



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 06:01 am BST

PDB ID : 1L9J  
Title : X-Ray Structure of the Cytochrome-c(2)-Photosynthetic Reaction Center Electron Transfer Complex from Rhodobacter sphaeroides in Type I Co-Crystals  
Authors : Axelrod, H.L.; Abresch, E.C.; Okamura, M.Y.; Yeh, A.P.; Rees, D.C.; Feher, G.  
Deposited on : 2002-03-24  
Resolution : 3.25 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.

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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	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

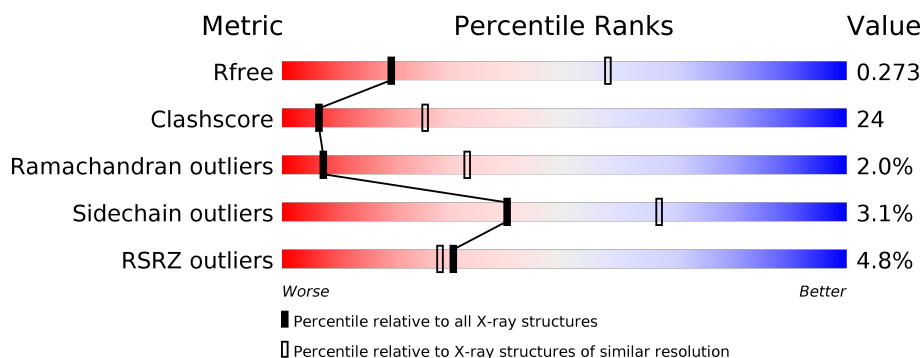
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.25 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.



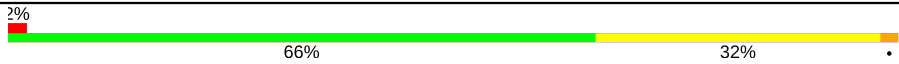

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)

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	L	281	<div> <div>0%</div> <div> <div>64%</div> <div>34%</div> <div>•</div> </div> </div>
1	R	281	<div> <div>3%</div> <div> <div>54%</div> <div>42%</div> <div>•</div> </div> </div>
2	M	307	<div> <div>2%</div> <div> <div>50%</div> <div>35%</div> <div>•</div> <div>13%</div> </div> </div>
2	S	307	<div> <div>2%</div> <div> <div>47%</div> <div>38%</div> <div>•</div> <div>13%</div> </div> </div>
3	H	260	<div> <div>8%</div> <div> <div>53%</div> <div>39%</div> <div>•</div> <div>5%</div> </div> </div>
3	T	260	<div> <div>14%</div> <div> <div>53%</div> <div>38%</div> <div>•</div> <div>5%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
4	C	124	
4	D	124	

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
10	LDA	M	1011	-	-	-	X
10	LDA	S	2011	-	-	-	X
6	BPH	L	1005	X	-	-	-
6	BPH	M	1006	X	-	-	-
6	BPH	R	2005	X	-	-	-
6	BPH	S	2006	X	-	-	-

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 15497 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 REACTION CENTER PROTEIN L CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	281	Total	C	N	O	S	0	0	0
			2232	1507	355	362	8			
1	R	281	Total	C	N	O	S	0	0	0
			2232	1507	355	362	8			

- Molecule 2 is a protein called REACTION CENTER PROTEIN M CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	267	Total	C	N	O	S	0	0	0
			2150	1450	347	344	9			
2	S	267	Total	C	N	O	S	0	0	0
			2150	1450	347	344	9			

- Molecule 3 is a protein called REACTION CENTER PROTEIN H CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	246	Total	C	N	O	S	0	0	0
			1871	1197	321	344	9			
3	T	246	Total	C	N	O	S	0	0	0
			1871	1197	321	344	9			

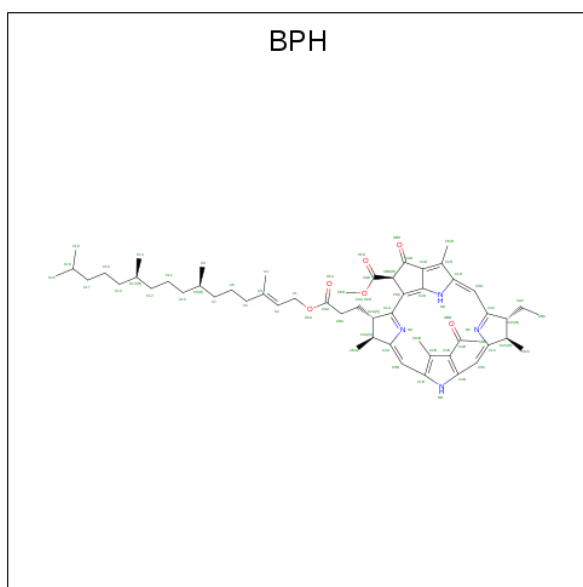
- Molecule 4 is a protein called cytochrome c-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	124	Total	C	N	O	S	0	0	0
			949	595	166	184	4			
4	D	124	Total	C	N	O	S	0	0	0
			949	595	166	184	4			

- Molecule 5 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: C<sub>55</sub>H<sub>74</sub>MgN<sub>4</sub>O<sub>6</sub>).



- Molecule 6 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula:  $C_{55}H_{76}N_4O_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	L	1	Total	C	N	O	0	0
			55	45	4	6		
6	M	1	Total	C	N	O	0	0
			65	55	4	6		
6	R	1	Total	C	N	O	0	0
			55	45	4	6		
6	S	1	Total	C	N	O	0	0
			65	55	4	6		

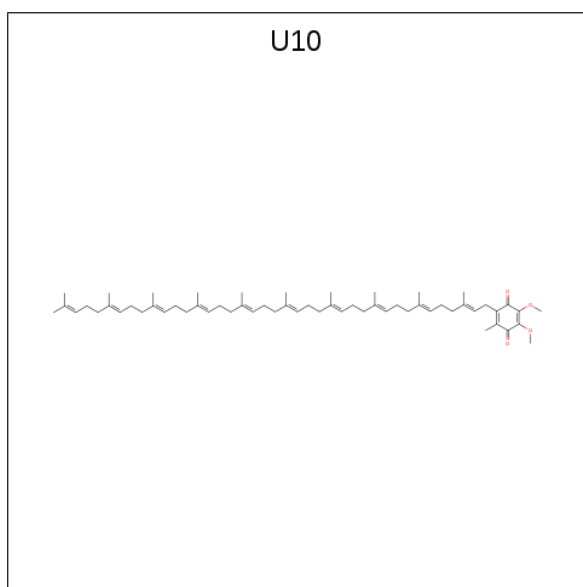
- Molecule 7 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	S	1	Total	Fe	0	0
			1	1		
7	M	1	Total	Fe	0	0
			1	1		

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

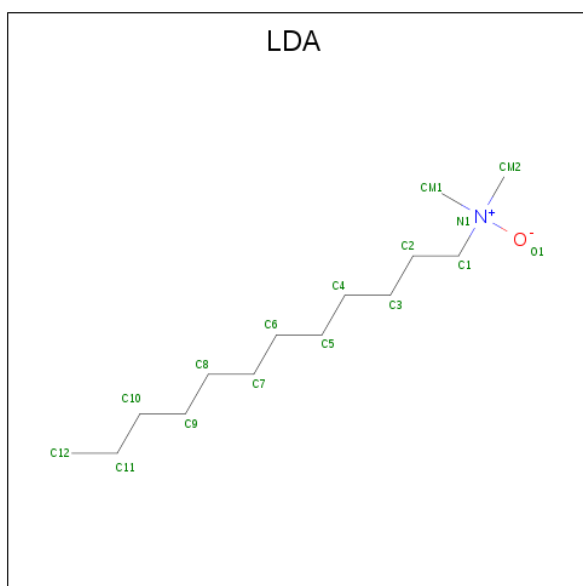
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	S	1	Total	Cl	0	0
			1	1		
8	M	1	Total	Cl	0	0
			1	1		

- Molecule 9 is UBIQUINONE-10 (three-letter code: U10) (formula: C<sub>59</sub>H<sub>90</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	M	1	Total	C	O	0	0
			37	33	4		
9	S	1	Total	C	O	0	0
			37	33	4		

- Molecule 10 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula:  $C_{14}H_{31}NO$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	M	1	Total	C	N	O	0	0
			16	14	1	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	M	1	Total 16	C 14	N 1	O 1	0	0
10	S	1	Total 16	C 14	N 1	O 1	0	0
10	S	1	Total 16	C 14	N 1	O 1	0	0

- # HEM

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	L	32	Total O 32 32	0	0
12	M	14	Total O 14 14	0	0
12	H	18	Total O 18 18	0	0
12	C	10	Total O 10 10	0	0





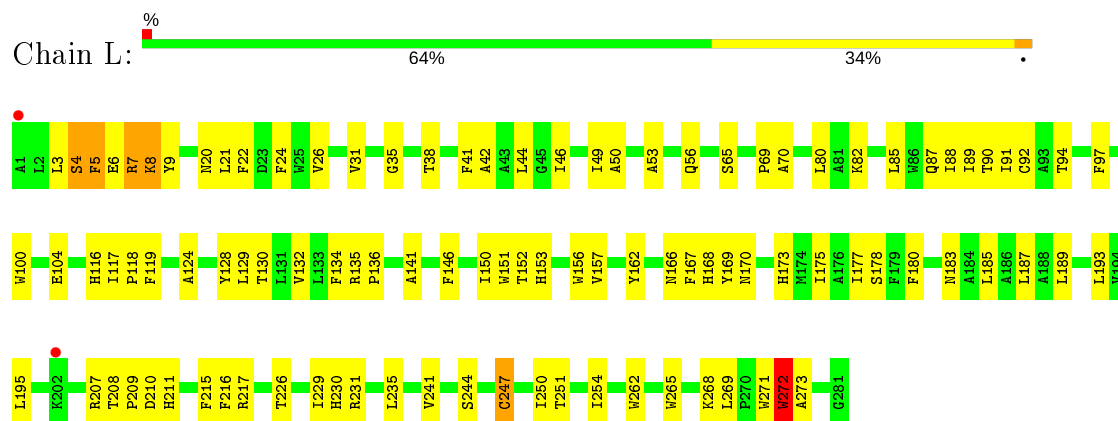
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	R	18	Total 18	O 18	0	0
12	S	15	Total 15	O 15	0	0
12	T	13	Total 13	O 13	0	0
12	D	9	Total 9	O 9	0	0

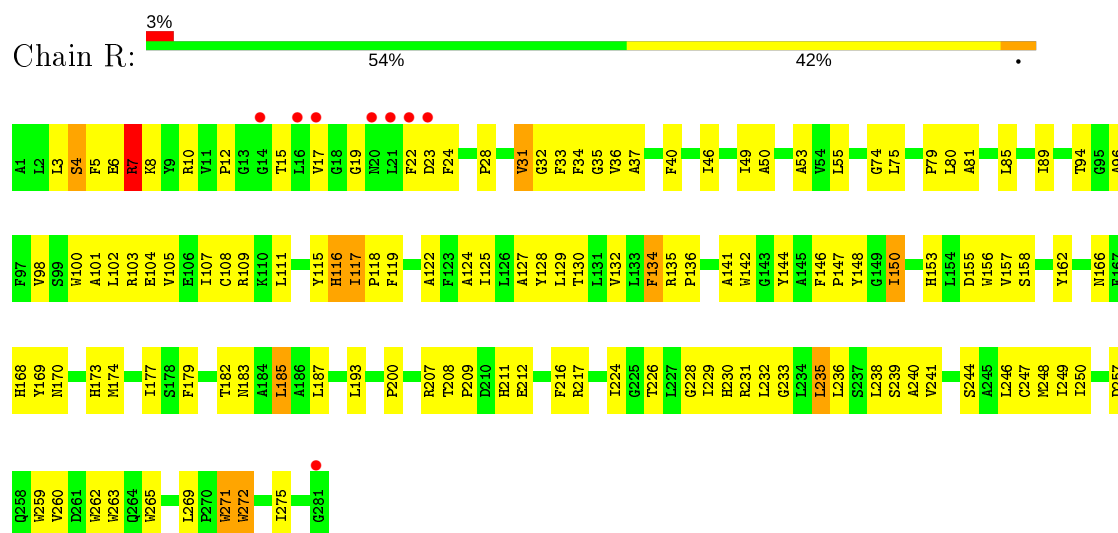
### 3 Residue-property plots [i](#)

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

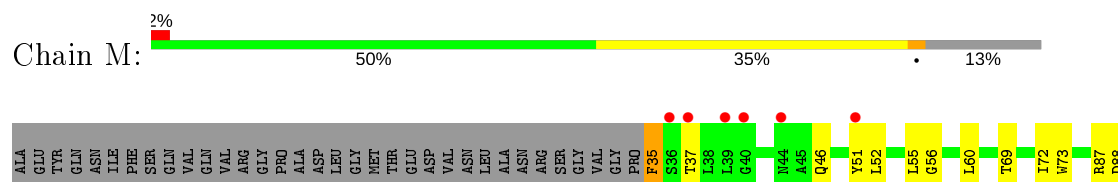
#### • Molecule 1: REACTION CENTER PROTEIN L CHAIN

