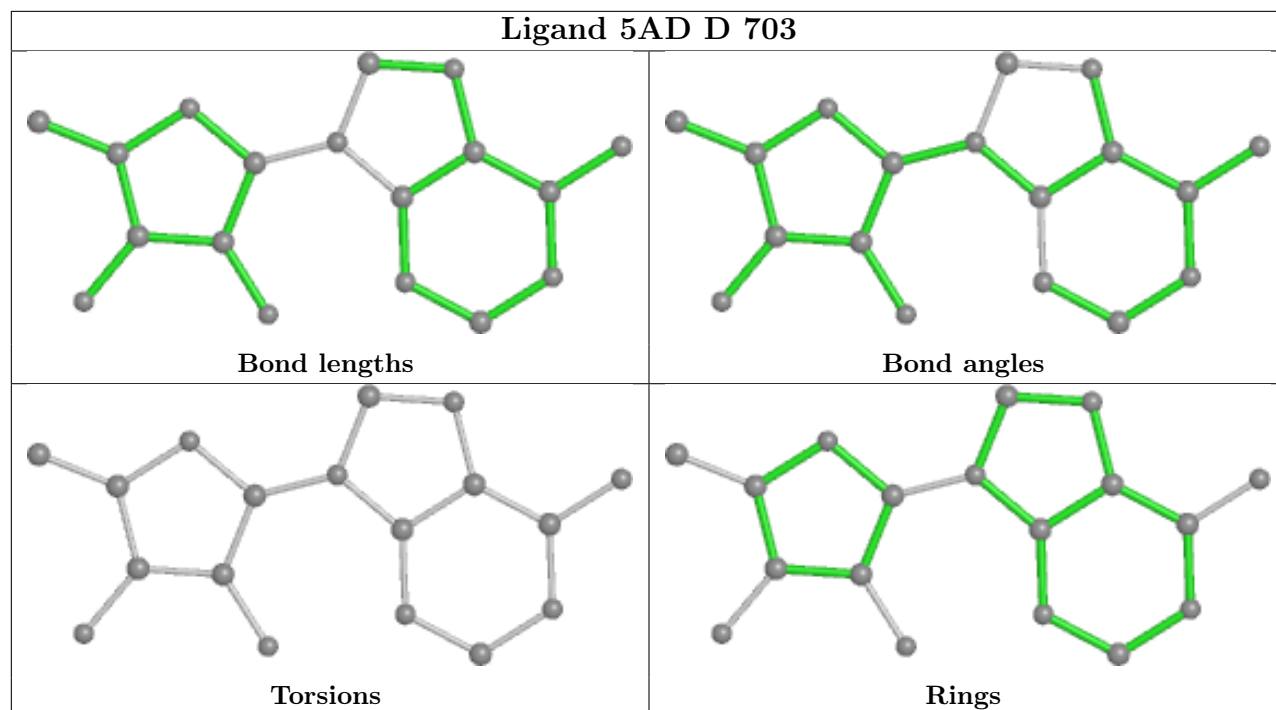


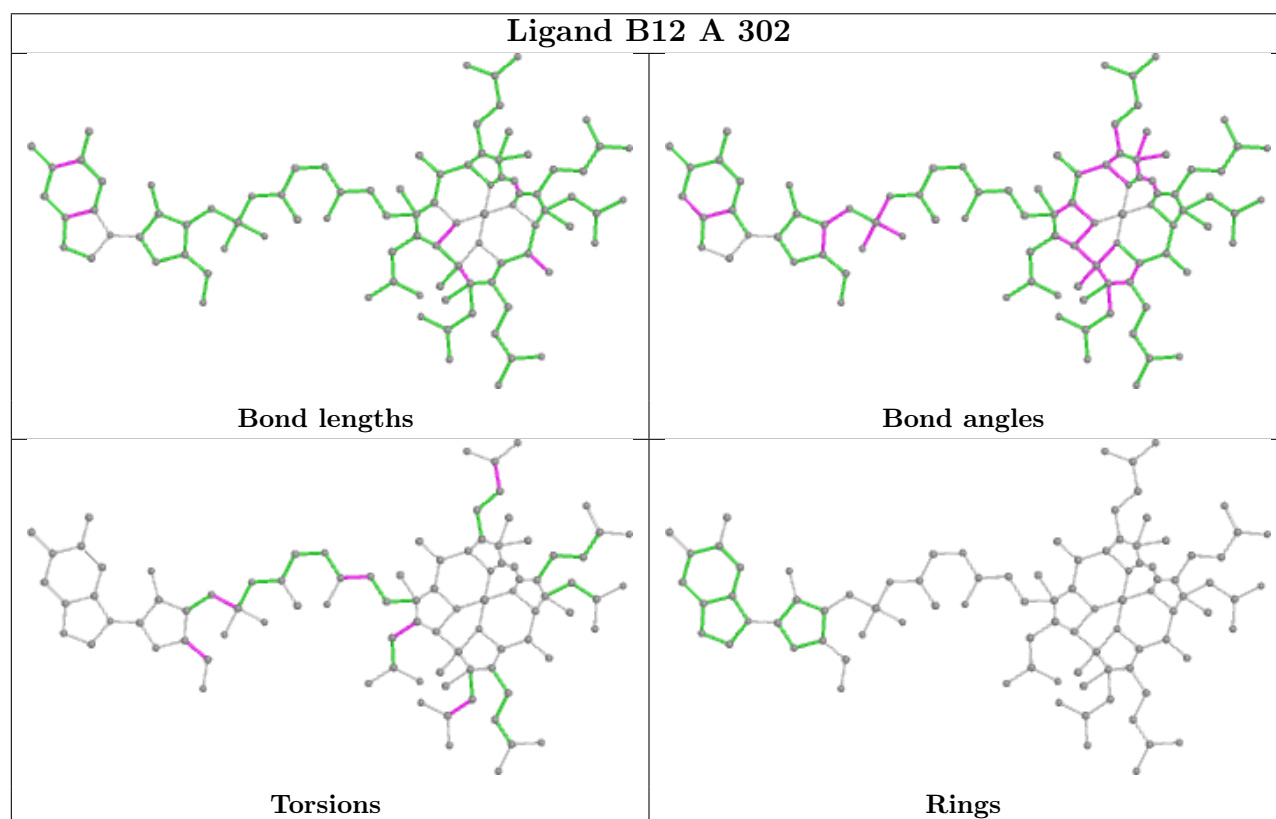
