



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 14, 2023 – 08:59 PM EDT

PDB ID : 1R2C  
Title : PHOTOSYNTHETIC REACTION CENTER BLASTOCHLORIS VIRIDIS (ATCC)  
Authors : Baxter, R.H.; Ponomarenko, N.; Pahl, R.; Srajer, V.; Moffat, K.; Norris, J.R.  
Deposited on : 2003-09-26  
Resolution : 2.86 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35

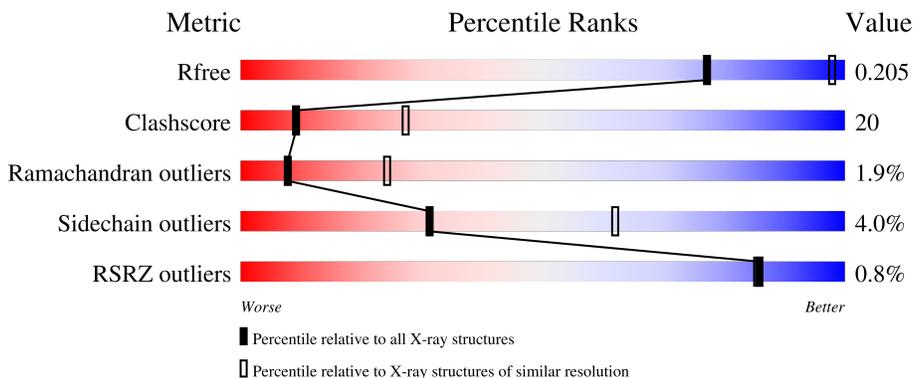
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.86 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C	336	 2% 67% 31% .
2	L	273	 67% 31% .
3	M	323	 65% 33% .
4	H	258	 2% 53% 42% 5%

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	BCB	L	304	X	-	-	-
6	BCB	M	1303	X	-	-	-
7	BPB	M	401	X	-	X	-
9	LDA	M	702	-	-	-	X

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 10140 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 precursor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	C	332	2602	1640	466	478	18	41	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	273	2171	1459	350	355	7	10	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	M	323	2555	1702	419	423	11	15	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	H	258	2018	1292	344	380	2	98	0	0

There is a discrepancy between the modelled and reference sequences:

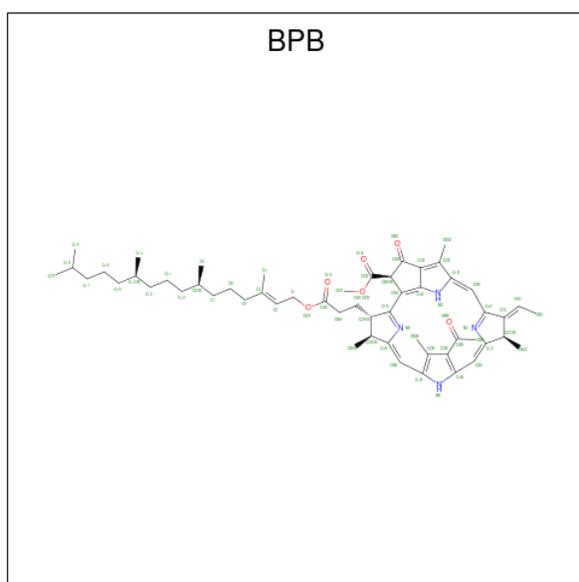
Chain	Residue	Modelled	Actual	Comment	Reference
H	1	FME	MET	modified residue	UNP P06008

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C<sub>34</sub>H<sub>32</sub>FeN<sub>4</sub>O<sub>4</sub>).



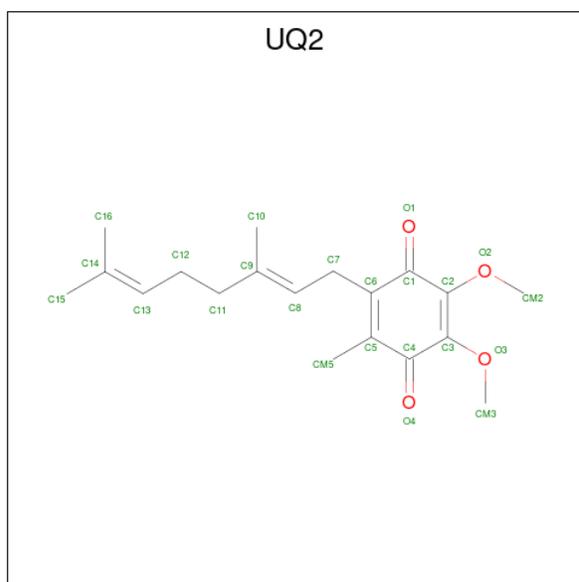
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
6	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
6	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
6	M	1	Total	C	Mg	N	O	15	0
			66	55	1	4	6		
6	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 7 is BACTERIOPHEOPHYTIN B (three-letter code: BPB) (formula:  $C_{55}H_{74}N_4O_6$ ).



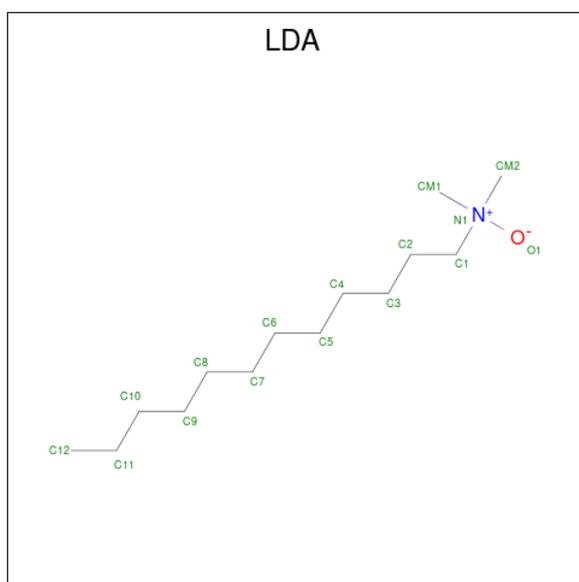
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	L	1	Total	C	N	O	0	0
			65	55	4	6		
7	M	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 8 is UBIQUINONE-2 (three-letter code: UQ2) (formula:  $C_{19}H_{26}O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	L	1	Total	C	O	0	0
			23	19	4		

- Molecule 9 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula:  $C_{14}H_{31}NO$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	L	1	Total	C	N	O	3	0
			16	14	1	1		
9	M	1	Total	C	N	O	0	0
			16	14	1	1		

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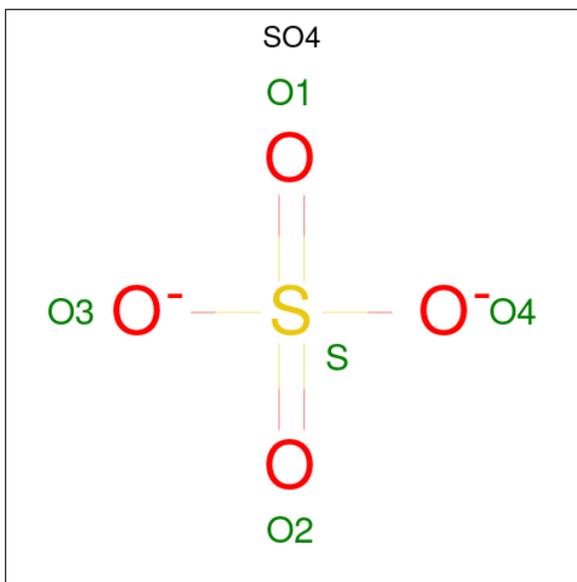
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	M	1	Total	C	N	O	0	0
			16	14	1	1		
9	M	1	Total	C	N	O	3	0
			16	14	1	1		
9	M	1	Total	C	N	O	0	0
			16	14	1	1		
9	H	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 10 is FE (II) ION (three-letter code: FE2) (formula: Fe).

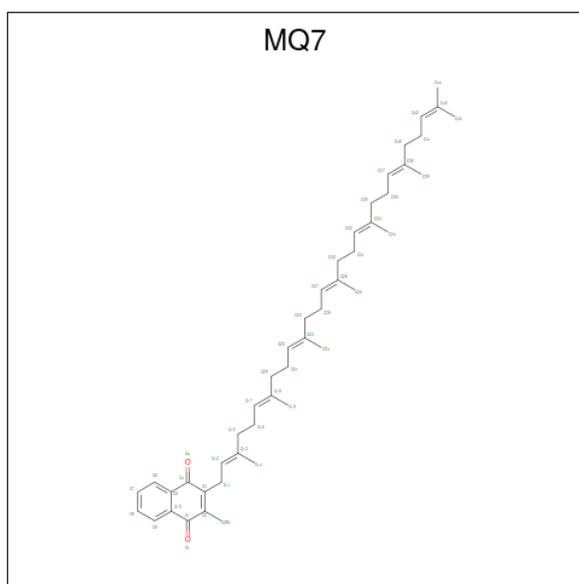
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	M	1	Total	Fe	0	0
			1	1		

- Molecule 11 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



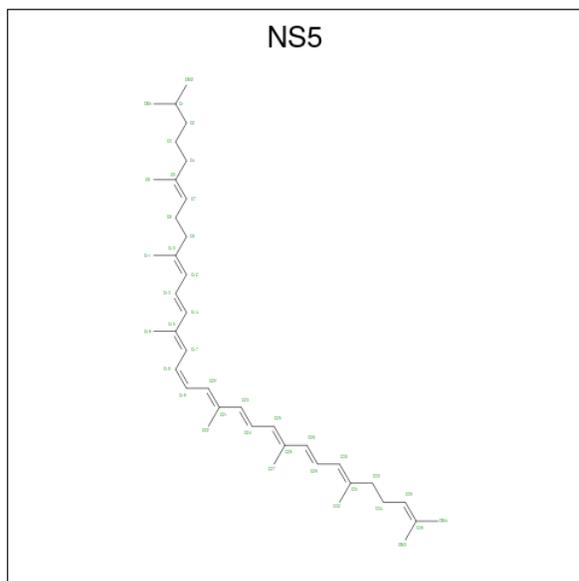
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	M	1	Total	O	S	0	0
			5	4	1		
11	M	1	Total	O	S	0	0
			5	4	1		
11	M	1	Total	O	S	0	0
			5	4	1		
11	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 12 is MENAQUINONE-7 (three-letter code: MQ7) (formula:  $C_{46}H_{64}O_2$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
12	M	1	Total	C	O	0	0
			48	46	2		

- Molecule 13 is 15-cis-1,2-dihydroneurosporene (three-letter code: NS5) (formula:  $C_{40}H_{60}$ ).