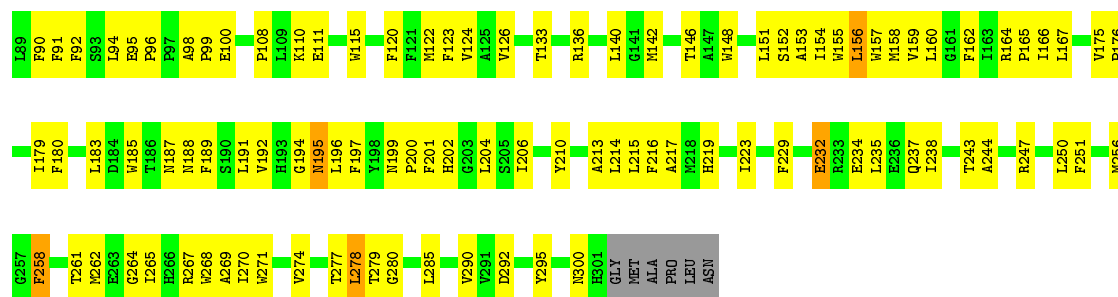


#### • Molecule 1: REACTION CENTER PROTEIN L CHAIN

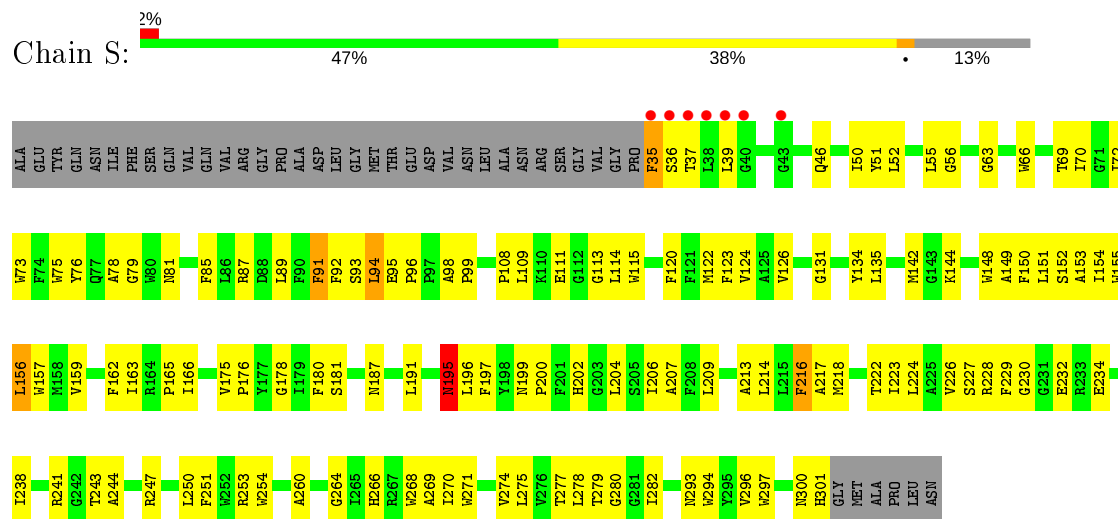


#### • Molecule 2: REACTION CENTER PROTEIN M CHAIN

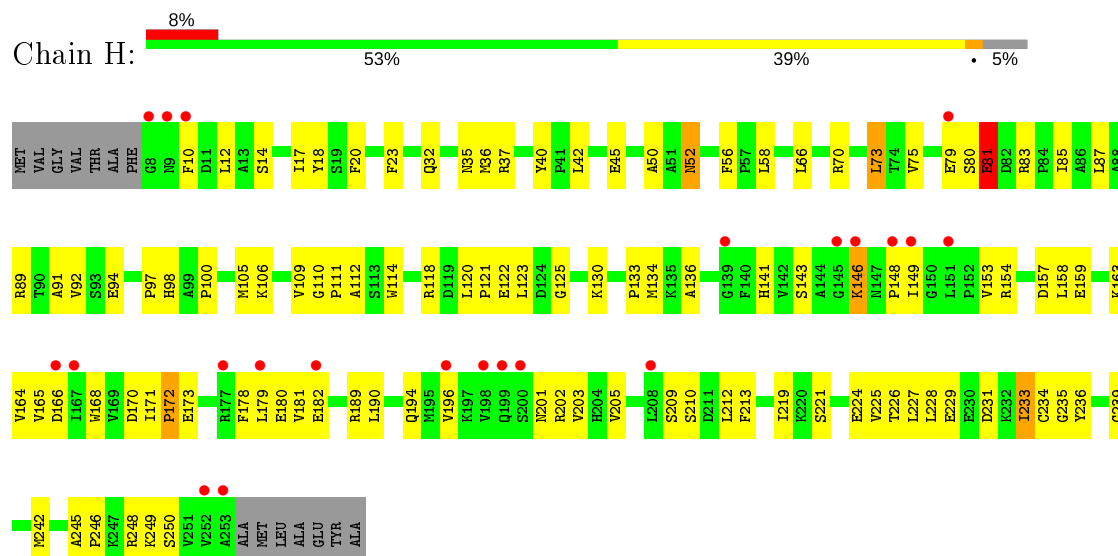




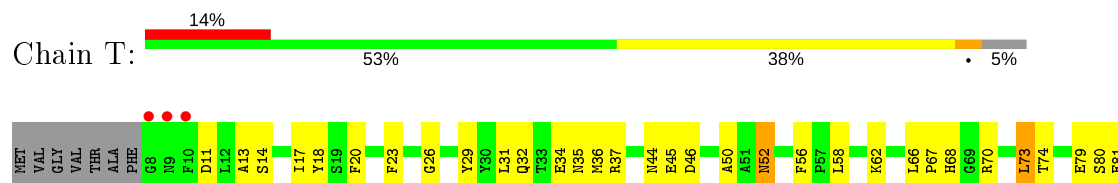
• Molecule 2: REACTION CENTER PROTEIN M CHAIN

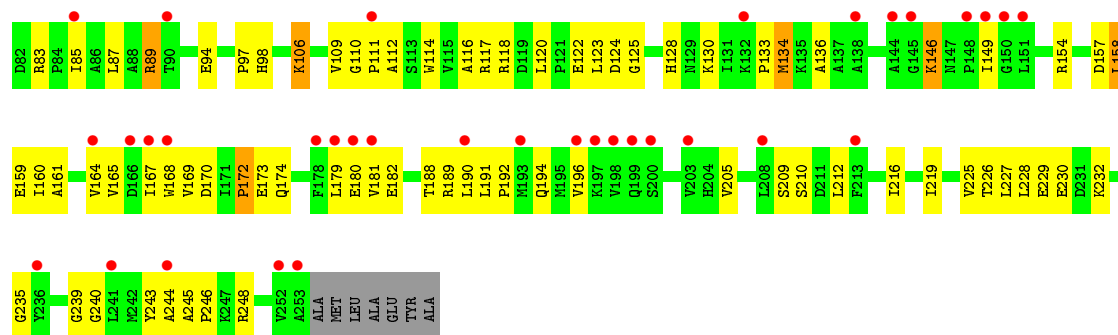


• Molecule 3: REACTION CENTER PROTEIN H CHAIN

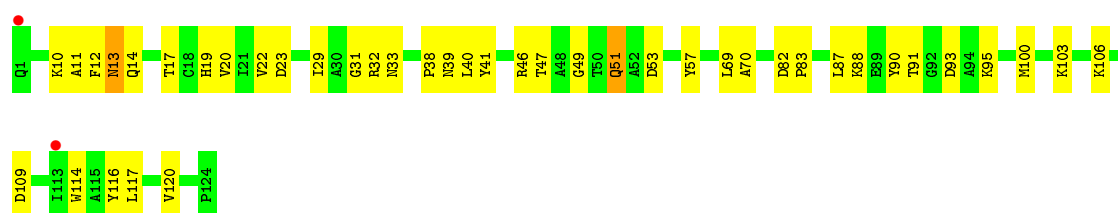


• Molecule 3: REACTION CENTER PROTEIN H CHAIN

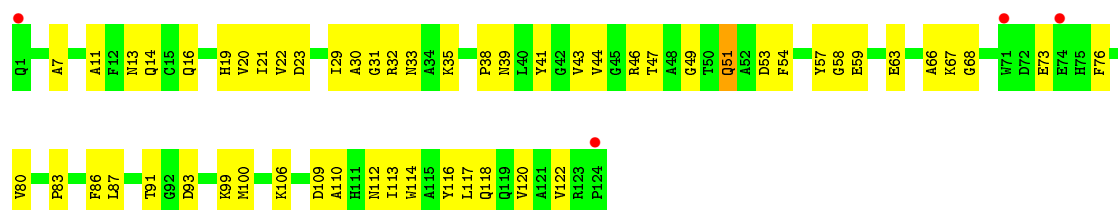




● Molecule 4: cytochrome c-2



● Molecule 4: cytochrome c-2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.93Å 80.31Å 246.57Å 90.00° 92.41° 90.00°	Depositor
Resolution (Å)	49.32 – 3.25 49.32 – 3.25	Depositor EDS
% Data completeness (in resolution range)	98.5 (49.32-3.25) 98.5 (49.32-3.25)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.31 (at 3.25Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.248 , 0.287 0.236 , 0.273	Depositor DCC
$R_{free}$ test set	2385 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	78.5	Xtriage
Anisotropy	0.711	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 53.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -k,-h,-l 0.000 for k,h,-l 0.027 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	15497	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.15 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.1270e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: BCL, LDA, CL, BPH, FE2, HEM, U10

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	L	0.35	0/2320	0.54	0/3175
1	R	0.35	0/2320	0.54	0/3175
2	M	0.36	0/2238	0.56	0/3057
2	S	0.36	0/2238	0.53	0/3057
3	H	0.30	0/1920	0.53	0/2612
3	T	0.30	0/1920	0.52	0/2612
4	C	0.32	0/969	0.57	0/1304
4	D	0.31	0/969	0.53	0/1304
All	All	0.34	0/14894	0.54	0/20296

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	L	2232	0	2187	93	0
1	R	2232	0	2187	123	0
2	M	2150	0	2073	118	0
2	S	2150	0	2073	145	0
3	H	1871	0	1877	105	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	T	1871	0	1877	103	0
4	C	949	0	916	36	0
4	D	949	0	916	46	0
5	L	132	0	148	15	0
5	M	116	0	115	17	0
5	R	132	0	148	16	0
5	S	116	0	115	13	0
6	L	55	0	53	2	0
6	M	65	0	74	3	0
6	R	55	0	53	2	0
6	S	65	0	74	6	0
7	M	1	0	0	0	0
7	S	1	0	0	0	0
8	M	1	0	0	0	0
8	S	1	0	0	0	0
9	M	37	0	47	1	0
9	S	37	0	47	1	0
10	M	32	0	62	5	0
10	S	32	0	62	3	0
11	C	43	0	30	2	0
11	D	43	0	30	2	0
12	C	10	0	0	3	0
12	D	9	0	0	0	0
12	H	18	0	0	2	0
12	L	32	0	0	6	0
12	M	14	0	0	1	0
12	R	18	0	0	4	0
12	S	15	0	0	2	0
12	T	13	0	0	1	0
All	All	15497	0	15164	727	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 24.

The worst 5 of 727 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:C:91:THR:HG23	4:C:93:ASP:H	1.20	1.03
2:S:280:GLY:HA3	5:S:2003:BCL:CED	1.91	1.01
2:S:280:GLY:HA3	5:S:2003:BCL:HED2	1.45	0.97
2:S:122:MET:HE3	2:S:157:TRP:HE1	1.33	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:208:THR:HG22	1:L:210:ASP:H	1.37	0.90

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	L	279/281 (99%)	227 (81%)	46 (16%)	6 (2%)	6	31
1	R	279/281 (99%)	231 (83%)	36 (13%)	12 (4%)	2	16
2	M	265/307 (86%)	228 (86%)	36 (14%)	1 (0%)	34	67
2	S	265/307 (86%)	220 (83%)	42 (16%)	3 (1%)	14	46
3	H	244/260 (94%)	198 (81%)	42 (17%)	4 (2%)	9	37
3	T	244/260 (94%)	199 (82%)	37 (15%)	8 (3%)	4	22
4	C	122/124 (98%)	109 (89%)	12 (10%)	1 (1%)	19	52
4	D	122/124 (98%)	105 (86%)	16 (13%)	1 (1%)	19	52
All	All	1820/1944 (94%)	1517 (83%)	267 (15%)	36 (2%)	7	33

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	7	ARG
1	R	23	ASP
1	R	116	HIS
3	T	80	SER
3	T	89	ARG



### 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	L	220/220 (100%)	216 (98%)	4 (2%)	59	77
1	R	220/220 (100%)	213 (97%)	7 (3%)	39	66
2	M	209/240 (87%)	199 (95%)	10 (5%)	25	56
2	S	209/240 (87%)	202 (97%)	7 (3%)	38	65
3	H	199/208 (96%)	191 (96%)	8 (4%)	31	61
3	T	199/208 (96%)	194 (98%)	5 (2%)	47	71
4	C	93/93 (100%)	91 (98%)	2 (2%)	52	74
4	D	93/93 (100%)	92 (99%)	1 (1%)	73	84
All	All	1442/1522 (95%)	1398 (97%)	44 (3%)	40	67

