



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 3, 2020 – 11:22 am GMT

PDB ID : 6ZI4  
Title : Ultrafast Structural Response to Charge Redistribution Within a Photosynthetic Reaction Centre - 5 ps (a) structure  
Authors : Baath, P.; Dods, R.; Braenden, G.; Neutze, R.  
Deposited on : 2020-06-24  
Resolution : 2.80 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 ⓘ symbol.

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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 : 2.14.6  
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) : 2.14.6

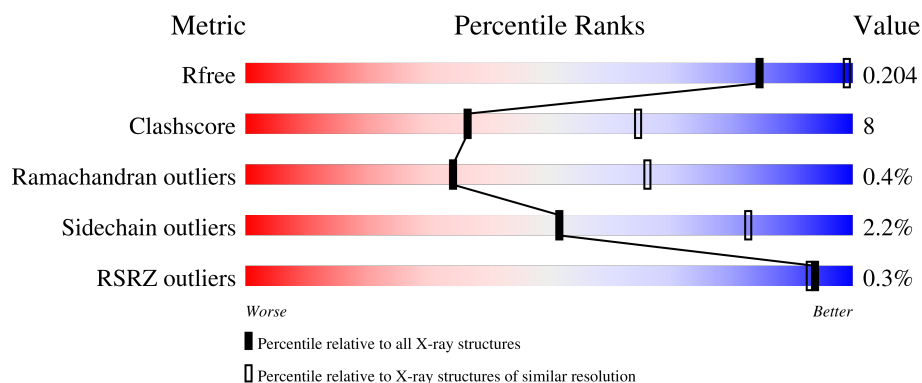
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 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.

Mol	Chain	Length	Quality of chain
1	C	336	<div> <div>83%</div> <div>15%</div> <div>..</div> </div>
2	H	258	<div> <div>%</div> <div>83%</div> <div>15%</div> <div>.</div> </div>
3	L	273	<div> <div>79%</div> <div>21%</div> </div>
4	M	323	<div> <div>88%</div> <div>11%</div> </div>

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:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	DGA	C	405	-	-	-	X
7	SO4	M	412	-	-	-	X
9	HTO	L	306	-	-	-	X

## 2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 11266 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 Photosynthetic reaction center cytochrome c subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	332	Total	C	N	O	S	0	0	0
			2602	1640	466	478	18			

- Molecule 2 is a protein called Reaction center protein H chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	258	Total	C	N	O	S	0	0	0
			2018	1292	344	380	2			

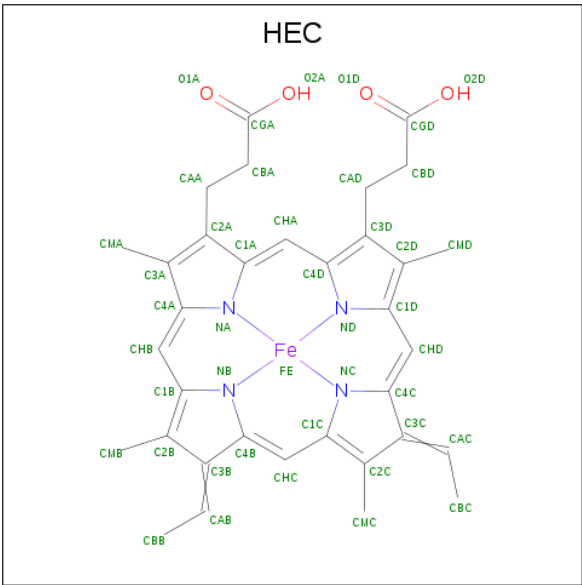
- Molecule 3 is a protein called Reaction center protein L chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	273	Total	C	N	O	S	0	41	0
			2508	1678	409	413	8			

- Molecule 4 is a protein called Reaction center protein M chain.

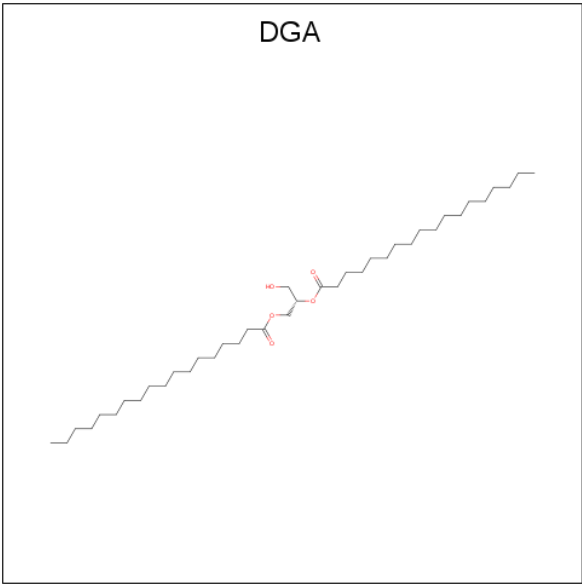
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	M	323	Total	C	N	O	S	0	51	0
			2977	1983	491	490	13			

- Molecule 5 is HEME C (three-letter code: HEC) (formula: C<sub>34</sub>H<sub>34</sub>FeN<sub>4</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 6 is DIACYL GLYCEROL (three-letter code: DGA) (formula: C<sub>39</sub>H<sub>76</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			37	33	4		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



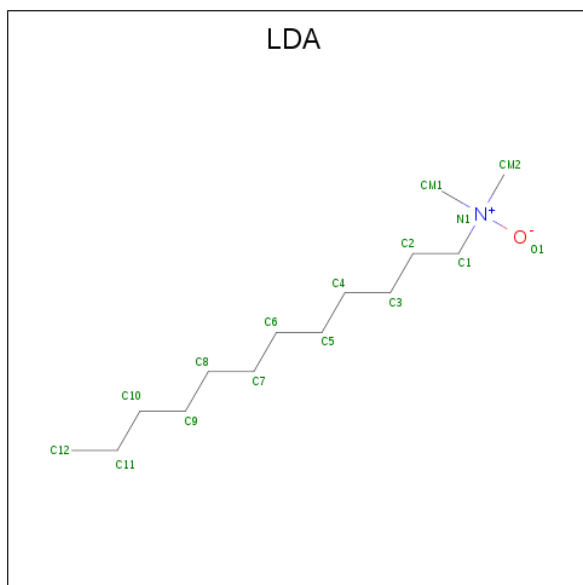
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	H	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		

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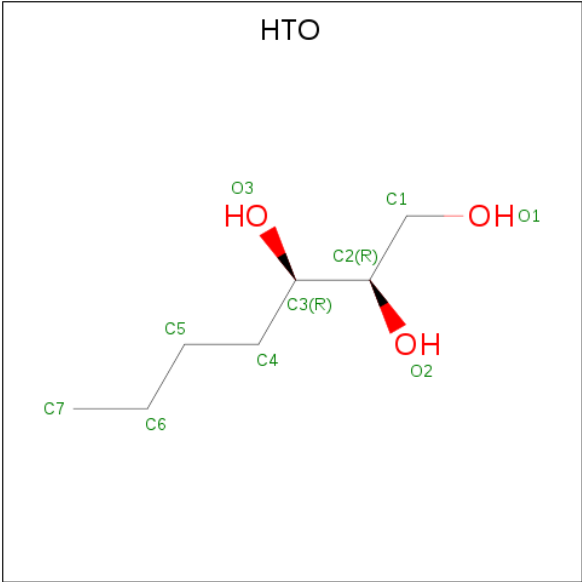
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	M	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula:  $C_{14}H_{31}NO$ ).



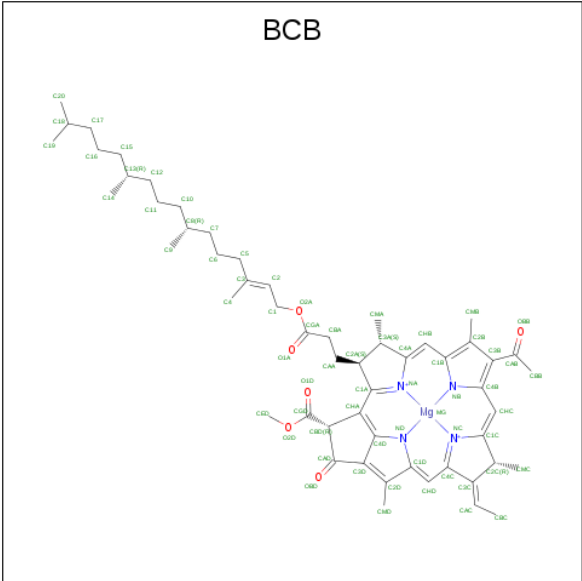
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	H	1	Total	C	N	O	0	0
			16	14	1	1		
8	H	1	Total	C	N	O	0	0
			16	14	1	1		
8	H	1	Total	C	N	O	0	0
			16	14	1	1		
8	L	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 9 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula:  $C_7H_{16}O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	H	1	Total	C	O		0	0
			10	7	3			
9	L	1	Total	C	O		0	0
			10	7	3			

- Molecule 10 is BACTERIOCHLOROPHYLL B (three-letter code: BCB) (formula: C<sub>55</sub>H<sub>72</sub>MgN<sub>4</sub>O<sub>6</sub>) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	L	1	Total	C	Mg	N	O	0	1
			132	110	2	8	12		

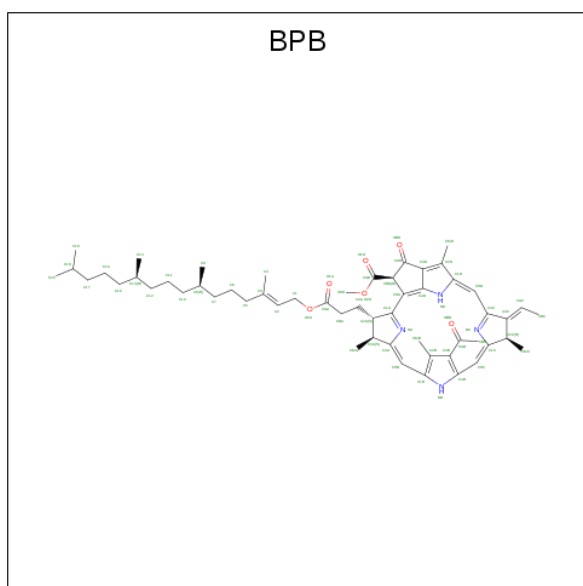
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	L	1	Total	C	Mg	N	O	0	1
			132	110	2	8	12		
10	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
10	M	1	Total	C	Mg	N	O	0	1
			132	110	2	8	12		

- Molecule 11 is BACTERIOPHEOPHYTIN B (three-letter code: BPB) (formula:  $C_{55}H_{74}N_4O_6$ ) (labeled as "Ligand of Interest" by author).

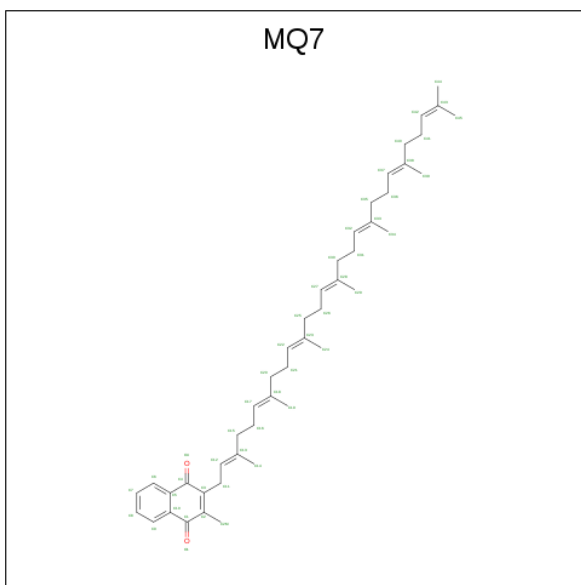


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	L	1	Total	C	N	O	0	1
			130	110	8	12		
11	M	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 12 is FE (III) ION (three-letter code: FE) (formula: Fe).

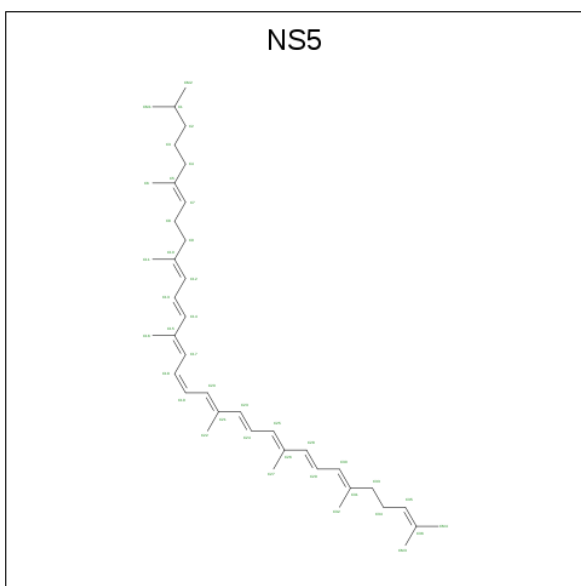
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	M	1	Total	Fe	0	1
			2	2		

- Molecule 13 is MENAQUINONE-7 (three-letter code: MQ7) (formula:  $C_{46}H_{64}O_2$ ) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	M	1	Total	C	O	0	1
			96	92	4		

- Molecule 14 is 15-cis-1,2-dihydroneurosporene (three-letter code: NS5) (formula: C<sub>40</sub>H<sub>60</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	M	1	Total	C	0	0
			40	40		

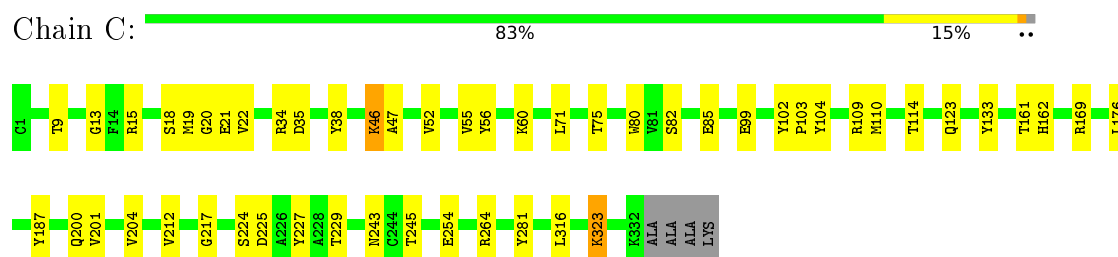
- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	C	3	Total 3	O 3	0	0
15	H	2	Total 2	O 2	0	0
15	L	4	Total 4	O 4	0	0
15	M	4	Total 4	O 4	0	0

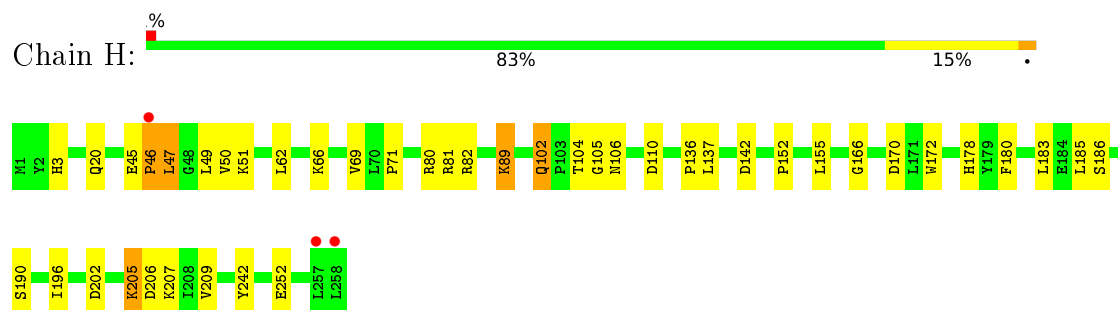
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

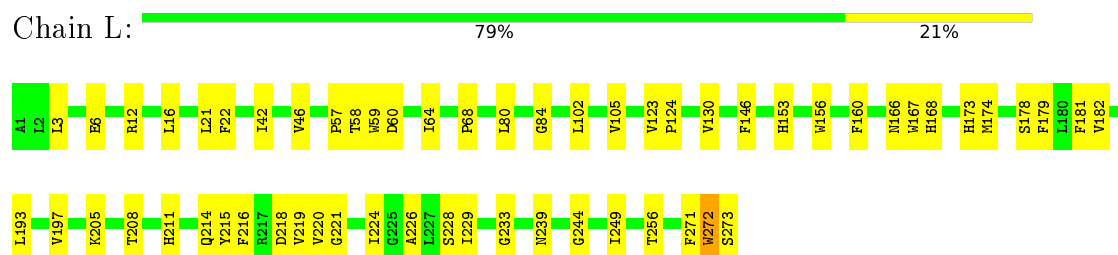
- Molecule 1: Photosynthetic reaction center cytochrome c subunit



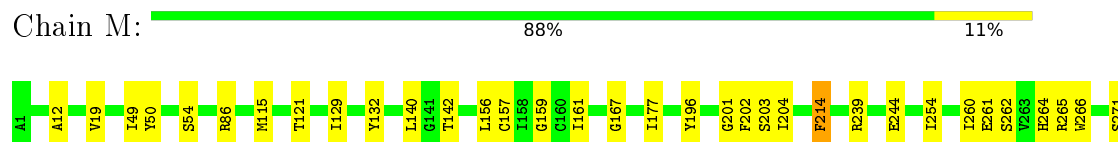
- Molecule 2: Reaction center protein H chain

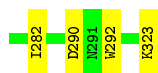


- Molecule 3: Reaction center protein L chain



- Molecule 4: Reaction center protein M chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	226.40 Å   226.40 Å   113.70 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	36.88 – 2.80 36.88 – 2.46	Depositor EDS
% Data completeness (in resolution range)	100.0 (36.88-2.80) 86.3 (36.88-2.46)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.04 (at 2.45 Å)	Xtriage
Refinement program	REFMAC 5.8.0158, PHENIX 1.17.1_3660	Depositor
R, $R_{free}$	0.176   ,   0.201 0.180   ,   0.204	Depositor DCC
$R_{free}$ test set	4542 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	75.4	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 63.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11266	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.74% 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: LDA, DGA, HTO, BCB, BPB, FE, MQ7, HEC, FME, NS5, SO4

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	C	0.44	0/2669	0.61	0/3637
2	H	0.41	0/2055	0.60	0/2807
3	L	0.43	0/2612	0.60	0/3568
4	M	0.47	0/3101	0.56	0/4242
All	All	0.44	0/10437	0.59	0/14254

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	C	2602	0	2578	57	0
2	H	2018	0	2020	40	0
3	L	2508	0	2390	51	0
4	M	2977	0	2832	29	0
5	C	172	0	120	8	0
6	C	37	0	58	0	0
7	C	5	0	0	0	0
7	H	20	0	0	0	0
7	M	35	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	48	0	93	2	0
8	L	16	0	31	1	0
9	H	10	0	16	0	0
9	L	10	0	16	0	0
10	L	330	0	360	14	0
10	M	132	0	144	5	0
11	L	130	0	148	8	0
11	M	65	0	74	5	0
12	M	2	0	0	0	0
13	M	96	0	128	2	0
14	M	40	0	60	3	0
15	C	3	0	0	0	0
15	H	2	0	0	0	0
15	L	4	0	0	0	0
15	M	4	0	0	0	0
All	All	11266	0	11068	176	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 8.

