



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 03:19 AM EDT

PDB ID : 2WX5  
Title : Hexa-coordination of a bacteriochlorophyll cofactor in the Rhodobacter sphaeroides reaction centre  
Authors : Marsh, M.; Frolov, D.; Crouch, L.I.; Fyfe, P.K.; Robert, B.; van Grondelle, R.; Jones, M.R.; Hadfield, A.T.  
Deposited on : 2009-11-02  
Resolution : 2.63 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>.

---

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

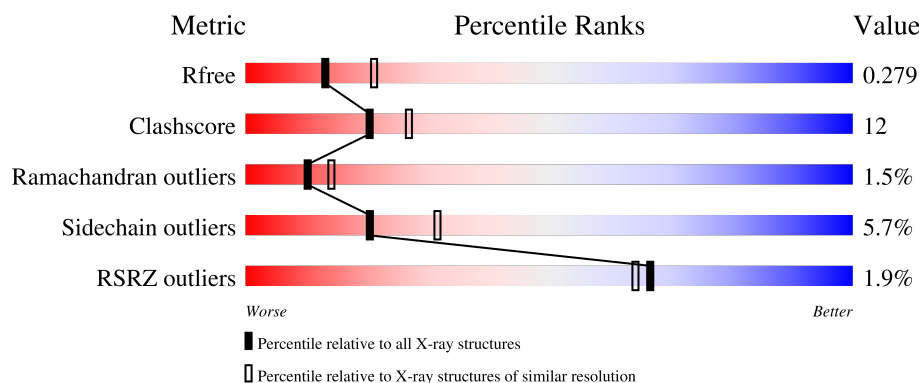
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

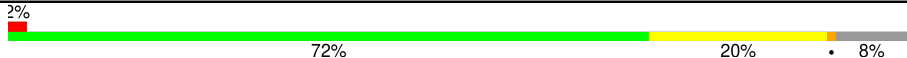
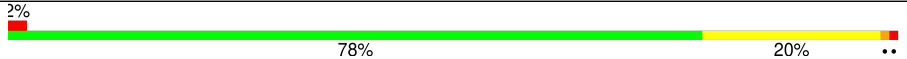

The reported resolution of this entry is 2.63 Å.

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	1426 (2.66-2.62)
Clashscore	141614	1472 (2.66-2.62)
Ramachandran outliers	138981	1446 (2.66-2.62)
Sidechain outliers	138945	1446 (2.66-2.62)
RSRZ outliers	127900	1408 (2.66-2.62)

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	H	260	 2% 72% 20% 8%
2	L	281	 2% 78% 20% ..
3	M	307	 2% 72% 23% ..

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
4	LDA	M	1309	-	-	-	X
4	LDA	M	1310	-	-	-	X
8	HTO	L	1286	X	-	-	-
8	HTO	L	1287	X	-	-	-
8	HTO	M	1313	X	-	X	-
9	BPH	L	1288	X	-	-	-
9	BPH	M	1314	X	-	-	-

## 2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 7468 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 H CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	240	Total	C	N	O	S	0	0	0
			1829	1169	314	337	9			

- Molecule 2 is a protein called REACTION CENTRE PROTEIN L CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	281	Total	C	N	O	S	0	0	0
			2232	1504	358	362	8			

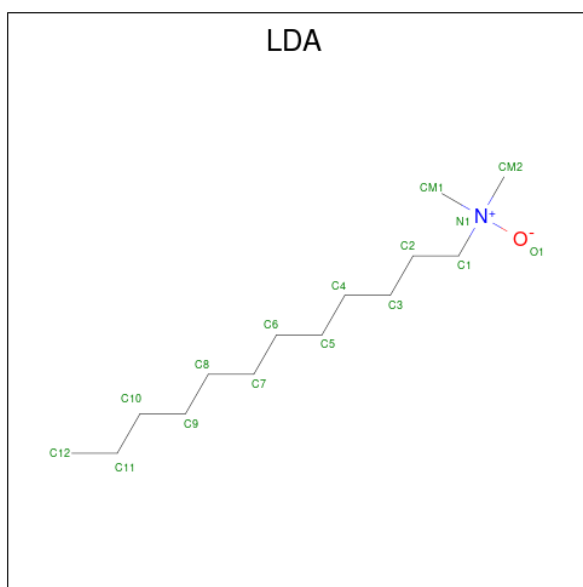
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	181	ARG	PHE	engineered mutation	UNP P0C0Y8

- Molecule 3 is a protein called REACTION CENTRE PROTEIN M CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	302	Total	C	N	O	S	0	0	0
			2408	1607	394	397	10			

- Molecule 4 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: C<sub>14</sub>H<sub>31</sub>NO).

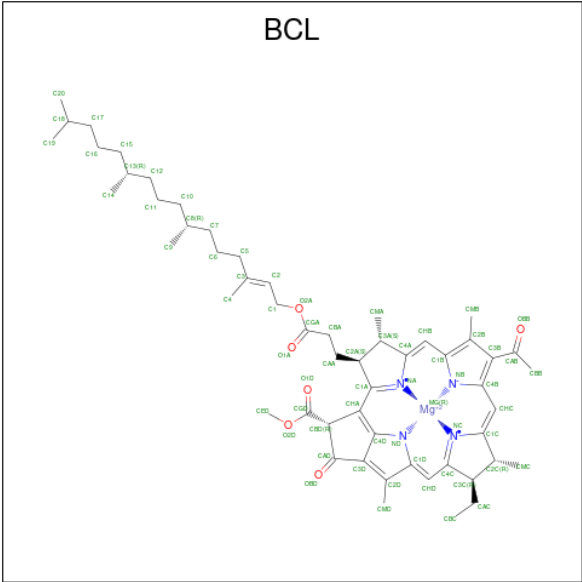


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	H	1	Total	C	N	O	0	0
			16	14	1	1		
4	M	1	Total	C	N	O	0	0
			16	14	1	1		
4	M	1	Total	C	N	O	0	0
			16	14	1	1		
4	M	1	Total	C	N	O	0	0
			16	14	1	1		
4	M	1	Total	C	N	O	0	0
			16	14	1	1		
4	M	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

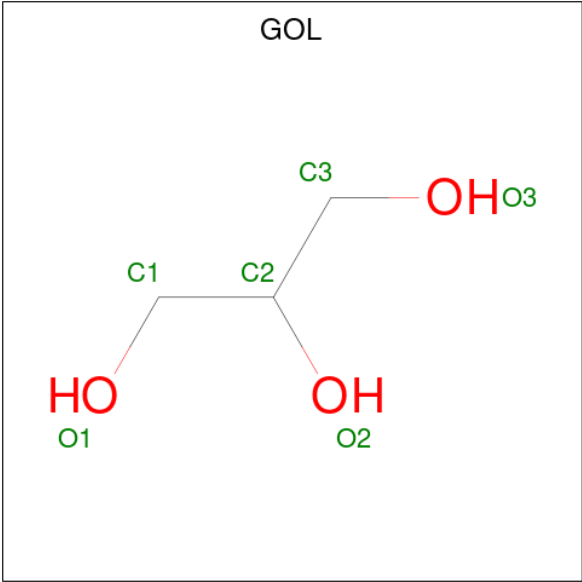
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Na	0	0
			1	1		
5	M	1	Total	Na	0	0
			1	1		

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



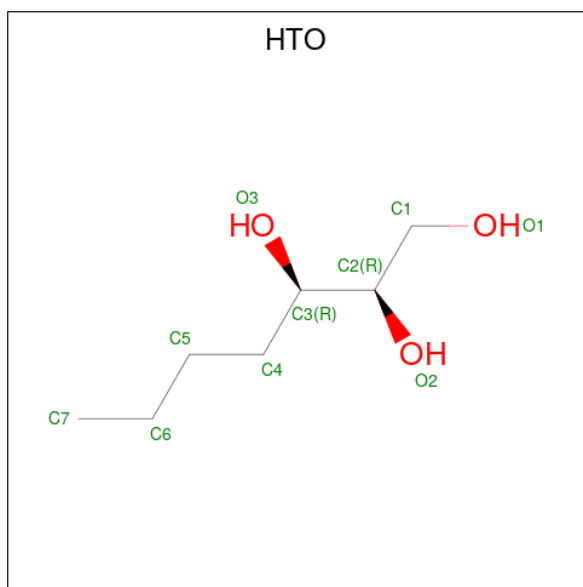
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
6	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
6	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
6	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



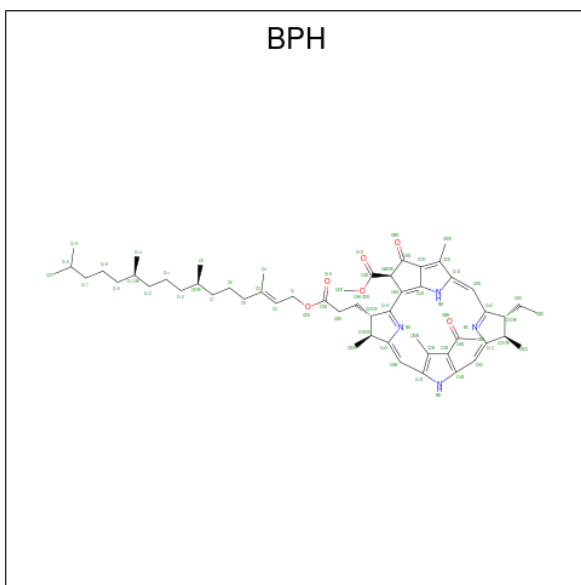
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	L	1	Total	C	O	0	0
			6	3	3		
7	L	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula:  $C_7H_{16}O_3$ ).



