



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 24, 2023 – 09:10 AM EDT

PDB ID : 5TZF  
Title : Structure of the BldD CTD(D116A)-(c-di-GMP)<sub>2</sub> intermediate, form 1  
Authors : Schumacher, M.A.  
Deposited on : 2016-11-21  
Resolution : 2.40 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

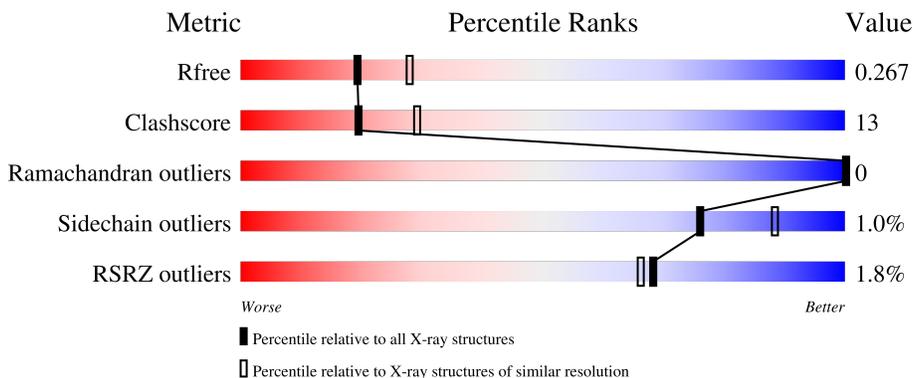
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	B	91	 2% 63% 21% 16%
1	D	91	 2% 66% 18% 15%
1	E	91	 2% 67% 16% 15%
1	H	91	 79% 16%
1	I	91	 3% 55% 30% 14%

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Mol	Chain	Length	Quality of chain
1	J	91	<p>% 74% 11% 14%</p>
1	M	91	<p>59% 24% 16%</p>
1	N	91	<p>3% 58% 27% 14%</p>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5353 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 DNA-binding protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	J	78	610	385	110	115	0	0	0
1	B	76	591	372	106	113	0	0	0
1	E	77	598	377	107	114	0	0	0
1	D	77	603	380	109	114	0	0	0
1	I	78	610	385	110	115	0	0	0
1	H	76	596	375	108	113	0	0	0
1	N	78	610	385	110	115	0	0	0
1	M	76	596	375	108	113	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

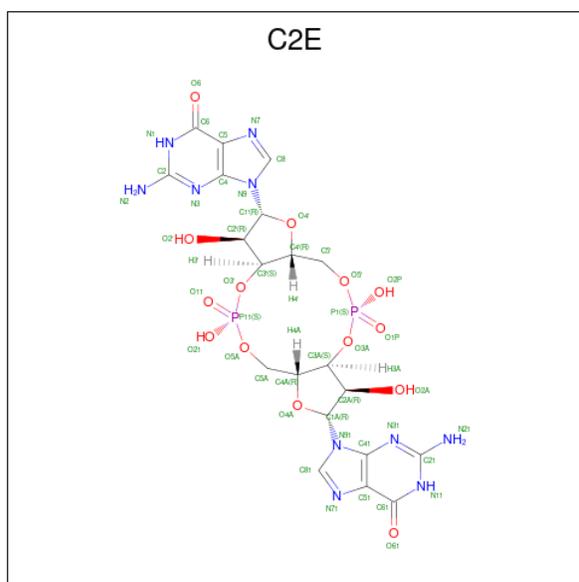
Chain	Residue	Modelled	Actual	Comment	Reference
J	76	GLY	-	expression tag	UNP F2RCL8
J	77	SER	-	expression tag	UNP F2RCL8
J	78	HIS	-	expression tag	UNP F2RCL8
J	79	MET	-	expression tag	UNP F2RCL8
J	116	ALA	ASP	engineered mutation	UNP F2RCL8
B	76	GLY	-	expression tag	UNP F2RCL8
B	77	SER	-	expression tag	UNP F2RCL8
B	78	HIS	-	expression tag	UNP F2RCL8
B	79	MET	-	expression tag	UNP F2RCL8
B	116	ALA	ASP	engineered mutation	UNP F2RCL8
E	76	GLY	-	expression tag	UNP F2RCL8
E	77	SER	-	expression tag	UNP F2RCL8
E	78	HIS	-	expression tag	UNP F2RCL8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	79	MET	-	expression tag	UNP F2RCL8
E	116	ALA	ASP	engineered mutation	UNP F2RCL8
D	76	GLY	-	expression tag	UNP F2RCL8
D	77	SER	-	expression tag	UNP F2RCL8
D	78	HIS	-	expression tag	UNP F2RCL8
D	79	MET	-	expression tag	UNP F2RCL8
D	116	ALA	ASP	engineered mutation	UNP F2RCL8
I	76	GLY	-	expression tag	UNP F2RCL8
I	77	SER	-	expression tag	UNP F2RCL8
I	78	HIS	-	expression tag	UNP F2RCL8
I	79	MET	-	expression tag	UNP F2RCL8
I	116	ALA	ASP	engineered mutation	UNP F2RCL8
H	76	GLY	-	expression tag	UNP F2RCL8
H	77	SER	-	expression tag	UNP F2RCL8
H	78	HIS	-	expression tag	UNP F2RCL8
H	79	MET	-	expression tag	UNP F2RCL8
H	116	ALA	ASP	engineered mutation	UNP F2RCL8
N	76	GLY	-	expression tag	UNP F2RCL8
N	77	SER	-	expression tag	UNP F2RCL8
N	78	HIS	-	expression tag	UNP F2RCL8
N	79	MET	-	expression tag	UNP F2RCL8
N	116	ALA	ASP	engineered mutation	UNP F2RCL8
M	76	GLY	-	expression tag	UNP F2RCL8
M	77	SER	-	expression tag	UNP F2RCL8
M	78	HIS	-	expression tag	UNP F2RCL8
M	79	MET	-	expression tag	UNP F2RCL8
M	116	ALA	ASP	engineered mutation	UNP F2RCL8