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	146	LYS
1	R	7	ARG
3	T	106	LYS
3	H	194	GLN
4	C	13	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
4	C	33	ASN
1	R	87	GLN
4	D	33	ASN
4	C	51	GLN
4	C	81	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 24 ligands modelled in this entry, 4 are monoatomic - leaving 20 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	BCL	M	1001	2	42,58,74	1.48	7 (16%)	48,95,115	2.23	15 (31%)
10	LDA	M	1010	-	12,15,15	2.07	1 (8%)	14,17,17	1.77	3 (21%)
11	HEM	D	2009	4	27,50,50	2.16	9 (33%)	17,82,82	2.65	10 (58%)
10	LDA	S	2010	-	12,15,15	1.94	1 (8%)	14,17,17	1.78	3 (21%)
10	LDA	M	1011	-	12,15,15	2.10	1 (8%)	14,17,17	1.74	4 (28%)
5	BCL	L	1004	1	58,74,74	1.35	8 (13%)	69,115,115	2.06	21 (30%)
5	BCL	L	1002	1	58,74,74	1.20	7 (12%)	69,115,115	1.99	21 (30%)
9	U10	S	2008	-	37,37,63	1.98	12 (32%)	44,47,79	1.89	12 (27%)
5	BCL	M	1003	2	58,74,74	1.40	8 (13%)	69,115,115	2.16	24 (34%)
9	U10	M	1008	-	37,37,63	1.89	10 (27%)	44,47,79	1.87	12 (27%)
5	BCL	R	2002	1	58,74,74	1.23	5 (8%)	69,115,115	2.04	21 (30%)
6	BPH	L	1005	-	54,60,70	1.46	9 (16%)	64,89,101	2.25	22 (34%)
5	BCL	S	2003	2	58,74,74	1.31	6 (10%)	69,115,115	2.10	19 (27%)
6	BPH	S	2006	-	64,70,70	1.53	10 (15%)	76,101,101	2.21	24 (31%)
11	HEM	C	1009	4	27,50,50	2.22	10 (37%)	17,82,82	2.73	10 (58%)
5	BCL	S	2001	2	42,58,74	1.48	6 (14%)	48,95,115	2.21	16 (33%)
10	LDA	S	2011	-	12,15,15	2.14	1 (8%)	14,17,17	1.54	4 (28%)
6	BPH	R	2005	-	54,60,70	1.54	9 (16%)	64,89,101	2.26	22 (34%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	BPH	M	1006	-	64,70,70	1.53	9 (14%)	76,101,101	2.17	23 (30%)
5	BCL	R	2004	1	58,74,74	1.36	9 (15%)	69,115,115	2.01	22 (31%)

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	BCL	M	1001	2	-	4/18/118/137	-
10	LDA	M	1010	-	-	6/13/13/13	-
11	HEM	D	2009	4	-	0/6/54/54	-
10	LDA	S	2010	-	-	5/13/13/13	-
10	LDA	M	1011	-	-	6/13/13/13	-
5	BCL	L	1004	1	-	11/37/137/137	-
5	BCL	L	1002	1	-	10/37/137/137	-
9	U10	S	2008	-	-	3/32/56/87	0/1/1/1
5	BCL	M	1003	2	-	9/37/137/137	-
9	U10	M	1008	-	-	3/32/56/87	0/1/1/1
6	BPH	R	2005	-	1/1/16/22	11/42/93/105	0/5/6/6
6	BPH	L	1005	-	1/1/16/22	14/42/93/105	0/5/6/6
5	BCL	S	2003	2	-	11/37/137/137	-
6	BPH	S	2006	-	2/2/18/22	21/54/105/105	0/5/6/6
11	HEM	C	1009	4	-	0/6/54/54	-
5	BCL	S	2001	2	-	5/18/118/137	-
10	LDA	S	2011	-	-	6/13/13/13	-
5	BCL	R	2002	1	-	12/37/137/137	-
6	BPH	M	1006	-	2/2/18/22	21/54/105/105	0/5/6/6
5	BCL	R	2004	1	-	12/37/137/137	-

The worst 5 of 138 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	S	2011	LDA	O1-N1	-7.16	1.25	1.42
10	M	1011	LDA	O1-N1	-7.01	1.25	1.42
10	M	1010	LDA	O1-N1	-6.82	1.26	1.42
10	S	2010	LDA	O1-N1	-6.31	1.27	1.42
6	M	1006	BPH	C11-C10	-5.41	1.29	1.52

The worst 5 of 308 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	S	2006	BPH	O2D-CGD-CBD	8.87	127.02	111.27
6	M	1006	BPH	O2D-CGD-CBD	8.46	126.30	111.27
6	R	2005	BPH	O2D-CGD-CBD	8.36	126.13	111.27
6	L	1005	BPH	O2D-CGD-CBD	8.34	126.09	111.27
6	M	1006	BPH	C1-C2-C3	6.63	137.50	126.04

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	S	2006	BPH	C8
6	S	2006	BPH	C13
6	R	2005	BPH	C8
6	L	1005	BPH	C8
6	M	1006	BPH	C8

5 of 170 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	R	2002	BCL	O2A-C1-C2-C3
6	S	2006	BPH	C4C-C3C-CAC-CBC
6	S	2006	BPH	C4B-C3B-CAB-CBB
6	S	2006	BPH	C4B-C3B-CAB-OB
6	S	2006	BPH	O2A-C1-C2-C3

There are no ring outliers.

20 monomers are involved in 79 short contacts:

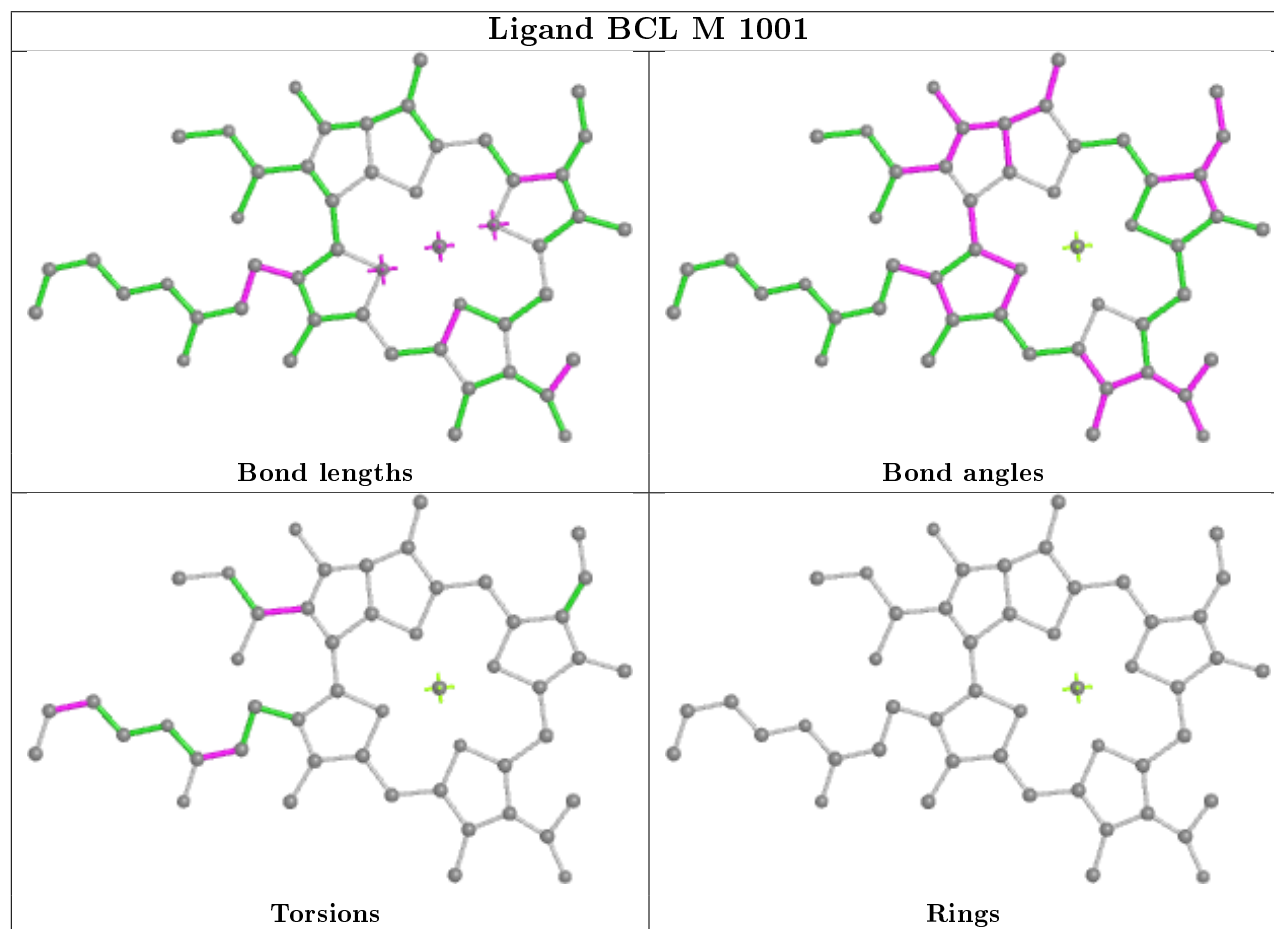
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	1001	BCL	4	0
10	M	1010	LDA	2	0
11	D	2009	HEM	2	0
10	S	2010	LDA	2	0
10	M	1011	LDA	3	0
5	L	1004	BCL	7	0
5	L	1002	BCL	11	0
9	S	2008	U10	1	0
5	M	1003	BCL	15	0
9	M	1008	U10	1	0
5	R	2002	BCL	10	0
6	L	1005	BPH	2	0
5	S	2003	BCL	11	0

*Continued on next page...*

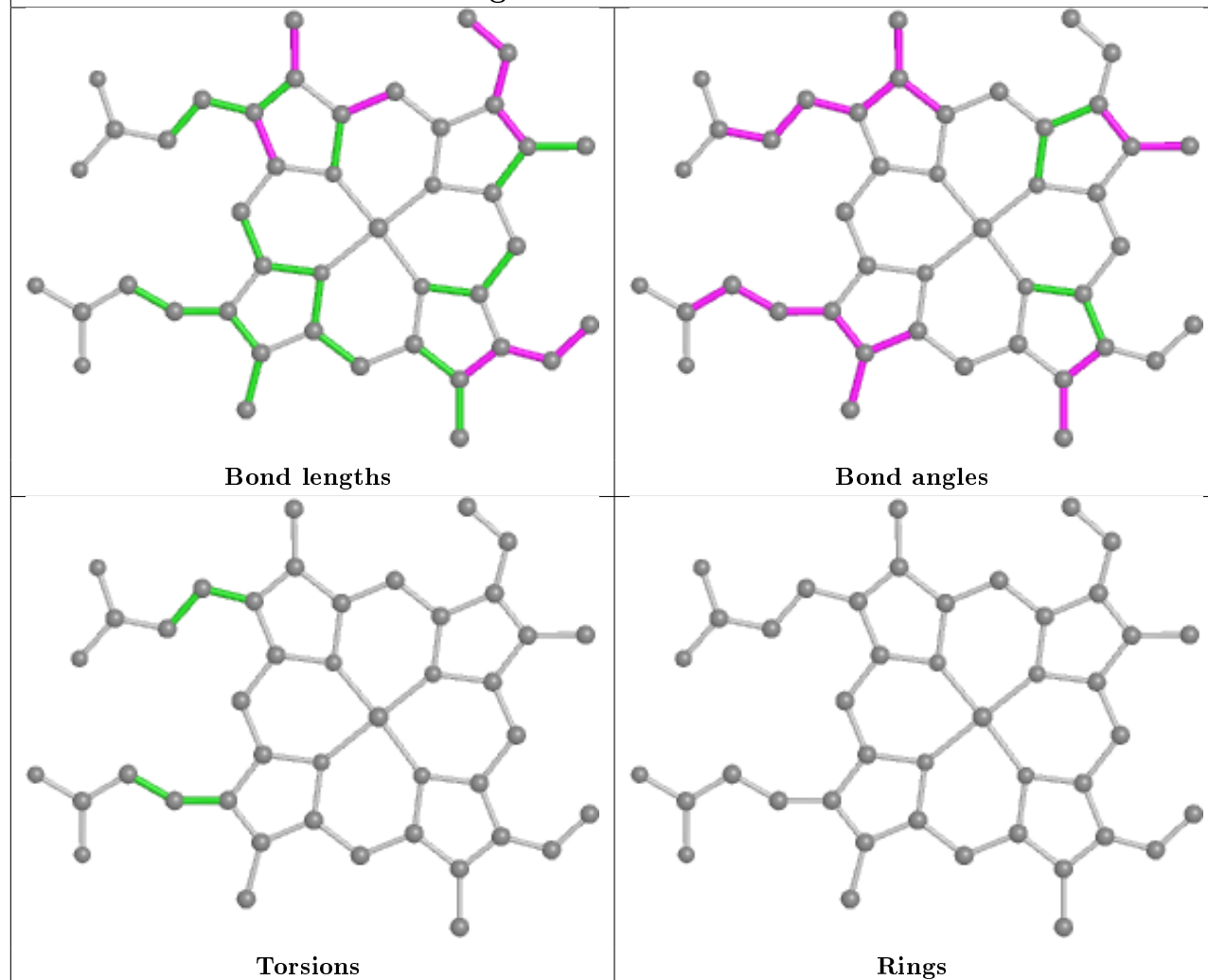
*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	S	2006	BPH	6	0
11	C	1009	HEM	2	0
5	S	2001	BCL	4	0
10	S	2011	LDA	1	0
6	R	2005	BPH	2	0
6	M	1006	BPH	3	0
5	R	2004	BCL	11	0