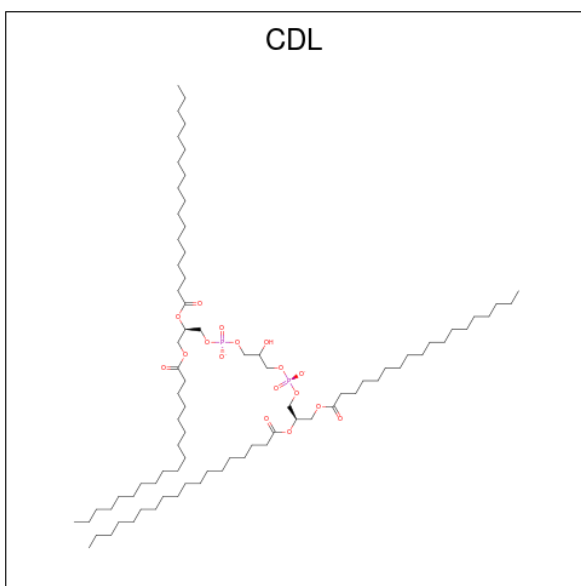
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	L	1	Total	C	O	0	0
			10	7	3		
8	L	1	Total	C	O	0	0
			10	7	3		
8	M	1	Total	C	O	0	0
			10	7	3		

- Molecule 9 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula:  $C_{55}H_{76}N_4O_6$ ).



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

- Molecule 10 is CARDIOLIPIN (three-letter code: CDL) (formula:  $C_{81}H_{156}O_{17}P_2$ ).



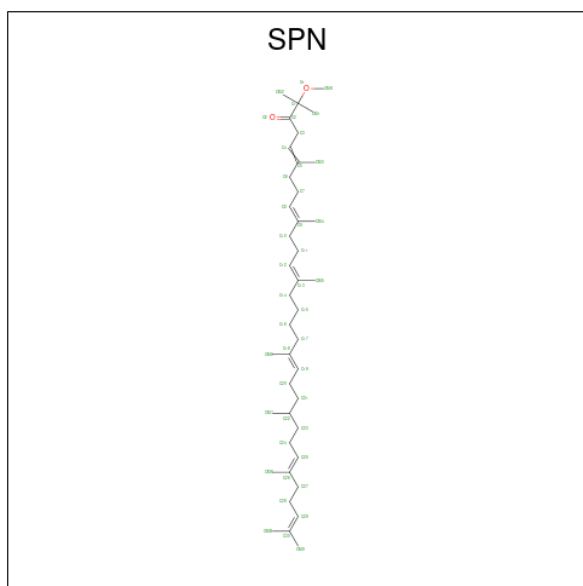
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	M	1	Total	C	O	P	0	0
			81	62	17	2		

- Molecule 11 is FE (III) ION (three-letter code: FE) (formula: Fe).



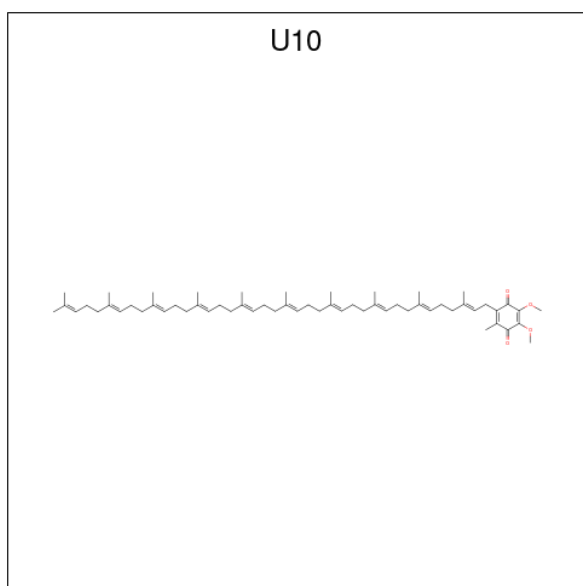
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	M	1	Total	Fe	0	0
			1	1		

- Molecule 12 is SPEROIDENONE (three-letter code: SPN) (formula:  $C_{41}H_{70}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	M	1	Total	C	O	0	0
			43	41	2		

- Molecule 13 is UBIQUINONE-10 (three-letter code: U10) (formula:  $C_{59}H_{90}O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	M	1	Total	C	O	0	0
			48	44	4		

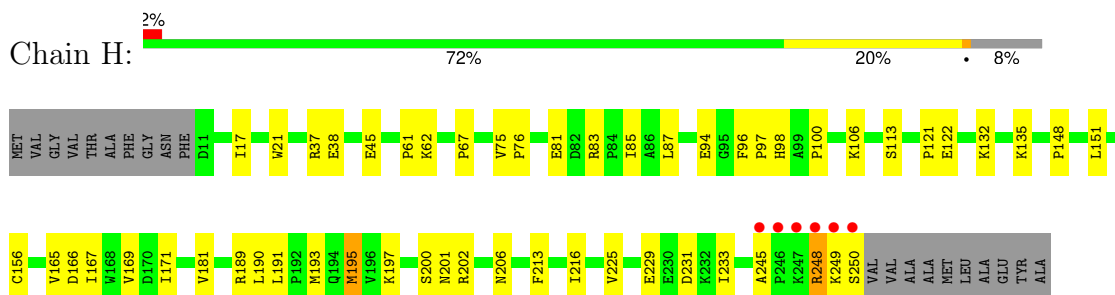
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	H	111	Total	O	0	0
			111	111		
14	L	99	Total	O	0	0
			99	99		
14	M	82	Total	O	0	0
			82	82		

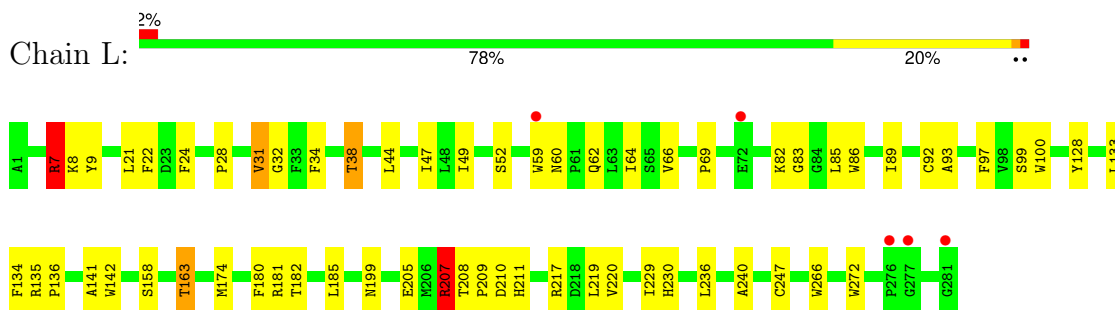
### 3 Residue-property plots [i](#)

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.