- Molecule 2 is 9,9'-[(2R,3R,3aS,5S,7aR,9R,10R,10aS,12S,14aR)-3,5,10,12-tetrahydroxy-5,12-dioxidoctahydro-2H,7H-difuro[3,2-d:3',2'-j][1,3,7,9,2,8]tetraoxadiphosphacyclododecine-2,9-diyl]bis(2-amino-1,9-dihydro-6H-purin-6-one) (three-letter code: C2E) (formula: C<sub>20</sub>H<sub>24</sub>N<sub>10</sub>O<sub>14</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	B	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
2	B	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
2	E	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
2	D	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
2	I	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
2	H	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
2	M	1	Total	C	N	O	P	0	0
			46	20	10	14	2		
2	M	1	Total	C	N	O	P	0	0
			46	20	10	14	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	18	Total	O	0	0
			18	18		
3	B	21	Total	O	0	0
			21	21		
3	E	16	Total	O	0	0
			16	16		
3	D	23	Total	O	0	0
			23	23		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
3	I	21	Total O 21 21	0	0
3	H	26	Total O 26 26	0	0
3	N	25	Total O 25 25	0	0
3	M	21	Total O 21 21	0	0



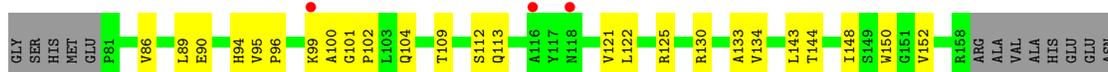
- Molecule 1: DNA-binding protein

Chain H:  79% .. 16%



- Molecule 1: DNA-binding protein

Chain N:  3% 58% 27% 14%



- Molecule 1: DNA-binding protein

Chain M:  59% 24% 16%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.13Å 93.06Å 94.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.17 – 2.40 66.17 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.6 (66.17-2.40) 96.6 (66.17-2.15)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.32 (at 2.14Å)	Xtrriage
Refinement program	PHENIX 1.6.4_486	Depositor
R, $R_{free}$	0.229 , 0.272 0.226 , 0.267	Depositor DCC
$R_{free}$ test set	1963 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.6	Xtrriage
Anisotropy	0.101	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 51.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.000 for -h,l,k	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5353	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	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 47.20 % 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 1.0267e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: C2E

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	B	0.22	0/599	0.38	0/813
1	D	0.22	0/613	0.40	0/833
1	E	0.22	0/607	0.40	0/825
1	H	0.22	0/605	0.38	0/821
1	I	0.23	0/621	0.40	0/845
1	J	0.33	0/621	0.44	0/845
1	M	0.21	0/605	0.37	0/821
1	N	0.24	0/621	0.41	0/845
All	All	0.24	0/4892	0.40	0/6648

There are no bond length outliers.

There are no bond angle outliers.

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	B	591	0	605	18	0
1	D	603	0	617	15	0
1	E	598	0	612	11	0
1	H	596	0	610	3	2
1	I	610	0	624	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	610	0	624	9	2
1	M	596	0	610	18	0
1	N	610	0	624	26	0
2	B	92	0	39	7	0
2	D	46	0	20	1	0
2	E	46	0	20	1	0
2	H	46	0	20	1	0
2	I	46	0	19	1	0
2	M	92	0	40	5	0
3	B	21	0	0	9	0
3	D	23	0	0	0	1
3	E	16	0	0	4	0
3	H	26	0	0	1	1
3	I	21	0	0	10	0
3	J	18	0	0	3	0
3	M	21	0	0	1	0
3	N	25	0	0	12	0
All	All	5353	0	5084	131	3

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 131 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:I:100:ALA:C	3:I:301:HOH:O	1.91	1.06
1:I:94:HIS:N	3:I:302:HOH:O	1.88	1.05
1:I:101:GLY:N	3:I:301:HOH:O	1.86	1.05
1:B:119:GLY:N	3:B:301:HOH:O	1.94	0.98
1:B:119:GLY:N	3:B:302:HOH:O	1.95	0.98

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:98:GLU:CG	1:H:97:GLN:NE2[3_544]	2.02	0.18
1:J:98:GLU:OE1	1:H:97:GLN:CG[3_544]	2.07	0.13
3:D:307:HOH:O	3:H:319:HOH:O[4_465]	2.10	0.10

## 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	B	74/91 (81%)	72 (97%)	2 (3%)	0	100	100
1	D	75/91 (82%)	70 (93%)	5 (7%)	0	100	100
1	E	75/91 (82%)	73 (97%)	2 (3%)	0	100	100
1	H	74/91 (81%)	72 (97%)	2 (3%)	0	100	100
1	I	76/91 (84%)	72 (95%)	4 (5%)	0	100	100
1	J	76/91 (84%)	73 (96%)	3 (4%)	0	100	100
1	M	74/91 (81%)	71 (96%)	3 (4%)	0	100	100
1	N	76/91 (84%)	71 (93%)	5 (7%)	0	100	100
All	All	600/728 (82%)	574 (96%)	26 (4%)	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	B	63/76 (83%)	63 (100%)	0	100	100
1	D	65/76 (86%)	64 (98%)	1 (2%)	65	80
1	E	64/76 (84%)	63 (98%)	1 (2%)	62	79
1	H	64/76 (84%)	63 (98%)	1 (2%)	62	79
1	I	66/76 (87%)	65 (98%)	1 (2%)	65	80
1	J	66/76 (87%)	65 (98%)	1 (2%)	65	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	64/76 (84%)	64 (100%)	0	100	100
1	N	66/76 (87%)	66 (100%)	0	100	100
All	All	518/608 (85%)	513 (99%)	5 (1%)	76	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	98	GLU
1	E	120	LYS
1	D	98	GLU
1	I	146	GLN
1	H	127	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	146	GLN
1	N	104	GLN
1	I	146	GLN
1	I	138	GLN
1	N	94	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](#)