All (176) 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)
2:H:89:LYS:HE2	2:H:110:ASP:CB	1.96	0.95
1:C:13:GLY:HA3	1:C:19:MET:CE	2.05	0.87
2:H:89:LYS:HE2	2:H:110:ASP:HB2	1.55	0.86
1:C:13:GLY:CA	1:C:19:MET:HE2	2.07	0.85
1:C:13:GLY:HA3	1:C:19:MET:HE2	1.60	0.82
1:C:13:GLY:CA	1:C:19:MET:CE	2.59	0.80
2:H:152:PRO:HA	2:H:155:LEU:HD13	1.60	0.80
11:M:404:BPB:HBBB	11:M:404:BPB:HHC	1.66	0.78
4:M:54:SER:HB3	4:M:129:ILE:HD11	1.64	0.77
1:C:20:GLY:N	1:C:245:THR:HG21	1.99	0.77
1:C:200:GLN:HE21	1:C:201:VAL:H	1.31	0.77
2:H:205:LYS:HD3	2:H:205:LYS:H	1.48	0.76
1:C:52:VAL:HA	1:C:55:VAL:HG12	1.68	0.75
3:L:233:GLY:HA3	4:M:214[A]:PHE:CZ	2.23	0.74
3:L:208:THR:HG22	3:L:211:HIS:ND1	2.04	0.72
1:C:110:MET:O	1:C:114:THR:HG23	1.88	0.72
1:C:243:ASN:OD1	1:C:245:THR:HB	1.89	0.72
1:C:200:GLN:HE21	1:C:201:VAL:N	1.88	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:233:GLY:HA3	4:M:214[A]:PHE:CE1	2.27	0.69
1:C:20:GLY:H	1:C:245:THR:HG21	1.55	0.69
1:C:204:VAL:HG11	1:C:254:GLU:HB3	1.76	0.68
1:C:204:VAL:CG1	1:C:254:GLU:HB3	2.24	0.68
1:C:169:ARG:HG3	1:C:169:ARG:HH11	1.58	0.67
1:C:46:LYS:HD3	1:C:47:ALA:H	1.59	0.66
1:C:46:LYS:HA	1:C:46:LYS:HE2	1.77	0.65
1:C:13:GLY:N	1:C:19:MET:HE2	2.10	0.65
2:H:89:LYS:HE2	2:H:110:ASP:HB3	1.77	0.63
3:L:42:ILE:O	3:L:46:VAL:HG12	1.98	0.63
2:H:252:GLU:N	2:H:252:GLU:OE2	2.27	0.63
1:C:13:GLY:CA	1:C:19:MET:HE1	2.29	0.63
8:H:701:LDA:HM11	8:L:305:LDA:HM21	1.81	0.62
2:H:47:LEU:C	2:H:47:LEU:HD13	2.21	0.60
1:C:201:VAL:O	1:C:229:THR:HG21	2.01	0.60
2:H:205:LYS:H	2:H:205:LYS:CD	2.14	0.60
1:C:18:SER:HB2	3:L:156[B]:TRP:CD1	2.37	0.60
2:H:45:GLU:HG3	2:H:46:PRO:HD2	1.85	0.58
3:L:166[B]:ASN:OD1	3:L:168[B]:HIS:HB2	2.04	0.58
1:C:52:VAL:HA	1:C:55:VAL:CG1	2.34	0.58
4:M:54:SER:HB3	4:M:129:ILE:CD1	2.33	0.58
1:C:19:MET:HB3	1:C:245:THR:HG23	1.86	0.57
3:L:197:VAL:HA	4:M:140:LEU:HD22	1.85	0.57
1:C:161:THR:HG21	3:L:273:SER:O	2.05	0.56
3:L:60:ASP:O	3:L:64:ILE:HD12	2.06	0.56
3:L:224:ILE:HG12	3:L:228:SER:HB2	1.86	0.56
3:L:181:PHE:HB3	11:M:404:BPB:HBBA	1.87	0.56
1:C:34:ARG:HD2	1:C:35:ASP:OD1	2.06	0.54
1:C:323:LYS:HD3	1:C:323:LYS:H	1.72	0.54
1:C:82:SER:HB2	1:C:85:GLU:HB2	1.89	0.54
1:C:80:TRP:CD1	1:C:133:TYR:HB2	2.43	0.54
1:C:109:ARG:HH11	1:C:281:TYR:HA	1.73	0.54
1:C:169:ARG:HG3	1:C:169:ARG:NH1	2.21	0.54
11:L:303[A]:BPB:HBBB	11:L:303[A]:BPB:HMB	1.90	0.53
2:H:136:PRO:HA	2:H:172:TRP:HA	1.89	0.53
4:M:196[B]:TYR:O	4:M:292:TRP:HB3	2.08	0.53
1:C:114:THR:HG21	5:C:402:HEC:HHC	1.90	0.53
1:C:225:ASP:O	1:C:229:THR:HG23	2.08	0.52
5:C:402:HEC:HMB1	5:C:402:HEC:HBB3	1.90	0.52
3:L:215:TYR:O	3:L:219:VAL:HG12	2.10	0.52
1:C:102:TYR:CG	1:C:103:PRO:HD3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:168[B]:HIS:CE1	10:L:301[B]:BCB:HMC2	2.45	0.51
3:L:16:LEU:HD11	3:L:105:VAL:CG2	2.40	0.51
10:L:304:BCB:HHC	10:L:304:BCB:HBB2	1.92	0.51
2:H:202:ASP:HB3	2:H:209:VAL:HB	1.92	0.51
2:H:196:ILE:HD12	2:H:242:TYR:CZ	2.45	0.51
3:L:181:PHE:HB3	11:M:404:BPB:CBB	2.40	0.51
3:L:80:LEU:HA	3:L:84:GLY:HA3	1.93	0.51
5:C:403:HEC:HBC1	5:C:404:HEC:HMA1	1.93	0.51
2:H:142:ASP:N	2:H:142:ASP:OD1	2.36	0.51
4:M:159:GLY:HA3	14:M:405:NS5:H272	1.91	0.51
3:L:226:ALA:O	3:L:229:ILE:HG22	2.11	0.51
4:M:260[B]:ILE:O	4:M:264[B]:HIS:ND1	2.36	0.50
1:C:99:GLU:HG2	1:C:104:TYR:CE1	2.45	0.50
4:M:157:CYS:HA	4:M:161:ILE:HB	1.92	0.50
4:M:204[B]:ILE:HG12	10:M:403[B]:BCB:HMB3	1.92	0.50
1:C:20:GLY:N	1:C:245:THR:CG2	2.72	0.50
4:M:121:THR:HG23	4:M:156:LEU:HD21	1.94	0.50
3:L:214:GLN:HG2	4:M:19:VAL:HB	1.94	0.49
5:C:402:HEC:O1D	5:C:402:HEC:HHA	2.13	0.49
2:H:89:LYS:HB2	2:H:104:THR:OG1	2.12	0.49
1:C:114:THR:HG22	5:C:402:HEC:HMC2	1.94	0.49
10:L:301[B]:BCB:H2C	10:M:403[B]:BCB:H2C	1.95	0.49
10:L:304:BCB:HBB3	10:M:403[A]:BCB:H62	1.95	0.49
3:L:178[A]:SER:O	3:L:182:VAL:HG12	2.13	0.48
1:C:13:GLY:HA2	1:C:19:MET:HE1	1.95	0.48
1:C:46:LYS:HD3	1:C:47:ALA:N	2.25	0.48
1:C:13:GLY:HA3	1:C:19:MET:HE1	1.90	0.48
2:H:166:GLY:HA3	2:H:186:SER:O	2.14	0.48
2:H:45:GLU:HG3	2:H:46:PRO:CD	2.43	0.48
3:L:174[B]:MET:HA	10:L:304:BCB:OBD	2.14	0.48
2:H:66:LYS:NZ	4:M:261[B]:GLU:OE2	2.47	0.48
10:L:301[B]:BCB:H143	11:L:303[B]:BPB:H5A	1.96	0.48
1:C:18:SER:HB2	3:L:156[A]:TRP:CD1	2.49	0.47
10:L:301[A]:BCB:H202	13:M:402[A]:MQ7:H261	1.96	0.47
3:L:179:PHE:CD2	3:L:239[B]:ASN:HB3	2.49	0.47
3:L:233:GLY:CA	4:M:214[A]:PHE:CZ	2.96	0.47
3:L:181:PHE:CD2	11:M:404:BPB:HBB	2.50	0.47
2:H:155:LEU:HD23	2:H:206:ASP:C	2.35	0.47
1:C:102:TYR:CD2	1:C:103:PRO:HD3	2.50	0.47
2:H:69:VAL:CG2	3:L:205:LYS:HA	2.45	0.47
4:M:132:TYR:CE2	4:M:142:THR:HG21	2.51	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:M:403[B]:BCB:HAA1	10:M:403[B]:BCB:HBD	1.97	0.46
10:L:302[B]:BCB:OBD	4:M:201[B]:GLY:HA2	2.15	0.46
10:L:302[A]:BCB:HMB1	10:L:302[A]:BCB:HBB2	1.97	0.46
2:H:62:LEU:O	8:H:707:LDA:HM21	2.16	0.46
2:H:80:ARG:NH2	2:H:82:ARG:HD2	2.31	0.46
11:L:303[A]:BPB:HEDB	4:M:254:ILE:HG21	1.96	0.46
2:H:49:LEU:O	2:H:51:LYS:N	2.50	0.45
1:C:109:ARG:NH1	1:C:281:TYR:HA	2.32	0.45
2:H:47:LEU:CD1	2:H:49:LEU:HB3	2.46	0.45
2:H:196:ILE:HD12	2:H:242:TYR:CE1	2.50	0.45
4:M:265[B]:ARG:NH1	7:M:408:SO4:O1	2.45	0.45
3:L:244[A]:GLY:O	10:L:301[A]:BCB:HED3	2.16	0.45
2:H:137:LEU:HB2	2:H:170:ASP:OD1	2.16	0.45
4:M:239:ARG:HD3	4:M:244[B]:GLU:HG2	1.99	0.45
2:H:80:ARG:CZ	2:H:82:ARG:HD2	2.47	0.44
2:H:89:LYS:CD	2:H:105:GLY:H	2.31	0.44
4:M:262[B]:SER:O	4:M:266[B]:TRP:HD1	2.00	0.44
1:C:71:LEU:O	1:C:75:THR:HG23	2.17	0.44
3:L:3:LEU:HB2	3:L:6:GLU:HB2	1.99	0.44
3:L:146:PHE:HB3	3:L:156[A]:TRP:CD2	2.53	0.44
3:L:153[B]:HIS:HD2	10:L:302[B]:BCB:HMC3	1.82	0.44
1:C:22:VAL:HG22	3:L:256:THR:HG22	2.00	0.44
3:L:146:PHE:HB3	3:L:156[B]:TRP:CE3	2.53	0.44
2:H:89:LYS:HZ3	2:H:106:ASN:C	2.21	0.44
2:H:81:ARG:HD2	2:H:81:ARG:H	1.83	0.44
14:M:405:NS5:H161	14:M:405:NS5:H18	1.82	0.44
3:L:244[B]:GLY:O	10:L:301[B]:BCB:HED3	2.17	0.43
11:L:303[B]:BPB:HHC	11:L:303[B]:BPB:OBB	2.18	0.43
1:C:35:ASP:OD2	1:C:316:LEU:HA	2.19	0.43
11:L:303[A]:BPB:HHC	11:L:303[A]:BPB:OBB	2.18	0.43
3:L:130:VAL:HG13	3:L:249:ILE:HG12	2.01	0.43
1:C:176:LEU:HD11	1:C:187:TYR:O	2.19	0.43
4:M:254:ILE:HD11	13:M:402[A]:MQ7:H142	2.01	0.43
2:H:20:GLN:HG2	4:M:202[A]:PHE:CE2	2.53	0.43
14:M:405:NS5:H29	14:M:405:NS5:H271	1.86	0.43
3:L:221:GLY:N	4:M:49:ILE:HD13	2.34	0.43
1:C:19:MET:HA	1:C:245:THR:HG21	2.00	0.42
1:C:204:VAL:HG13	1:C:254:GLU:HB3	2.01	0.42
2:H:89:LYS:HD2	2:H:105:GLY:H	1.84	0.42
4:M:239:ARG:HD3	4:M:244[A]:GLU:HG2	1.99	0.42
1:C:161:THR:OG1	1:C:162:HIS:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:16:LEU:HD11	3:L:105:VAL:HG23	2.01	0.42
1:C:15:ARG:HD2	3:L:68:PRO:O	2.19	0.42
3:L:102:LEU:O	3:L:105:VAL:HG22	2.20	0.42
10:L:301[B]:BCB:H162	10:L:301[B]:BCB:H192	1.75	0.42
5:C:404:HEC:HAD2	5:C:404:HEC:HMD1	1.93	0.42
4:M:282:ILE:HD11	10:M:403[B]:BCB:OBD	2.20	0.42
2:H:183:LEU:HB2	2:H:196:ILE:CG2	2.50	0.42
3:L:124:PRO:HD3	11:L:303[A]:BPB:HAC	2.01	0.42
1:C:56:TYR:HB3	5:C:401:HEC:O2A	2.20	0.42
2:H:47:LEU:CD1	2:H:47:LEU:C	2.86	0.42
1:C:9:THR:HA	1:C:21:GLU:O	2.19	0.41
3:L:174[A]:MET:HE3	10:L:304:BCB:O1D	2.20	0.41
1:C:264:ARG:HG2	5:C:403:HEC:HMD3	2.01	0.41
1:C:217:GLY:HA2	4:M:167:GLY:O	2.20	0.41
1:C:323:LYS:H	1:C:323:LYS:CD	2.32	0.41
1:C:224:SER:HA	1:C:227:TYR:HD1	1.85	0.41
3:L:21:LEU:HD12	3:L:22:PHE:CE2	2.55	0.41
2:H:180:PHE:CE2	4:M:12:ALA:HB2	2.56	0.41
2:H:89:LYS:HZ2	2:H:105:GLY:C	2.23	0.41
1:C:18:SER:HB2	3:L:156[B]:TRP:NE1	2.35	0.41
3:L:193:LEU:HD22	3:L:216:PHE:HE2	1.84	0.41
11:L:303[B]:BPB:H11A	11:L:303[B]:BPB:H7A	1.89	0.41
3:L:58:THR:OG1	3:L:59:TRP:N	2.54	0.41
2:H:45:GLU:O	2:H:47:LEU:N	2.54	0.41
3:L:123:VAL:HG22	3:L:124:PRO:HD3	2.02	0.41
2:H:155:LEU:HD23	2:H:207:LYS:N	2.36	0.41
3:L:218:ASP:O	4:M:50:TYR:HB3	2.20	0.41
2:H:47:LEU:HD12	2:H:49:LEU:HB3	2.02	0.41
2:H:102:GLN:HE21	3:L:12:ARG:HD3	1.86	0.40
3:L:220:VAL:HG11	11:M:404:BPB:HEDA	2.04	0.40
1:C:212:VAL:HG22	2:H:3:HIS:CD2	2.56	0.40
3:L:146:PHE:HB3	3:L:156[B]:TRP:CD2	2.55	0.40
3:L:272:TRP:CE2	4:M:86:ARG:HG3	2.56	0.40
3:L:167[A]:TRP:HE1	3:L:173[A]:HIS:CD2	2.40	0.40
3:L:42:ILE:HG12	11:L:303[B]:BPB:H6A	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	C	330/336 (98%)	319 (97%)	11 (3%)	0	100	100
2	H	256/258 (99%)	245 (96%)	8 (3%)	3 (1%)	13	39
3	L	312/273 (114%)	298 (96%)	13 (4%)	1 (0%)	41	72
4	M	372/323 (115%)	358 (96%)	13 (4%)	1 (0%)	41	72
All	All	1270/1190 (107%)	1220 (96%)	45 (4%)	5 (0%)	34	66

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	47	LEU
2	H	50	VAL
2	H	46	PRO
4	M	177	ILE
3	L	57	PRO

### 5.3.2 Protein sidechains

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	C	281/282 (100%)	276 (98%)	5 (2%)	59	86
2	H	212/212 (100%)	205 (97%)	7 (3%)	38	72
3	L	253/218 (116%)	249 (98%)	4 (2%)	62	88
4	M	288/249 (116%)	280 (97%)	8 (3%)	43	77
All	All	1034/961 (108%)	1010 (98%)	24 (2%)	52	82

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	38	TYR
1	C	46	LYS
1	C	60	LYS
1	C	123	GLN
1	C	323	LYS
2	H	71	PRO
2	H	89	LYS
2	H	102	GLN
2	H	178	HIS
2	H	185	LEU
2	H	190	SER
2	H	205	LYS
3	L	160[A]	PHE
3	L	160[B]	PHE
3	L	271	PHE
3	L	272	TRP
4	M	115	MET
4	M	203[A]	SER
4	M	203[B]	SER
4	M	214[A]	PHE
4	M	214[B]	PHE
4	M	271	SER
4	M	290	ASP
4	M	323	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	24	HIS
1	C	123	GLN
1	C	200	GLN
1	C	310	GLN
2	H	8	GLN
2	H	102	GLN
2	H	106	ASN
2	H	220	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	FME	H	1	2	8,9,10	1.01	0	7,9,11	0.94	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
2	FME	H	1	2	-	1/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	1	FME	CB-CG-SD-CE

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 38 ligands modelled in this entry, 2 are monoatomic - leaving 36 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$
5	HEC	C	402	1	26,50,50	1.44	2 (7%)	18,82,82	2.17	7 (38%)
11	BPB	L	303[A]	-	64,70,70	2.16	16 (25%)	64,101,101	2.00	17 (26%)
5	HEC	C	401	1	26,50,50	1.53	3 (11%)	18,82,82	2.37	7 (38%)
11	BPB	L	303[B]	-	64,70,70	2.16	15 (23%)	64,101,101	1.98	16 (25%)
7	SO4	H	704	-	4,4,4	0.12	0	6,6,6	0.14	0
10	BCB	L	304	-	60,74,74	2.73	21 (35%)	48,115,115	2.16	12 (25%)
7	SO4	M	406	-	4,4,4	0.13	0	6,6,6	0.41	0
5	HEC	C	403	1	26,50,50	1.58	4 (15%)	18,82,82	2.01	9 (50%)
9	HTO	H	708	-	9,9,9	0.79	0	10,10,10	0.79	0
10	BCB	L	301[A]	-	60,74,74	2.84	20 (33%)	48,115,115	2.37	17 (35%)
7	SO4	H	705	-	4,4,4	0.15	0	6,6,6	0.15	0
7	SO4	C	406	-	4,4,4	0.24	0	6,6,6	0.18	0
7	SO4	M	407	-	4,4,4	0.11	0	6,6,6	0.14	0
14	NS5	M	405	-	39,39,39	1.38	1 (2%)	44,46,46	2.04	12 (27%)
6	DGA	C	405	1	36,36,43	1.17	3 (8%)	38,38,45	1.22	4 (10%)
10	BCB	M	403[A]	-	60,74,74	2.74	19 (31%)	48,115,115	2.43	14 (29%)
13	MQ7	M	402[B]	-	49,49,49	1.46	2 (4%)	60,63,63	1.38	10 (16%)
7	SO4	H	703	-	4,4,4	0.22	0	6,6,6	0.19	0
7	SO4	M	411	-	4,4,4	0.32	0	6,6,6	0.33	0
7	SO4	M	409	-	4,4,4	0.26	0	6,6,6	0.21	0
11	BPB	M	404	-	64,70,70	2.21	16 (25%)	64,101,101	1.93	14 (21%)
8	LDA	H	706	-	12,15,15	0.38	0	14,17,17	0.79	0
8	LDA	H	707	-	12,15,15	0.31	0	14,17,17	1.17	1 (7%)
10	BCB	L	302[B]	-	60,74,74	2.76	20 (33%)	48,115,115	2.32	16 (33%)
10	BCB	L	301[B]	-	60,74,74	2.78	19 (31%)	48,115,115	2.28	15 (31%)
9	HTO	L	306	-	9,9,9	0.75	0	10,10,10	0.89	1 (10%)
7	SO4	M	412	-	4,4,4	0.22	0	6,6,6	0.14	0
10	BCB	L	302[A]	-	60,74,74	2.75	20 (33%)	48,115,115	2.31	16 (33%)
7	SO4	H	702	-	4,4,4	0.21	0	6,6,6	0.28	0
13	MQ7	M	402[A]	-	49,49,49	1.54	2 (4%)	60,63,63	1.49	10 (16%)
7	SO4	M	410	-	4,4,4	0.27	0	6,6,6	0.24	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	SO4	M	408	-	4,4,4	0.20	0	6,6,6	0.26	0
10	BCB	M	403[B]	-	60,74,74	2.80	21 (35%)	48,115,115	2.56	16 (33%)
8	LDA	H	701	-	12,15,15	0.36	0	14,17,17	0.68	0
8	LDA	L	305	-	12,15,15	0.37	0	14,17,17	0.73	0
5	HEC	C	404	1	26,50,50	1.58	4 (15%)	18,82,82	2.31	8 (44%)

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
5	HEC	C	402	1	-	1/6/54/54	-
11	BPB	L	303[A]	-	-	8/47/105/105	0/5/6/6
5	HEC	C	401	1	-	1/6/54/54	-
11	BPB	L	303[B]	-	-	6/47/105/105	0/5/6/6
10	BCB	M	403[B]	-	-	11/41/177/177	-
10	BCB	L	304	-	-	14/41/177/177	-
5	HEC	C	403	1	-	0/6/54/54	-
9	HTO	H	708	-	-	1/10/10/10	-
10	BCB	M	403[A]	-	-	13/41/177/177	-
14	NS5	M	405	-	-	10/43/43/43	-
6	DGA	C	405	1	-	15/37/37/45	-
13	MQ7	M	402[A]	-	-	0/41/61/61	0/2/2/2
13	MQ7	M	402[B]	-	-	2/41/61/61	0/2/2/2
10	BCB	L	301[A]	-	-	11/41/177/177	-
11	BPB	M	404	-	-	8/47/105/105	0/5/6/6
8	LDA	H	706	-	-	6/13/13/13	-
8	LDA	H	707	-	-	11/13/13/13	-
10	BCB	L	302[B]	-	-	14/41/177/177	-
10	BCB	L	301[B]	-	-	15/41/177/177	-
9	HTO	L	306	-	-	4/10/10/10	-
10	BCB	L	302[A]	-	-	10/41/177/177	-
8	LDA	H	701	-	-	4/13/13/13	-
8	LDA	L	305	-	-	6/13/13/13	-
5	HEC	C	404	1	-	2/6/54/54	-

