



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 08:24 AM UTC

PDB ID : 2BOZ / pdb_00002boz
Title : Photosynthetic Reaction Center Mutant With Gly M203 Replaced With Leu
Authors : Potter, J.P.; Fyfe, P.K.; Jones, M.R.
Deposited on : 2005-04-15
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 ⓘ](#)) 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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

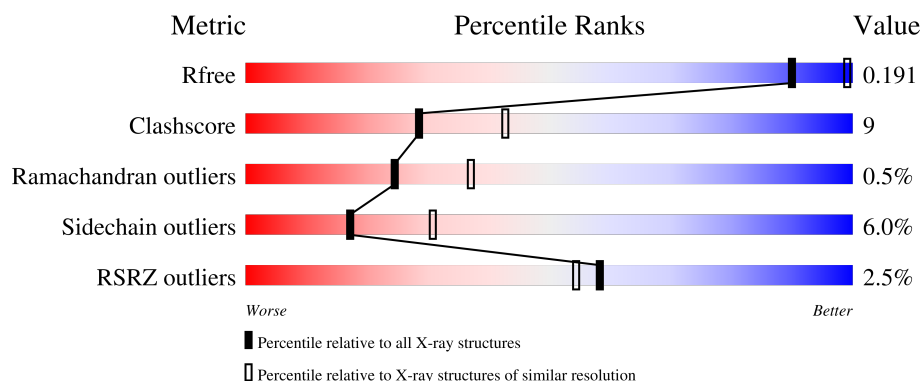
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

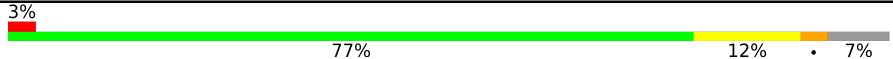
The reported resolution of this entry is 2.40 Å.

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	H	260	
2	L	281	
3	M	307	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 7475 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	241	Total	C	N	O	S	0	0	1
			1830	1169	315	337	9			

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

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

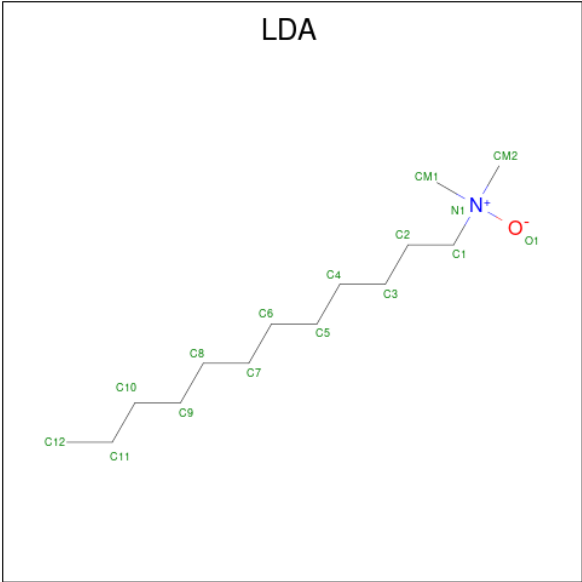
- Molecule 3 is a protein called REACTION CENTER PROTEIN M CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	303	Total	C	N	O	S	0	0	1
			2413	1611	395	397	10			

There is a discrepancy between the modelled and reference sequences:

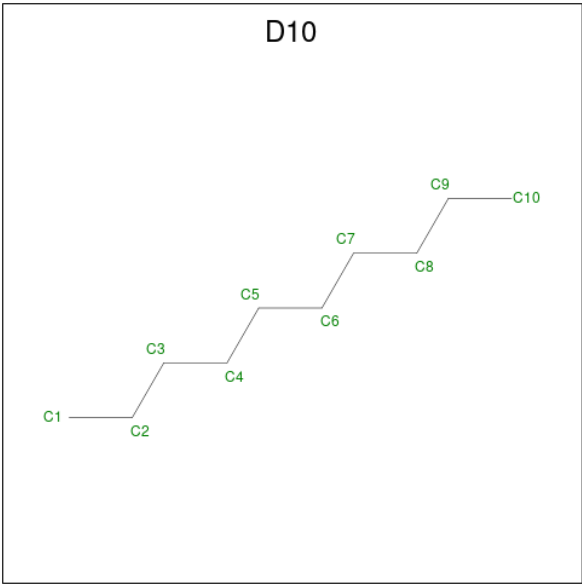
Chain	Residue	Modelled	Actual	Comment	Reference
M	203	LEU	GLY	engineered mutation	UNP P11846

- Molecule 4 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: C₁₄H₃₁NO).