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	C2E	B	202	-	44,52,52	2.97	16 (36%)	52,82,82	2.06	17 (32%)
2	C2E	I	201	-	44,52,52	3.86	16 (36%)	52,82,82	2.60	18 (34%)
2	C2E	H	201	-	44,52,52	3.56	17 (38%)	52,82,82	1.97	16 (30%)
2	C2E	M	201	-	44,52,52	3.58	18 (40%)	52,82,82	2.06	14 (26%)
2	C2E	D	201	-	44,52,52	2.24	15 (34%)	52,82,82	1.80	14 (26%)
2	C2E	M	202	-	44,52,52	2.63	16 (36%)	52,82,82	1.75	15 (28%)
2	C2E	E	201	-	44,52,52	2.52	15 (34%)	52,82,82	1.67	14 (26%)
2	C2E	B	201	-	44,52,52	3.72	15 (34%)	52,82,82	1.89	15 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	C2E	B	202	-	-	1/22/62/62	0/6/7/7
2	C2E	I	201	-	-	1/22/62/62	0/6/7/7
2	C2E	H	201	-	-	3/22/62/62	0/6/7/7
2	C2E	M	201	-	-	3/22/62/62	0/6/7/7
2	C2E	D	201	-	-	1/22/62/62	0/6/7/7
2	C2E	M	202	-	-	6/22/62/62	0/6/7/7
2	C2E	E	201	-	-	3/22/62/62	0/6/7/7
2	C2E	B	201	-	-	1/22/62/62	0/6/7/7

The worst 5 of 128 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	201	C2E	C2'-C1'	-21.73	1.20	1.53
2	B	201	C2E	O2'-C2'	-20.38	0.95	1.43
2	M	201	C2E	O2'-C2'	-19.04	0.98	1.43
2	H	201	C2E	C2'-C1'	-15.19	1.30	1.53
2	H	201	C2E	O2'-C2'	-11.99	1.14	1.43

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	201	C2E	C3'-C2'-C1'	10.14	122.35	99.89
2	M	201	C2E	O2'-C2'-C3'	8.10	134.18	111.17
2	I	201	C2E	O2'-C2'-C3'	-6.97	91.38	111.17
2	I	201	C2E	C2'-C3'-C4'	-6.01	92.57	103.22
2	H	201	C2E	C3'-C2'-C1'	5.08	111.13	99.89

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

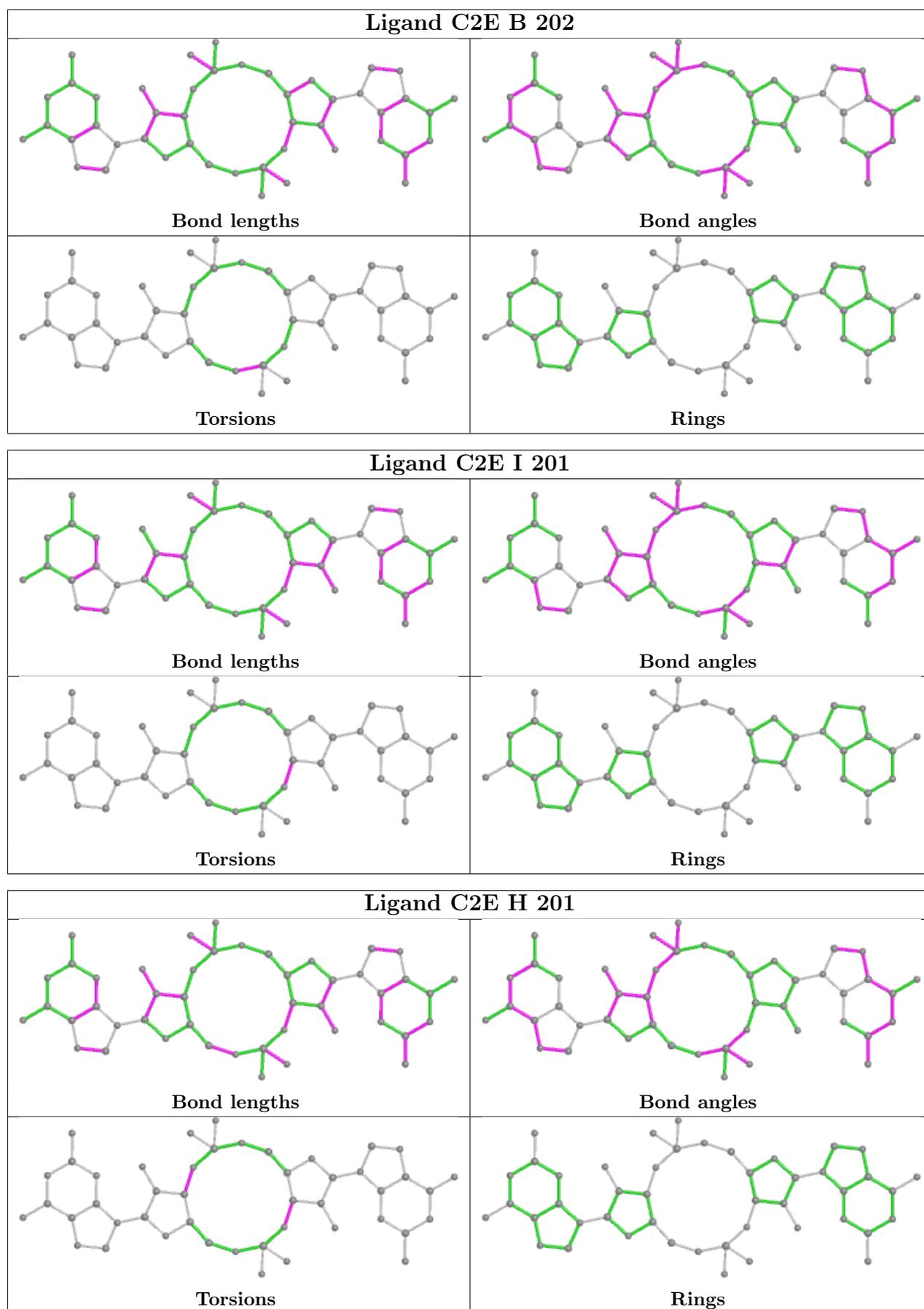
Mol	Chain	Res	Type	Atoms
2	M	202	C2E	O4A-C4A-C5A-O5A
2	M	202	C2E	C3A-C4A-C5A-O5A
2	H	201	C2E	C2A-C3A-O3A-P1
2	M	201	C2E	C2A-C3A-O3A-P1
2	M	202	C2E	C5A-O5A-P11-O3'