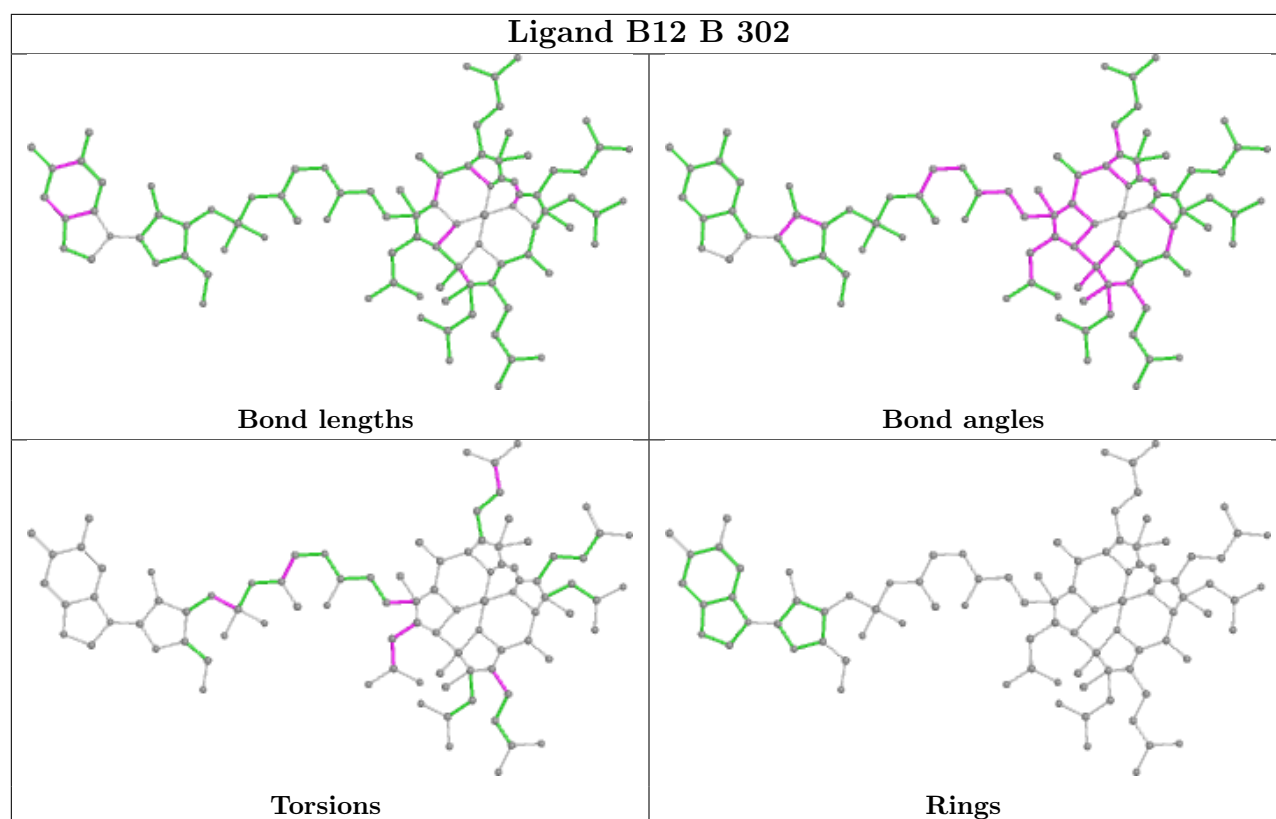
*Continued from previous page...*