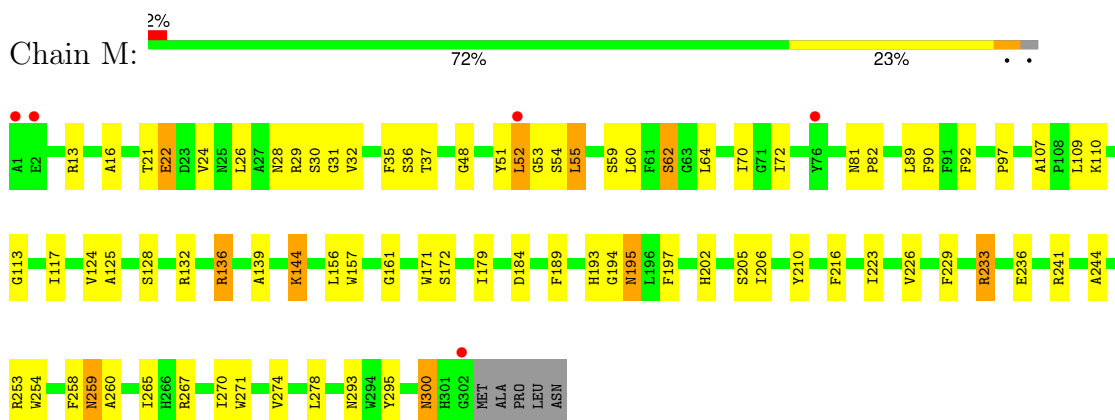
#### • Molecule 1: REACTION CENTER PROTEIN H CHAIN



#### • Molecule 2: REACTION CENTRE PROTEIN L CHAIN



#### • Molecule 3: REACTION CENTRE PROTEIN M CHAIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	140.18Å 140.18Å 185.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.40 – 2.63 20.31 – 2.63	Depositor EDS
% Data completeness (in resolution range)	98.5 (20.40-2.63) 95.6 (20.31-2.63)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.78 (at 2.63Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.237 , 0.279 0.240 , 0.279	Depositor DCC
$R_{free}$ test set	3047 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	64.3	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 67.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	7468	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LDA, BCL, U10, CDL, GOL, NA, BPH, FE, HTO, SPN

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	H	0.92	1/1877 (0.1%)	0.88	1/2553 (0.0%)
2	L	0.92	0/2319	0.89	3/3173 (0.1%)
3	M	0.87	2/2500 (0.1%)	0.84	3/3413 (0.1%)
All	All	0.90	3/6696 (0.0%)	0.87	7/9139 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	M	226	VAL	CB-CG2	7.00	1.67	1.52
3	M	236	GLU	CG-CD	6.00	1.60	1.51
1	H	94	GLU	CG-CD	5.13	1.59	1.51

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	7	ARG	NE-CZ-NH2	-9.86	115.37	120.30
2	L	7	ARG	NE-CZ-NH1	8.20	124.40	120.30
1	H	195	MET	CG-SD-CE	-6.10	90.44	100.20
3	M	233	ARG	NE-CZ-NH1	-5.50	117.55	120.30
2	L	207	ARG	NE-CZ-NH2	-5.39	117.61	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	H	1829	0	1836	30	0
2	L	2232	0	2191	58	0
3	M	2408	0	2321	65	0
4	H	16	0	31	2	0
4	M	80	0	155	8	0
5	H	1	0	0	0	0
5	M	1	0	0	0	0
6	L	132	0	148	18	0
6	M	132	0	148	19	0
7	L	12	0	16	0	0
8	L	20	0	32	4	0
8	M	10	0	16	7	0
9	L	65	0	76	8	0
9	M	65	0	76	8	0
10	M	81	0	106	3	0
11	M	1	0	0	0	0
12	M	43	0	70	10	0
13	M	48	0	63	4	0
14	H	111	0	0	1	0
14	L	99	0	0	6	0
14	M	82	0	0	5	0
All	All	7468	0	7285	178	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 12.

The worst 5 of 178 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:248:ARG:HD2	1:H:250:SER:HB2	1.46	0.98
4:M:1306:LDA:H91	4:M:1307:LDA:H121	1.43	0.97
2:L:182:THR:HG22	2:L:236:LEU:HD13	1.50	0.91
2:L:34:PHE:O	2:L:38:THR:HG23	1.71	0.89
2:L:69:PRO:HG2	2:L:142:TRP:HB2	1.56	0.86

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	H	238/260 (92%)	221 (93%)	14 (6%)	3 (1%)	12	17
2	L	279/281 (99%)	250 (90%)	26 (9%)	3 (1%)	14	20
3	M	300/307 (98%)	273 (91%)	21 (7%)	6 (2%)	7	10
All	All	817/848 (96%)	744 (91%)	61 (8%)	12 (2%)	10	14

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	245	ALA
3	M	48	GLY
3	M	124	VAL
2	L	163	THR
3	M	22	GLU

### 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	H	195/208 (94%)	185 (95%)	10 (5%)	24	37
2	L	220/220 (100%)	209 (95%)	11 (5%)	24	38
3	M	236/240 (98%)	220 (93%)	16 (7%)	16	24
All	All	651/668 (98%)	614 (94%)	37 (6%)	20	31

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	M	109	LEU
3	M	265	ILE
3	M	136	ARG
3	M	216	PHE
2	L	38	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	199	ASN
3	M	193	HIS
3	M	300	ASN
2	L	62	GLN
1	H	98	HIS

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 3 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
8	HTO	L	1286	-	9,9,9	1.25	1 (11%)	10,10,10	2.18	4 (40%)
4	LDA	M	1309	-	13,15,15	2.17	2 (15%)	14,17,17	0.57	0
12	SPN	M	1315	-	42,42,42	0.65	0	50,52,52	1.66	12 (24%)
4	LDA	H	1251	-	13,15,15	2.28	2 (15%)	14,17,17	0.44	0
4	LDA	M	1306	-	13,15,15	1.98	1 (7%)	14,17,17	1.00	1 (7%)
7	GOL	L	1285	-	5,5,5	0.46	0	5,5,5	0.49	0
6	BCL	L	1283	2	64,74,74	1.35	3 (4%)	74,115,115	1.87	15 (20%)
8	HTO	M	1313	-	9,9,9	1.08	1 (11%)	10,10,10	1.24	1 (10%)
9	BPH	L	1288	-	51,70,70	0.80	1 (1%)	52,101,101	1.50	8 (15%)
6	BCL	L	1282	14,3	64,74,74	1.09	3 (4%)	74,115,115	2.00	18 (24%)
4	LDA	M	1308	-	13,15,15	2.05	2 (15%)	14,17,17	0.68	0
8	HTO	L	1287	-	9,9,9	0.77	0	10,10,10	1.47	3 (30%)
4	LDA	M	1310	-	13,15,15	2.04	2 (15%)	14,17,17	0.77	0
6	BCL	M	1304	2	64,74,74	1.36	7 (10%)	74,115,115	2.57	25 (33%)
10	CDL	M	1305	-	80,80,99	1.28	4 (5%)	86,92,111	1.31	11 (12%)
7	GOL	L	1284	-	5,5,5	0.41	0	5,5,5	0.29	0
6	BCL	M	1303	3	64,74,74	1.07	4 (6%)	74,115,115	2.01	13 (17%)
4	LDA	M	1307	-	13,15,15	2.15	2 (15%)	14,17,17	0.70	0
9	BPH	M	1314	-	51,70,70	1.13	3 (5%)	52,101,101	1.91	13 (25%)
13	U10	M	1316	-	48,48,63	2.80	15 (31%)	60,61,79	1.93	16 (26%)

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	HTO	L	1286	-	1/1/2/2	2/10/10/10	-
4	LDA	M	1309	-	-	11/13/13/13	-
12	SPN	M	1315	-	-	18/50/51/51	-
4	LDA	H	1251	-	-	7/13/13/13	-
4	LDA	M	1306	-	-	7/13/13/13	-
7	GOL	L	1285	-	-	0/4/4/4	-
6	BCL	L	1283	2	-	4/37/137/137	-
8	HTO	M	1313	-	1/1/2/2	4/10/10/10	-
9	BPH	L	1288	-	2/2/18/22	12/37/105/105	0/5/6/6

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	BCL	L	1282	14,3	-	9/37/137/137	-
8	HTO	L	1287	-	1/1/2/2	2/10/10/10	-
4	LDA	M	1308	-	-	4/13/13/13	-
4	LDA	M	1310	-	-	6/13/13/13	-
6	BCL	M	1304	2	-	8/37/137/137	-
10	CDL	M	1305	-	-	40/91/91/110	-
7	GOL	L	1284	-	-	2/4/4/4	-
6	BCL	M	1303	3	-	3/37/137/137	-
4	LDA	M	1307	-	-	3/13/13/13	-
9	BPH	M	1314	-	2/2/18/22	13/37/105/105	0/5/6/6
13	U10	M	1316	-	-	8/45/69/87	0/1/1/1