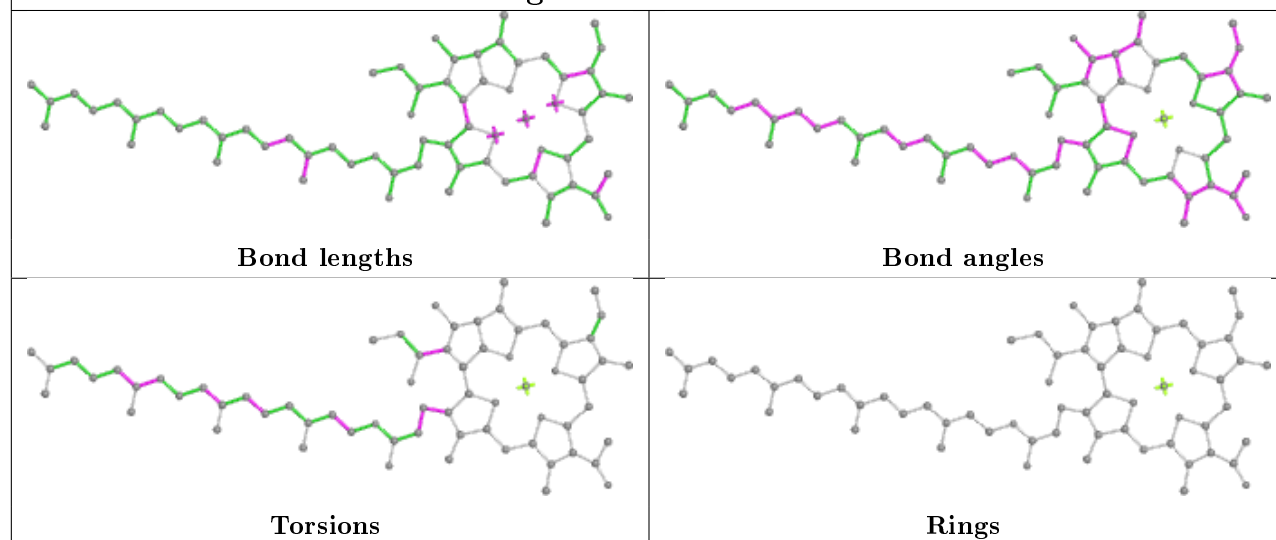
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

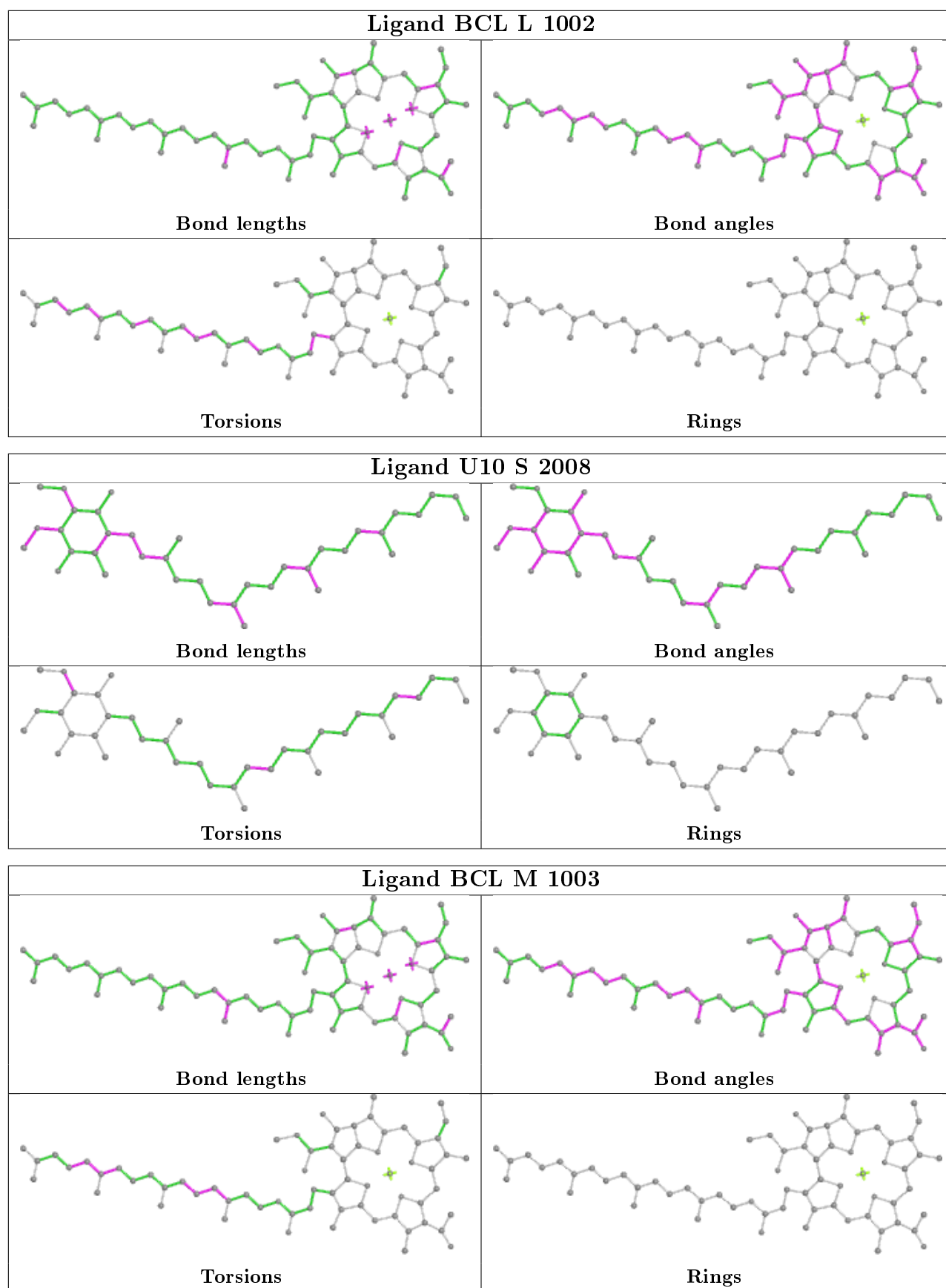


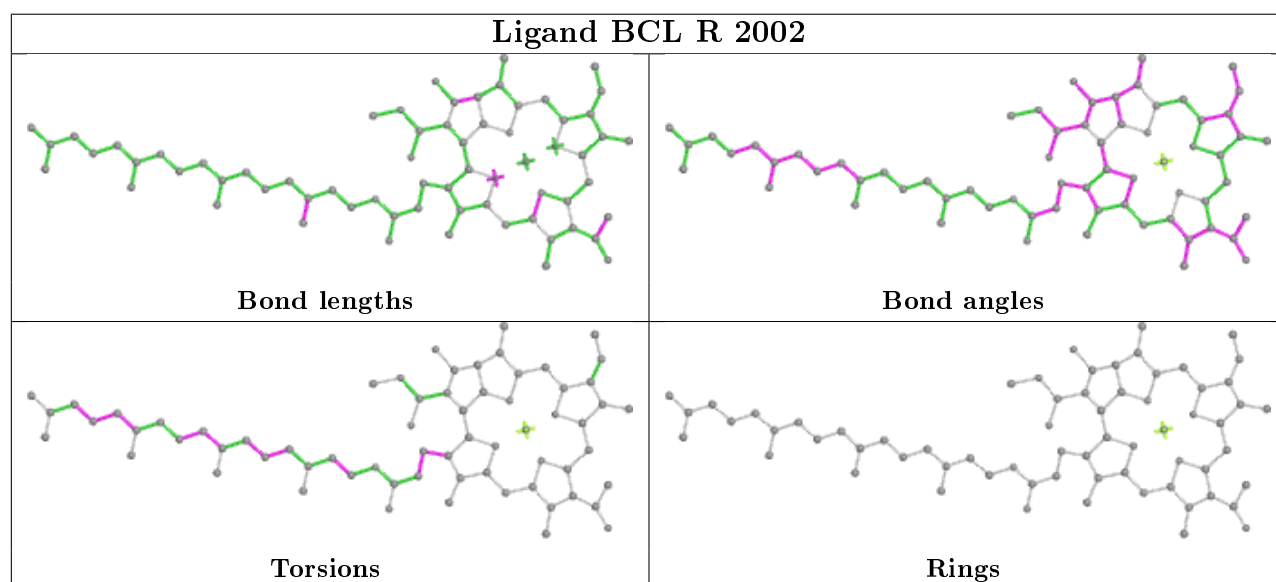
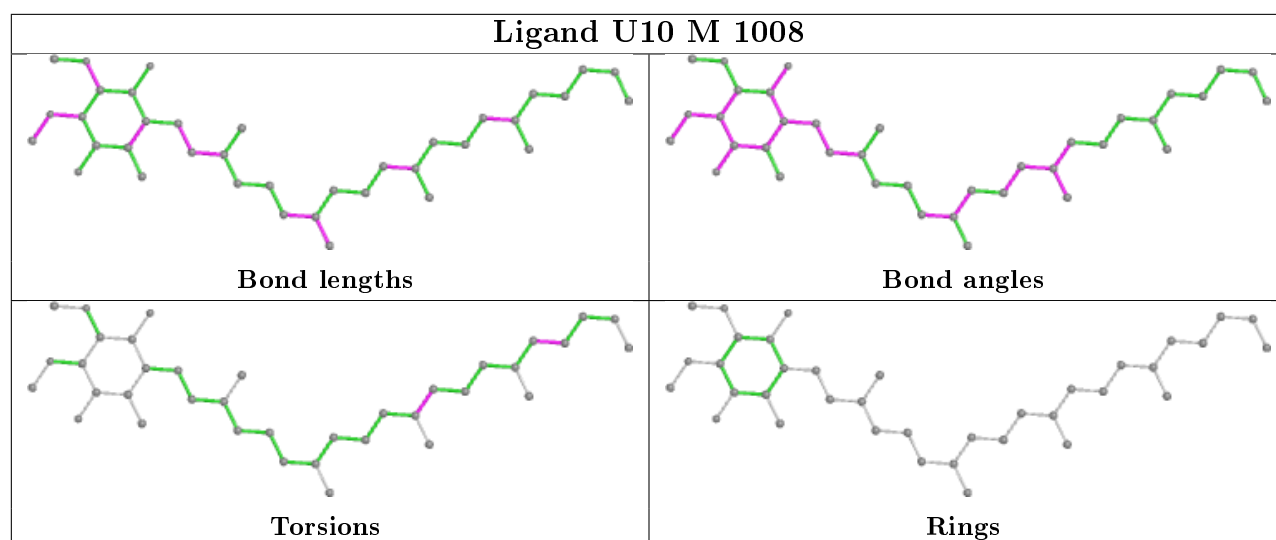
## Ligand HEM D 2009



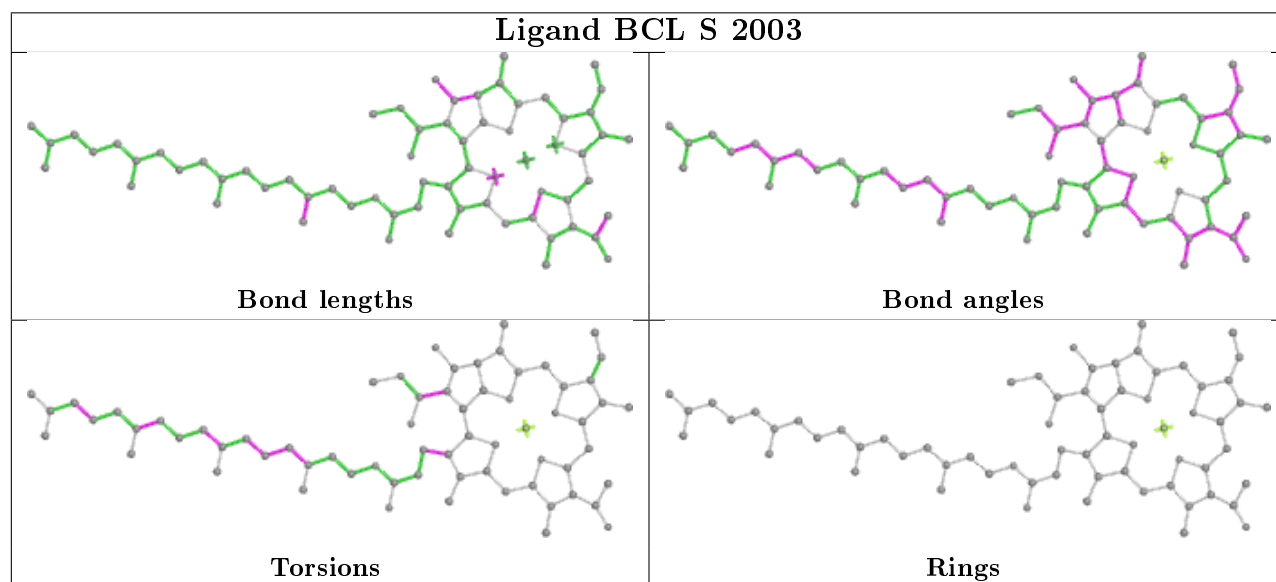
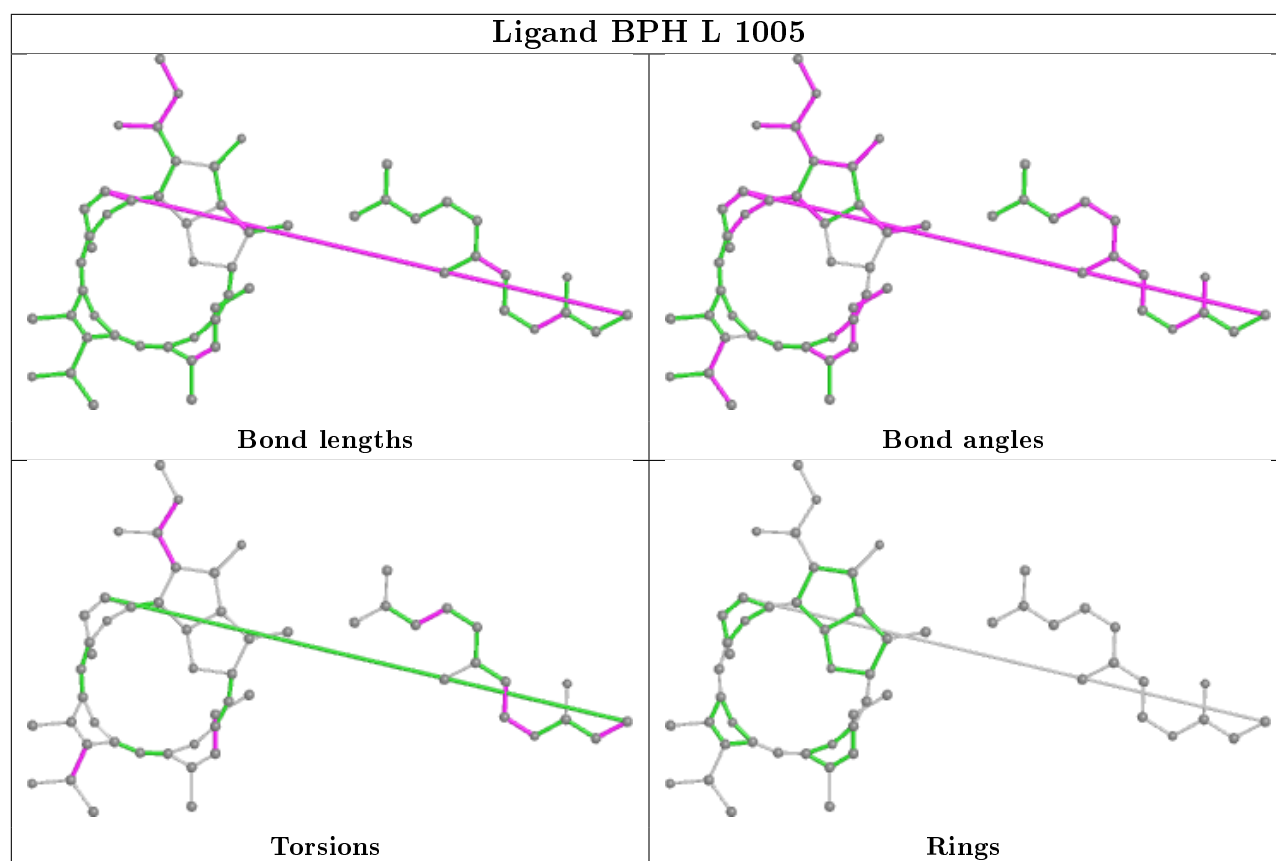
## Ligand BCL L 1004

