



# Full wwPDB X-ray Structure Validation Report i

May 16, 2020 – 01:58 pm BST

PDB ID : 3W78  
Title : Crystal Structure of azoreductase AzrC in complex with NAD(P)-inhibitor Cibacron Blue  
Authors : Yu, J.; Ogata, D.; Ooi, T.; Yao, M.  
Deposited on : 2013-02-27  
Resolution : 2.62 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](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 i symbol.

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The following versions of software and data (see [references](#) i) 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	:	2.11
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)	:	2.11

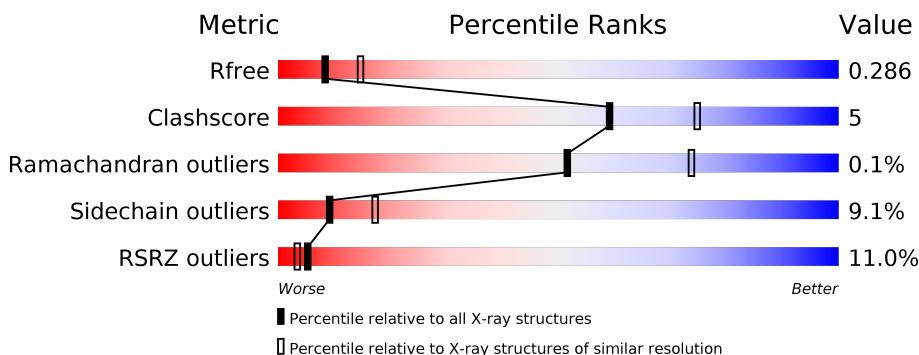
## 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

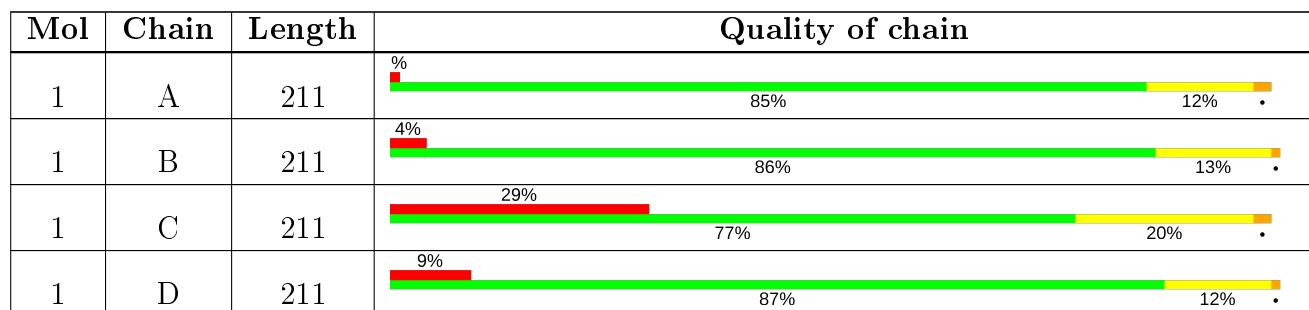
The reported resolution of this entry is 2.62 Å.

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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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.



## 2 Entry composition (i)

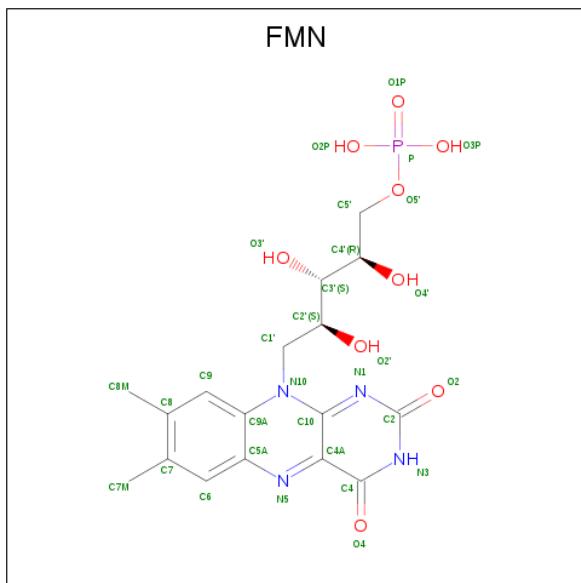
There are 4 unique types of molecules in this entry. The entry contains 6789 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FMN-dependent NADH-azoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total 1610	C 1032	N 264	O 309	S 5	0	0	0
1	D	210	Total 1610	C 1032	N 264	O 309	S 5	0	0	0
1	B	210	Total 1610	C 1032	N 264	O 309	S 5	0	0	0
1	C	210	Total 1610	C 1032	N 264	O 309	S 5	0	0	0

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P).



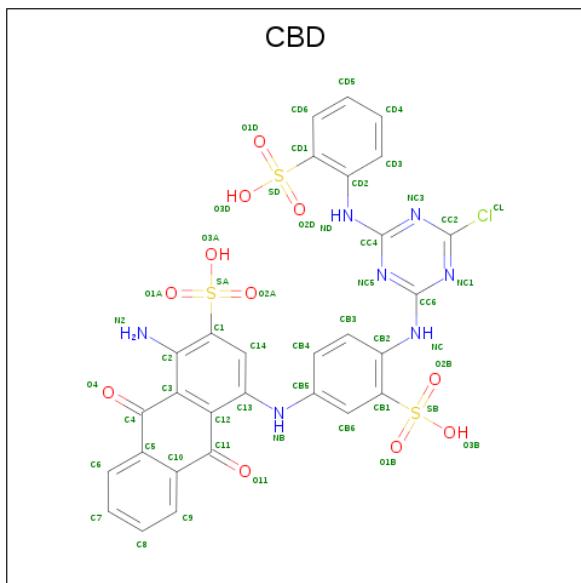
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 31	C 17	N 4	O 9	P 1	0	0
2	D	1	Total 31	C 17	N 4	O 9	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2		B		1	Total	C	N	O	P
				31	17	4	9	1	
2		C		1	Total	C	N	O	P
				31	17	4	9	1	

- Molecule 3 is CIBACRON BLUE (three-letter code: CBD) (formula:  $C_{29}H_{20}ClN_7O_{11}S_3$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	S	0	0
			51	29	1	7	11	3		
3	D	1	Total	C	Cl	N	O	S	0	0
			51	29	1	7	11	3		
3	B	1	Total	C	Cl	N	O	S	0	0
			51	29	1	7	11	3		
3	C	1	Total	C	Cl	N	O	S	0	0
			51	29	1	7	11	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	6	Total 6	O 6	0	0
4	D	6	Total 6	O 6	0	0
4	B	4	Total 4	O 4	0	0

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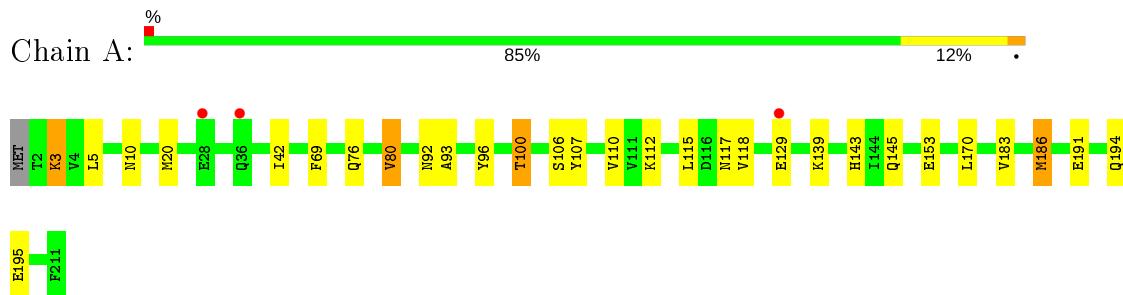
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	5	Total    O 5      5	0	0

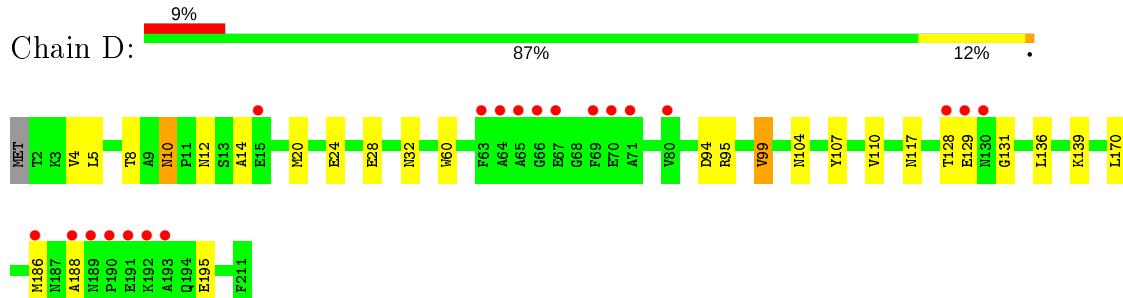
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

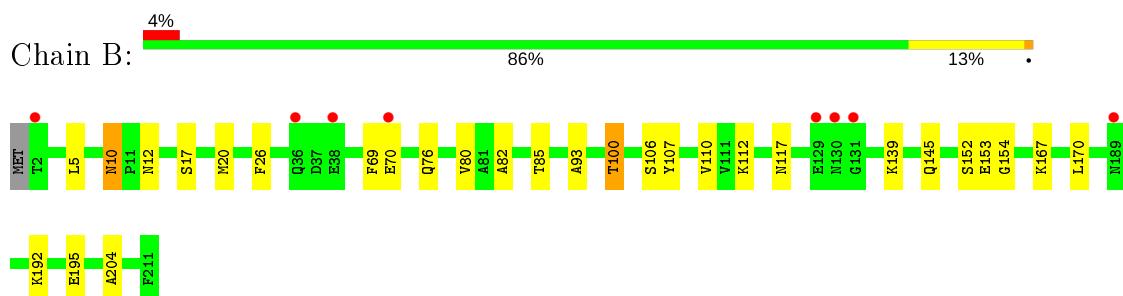
- Molecule 1: FMN-dependent NADH-azoreductase



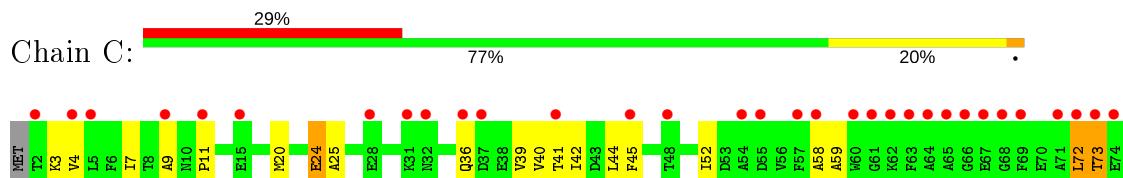
- Molecule 1: FMN-dependent NADH-azoreductase

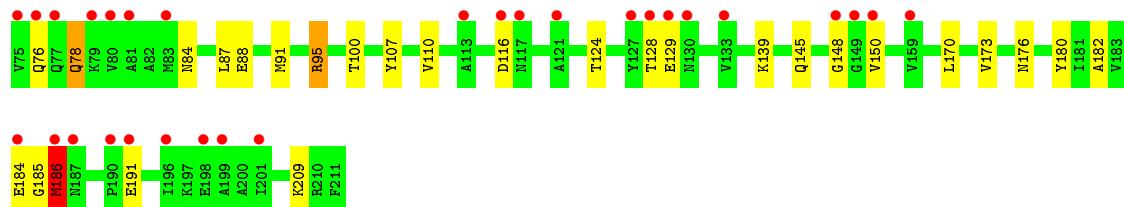


- Molecule 1: FMN-dependent NADH-azoreductase



- Molecule 1: FMN-dependent NADH-azoreductase





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	146.37 Å    146.37 Å    116.20 Å 90.00°    90.00°    120.00°	Depositor
Resolution (Å)	50.00 – 2.62 47.91 – 2.62	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.00-2.62) 99.3 (47.91-2.62)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle^1$	1.76 (at 2.61 Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
$R$ , $R_{free}$	0.253 , 0.285 0.254 , 0.286	Depositor DCC
$R_{free}$ test set	3079 reflections (7.15%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	50.2	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 38.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.020 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6789	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% 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: FMN, CBD

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	0.42	0/1646	0.50	0/2236
1	B	0.41	0/1646	0.48	0/2236
1	C	0.41	0/1646	0.52	0/2236
1	D	0.41	1/1646 (0.1%)	0.48	0/2236
All	All	0.41	1/6584 (0.0%)	0.49	0/8944

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	60	TRP	CD2-CE2	5.04	1.47	1.41

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	A	1610	0	1562	14	0
1	B	1610	0	1562	10	0
1	C	1610	0	1562	29	0
1	D	1610	0	1562	11	0
2	A	31	0	19	0	0
2	B	31	0	19	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	31	0	19	0	0
2	D	31	0	19	0	0
3	A	51	0	20	0	0
3	B	51	0	20	0	0
3	C	51	0	20	0	0
3	D	51	0	20	2	0
4	A	6	0	0	0	0
4	B	4	0	0	0	0
4	C	5	0	0	0	0
4	D	6	0	0	0	0
All	All	6789	0	6404	62	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 5.