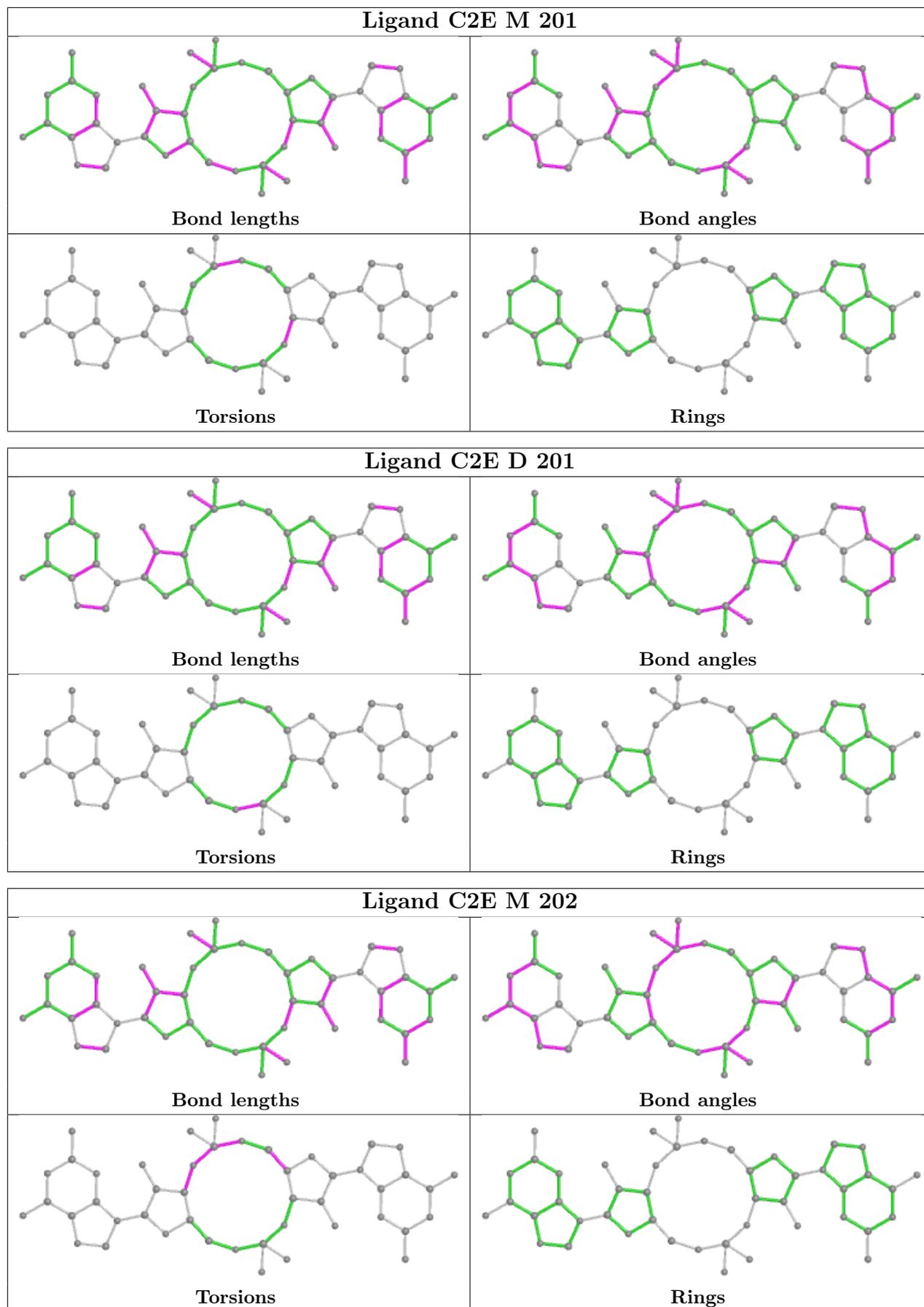
There are no ring outliers.