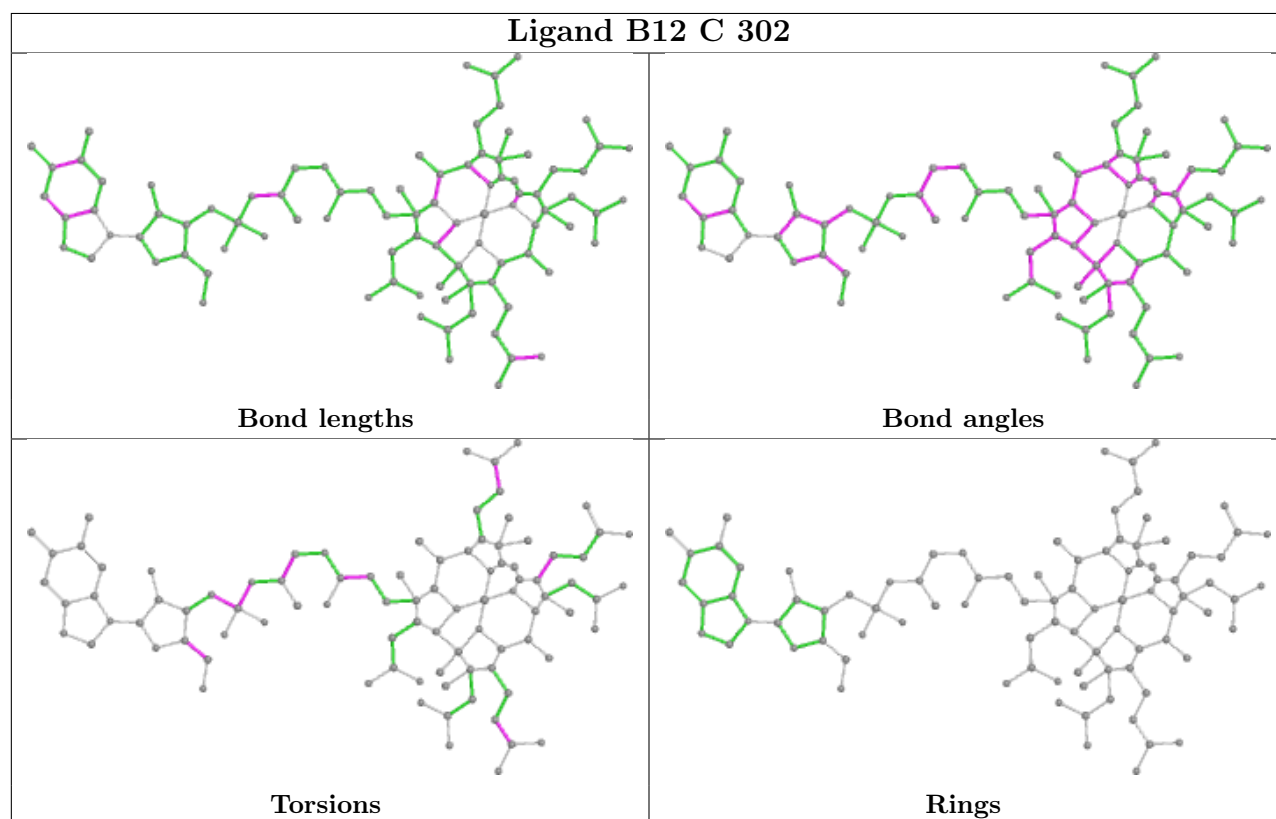
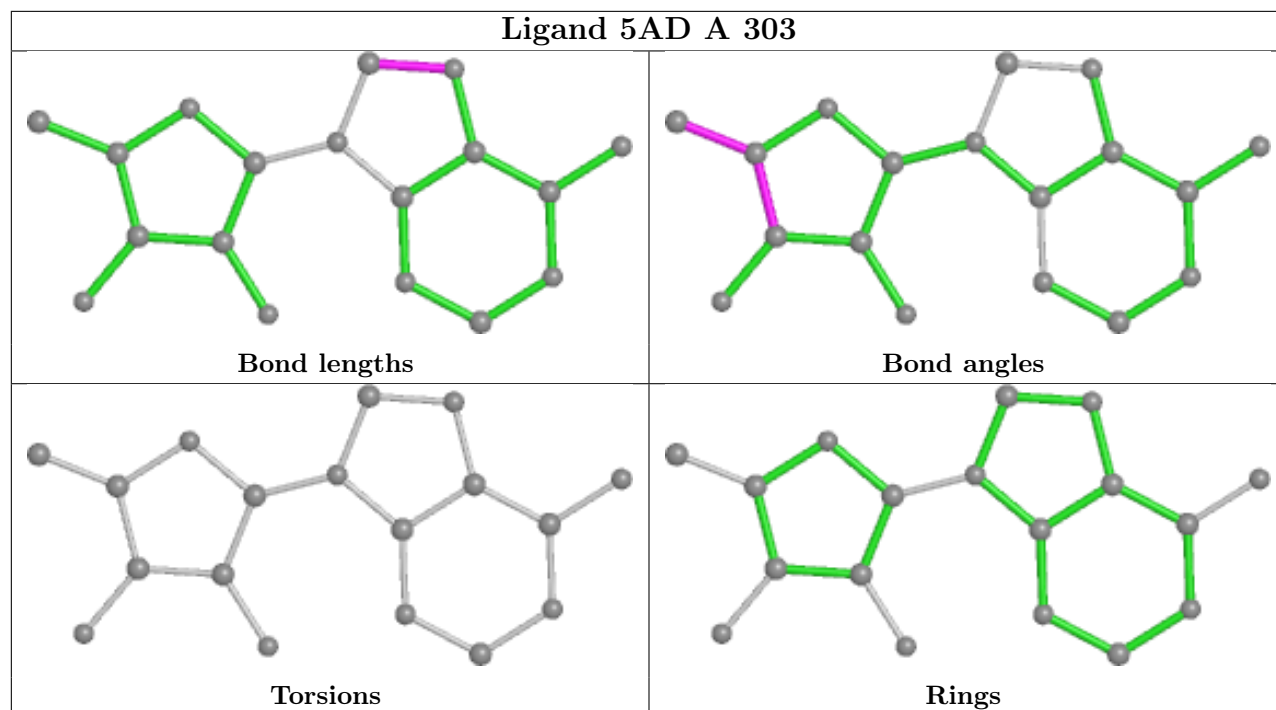
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	703	5AD	1	0
3	D	702	B12	6	0
5	A	304	IMD	2	0
3	B	302	B12	12	0
3	A	302	B12	14	0
4	A	303	5AD	2	0
3	C	302	B12	10	0