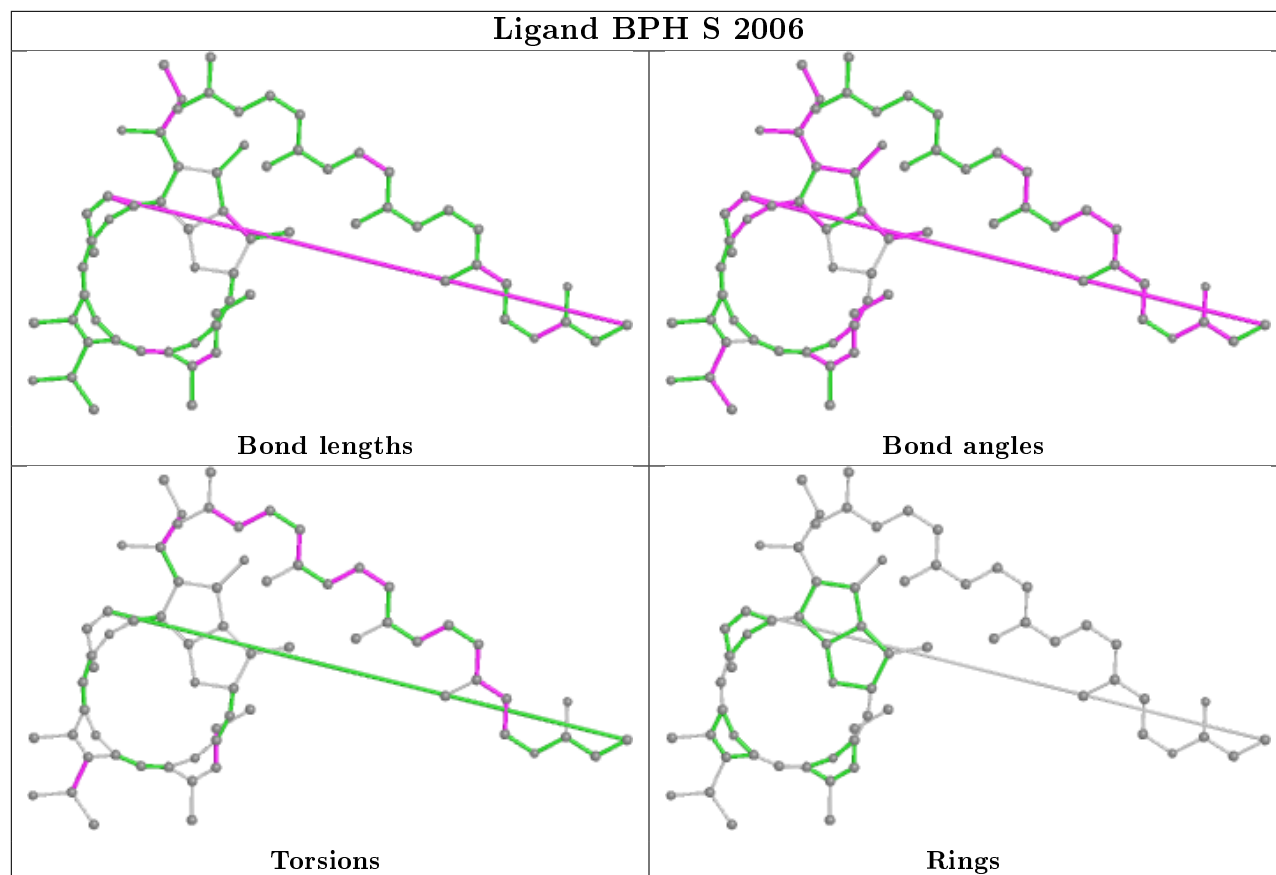




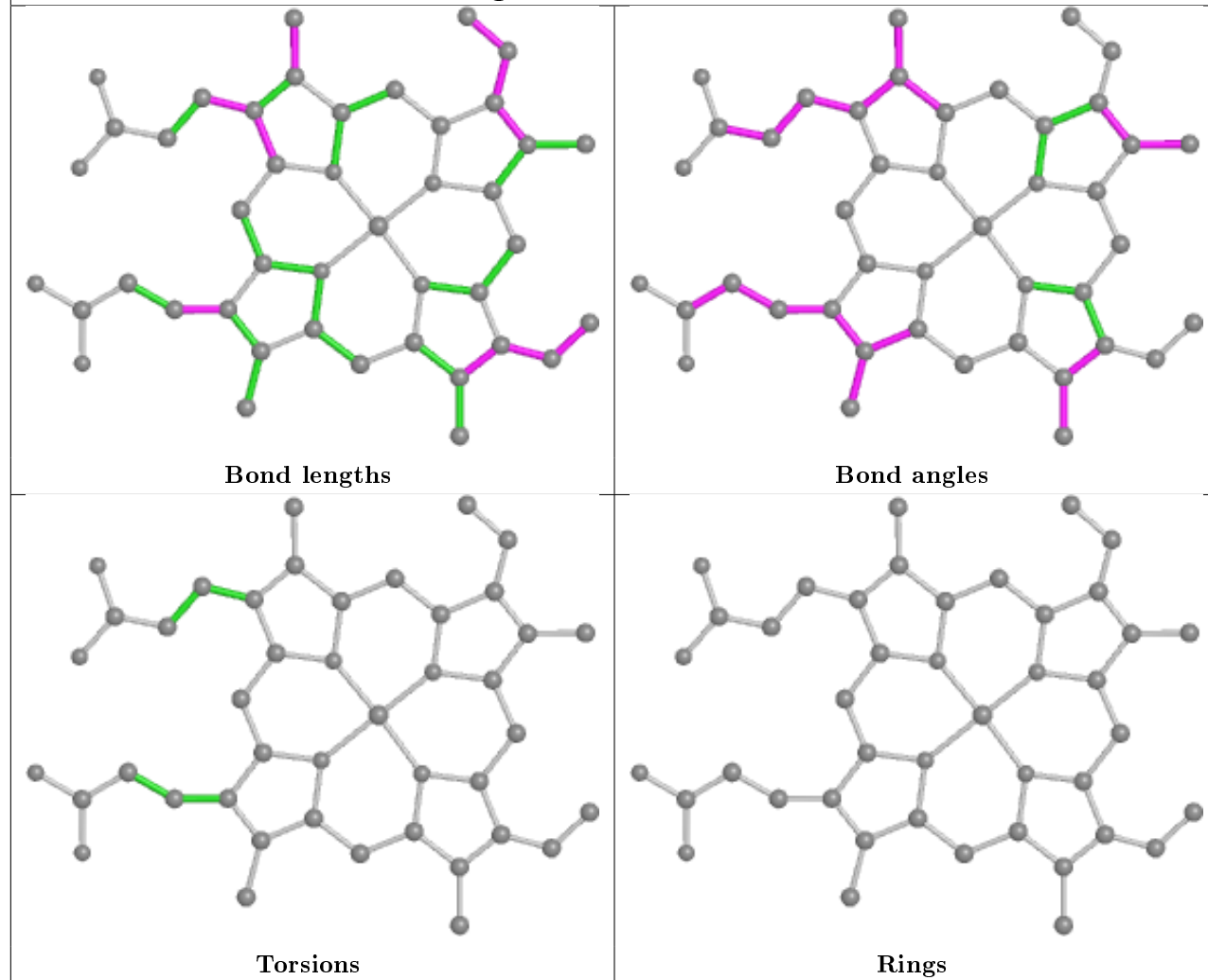




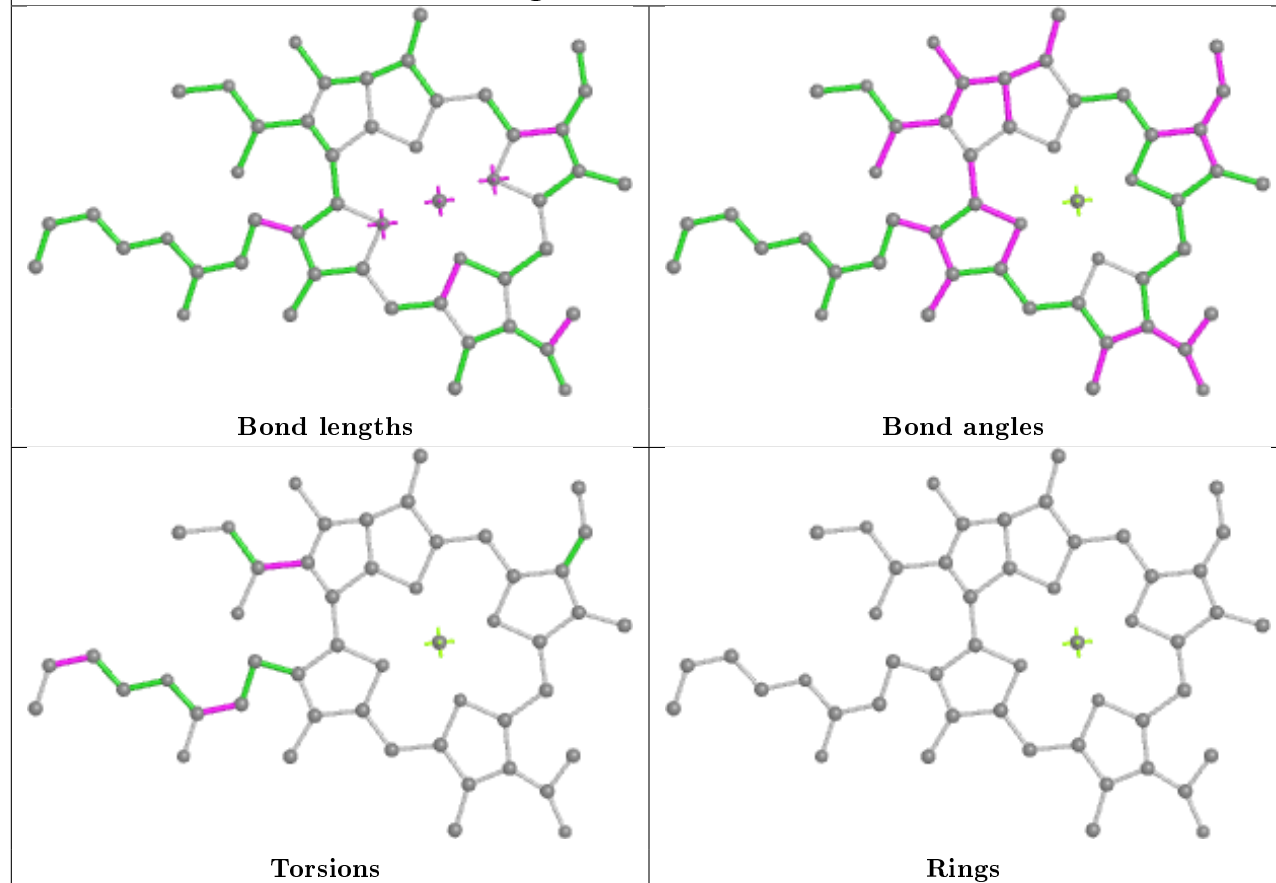




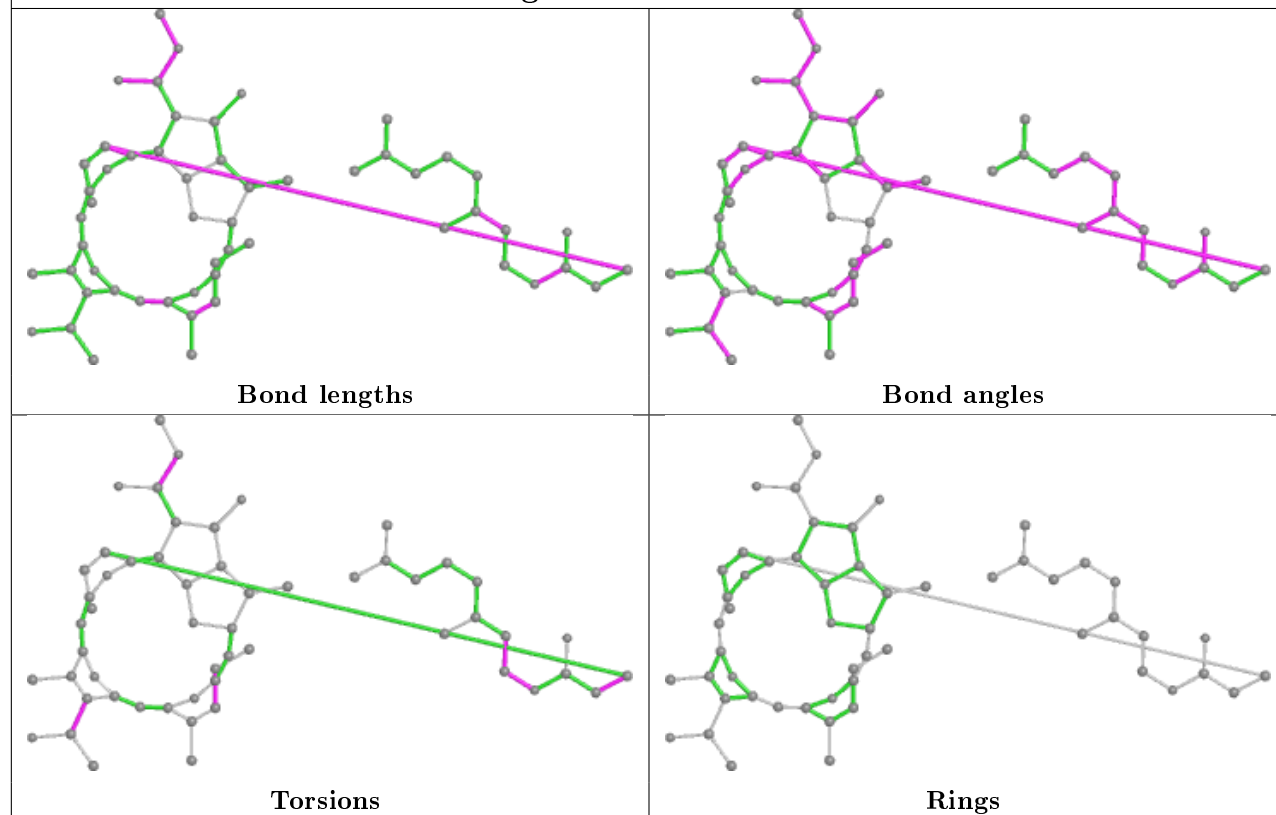
## Ligand HEM C 1009

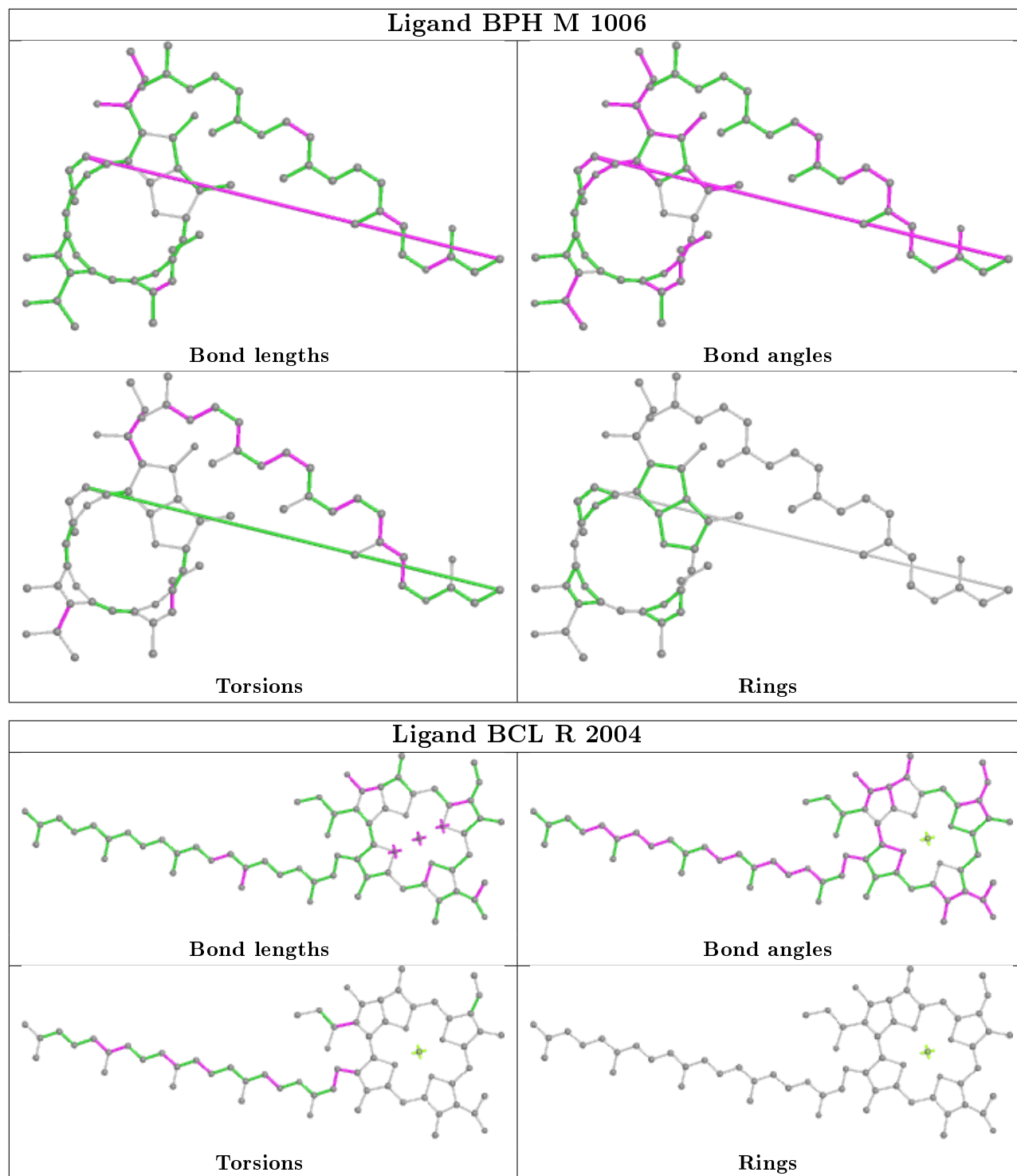


## Ligand BCL S 2001



## Ligand BPH R 2005





## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	L	281/281 (100%)	-0.28	2 (0%) 87 88	34, 59, 84, 103	0
1	R	281/281 (100%)	-0.24	8 (2%) 53 50	38, 72, 106, 122	0
2	M	267/307 (86%)	-0.29	6 (2%) 62 59	25, 52, 109, 134	0
2	S	267/307 (86%)	-0.15	7 (2%) 56 52	33, 61, 110, 139	0
3	H	246/260 (94%)	0.26	22 (8%) 9 10	44, 98, 148, 167	0
3	T	246/260 (94%)	0.70	37 (15%) 2 2	42, 121, 157, 172	0
4	C	124/124 (100%)	0.14	2 (1%) 72 69	40, 70, 95, 140	0
4	D	124/124 (100%)	0.16	4 (3%) 47 45	50, 82, 105, 146	0
All	All	1836/1944 (94%)	0.00	88 (4%) 30 28	25, 71, 131, 172	0

The worst 5 of 88 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	T	8	GLY	8.2
3	T	9	ASN	7.2
2	S	37	THR	6.9
3	T	179	LEU	6.7
3	T	167	ILE	6.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates 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.

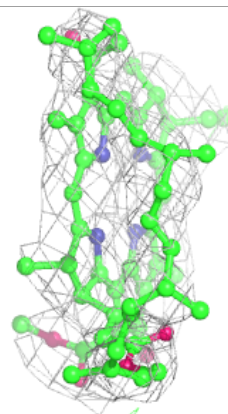
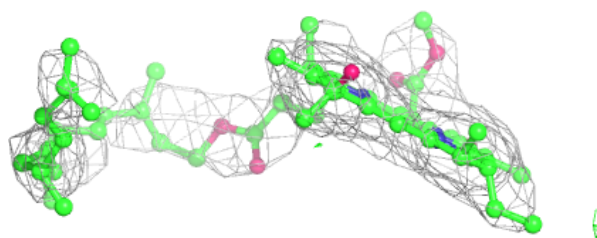
