



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 22, 2026 – 03:25 PM EDT

PDB ID : 1L9B / pdb_00001l9b
Title : X-Ray Structure of the Cytochrome-c(2)-Photosynthetic Reaction Center Electron Transfer Complex from Rhodobacter sphaeroides in Type II Crystals
Authors : Axelrod, H.L.; Abresch, E.C.; Okamura, M.Y.; Yeh, A.P.; Rees, D.C.; Feher, G.
Deposited on : 2002-03-22
Resolution : 2.40 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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>.

The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

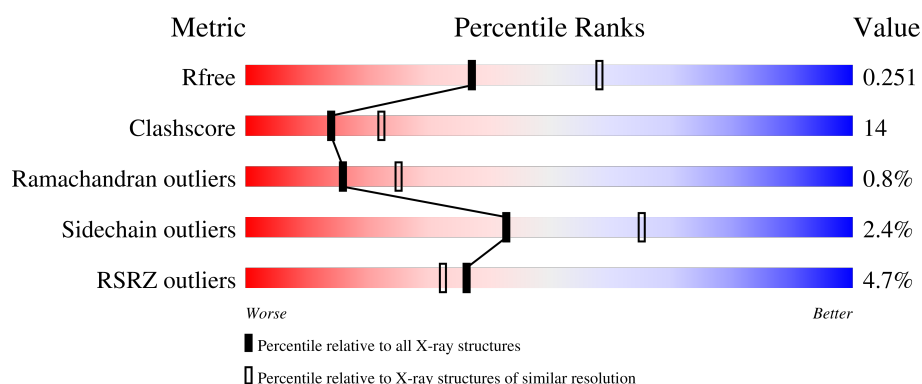
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	3% 73% 25% •
2	M	307	3% 66% 20% • 13%
3	H	260	10% 63% 29% • 5%
4	C	124	% 71% 27% •

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
13	HEC	C	1009	X	-	-	-
7	BPH	L	1005	X	-	-	-
7	BPH	M	1006	X	-	-	-
9	HTO	C	1022	-	-	X	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 8102 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			

- 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			

- 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			

- 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			

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	1	Total	Na	0	0
			1	1		

- Molecule 6 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: C₅₅H₇₄MgN₄O₆).

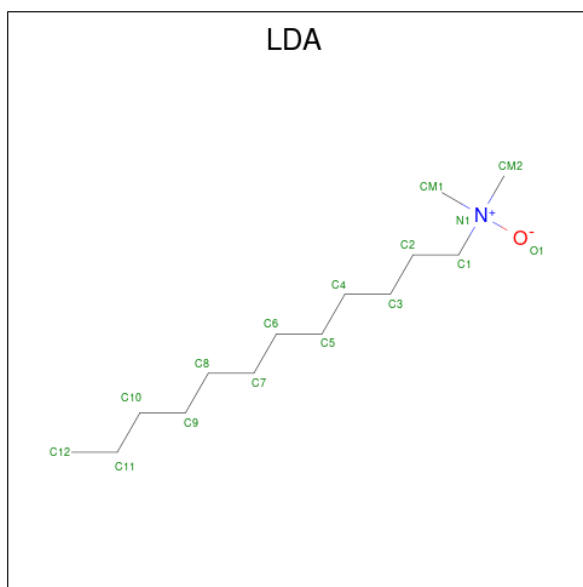


- Molecule 7 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$).



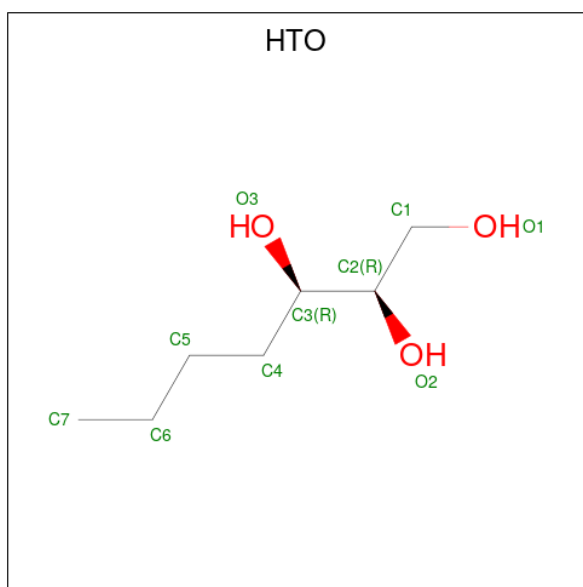
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	L	1	Total	C	N	O	0	0
			55	45	4	6		
7	M	1	Total	C	N	O	0	0
			65	55	4	6		

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



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

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



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

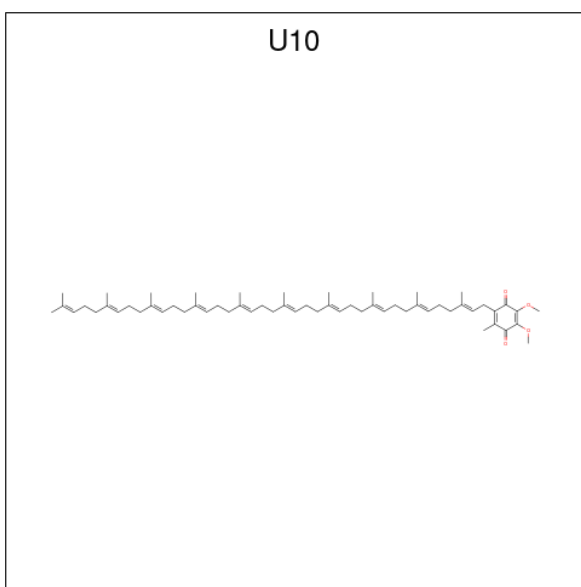
- Molecule 10 is FE (II) ION (CCD ID: FE2) (formula: Fe).

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

- Molecule 11 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

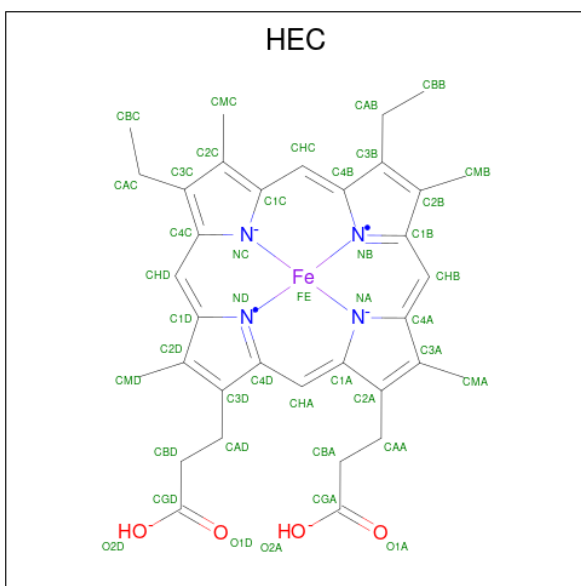
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	M	1	Total	Cl	0	0
			1	1		

- Molecule 12 is UBIQUINONE-10 (CCD ID: U10) (formula: C₅₉H₉₀O₄).