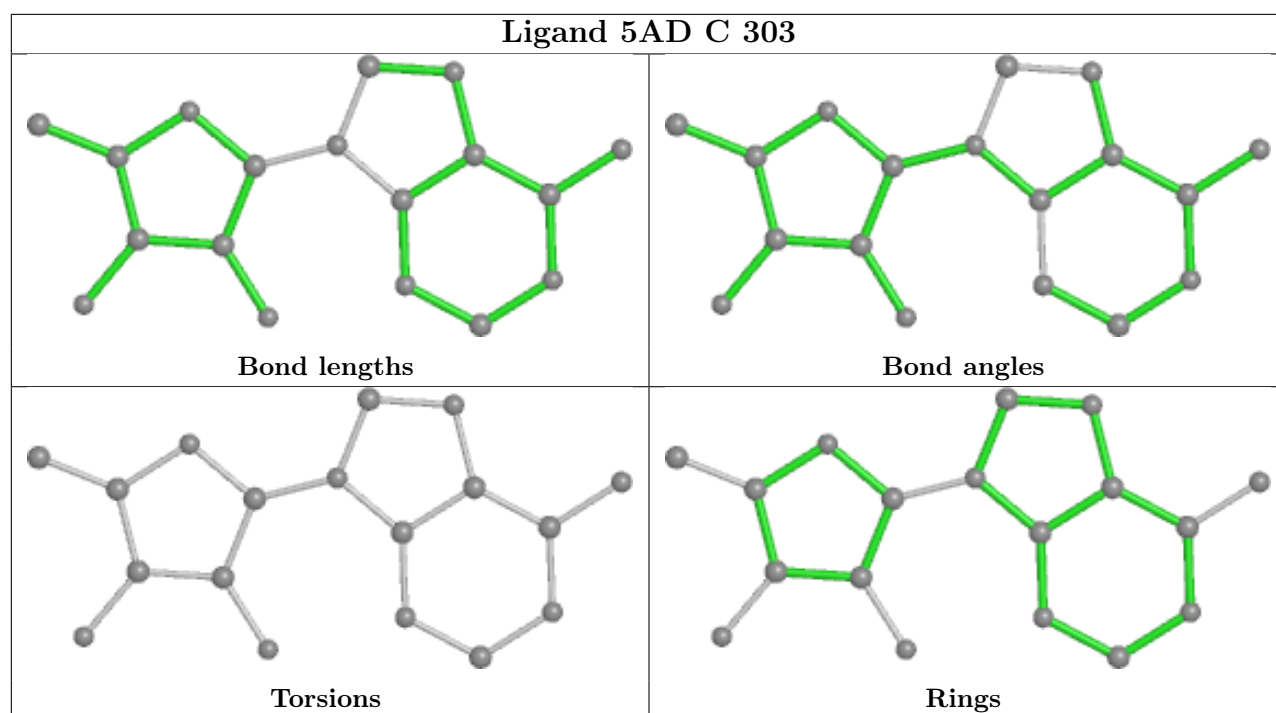
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	194/215 (90%)	0.20	11 (5%) 23 19	26, 44, 84, 92	0
1	B	198/215 (92%)	-0.01	4 (2%) 65 61	27, 46, 80, 101	0
1	C	197/215 (91%)	-0.27	1 (0%) 91 89	26, 39, 66, 92	0
1	D	194/215 (90%)	-0.22	3 (1%) 73 70	25, 38, 59, 80	0
All	All	783/860 (91%)	-0.07	19 (2%) 59 54	25, 41, 75, 101	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	241	ALA	4.9
1	A	257	ARG	4.6
1	A	208	ARG	4.4
1	D	275	TRP	3.6
1	A	207	LEU	3.4