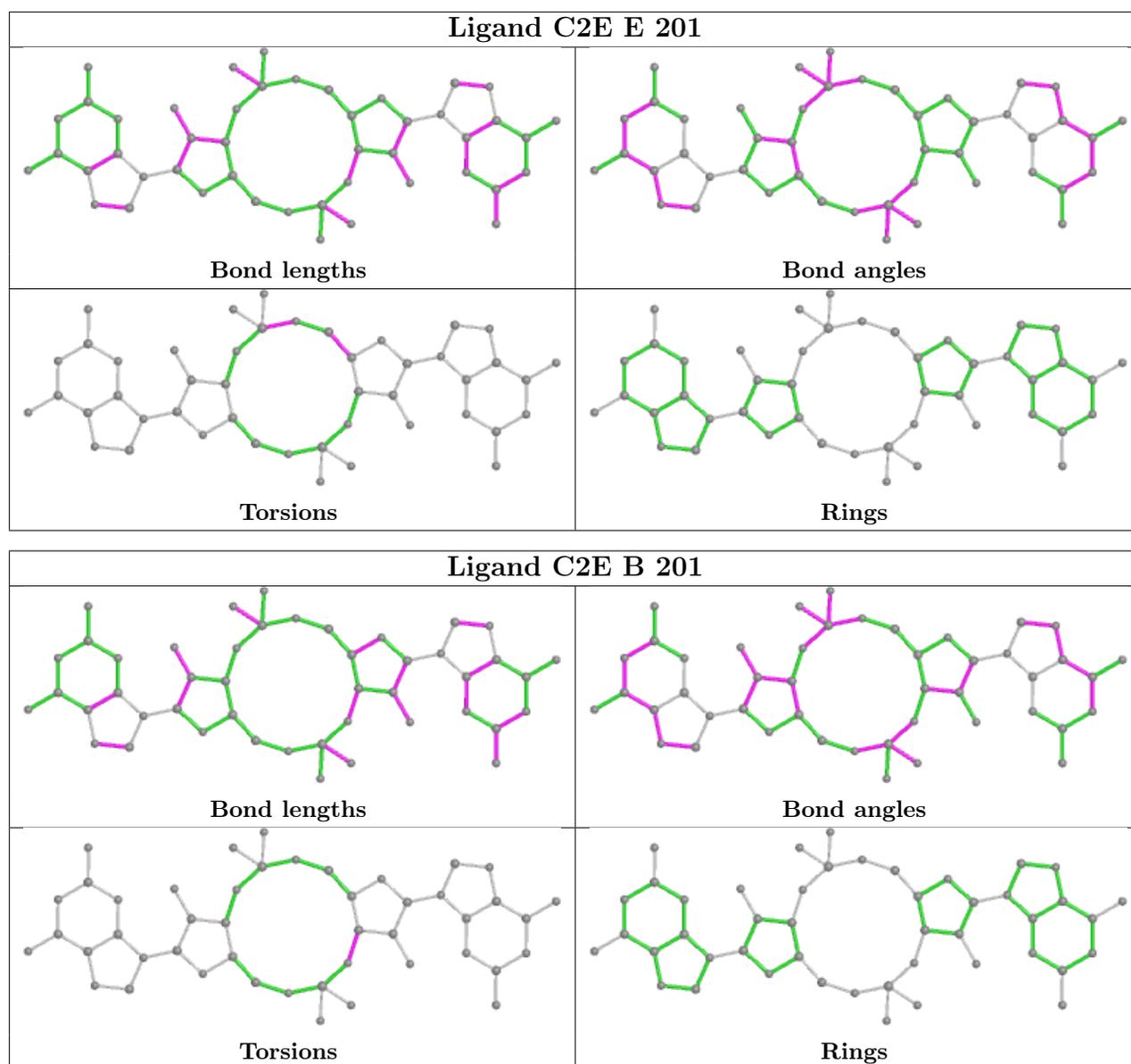
8 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	202	C2E	5	0
2	I	201	C2E	1	0
2	H	201	C2E	1	0
2	M	201	C2E	1	0
2	D	201	C2E	1	0
2	M	202	C2E	4	0
2	E	201	C2E	1	0
2	B	201	C2E	2	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	B	76/91 (83%)	-0.38	0 <b>100</b> <b>100</b>	32, 52, 94, 109	0
1	D	77/91 (84%)	-0.43	2 (2%) 56 54	29, 48, 96, 114	0
1	E	77/91 (84%)	-0.38	2 (2%) 56 54	32, 51, 95, 135	0
1	H	76/91 (83%)	-0.42	0 <b>100</b> <b>100</b>	30, 46, 74, 101	0
1	I	78/91 (85%)	-0.01	3 (3%) 40 39	27, 67, 118, 136	0
1	J	78/91 (85%)	-0.36	1 (1%) 77 75	33, 46, 91, 132	0
1	M	76/91 (83%)	-0.20	0 <b>100</b> <b>100</b>	34, 62, 100, 122	0
1	N	78/91 (85%)	-0.08	3 (3%) 40 39	30, 58, 127, 156	0
All	All	616/728 (84%)	-0.28	11 (1%) 68 66	27, 55, 105, 156	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	118	ASN	6.3
1	I	118	ASN	3.7
1	D	116	ALA	3.1
1	E	118	ASN	2.9
1	J	97	GLN	2.9

### 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 monosaccharides in this entry.

## 6.4 Ligands

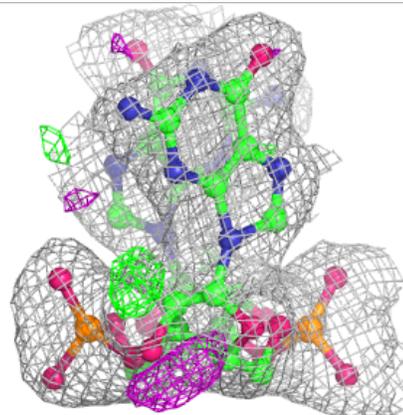
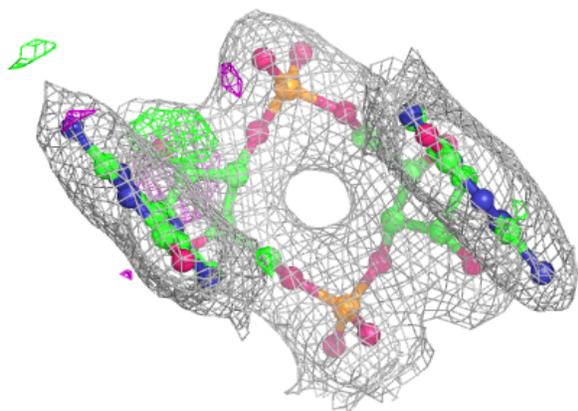
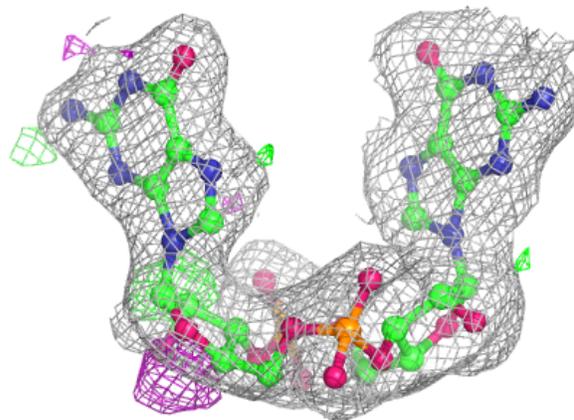
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	C2E	I	201	46/46	0.95	0.12	22,37,49,73	0
2	C2E	D	201	46/46	0.96	0.11	22,36,45,52	0
2	C2E	M	202	46/46	0.96	0.13	26,39,52,150	0
2	C2E	B	201	46/46	0.97	0.11	27,37,43,52	0
2	C2E	B	202	46/46	0.97	0.12	22,36,49,67	0
2	C2E	M	201	46/46	0.97	0.12	23,36,47,60	0
2	C2E	E	201	46/46	0.97	0.11	27,38,50,55	0
2	C2E	H	201	46/46	0.98	0.13	17,33,44,58	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.