All (208) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	L	301[B]	BCB	CHB-C4A	-8.31	1.33	1.52
10	L	304	BCB	CHB-C4A	-8.30	1.33	1.52
10	L	301[A]	BCB	CHB-C4A	-8.30	1.33	1.52
13	M	402[B]	MQ7	C3-C2	8.26	1.50	1.35
10	L	302[B]	BCB	CHB-C4A	-8.24	1.34	1.52
10	M	403[A]	BCB	CHB-C4A	-8.21	1.34	1.52
10	L	302[A]	BCB	CHB-C4A	-8.11	1.34	1.52
13	M	402[A]	MQ7	C3-C2	8.08	1.50	1.35
10	M	403[B]	BCB	CHB-C4A	-8.05	1.34	1.52
10	L	301[A]	BCB	C1D-ND	-8.01	1.33	1.50
10	L	301[B]	BCB	C1D-ND	-7.75	1.34	1.50
10	M	403[B]	BCB	C1D-ND	-7.63	1.34	1.50
10	L	304	BCB	C1D-ND	-7.60	1.34	1.50
10	L	302[A]	BCB	C1D-ND	-7.59	1.34	1.50
10	L	302[B]	BCB	C1D-ND	-7.45	1.34	1.50
10	M	403[A]	BCB	C1D-ND	-7.40	1.34	1.50
14	M	405	NS5	C35-C36	7.33	1.53	1.32
10	L	302[B]	BCB	C1B-NB	-7.01	1.35	1.50
10	L	304	BCB	C4B-NB	-6.98	1.35	1.50
10	M	403[B]	BCB	C1B-NB	-6.96	1.35	1.50
10	M	403[B]	BCB	C4B-NB	-6.95	1.35	1.50
10	L	301[B]	BCB	C1B-NB	-6.86	1.35	1.50
11	M	404	BPB	CAC-C3C	6.77	1.52	1.33
10	M	403[A]	BCB	C4B-NB	-6.75	1.36	1.50
11	L	303[A]	BPB	CAC-C3C	6.74	1.52	1.33
11	L	303[B]	BPB	CAC-C3C	6.73	1.52	1.33
10	L	301[A]	BCB	C1B-NB	-6.73	1.36	1.50
10	L	301[A]	BCB	C4B-NB	-6.72	1.36	1.50
10	M	403[A]	BCB	C1B-NB	-6.64	1.36	1.50
10	L	302[A]	BCB	C1B-NB	-6.40	1.36	1.50
10	L	302[A]	BCB	C4B-NB	-6.39	1.36	1.50
10	L	301[B]	BCB	C4B-NB	-6.37	1.36	1.50
10	L	304	BCB	C1B-NB	-6.32	1.36	1.50
10	L	302[B]	BCB	C4B-NB	-6.06	1.37	1.50
11	L	303[B]	BPB	C3B-C2B	5.66	1.49	1.39
10	L	301[A]	BCB	C4D-ND	-5.61	1.38	1.50
10	M	403[B]	BCB	O2D-CGD	5.55	1.46	1.33
11	L	303[A]	BPB	C3B-C4B	5.49	1.48	1.41
10	L	301[B]	BCB	C4D-ND	-5.47	1.38	1.50
10	M	403[A]	BCB	O2D-CGD	5.46	1.46	1.33
10	L	301[B]	BCB	O2D-CGD	5.46	1.46	1.33
10	L	301[A]	BCB	O2D-CGD	5.44	1.46	1.33
10	L	302[A]	BCB	C4D-ND	-5.44	1.38	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	L	303[B]	BPB	C3B-C4B	5.41	1.48	1.41
11	M	404	BPB	O2A-CGA	5.35	1.49	1.33
13	M	402[A]	MQ7	C10-C5	5.33	1.49	1.40
11	M	404	BPB	C3B-C4B	5.25	1.48	1.41
11	L	303[B]	BPB	O2D-CGD	5.19	1.45	1.33
10	L	304	BCB	CHD-C1D	-5.16	1.45	1.53
11	L	303[A]	BPB	C1A-NA	-5.16	1.26	1.36
10	L	304	BCB	C4D-ND	-5.16	1.39	1.50
10	M	403[B]	BCB	C4D-ND	-5.15	1.39	1.50
10	L	301[A]	BCB	CHD-C1D	-5.15	1.45	1.53
11	M	404	BPB	C1A-NA	-5.13	1.26	1.36
10	M	403[A]	BCB	C4D-ND	-5.10	1.39	1.50
11	L	303[A]	BPB	C3B-C2B	5.08	1.48	1.39
11	L	303[A]	BPB	O2D-CGD	5.07	1.45	1.33
10	L	302[B]	BCB	C4D-ND	-5.07	1.39	1.50
11	L	303[A]	BPB	CHD-C1D	5.06	1.48	1.38
10	L	301[A]	BCB	CHD-C4C	-5.06	1.44	1.53
10	M	403[A]	BCB	CHD-C1D	-5.02	1.45	1.53
5	C	401	HEC	C3B-C2B	-5.02	1.35	1.40
11	M	404	BPB	CHD-C1D	5.02	1.48	1.38
10	M	403[B]	BCB	CHD-C1D	-5.01	1.45	1.53
11	L	303[B]	BPB	C1A-NA	-4.97	1.27	1.36
11	M	404	BPB	O2D-CGD	4.96	1.45	1.33
10	L	302[A]	BCB	CHD-C1D	-4.95	1.45	1.53
10	L	302[B]	BCB	OBD-CAD	4.90	1.29	1.21
10	L	302[B]	BCB	O2D-CGD	4.90	1.45	1.33
10	L	304	BCB	O2D-CGD	4.83	1.45	1.33
10	L	301[B]	BCB	CHD-C1D	-4.83	1.46	1.53
10	M	403[B]	BCB	OBD-CAD	4.82	1.29	1.21
10	L	301[B]	BCB	OBD-CAD	4.81	1.29	1.21
10	L	302[B]	BCB	CHD-C1D	-4.78	1.46	1.53
11	M	404	BPB	C3B-C2B	4.75	1.47	1.39
11	L	303[B]	BPB	CHD-C1D	4.75	1.47	1.38
10	L	302[A]	BCB	O2D-CGD	4.72	1.44	1.33
5	C	403	HEC	C3B-C2B	-4.69	1.35	1.40
10	L	301[A]	BCB	OBD-CAD	4.65	1.29	1.21
13	M	402[B]	MQ7	C10-C5	4.62	1.48	1.40
5	C	404	HEC	C3B-C2B	-4.58	1.36	1.40
10	M	403[A]	BCB	OBD-CAD	4.54	1.28	1.21
10	L	302[A]	BCB	OBD-CAD	4.50	1.28	1.21
10	L	301[B]	BCB	CHD-C4C	-4.46	1.45	1.53
5	C	402	HEC	C3B-C2B	-4.46	1.36	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	403[A]	BCB	CHD-C4C	-4.45	1.45	1.53
10	L	302[B]	BCB	O2A-CGA	4.38	1.46	1.33
10	M	403[B]	BCB	CHD-C4C	-4.33	1.45	1.53
10	M	403[A]	BCB	O2A-CGA	4.33	1.46	1.33
10	L	301[A]	BCB	O2A-CGA	4.32	1.46	1.33
10	M	403[B]	BCB	CHB-C1B	-4.27	1.47	1.53
10	L	304	BCB	O2A-CGA	4.26	1.45	1.33
10	L	302[A]	BCB	CHD-C4C	-4.25	1.46	1.53
10	L	301[B]	BCB	O2A-CGA	4.23	1.45	1.33
10	L	304	BCB	CHD-C4C	-4.21	1.46	1.53
11	M	404	BPB	C4C-NC	-4.21	1.27	1.36
11	L	303[A]	BPB	O2A-CGA	4.19	1.45	1.33
10	L	302[B]	BCB	C1A-CHA	-4.16	1.47	1.54
10	L	301[A]	BCB	CHB-C1B	-4.15	1.47	1.53
11	L	303[B]	BPB	O2A-CGA	4.11	1.45	1.33
10	L	304	BCB	OBD-CAD	4.10	1.28	1.21
10	M	403[A]	BCB	CHB-C1B	-4.09	1.47	1.53
10	L	302[A]	BCB	CHB-C1B	-4.09	1.47	1.53
10	L	302[A]	BCB	C1A-CHA	-4.08	1.47	1.54
10	L	302[B]	BCB	CHB-C1B	-4.05	1.47	1.53
10	M	403[B]	BCB	O2A-CGA	4.05	1.45	1.33
10	L	301[B]	BCB	CHB-C1B	-4.03	1.47	1.53
11	L	303[B]	BPB	OBD-CAD	3.94	1.29	1.22
10	L	302[A]	BCB	O2A-CGA	3.92	1.44	1.33
10	M	403[A]	BCB	CBD-CAD	-3.85	1.47	1.53
10	M	403[B]	BCB	CHC-C4B	-3.80	1.47	1.53
5	C	404	HEC	C3C-C2C	-3.80	1.36	1.40
11	L	303[B]	BPB	C4C-NC	-3.78	1.28	1.36
11	L	303[A]	BPB	C4C-NC	-3.74	1.28	1.36
11	M	404	BPB	OBD-CAD	3.74	1.28	1.22
10	L	302[A]	BCB	CHC-C4B	-3.57	1.48	1.53
10	M	403[B]	BCB	CBD-CAD	-3.54	1.47	1.53
10	L	301[B]	BCB	CHC-C4B	-3.53	1.48	1.53
10	L	302[B]	BCB	CHD-C4C	-3.51	1.47	1.53
10	L	301[A]	BCB	CBD-CAD	-3.49	1.47	1.53
10	L	304	BCB	CHB-C1B	-3.46	1.48	1.53
10	L	301[A]	BCB	C2D-C1D	-3.45	1.47	1.53
11	L	303[B]	BPB	C3D-C2D	3.42	1.48	1.39
11	M	404	BPB	C3D-C2D	3.42	1.48	1.39
10	L	302[B]	BCB	C4A-C3A	-3.42	1.49	1.53
10	M	403[A]	BCB	CHC-C4B	-3.41	1.48	1.53
11	L	303[A]	BPB	OBD-CAD	3.40	1.28	1.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	403	HEC	C3C-C2C	-3.38	1.37	1.40
11	L	303[A]	BPB	C3D-C2D	3.31	1.48	1.39
10	L	302[B]	BCB	CHC-C4B	-3.25	1.48	1.53
10	L	304	BCB	C1A-CHA	-3.24	1.48	1.54
10	L	301[B]	BCB	C2D-C1D	-3.22	1.47	1.53
10	L	302[A]	BCB	C2D-C1D	-3.14	1.47	1.53
10	L	301[B]	BCB	CBD-CAD	-3.13	1.48	1.53
6	C	405	DGA	OG1-CA1	3.12	1.42	1.33
6	C	405	DGA	OG2-CB1	3.08	1.43	1.34
11	M	404	BPB	C1C-NC	-3.07	1.33	1.38
10	L	301[A]	BCB	CHC-C4B	-3.05	1.48	1.53
10	L	302[B]	BCB	C2D-C1D	-2.97	1.47	1.53
10	L	304	BCB	C2D-C1D	-2.90	1.48	1.53
11	L	303[B]	BPB	CHD-C4C	2.87	1.47	1.40
5	C	401	HEC	C3C-C2C	-2.85	1.37	1.40
10	L	304	BCB	CHC-C4B	-2.85	1.49	1.53
10	M	403[A]	BCB	C2D-C1D	-2.84	1.48	1.53
11	L	303[A]	BPB	CHD-C4C	2.83	1.47	1.40
10	L	302[A]	BCB	C4A-C3A	-2.80	1.50	1.53
10	L	304	BCB	C3B-C2B	-2.79	1.48	1.55
10	M	403[B]	BCB	C2D-C1D	-2.78	1.48	1.53
10	L	301[A]	BCB	C4A-C3A	-2.77	1.50	1.53
10	L	301[B]	BCB	C3D-C2D	-2.77	1.48	1.55
6	C	405	DGA	OG2-CG2	-2.76	1.42	1.47
10	L	302[B]	BCB	C1A-C2A	-2.75	1.50	1.53
10	L	302[B]	BCB	C3D-C2D	-2.71	1.48	1.55
11	L	303[A]	BPB	C1C-NC	-2.67	1.33	1.38
10	L	301[A]	BCB	C1A-CHA	-2.65	1.49	1.54
10	L	301[B]	BCB	C1A-CHA	-2.62	1.49	1.54
10	L	302[A]	BCB	C3D-C2D	-2.62	1.48	1.55
10	M	403[B]	BCB	CHC-C1C	-2.59	1.46	1.52
11	M	404	BPB	CHD-C4C	2.57	1.46	1.40
10	L	304	BCB	CBD-CAD	-2.57	1.49	1.53
10	L	302[B]	BCB	C3B-C2B	-2.57	1.48	1.55
10	L	302[A]	BCB	C3B-C2B	-2.55	1.48	1.55
10	L	301[A]	BCB	C3B-C2B	-2.53	1.48	1.55
10	L	301[A]	BCB	C2B-C1B	-2.51	1.48	1.53
10	L	304	BCB	C2B-C1B	-2.49	1.48	1.53
5	C	402	HEC	C3C-C2C	-2.47	1.38	1.40
10	L	304	BCB	CHC-C1C	-2.46	1.47	1.52
5	C	403	HEC	C3C-C4C	2.45	1.47	1.43
10	L	301[B]	BCB	C3B-C2B	-2.45	1.48	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	L	303[B]	BPB	C1C-NC	-2.44	1.34	1.38
10	L	302[A]	BCB	CBD-CAD	-2.43	1.49	1.53
10	M	403[B]	BCB	C3B-C2B	-2.40	1.49	1.55
10	M	403[B]	BCB	C3D-C2D	-2.39	1.49	1.55
10	M	403[A]	BCB	C3B-C2B	-2.38	1.49	1.55
10	M	403[B]	BCB	CHA-CBD	-2.37	1.46	1.53
10	M	403[B]	BCB	C1A-CHA	-2.34	1.50	1.54
11	L	303[B]	BPB	C4D-ND	2.33	1.41	1.36
10	L	302[A]	BCB	CHC-C1C	-2.29	1.47	1.52
10	M	403[B]	BCB	C4A-C3A	-2.29	1.51	1.53
11	L	303[A]	BPB	C4C-C3C	2.28	1.50	1.45
10	M	403[A]	BCB	C2B-C1B	-2.28	1.49	1.53
5	C	404	HEC	C3C-C4C	2.28	1.47	1.43
10	L	302[B]	BCB	CBD-CAD	-2.27	1.49	1.53
10	M	403[B]	BCB	C2B-C1B	-2.26	1.49	1.53
10	L	304	BCB	C4A-C3A	-2.26	1.51	1.53
11	L	303[A]	BPB	C4D-ND	2.25	1.41	1.36
11	M	404	BPB	C4C-C3C	2.24	1.50	1.45
10	L	304	BCB	C3B-CAB	-2.23	1.49	1.52
10	L	301[B]	BCB	C4A-C3A	-2.22	1.51	1.53
10	L	301[A]	BCB	C3D-C2D	-2.20	1.49	1.55
10	L	304	BCB	C3D-C2D	-2.19	1.49	1.55
5	C	403	HEC	C1A-C2A	2.17	1.47	1.42
5	C	401	HEC	C3C-C4C	2.15	1.46	1.43
11	M	404	BPB	CHC-C1C	-2.15	1.33	1.37
10	L	302[A]	BCB	C3B-CAB	-2.13	1.49	1.52
11	L	303[B]	BPB	C4B-CHC	2.13	1.49	1.41
11	M	404	BPB	C1B-CHB	2.13	1.49	1.41
10	L	301[A]	BCB	C3B-CAB	-2.11	1.49	1.52
10	M	403[A]	BCB	CHC-C1C	-2.11	1.47	1.52
5	C	404	HEC	C4D-ND	2.10	1.40	1.36
10	M	403[A]	BCB	C4A-C3A	-2.09	1.51	1.53
10	M	403[A]	BCB	C3D-C2D	-2.06	1.49	1.55
11	M	404	BPB	C4D-ND	2.04	1.40	1.36
11	L	303[B]	BPB	C1B-CHB	2.04	1.49	1.41
11	L	303[A]	BPB	C4B-CHC	2.03	1.49	1.41
10	L	302[B]	BCB	C2B-C1B	-2.01	1.49	1.53
11	L	303[A]	BPB	C1B-CHB	2.01	1.48	1.41
10	L	301[B]	BCB	C2A-C3A	-2.01	1.51	1.54