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

- Molecule 13 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



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

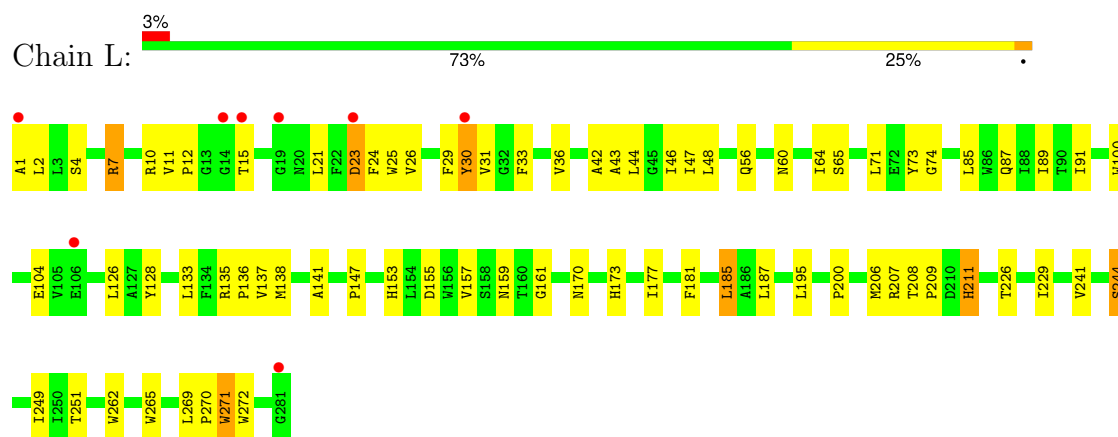
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	L	91	Total 91	O 91	0	0
14	M	70	Total 70	O 70	0	0
14	H	66	Total 66	O 66	0	0
14	C	58	Total 58	O 58	0	0

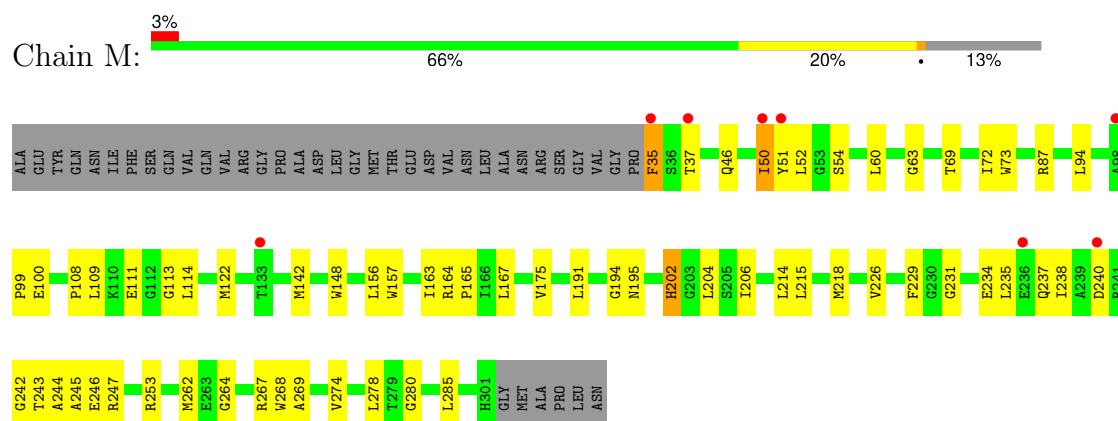
3 Residue-property plots

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.

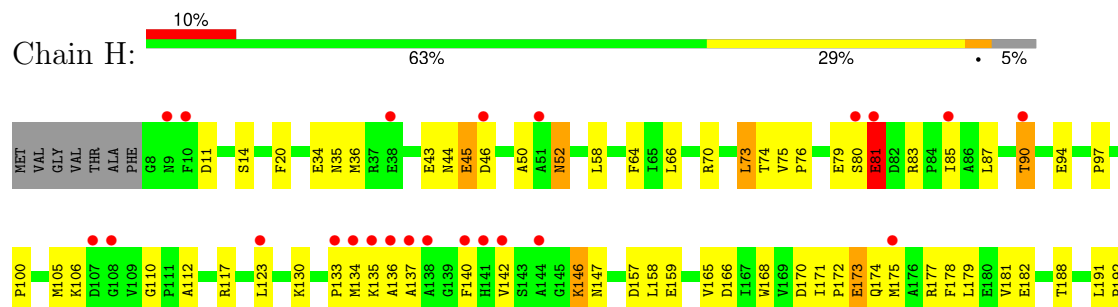
• Molecule 1: REACTION CENTER PROTEIN L CHAIN

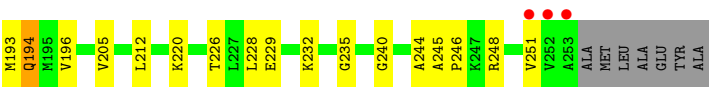


• Molecule 2: REACTION CENTER PROTEIN M CHAIN



• Molecule 3: REACTION CENTER PROTEIN H CHAIN





● 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, α , β , γ	78.22Å 115.65Å 79.68Å 90.00° 110.29° 90.00°	Depositor
Resolution (Å)	45.73 – 2.40 45.73 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.7 (45.73-2.40) 96.7 (45.73-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.39Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.220 , 0.264 0.209 , 0.251	Depositor DCC
R_{free} test set	2523 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	49.1	Xtriage
Anisotropy	0.703	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 77.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8102	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: BPH, LDA, CL, HTO, HEC, BCL, NA, U10, FE2

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	0.41	0/2320	0.90	5/3175 (0.2%)
2	M	0.44	0/2238	0.86	2/3057 (0.1%)
3	H	0.37	0/1920	0.85	0/2612
4	C	0.42	0/969	0.92	2/1304 (0.2%)
All	All	0.41	0/7447	0.88	9/10148 (0.1%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	271	TRP	N-CA-C	6.82	120.86	112.54
1	L	29	PHE	N-CA-C	5.84	119.05	109.76
2	M	202	HIS	N-CA-C	-5.73	105.01	112.23
2	M	163	ILE	N-CA-C	5.38	115.58	110.42
4	C	32	ARG	N-CA-C	-5.38	104.00	110.88

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	59	0
2	M	2150	0	2073	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	1871	0	1877	72	0
4	C	949	0	916	32	0
5	L	1	0	0	0	0
6	L	132	0	148	10	0
6	M	116	0	115	15	0
7	L	55	0	53	5	0
7	M	65	0	74	2	0
8	H	32	0	62	2	0
8	L	64	0	124	0	0
8	M	48	0	93	5	0
9	C	10	0	16	6	0
9	L	10	0	16	0	0
10	M	1	0	0	0	0
11	M	1	0	0	0	0
12	M	37	0	47	0	0
13	C	43	0	30	0	0
14	C	58	0	0	8	0
14	H	66	0	0	3	0
14	L	91	0	0	10	0
14	M	70	0	0	9	0
All	All	8102	0	7831	224	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 14.

The worst 5 of 224 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:M:280:GLY:HA3	6:M:1003:BCL:HED3	1.40	1.02
2:M:280:GLY:HA3	6:M:1003:BCL:CED	1.93	0.98
2:M:157:TRP:HB2	6:M:1003:BCL:H62	1.49	0.93
2:M:218:MET:N	14:M:1085:HOH:O	2.03	0.91
2:M:268:TRP:HE1	3:H:35:ASN:ND2	1.69	0.90

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	L	279/281 (99%)	261 (94%)	15 (5%)	3 (1%)	11	18
2	M	265/307 (86%)	256 (97%)	9 (3%)	0	100	100
3	H	244/260 (94%)	218 (89%)	22 (9%)	4 (2%)	7	11
4	C	122/124 (98%)	112 (92%)	10 (8%)	0	100	100
All	All	910/972 (94%)	847 (93%)	56 (6%)	7 (1%)	16	25

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	81	GLU
3	H	220	LYS
3	H	83	ARG
1	L	7	ARG
1	L	23	ASP

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%)	217 (99%)	3 (1%)	59	79
2	M	209/240 (87%)	204 (98%)	5 (2%)	43	65
3	H	199/208 (96%)	191 (96%)	8 (4%)	28	47
4	C	93/93 (100%)	92 (99%)	1 (1%)	65	82
All	All	721/761 (95%)	704 (98%)	17 (2%)	43	65