All (62) 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:C:95:ARG:HH11	1:C:95:ARG:HG3	1.15	1.09
1:C:95:ARG:CG	1:C:95:ARG:HH11	1.87	0.87
1:C:185:GLY:HA2	1:C:186:MET:CB	2.10	0.81
1:C:185:GLY:HA2	1:C:186:MET:CG	2.10	0.81
1:C:95:ARG:NH1	1:C:95:ARG:HG3	1.90	0.78
1:B:10:ASN:HD22	1:B:12:ASN:H	1.35	0.75
1:D:10:ASN:HD22	1:D:12:ASN:H	1.35	0.73
1:C:185:GLY:HA2	1:C:186:MET:HG2	1.72	0.70
1:A:100:THR:HB	1:A:143:HIS:HE1	1.62	0.65
1:A:5:LEU:HD13	1:A:93:ALA:HB2	1.79	0.64
1:A:112:LYS:HE3	1:B:106:SER:HB3	1.81	0.62
1:C:58:ALA:HB3	1:C:76:GLN:HE22	1.64	0.61
1:C:148:GLY:O	1:C:185:GLY:HA3	2.01	0.60
1:B:100:THR:HG22	1:B:145:GLN:HG3	1.84	0.59
1:C:11:PRO:HA	1:C:45:PHE:CE2	2.37	0.59
1:C:185:GLY:HA2	1:C:186:MET:HB3	1.84	0.59
1:C:59:ALA:HA	1:C:72:LEU:HD11	1.85	0.58
1:D:104:ASN:HD22	3:D:302:CBD:H8	1.68	0.58
1:B:82:ALA:HA	1:B:85:THR:HG22	1.86	0.57
1:C:52:ILE:HD11	1:C:116:ASP:HB3	1.87	0.55
1:C:124:THR:HG22	1:C:173:VAL:HB	1.91	0.52
1:C:40:VAL:HB	1:C:41:THR:HB	1.92	0.52
1:B:93:ALA:O	1:B:139:LYS:HE3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:LYS:HE3	1:A:92:ASN:HD22	1.76	0.51
1:C:84:ASN:O	1:C:88:GLU:HG2	2.11	0.51
1:A:106:SER:HB3	1:B:112:LYS:HE3	1.94	0.50
1:C:150:VAL:HG12	1:C:184:GLU:HB3	1.94	0.49
1:D:4:VAL:HG22	1:D:95:ARG:HB2	1.94	0.49
1:D:128:THR:HG22	1:D:129:GLU:N	2.27	0.49
1:D:14:ALA:HA	1:D:20:MET:HB3	1.95	0.48
1:C:52:ILE:CD1	1:C:116:ASP:HB3	2.43	0.48
1:C:73:THR:HB	1:C:76:GLN:HG3	1.96	0.47
1:A:5:LEU:HG	1:A:42:ILE:CD1	2.45	0.47
1:B:26:PHE:HB2	1:B:204:ALA:HB1	1.97	0.47
1:C:95:ARG:NH1	1:C:95:ARG:CG	2.57	0.47
1:A:3:LYS:CE	1:A:92:ASN:HD22	2.28	0.46
1:A:100:THR:HG22	1:A:145:GLN:HG3	1.98	0.45
1:D:14:ALA:HB2	1:D:24:GLU:HG3	1.99	0.45
1:C:100:THR:HG22	1:C:145:GLN:HG3	1.99	0.45
1:B:100:THR:O	1:B:145:GLN:HA	2.17	0.45
1:C:58:ALA:HB3	1:C:76:GLN:NE2	2.32	0.45
1:A:76:GLN:O	1:A:80:VAL:HG13	2.17	0.44
1:A:183:VAL:HG12	1:A:186:MET:HE1	1.99	0.44
1:C:4:VAL:HG13	1:C:39:VAL:HA	2.00	0.44
1:C:9:ALA:HB2	1:C:44:LEU:HD12	1.99	0.44
1:D:136:LEU:HB3	1:D:139:LYS:HD3	2.00	0.44
1:D:188:ALA:HA	3:D:302:CBD:CC6	2.48	0.44
1:A:69:PHE:HE1	1:A:80:VAL:CG2	2.30	0.43
1:A:93:ALA:O	1:A:139:LYS:HE2	2.19	0.43
1:B:153:GLU:HG2	1:B:154:GLY:N	2.33	0.43
1:C:87:LEU:O	1:C:91:MET:HB2	2.19	0.43
1:C:78:GLN:HG3	1:C:78:GLN:H	1.72	0.43
1:C:100:THR:O	1:C:145:GLN:HA	2.20	0.42
1:C:180:TYR:CE2	1:C:182:ALA:HB2	2.54	0.42
1:A:115:LEU:HA	1:A:118:VAL:HG22	2.01	0.41
1:A:96:TYR:CE2	1:A:139:LYS:HG2	2.55	0.41
1:D:8:THR:HG22	1:D:99:VAL:CG1	2.50	0.41
1:C:24:GLU:HG3	1:C:25:ALA:N	2.36	0.41
1:C:7:ILE:HA	1:C:42:ILE:HG23	2.02	0.41
1:D:128:THR:HB	1:D:131:GLY:O	2.20	0.40
1:D:94:ASP:C	1:D:95:ARG:HD3	2.42	0.40
1:B:76:GLN:O	1:B:80:VAL:HG12	2.22	0.40

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	208/211 (99%)	202 (97%)	6 (3%)	0	100 100
1	B	208/211 (99%)	202 (97%)	6 (3%)	0	100 100
1	C	208/211 (99%)	199 (96%)	8 (4%)	1 (0%)	29 50
1	D	208/211 (99%)	203 (98%)	5 (2%)	0	100 100
All	All	832/844 (99%)	806 (97%)	25 (3%)	1 (0%)	51 74

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	186	MET

### 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	162/163 (99%)	147 (91%)	15 (9%)	9 16
1	B	162/163 (99%)	147 (91%)	15 (9%)	9 16
1	C	162/163 (99%)	144 (89%)	18 (11%)	6 10
1	D	162/163 (99%)	151 (93%)	11 (7%)	16 30
All	All	648/652 (99%)	589 (91%)	59 (9%)	9 17

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	10	ASN
1	A	20	MET
1	A	80	VAL
1	A	100	THR
1	A	107	TYR
1	A	110	VAL
1	A	117	ASN
1	A	129	GLU
1	A	153	GLU
1	A	170	LEU
1	A	186	MET
1	A	191	GLU
1	A	194	GLN
1	A	195	GLU
1	D	5	LEU
1	D	10	ASN
1	D	28	GLU
1	D	32	ASN
1	D	99	VAL
1	D	107	TYR
1	D	110	VAL
1	D	117	ASN
1	D	170	LEU
1	D	186	MET
1	D	195	GLU
1	B	5	LEU
1	B	10	ASN
1	B	17	SER
1	B	20	MET
1	B	69	PHE
1	B	70	GLU
1	B	100	THR
1	B	107	TYR
1	B	110	VAL
1	B	117	ASN
1	B	152	SER
1	B	167	LYS
1	B	170	LEU
1	B	192	LYS
1	B	195	GLU
1	C	3	LYS
1	C	20	MET

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Mol	Chain	Res	Type
1	C	24	GLU
1	C	36	GLN
1	C	72	LEU
1	C	73	THR
1	C	78	GLN
1	C	95	ARG
1	C	107	TYR
1	C	110	VAL
1	C	128	THR
1	C	129	GLU
1	C	139	LYS
1	C	170	LEU
1	C	176	ASN
1	C	186	MET
1	C	191	GLU
1	C	209	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	84	ASN
1	A	92	ASN
1	A	143	HIS
1	A	145	GLN
1	D	10	ASN
1	D	32	ASN
1	D	84	ASN
1	D	104	ASN
1	D	189	ASN
1	B	10	ASN
1	B	32	ASN
1	B	84	ASN
1	B	187	ASN
1	C	32	ASN
1	C	84	ASN
1	C	86	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 carbohydrates 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	CBD	A	302	-	53,56,56	2.35	12 (22%)	78,87,87	2.17	16 (20%)
3	CBD	D	302	-	53,56,56	2.27	11 (20%)	78,87,87	2.14	15 (19%)
3	CBD	B	302	-	53,56,56	2.31	12 (22%)	78,87,87	2.08	16 (20%)
2	FMN	C	301	-	31,33,33	2.45	6 (19%)	40,50,50	2.19	8 (20%)
2	FMN	A	301	-	31,33,33	2.30	6 (19%)	40,50,50	2.12	9 (22%)
2	FMN	D	301	-	31,33,33	2.37	7 (22%)	40,50,50	2.28	8 (20%)
2	FMN	B	301	-	31,33,33	2.36	5 (16%)	40,50,50	2.30	8 (20%)
3	CBD	C	302	-	53,56,56	2.34	12 (22%)	78,87,87	2.06	14 (17%)

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	CBD	A	302	-	-	10/30/46/46	0/6/6/6
3	CBD	D	302	-	-	1/30/46/46	0/6/6/6
3	CBD	B	302	-	-	13/30/46/46	0/6/6/6
2	FMN	C	301	-	-	7/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FMN	A	301	-	-	1/18/18/18	0/3/3/3
2	FMN	D	301	-	-	1/18/18/18	0/3/3/3
2	FMN	B	301	-	-	1/18/18/18	0/3/3/3
3	CBD	C	302	-	-	13/30/46/46	0/6/6/6