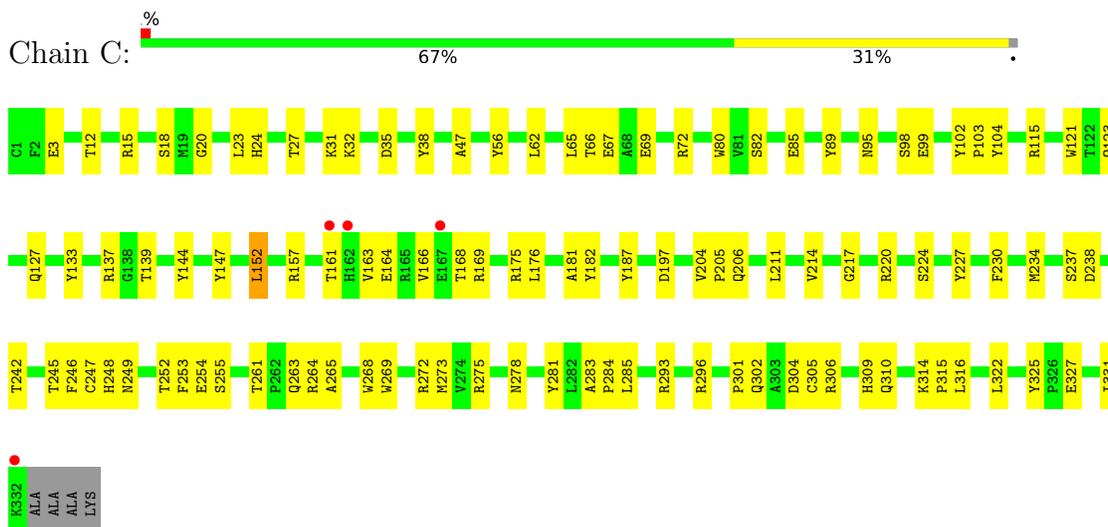


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
13	M	1	Total	C		11	0
			40	40			

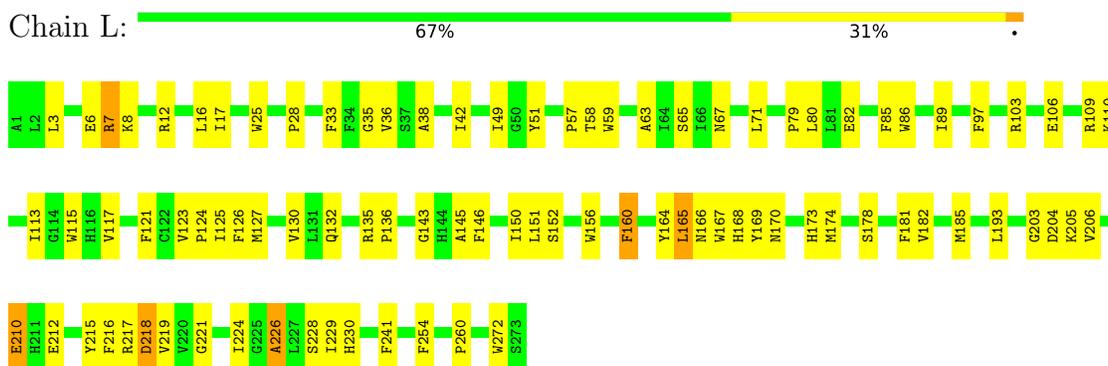
### 3 Residue-property plots [i](#)

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.

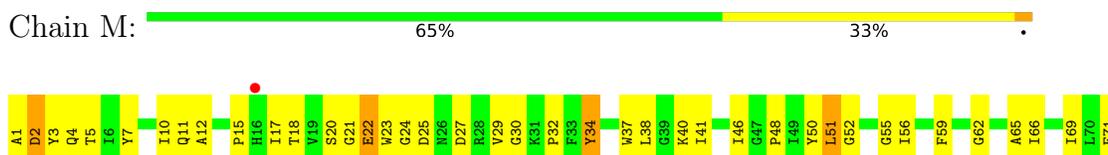
- Molecule 1: Photosynthetic reaction center cytochrome C subunit precursor

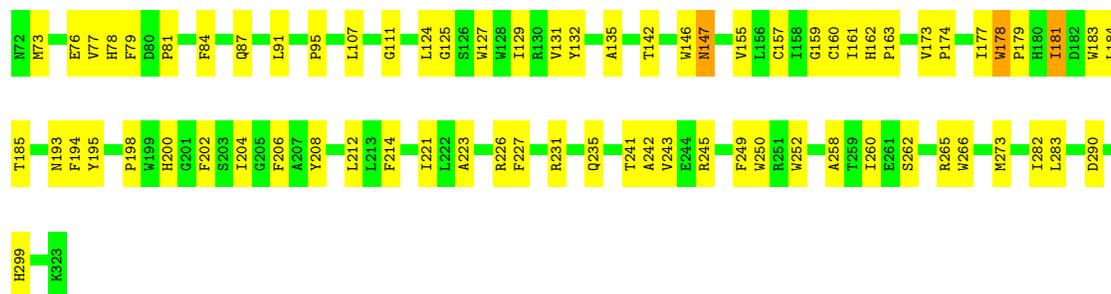


- Molecule 2: Reaction center protein L chain

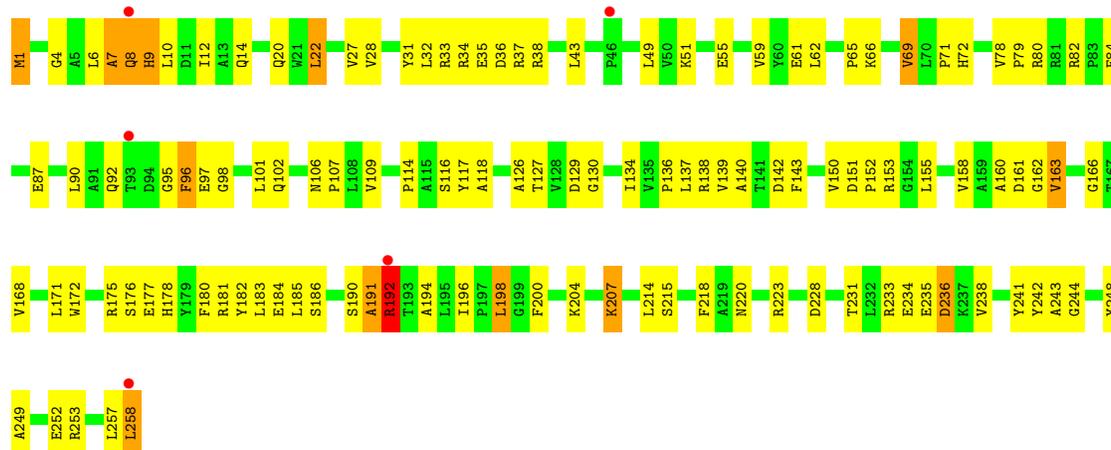


- Molecule 3: Reaction center protein M chain





- Molecule 4: Reaction center protein H chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	223.50Å 223.50Å 112.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.83 – 2.86 48.83 – 2.86	Depositor EDS
% Data completeness (in resolution range)	97.3 (48.83-2.86) 97.4 (48.83-2.86)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.90 (at 2.86Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.202 , 0.228 0.184 , 0.205	Depositor DCC
$R_{free}$ test set	6311 reflections (9.82%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	59.3	Xtrriage
Anisotropy	0.312	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 56.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10140	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.10% 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: HEM, LDA, BPB, MQ7, NS5, SO4, UQ2, FME, FE2, BCB

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	0.35	0/2669	0.62	1/3637 (0.0%)
2	L	0.41	0/2259	0.60	0/3084
3	M	0.42	0/2659	0.58	0/3637
4	H	0.35	0/2055	0.62	0/2807
All	All	0.38	0/9642	0.61	1/13165 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	249	ASN	N-CA-C	-6.50	93.44	111.00

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	2579	74	0
2	L	2171	0	2098	90	0
3	M	2555	0	2452	112	0
4	H	2018	0	2020	113	0
5	C	172	0	120	7	0
6	L	132	0	144	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	M	132	0	143	29	0
7	L	65	0	74	12	0
7	M	65	0	74	22	0
8	L	23	0	26	4	0
9	H	16	0	31	4	0
9	L	16	0	31	2	0
9	M	64	0	124	11	0
10	M	1	0	0	0	0
11	H	5	0	0	0	0
11	M	15	0	0	0	0
12	M	48	0	64	0	0
13	M	40	0	60	5	0
All	All	10140	0	10040	393	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 20.

The worst 5 of 393 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)
4:H:152:PRO:HA	4:H:155:LEU:HD12	1.31	1.05
7:M:401:BPB:H14	7:M:401:BPB:H17	1.39	1.03
3:M:32:PRO:HG3	3:M:48:PRO:HD3	1.39	1.02
6:L:302:BCB:HBD	6:L:302:BCB:HBA1	1.46	0.94
7:L:402:BPB:HBBA	3:M:208:TYR:HB3	1.47	0.94

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	C	330/336 (98%)	299 (91%)	30 (9%)	1 (0%)	41	68
2	L	271/273 (99%)	251 (93%)	17 (6%)	3 (1%)	14	38
3	M	321/323 (99%)	299 (93%)	19 (6%)	3 (1%)	17	43
4	H	256/258 (99%)	216 (84%)	25 (10%)	15 (6%)	1	4
All	All	1178/1190 (99%)	1065 (90%)	91 (8%)	22 (2%)	8	24

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	57	PRO
4	H	7	ALA
4	H	8	GLN
4	H	9	HIS
4	H	96	PHE

### 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	C	281/282 (100%)	276 (98%)	5 (2%)	59	82
2	L	218/218 (100%)	209 (96%)	9 (4%)	30	61
3	M	249/249 (100%)	239 (96%)	10 (4%)	31	62
4	H	212/212 (100%)	198 (93%)	14 (7%)	16	40
All	All	960/961 (100%)	922 (96%)	38 (4%)	31	62

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	92	GLN
4	H	236	ASP
4	H	96	PHE
4	H	198	LEU
4	H	258	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
4	H	106	ASN
4	H	102	GLN
3	M	16	HIS
4	H	72	HIS
2	L	239	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](#)

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
4	FME	H	1	4	8,9,10	0.67	0	7,9,11	3.47	3 (42%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FME	H	1	4	-	2/7/9/11	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	1	FME	CA-N-CN	-7.21	111.74	122.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	1	FME	O1-CN-N	-3.99	114.75	125.27
4	H	1	FME	CE-SD-CG	-3.30	89.07	100.40