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	173	GLU
4	C	20	VAL
2	M	191	LEU
3	H	52	ASN
3	H	73	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
4	C	14	GLN
4	C	81	GLN
4	C	119	GLN
4	C	112	ASN
4	C	51	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 3 are monoatomic - leaving 19 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
8	LDA	M	1013	-	13,15,15	1.89	1 (7%)	14,17,17	1.69	4 (28%)
8	LDA	L	1018	-	13,15,15	1.96	1 (7%)	14,17,17	1.70	4 (28%)
9	HTO	L	1021	-	9,9,9	1.50	2 (22%)	10,10,10	0.58	0
8	LDA	M	1015	-	13,15,15	1.94	1 (7%)	14,17,17	1.68	4 (28%)
7	BPH	L	1005	-	49,60,70	2.30	14 (28%)	47,89,101	3.15	21 (44%)
8	LDA	L	1016	-	13,15,15	1.96	1 (7%)	14,17,17	1.71	4 (28%)
8	LDA	H	1014	-	13,15,15	1.94	1 (7%)	14,17,17	1.72	4 (28%)
6	BCL	M	1001	2	53,58,74	2.10	14 (26%)	58,95,115	1.97	12 (20%)
7	BPH	M	1006	-	59,70,70	2.24	13 (22%)	59,101,101	2.91	19 (32%)
9	HTO	C	1022	-	9,9,9	1.31	1 (11%)	10,10,10	0.66	0
6	BCL	M	1003	2	69,74,74	1.83	16 (23%)	79,115,115	1.93	23 (29%)
13	HEC	C	1009	4	50,50,50	1.39	8 (16%)	68,82,82	1.35	10 (14%)
8	LDA	L	1017	-	13,15,15	1.96	1 (7%)	14,17,17	1.75	4 (28%)
6	BCL	L	1004	1	69,74,74	1.86	13 (18%)	79,115,115	1.80	18 (22%)
8	LDA	M	1012	-	13,15,15	1.94	1 (7%)	14,17,17	1.74	4 (28%)
6	BCL	L	1002	1	69,74,74	1.89	14 (20%)	79,115,115	1.80	19 (24%)
8	LDA	H	1019	-	13,15,15	1.92	1 (7%)	14,17,17	1.73	4 (28%)
8	LDA	L	1020	-	13,15,15	1.95	1 (7%)	14,17,17	1.69	4 (28%)
12	U10	M	1008	-	37,37,63	2.00	10 (27%)	46,47,79	1.76	10 (21%)

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
8	LDA	M	1013	-	-	6/13/13/13	-
8	LDA	L	1018	-	-	9/13/13/13	-
9	HTO	L	1021	-	-	1/10/10/10	-
8	LDA	M	1015	-	-	6/13/13/13	-
7	BPH	L	1005	-	1/1/16/22	11/25/93/105	0/5/6/6
8	LDA	L	1016	-	-	9/13/13/13	-
8	LDA	H	1014	-	-	9/13/13/13	-
7	BPH	M	1006	-	2/2/18/22	16/37/105/105	0/5/6/6
6	BCL	M	1001	2	-	5/22/118/137	-
9	HTO	C	1022	-	-	1/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	BCL	M	1003	2	-	11/41/137/137	-
13	HEC	C	1009	4	1/1/3/7	4/14/54/54	-
8	LDA	L	1017	-	-	8/13/13/13	-
6	BCL	L	1004	1	-	12/41/137/137	-
8	LDA	M	1012	-	-	5/13/13/13	-
6	BCL	L	1002	1	-	13/41/137/137	-
8	LDA	H	1019	-	-	9/13/13/13	-
8	LDA	L	1020	-	-	8/13/13/13	-
12	U10	M	1008	-	-	4/32/56/87	0/1/1/1

The worst 5 of 114 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	L	1005	BPH	C2C-C3C	-8.64	1.47	1.54
7	M	1006	BPH	C2C-C3C	-7.77	1.48	1.54
6	L	1002	BCL	MG-NB	-7.13	1.91	2.05
8	M	1012	LDA	O1-N1	-6.71	1.25	1.42
8	L	1016	LDA	O1-N1	-6.70	1.25	1.42

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	M	1006	BPH	O2D-CGD-CBD	14.76	127.16	110.95
7	L	1005	BPH	O2D-CGD-CBD	14.27	126.62	110.95
6	M	1001	BCL	CBC-CAC-C3C	-6.76	99.07	113.41
12	M	1008	U10	C3M-O3-C3	6.50	139.30	116.47
7	M	1006	BPH	C1-C2-C3	6.37	136.63	126.20

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	L	1005	BPH	C8
7	M	1006	BPH	C13
7	M	1006	BPH	C8
13	C	1009	HEC	NA

5 of 147 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	1004	BCL	C1A-C2A-CAA-CBA