### 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 [i](#)

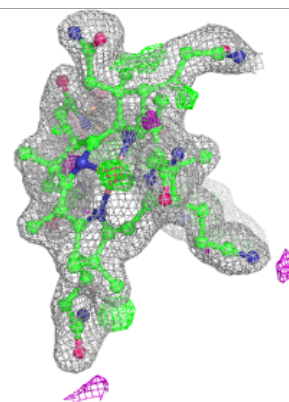
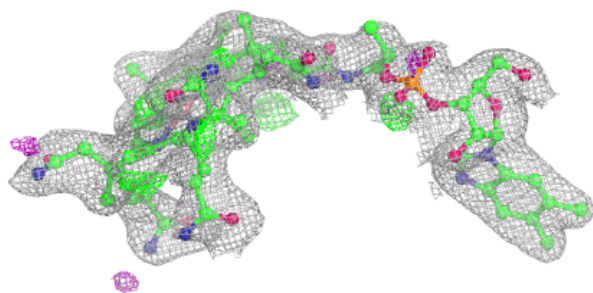
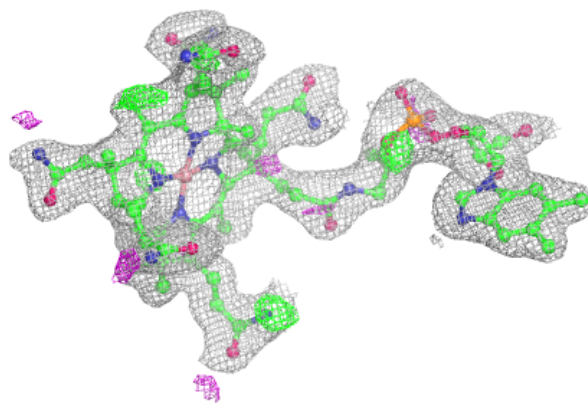
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 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
5	IMD	A	304	5/5	0.56	0.27	73,74,77,79	0
7	EDO	C	306	4/4	0.61	0.24	65,73,74,74	0
6	PGE	C	305	10/10	0.68	0.29	64,84,90,90	0
5	IMD	C	304	5/5	0.71	0.23	64,74,75,81	0
7	EDO	D	704	4/4	0.79	0.24	71,72,73,74	0
7	EDO	D	706	4/4	0.79	0.21	62,70,75,78	0
7	EDO	D	705	4/4	0.89	0.11	39,48,50,54	0
7	EDO	D	701	4/4	0.91	0.12	57,63,63,66	0
2	BR	B	301	1/1	0.95	0.04	69,69,69,69	0
3	B12	B	302	91/91	0.95	0.11	34,48,63,69	0
4	5AD	B	303	18/18	0.96	0.11	46,50,54,56	0
3	B12	A	302	91/91	0.97	0.09	28,37,55,64	0
4	5AD	D	703	18/18	0.97	0.08	34,36,39,40	0
3	B12	C	302	91/91	0.97	0.08	24,33,59,77	0
3	B12	D	702	91/91	0.97	0.08	26,35,48,56	0
4	5AD	A	303	18/18	0.97	0.09	30,31,33,33	0
4	5AD	C	303	18/18	0.98	0.08	26,30,32,32	0
2	BR	A	301	1/1	0.99	0.05	45,45,45,45	0
2	BR	C	301	1/1	0.99	0.03	49,49,49,49	0