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1251	LDA	O1-N1	-6.91	1.25	1.42
13	M	1316	U10	C33-C34	6.86	1.48	1.33
13	M	1316	U10	C13-C14	6.79	1.48	1.33
13	M	1316	U10	C18-C19	6.78	1.48	1.33
4	M	1309	LDA	O1-N1	-6.71	1.25	1.42

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	1304	BCL	C1D-ND-C4D	-12.59	97.47	106.31
6	L	1282	BCL	C1D-ND-C4D	-8.53	100.33	106.31
6	M	1303	BCL	C1D-ND-C4D	-8.24	100.53	106.31
6	L	1283	BCL	C1D-ND-C4D	-7.49	101.06	106.31
6	M	1303	BCL	C1C-NC-C4C	7.31	110.01	106.68

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	L	1286	HTO	C2
8	L	1287	HTO	C2
8	M	1313	HTO	C2
9	L	1288	BPH	C8
9	L	1288	BPH	C13

5 of 163 torsion outliers are listed below:

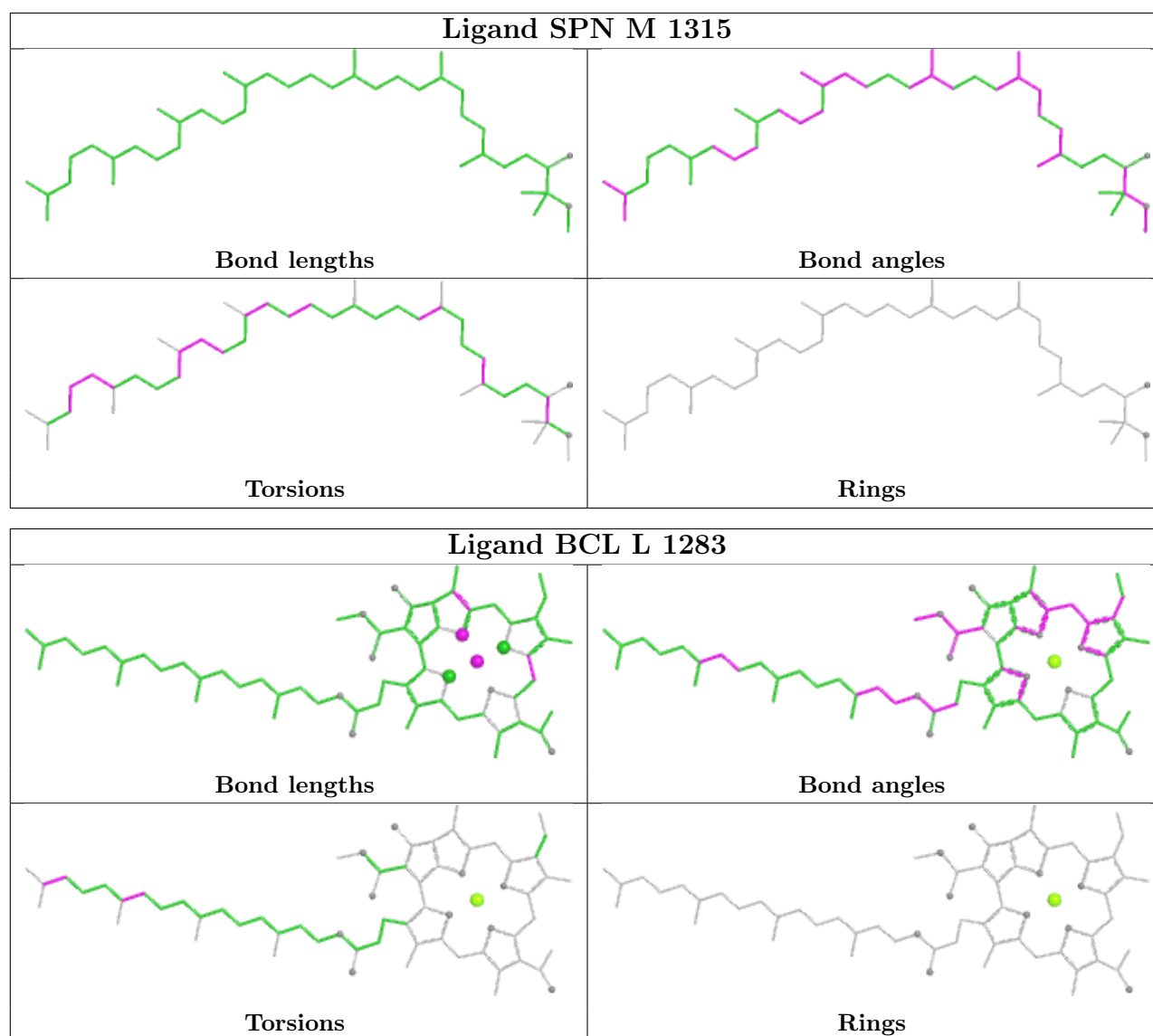
Mol	Chain	Res	Type	Atoms
4	M	1306	LDA	C2-C1-N1-CM1
4	M	1309	LDA	C2-C1-N1-O1
4	M	1309	LDA	C2-C1-N1-CM1
4	M	1309	LDA	C2-C1-N1-CM2
4	M	1309	LDA	N1-C1-C2-C3

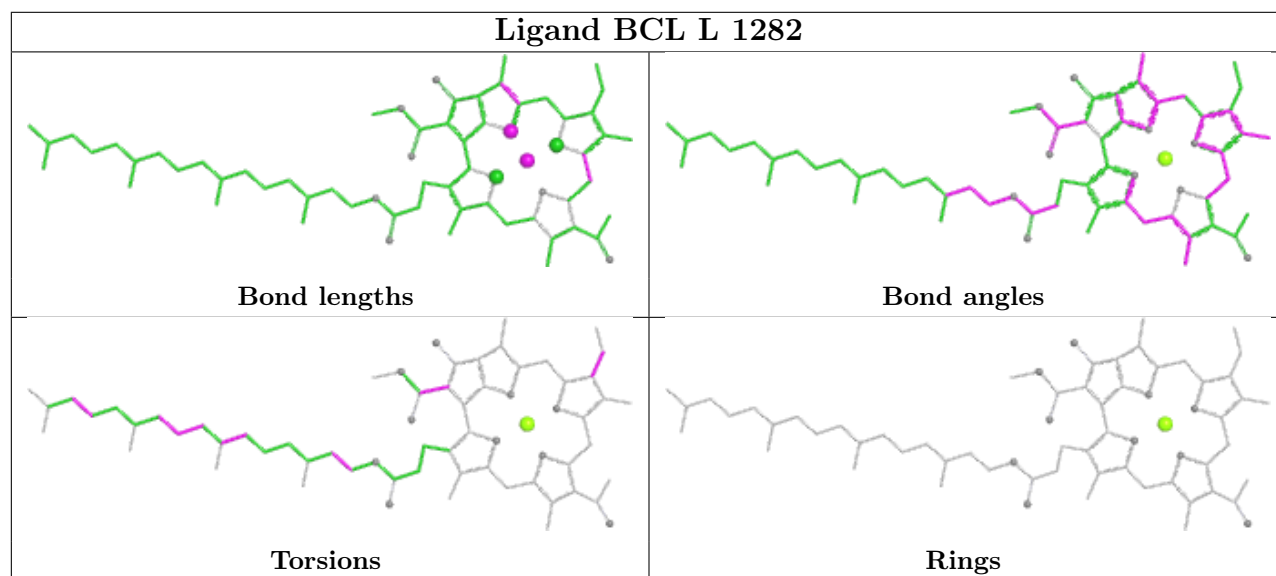
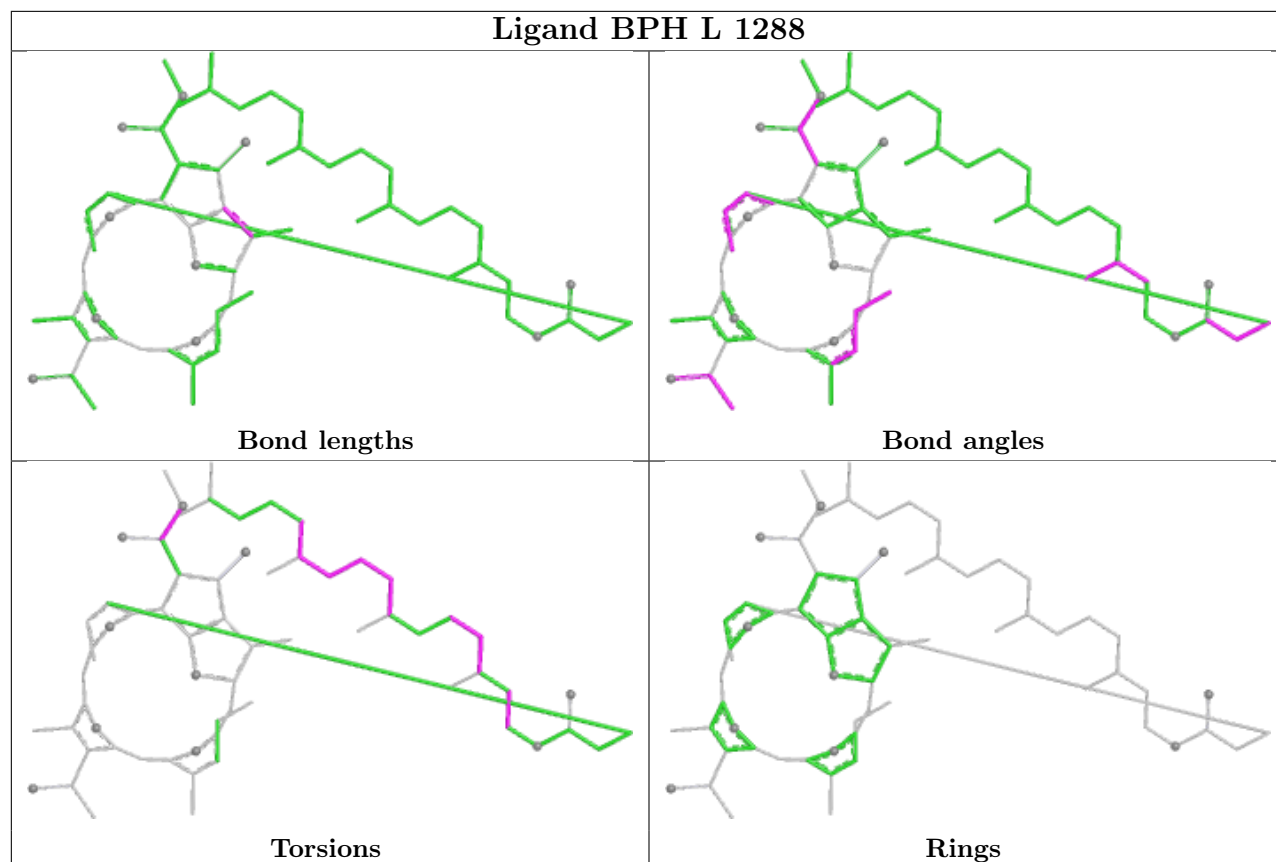
There are no ring outliers.