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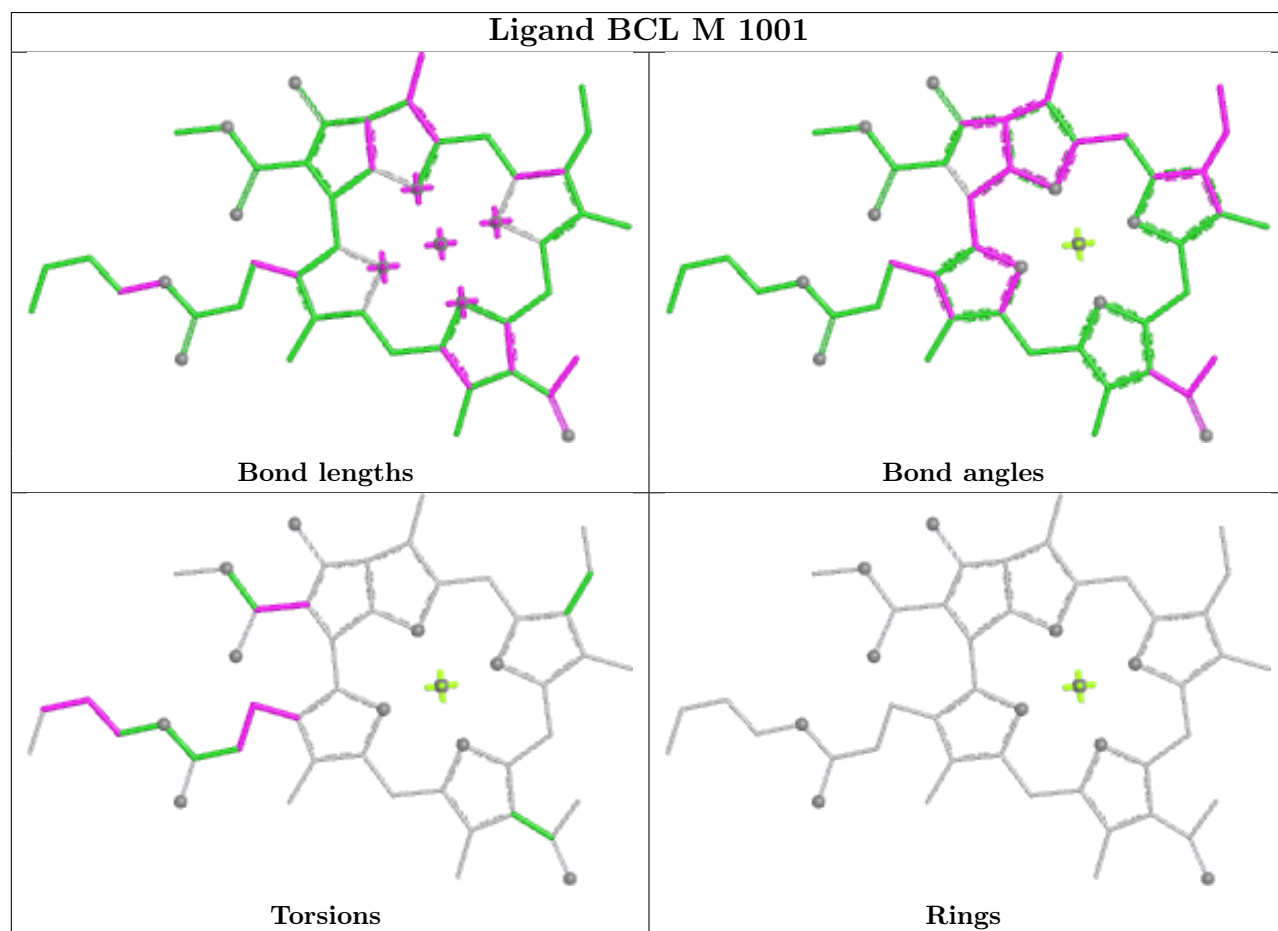
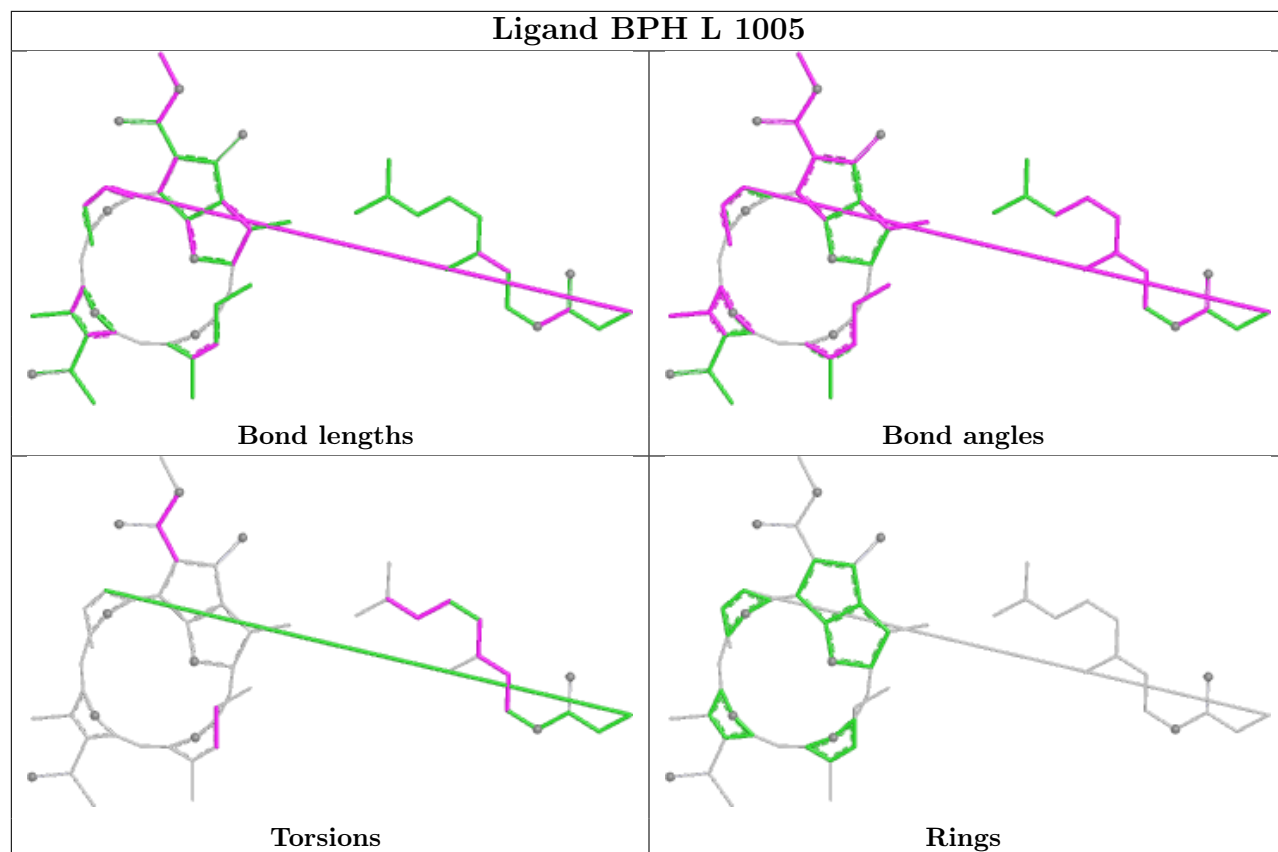
Mol	Chain	Res	Type	Atoms
6	L	1004	BCL	C3A-C2A-CAA-CBA
6	L	1004	BCL	CHA-CBD-CGD-O2D
7	L	1005	BPH	C2C-C3C-CAC-CBC
7	L	1005	BPH	C2-C3-C5-C6

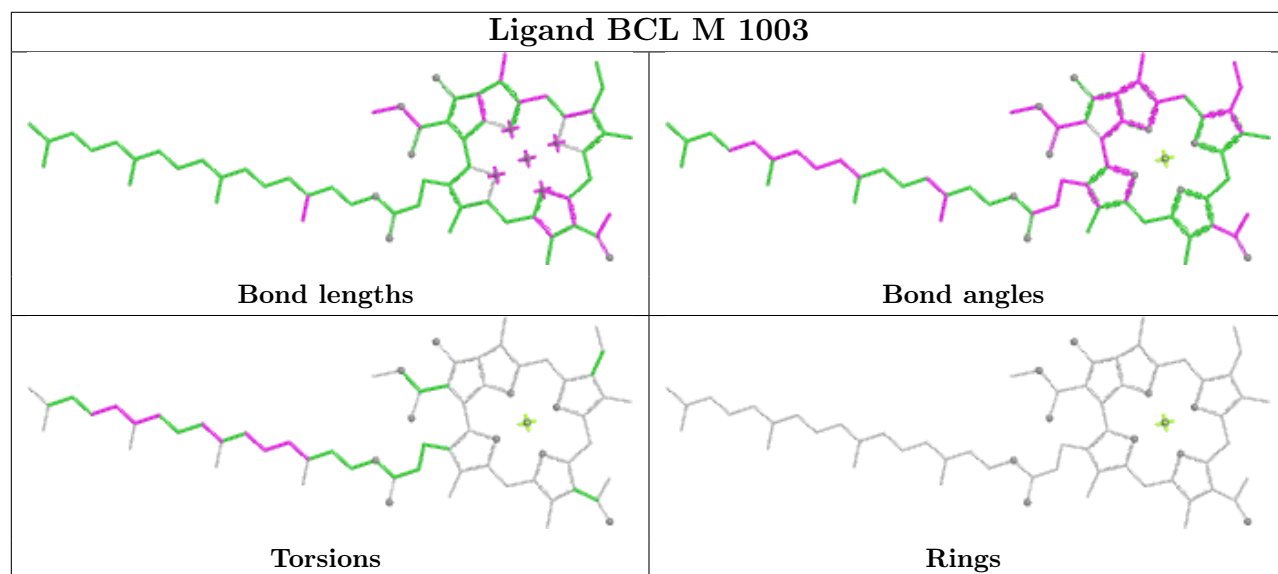
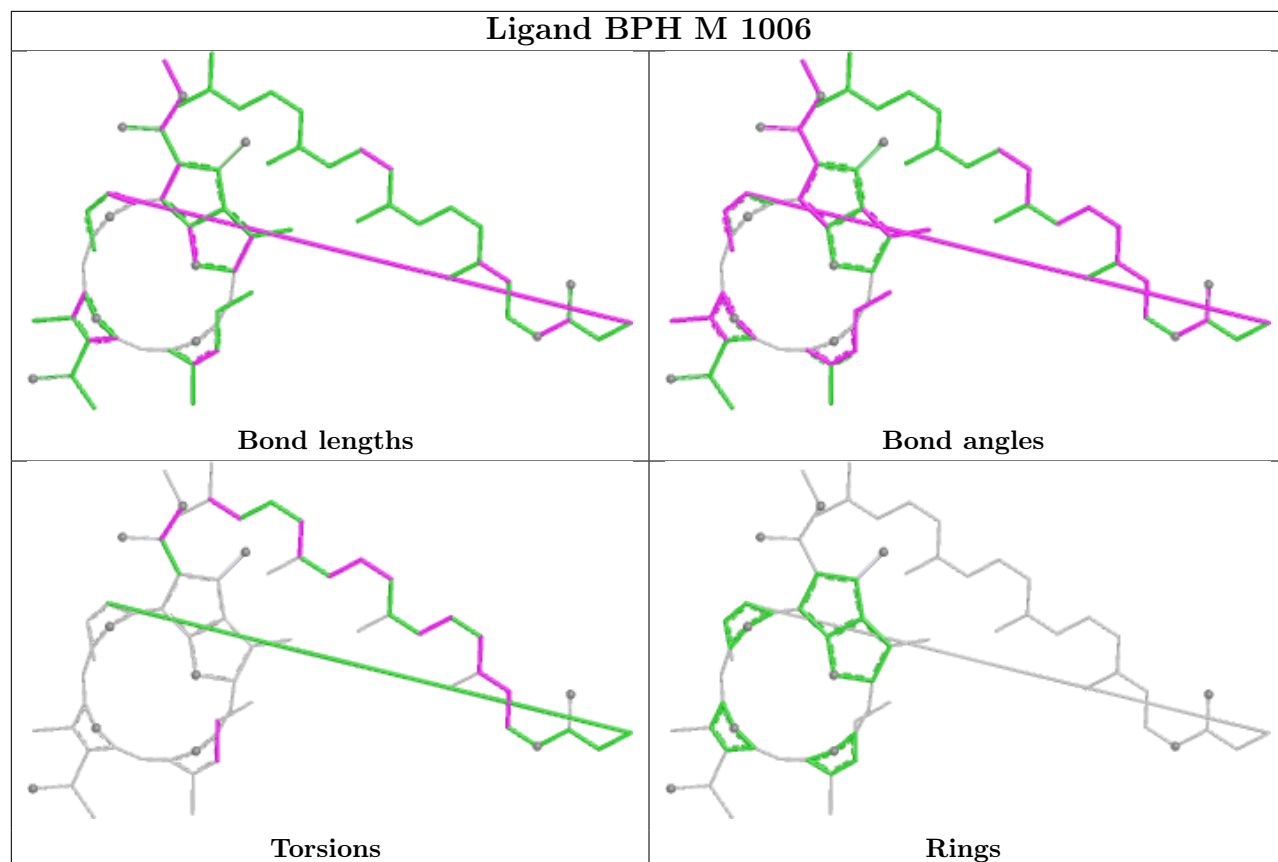
There are no ring outliers.