All (222) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	301[A]	BCB	CMB-C2B-C3B	7.94	134.01	114.29
10	L	301[B]	BCB	CMB-C2B-C3B	7.74	133.51	114.29
10	M	403[B]	BCB	CHA-CBD-CGD	-7.43	98.22	115.02
10	M	403[B]	BCB	CMB-C2B-C3B	7.39	132.64	114.29
10	L	302[B]	BCB	CMB-C2B-C3B	7.19	132.14	114.29
10	M	403[A]	BCB	CMB-C2B-C3B	7.05	131.80	114.29
10	L	302[A]	BCB	CMB-C2B-C3B	6.91	131.44	114.29
10	L	304	BCB	CMB-C2B-C3B	6.51	130.45	114.29
11	L	303[B]	BPB	CMD-C2D-C1D	6.45	134.99	125.06
11	L	303[A]	BPB	CMD-C2D-C1D	6.33	134.81	125.06
11	M	404	BPB	O2D-CGD-CBD	6.30	122.46	111.27
11	M	404	BPB	CMD-C2D-C1D	6.17	134.57	125.06
11	L	303[B]	BPB	CBC-CAC-C3C	-5.68	110.09	126.72
10	L	302[B]	BCB	C3B-C4B-NB	5.64	114.04	103.75
11	L	303[A]	BPB	O2D-CGD-CBD	5.63	121.28	111.27
11	L	303[A]	BPB	CBC-CAC-C3C	-5.63	110.26	126.72
10	M	403[A]	BCB	CHA-CBD-CGD	-5.60	102.35	115.02
10	L	302[A]	BCB	C3B-C4B-NB	5.58	113.94	103.75
10	M	403[B]	BCB	C3B-C4B-NB	5.57	113.92	103.75
11	M	404	BPB	CBC-CAC-C3C	-5.53	110.53	126.72
14	M	405	NS5	C19-C20-C21	-5.52	119.44	127.31
10	L	301[B]	BCB	C3B-C4B-NB	5.46	113.71	103.75
10	M	403[A]	BCB	C3B-C4B-NB	5.45	113.70	103.75
10	M	403[B]	BCB	O2D-CGD-CBD	5.07	123.02	111.11
10	M	403[A]	BCB	CBB-CAB-C3B	5.04	121.94	116.80
10	L	301[A]	BCB	C3B-C4B-NB	4.98	112.83	103.75
10	M	403[A]	BCB	O2D-CGD-CBD	4.95	122.74	111.11
10	L	304	BCB	C3B-C4B-NB	4.88	112.66	103.75
10	M	403[B]	BCB	O2D-CGD-O1D	-4.87	114.33	123.84
5	C	401	HEC	CBA-CAA-C2A	-4.79	103.66	112.48
5	C	404	HEC	CAD-CBD-CGD	-4.78	104.65	112.67
10	L	304	BCB	CBA-CAA-C2A	-4.72	109.30	115.72
10	L	301[B]	BCB	CHA-CBD-CGD	-4.72	104.35	115.02
10	L	302[A]	BCB	O2D-CGD-CBD	4.65	122.03	111.11
10	L	302[A]	BCB	C1-C2-C3	-4.64	118.02	126.04
11	L	303[B]	BPB	O2D-CGD-CBD	4.60	119.44	111.27
10	L	302[B]	BCB	O2D-CGD-CBD	4.52	121.71	111.11
5	C	401	HEC	CBD-CAD-C3D	-4.44	104.29	112.49
6	C	405	DGA	OG2-CB1-CB2	4.33	120.84	111.50
10	L	304	BCB	OBD-CAD-C3D	-4.32	119.13	126.73
14	M	405	NS5	CM4-C36-C35	-4.26	110.32	122.65
11	L	303[B]	BPB	CMB-C2B-C3B	4.26	132.65	124.68
10	M	403[A]	BCB	O2D-CGD-O1D	-4.25	115.53	123.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	402	HEC	CBA-CAA-C2A	-4.14	104.84	112.48
10	L	302[B]	BCB	C1-C2-C3	-4.08	118.98	126.04
10	L	301[A]	BCB	CHA-CBD-CGD	-4.08	105.78	115.02
5	C	401	HEC	CMC-C2C-C1C	-4.08	122.19	128.46
10	L	302[B]	BCB	CBB-CAB-C3B	4.08	120.96	116.80
11	L	303[B]	BPB	CMD-C2D-C3D	-4.06	118.28	127.61
10	L	304	BCB	C1D-CHD-C4C	4.06	121.02	112.37
14	M	405	NS5	C18-C17-C15	-4.06	121.52	127.31
10	L	301[A]	BCB	C4-C3-C5	4.00	122.01	115.27
10	L	302[B]	BCB	C1D-CHD-C4C	3.98	120.86	112.37
10	M	403[B]	BCB	OBD-CAD-C3D	-3.98	119.73	126.73
14	M	405	NS5	C34-C35-C36	-3.92	114.34	127.75
14	M	405	NS5	CM3-C36-C35	-3.86	111.49	122.65
10	L	301[B]	BCB	C1D-CHD-C4C	3.85	120.57	112.37
10	L	301[A]	BCB	C1D-CHD-C4C	3.83	120.54	112.37
10	L	304	BCB	O2D-CGD-CBD	3.82	120.08	111.11
10	M	403[B]	BCB	CBB-CAB-C3B	3.78	120.65	116.80
10	L	302[A]	BCB	OBD-CAD-C3D	-3.76	120.12	126.73
11	L	303[A]	BPB	CMB-C2B-C3B	3.76	131.71	124.68
11	M	404	BPB	CMD-C2D-C3D	-3.72	119.05	127.61
10	L	302[B]	BCB	OBD-CAD-C3D	-3.71	120.20	126.73
11	L	303[A]	BPB	CMD-C2D-C3D	-3.71	119.08	127.61
10	L	302[A]	BCB	O1D-CGD-CBD	-3.71	117.20	124.54
11	M	404	BPB	O2A-CGA-CBA	3.68	123.45	111.91
10	M	403[B]	BCB	CBA-CAA-C2A	-3.67	110.72	115.72
10	L	301[A]	BCB	O2D-CGD-CBD	3.67	119.74	111.11
5	C	401	HEC	CMC-C2C-C3C	3.63	130.09	125.82
10	L	301[B]	BCB	C4-C3-C5	3.62	121.37	115.27
14	M	405	NS5	C11-C10-C9	3.61	121.35	115.27
10	M	403[B]	BCB	C1-C2-C3	-3.60	119.83	126.04
10	L	301[B]	BCB	O2D-CGD-CBD	3.58	119.51	111.11
10	L	302[A]	BCB	C1D-CHD-C4C	3.58	119.99	112.37
10	L	301[B]	BCB	OBD-CAD-C3D	-3.54	120.51	126.73
5	C	404	HEC	CMB-C2B-C1B	-3.53	123.04	128.46
10	L	301[A]	BCB	O2A-CGA-CBA	3.52	122.94	111.91
10	L	301[A]	BCB	CBB-CAB-C3B	3.49	120.36	116.80
5	C	403	HEC	CBD-CAD-C3D	-3.48	106.06	112.49
5	C	402	HEC	CAD-CBD-CGD	-3.43	106.91	112.67
11	L	303[A]	BPB	C3C-C4C-NC	3.39	115.00	109.58
5	C	402	HEC	CMC-C2C-C1C	-3.35	123.31	128.46
10	L	302[B]	BCB	C6-C5-C3	-3.29	104.82	113.45
5	C	404	HEC	CBD-CAD-C3D	3.28	118.54	112.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	301[A]	BCB	OBD-CAD-C3D	-3.28	120.95	126.73
11	L	303[B]	BPB	OBD-CAD-C3D	-3.26	120.67	128.52
5	C	402	HEC	CMD-C2D-C1D	-3.25	123.47	128.46
5	C	403	HEC	CMC-C2C-C1C	-3.24	123.48	128.46
13	M	402[A]	MQ7	C39-C38-C40	3.24	120.72	115.27
10	L	301[A]	BCB	CMD-C2D-C3D	3.22	122.28	114.29
13	M	402[A]	MQ7	C29-C28-C30	3.17	120.61	115.27
10	M	403[B]	BCB	C1D-CHD-C4C	3.15	119.08	112.37
11	M	404	BPB	C1-O2A-CGA	3.14	124.67	116.44
13	M	402[B]	MQ7	C39-C38-C40	3.12	120.52	115.27
10	L	302[A]	BCB	CBA-CAA-C2A	-3.11	111.50	115.72
5	C	404	HEC	CMB-C2B-C3B	3.08	129.44	125.82
10	L	302[A]	BCB	CBB-CAB-C3B	3.08	119.94	116.80
10	L	302[B]	BCB	O2A-CGA-CBA	3.04	121.46	111.91
5	C	404	HEC	CBA-CAA-C2A	-3.03	106.89	112.48
10	L	304	BCB	C1-C2-C3	-3.03	120.80	126.04
10	M	403[A]	BCB	C1D-CHD-C4C	3.02	118.81	112.37
10	M	403[A]	BCB	OBD-CAD-C3D	-3.01	121.43	126.73
5	C	404	HEC	CMC-C2C-C1C	-3.00	123.85	128.46
10	L	302[A]	BCB	C6-C5-C3	-3.00	105.60	113.45
10	L	301[B]	BCB	O2A-CGA-CBA	2.98	121.25	111.91
6	C	405	DGA	OG1-CA1-CA2	2.97	121.24	111.91
10	L	301[A]	BCB	O2D-CGD-O1D	-2.97	118.04	123.84
5	C	403	HEC	CAA-CBA-CGA	-2.95	107.71	112.67
11	L	303[B]	BPB	C3C-C4C-NC	2.93	114.27	109.58
11	M	404	BPB	CAD-C3D-C2D	2.93	154.92	140.80
14	M	405	NS5	C32-C31-C33	2.92	120.18	115.27
10	L	301[B]	BCB	O2D-CGD-O1D	-2.92	118.14	123.84
11	L	303[A]	BPB	OBD-CAD-C3D	-2.91	121.51	128.52
5	C	402	HEC	CMB-C2B-C1B	-2.90	124.01	128.46
10	L	304	BCB	O2A-CGA-CBA	2.89	120.99	111.91
13	M	402[A]	MQ7	C34-C33-C35	2.89	120.14	115.27
11	M	404	BPB	OBD-CAD-C3D	-2.89	121.57	128.52
10	L	304	BCB	C4-C3-C5	2.88	120.12	115.27
10	L	302[B]	BCB	O1D-CGD-CBD	-2.83	118.94	124.54
11	L	303[B]	BPB	CED-O2D-CGD	2.83	122.33	115.94
11	M	404	BPB	C3C-C4C-NC	2.81	114.08	109.58
11	L	303[B]	BPB	CAD-C3D-C2D	2.81	154.35	140.80
13	M	402[B]	MQ7	C29-C28-C30	2.81	120.00	115.27
10	L	301[B]	BCB	C1-C2-C3	-2.80	121.20	126.04
5	C	402	HEC	CMC-C2C-C3C	2.79	129.11	125.82
10	M	403[A]	BCB	CMD-C2D-C3D	2.77	121.17	114.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	304	BCB	CMD-C2D-C3D	2.77	121.16	114.29
11	L	303[A]	BPB	CAD-C3D-C2D	2.76	154.14	140.80
6	C	405	DGA	OG2-CG2-CG1	2.76	112.52	106.13
11	L	303[A]	BPB	O2A-CGA-CBA	2.75	120.54	111.91
10	L	301[B]	BCB	CBB-CAB-C3B	2.75	119.60	116.80
10	M	403[A]	BCB	O2A-CGA-O1A	-2.74	116.67	123.59
13	M	402[A]	MQ7	C16-C17-C18	-2.73	121.09	127.66
13	M	402[B]	MQ7	C31-C32-C33	-2.72	121.11	127.66
11	M	404	BPB	O2D-CGD-O1D	-2.71	118.54	123.84
13	M	402[A]	MQ7	C19-C18-C20	2.70	119.81	115.27
11	M	404	BPB	O1D-CGD-CBD	-2.68	119.00	124.48
11	L	303[B]	BPB	C4D-ND-C1D	-2.68	101.95	106.76
10	L	302[A]	BCB	C4A-C3A-C2A	-2.67	99.77	103.86
11	L	303[A]	BPB	C4B-CHC-C1C	2.67	132.01	128.57
10	M	403[A]	BCB	O2A-CGA-CBA	2.64	120.20	111.91
11	L	303[A]	BPB	O2D-CGD-O1D	-2.63	118.69	123.84
11	L	303[A]	BPB	C4D-ND-C1D	-2.61	102.07	106.76
10	L	301[A]	BCB	CHC-C4B-C3B	2.60	124.56	118.17
10	L	302[A]	BCB	O2A-CGA-O1A	-2.60	117.03	123.59
13	M	402[A]	MQ7	C12-C11-C3	-2.59	105.05	112.05
11	M	404	BPB	C4D-ND-C1D	-2.58	102.12	106.76
13	M	402[B]	MQ7	C16-C17-C18	-2.57	121.46	127.66
10	L	302[A]	BCB	C4-C3-C5	2.57	119.60	115.27
5	C	401	HEC	CMB-C2B-C1B	-2.57	124.52	128.46
11	L	303[B]	BPB	C4-C3-C5	2.56	119.58	115.27
5	C	403	HEC	CBA-CAA-C2A	-2.55	107.78	112.48
11	L	303[B]	BPB	CHD-C4C-C3C	-2.54	121.05	125.11
10	L	302[A]	BCB	O2A-CGA-CBA	2.52	119.81	111.91
10	L	301[A]	BCB	O2A-CGA-O1A	-2.52	117.24	123.59
11	L	303[B]	BPB	O2A-CGA-CBA	2.51	119.80	111.91
13	M	402[B]	MQ7	C24-C23-C25	2.51	119.49	115.27
5	C	403	HEC	CMC-C2C-C3C	2.50	128.76	125.82
11	M	404	BPB	O2A-C1-C2	2.49	115.17	108.64
10	L	301[B]	BCB	CHC-C4B-C3B	2.48	124.24	118.17
13	M	402[A]	MQ7	C45-C43-C44	2.48	120.07	114.60
10	L	301[A]	BCB	C4A-C3A-C2A	-2.47	100.08	103.86
10	L	301[A]	BCB	CED-O2D-CGD	2.47	121.52	115.94
5	C	403	HEC	CMD-C2D-C1D	-2.47	124.67	128.46
10	M	403[A]	BCB	C4A-C3A-C2A	-2.46	100.10	103.86
13	M	402[B]	MQ7	C21-C22-C23	-2.45	121.75	127.66
14	M	405	NS5	C6-C5-C4	2.45	119.39	115.27
10	L	301[B]	BCB	O2A-CGA-O1A	-2.45	117.42	123.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	304	BCB	O2D-CGD-O1D	-2.45	119.05	123.84
13	M	402[B]	MQ7	C14-C13-C15	2.44	119.38	115.27
14	M	405	NS5	C18-C19-C20	2.43	128.46	123.47
5	C	404	HEC	CMA-C3A-C2A	2.43	129.52	124.94
13	M	402[B]	MQ7	C26-C27-C28	-2.37	121.95	127.66
10	M	403[B]	BCB	O2A-CGA-O1A	-2.35	117.65	123.59
11	L	303[A]	BPB	C4-C3-C5	2.35	119.23	115.27
11	L	303[B]	BPB	O1D-CGD-CBD	-2.35	119.68	124.48
10	L	301[A]	BCB	CAA-CBA-CGA	-2.34	106.41	113.25
13	M	402[A]	MQ7	C24-C23-C25	2.33	119.20	115.27
5	C	403	HEC	CMA-C3A-C2A	2.33	129.34	124.94
14	M	405	NS5	C12-C13-C14	-2.32	115.98	123.22
9	L	306	HTO	C5-C4-C3	-2.32	110.37	114.18
10	M	403[B]	BCB	CMD-C2D-C3D	2.31	120.03	114.29
10	L	302[B]	BCB	O2D-CGD-O1D	-2.30	119.35	123.84
11	L	303[A]	BPB	CHD-C4C-C3C	-2.29	121.45	125.11
10	L	301[B]	BCB	CMD-C2D-C3D	2.28	119.95	114.29
10	L	302[B]	BCB	C4-C3-C5	2.27	119.09	115.27
8	H	707	LDA	CM2-N1-C1	-2.26	105.49	110.23
5	C	401	HEC	CAD-CBD-CGD	2.26	116.46	112.67
10	L	302[B]	BCB	C4A-C3A-C2A	-2.25	100.42	103.86
5	C	404	HEC	CMC-C2C-C3C	2.23	128.44	125.82
10	M	403[B]	BCB	CHC-C4B-C3B	2.23	123.63	118.17
14	M	405	NS5	C8-C9-C10	-2.22	105.66	112.98
13	M	402[A]	MQ7	C14-C13-C15	2.22	119.01	115.27
13	M	402[A]	MQ7	C26-C27-C28	-2.22	122.31	127.66
10	M	403[A]	BCB	CHC-C4B-C3B	2.21	123.59	118.17
10	L	301[B]	BCB	C4A-C3A-C2A	-2.21	100.48	103.86
10	L	302[B]	BCB	CHC-C4B-C3B	2.21	123.58	118.17
11	L	303[A]	BPB	CBA-CAA-C2A	-2.20	107.36	113.86
13	M	402[B]	MQ7	C34-C33-C35	2.18	118.94	115.27
11	L	303[A]	BPB	O1D-CGD-CBD	-2.18	120.03	124.48
11	L	303[B]	BPB	C4B-CHC-C1C	2.17	131.36	128.57
10	L	302[A]	BCB	CED-O2D-CGD	2.15	120.79	115.94
10	M	403[B]	BCB	C4-C3-C5	2.14	118.87	115.27
5	C	403	HEC	C1D-C2D-C3D	2.14	108.48	107.00
11	L	303[B]	BPB	C16-C15-C13	-2.13	109.03	115.92
14	M	405	NS5	C22-C21-C20	-2.10	119.98	122.92
13	M	402[B]	MQ7	C45-C43-C44	2.09	119.22	114.60
10	L	302[B]	BCB	OBB-CAB-C3B	-2.09	119.31	121.52
10	M	403[B]	BCB	C4D-C3D-CAD	-2.08	100.00	104.73
10	L	304	BCB	CHC-C4B-C3B	2.08	123.28	118.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	L	302[A]	BCB	CHC-C4B-C3B	2.07	123.25	118.17
5	C	401	HEC	CMB-C2B-C3B	2.07	128.26	125.82
10	L	302[B]	BCB	CED-O2D-CGD	2.03	120.53	115.94
5	C	403	HEC	CMB-C2B-C1B	-2.03	125.34	128.46
6	C	405	DGA	OG1-CA1-OA1	-2.02	118.48	123.59
10	M	403[A]	BCB	C4D-C3D-CAD	-2.02	100.15	104.73
5	C	402	HEC	CMB-C2B-C3B	2.02	128.19	125.82
10	M	403[B]	BCB	O2A-CGA-CBA	2.01	118.22	111.91
10	L	301[A]	BCB	C1-C2-C3	-2.01	122.56	126.04
11	M	404	BPB	CMB-C2B-C3B	2.01	128.44	124.68
11	L	303[A]	BPB	CAA-C2A-C3A	-2.01	107.28	112.78

There are no chirality outliers.

All (173) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	L	303[A]	BPB	C2C-C3C-CAC-CBC
11	L	303[B]	BPB	C2C-C3C-CAC-CBC
8	H	706	LDA	C2-C1-N1-O1
8	H	706	LDA	C2-C1-N1-CM1
8	H	706	LDA	C2-C1-N1-CM2
8	H	706	LDA	N1-C1-C2-C3
10	L	301[A]	BCB	C2B-C3B-CAB-OBB
10	L	301[A]	BCB	C2B-C3B-CAB-CBB
10	L	301[A]	BCB	C2-C3-C5-C6
10	L	301[A]	BCB	C4-C3-C5-C6
14	M	405	NS5	C13-C14-C15-C16
14	M	405	NS5	C13-C14-C15-C17
14	M	405	NS5	C34-C35-C36-CM3
6	C	405	DGA	OG1-CG1-CG2-OG2
6	C	405	DGA	OG1-CG1-CG2-CG3
10	M	403[A]	BCB	C2B-C3B-CAB-OBB
10	M	403[A]	BCB	C2B-C3B-CAB-CBB
10	M	403[A]	BCB	C2C-C3C-CAC-CBC
10	M	403[A]	BCB	CAD-CBD-CGD-O1D
10	M	403[A]	BCB	CAD-CBD-CGD-O2D
11	M	404	BPB	C2C-C3C-CAC-CBC
8	H	707	LDA	C2-C1-N1-O1
8	H	707	LDA	C2-C1-N1-CM1
8	H	707	LDA	N1-C1-C2-C3
10	L	301[B]	BCB	C2B-C3B-CAB-OBB
10	L	301[B]	BCB	C2B-C3B-CAB-CBB

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Mol	Chain	Res	Type	Atoms
10	L	301[B]	BCB	C4-C3-C5-C6
10	L	302[B]	BCB	C2B-C3B-CAB-OBB
10	L	302[B]	BCB	C2B-C3B-CAB-CBB
9	L	306	HTO	O2-C2-C3-C4
10	L	302[A]	BCB	C2B-C3B-CAB-OBB
10	L	302[A]	BCB	C2B-C3B-CAB-CBB
10	M	403[B]	BCB	C2B-C3B-CAB-OBB
10	M	403[B]	BCB	C2B-C3B-CAB-CBB
10	M	403[B]	BCB	C2C-C3C-CAC-CBC
10	L	304	BCB	CBD-CGD-O2D-CED
10	L	301[B]	BCB	C2-C3-C5-C6
10	M	403[A]	BCB	C2A-CAA-CBA-CGA
14	M	405	NS5	C34-C35-C36-CM4
11	M	404	BPB	CBA-CGA-O2A-C1
11	M	404	BPB	O1A-CGA-O2A-C1
10	L	304	BCB	O1D-CGD-O2D-CED
6	C	405	DGA	CA2-CA1-OG1-CG1
6	C	405	DGA	OA1-CA1-OG1-CG1
10	L	304	BCB	C5-C6-C7-C8
10	L	302[B]	BCB	C13-C15-C16-C17
10	L	301[B]	BCB	C15-C16-C17-C18
10	M	403[A]	BCB	C15-C16-C17-C18
10	M	403[B]	BCB	C8-C10-C11-C12
14	M	405	NS5	C7-C8-C9-C10
10	L	301[A]	BCB	C13-C15-C16-C17
10	L	304	BCB	C3-C5-C6-C7
8	H	707	LDA	C2-C3-C4-C5
8	H	707	LDA	C4-C5-C6-C7
8	L	305	LDA	C2-C3-C4-C5
6	C	405	DGA	CCB-CDB-CEB-CFB
10	L	302[B]	BCB	CHA-CBD-CGD-O1D
11	L	303[A]	BPB	C4-C3-C5-C6
10	L	302[A]	BCB	C14-C13-C15-C16
8	H	707	LDA	C6-C7-C8-C9
14	M	405	NS5	C31-C33-C34-C35
6	C	405	DGA	CBB-CAB-CB9-CB8
11	L	303[A]	BPB	O2A-C1-C2-C3
11	L	303[B]	BPB	C8-C10-C11-C12
11	L	303[A]	BPB	C2-C3-C5-C6
11	L	303[A]	BPB	C8-C10-C11-C12
10	M	403[A]	BCB	C8-C10-C11-C12
6	C	405	DGA	CAB-CBB-CCB-CDB