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	FMN	C4A-C10	10.33	1.49	1.38
2	D	301	FMN	C4A-C10	9.93	1.48	1.38
2	B	301	FMN	C4A-C10	9.80	1.48	1.38
2	A	301	FMN	C4A-C10	9.68	1.48	1.38
3	A	302	CBD	C2-C1	7.07	1.50	1.42
3	B	302	CBD	C2-C1	6.87	1.49	1.42
3	C	302	CBD	C2-C1	6.83	1.49	1.42
3	D	302	CBD	C2-C1	6.48	1.49	1.42
3	A	302	CBD	CD2-CD1	6.24	1.50	1.40
3	C	302	CBD	CD2-CD1	6.18	1.50	1.40
3	D	302	CBD	CB2-CB1	5.93	1.50	1.40
3	B	302	CBD	CD2-CD1	5.89	1.49	1.40
3	A	302	CBD	CB2-CB1	5.86	1.49	1.40
3	D	302	CBD	CD2-CD1	5.80	1.49	1.40
3	B	302	CBD	CB2-CB1	5.77	1.49	1.40
3	C	302	CBD	CB2-CB1	5.73	1.49	1.40
3	C	302	CBD	C3-C2	5.60	1.49	1.42
3	D	302	CBD	C10-C5	5.56	1.49	1.40
3	C	302	CBD	C10-C5	5.56	1.49	1.40
3	B	302	CBD	C10-C5	5.55	1.49	1.40
3	A	302	CBD	C10-C5	5.49	1.49	1.40
3	A	302	CBD	C3-C2	5.48	1.49	1.42
3	B	302	CBD	C3-C2	5.39	1.49	1.42
3	D	302	CBD	C3-C2	4.89	1.48	1.42
2	D	301	FMN	C4-C4A	4.79	1.49	1.41
2	B	301	FMN	C4-C4A	4.76	1.49	1.41
2	C	301	FMN	C4-C4A	4.61	1.49	1.41
3	A	302	CBD	C12-C13	4.51	1.50	1.41
2	A	301	FMN	C4-C4A	4.49	1.49	1.41
3	D	302	CBD	C12-C13	4.46	1.50	1.41
3	C	302	CBD	C12-C13	4.41	1.50	1.41
3	B	302	CBD	C12-C13	4.34	1.49	1.41
2	C	301	FMN	C9A-C5A	3.85	1.50	1.42
2	B	301	FMN	C9A-C5A	3.81	1.50	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	302	CBD	O3A-SA	3.76	1.64	1.45
3	B	302	CBD	O3B-SB	3.75	1.64	1.45
3	C	302	CBD	O3B-SB	3.73	1.64	1.45
3	C	302	CBD	C12-C3	3.73	1.49	1.41
3	D	302	CBD	O3B-SB	3.73	1.64	1.45
3	D	302	CBD	O3A-SA	3.72	1.64	1.45
2	D	301	FMN	C9A-C5A	3.71	1.50	1.42
2	C	301	FMN	C8-C7	3.70	1.50	1.40
3	C	302	CBD	O3D-SD	3.70	1.64	1.45
3	C	302	CBD	O3A-SA	3.69	1.64	1.45
3	A	302	CBD	O3B-SB	3.68	1.64	1.45
3	A	302	CBD	O3D-SD	3.66	1.63	1.45
3	A	302	CBD	O3A-SA	3.65	1.63	1.45
3	D	302	CBD	C12-C3	3.64	1.49	1.41
2	B	301	FMN	C8-C7	3.63	1.50	1.40
3	B	302	CBD	O3D-SD	3.63	1.63	1.45
3	D	302	CBD	O3D-SD	3.63	1.63	1.45
2	A	301	FMN	C9A-C5A	3.61	1.49	1.42
3	A	302	CBD	C12-C3	3.59	1.49	1.41
2	D	301	FMN	C8-C7	3.59	1.49	1.40
3	B	302	CBD	C12-C3	3.55	1.49	1.41
2	A	301	FMN	C8-C7	3.42	1.49	1.40
2	C	301	FMN	C9A-N10	3.13	1.42	1.38
2	B	301	FMN	C9A-N10	3.02	1.42	1.38
2	A	301	FMN	C9A-N10	2.98	1.42	1.38
3	A	302	CBD	CC2-CL	2.60	1.80	1.73
2	D	301	FMN	C9A-N10	2.55	1.42	1.38
3	C	302	CBD	CC2-CL	2.42	1.80	1.73
3	D	302	CBD	CC2-CL	2.40	1.80	1.73
3	B	302	CBD	CC2-CL	2.36	1.80	1.73
3	B	302	CBD	CB5-NB	-2.11	1.36	1.40
2	D	301	FMN	C10-N1	2.11	1.36	1.33
2	C	301	FMN	C10-N1	2.10	1.36	1.33
2	D	301	FMN	C4A-N5	2.10	1.36	1.33
3	C	302	CBD	CB5-NB	-2.06	1.36	1.40
2	A	301	FMN	C10-N1	2.03	1.35	1.33
3	A	302	CBD	CC2-NC3	2.02	1.36	1.32

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	302	CBD	CC6-NC1-CC2	9.02	121.11	112.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	CBD	CC6-NC1-CC2	8.99	121.08	112.43
2	D	301	FMN	C4-N3-C2	8.75	122.53	115.14
3	A	302	CBD	CC4-NC3-CC2	8.62	120.73	112.43
2	B	301	FMN	C4-N3-C2	8.59	122.40	115.14
3	D	302	CBD	CC4-NC3-CC2	8.55	120.66	112.43
2	C	301	FMN	C4-N3-C2	8.45	122.28	115.14
3	B	302	CBD	CC6-NC1-CC2	8.44	120.55	112.43
3	C	302	CBD	CC6-NC1-CC2	8.26	120.38	112.43
3	B	302	CBD	CC4-NC3-CC2	8.20	120.32	112.43
2	A	301	FMN	C4-N3-C2	8.12	122.00	115.14
3	C	302	CBD	CC4-NC3-CC2	8.12	120.25	112.43
2	D	301	FMN	C4-C4A-C10	-5.87	116.07	119.95
2	B	301	FMN	C4-C4A-C10	-5.86	116.07	119.95
3	A	302	CBD	NC3-CC2-NC1	-5.86	119.23	129.57
3	D	302	CBD	NC3-CC2-NC1	-5.67	119.57	129.57
3	C	302	CBD	NC3-CC2-NC1	-5.50	119.87	129.57
3	B	302	CBD	NC3-CC2-NC1	-5.46	119.93	129.57
2	B	301	FMN	C1'-N10-C9A	4.91	122.16	118.29
2	D	301	FMN	C4A-N5-C5A	4.79	121.56	116.77
2	A	301	FMN	C4-C4A-C10	-4.75	116.81	119.95
2	A	301	FMN	C4A-N5-C5A	4.73	121.50	116.77
2	C	301	FMN	C1'-N10-C9A	4.72	122.01	118.29
3	D	302	CBD	NC5-CC6-NC1	-4.66	118.86	126.23
2	B	301	FMN	C4A-N5-C5A	4.66	121.42	116.77
2	C	301	FMN	C4-C4A-C10	-4.63	116.89	119.95
3	A	302	CBD	NC5-CC6-NC1	-4.40	119.27	126.23
3	A	302	CBD	NC5-CC4-NC3	-4.39	119.30	126.23
3	B	302	CBD	NC5-CC6-NC1	-4.39	119.30	126.23
3	B	302	CBD	NC5-CC4-NC3	-4.36	119.34	126.23
3	C	302	CBD	NC5-CC4-NC3	-4.34	119.36	126.23
3	C	302	CBD	NC5-CC6-NC1	-4.28	119.46	126.23
2	C	301	FMN	C4A-N5-C5A	4.20	120.97	116.77
3	D	302	CBD	NC5-CC4-NC3	-4.20	119.59	126.23
2	B	301	FMN	C4-C4A-N5	4.17	123.36	118.60
3	D	302	CBD	CL-CC2-NC1	4.13	121.05	115.15
2	D	301	FMN	C4-C4A-N5	4.11	123.30	118.60
3	A	302	CBD	CL-CC2-NC3	4.08	120.98	115.15
3	C	302	CBD	CC6-NC5-CC4	4.00	120.68	113.89
3	B	302	CBD	CC6-NC5-CC4	3.93	120.56	113.89
2	D	301	FMN	C1'-N10-C9A	3.88	121.35	118.29
3	B	302	CBD	CL-CC2-NC3	3.83	120.63	115.15
3	A	302	CBD	CC6-NC5-CC4	3.83	120.39	113.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	302	CBD	CL-CC2-NC3	3.75	120.51	115.15
3	D	302	CBD	CC6-NC5-CC4	3.73	120.21	113.89
2	C	301	FMN	C4A-C4-N3	-3.68	118.41	123.43
2	B	301	FMN	C4A-C4-N3	-3.59	118.52	123.43
2	A	301	FMN	C1'-N10-C9A	3.57	121.10	118.29
2	D	301	FMN	C4A-C4-N3	-3.48	118.68	123.43
3	C	302	CBD	C12-C3-C2	-3.34	118.05	119.95
2	A	301	FMN	C4A-C4-N3	-3.29	118.93	123.43
3	A	302	CBD	CL-CC2-NC1	3.25	119.79	115.15
2	A	301	FMN	C4-C4A-N5	3.14	122.18	118.60
3	C	302	CBD	CL-CC2-NC1	3.13	119.62	115.15
3	A	302	CBD	C12-C3-C2	-3.11	118.18	119.95
3	D	302	CBD	C12-C3-C2	-3.03	118.23	119.95
3	B	302	CBD	CB1-CB2-NC	-3.01	118.61	121.45
3	B	302	CBD	CL-CC2-NC1	3.00	119.44	115.15
2	C	301	FMN	C4-C4A-N5	3.00	122.02	118.60
3	D	302	CBD	CL-CC2-NC3	2.96	119.38	115.15
2	C	301	FMN	C9A-N10-C10	-2.96	118.04	121.91
3	D	302	CBD	C2-C1-SA	-2.95	118.19	121.56
2	A	301	FMN	C9A-N10-C10	-2.74	118.32	121.91
3	B	302	CBD	O1D-SD-CD1	2.72	111.10	106.51
3	B	302	CBD	O2A-SA-C1	2.62	110.93	106.51
3	B	302	CBD	C13-C14-C1	2.61	123.59	119.47
3	A	302	CBD	CB1-CB2-NC	-2.57	119.02	121.45
3	C	302	CBD	O2D-SD-CD1	2.51	110.75	106.51
3	A	302	CBD	C13-C14-C1	2.49	123.40	119.47
2	B	301	FMN	C9A-N10-C10	-2.48	118.66	121.91
3	D	302	CBD	O1A-SA-C1	2.44	110.63	106.51
2	A	301	FMN	C1'-N10-C10	2.42	120.58	118.41
3	C	302	CBD	C13-C14-C1	2.34	123.17	119.47
3	C	302	CBD	O1A-SA-C1	2.32	110.42	106.51
3	C	302	CBD	O1D-SD-CD1	2.26	110.34	106.51
2	A	301	FMN	C5A-C9A-N10	2.26	119.36	117.72
3	D	302	CBD	C13-C14-C1	2.24	123.00	119.47
3	A	302	CBD	CD6-CD1-CD2	-2.20	118.47	120.28
3	B	302	CBD	C12-C3-C2	-2.19	118.71	119.95
3	D	302	CBD	ND-CC4-NC5	2.18	124.31	116.92
3	B	302	CBD	C12-C13-NB	-2.18	118.14	120.52
2	D	301	FMN	C9A-N10-C10	-2.16	119.08	121.91
3	D	302	CBD	O2D-SD-CD1	2.15	110.15	106.51
3	B	302	CBD	O2B-SB-CB1	2.14	110.13	106.51
3	A	302	CBD	O1A-SA-C1	2.14	110.13	106.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	302	CBD	NC-CC6-NC5	2.13	124.15	116.92
2	B	301	FMN	O3P-P-O2P	2.10	115.67	107.64
3	A	302	CBD	O2A-SA-C1	2.09	110.04	106.51
3	C	302	CBD	C1-C2-N2	-2.06	120.56	122.64
3	B	302	CBD	C3-C2-N2	-2.06	119.74	122.65
2	C	301	FMN	C5A-C9A-N10	2.06	119.21	117.72
3	A	302	CBD	O2D-SD-CD1	2.04	109.96	106.51
3	A	302	CBD	NC-CC6-NC5	2.03	123.81	116.92
2	D	301	FMN	O3P-P-O2P	2.03	115.39	107.64

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	CBD	CD2-CD1-SD-O3D
3	A	302	CBD	CD6-CD1-SD-O1D
3	A	302	CBD	CD6-CD1-SD-O2D
3	D	302	CBD	CD1-CD2-ND-CC4
3	B	302	CBD	C2-C1-SA-O1A
3	B	302	CBD	C14-C1-SA-O1A
3	B	302	CBD	C14-C1-SA-O2A
3	B	302	CBD	C14-C1-SA-O3A
3	B	302	CBD	CB2-CB1-SB-O3B
2	C	301	FMN	N10-C1'-C2'-O2'
2	C	301	FMN	O3'-C3'-C4'-C5'
3	C	302	CBD	CB2-CB1-SB-O3B
3	C	302	CBD	CB6-CB1-SB-O1B
3	C	302	CBD	CB6-CB1-SB-O2B
3	C	302	CBD	CD1-CD2-ND-CC4
3	C	302	CBD	CD2-CD1-SD-O3D
3	C	302	CBD	CD6-CD1-SD-O1D
3	C	302	CBD	CD6-CD1-SD-O2D
2	C	301	FMN	O3'-C3'-C4'-O4'
2	C	301	FMN	C2'-C3'-C4'-C5'
2	C	301	FMN	C2'-C3'-C4'-O4'
3	A	302	CBD	CB6-CB1-SB-O1B
3	B	302	CBD	CB6-CB1-SB-O2B
3	B	302	CBD	CD1-CD2-ND-CC4
3	C	302	CBD	CB2-CB1-SB-O1B
2	A	301	FMN	C4'-C5'-O5'-P
3	A	302	CBD	CB2-CB1-SB-O3B
3	A	302	CBD	CB6-CB1-SB-O3B