12 monomers are involved in 43 short contacts:

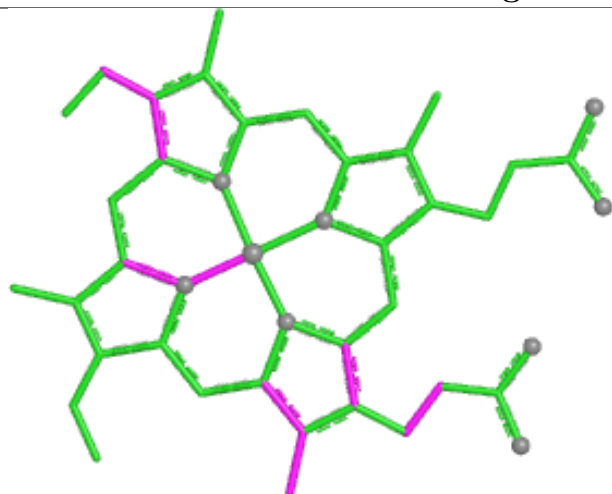
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	M	1013	LDA	1	0
8	M	1015	LDA	1	0
7	L	1005	BPH	5	0
8	H	1014	LDA	1	0
6	M	1001	BCL	7	0
7	M	1006	BPH	2	0
9	C	1022	HTO	6	0
6	M	1003	BCL	11	0
6	L	1004	BCL	5	0
8	M	1012	LDA	3	0
6	L	1002	BCL	8	0
8	H	1019	LDA	1	0

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.