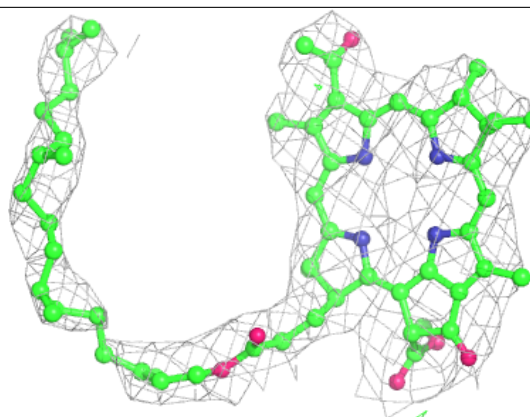
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
10	LDA	S	2011	16/16	0.77	0.56	91,98,110,111	0
10	LDA	M	1011	16/16	0.78	0.54	86,89,95,95	0
10	LDA	S	2010	16/16	0.87	0.35	59,82,94,94	0
10	LDA	M	1010	16/16	0.90	0.27	50,54,57,59	0
6	BPH	S	2006	65/65	0.92	0.29	50,57,67,70	0
6	BPH	R	2005	55/65	0.92	0.29	63,70,94,96	0
9	U10	M	1008	37/63	0.93	0.26	44,54,68,69	0
5	BCL	M	1003	66/66	0.93	0.26	33,40,55,59	0
5	BCL	L	1004	66/66	0.93	0.28	42,48,67,71	0
5	BCL	R	2004	66/66	0.94	0.29	46,52,69,74	0
9	U10	S	2008	37/63	0.94	0.27	52,62,87,87	0
5	BCL	R	2002	66/66	0.94	0.27	38,43,56,58	0
6	BPH	L	1005	55/65	0.94	0.28	43,52,91,93	0
5	BCL	S	2001	50/66	0.94	0.23	51,60,71,76	0
5	BCL	M	1001	50/66	0.95	0.22	37,46,58,61	0
5	BCL	L	1002	66/66	0.95	0.25	29,40,50,55	0
8	CL	S	2012	1/1	0.95	0.39	71,71,71,71	0
5	BCL	S	2003	66/66	0.95	0.25	36,42,73,75	0
8	CL	M	1012	1/1	0.95	0.35	66,66,66,66	0
6	BPH	M	1006	65/65	0.95	0.23	48,56,67,69	0
11	HEM	D	2009	43/43	0.96	0.26	49,52,64,70	0
11	HEM	C	1009	43/43	0.97	0.23	35,42,52,55	0
7	FE2	S	2007	1/1	0.99	0.14	54,54,54,54	0
7	FE2	M	1007	1/1	0.99	0.15	45,45,45,45	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.