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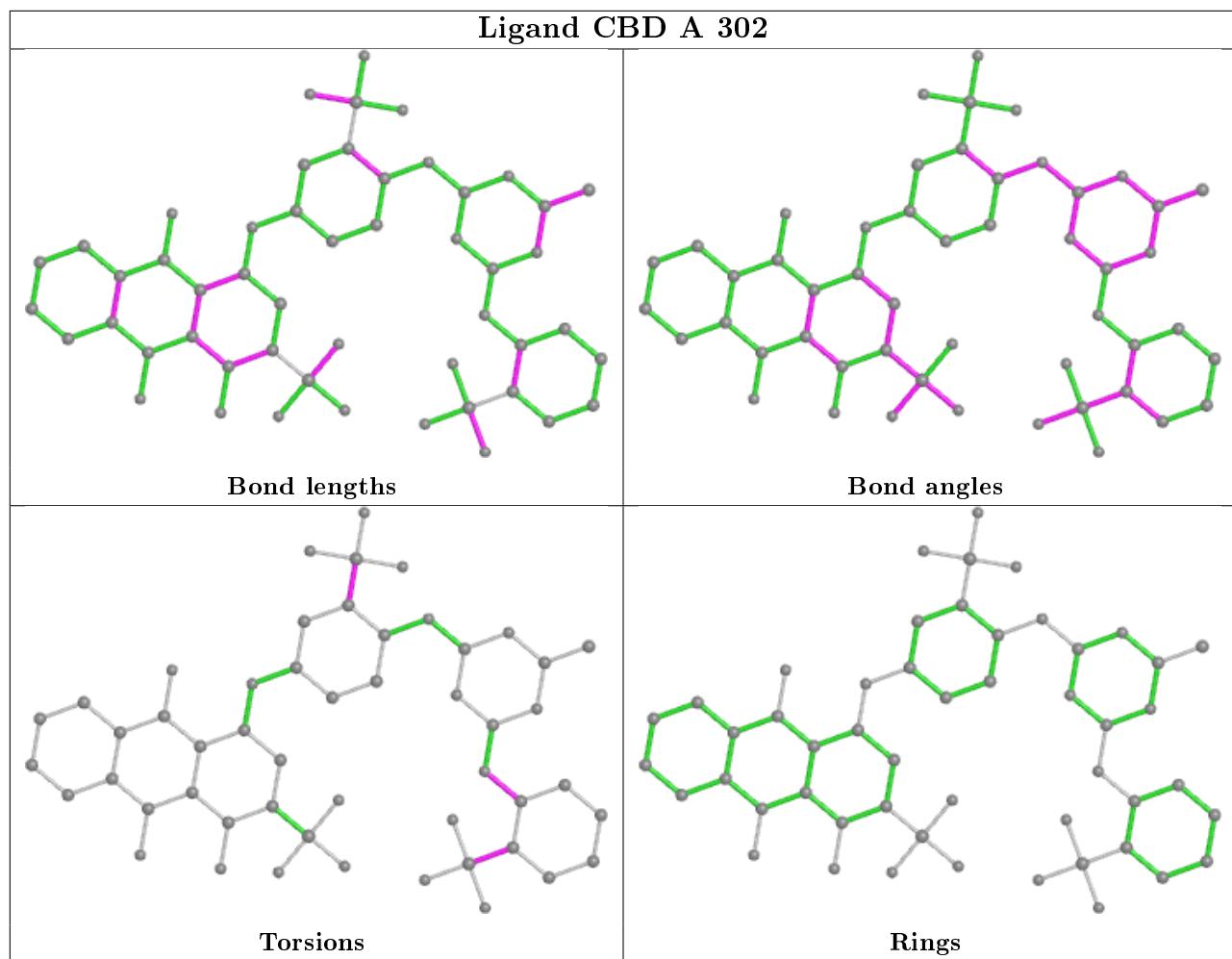
Mol	Chain	Res	Type	Atoms
3	A	302	CBD	CD6-CD1-SD-O3D
3	B	302	CBD	C2-C1-SA-O3A
3	B	302	CBD	CB6-CB1-SB-O3B
2	C	301	FMN	N10-C1'-C2'-C3'
3	C	302	CBD	CB6-CB1-SB-O3B
3	C	302	CBD	CD6-CD1-SD-O3D
2	D	301	FMN	C4'-C5'-O5'-P
3	C	302	CBD	CB2-CB1-SB-O2B
3	A	302	CBD	CB6-CB1-SB-O2B
3	B	302	CBD	CB6-CB1-SB-O1B
3	A	302	CBD	CD1-CD2-ND-CC4
2	B	301	FMN	C4'-C5'-O5'-P
3	A	302	CBD	CD2-CD1-SD-O1D
3	B	302	CBD	C2-C1-SA-O2A
3	C	302	CBD	CD2-CD1-SD-O1D
3	B	302	CBD	CD3-CD2-ND-CC4
3	C	302	CBD	CD3-CD2-ND-CC4
3	B	302	CBD	CB2-CB1-SB-O1B
2	C	301	FMN	C3'-C4'-C5'-O5'

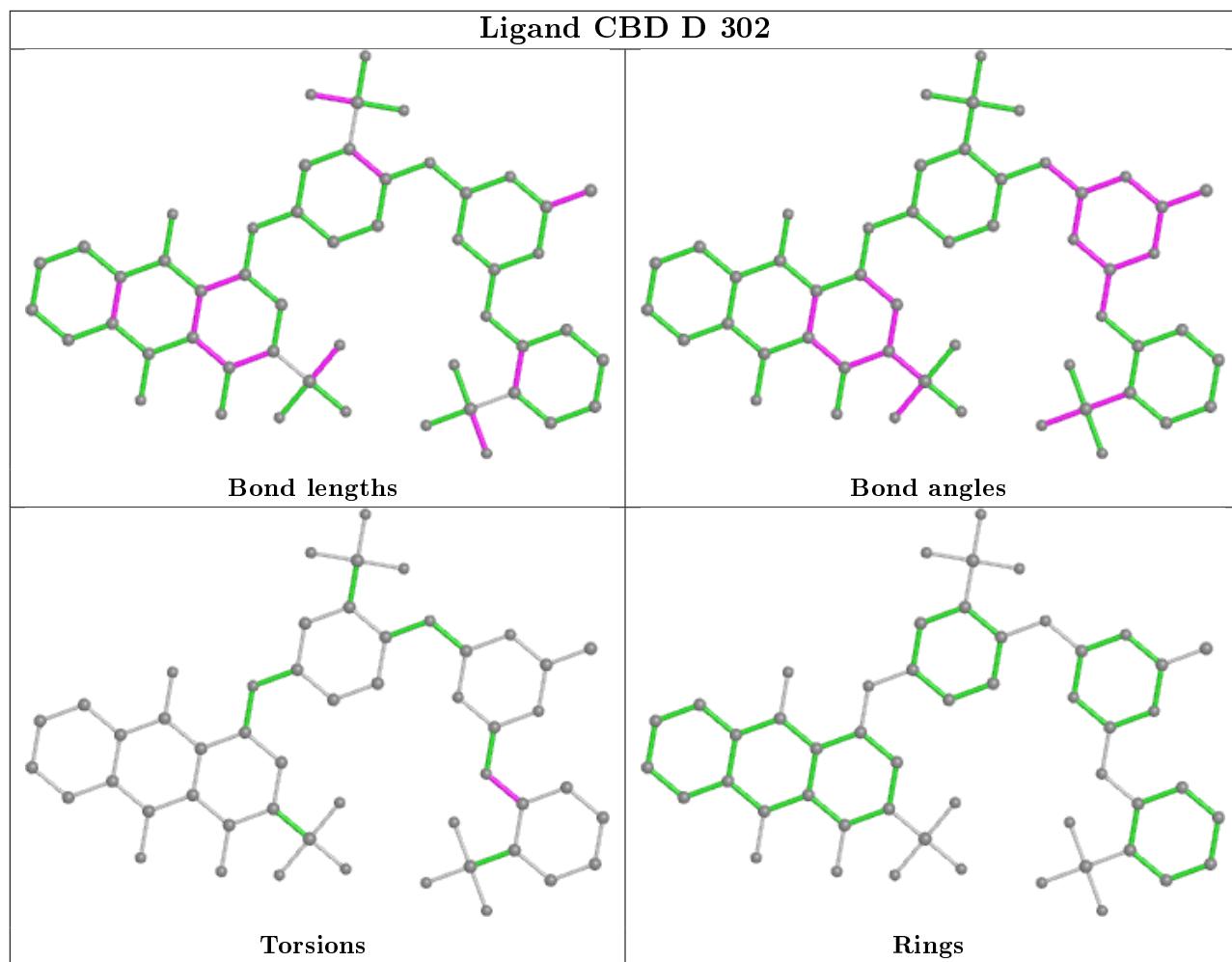
There are no ring outliers.

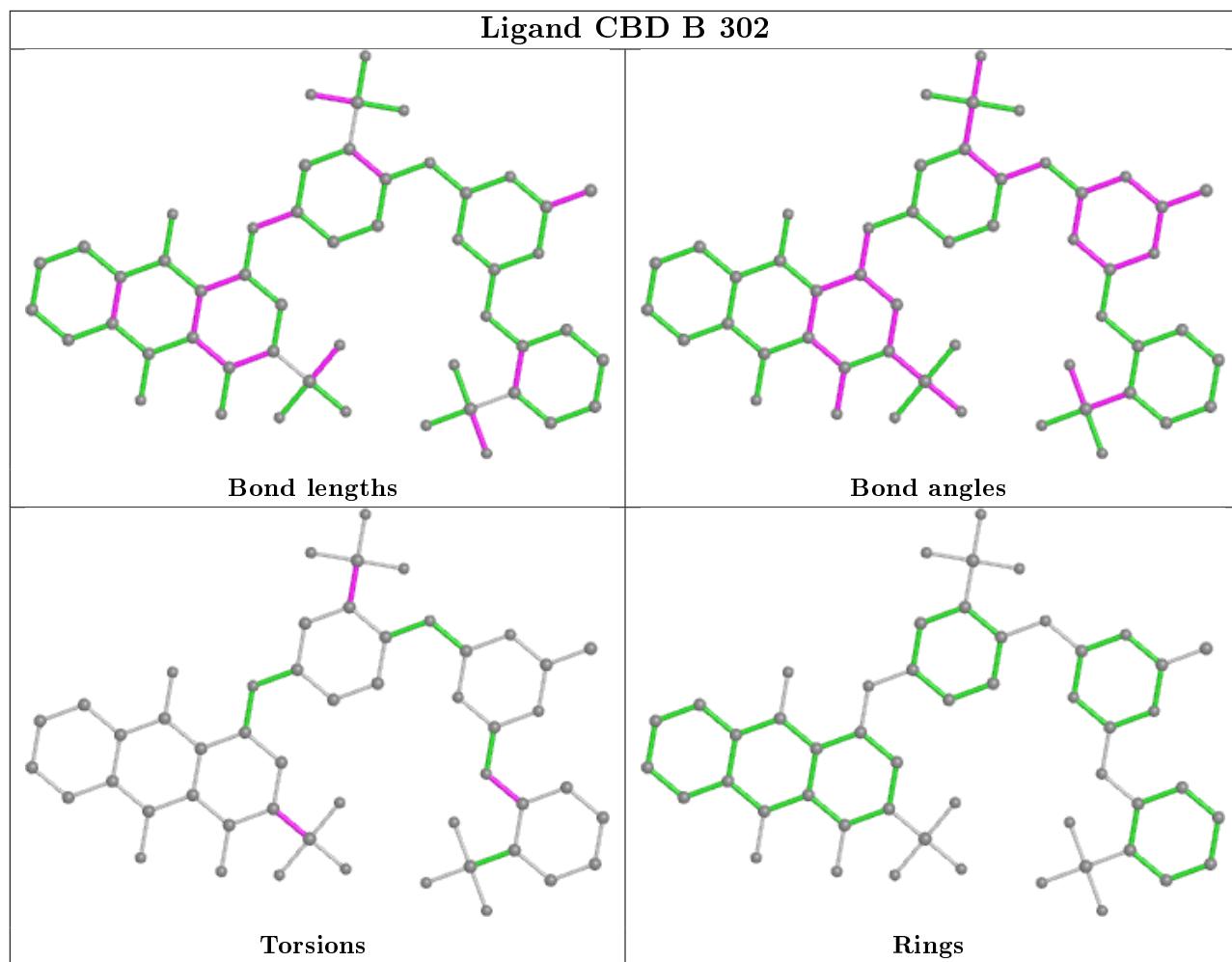
1 monomer is involved in 2 short contacts:

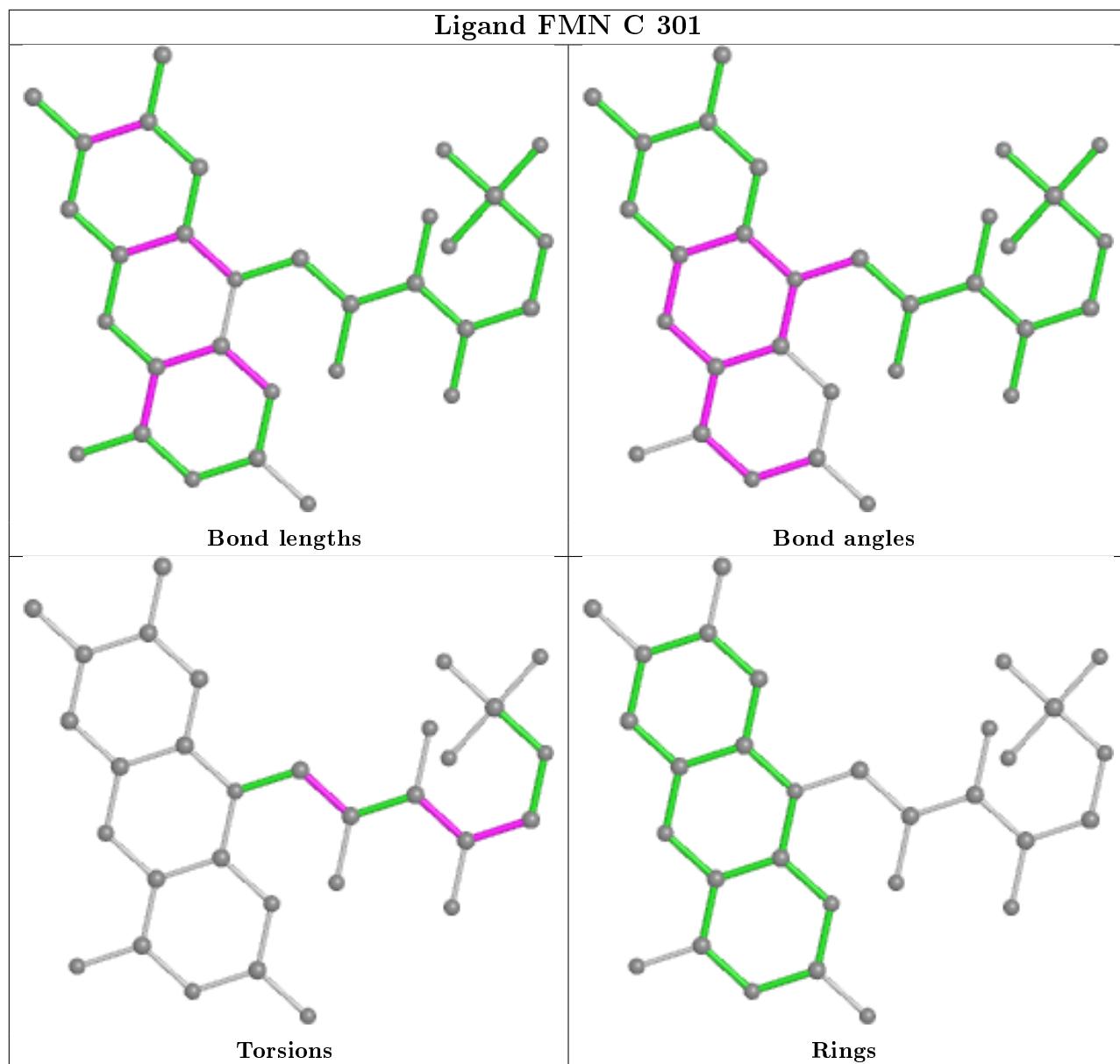
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	302	CBD	2	0

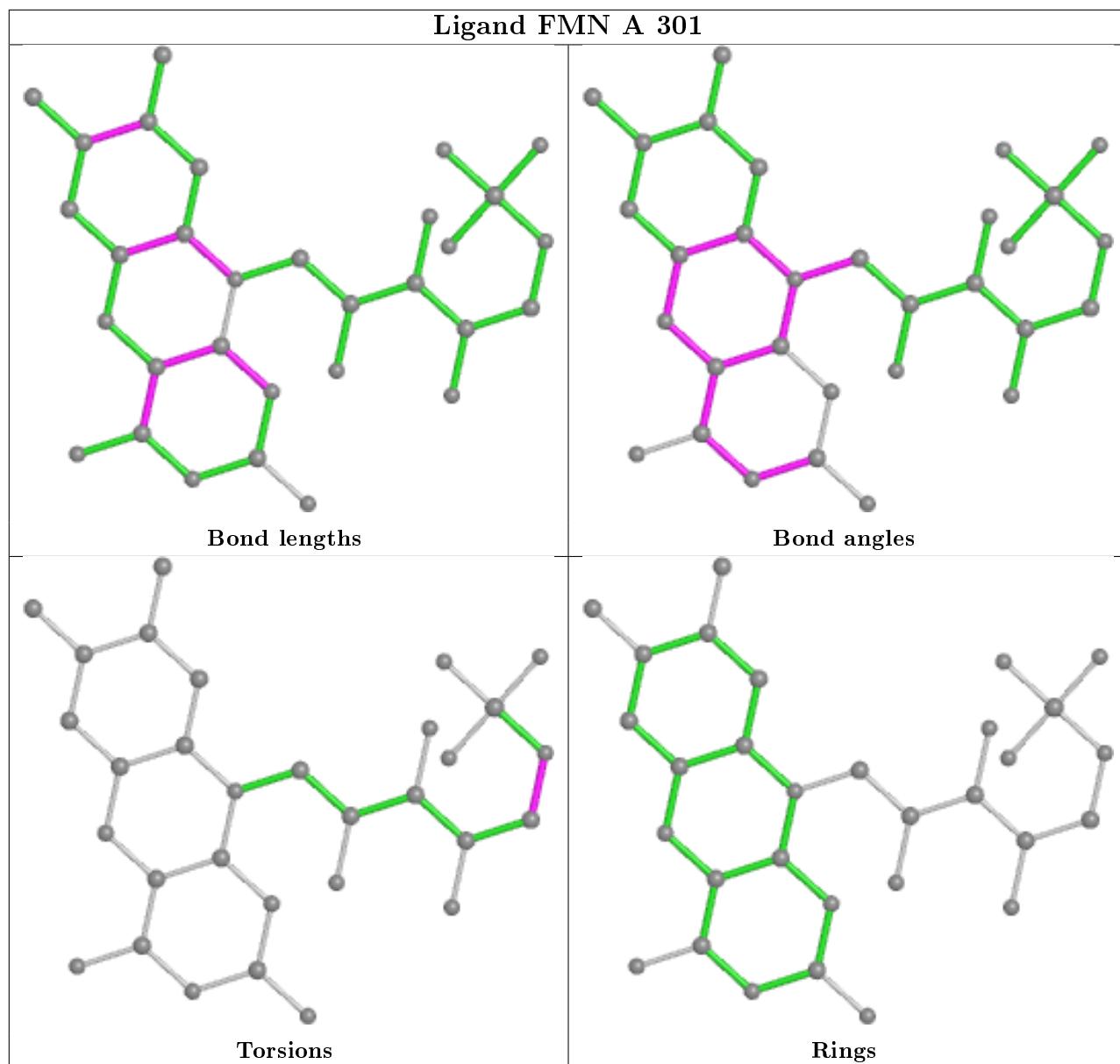
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