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Mol	Chain	Res	Type	Atoms
10	M	403[A]	BCB	C13-C15-C16-C17
8	L	305	LDA	C1-C2-C3-C4
10	L	302[A]	BCB	C12-C13-C15-C16
11	L	303[A]	BPB	CBD-CGD-O2D-CED
8	H	706	LDA	C3-C4-C5-C6
10	L	302[B]	BCB	C8-C10-C11-C12
14	M	405	NS5	C3-C4-C5-C6
8	H	701	LDA	C6-C7-C8-C9
8	L	305	LDA	C5-C6-C7-C8
9	H	708	HTO	O1-C1-C2-O2
10	L	302[B]	BCB	CHA-CBD-CGD-O2D
10	L	301[A]	BCB	C15-C16-C17-C18
10	M	403[A]	BCB	C12-C13-C15-C16
10	M	403[A]	BCB	C14-C13-C15-C16
8	H	706	LDA	C6-C7-C8-C9
9	L	306	HTO	C4-C5-C6-C7
14	M	405	NS5	C10-C12-C13-C14
8	H	707	LDA	C11-C10-C9-C8
11	L	303[B]	BPB	O2A-C1-C2-C3
8	L	305	LDA	C4-C5-C6-C7
9	L	306	HTO	O1-C1-C2-O2
11	M	404	BPB	C10-C11-C12-C13
11	L	303[B]	BPB	C4-C3-C5-C6
10	L	302[A]	BCB	C13-C15-C16-C17
10	L	301[B]	BCB	C13-C15-C16-C17
11	M	404	BPB	C15-C16-C17-C18
11	L	303[A]	BPB	O1D-CGD-O2D-CED
11	L	303[B]	BPB	C2-C3-C5-C6
10	L	304	BCB	C11-C10-C8-C7
10	L	301[B]	BCB	C11-C12-C13-C15
10	L	302[B]	BCB	C11-C10-C8-C7
10	M	403[B]	BCB	CBA-CGA-O2A-C1
11	M	404	BPB	C16-C17-C18-C20
10	L	302[B]	BCB	C2C-C3C-CAC-CBC
10	L	302[A]	BCB	C2C-C3C-CAC-CBC
10	L	304	BCB	C3A-C2A-CAA-CBA
6	C	405	DGA	CBB-CCB-CDB-CEB
8	H	707	LDA	C2-C1-N1-CM2
6	C	405	DGA	CB9-CAB-CBB-CCB
10	L	304	BCB	C8-C10-C11-C12
10	M	403[B]	BCB	O1A-CGA-O2A-C1
10	L	301[B]	BCB	CBA-CGA-O2A-C1

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Mol	Chain	Res	Type	Atoms
8	H	707	LDA	C5-C6-C7-C8
10	M	403[B]	BCB	C12-C13-C15-C16
10	L	301[B]	BCB	O1A-CGA-O2A-C1
5	C	404	HEC	C2D-C3D-CAD-CBD
5	C	404	HEC	C4D-C3D-CAD-CBD
8	H	701	LDA	C2-C3-C4-C5
10	L	301[B]	BCB	C16-C17-C18-C19
10	L	304	BCB	C4-C3-C5-C6
14	M	405	NS5	C3-C4-C5-C7
9	L	306	HTO	O2-C2-C3-O3
10	L	301[A]	BCB	CAD-CBD-CGD-O1D
10	L	301[B]	BCB	CAD-CBD-CGD-O1D
10	L	304	BCB	C11-C10-C8-C9
10	M	403[B]	BCB	C14-C13-C15-C16
6	C	405	DGA	CA6-CA7-CA8-CA9
6	C	405	DGA	CA7-CA8-CA9-CAA
11	M	404	BPB	C16-C17-C18-C19
8	H	701	LDA	C9-C10-C11-C12
14	M	405	NS5	C23-C24-C25-C26
6	C	405	DGA	CB2-CB3-CB4-CB5
8	L	305	LDA	C3-C4-C5-C6
11	M	404	BPB	C14-C13-C15-C16
10	L	301[A]	BCB	C1A-C2A-CAA-CBA
10	L	301[B]	BCB	C1A-C2A-CAA-CBA
10	L	302[B]	BCB	C1A-C2A-CAA-CBA
11	L	303[B]	BPB	C5-C6-C7-C8
10	L	304	BCB	CHA-CBD-CGD-O1D
10	L	302[A]	BCB	CHA-CBD-CGD-O1D
6	C	405	DGA	CB6-CB7-CB8-CB9
10	L	304	BCB	C2-C3-C5-C6
5	C	402	HEC	C3D-CAD-CBD-CGD
10	L	302[A]	BCB	CBD-CGD-O2D-CED
10	M	403[A]	BCB	C5-C6-C7-C8
10	L	301[B]	BCB	C11-C12-C13-C14
10	L	302[B]	BCB	C11-C10-C8-C9
8	H	707	LDA	C3-C4-C5-C6
11	L	303[A]	BPB	CAD-CBD-CGD-O2D
10	L	304	BCB	C2C-C3C-CAC-CBC
10	L	301[A]	BCB	C2C-C3C-CAC-CBC
8	H	701	LDA	C5-C6-C7-C8
13	M	402[B]	MQ7	C39-C38-C40-C41
10	L	302[A]	BCB	C3A-C2A-CAA-CBA

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Mol	Chain	Res	Type	Atoms
10	M	403[B]	BCB	C3A-C2A-CAA-CBA
10	M	403[B]	BCB	C16-C17-C18-C20
6	C	405	DGA	CB4-CB5-CB6-CB7
10	M	403[A]	BCB	O2A-C1-C2-C3
10	M	403[B]	BCB	O2A-C1-C2-C3
10	L	304	BCB	CHA-CBD-CGD-O2D
13	M	402[B]	MQ7	C37-C38-C40-C41
10	L	301[A]	BCB	CAD-CBD-CGD-O2D
10	L	301[B]	BCB	CAD-CBD-CGD-O2D
10	L	302[B]	BCB	C16-C17-C18-C19
5	C	401	HEC	C2A-CAA-CBA-CGA
8	L	305	LDA	C2-C1-N1-O1
10	L	304	BCB	C11-C12-C13-C14
10	L	302[B]	BCB	C14-C13-C15-C16
6	C	405	DGA	CA3-CA4-CA5-CA6
10	L	301[B]	BCB	CAA-CBA-CGA-O2A
10	L	301[A]	BCB	C6-C7-C8-C10
10	L	302[B]	BCB	C12-C13-C15-C16
10	L	302[A]	BCB	CHA-CBD-CGD-O2D
10	L	302[B]	BCB	C2A-CAA-CBA-CGA
8	H	707	LDA	C9-C10-C11-C12

There are no ring outliers.

20 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	402	HEC	4	0
11	L	303[A]	BPB	4	0
5	C	401	HEC	1	0
11	L	303[B]	BPB	4	0
10	L	304	BCB	4	0
5	C	403	HEC	2	0
10	L	301[A]	BCB	2	0
14	M	405	NS5	3	0
10	M	403[A]	BCB	1	0
11	M	404	BPB	5	0
8	H	707	LDA	1	0
10	L	302[B]	BCB	2	0
10	L	301[B]	BCB	5	0
10	L	302[A]	BCB	1	0
13	M	402[A]	MQ7	2	0
7	M	408	SO4	1	0

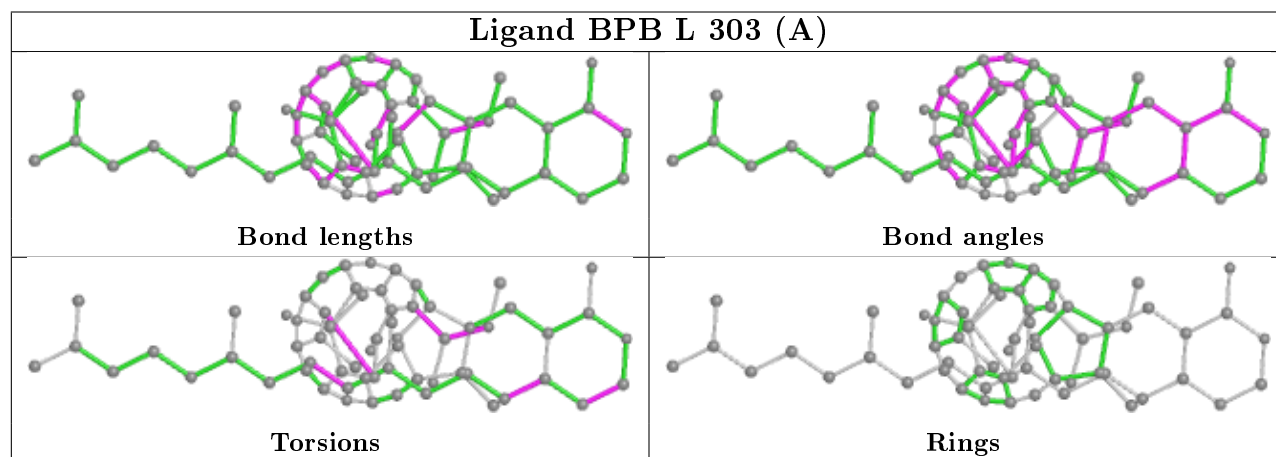
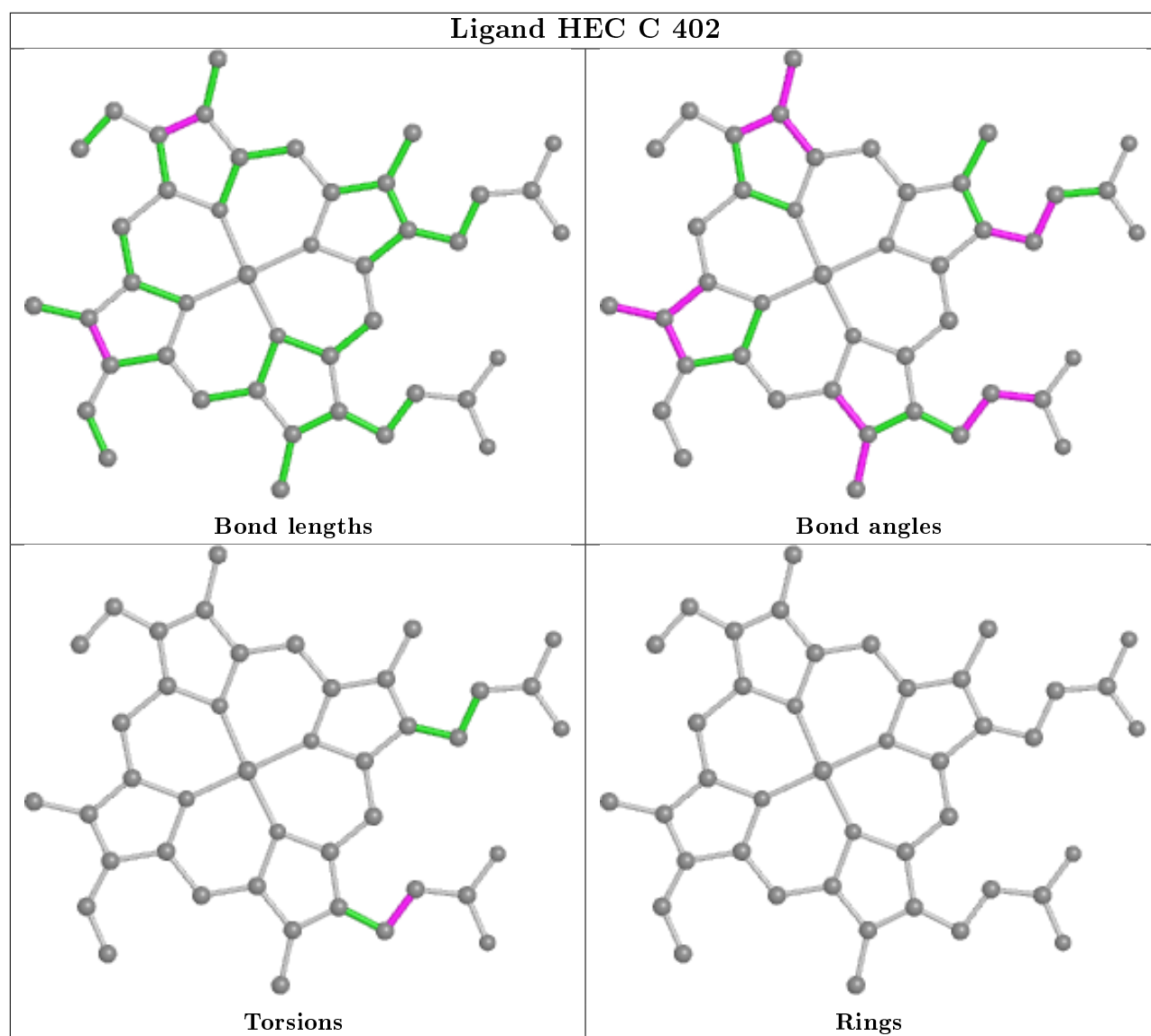
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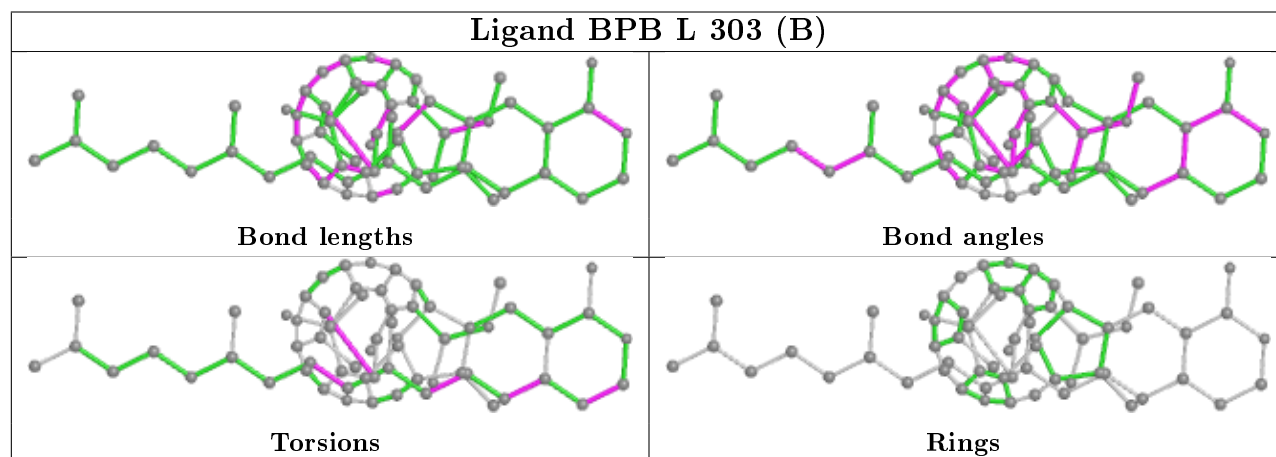
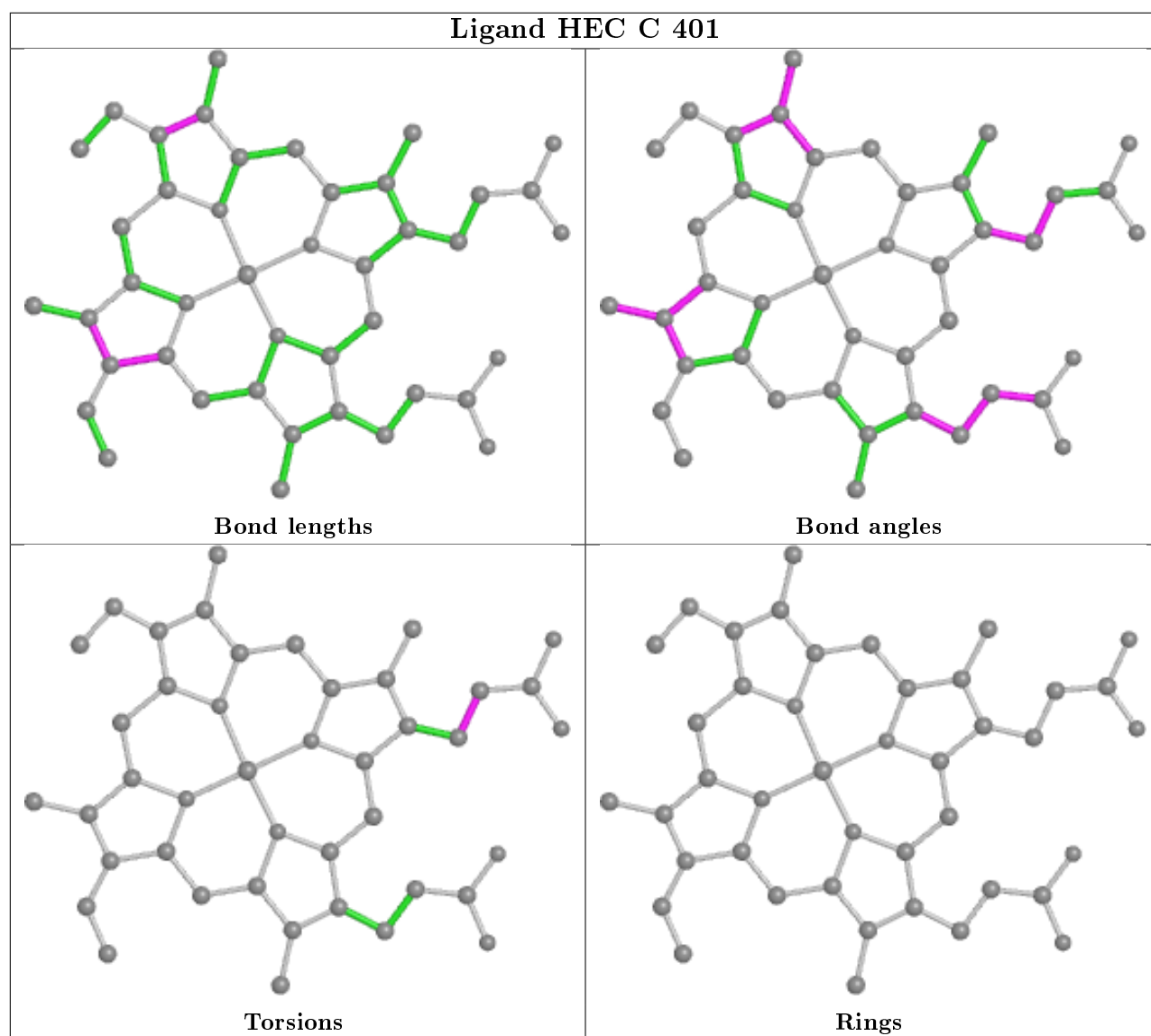


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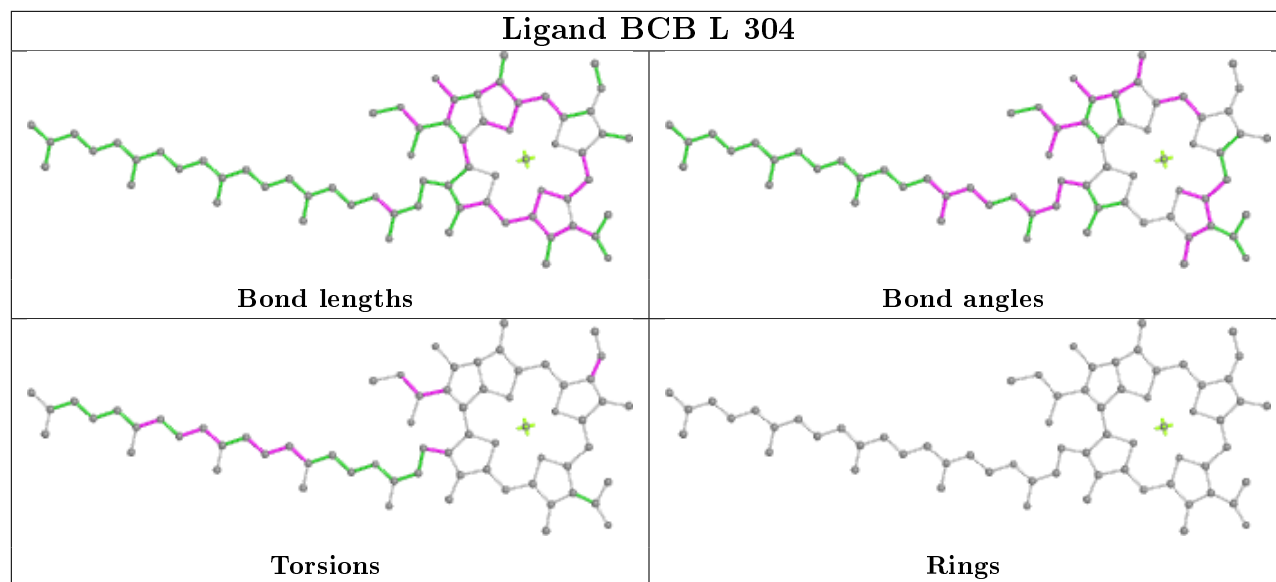
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	M	403[B]	BCB	4	0
8	H	701	LDA	1	0
8	L	305	LDA	1	0
5	C	404	HEC	2	0

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.