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	1	FME	CB-CG-SD-CE
4	H	1	FME	O1-CN-N-CA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	1	FME	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 1 is monoatomic - leaving 23 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
9	LDA	M	702	-	12,15,15	2.26	1 (8%)	14,17,17	0.51	0
11	SO4	H	801	-	4,4,4	0.35	0	6,6,6	0.38	0
5	HEM	C	1203	1	41,50,50	1.43	5 (12%)	45,82,82	1.22	7 (15%)
11	SO4	M	803	-	4,4,4	0.47	0	6,6,6	0.09	0
7	BPB	M	401	-	49,70,70	1.43	8 (16%)	47,101,101	2.71	13 (27%)
11	SO4	M	802	-	4,4,4	0.51	0	6,6,6	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
9	LDA	L	705	-	12,15,15	2.16	1 (8%)	14,17,17	0.57	0
5	HEM	C	1202	1	41,50,50	1.42	3 (7%)	45,82,82	1.20	5 (11%)
6	BCB	M	1303	3	54,74,74	1.51	7 (12%)	52,115,115	2.22	13 (25%)
13	NS5	M	600	-	39,39,39	0.79	0	44,46,46	1.08	4 (9%)
6	BCB	L	304	2	54,74,74	1.59	8 (14%)	52,115,115	2.50	12 (23%)
9	LDA	H	703	-	12,15,15	2.50	1 (8%)	14,17,17	0.50	0
5	HEM	C	1204	1	41,50,50	1.50	6 (14%)	45,82,82	1.50	8 (17%)
9	LDA	M	706	-	12,15,15	2.39	1 (8%)	14,17,17	0.51	0
5	HEM	C	1201	1	41,50,50	1.45	4 (9%)	45,82,82	1.28	5 (11%)
6	BCB	L	302	2	54,74,74	1.62	6 (11%)	52,115,115	2.66	17 (32%)
12	MQ7	M	501	-	49,49,49	1.65	16 (32%)	60,63,63	1.54	7 (11%)
9	LDA	M	701	-	12,15,15	2.43	1 (8%)	14,17,17	0.63	0
7	BPB	L	402	-	49,70,70	1.33	7 (14%)	47,101,101	3.24	12 (25%)
8	UQ2	L	502	-	23,23,23	1.83	5 (21%)	28,31,31	1.26	2 (7%)
11	SO4	M	804	-	4,4,4	0.51	0	6,6,6	0.39	0
6	BCB	M	1301	3	54,74,74	1.48	7 (12%)	52,115,115	2.37	11 (21%)
9	LDA	M	704	-	12,15,15	2.47	1 (8%)	14,17,17	0.54	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
9	LDA	M	702	-	-	0/13/13/13	-
5	HEM	C	1203	1	-	6/12/54/54	-
7	BPB	M	401	-	1/1/18/23	13/37/105/105	0/5/6/6
9	LDA	L	705	-	-	0/13/13/13	-
5	HEM	C	1202	1	-	6/12/54/54	-
6	BCB	M	1303	3	1/1/31/36	6/37/177/177	-
13	NS5	M	600	-	-	10/43/43/43	-
6	BCB	L	304	2	1/1/31/36	13/37/177/177	-
9	LDA	H	703	-	-	1/13/13/13	-
5	HEM	C	1204	1	-	6/12/54/54	-
9	LDA	M	706	-	-	0/13/13/13	-
5	HEM	C	1201	1	-	3/12/54/54	-
6	BCB	L	302	2	-	9/37/177/177	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	MQ7	M	501	-	-	2/41/61/61	0/2/2/2
9	LDA	M	701	-	-	0/13/13/13	-
7	BPB	L	402	-	-	6/37/105/105	0/5/6/6
8	UQ2	L	502	-	-	3/15/39/39	0/1/1/1
6	BCB	M	1301	3	-	6/37/177/177	-
9	LDA	M	704	-	-	3/13/13/13	-

The worst 5 of 88 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	H	703	LDA	O1-N1	-8.63	1.22	1.42
9	M	704	LDA	O1-N1	-8.51	1.22	1.42
9	M	701	LDA	O1-N1	-8.36	1.22	1.42
9	M	706	LDA	O1-N1	-8.26	1.22	1.42
9	M	702	LDA	O1-N1	-7.77	1.24	1.42

The worst 5 of 116 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	402	BPB	C1-C2-C3	10.85	144.81	126.04
7	L	402	BPB	O2D-CGD-CBD	10.17	123.89	111.00
7	M	401	BPB	C1-C2-C3	9.90	143.17	126.04
6	L	304	BCB	O2D-CGD-CBD	9.74	123.34	111.00
7	M	401	BPB	O2D-CGD-CBD	9.65	123.22	111.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	L	304	BCB	C8
6	M	1303	BCB	C13
7	M	401	BPB	C13

5 of 93 torsion outliers are listed below:

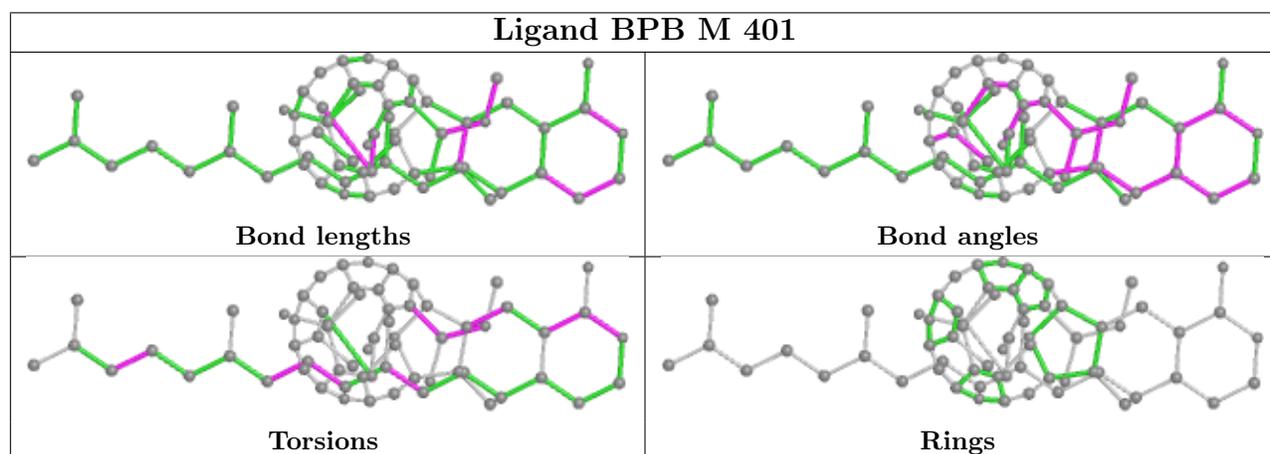
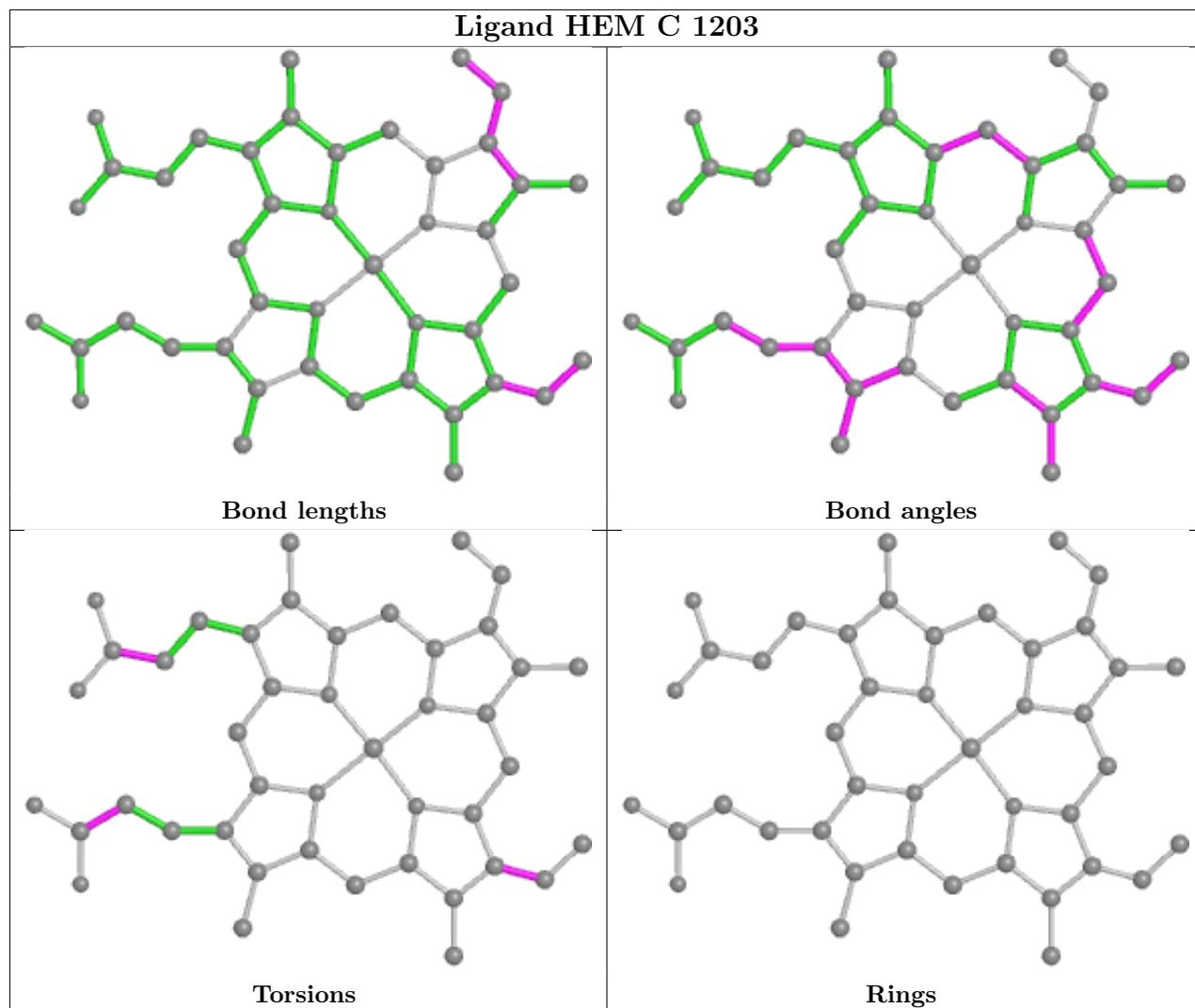
Mol	Chain	Res	Type	Atoms
6	L	302	BCB	CAD-CBD-CGD-O1D
6	L	302	BCB	C4-C3-C5-C6
6	L	304	BCB	O2A-C1-C2-C3
6	L	304	BCB	C2-C3-C5-C6
6	L	304	BCB	C4-C3-C5-C6