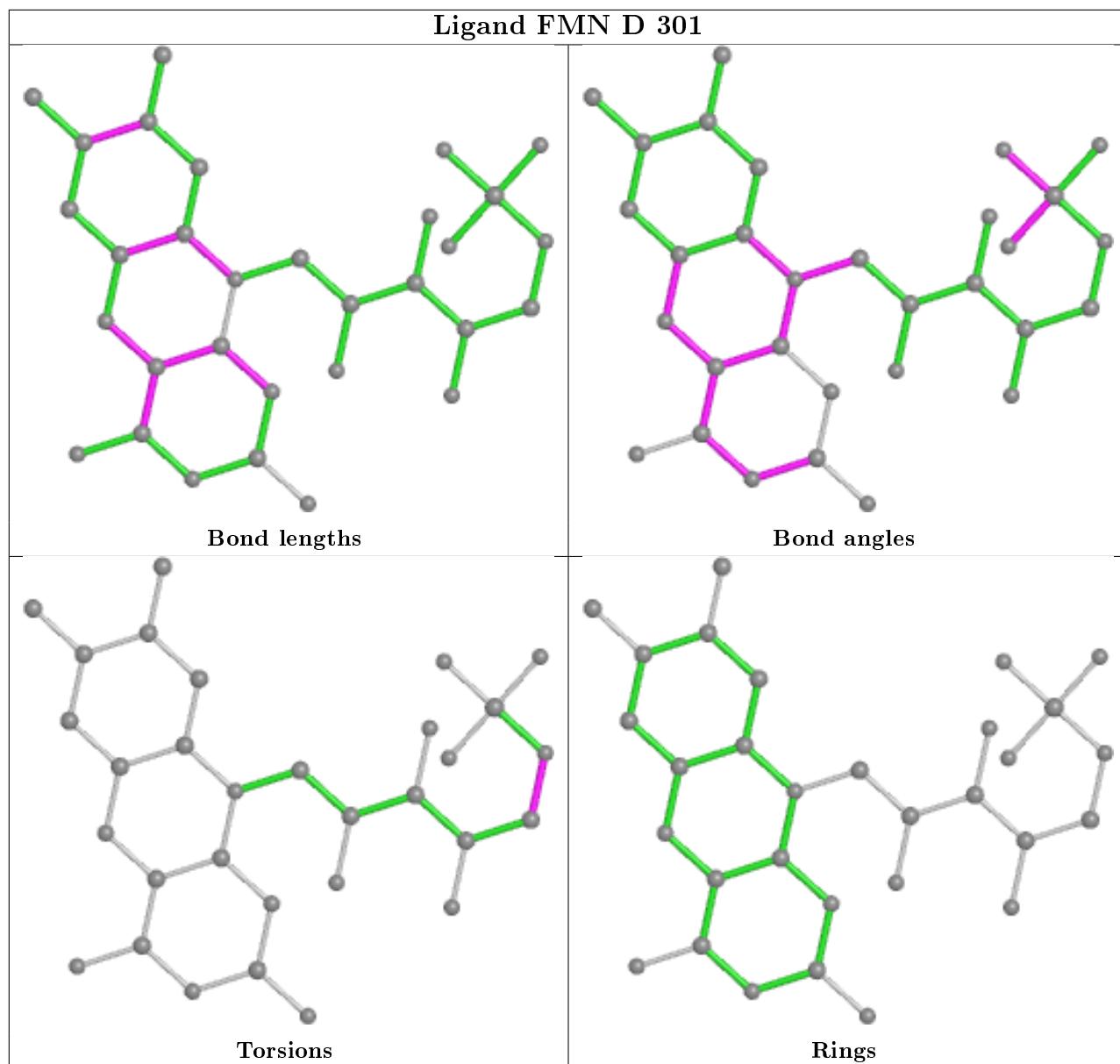


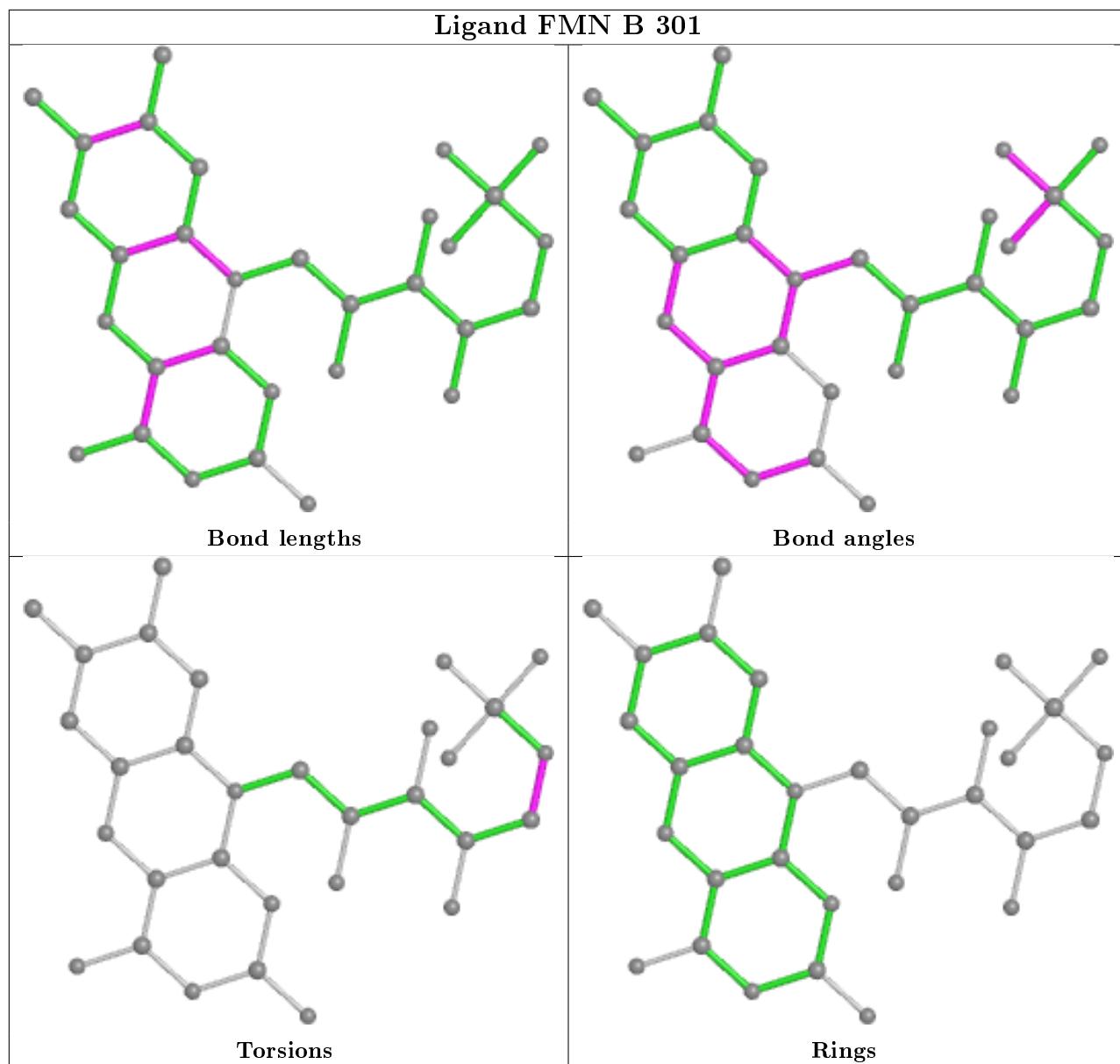


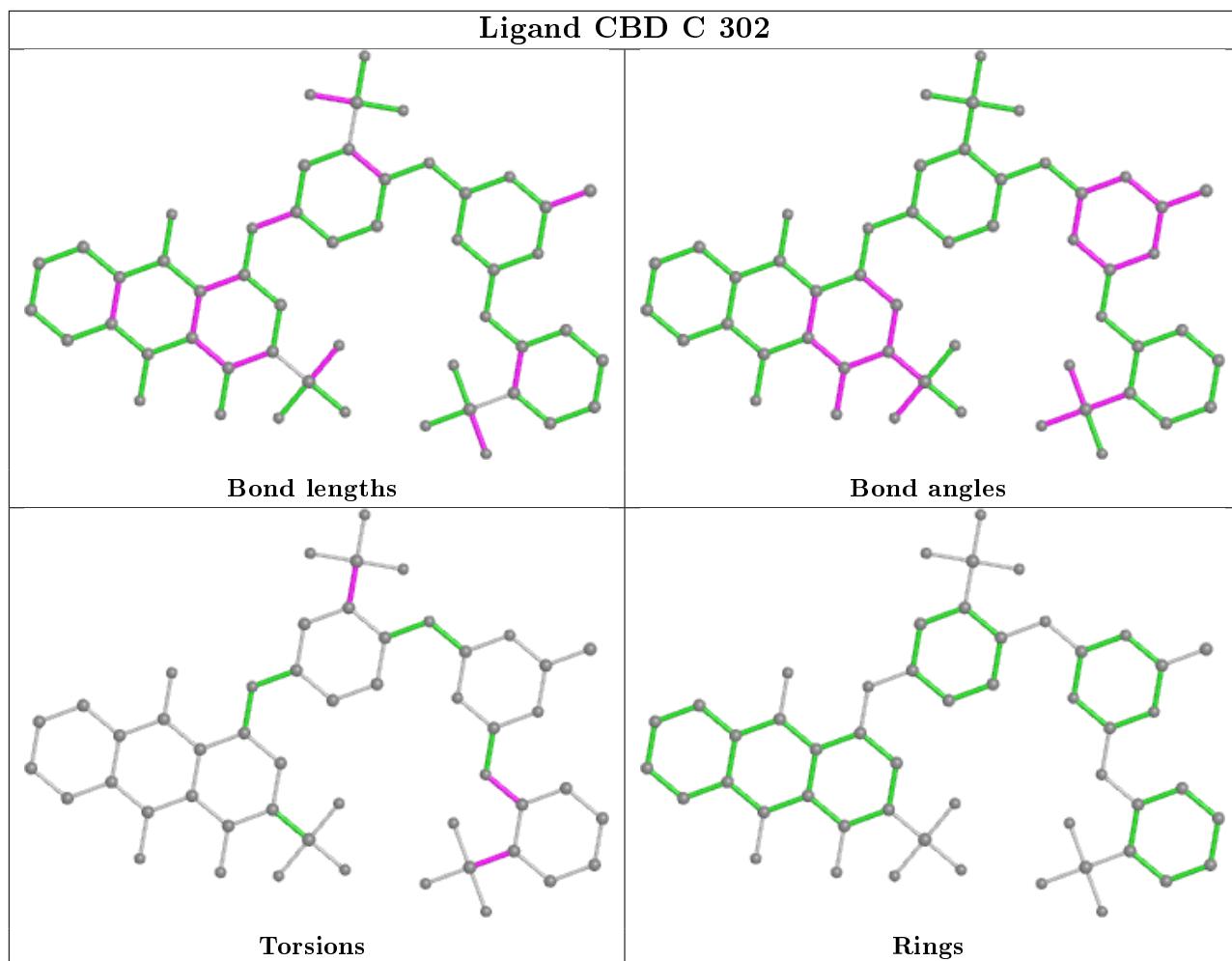












## 5.7 Other polymers [\(i\)](#)

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	A	210/211 (99%)	0.12	3 (1%) 75 71	30, 41, 59, 73	0
1	B	210/211 (99%)	0.27	8 (3%) 40 34	35, 62, 89, 107	0
1	C	210/211 (99%)	1.68	61 (29%) 0 0	70, 110, 175, 202	0
1	D	210/211 (99%)	0.43	20 (9%) 8 5	35, 54, 101, 129	0
All	All	840/844 (99%)	0.63	92 (10%) 5 3	30, 59, 135, 202	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	71	ALA	15.2
1	C	65	ALA	8.5
1	D	65	ALA	7.4
1	C	81	ALA	7.2
1	C	149	GLY	6.8
1	C	66	GLY	6.4
1	C	77	GLN	6.0
1	C	67	GLU	5.8
1	D	64	ALA	5.2
1	D	191	GLU	5.2
1	B	130	ASN	5.1
1	C	80	VAL	5.1
1	C	58	ALA	5.1
1	C	127	TYR	5.0
1	D	67	GLU	4.7
1	C	54	ALA	4.7
1	D	70	GLU	4.6
1	C	61	GLY	4.6
1	C	45	PHE	4.5
1	D	71	ALA	4.5
1	C	9	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
1	C	37	ASP	4.3
1	D	193	ALA	4.3
1	C	68	GLY	4.2
1	C	76	GLN	4.1
1	D	189	ASN	4.0
1	C	60	TRP	4.0
1	C	72	LEU	4.0
1	C	75	VAL	4.0
1	C	198	GLU	3.9
1	C	83	MET	3.8
1	C	79	LYS	3.7
1	C	121	ALA	3.7
1	B	2	THR	3.7
1	C	74	GLU	3.5
1	C	117	ASN	3.5
1	C	15	GLU	3.4
1	C	191	GLU	3.4
1	C	64	ALA	3.4
1	C	36	GLN	3.3
1	B	131	GLY	3.3
1	C	190	PRO	3.2
1	D	188	ALA	3.2
1	D	129	GLU	3.1
1	C	148	GLY	3.1
1	C	130	ASN	3.1
1	D	190	PRO	3.0
1	D	63	PHE	3.0
1	D	69	PHE	3.0
1	C	128	THR	2.9
1	C	133	VAL	2.9
1	C	69	PHE	2.9
1	C	11	PRO	2.8
1	C	57	PHE	2.8
1	C	62	LYS	2.8
1	A	129	GLU	2.7
1	A	36	GLN	2.7
1	B	189	ASN	2.6
1	D	128	THR	2.6
1	C	150	VAL	2.6
1	D	130	ASN	2.6
1	C	28	GLU	2.5
1	C	186	MET	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	80	VAL	2.5
1	C	129	GLU	2.5
1	C	48	THR	2.5
1	C	32	ASN	2.5
1	C	184	GLU	2.5
1	C	63	PHE	2.4
1	C	2	THR	2.4
1	B	36	GLN	2.4
1	C	4	VAL	2.4
1	C	55	ASP	2.3
1	D	192	LYS	2.3
1	C	199	ALA	2.3
1	B	38	GLU	2.3
1	C	201	ILE	2.3
1	C	196	ILE	2.2
1	C	73	THR	2.2
1	C	5	LEU	2.2
1	C	31	LYS	2.2
1	D	66	GLY	2.2
1	C	116	ASP	2.2
1	C	159	VAL	2.1
1	A	28	GLU	2.1
1	D	15	GLU	2.1
1	C	113	ALA	2.1
1	D	186	MET	2.1
1	B	129	GLU	2.1
1	C	187	ASN	2.0
1	B	70	GLU	2.0
1	C	41	THR	2.0

## 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 [\(i\)](#)

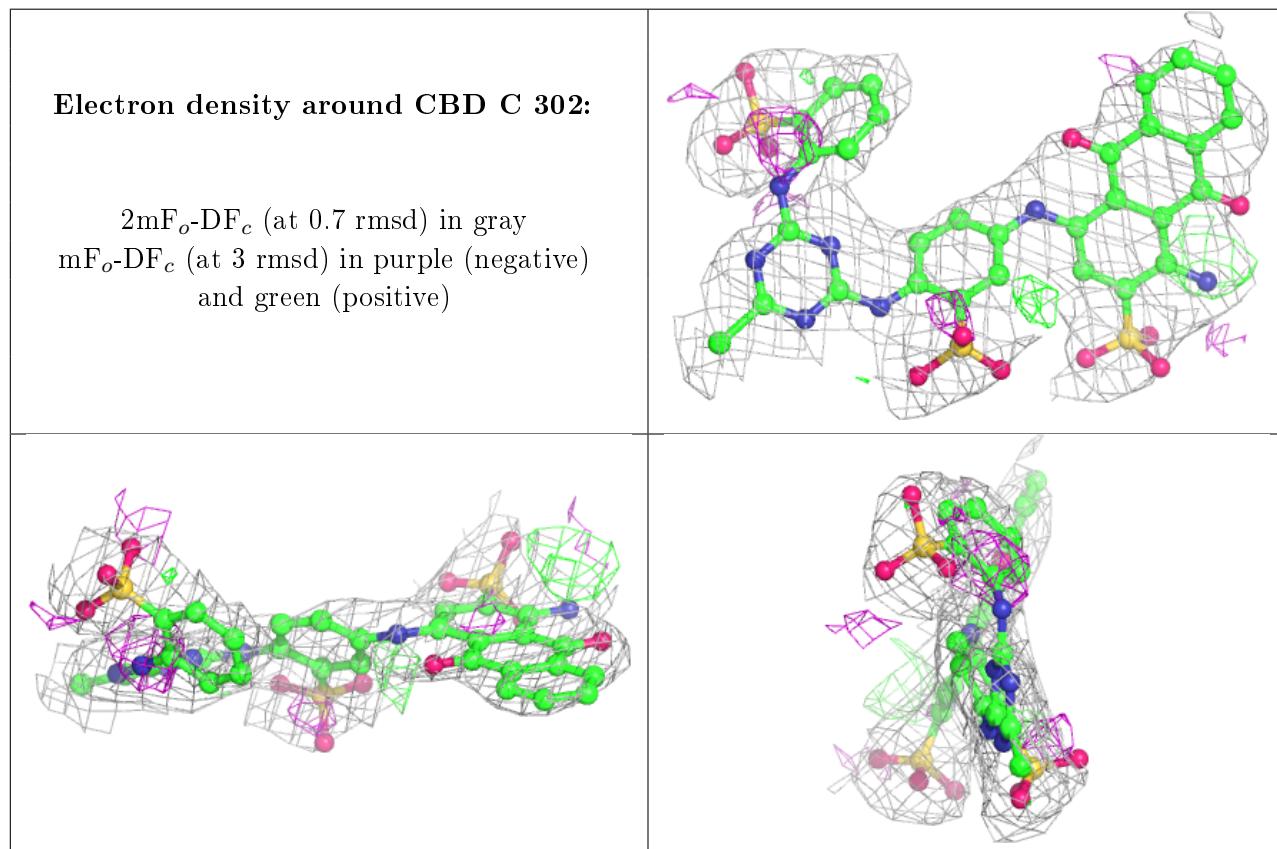
There are no carbohydrates in this entry.