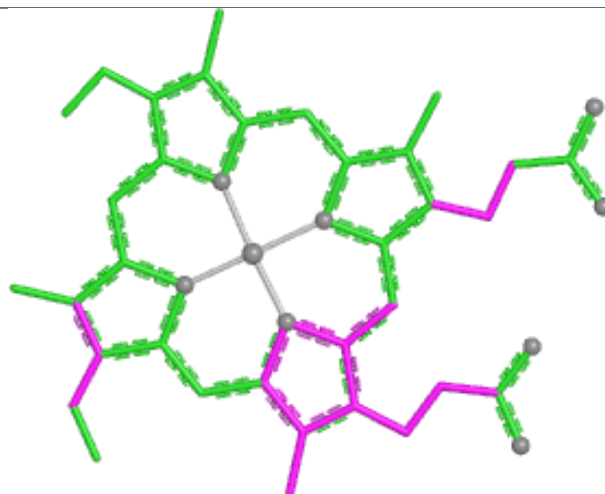




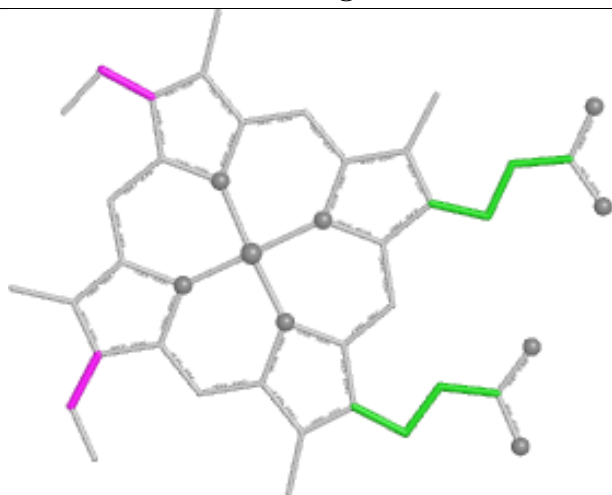
Ligand HEC C 1009



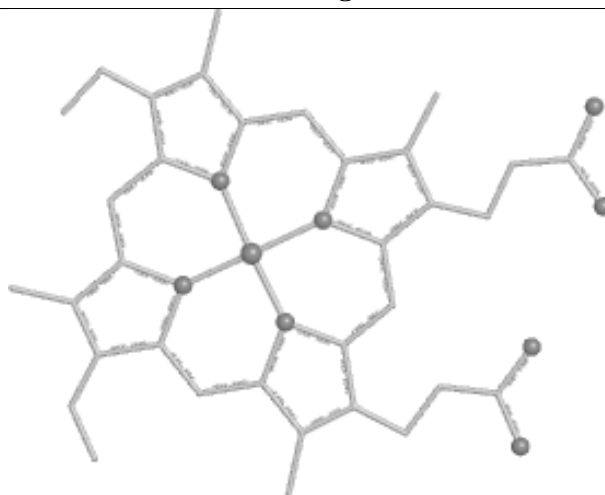
Bond lengths



Bond angles

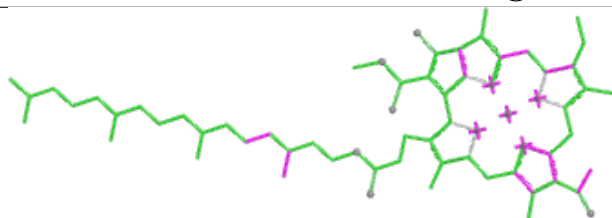


Torsions

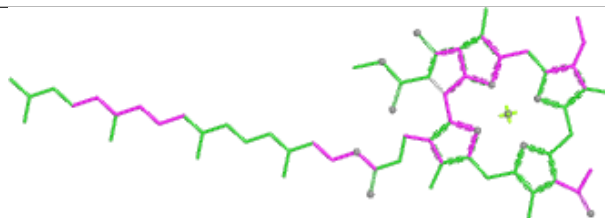


Rings

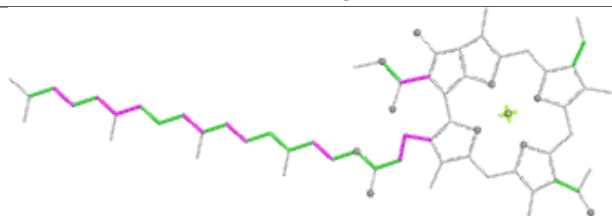
Ligand BCL L 1004



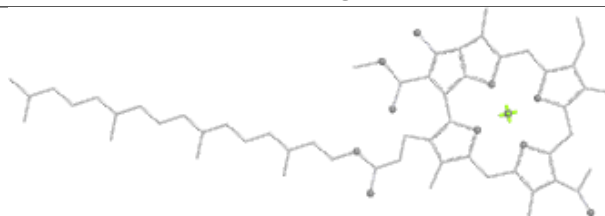
Bond lengths



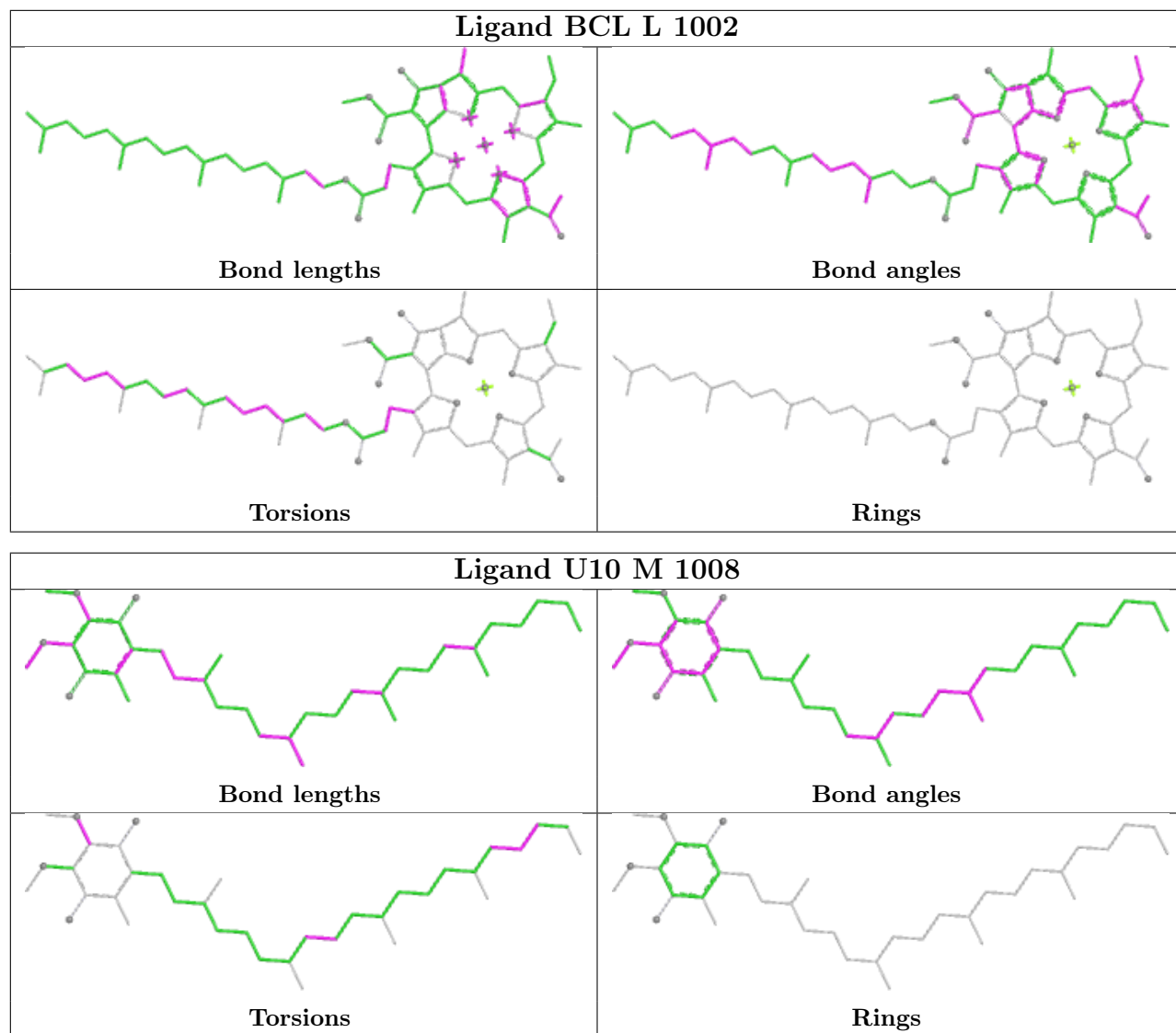
Bond angles



Torsions



Rings



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, 95th 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 ²)	Q<0.9
1	L	281/281 (100%)	0.37	8 (2%) 55 51	36, 56, 75, 85	0
2	M	267/307 (86%)	0.29	8 (2%) 52 48	34, 52, 71, 86	0
3	H	246/260 (94%)	0.85	26 (10%) 11 8	50, 73, 113, 139	0
4	C	124/124 (100%)	0.34	1 (0%) 82 80	38, 58, 82, 103	0
All	All	918/972 (94%)	0.47	43 (4%) 36 32	34, 60, 88, 139	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	M	240	ASP	5.8
3	H	144	ALA	4.0
3	H	90	THR	3.9
3	H	251	VAL	3.8
3	H	252	VAL	3.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

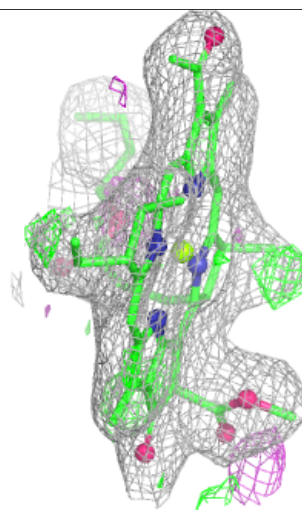
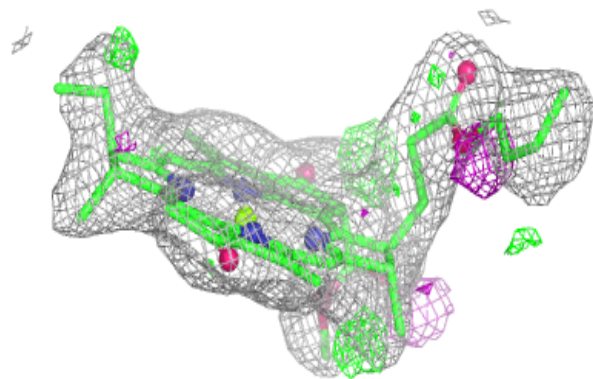
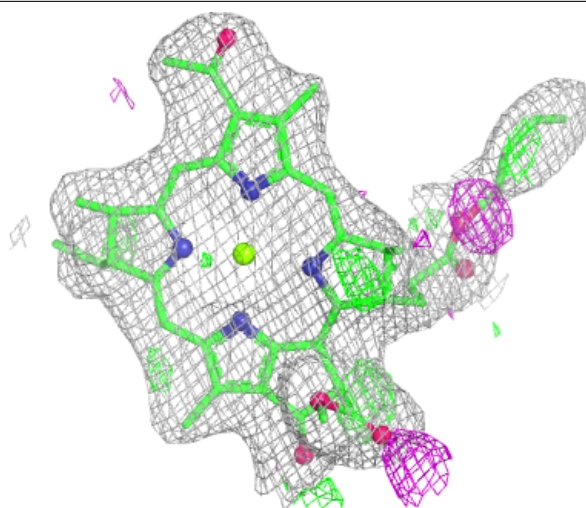
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	LDA	H	1014	16/16	0.74	0.27	132,133,134,134	0
8	LDA	L	1017	16/16	0.75	0.30	101,105,114,114	0
8	LDA	L	1018	16/16	0.77	0.28	94,95,102,102	0
8	LDA	L	1016	16/16	0.77	0.25	120,122,124,125	0
9	HTO	C	1022	10/10	0.77	0.29	77,81,84,86	0
5	NA	L	1011	1/1	0.78	0.32	81,81,81,81	0
8	LDA	H	1019	16/16	0.79	0.21	115,117,120,121	0
9	HTO	L	1021	10/10	0.80	0.23	97,103,104,104	0
8	LDA	L	1020	16/16	0.81	0.24	82,87,93,93	0
8	LDA	M	1012	16/16	0.84	0.25	75,78,87,87	0
8	LDA	M	1015	16/16	0.85	0.24	84,88,90,92	0
8	LDA	M	1013	16/16	0.88	0.20	68,83,96,97	0
6	BCL	M	1001	50/66	0.91	0.12	43,47,71,73	0
6	BCL	L	1002	66/66	0.91	0.13	17,34,69,74	0
6	BCL	M	1003	66/66	0.92	0.13	23,32,78,80	0
12	U10	M	1008	37/63	0.92	0.14	41,54,87,87	0
6	BCL	L	1004	66/66	0.93	0.12	36,48,75,77	0
7	BPH	L	1005	55/65	0.93	0.11	38,46,78,78	0
7	BPH	M	1006	65/65	0.93	0.12	42,53,77,81	0
11	CL	M	1010	1/1	0.97	0.16	72,72,72,72	0
13	HEC	C	1009	43/43	0.98	0.08	38,42,46,50	0
10	FE2	M	1007	1/1	1.00	0.01	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.