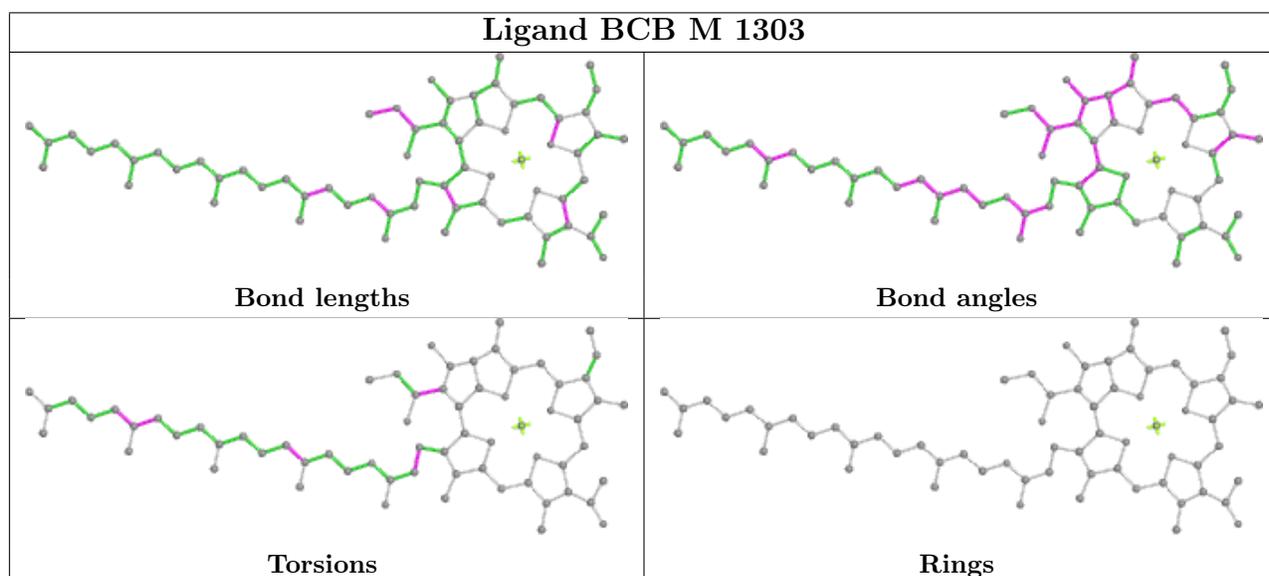
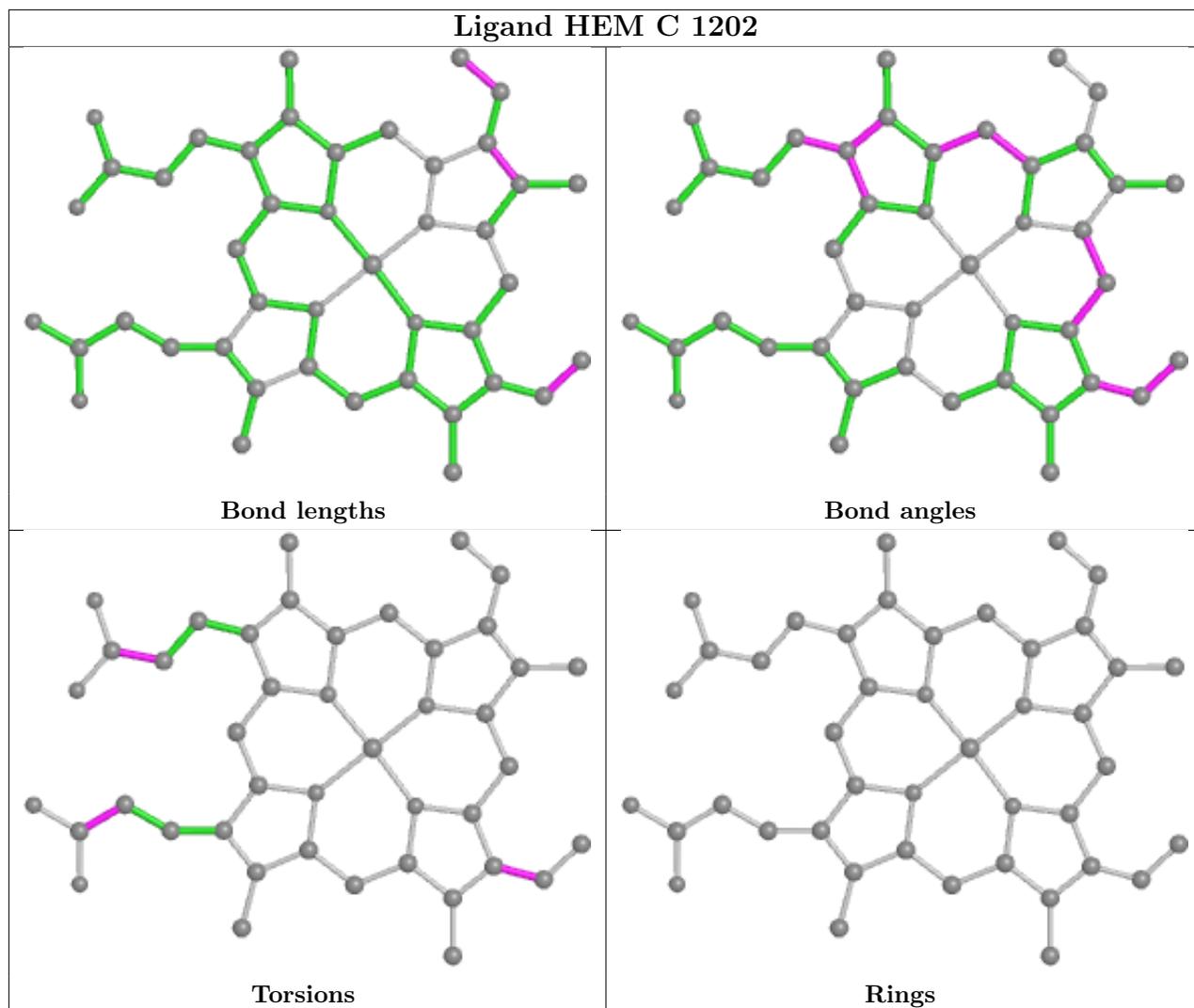
There are no ring outliers.

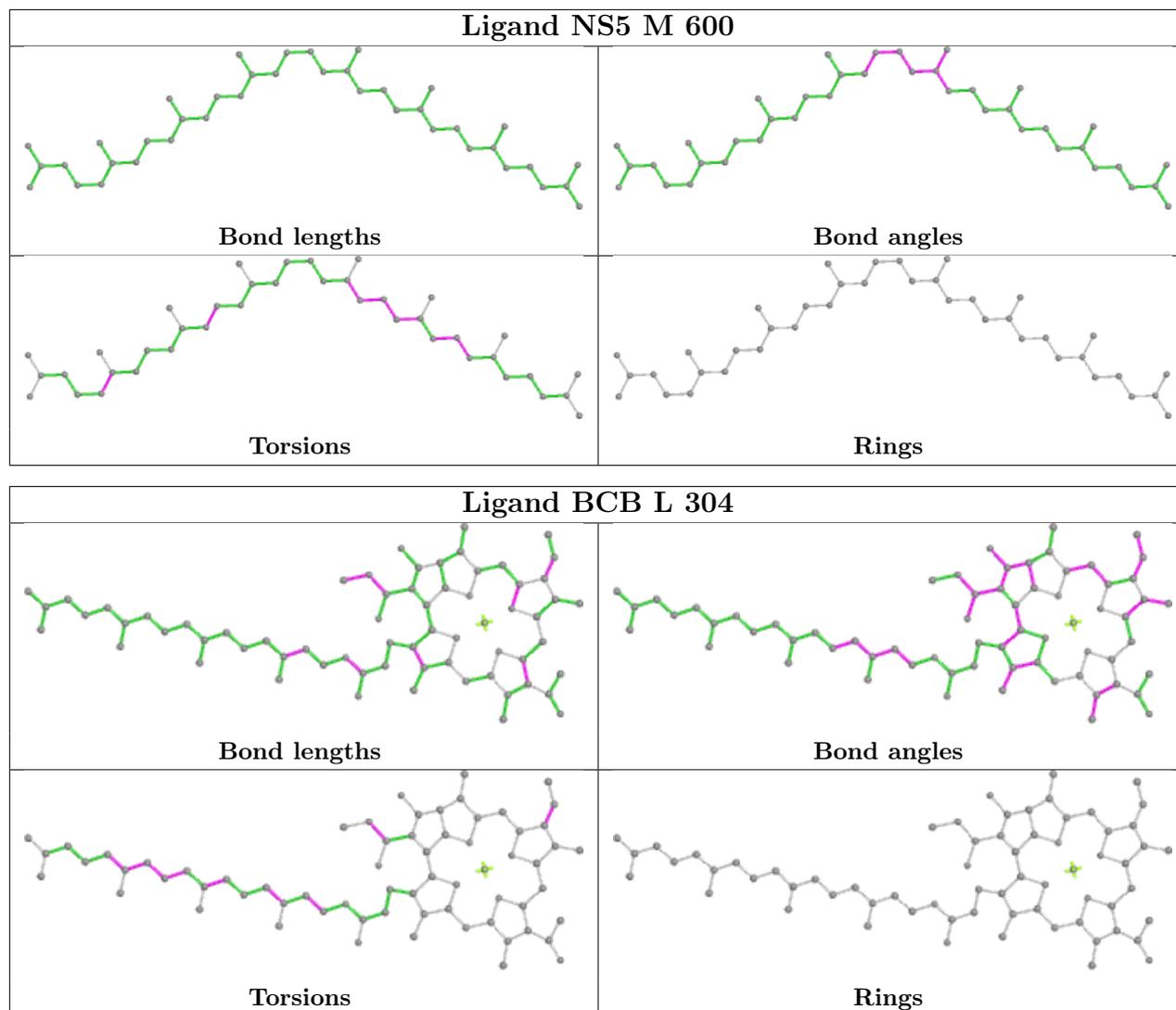
17 monomers are involved in 113 short contacts:

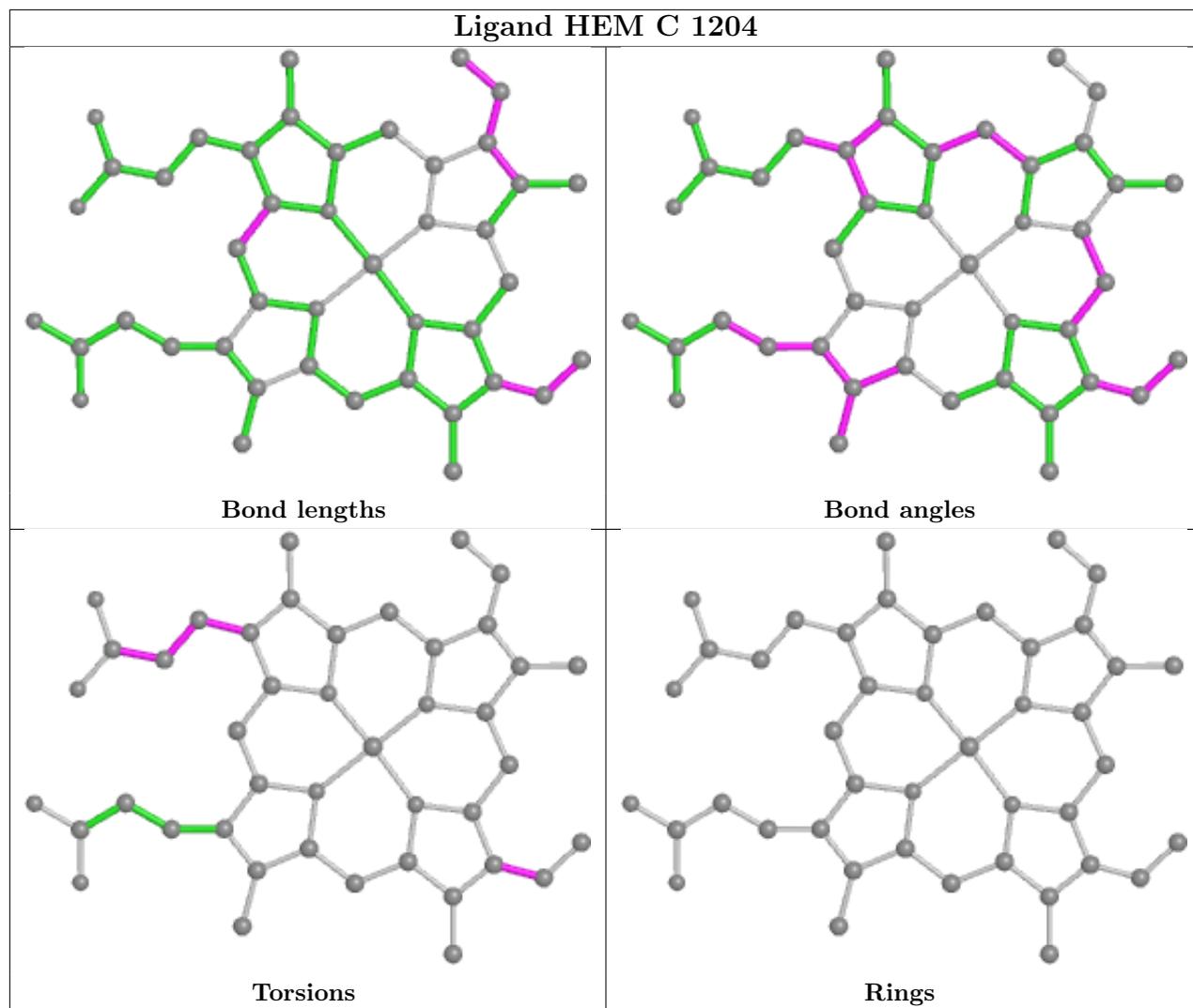
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	M	702	LDA	7	0
5	C	1203	HEM	1	0
7	M	401	BPB	22	0
9	L	705	LDA	2	0
5	C	1202	HEM	1	0
6	M	1303	BCB	19	0
13	M	600	NS5	5	0
6	L	304	BCB	8	0
9	H	703	LDA	4	0
5	C	1204	HEM	3	0
9	M	706	LDA	1	0
5	C	1201	HEM	2	0
6	L	302	BCB	15	0
9	M	701	LDA	3	0
7	L	402	BPB	12	0
8	L	502	UQ2	4	0
6	M	1301	BCB	12	0

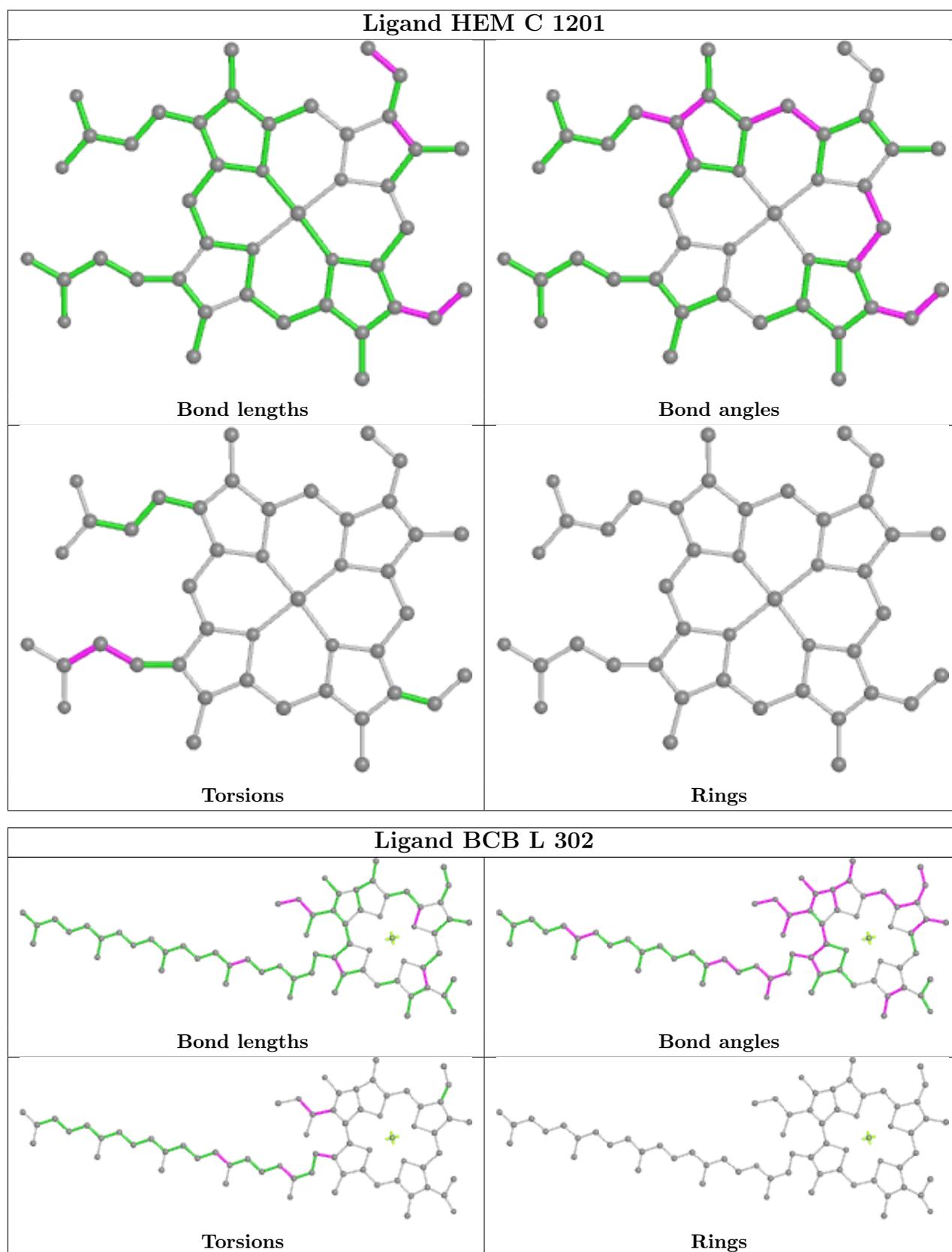
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

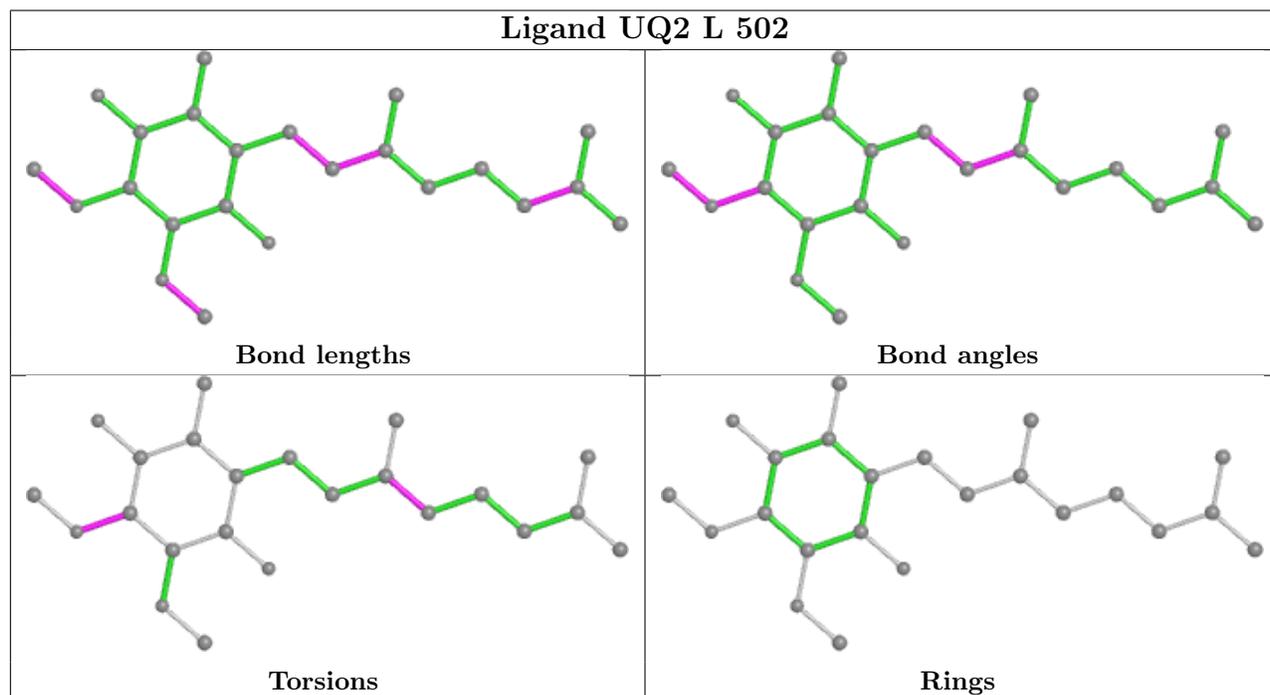
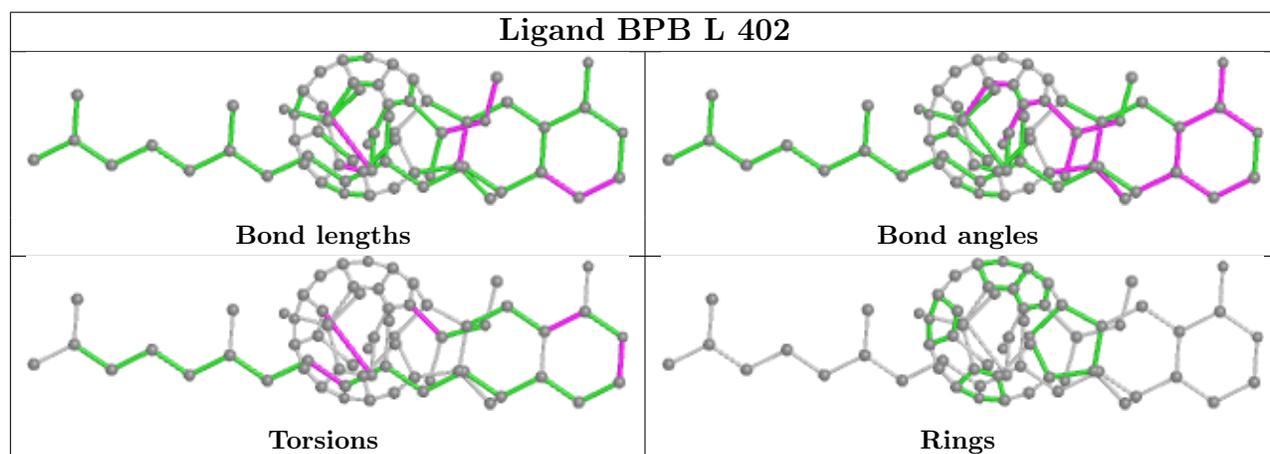
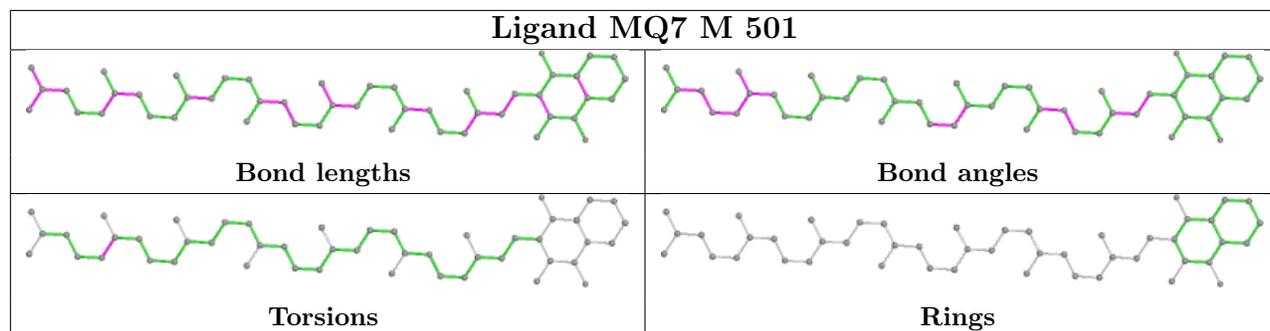