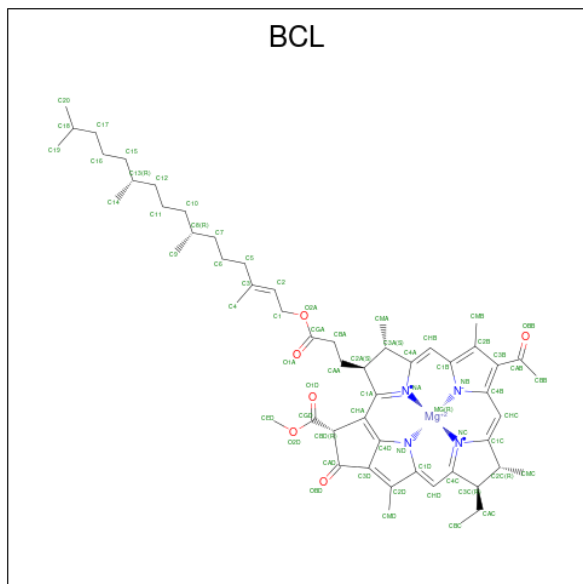
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	H	1	Total	C	N	O	0	0
			16	14	1	1		
4	M	1	Total	C	N	O	0	0
			16	14	1	1		
4	M	1	Total	C	N	O	0	0
			16	14	1	1		
4	M	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 5 is DECANE (CCD ID: D10) (formula: C₁₀H₂₂).



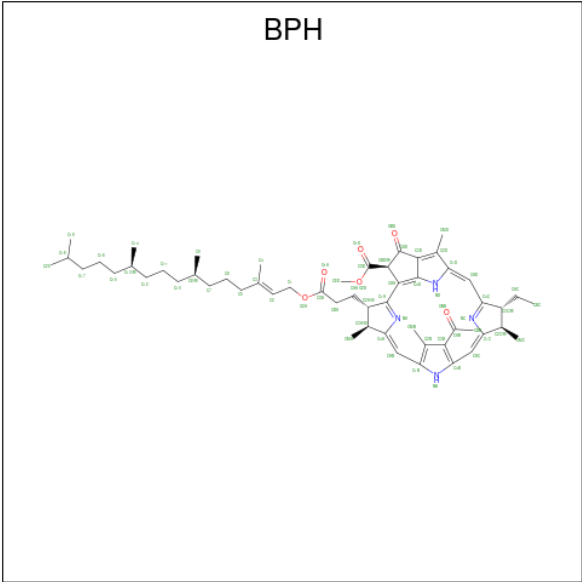
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	1	Total C 9 9	0	0
5	H	1	Total C 8 8	0	0
5	H	1	Total C 7 7	0	0

- Molecule 6 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $\text{C}_{55}\text{H}_{74}\text{MgN}_4\text{O}_6$).



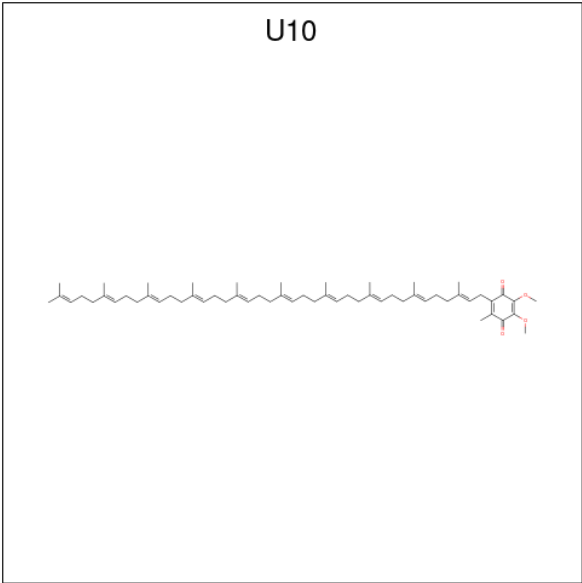
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
6	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
6	M	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
6	M	1	Total 66	C 55	Mg 1	N 4	O 6	0	0

- 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
			65	55	4	6		
7	M	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 8 is UBIQUINONE-10 (CCD ID: U10) (formula: C₅₉H₉₀O₄).