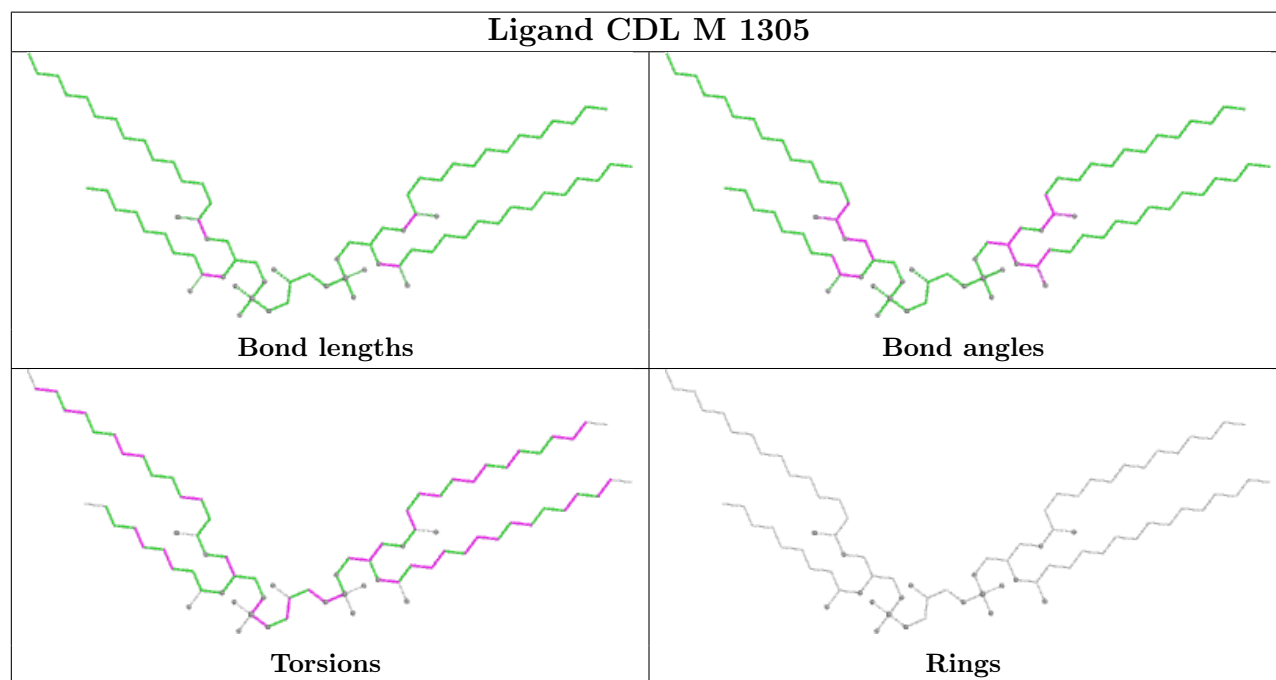
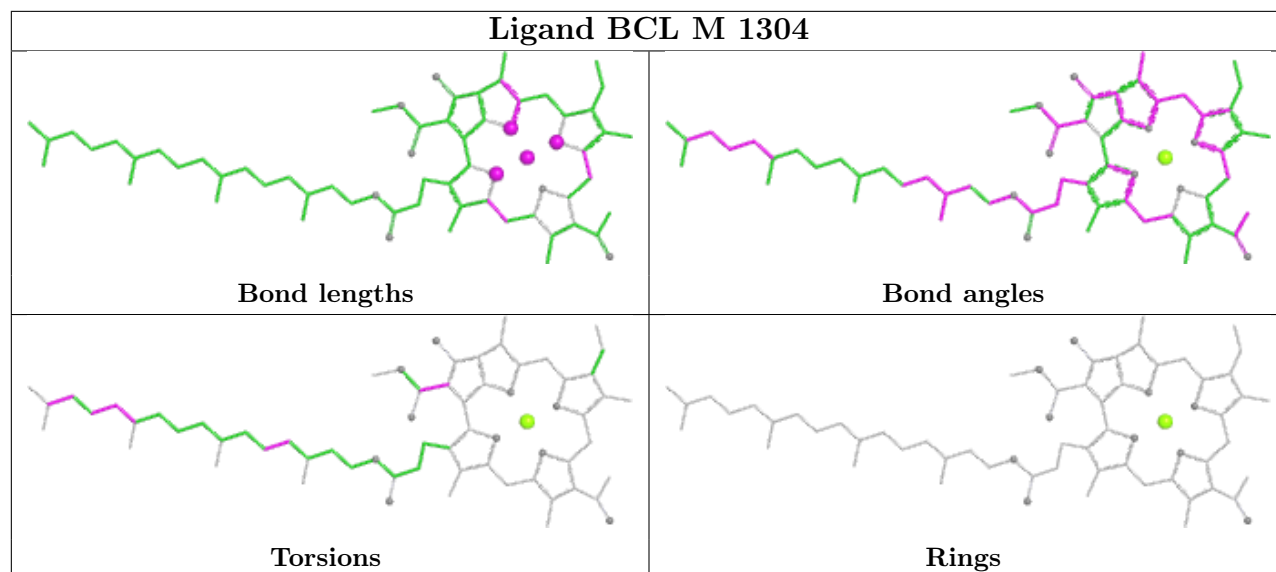
17 monomers are involved in 76 short contacts:

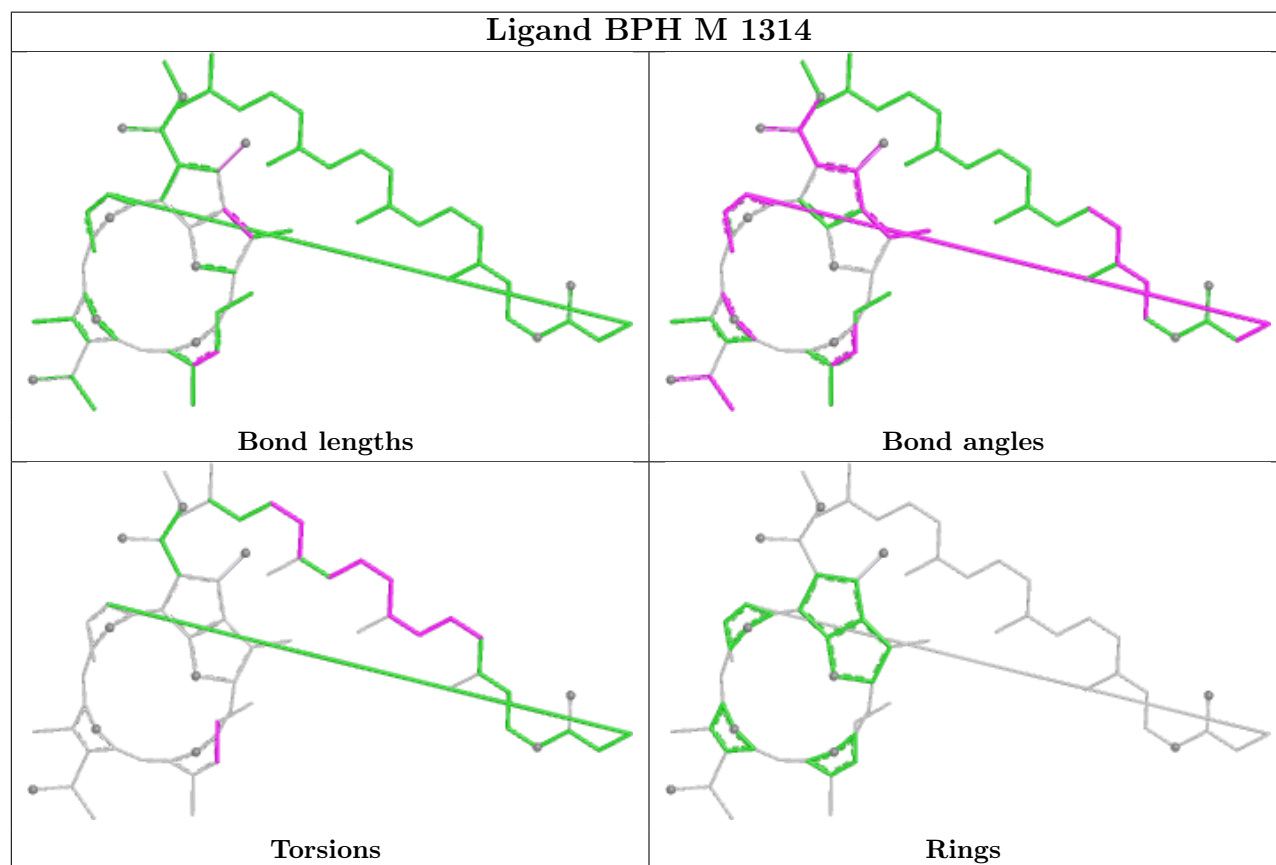
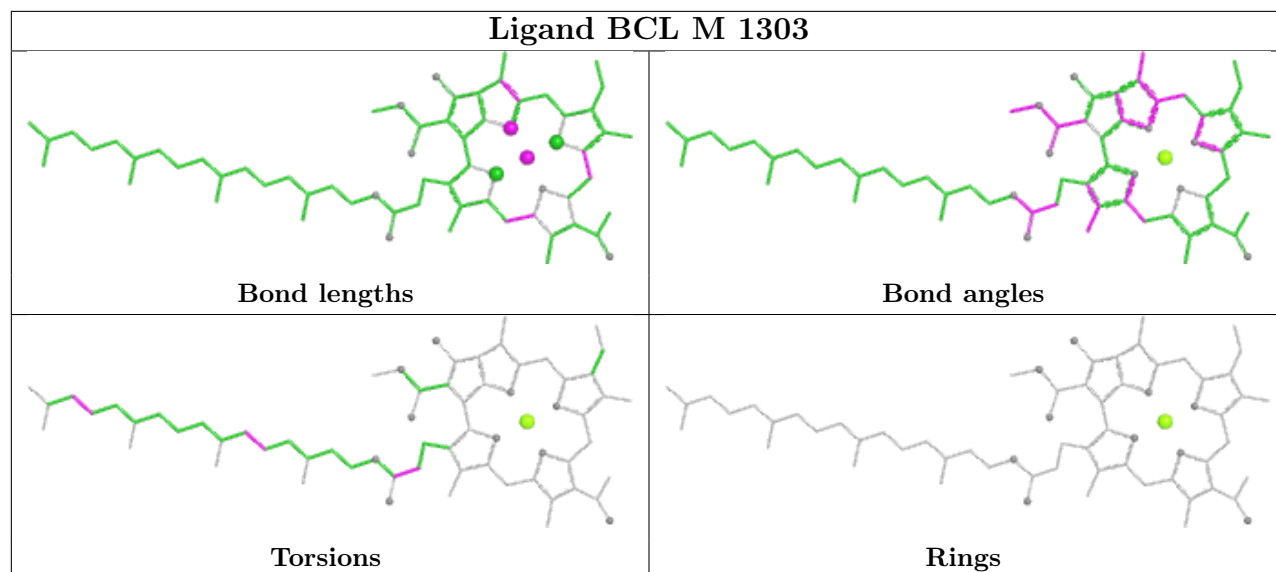
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	L	1286	HTO	1	0
4	M	1309	LDA	2	0
12	M	1315	SPN	10	0
4	H	1251	LDA	2	0
4	M	1306	LDA	3	0
6	L	1283	BCL	6	0
8	M	1313	HTO	7	0
9	L	1288	BPH	8	0
6	L	1282	BCL	12	0
8	L	1287	HTO	3	0
4	M	1310	LDA	2	0
6	M	1304	BCL	6	0
10	M	1305	CDL	3	0
6	M	1303	BCL	13	0
4	M	1307	LDA	4	0
9	M	1314	BPH	8	0
13	M	1316	U10	4	0

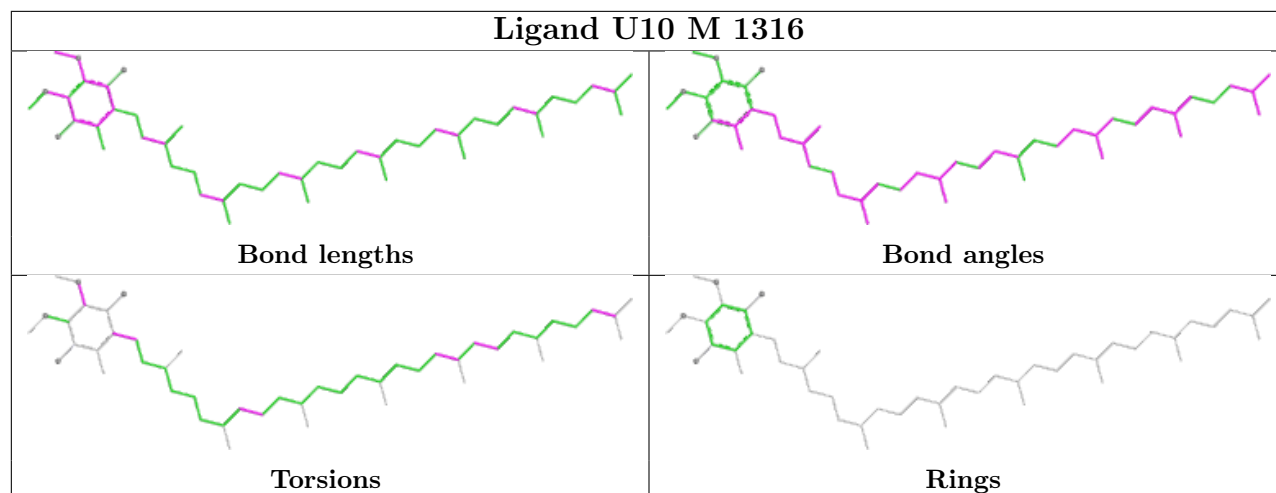
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	H	240/260 (92%)	-0.35	6 (2%) 57 53	48, 63, 84, 171	0
2	L	281/281 (100%)	-0.40	5 (1%) 68 66	42, 62, 103, 129	0
3	M	302/307 (98%)	-0.46	5 (1%) 70 67	42, 64, 101, 118	0
All	All	823/848 (97%)	-0.41	16 (1%) 66 64	42, 63, 99, 171	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	249	LYS	8.1
1	H	250	SER	7.1
3	M	1	ALA	6.7
1	H	246	PRO	5.8
1	H	247	LYS	5.0