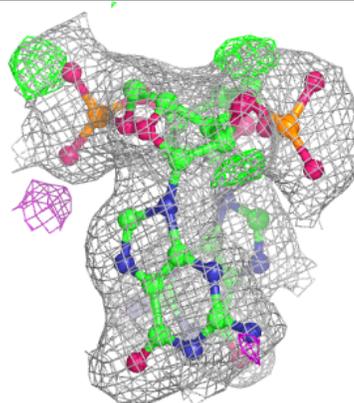
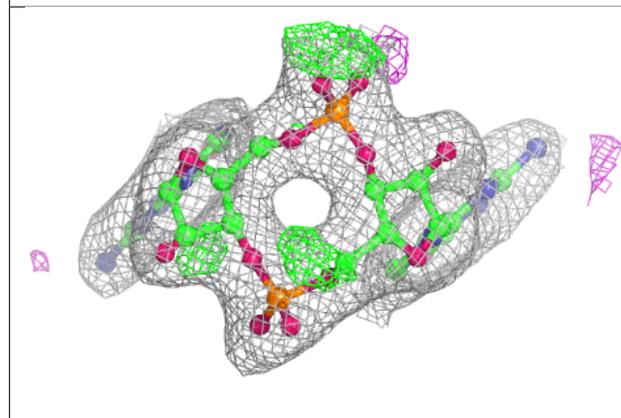
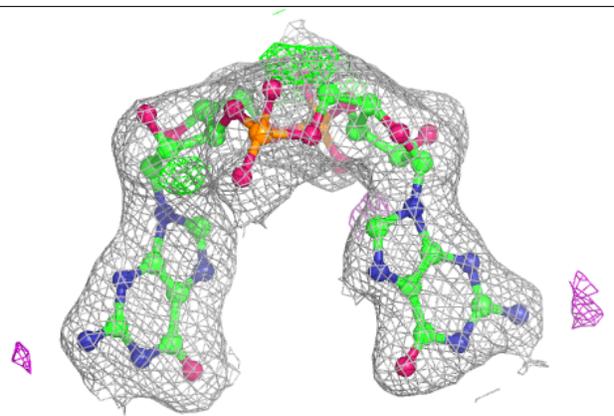
**Electron density around C2E I 201:**

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



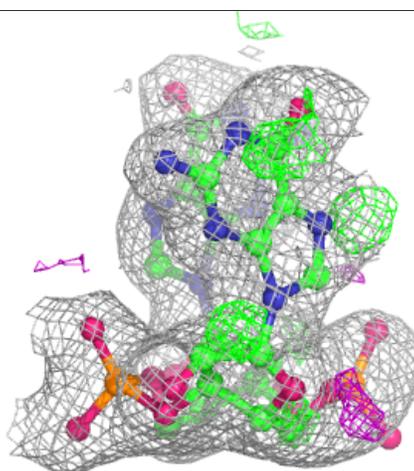
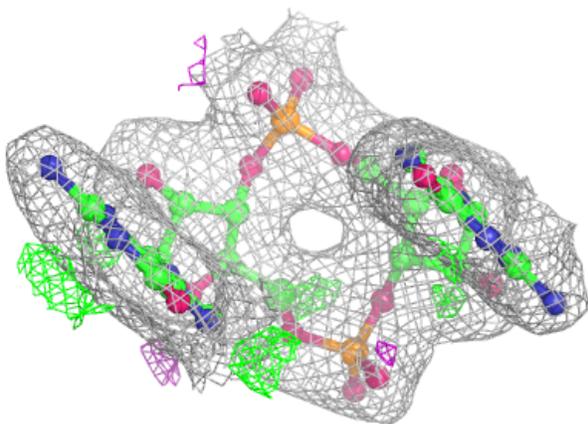
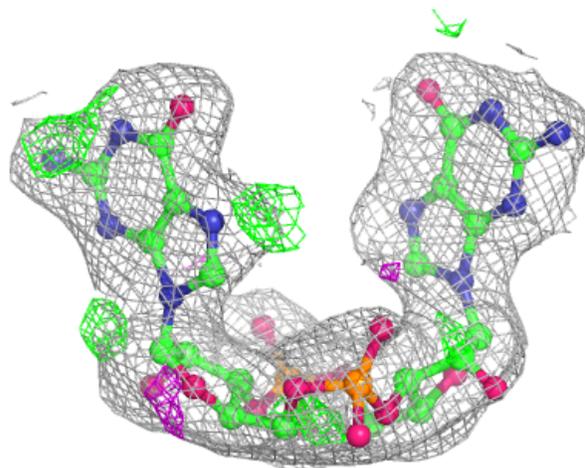
**Electron density around C2E D 201:**

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



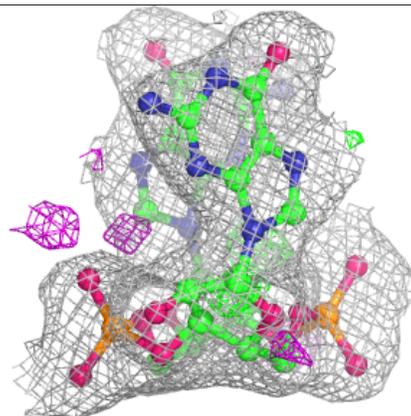
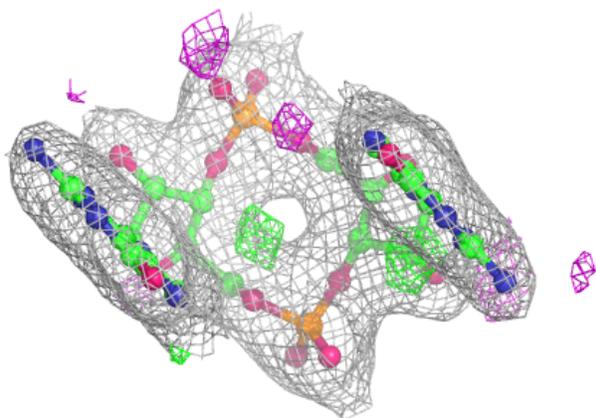
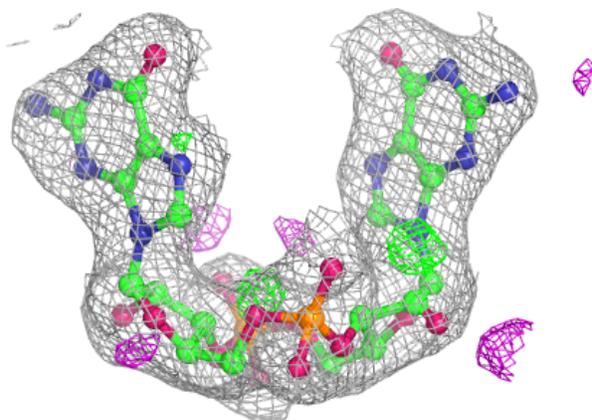
**Electron density around C2E M 202:**