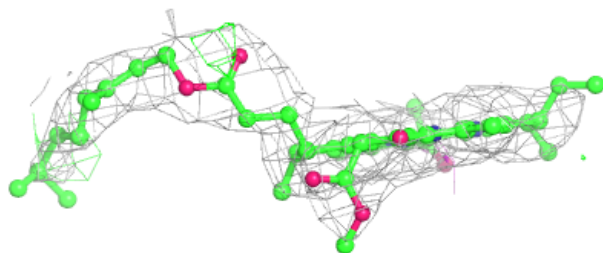
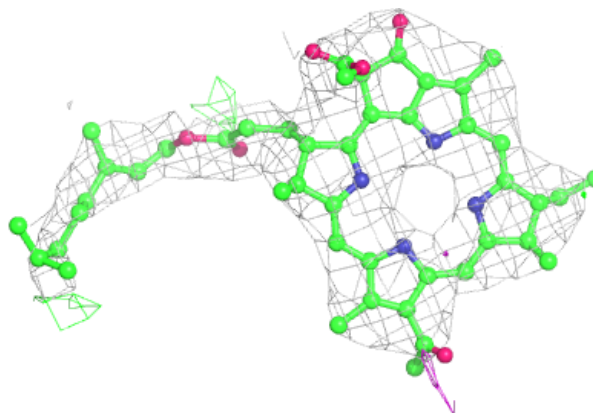


**Electron density around BPH S 2006:**

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

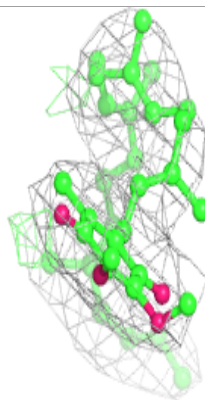
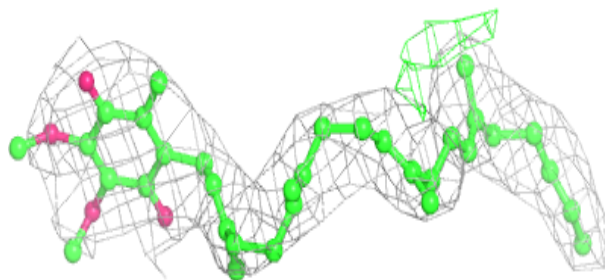
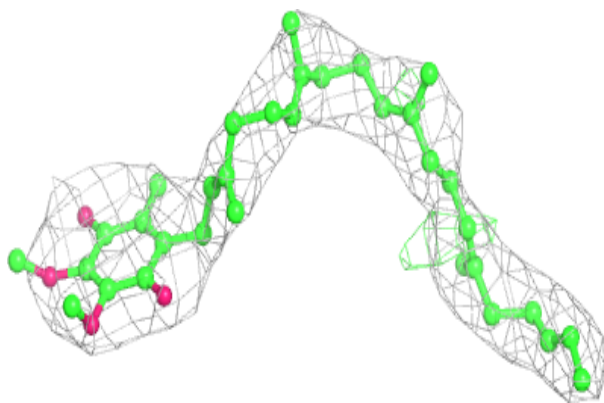
**Electron density around BPH R 2005:**

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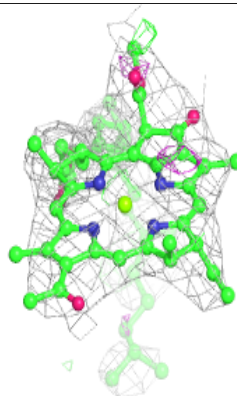
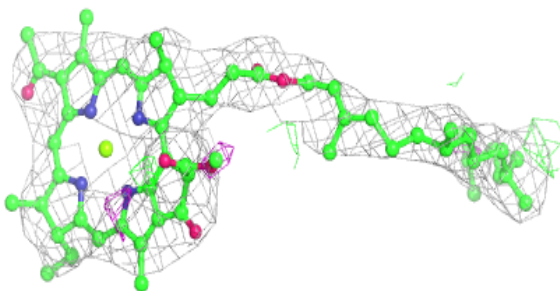
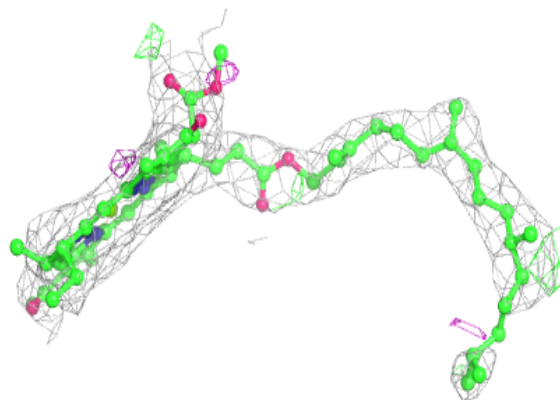


**Electron density around U10 M 1008:**

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and green (positive)

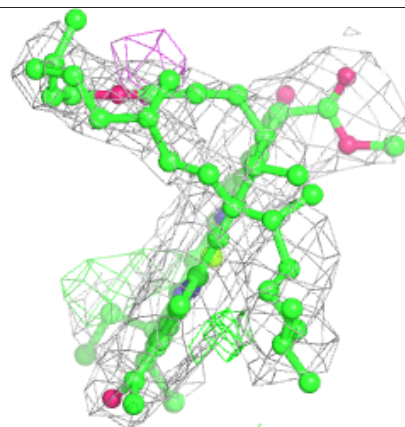
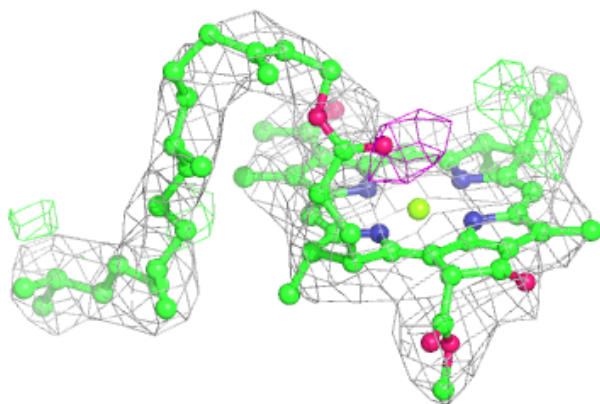
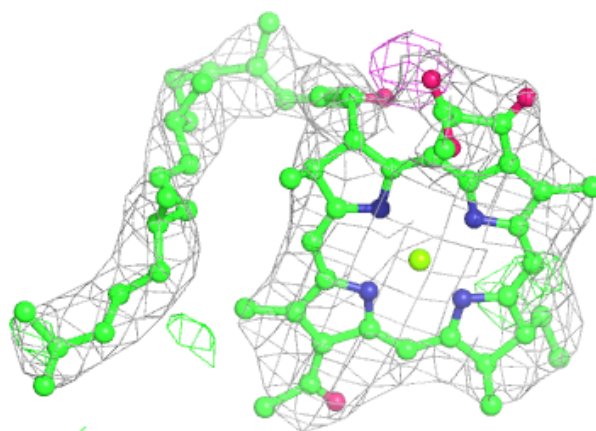
**Electron density around BCL M 1003:**

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and green (positive)

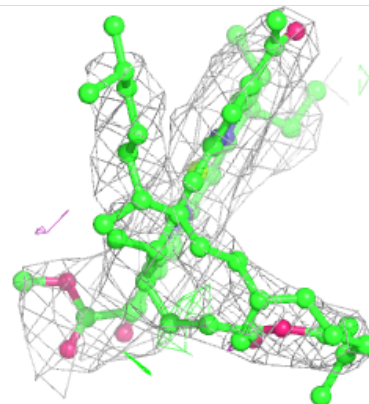
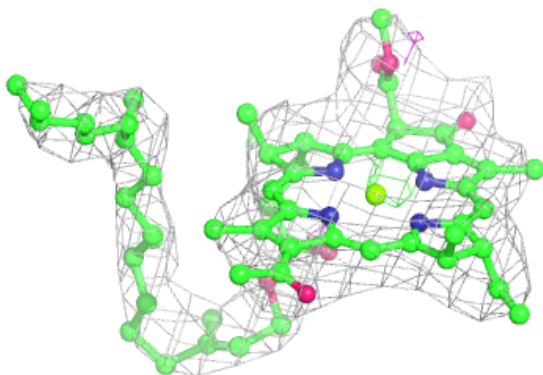
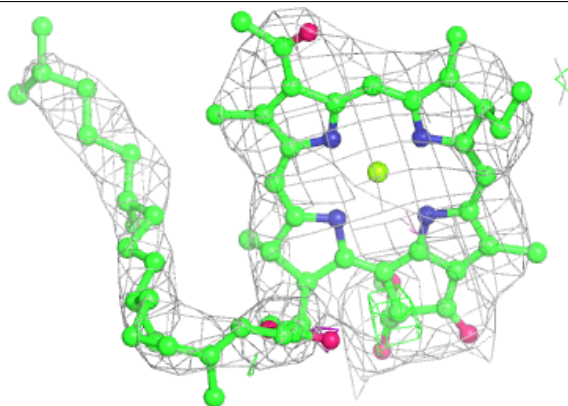


**Electron density around BCL L 1004:**

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and green (positive)

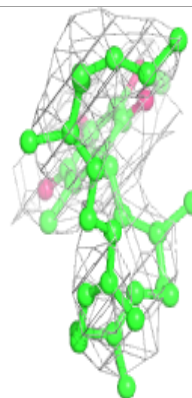
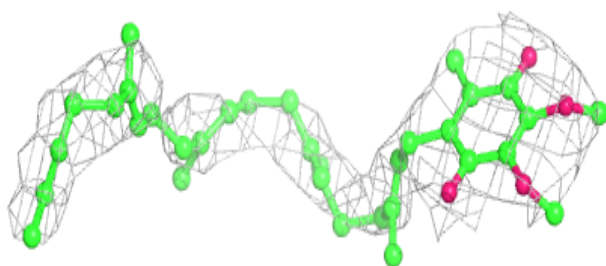
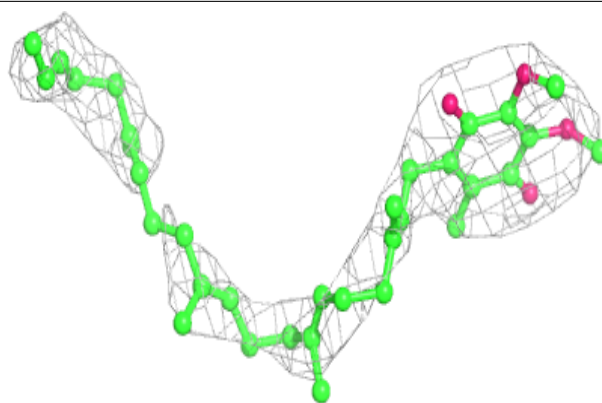
**Electron density around BCL R 2004:**

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and green (positive)

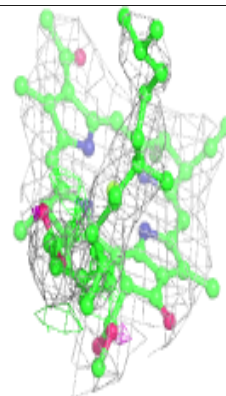
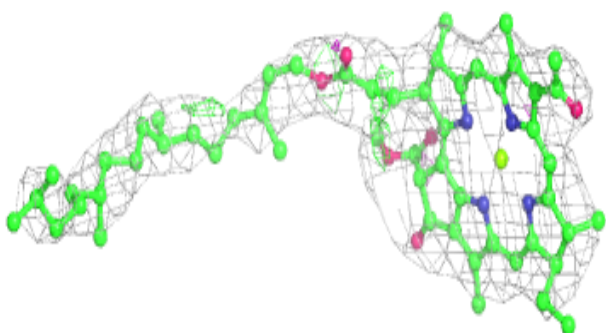
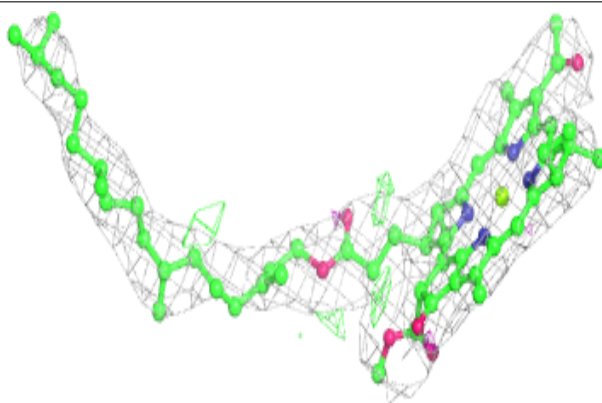


**Electron density around U10 S 2008:**

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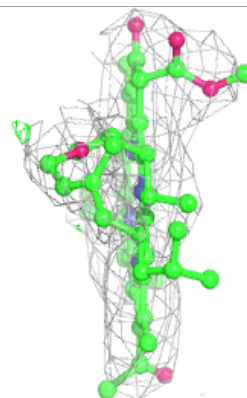
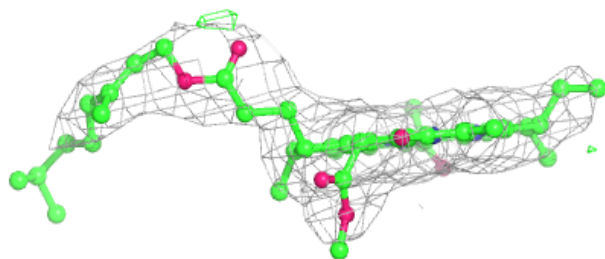
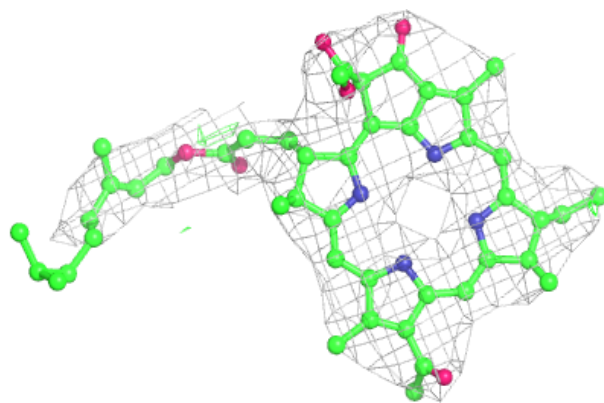
**Electron density around BCL R 2002:**

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and green (positive)