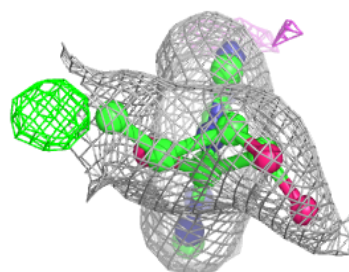
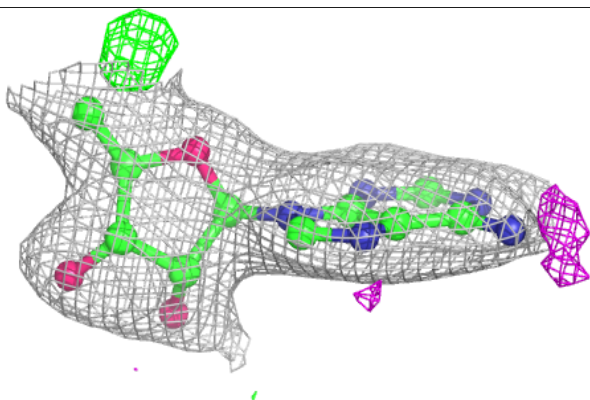
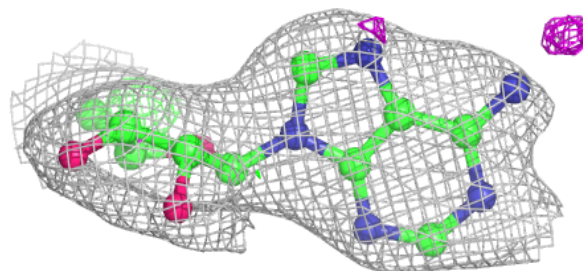
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around B12 B 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 5AD B 303:**

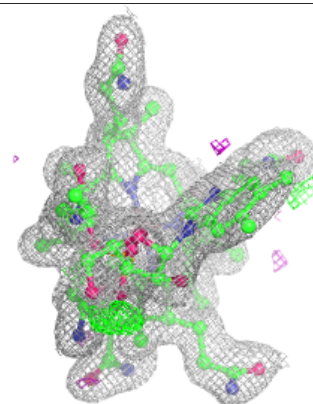
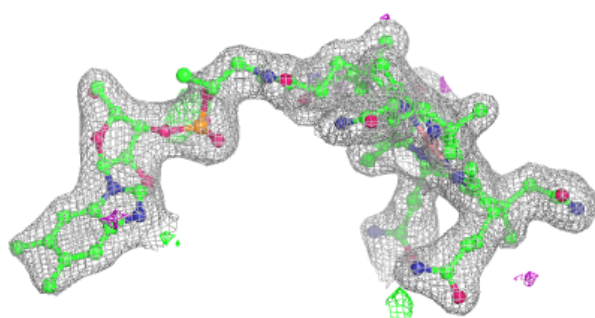
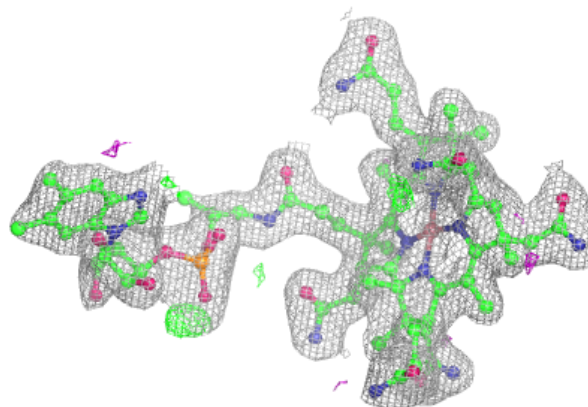
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