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



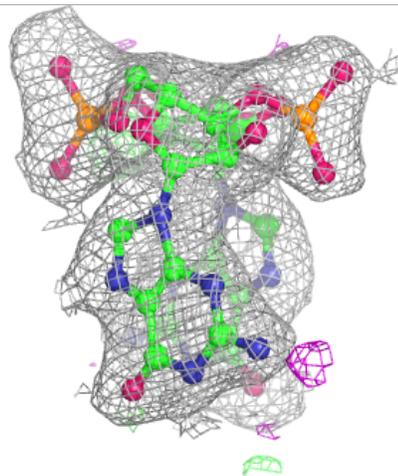
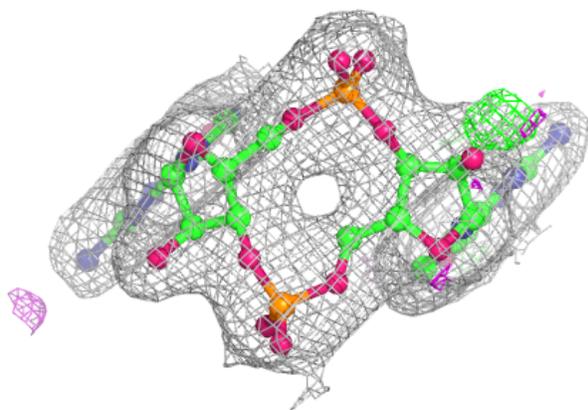
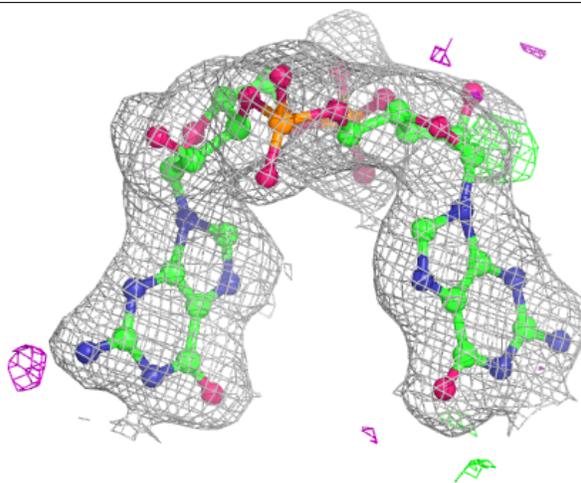
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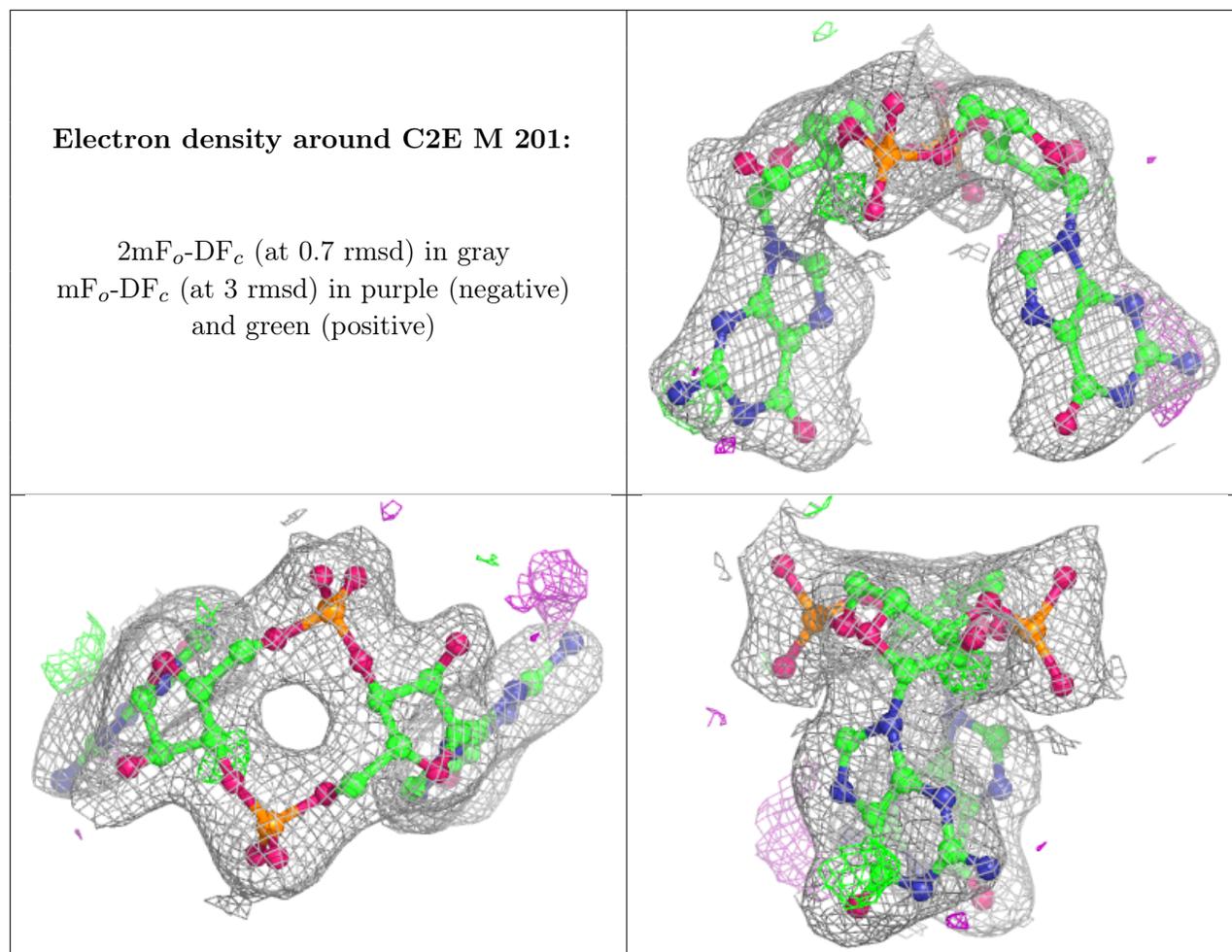
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around C2E B 202:**