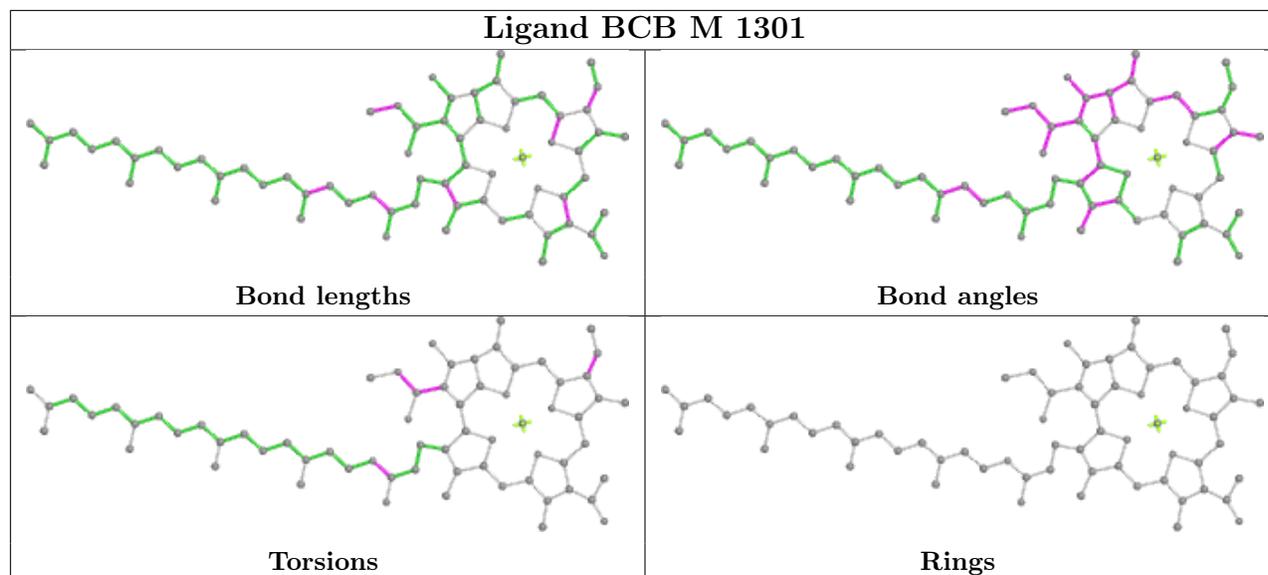












## 5.7 Other polymers [i](#)

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	C	332/336 (98%)	-0.35	4 (1%) 79 78	23, 45, 67, 78	15 (4%)
2	L	273/273 (100%)	-0.52	0 100 100	25, 42, 65, 76	6 (2%)
3	M	323/323 (100%)	-0.54	1 (0%) 94 94	25, 42, 68, 77	8 (2%)
4	H	251/258 (97%)	-0.19	5 (1%) 65 62	30, 56, 84, 93	19 (7%)
All	All	1179/1190 (99%)	-0.41	10 (0%) 86 85	23, 46, 71, 93	48 (4%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	H	8	GLN	5.3
4	H	46	PRO	3.1
4	H	258	LEU	3.0
1	C	162	HIS	2.7
4	H	93	THR	2.7

### 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
4	FME	H	1	10/11	0.96	0.32	53,55,63,65	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands

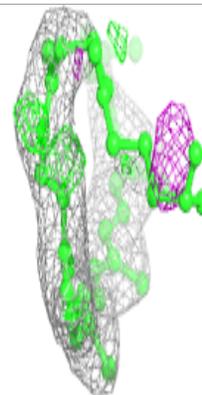
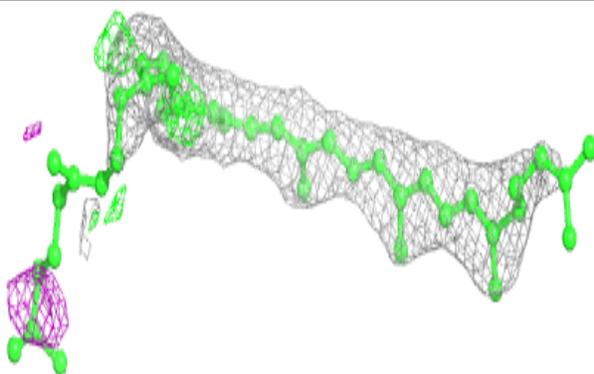
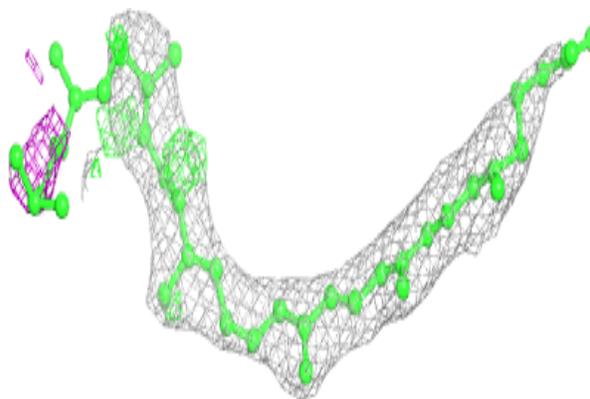
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
9	LDA	M	702	16/16	0.49	0.49	73,87,100,101	0
9	LDA	M	706	16/16	0.73	0.38	99,105,114,114	0
9	LDA	L	705	16/16	0.74	0.36	71,78,94,95	3
9	LDA	M	704	16/16	0.83	0.44	79,82,83,84	3
9	LDA	H	703	16/16	0.90	0.30	74,79,85,85	0
13	NS5	M	600	40/40	0.90	0.23	39,58,67,68	11
12	MQ7	M	501	48/48	0.93	0.22	36,45,67,70	0
8	UQ2	L	502	23/23	0.93	0.28	48,49,50,50	23
7	BPB	M	401	65/65	0.94	0.21	37,45,94,95	0
9	LDA	M	701	16/16	0.95	0.20	48,50,52,52	0
11	SO4	M	803	5/5	0.95	0.13	102,102,103,103	0
7	BPB	L	402	65/65	0.96	0.20	31,41,45,47	0
11	SO4	M	804	5/5	0.97	0.11	81,82,82,83	0
11	SO4	H	801	5/5	0.97	0.11	73,76,76,77	0
6	BCB	L	304	66/66	0.97	0.18	23,29,54,57	0
6	BCB	M	1303	66/66	0.97	0.16	17,25,46,48	0
6	BCB	M	1301	66/66	0.98	0.18	33,43,59,63	15
6	BCB	L	302	66/66	0.98	0.16	10,20,42,43	0
11	SO4	M	802	5/5	0.98	0.11	57,59,61,61	0
5	HEM	C	1201	43/43	0.98	0.14	47,51,61,65	0
5	HEM	C	1202	43/43	0.99	0.14	39,43,55,58	0
10	FE2	M	500	1/1	0.99	0.06	33,33,33,33	0
5	HEM	C	1203	43/43	0.99	0.16	26,33,41,44	0
5	HEM	C	1204	43/43	0.99	0.14	32,36,48,53	0

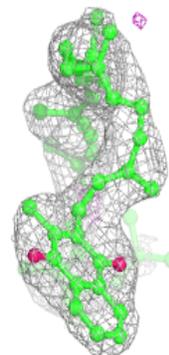
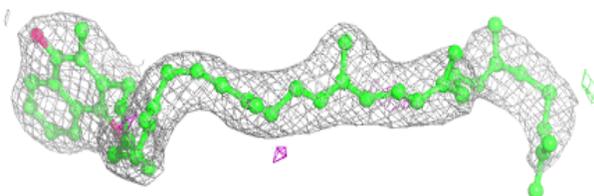
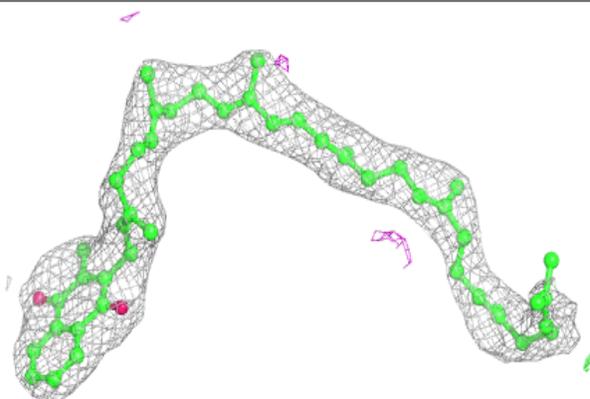
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around NS5 M 600:**