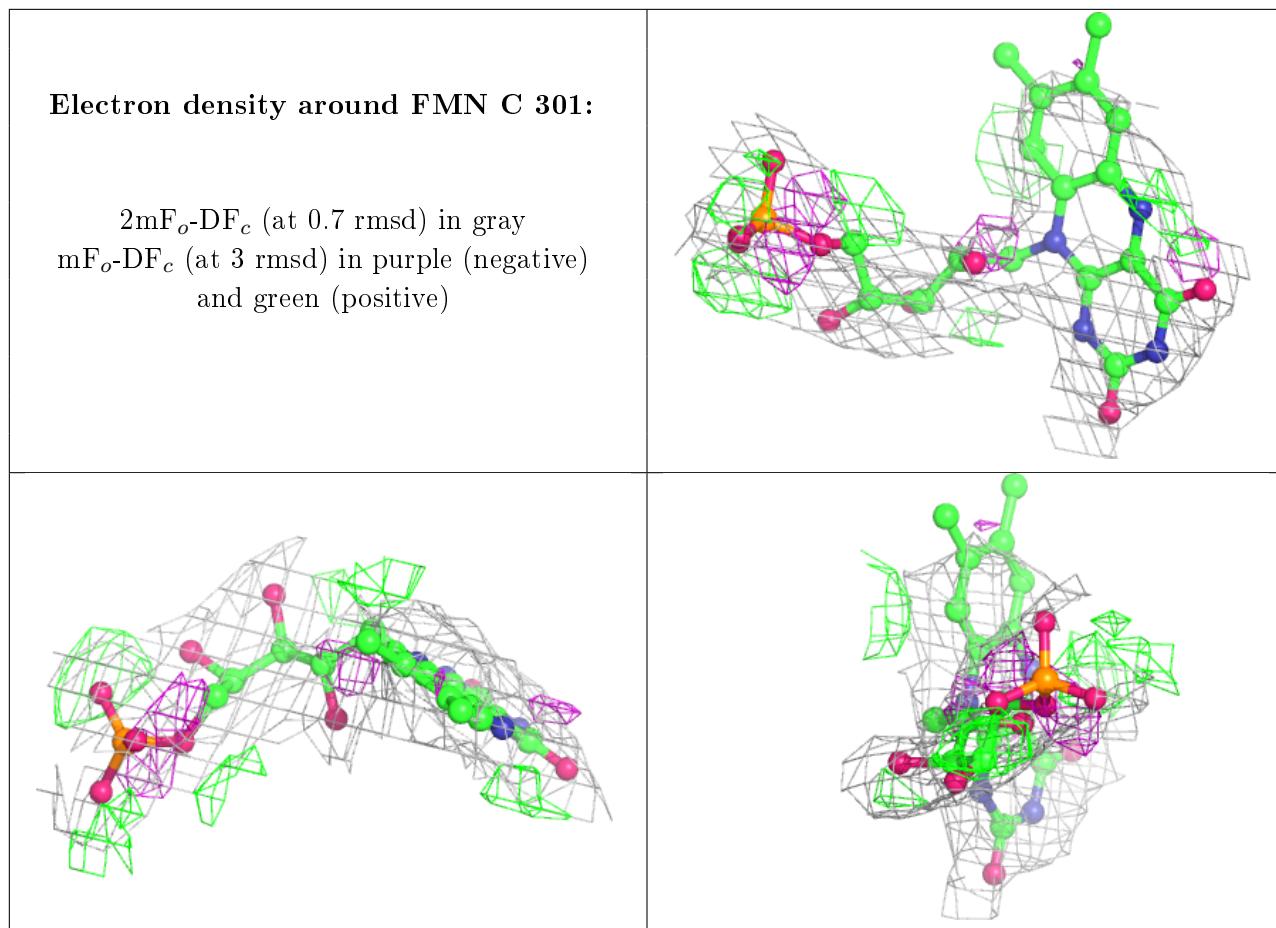
## 6.4 Ligands [\(i\)](#)

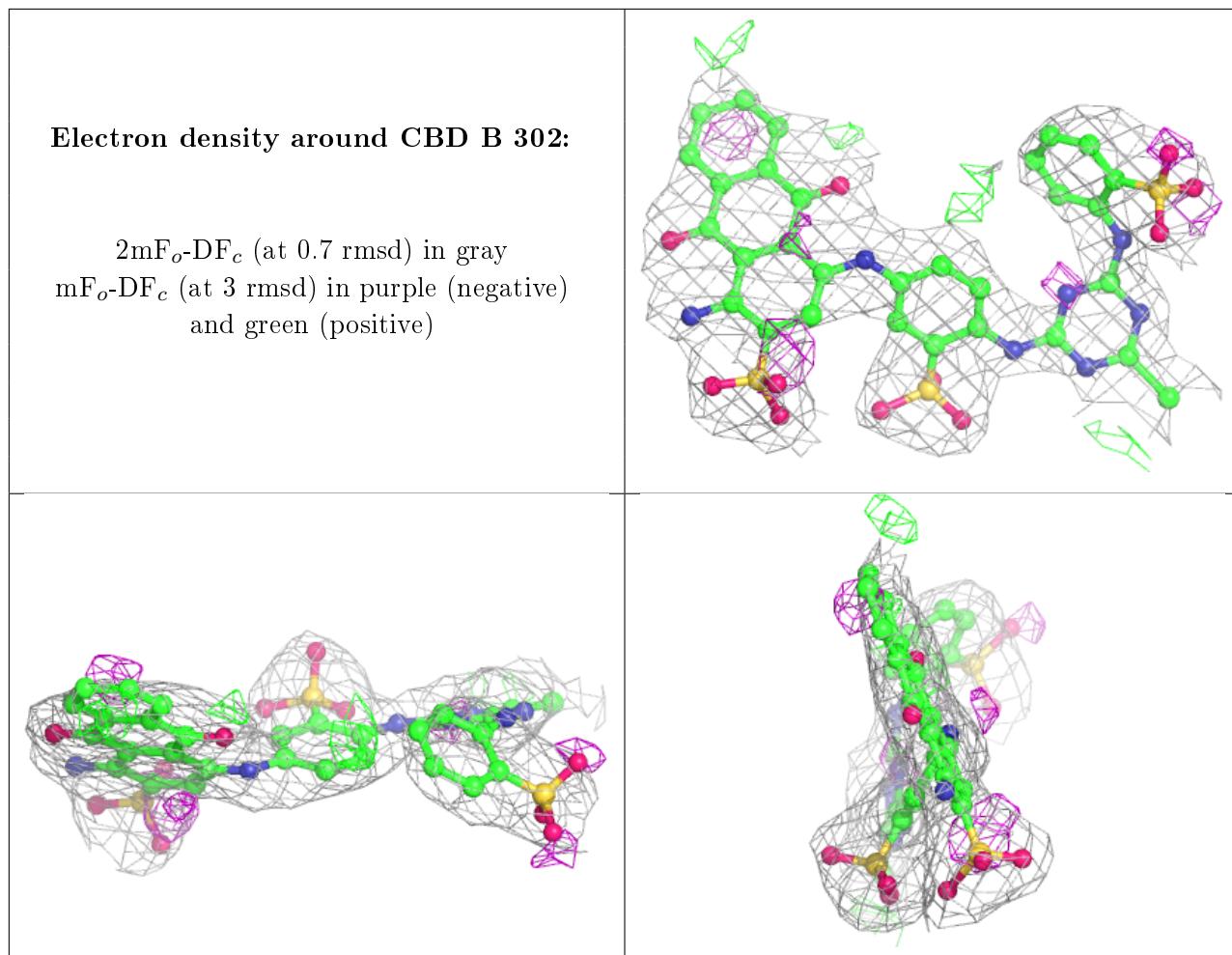
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

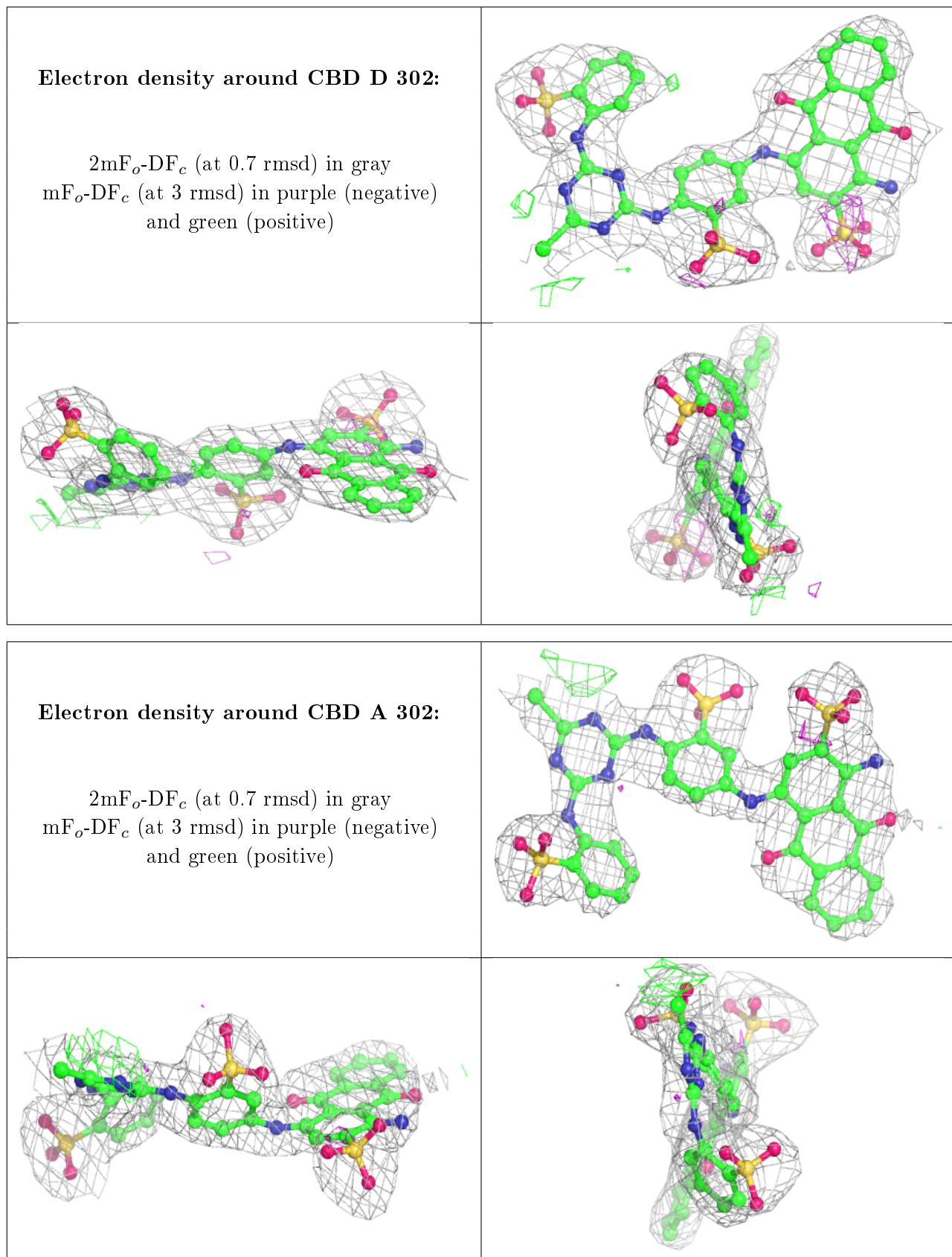
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	CBD	C	302	51/51	0.70	0.32	93,101,112,114	0
2	FMN	C	301	31/31	0.78	0.30	71,78,84,85	0
3	CBD	B	302	51/51	0.84	0.25	60,76,88,99	0
3	CBD	D	302	51/51	0.91	0.22	57,59,64,74	0
3	CBD	A	302	51/51	0.92	0.19	54,63,72,81	0
2	FMN	D	301	31/31	0.96	0.16	40,43,45,47	0
2	FMN	B	301	31/31	0.96	0.16	46,47,48,49	0
2	FMN	A	301	31/31	0.96	0.19	32,34,35,37	0