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

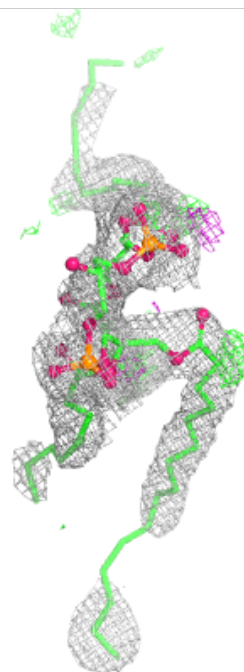
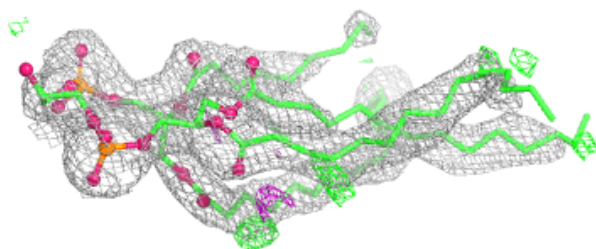
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	LDA	M	1309	16/16	0.60	0.59	115,132,147,148	0
7	GOL	L	1285	6/6	0.67	0.31	86,106,108,109	0
4	LDA	M	1310	16/16	0.70	0.42	74,88,126,127	0
8	HTO	L	1286	10/10	0.75	0.28	71,75,90,97	0
4	LDA	M	1308	16/16	0.79	0.35	74,113,155,156	0
4	LDA	M	1306	16/16	0.80	0.25	52,89,101,102	0
4	LDA	H	1251	16/16	0.80	0.41	98,130,149,151	0
4	LDA	M	1307	16/16	0.85	0.21	88,98,122,123	0
8	HTO	L	1287	10/10	0.85	0.26	92,97,101,102	0
10	CDL	M	1305	81/100	0.85	0.28	52,98,114,118	0
7	GOL	L	1284	6/6	0.87	0.21	84,90,95,95	0
9	BPH	M	1314	65/65	0.89	0.18	44,71,128,133	0
12	SPN	M	1315	43/43	0.89	0.22	47,77,114,118	0
8	HTO	M	1313	10/10	0.91	0.18	77,89,95,97	0
6	BCL	L	1282	66/66	0.91	0.16	42,57,125,132	0
13	U10	M	1316	48/63	0.94	0.15	40,68,98,105	0
5	NA	M	1311	1/1	0.96	0.06	71,71,71,71	0
5	NA	H	1252	1/1	0.96	0.04	45,45,45,45	0
6	BCL	L	1283	66/66	0.96	0.17	39,56,67,83	0
6	BCL	M	1303	66/66	0.97	0.15	39,56,78,103	0
9	BPH	L	1288	65/65	0.97	0.14	30,52,77,81	0
6	BCL	M	1304	66/66	0.97	0.09	14,45,78,88	0
11	FE	M	1312	1/1	1.00	0.05	49,49,49,49	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.

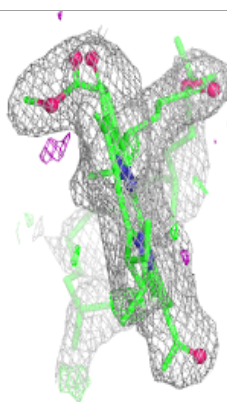
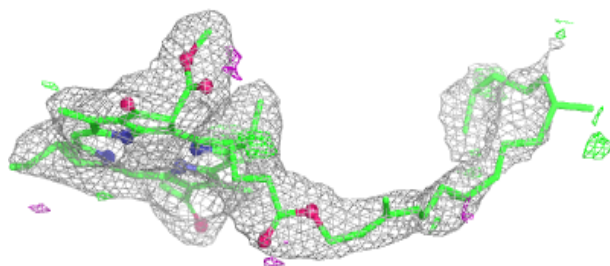
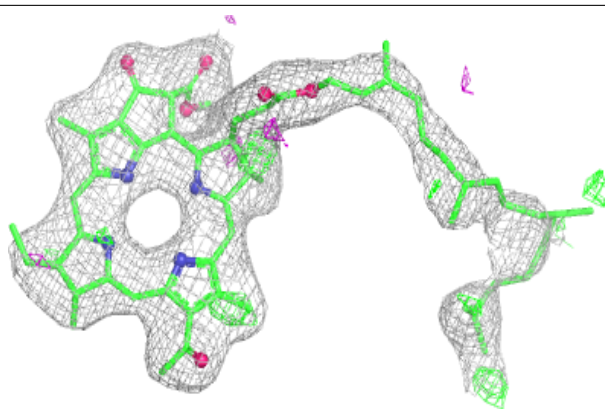
**Electron density around CDL M 1305:**

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

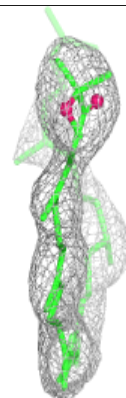
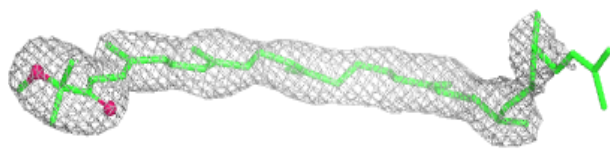
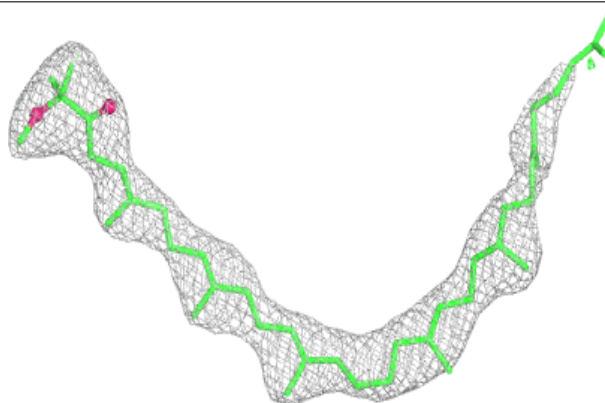


**Electron density around BPH M 1314:**

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

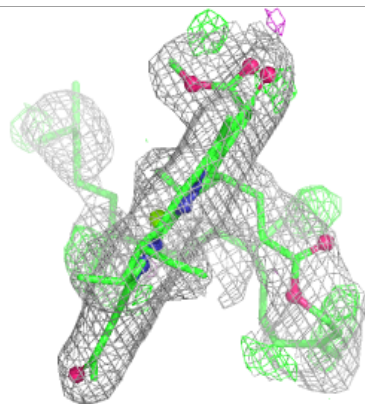
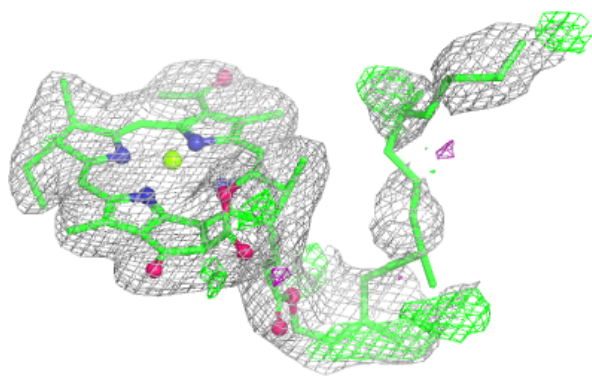
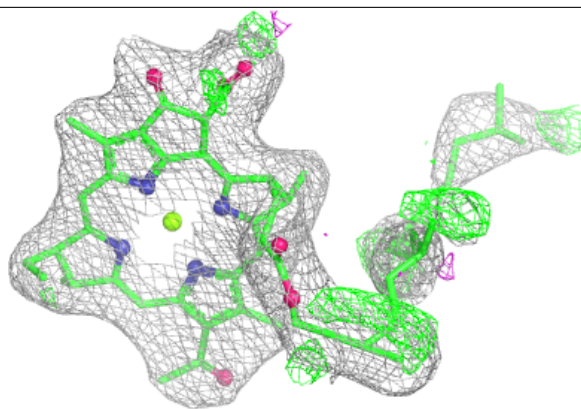
**Electron density around SPN M 1315:**