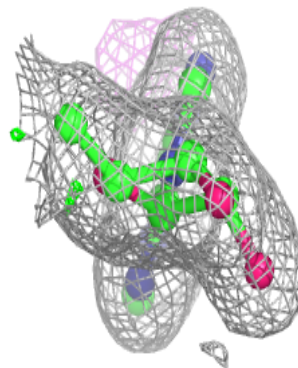
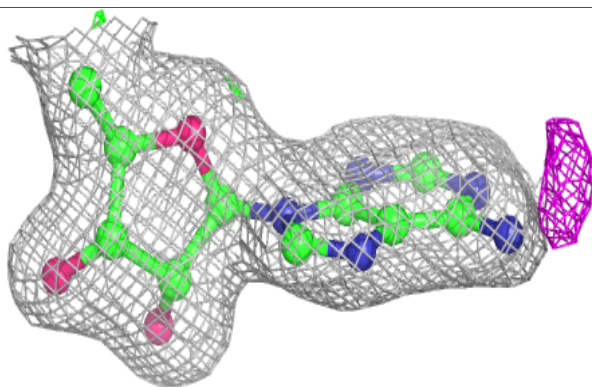
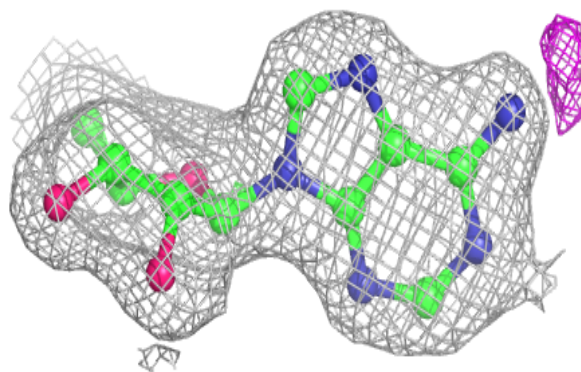


**Electron density around B12 A 302:**

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

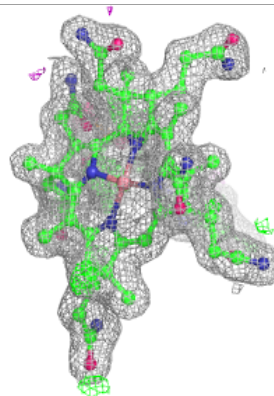
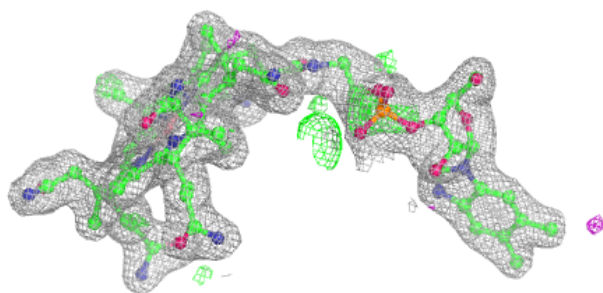
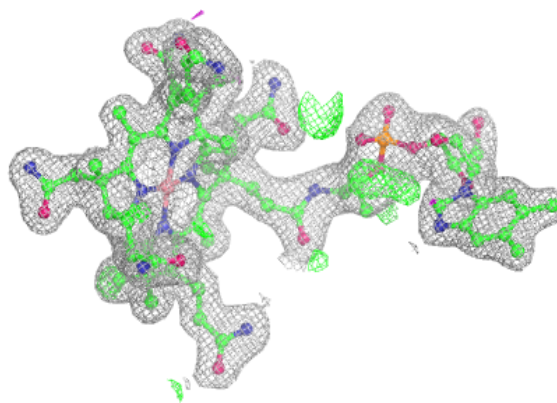
**Electron density around 5AD D 703:**

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

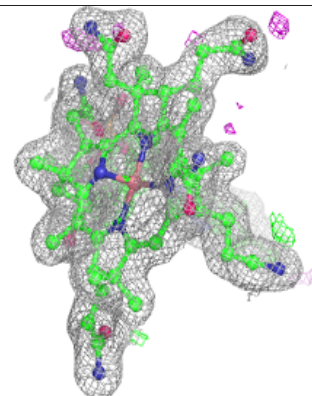
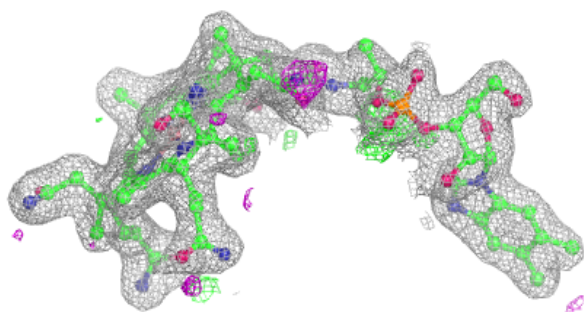
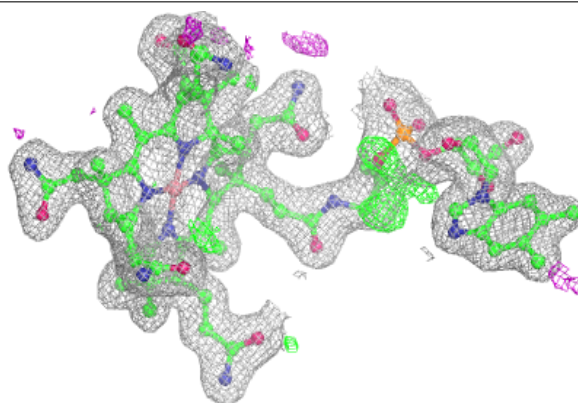