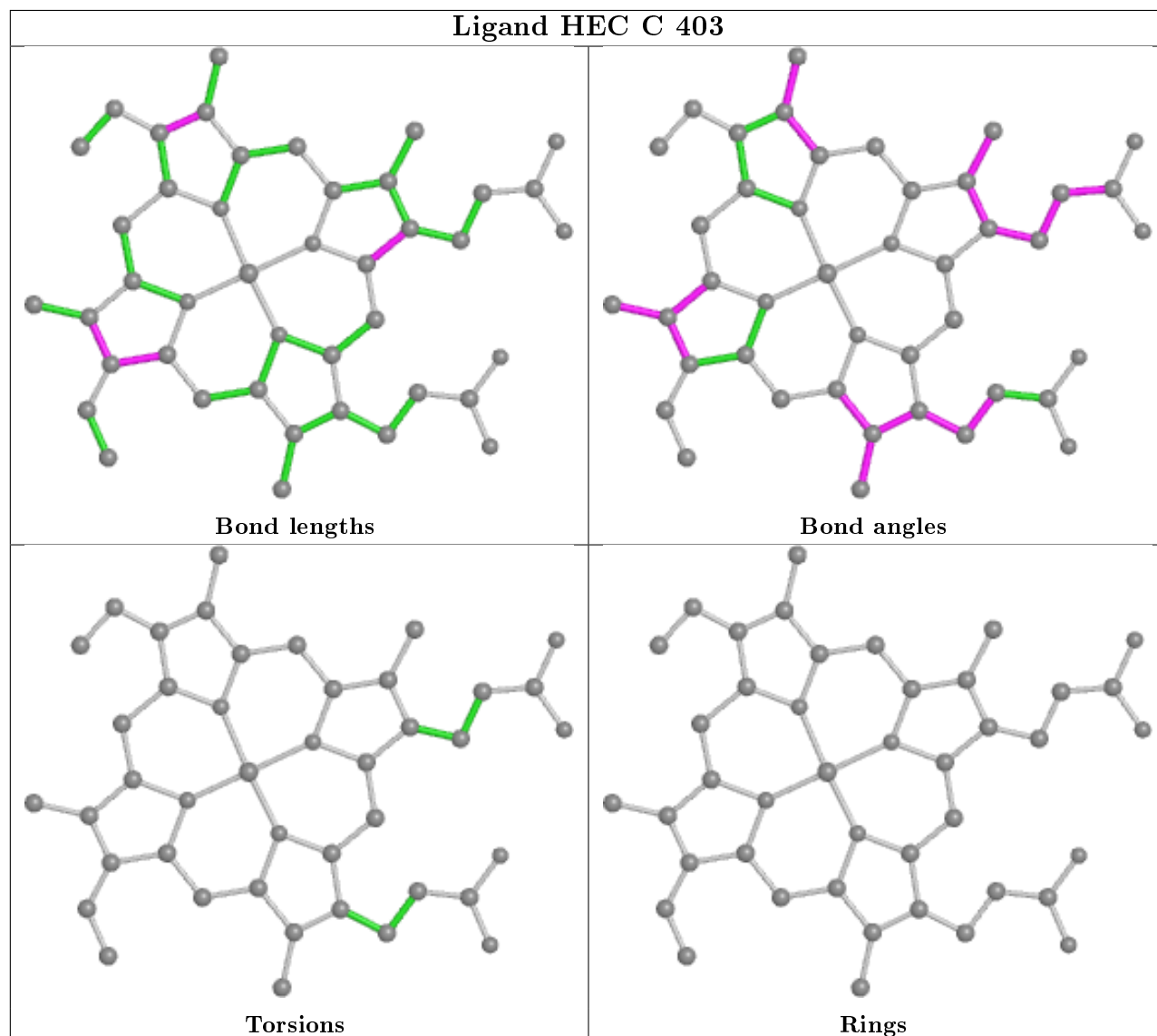


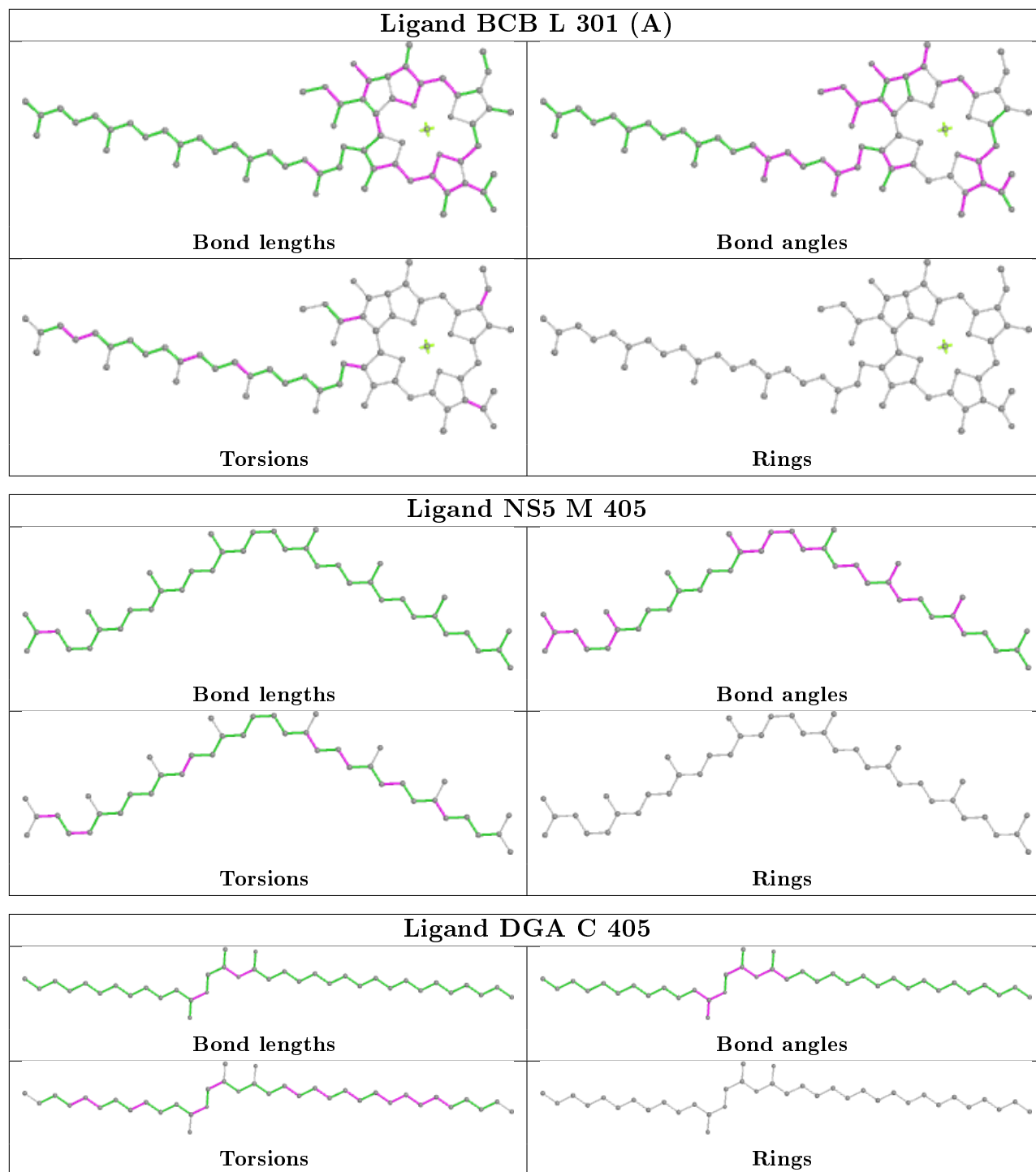


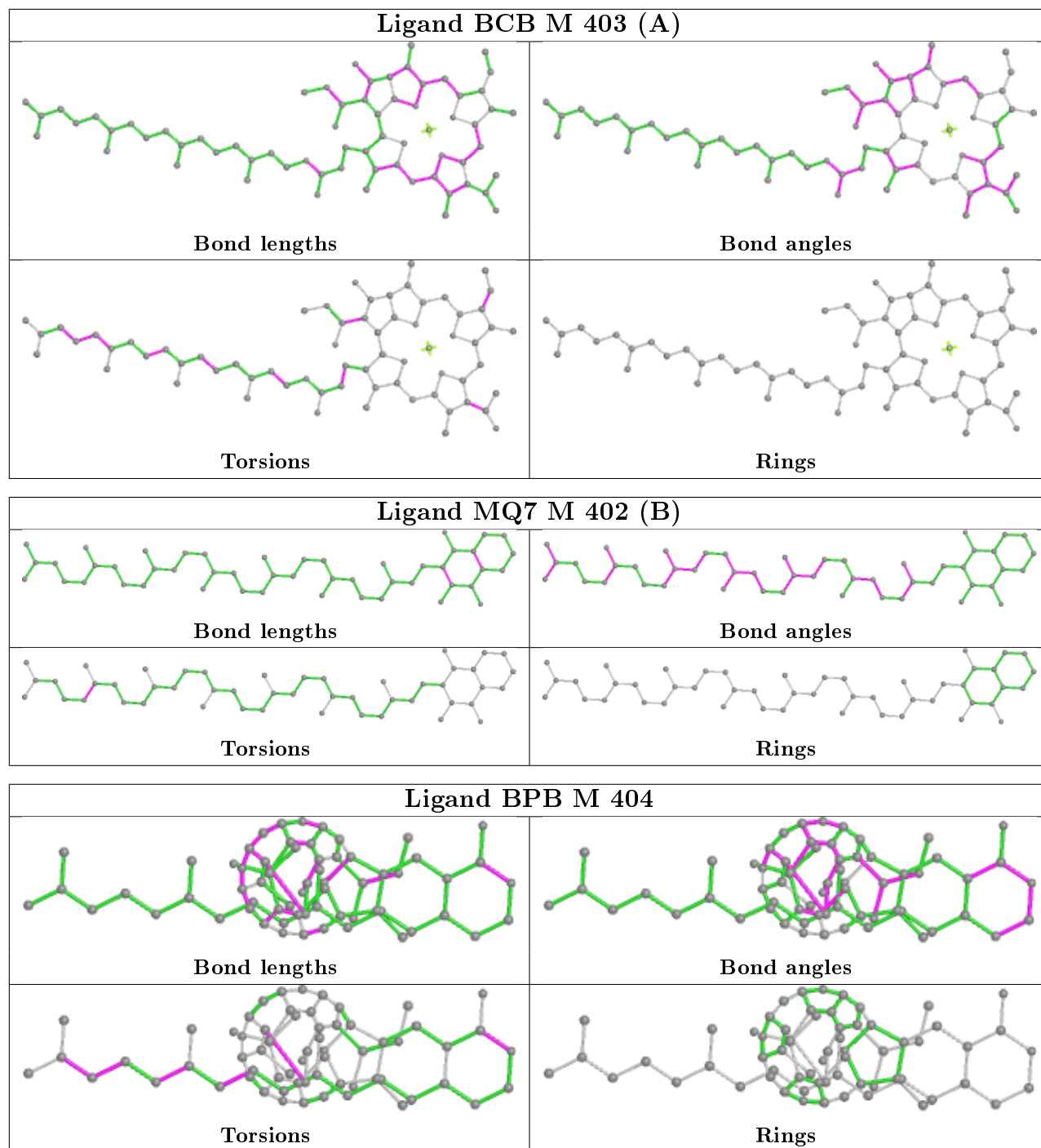
## Ligand BCB L 304

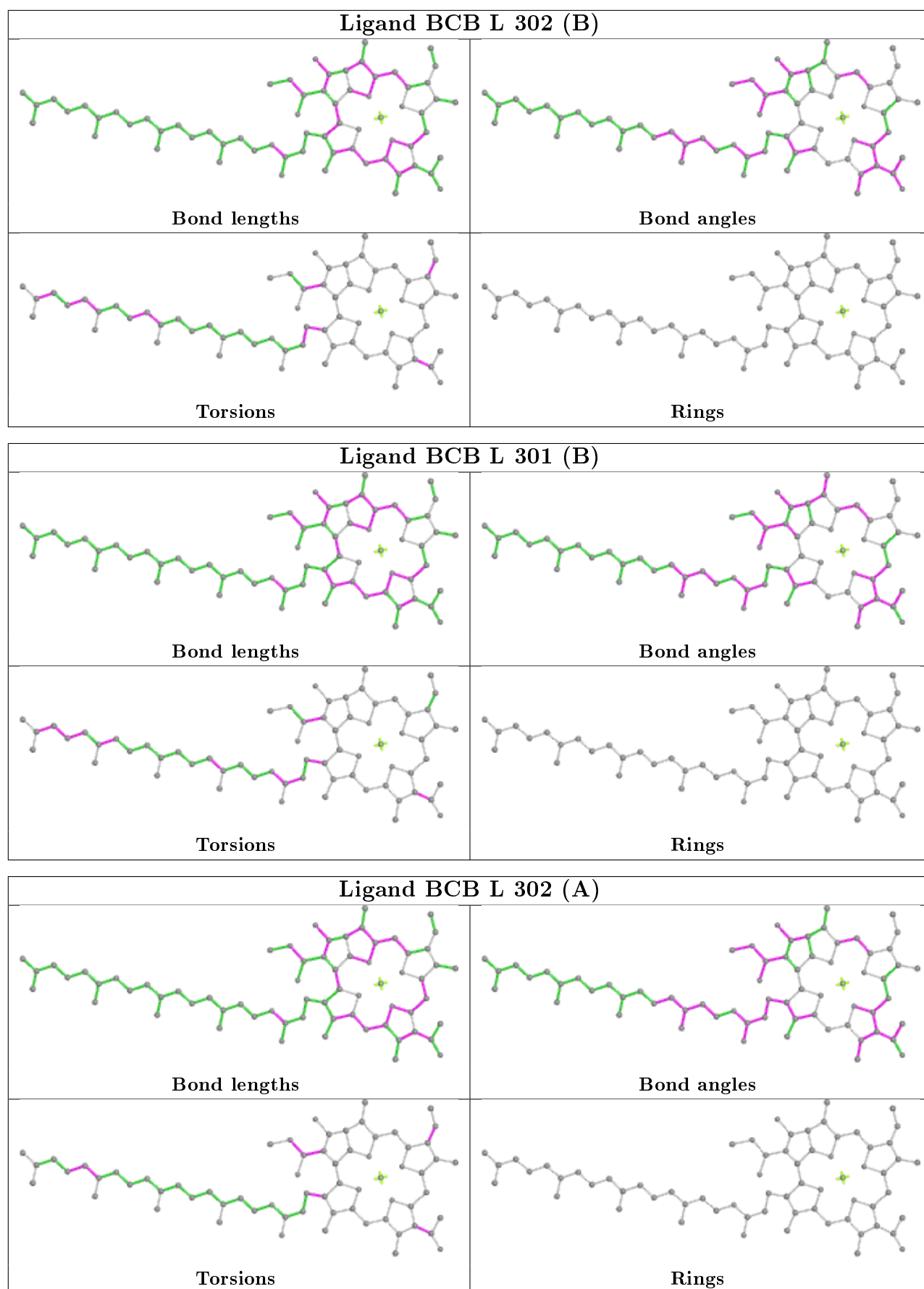


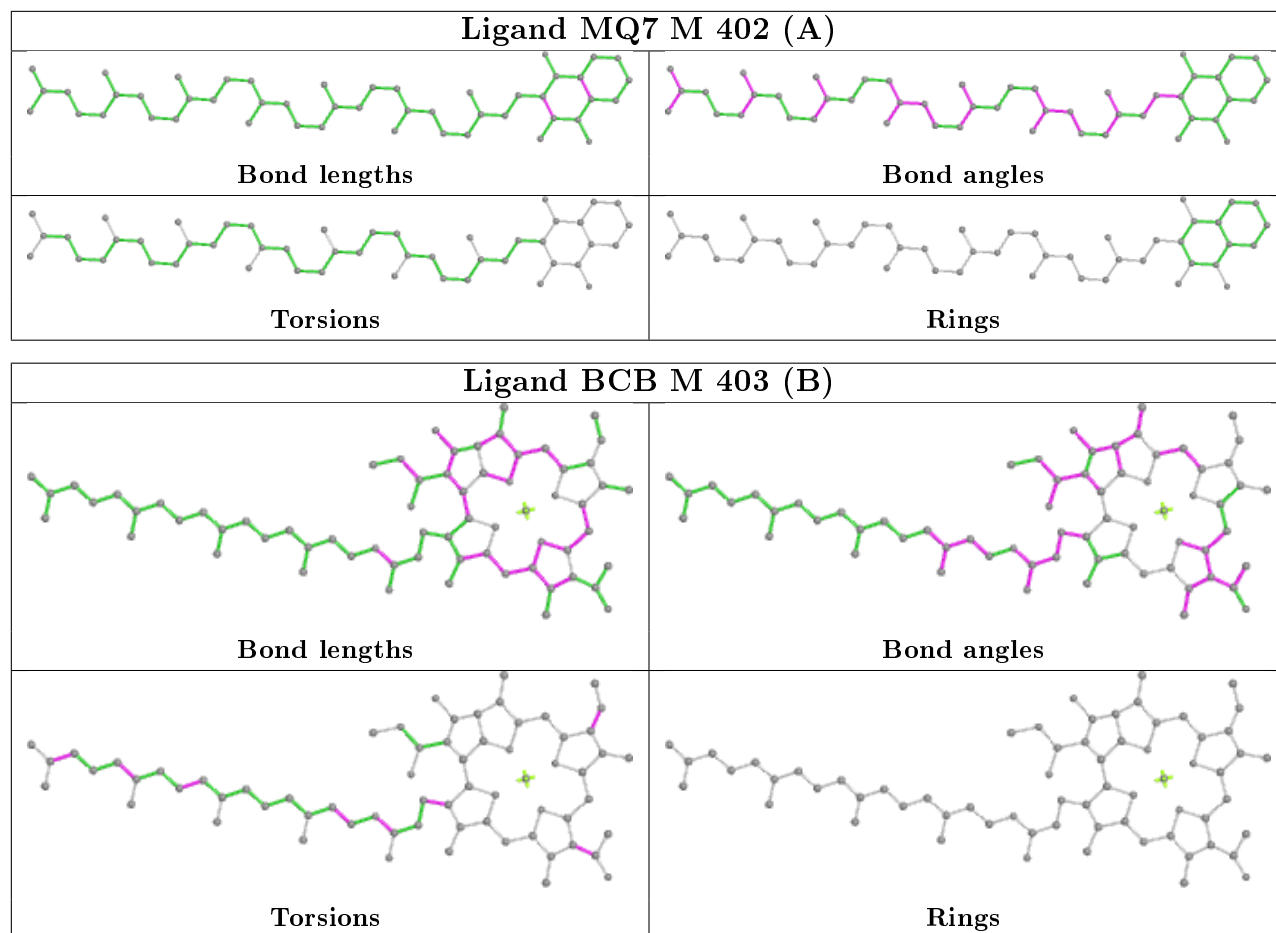
## Ligand HEC C 403



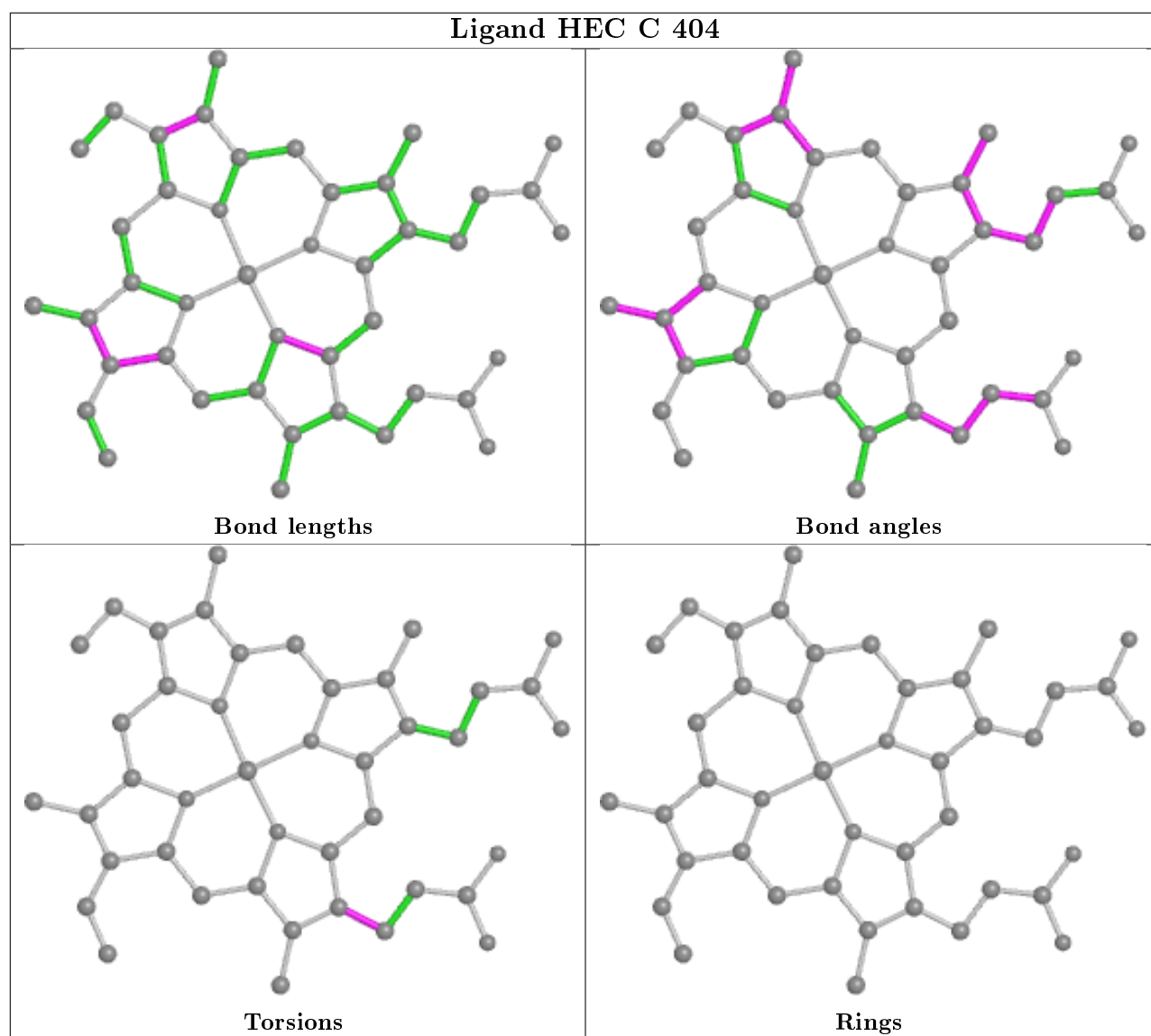












## 5.7 Other polymers [i](#)

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	C	332/336 (98%)	-0.77	0 <span>100</span> <span>100</span>	64, 83, 110, 135	0
2	H	257/258 (99%)	-0.59	3 (1%) <span>79</span> <span>73</span>	71, 93, 133, 185	0
3	L	273/273 (100%)	-0.81	0 <span>100</span> <span>100</span>	66, 80, 105, 122	0
4	M	323/323 (100%)	-0.60	0 <span>100</span> <span>100</span>	66, 80, 106, 134	0
All	All	1185/1190 (99%)	-0.69	3 (0%) <span>94</span> <span>93</span>	64, 84, 114, 185	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	46	PRO	2.7
2	H	258	LEU	2.2
2	H	257	LEU	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
2	FME	H	1	10/11	0.97	0.13	81,93,103,118	0