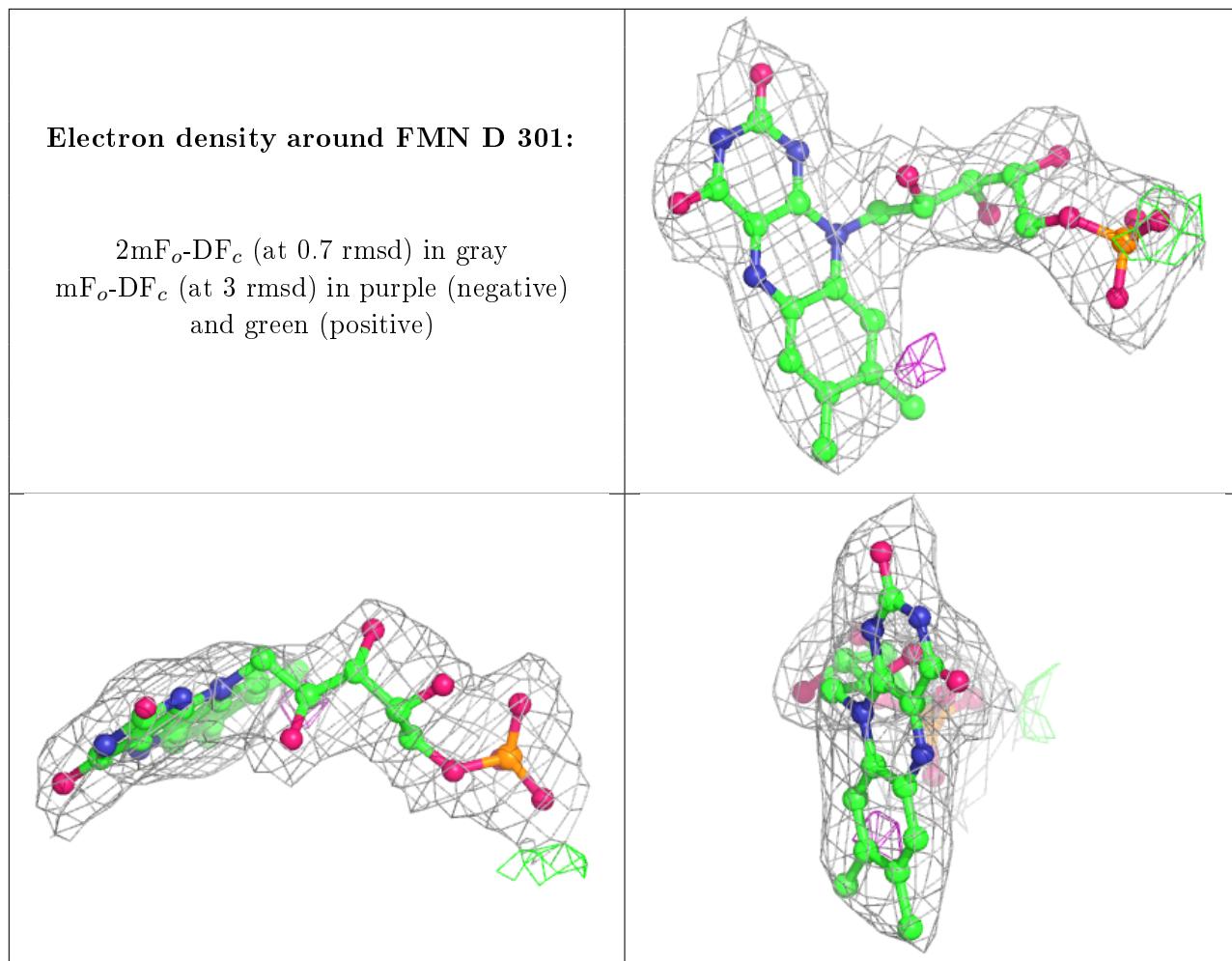
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

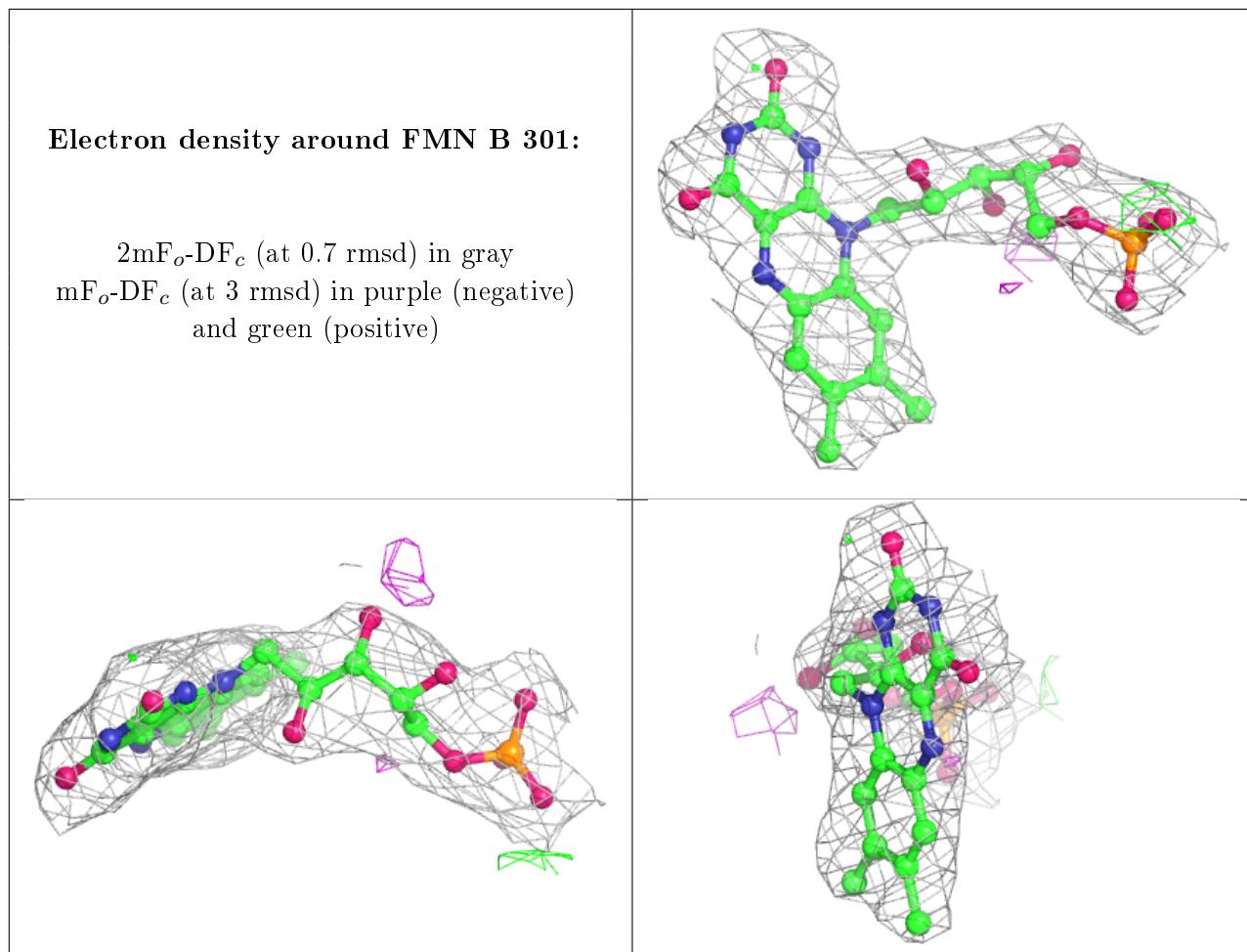


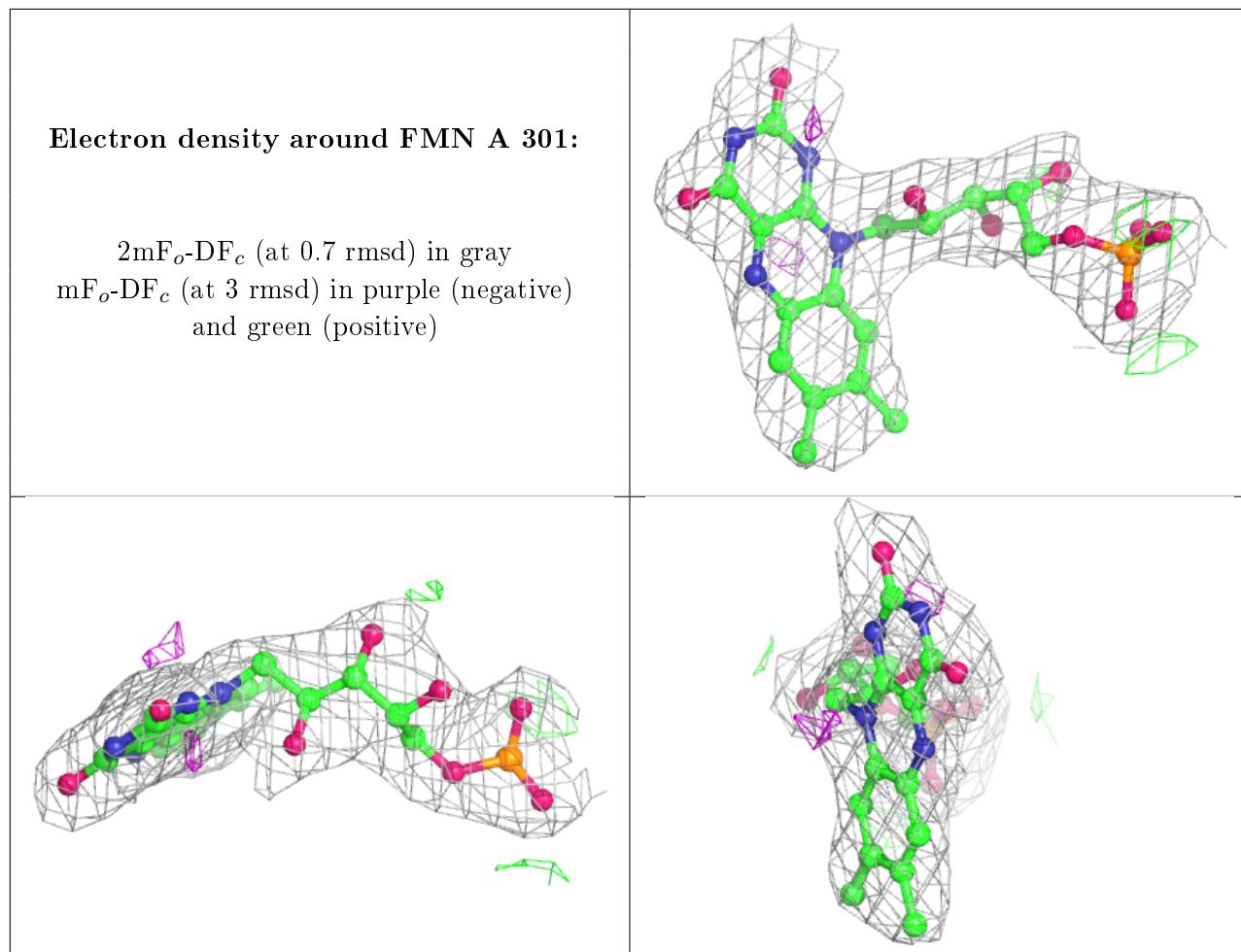












## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.