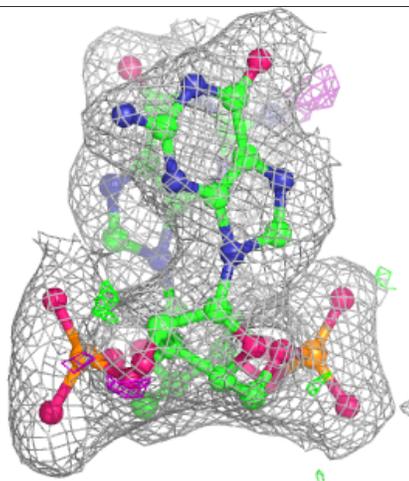
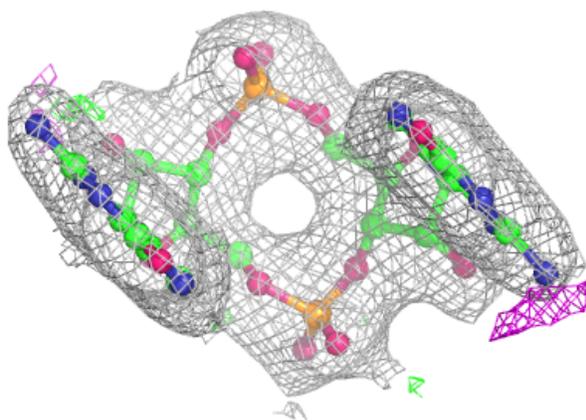
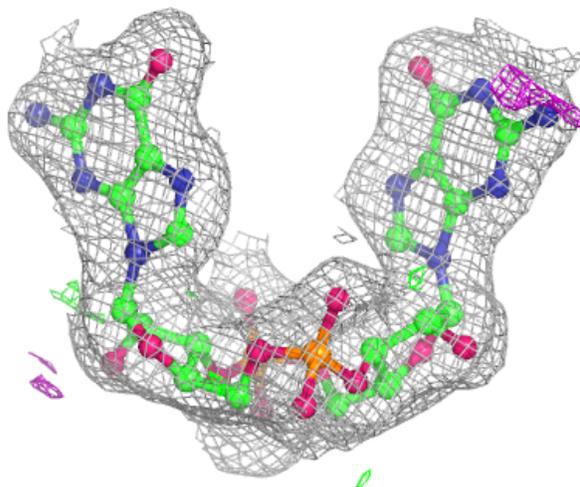
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





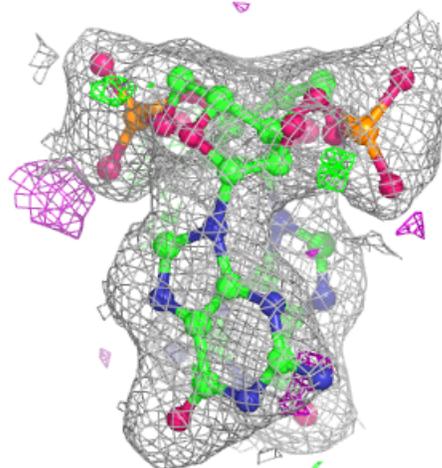
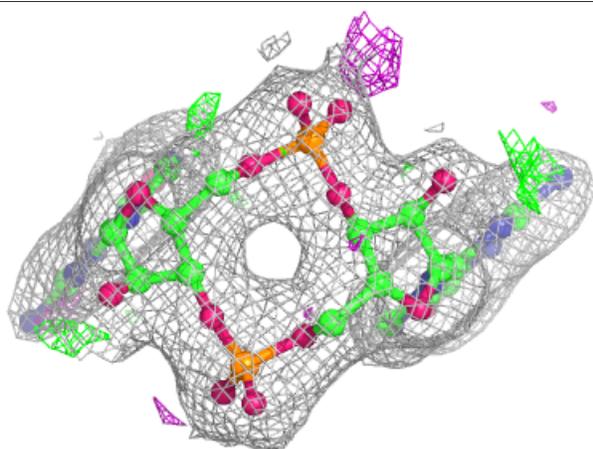
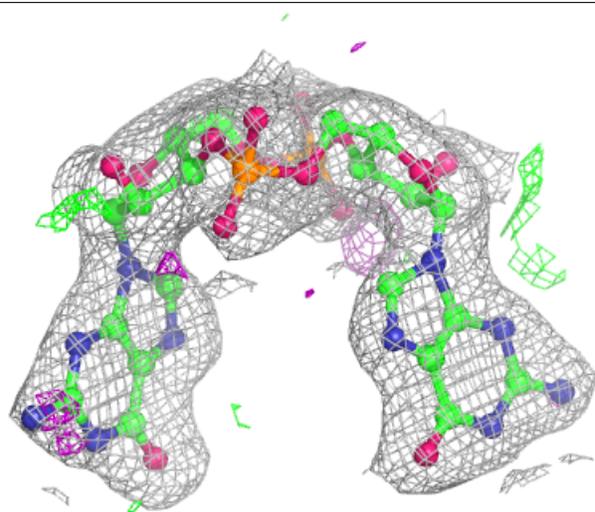
**Electron density around C2E E 201:**

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



**Electron density around C2E H 201:**

$2mF_o-DF_c$  (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.