### 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.

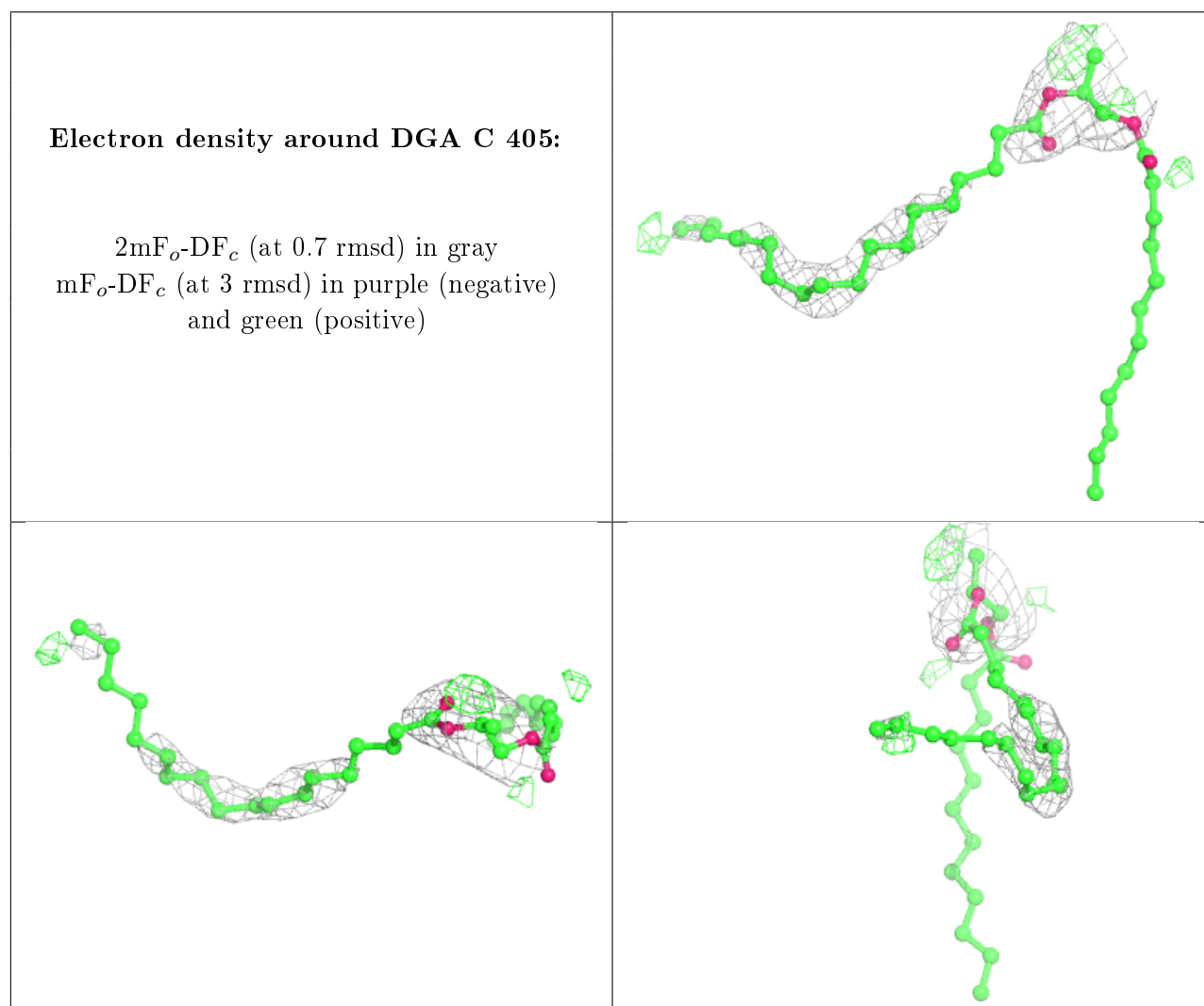
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	DGA	C	405	37/44	0.67	0.55	88,122,155,160	0
7	SO4	M	412	5/5	0.72	0.50	140,155,161,174	0
9	HTO	L	306	10/10	0.79	0.53	86,109,119,121	0
7	SO4	M	409	5/5	0.80	0.31	122,128,141,155	0
8	LDA	H	706	16/16	0.81	0.42	75,91,159,160	0
8	LDA	L	305	16/16	0.81	0.29	94,116,141,145	0
7	SO4	M	410	5/5	0.83	0.30	122,148,161,167	0
14	NS5	M	405	40/40	0.87	0.21	69,84,125,127	0
9	HTO	H	708	10/10	0.88	0.23	95,107,121,123	0
7	SO4	M	411	5/5	0.89	0.44	119,121,146,173	0
7	SO4	H	704	5/5	0.90	0.48	89,93,107,107	5
7	SO4	C	406	5/5	0.91	0.27	121,135,142,155	0
13	MQ7	M	402[B]	48/48	0.93	0.21	67,75,112,135	48
13	MQ7	M	402[A]	48/48	0.93	0.21	67,75,113,135	48
10	BCB	L	304	66/66	0.95	0.21	65,74,156,167	0
7	SO4	H	705	5/5	0.95	0.06	97,98,110,110	5
8	LDA	H	707	16/16	0.95	0.35	89,107,124,127	0
7	SO4	H	703	5/5	0.95	0.45	143,146,151,163	0
7	SO4	M	407	5/5	0.96	0.07	106,107,116,138	0
8	LDA	H	701	16/16	0.96	0.18	72,86,101,101	0
11	BPB	M	404	65/65	0.96	0.17	69,82,163,171	0
5	HEC	C	403	43/43	0.97	0.17	63,73,83,87	0
10	BCB	L	301[B]	66/66	0.98	0.20	56,66,82,99	66
10	BCB	L	302[B]	66/66	0.98	0.21	62,70,102,105	66
7	SO4	M	406	5/5	0.98	0.06	90,104,114,115	0
11	BPB	L	303[B]	65/65	0.98	0.21	67,73,82,87	65
10	BCB	L	302[A]	66/66	0.98	0.21	62,70,102,105	66
11	BPB	L	303[A]	65/65	0.98	0.21	67,73,82,87	65
5	HEC	C	401	43/43	0.98	0.14	80,88,103,117	0
10	BCB	M	403[B]	66/66	0.98	0.18	52,66,97,103	66
10	BCB	L	301[A]	66/66	0.98	0.20	56,66,82,99	66
10	BCB	M	403[A]	66/66	0.98	0.18	52,66,97,103	66
12	FE	M	401[B]	1/1	0.99	0.09	78,78,78,78	1
7	SO4	M	408	5/5	0.99	0.08	78,86,92,93	0
12	FE	M	401[A]	1/1	0.99	0.09	78,78,78,78	1
7	SO4	H	702	5/5	0.99	0.06	94,104,112,115	0
5	HEC	C	402	43/43	0.99	0.13	71,82,93,119	0

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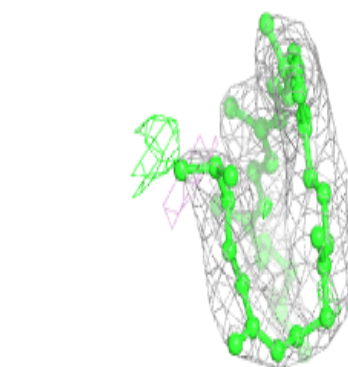
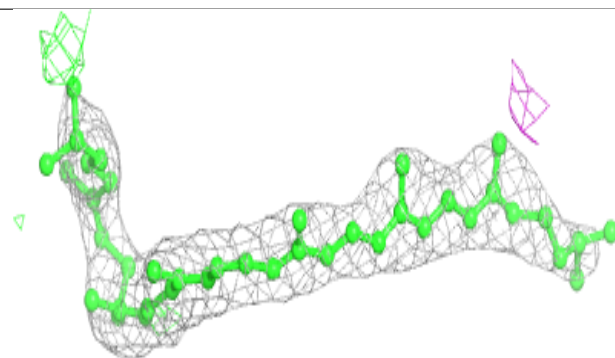
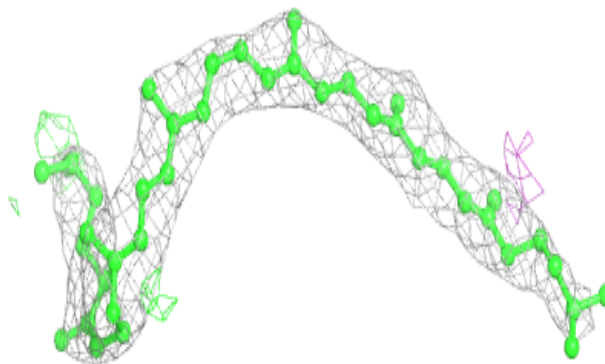
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	HEC	C	404	43/43	0.99	0.12	65,74,91,113	0

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.

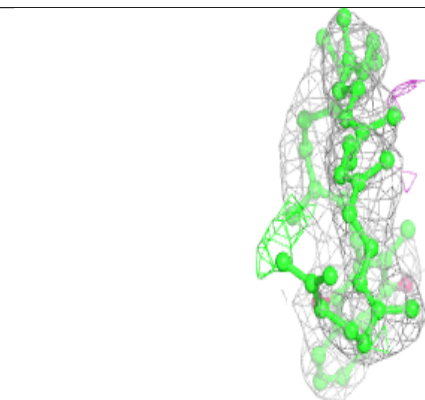
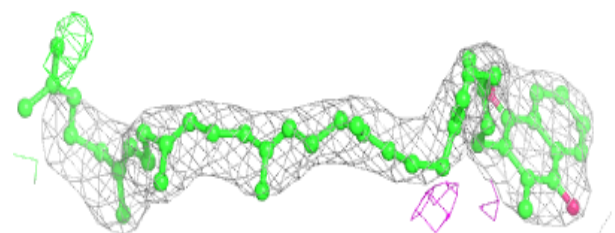
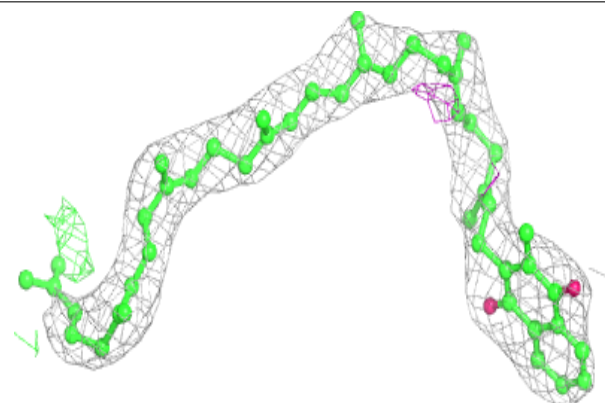


**Electron density around NS5 M 405:**

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

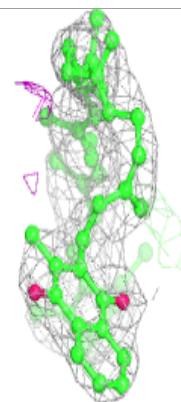
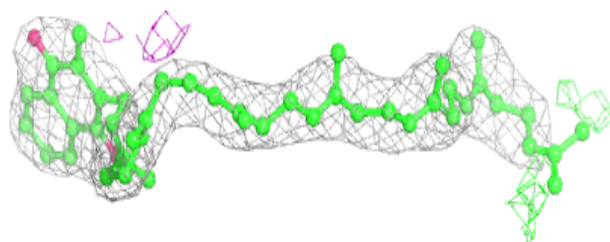
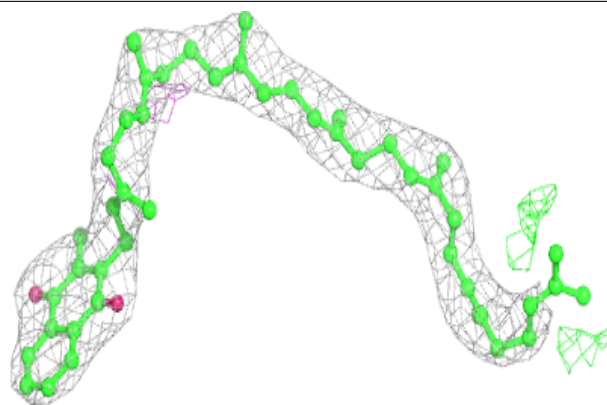
**Electron density around MQ7 M 402 (B):**

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

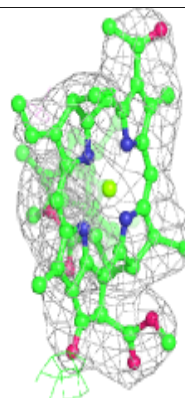
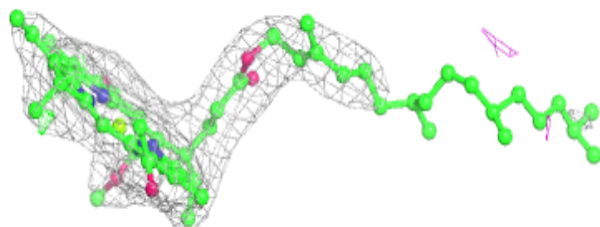
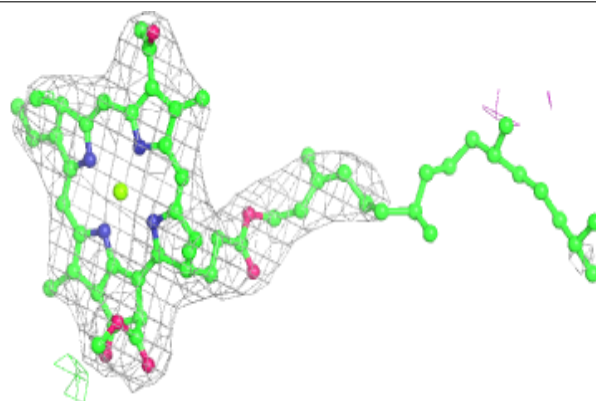


**Electron density around MQ7 M 402 (A):**

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and green (positive)

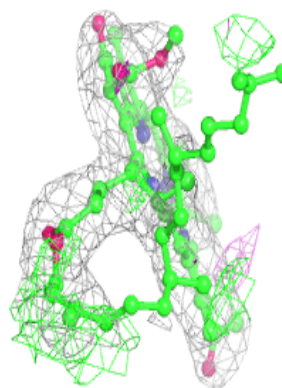
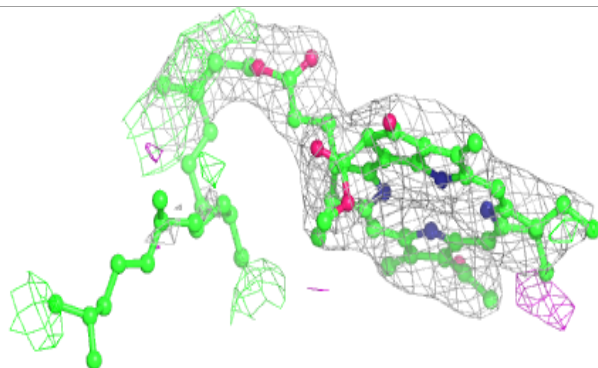
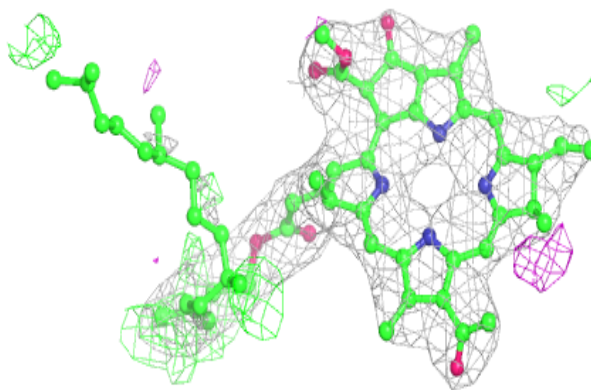
**Electron density around BCB L 304:**

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and green (positive)

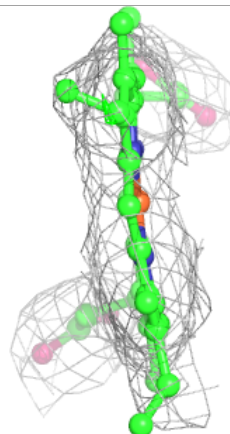
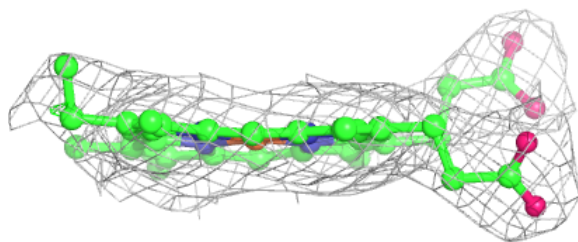
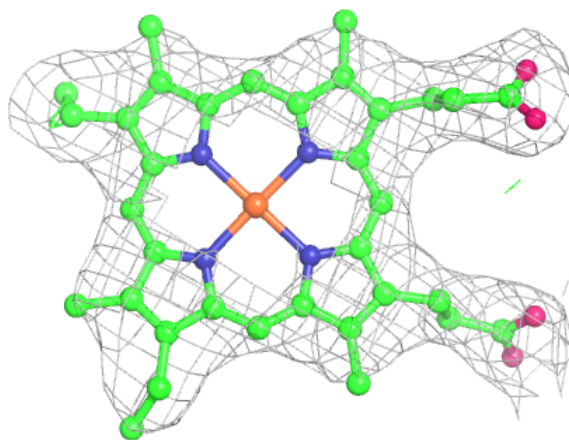


**Electron density around BPB M 404:**

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

**Electron density around HEC C 403:**

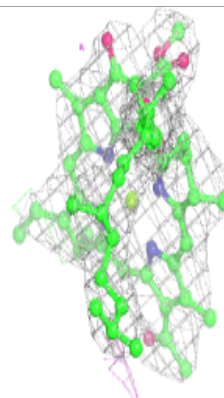
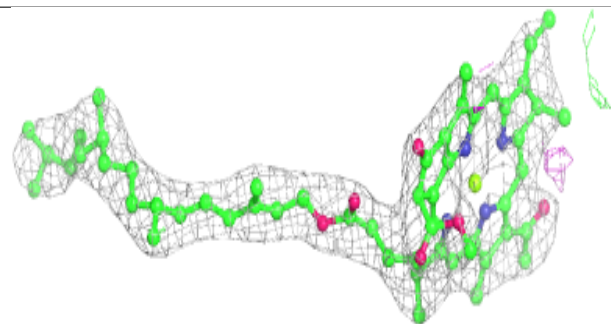
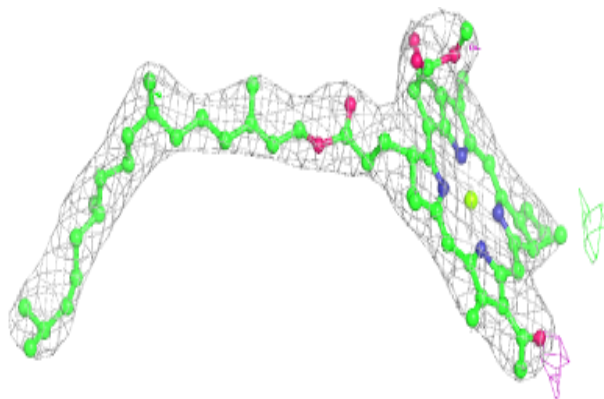
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