**Electron density around BPH L 1005:**

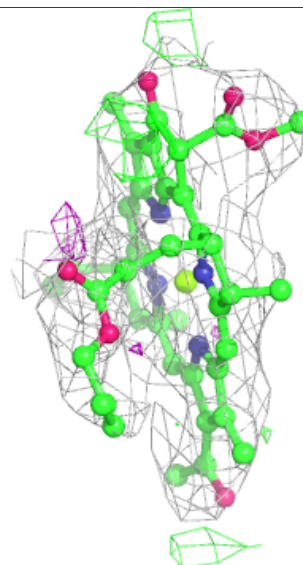
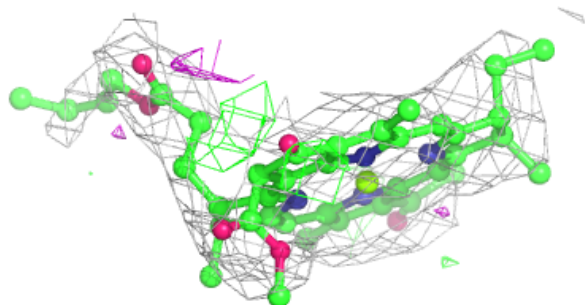
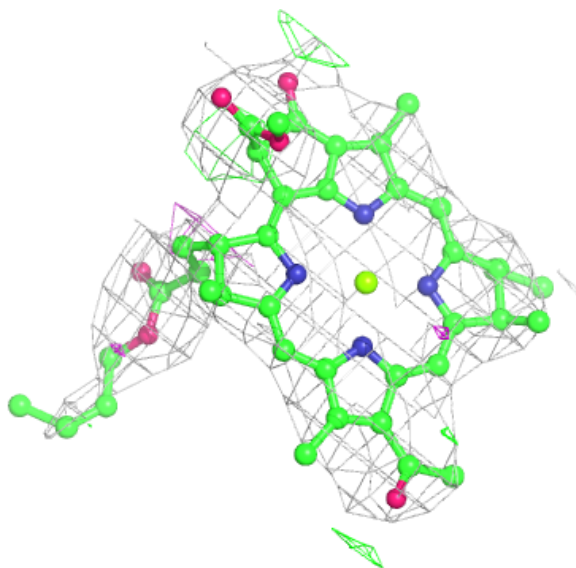
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





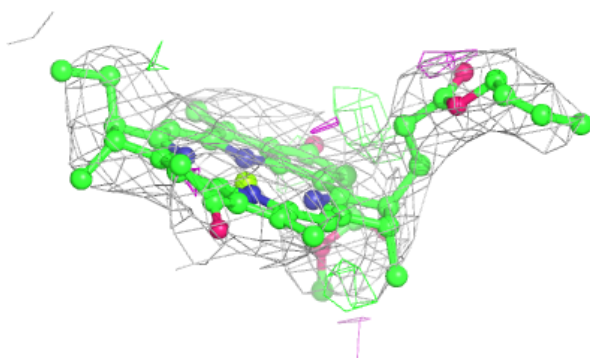
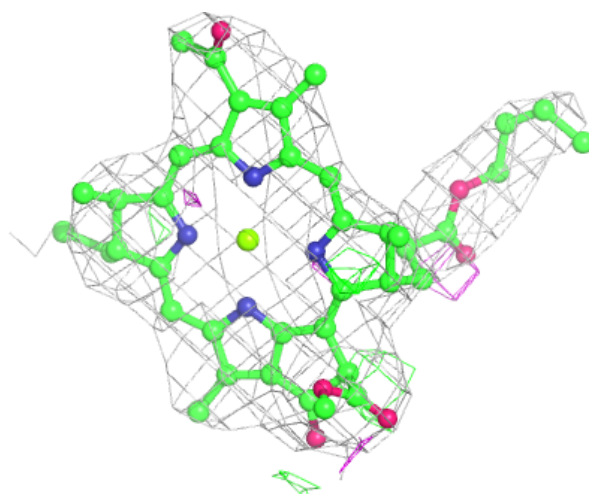
**Electron density around BCL S 2001:**

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



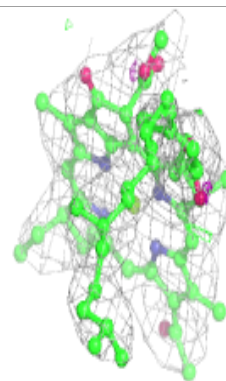
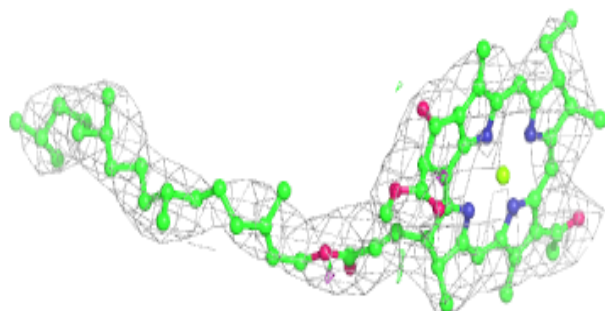
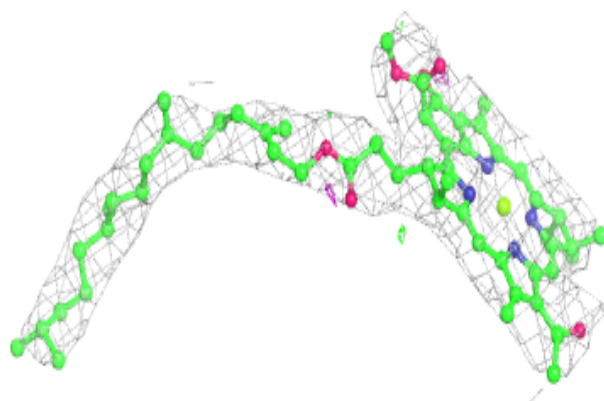
**Electron density around BCL M 1001:**

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

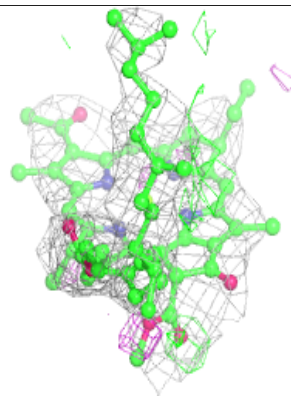
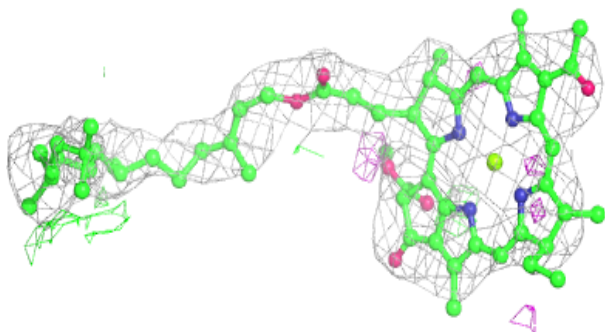
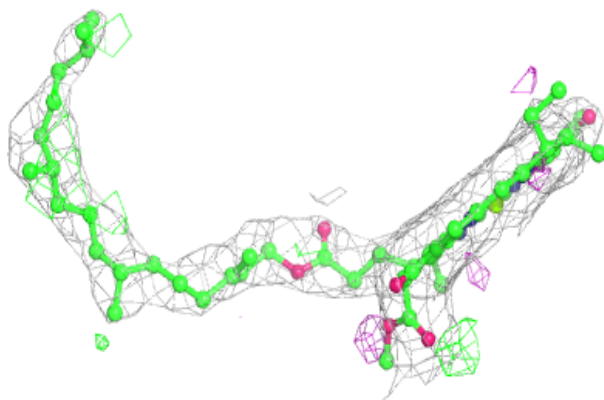


**Electron density around BCL L 1002:**

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

**Electron density around BCL S 2003:**

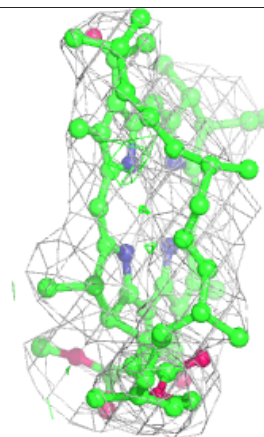
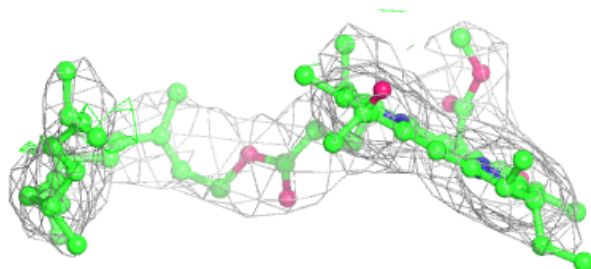
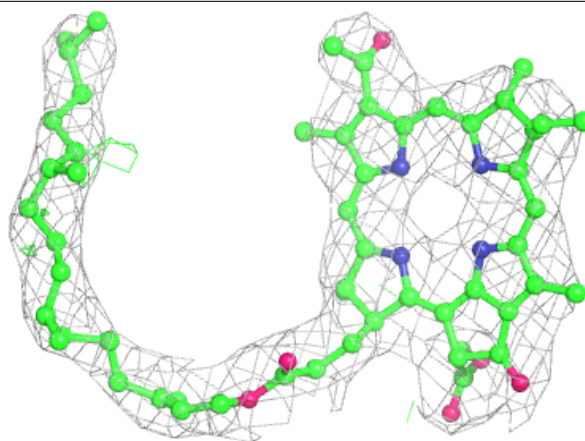
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





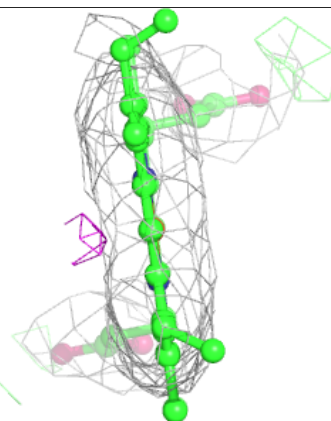
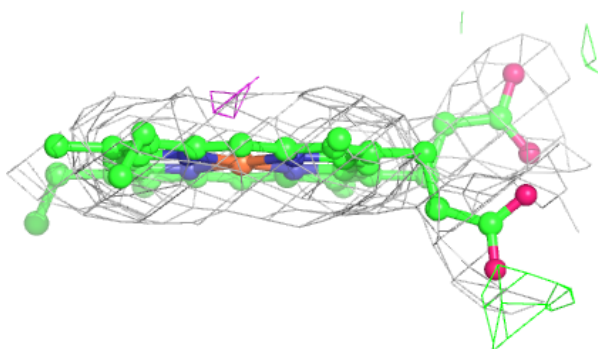
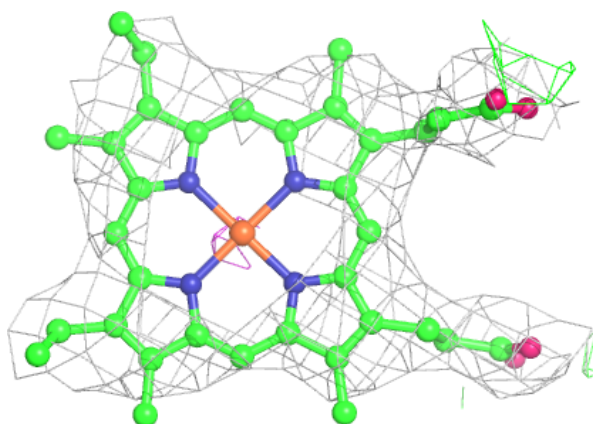
**Electron density around BPH M 1006:**

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

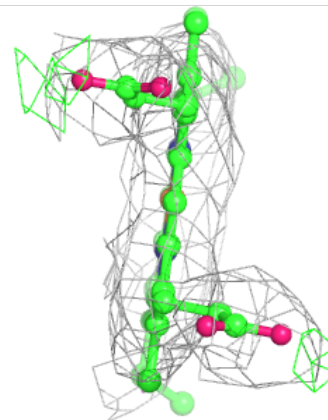
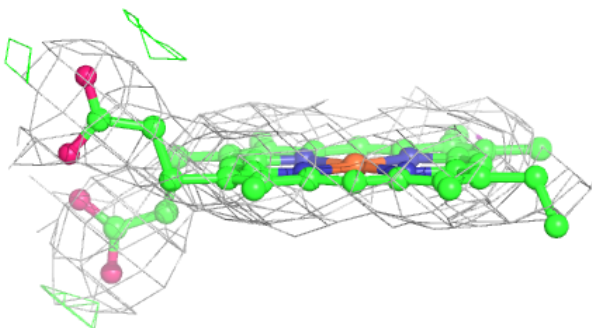
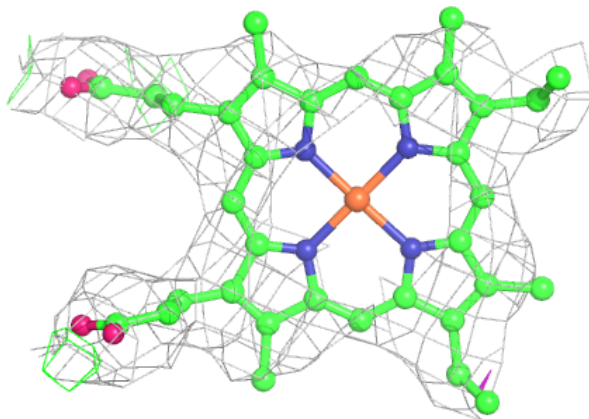


**Electron density around HEM D 2009:**

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

**Electron density around HEM C 1009:**

$2mF_o-DF_c$  (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.