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

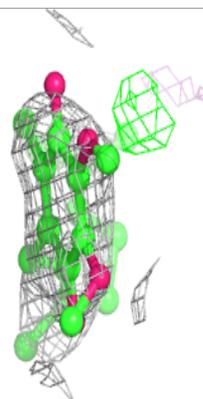
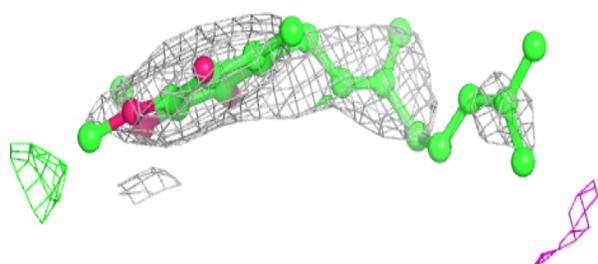
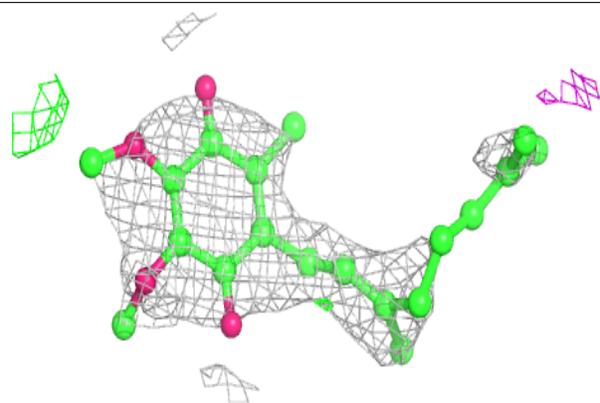
**Electron density around MQ7 M 501:**

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

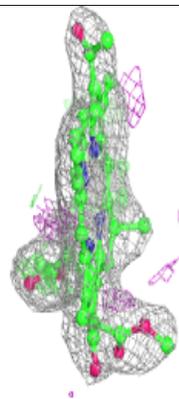
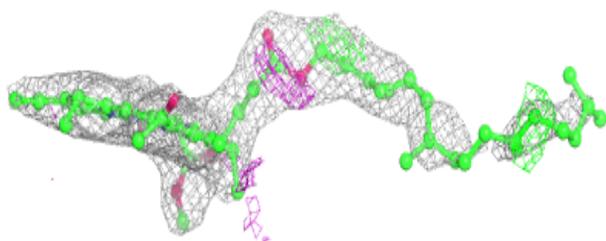
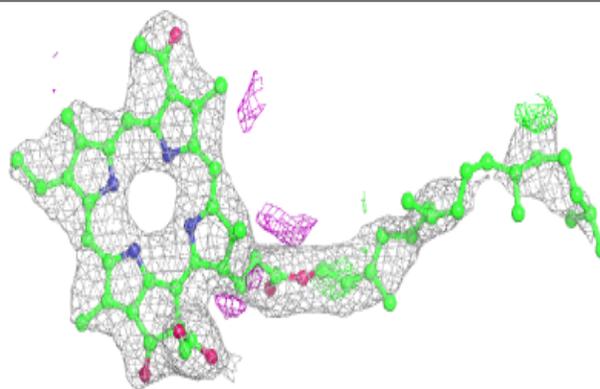


**Electron density around UQ2 L 502:**

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

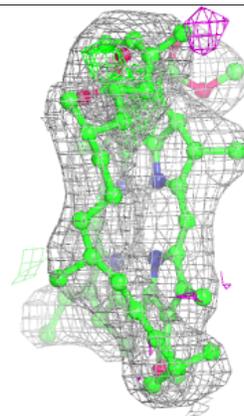
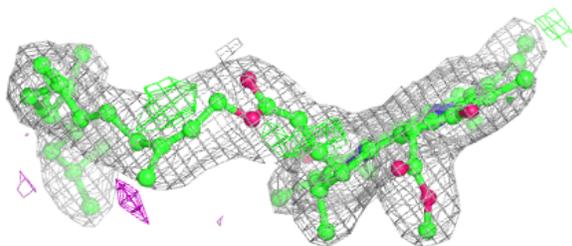
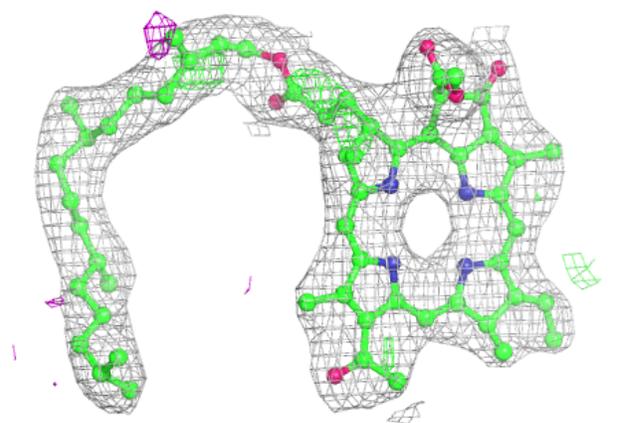
**Electron density around BPB M 401:**

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



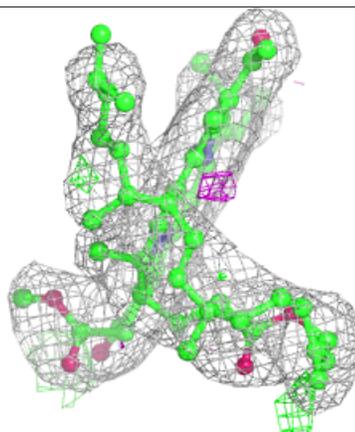
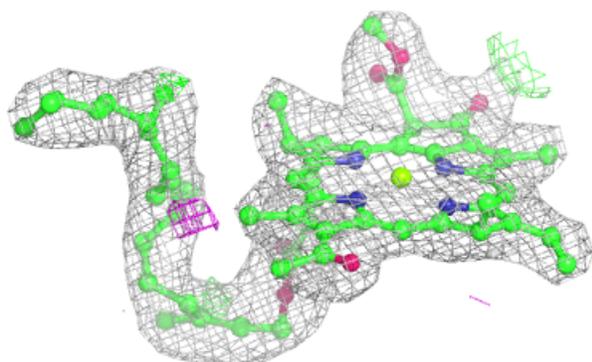
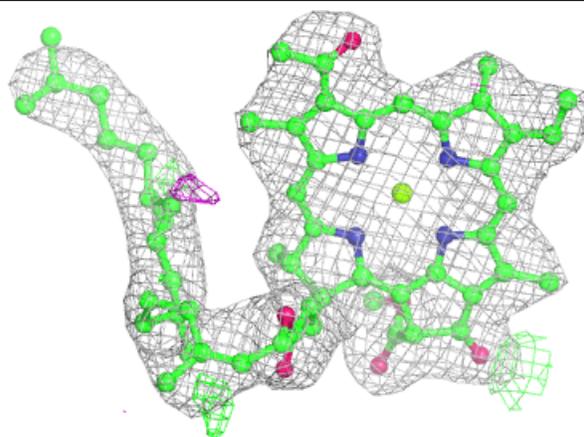
**Electron density around BPB L 402:**

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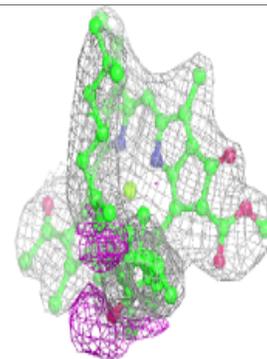
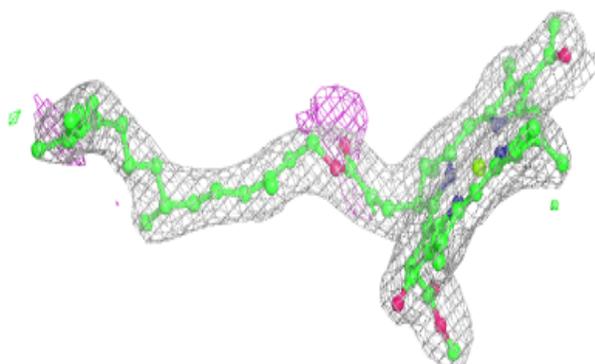
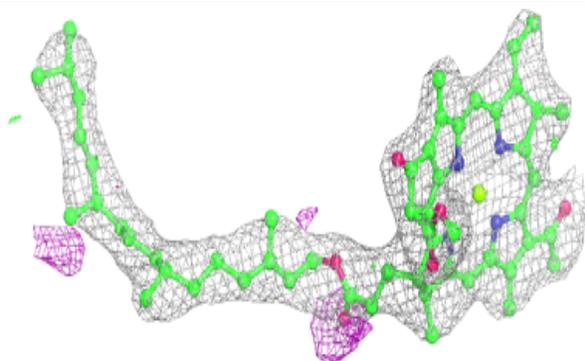


**Electron density around BCB L 304:**

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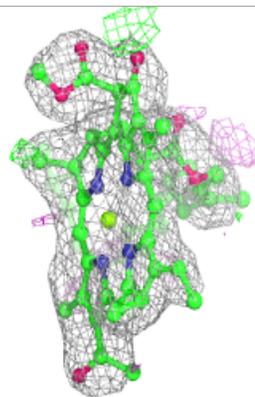
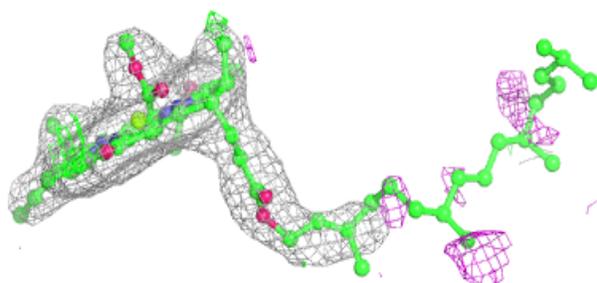
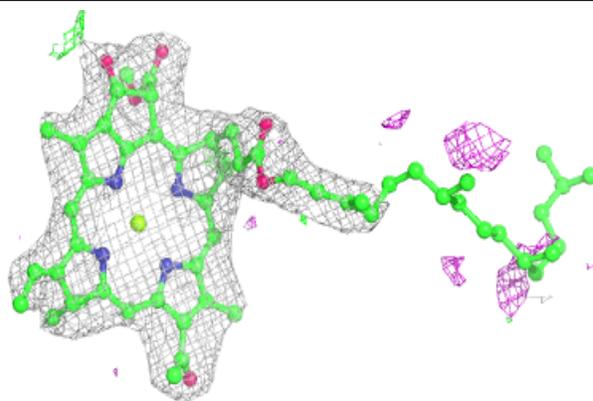
**Electron density around BCB M 1303:**

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and green (positive)