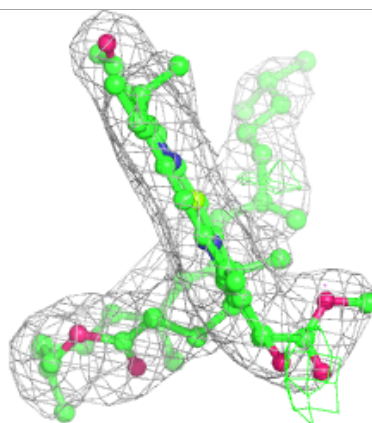
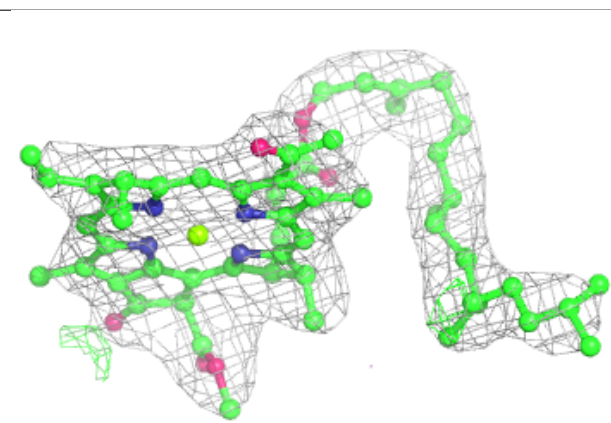
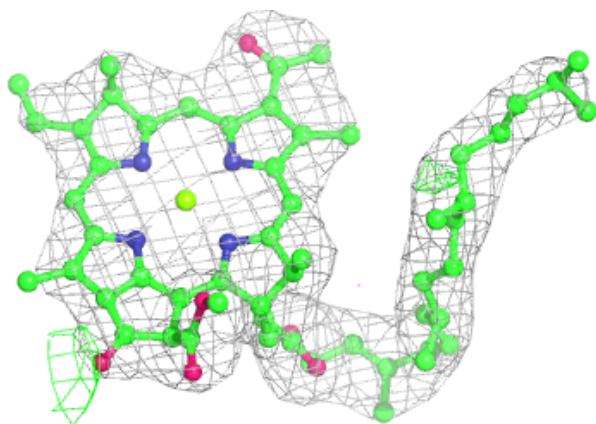


**Electron density around BCB L 301 (B):**

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

**Electron density around BCB L 302 (B):**

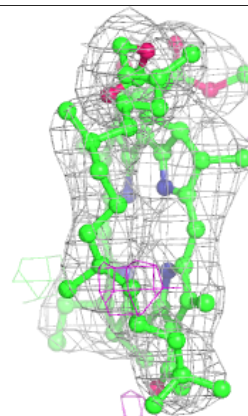
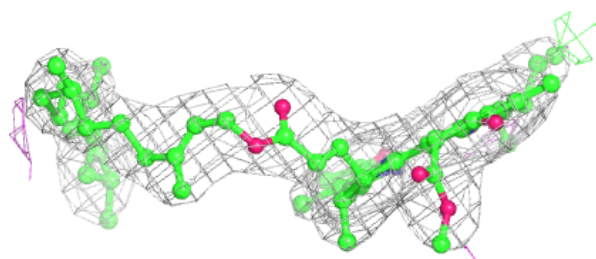
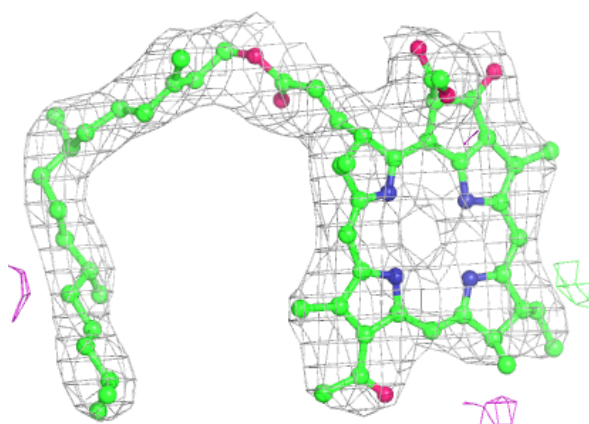
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



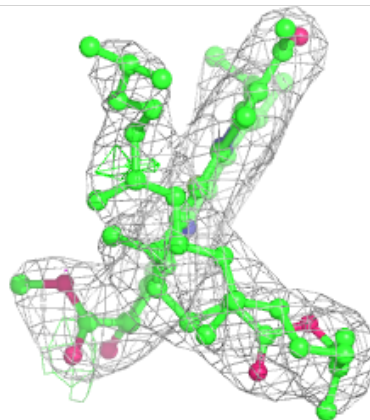
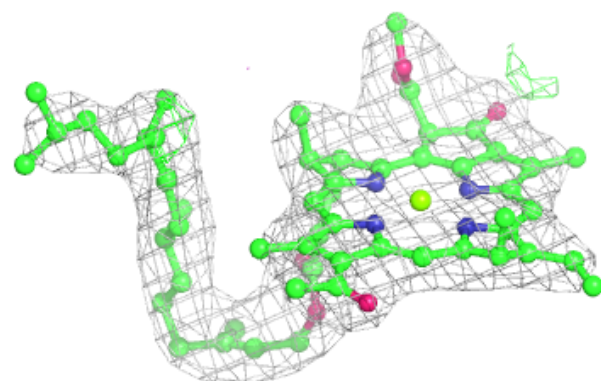
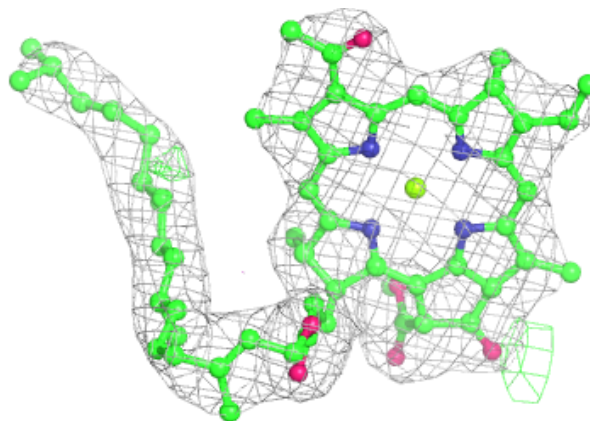


**Electron density around BPB L 303 (B):**

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

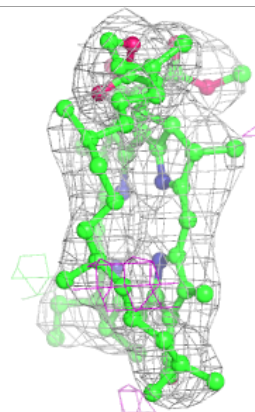
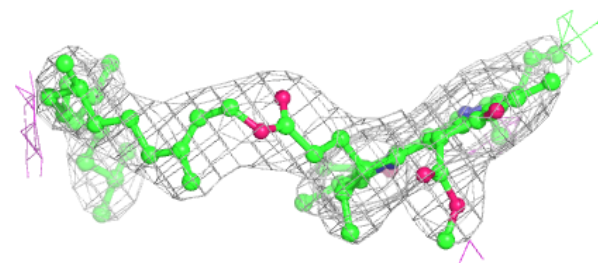
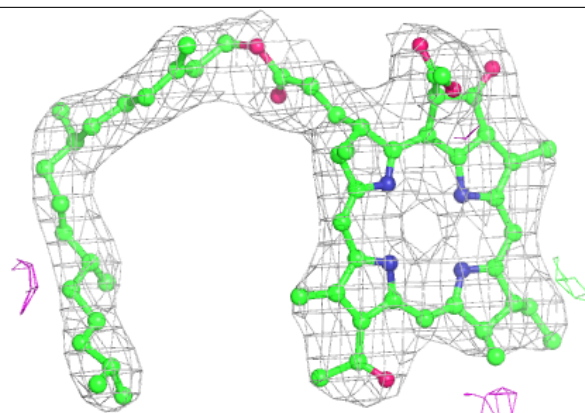
**Electron density around BCB L 302 (A):**

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



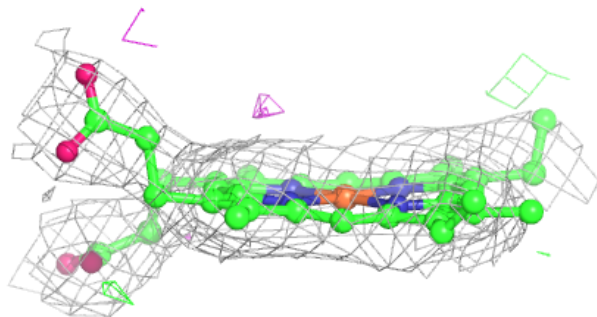
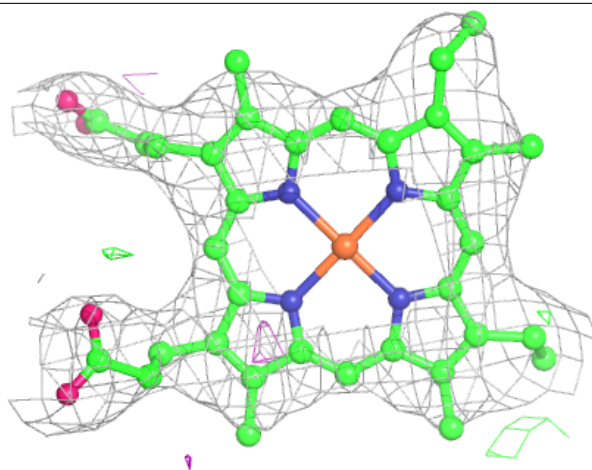
**Electron density around BPB L 303 (A):**

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



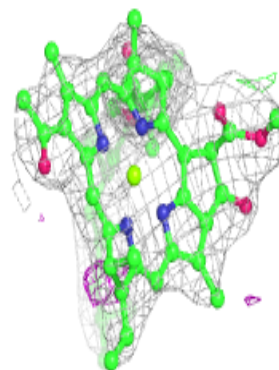
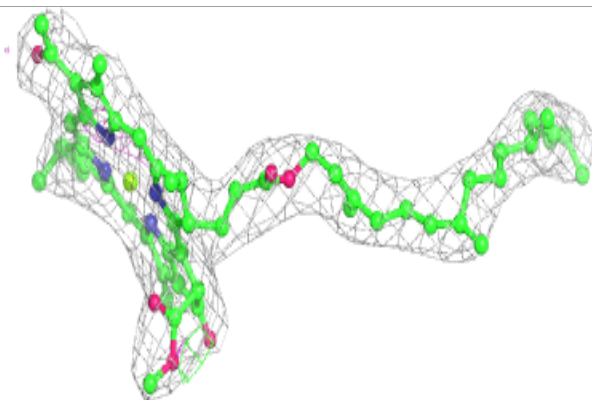
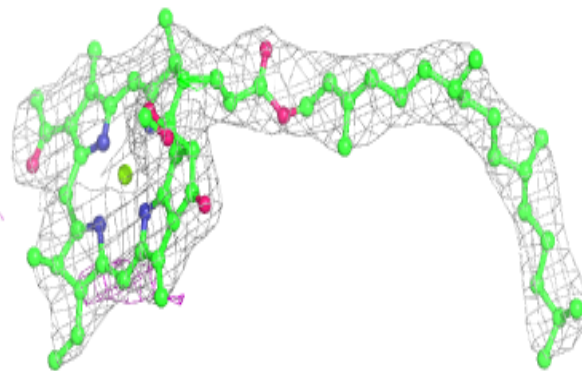
**Electron density around HEC C 401:**

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

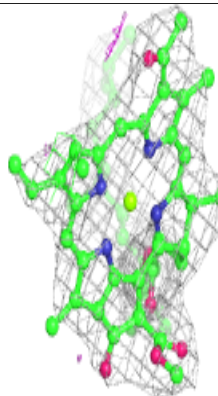
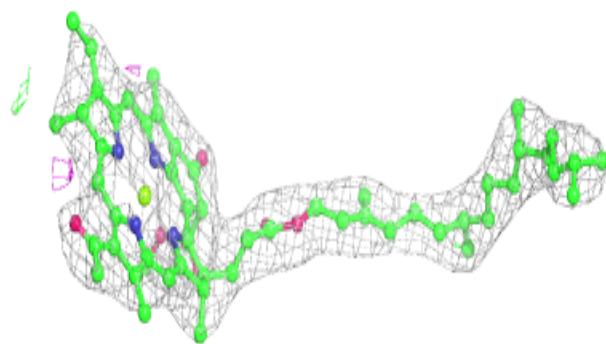
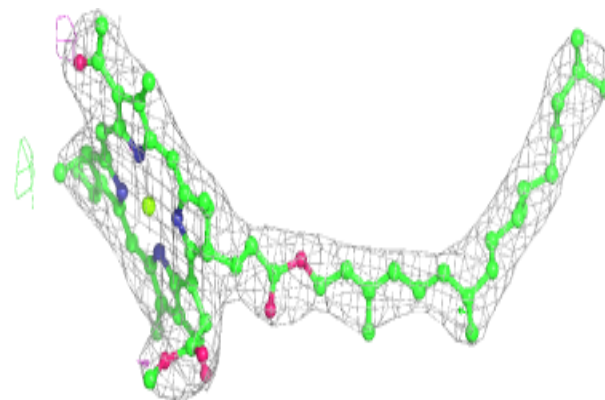


**Electron density around BCB M 403 (B):**

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

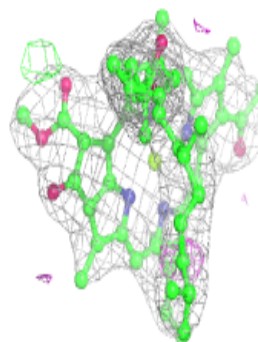
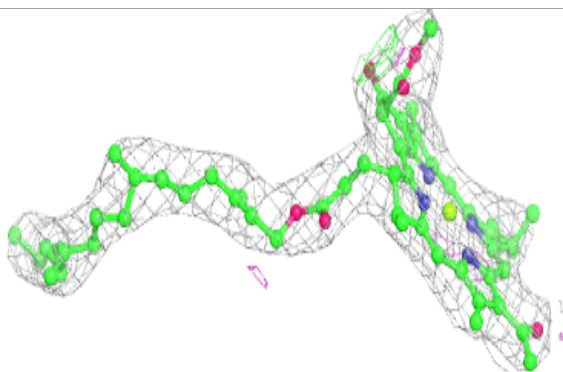
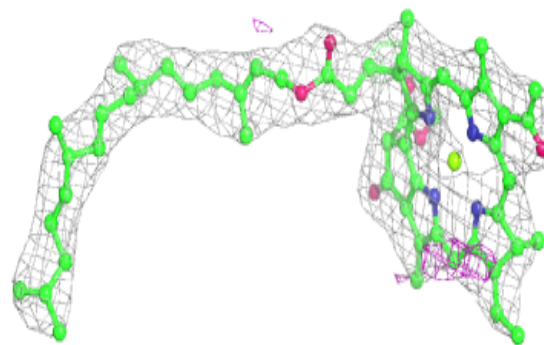
**Electron density around BCB L 301 (A):**

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

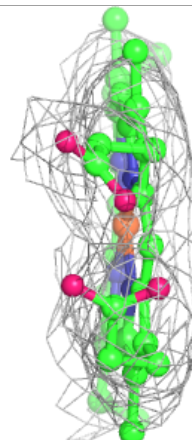
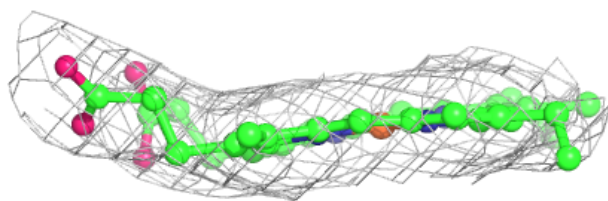
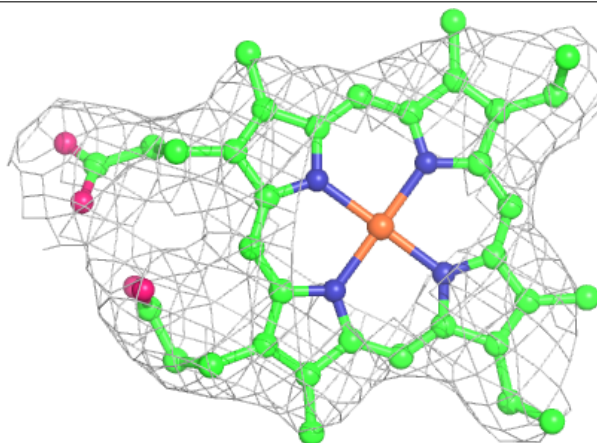


**Electron density around BCB M 403 (A):**

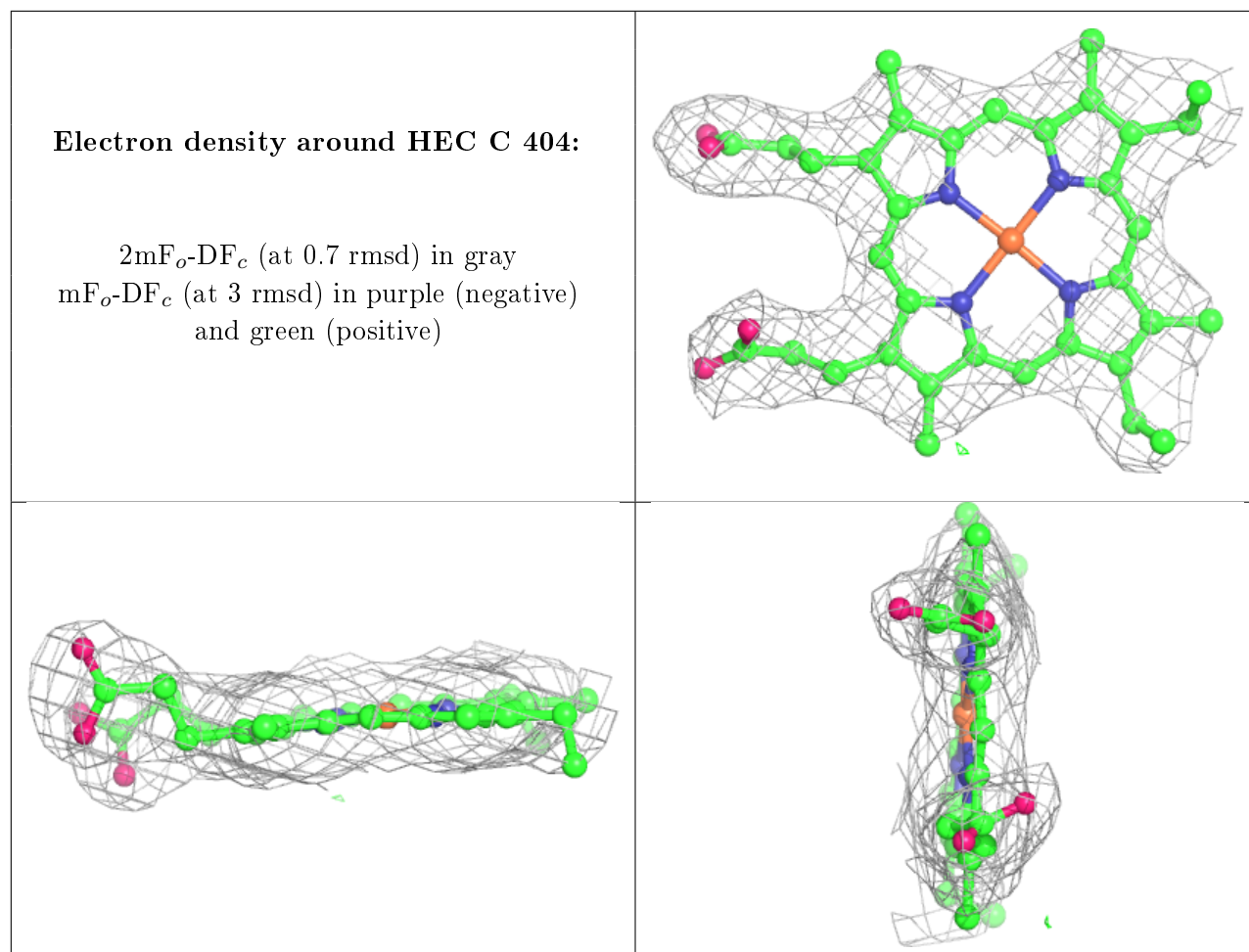
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around HEC C 402:**

$2mF_o-DF_c$  (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.