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

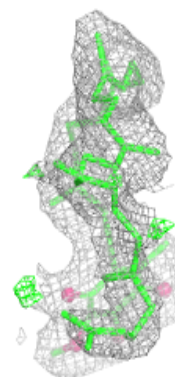
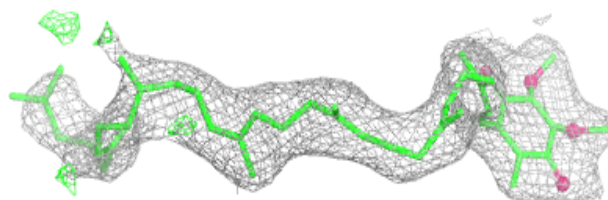
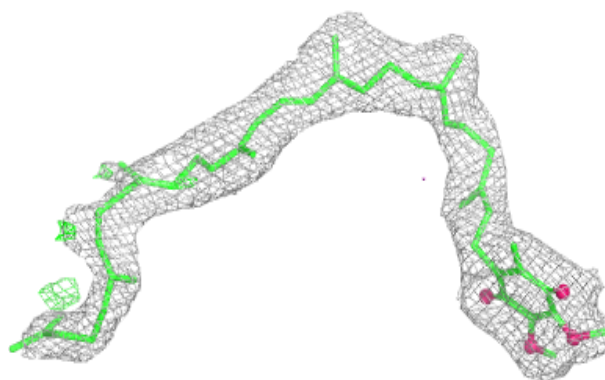


**Electron density around BCL L 1282:**

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

**Electron density around U10 M 1316:**

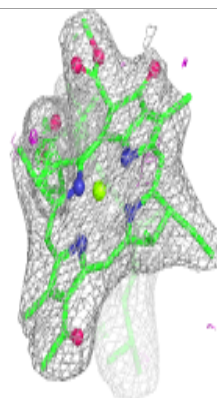
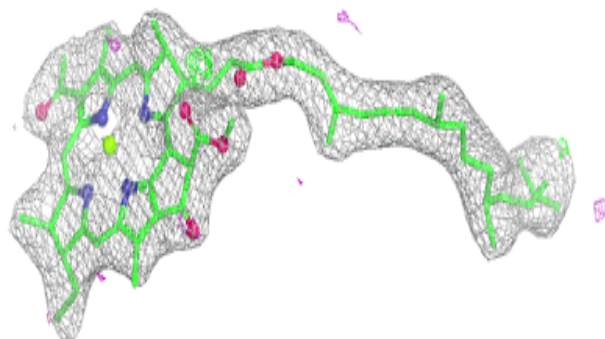
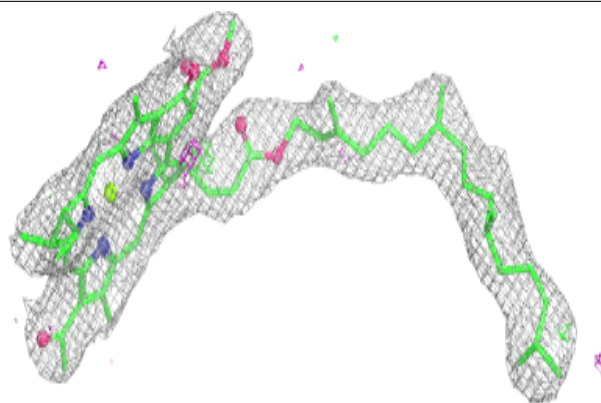
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



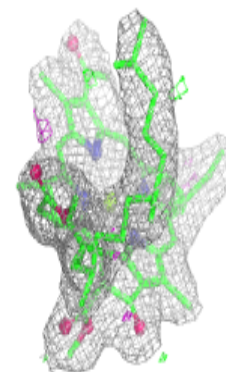
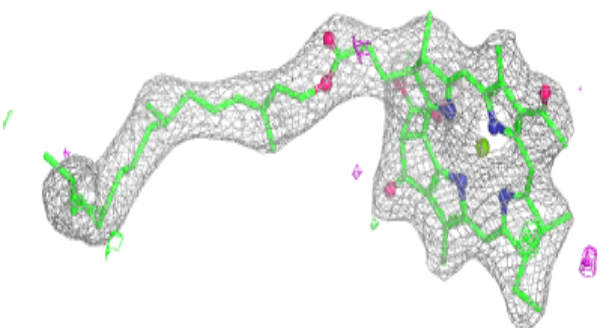
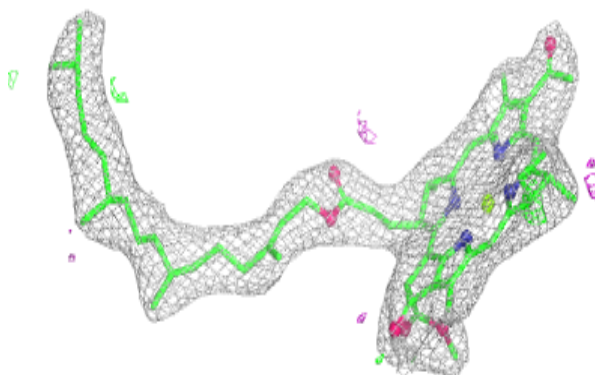


**Electron density around BCL L 1283:**

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

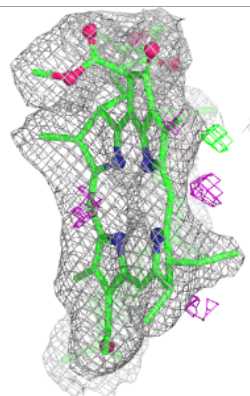
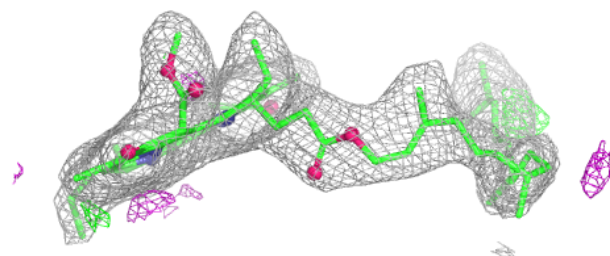
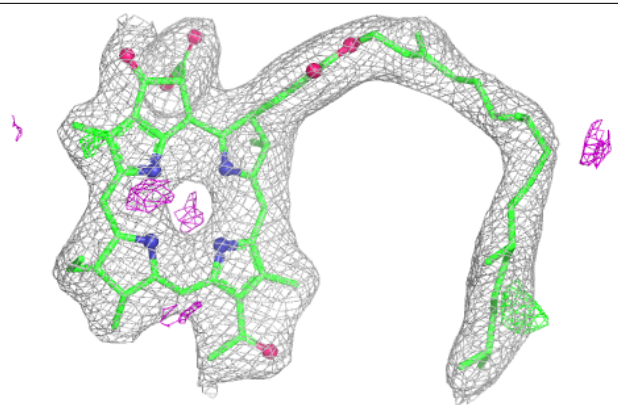
**Electron density around BCL M 1303:**

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



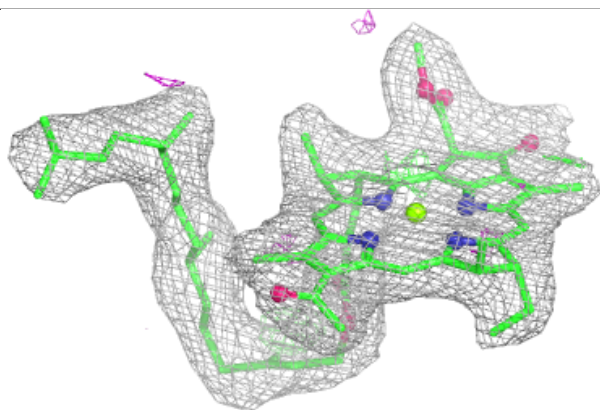
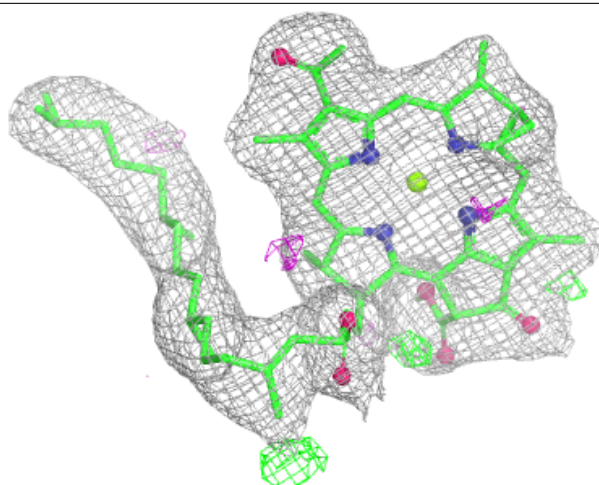
**Electron density around BPH L 1288:**

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



**Electron density around BCL M 1304:**

$2mF_o-DF_c$  (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.