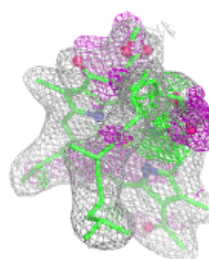
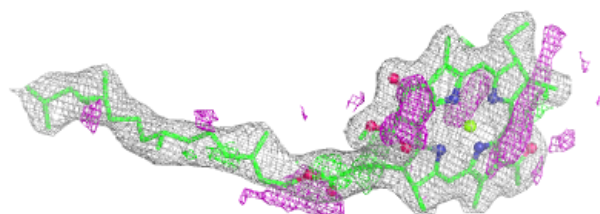
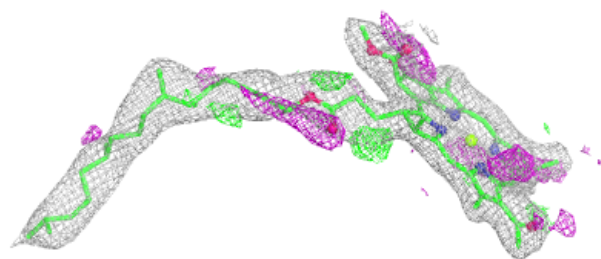
Electron density around BCL M 1001:

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

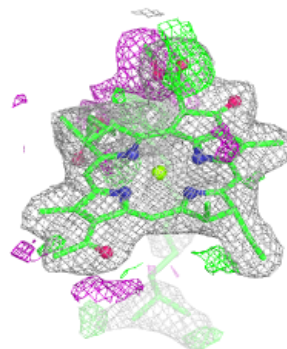
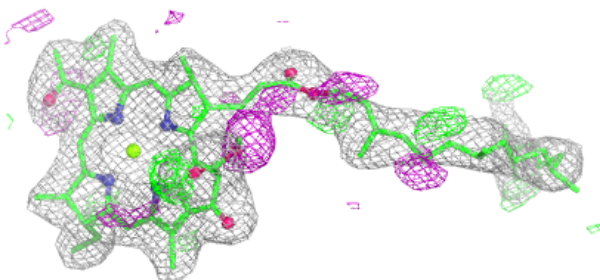
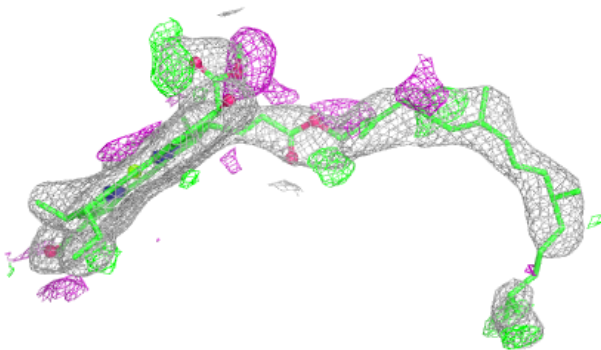


Electron density around BCL L 1002:

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

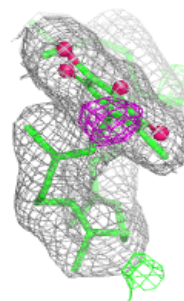
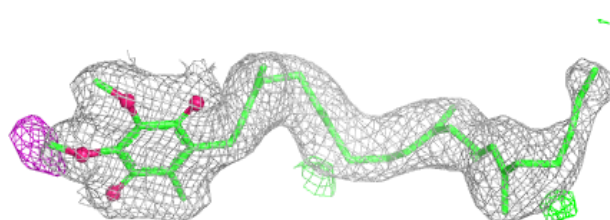
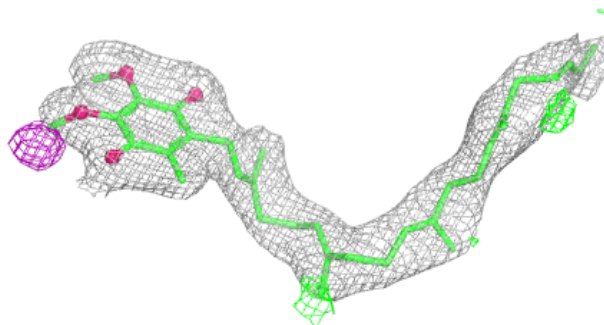
**Electron density around BCL M 1003:**

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



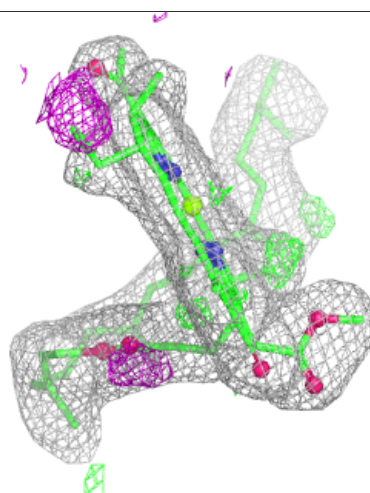
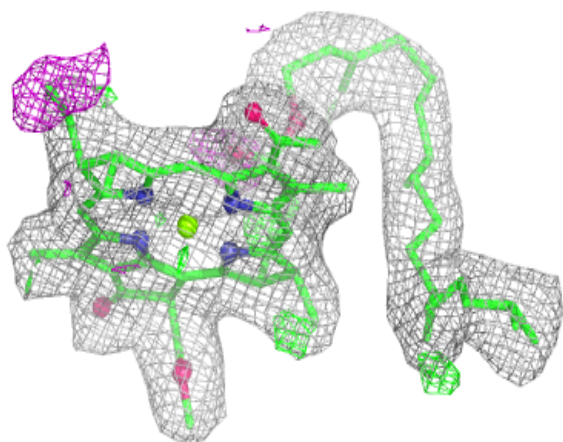
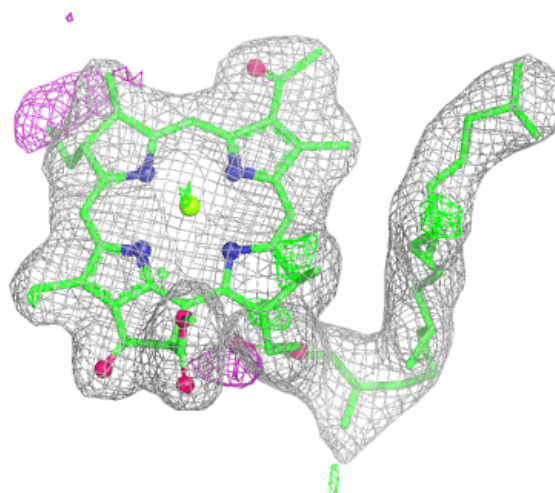
Electron density around U10 M 1008:

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



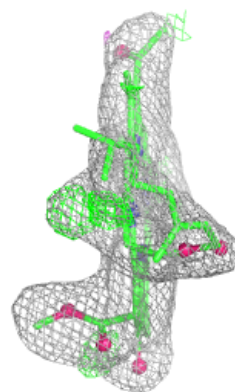
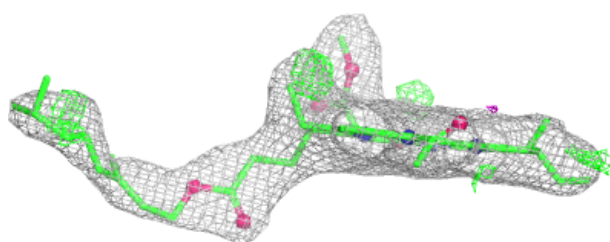
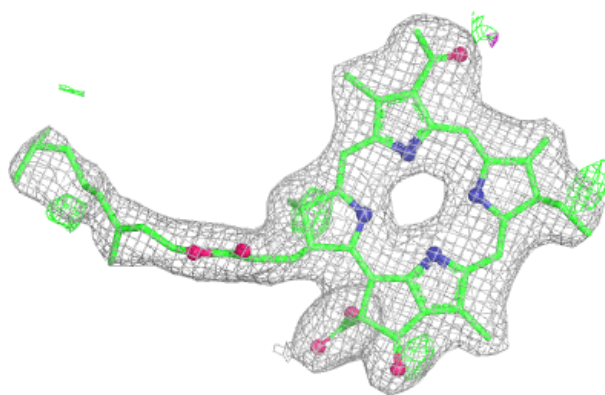
Electron density around BCL L 1004:

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

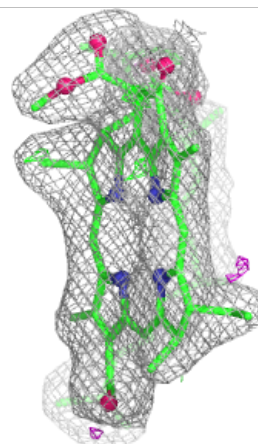
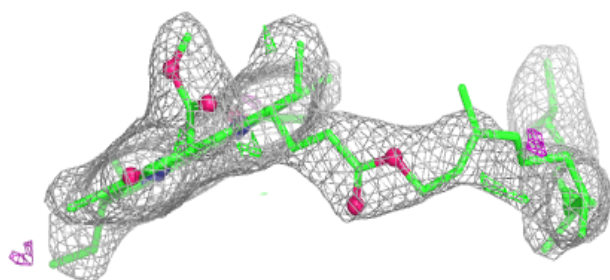
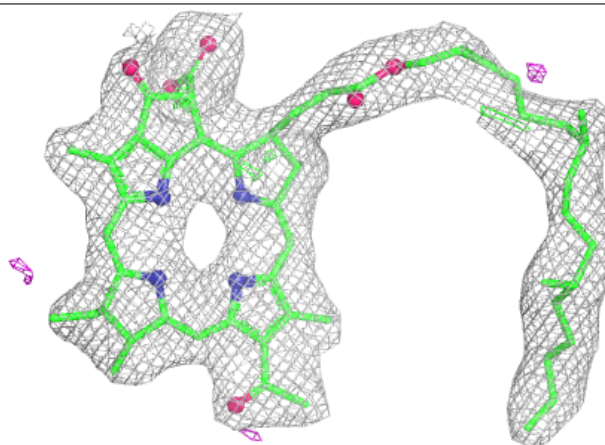


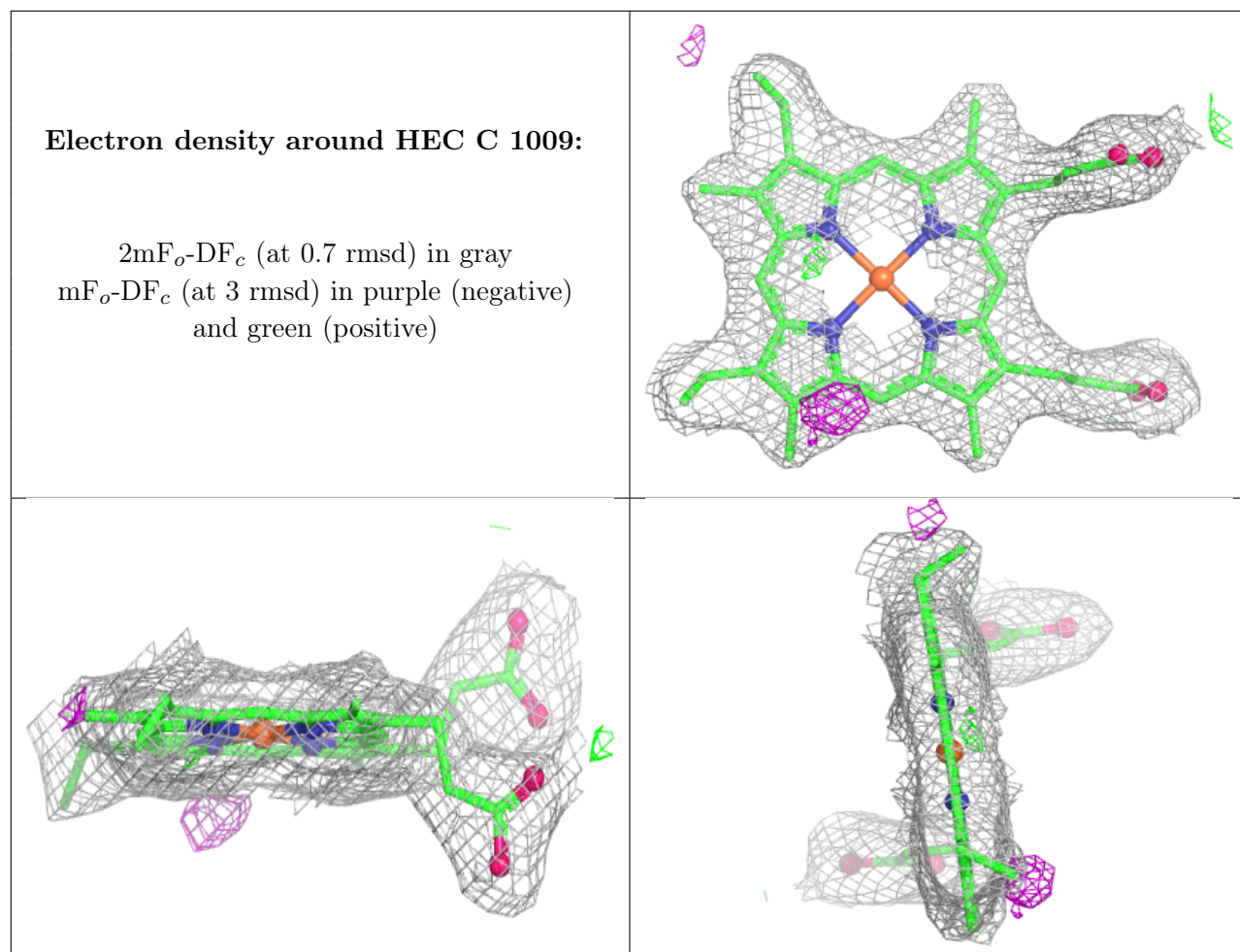
Electron density around BPH L 1005:

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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)





6.5 Other polymers [i](#)

There are no such residues in this entry.