**Electron density around B12 C 302:**

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

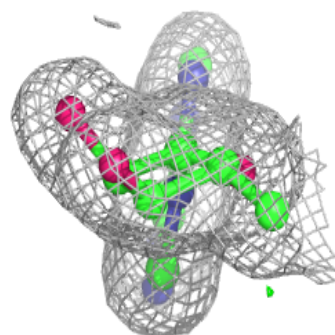
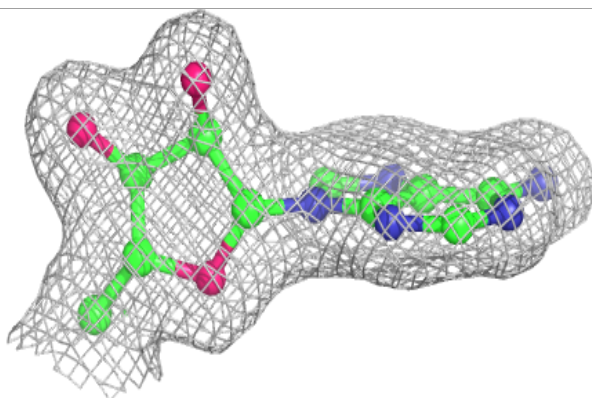
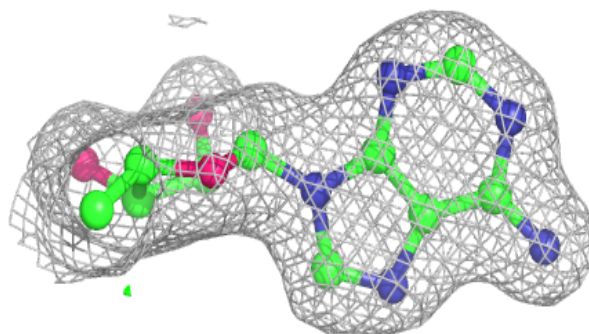
**Electron density around B12 D 702:**

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

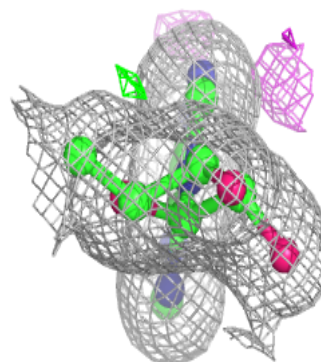
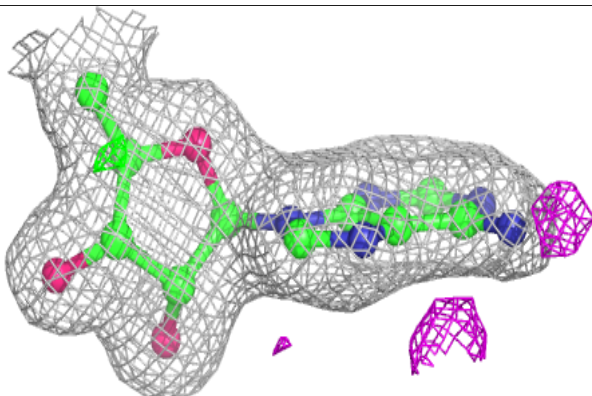
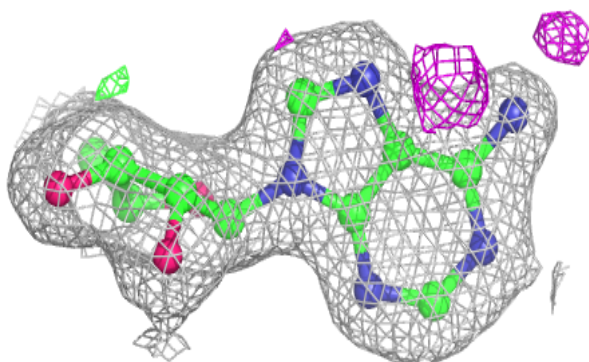


**Electron density around 5AD A 303:**

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

**Electron density around 5AD C 303:**

$2mF_o-DF_c$  (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.