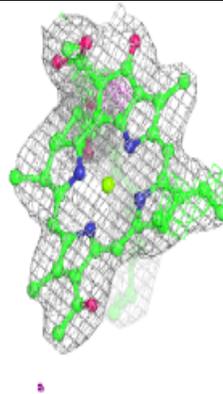
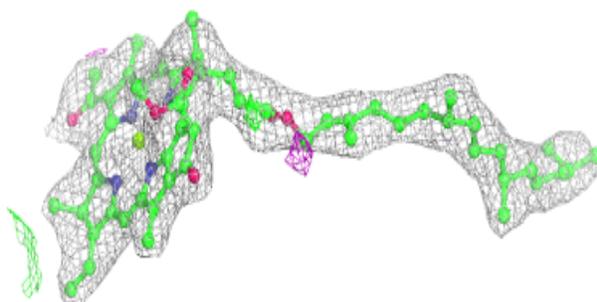
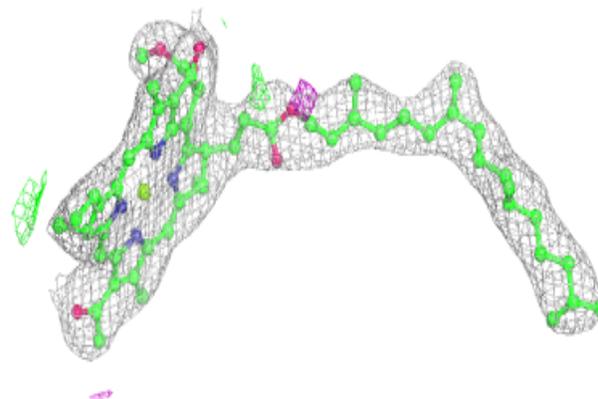


**Electron density around BCB M 1301:**

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and green (positive)

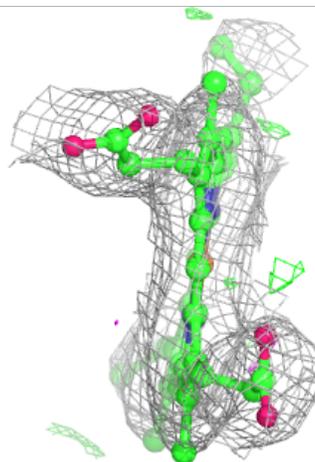
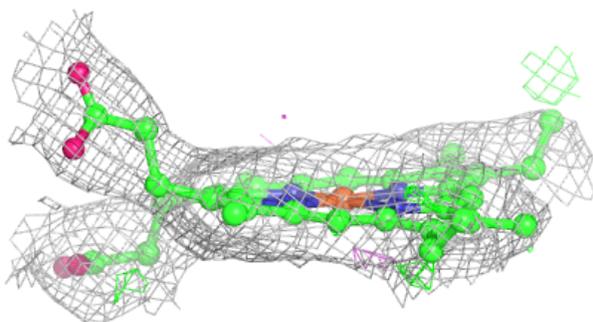
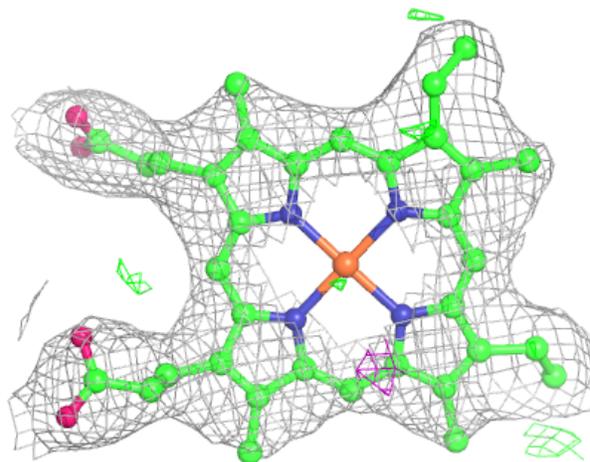
**Electron density around BCB L 302:**

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



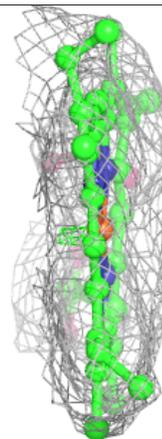
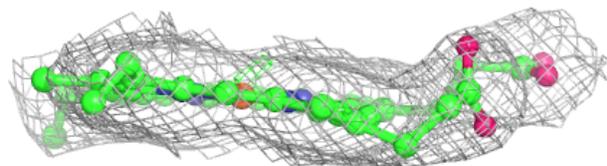
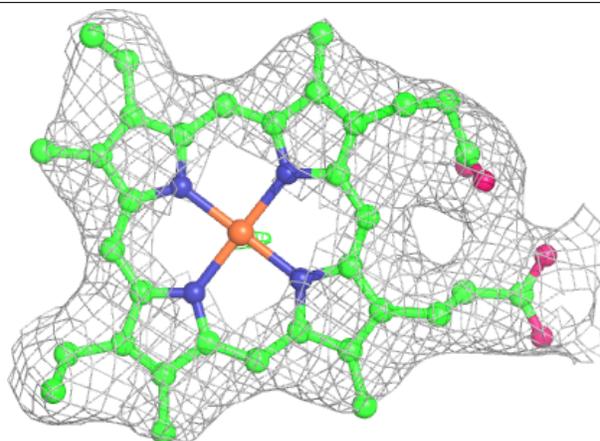
**Electron density around HEM C 1201:**

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



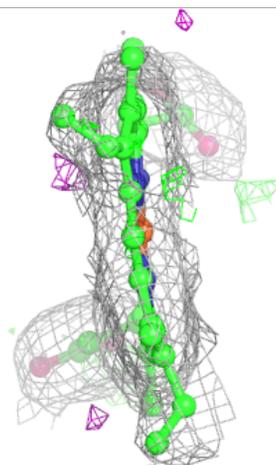
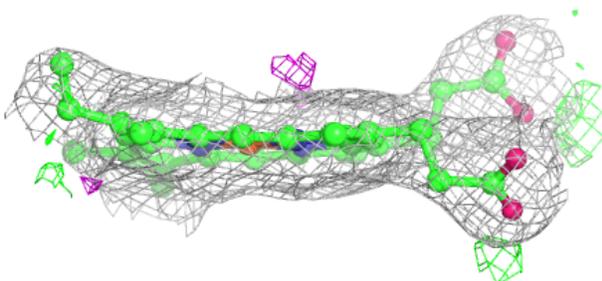
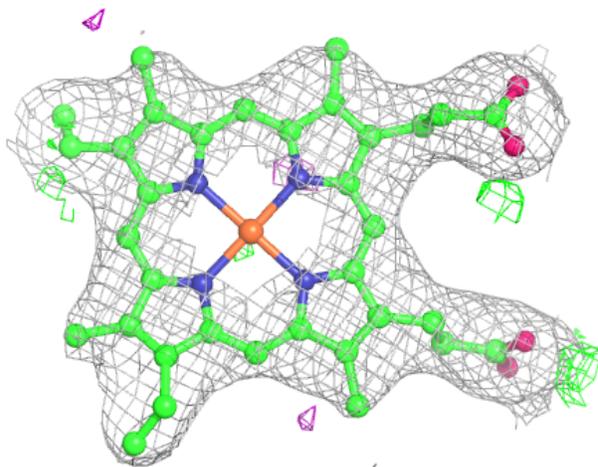
**Electron density around HEM C 1202:**

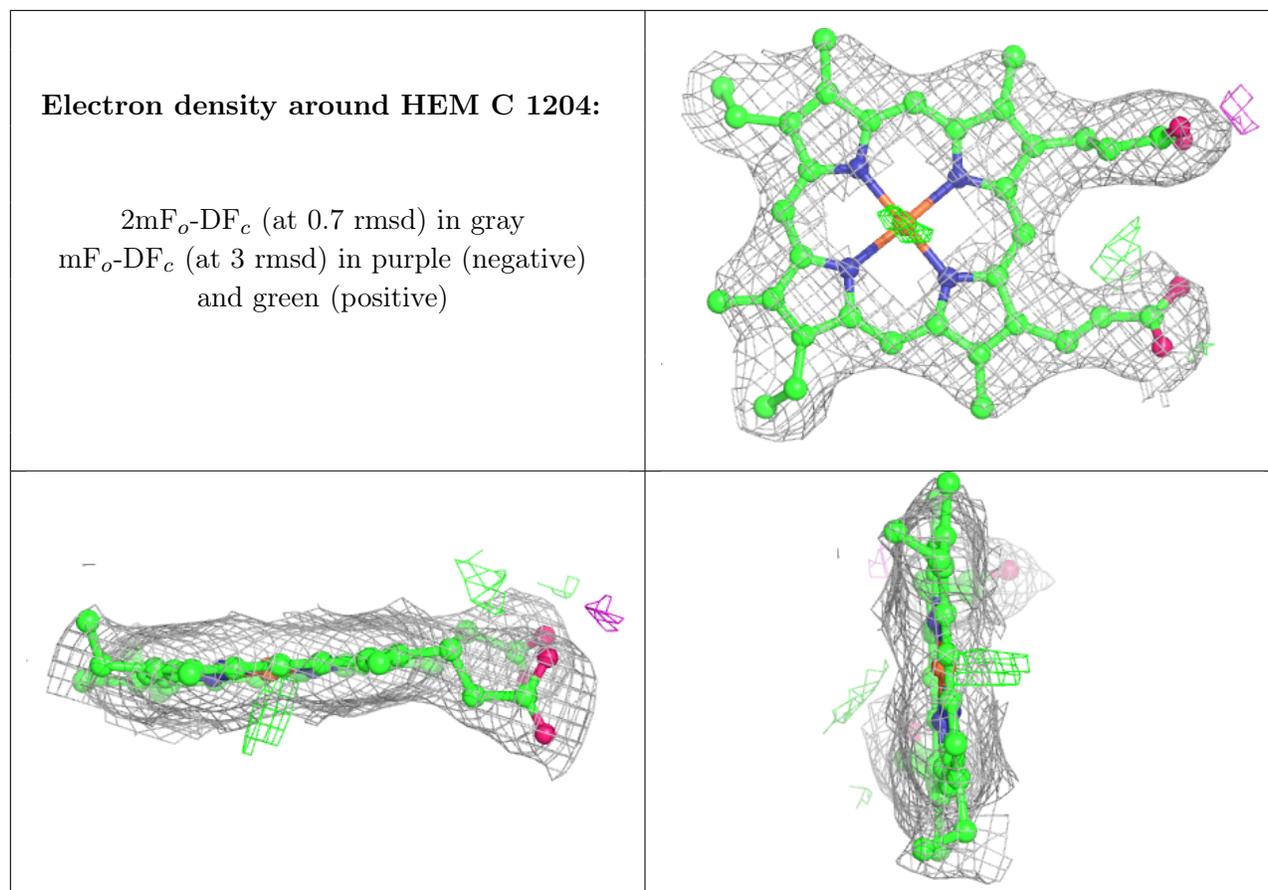
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEM C 1203:**

$2mF_o-DF_c$  (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.