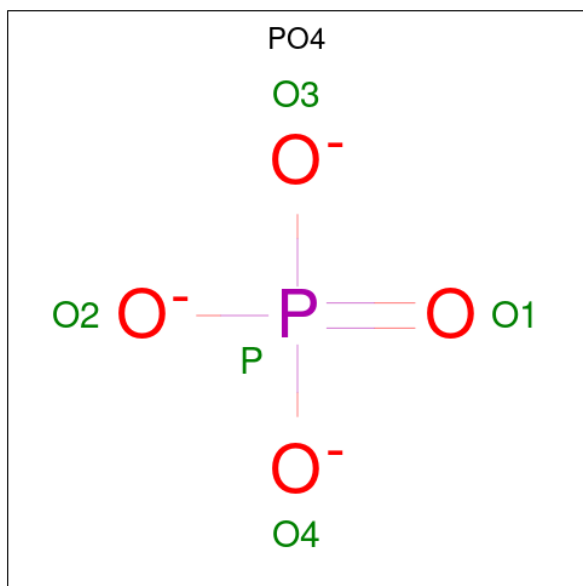


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	L	1	Total	C	O	14	0
			48	44	4		
8	M	1	Total	C	O	0	0
			48	44	4		

- Molecule 9 is FE (III) ION (CCD ID: FE) (formula: Fe).

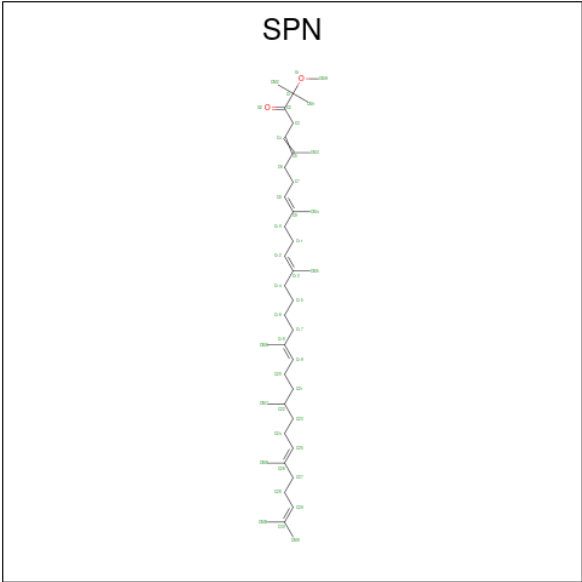
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	M	1	Total	Fe	0	0
			1	1		

- Molecule 10 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	M	1	Total	O	P	0	0
			5	4	1		
10	M	1	Total	O	P	0	0
			5	4	1		

- Molecule 11 is SPEROIDENONE (CCD ID: SPN) (formula: C₄₁H₇₀O₂).



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

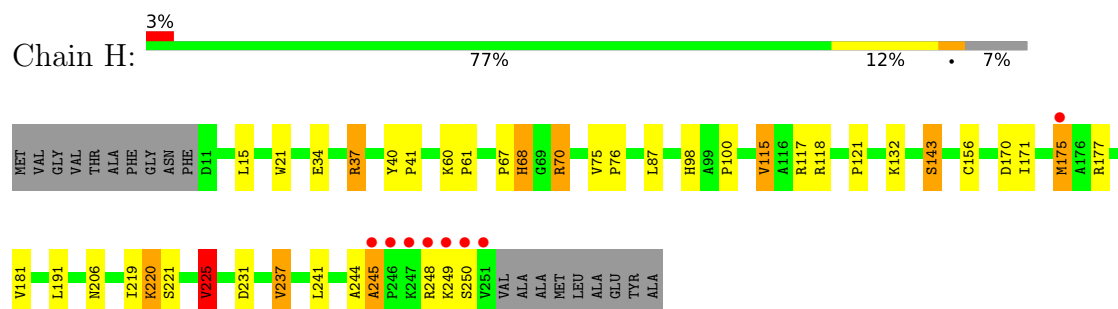
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	H	174	Total	O	0	0
			174	174		
12	L	95	Total	O	0	0
			95	95		
12	M	99	Total	O	0	0
			99	99		

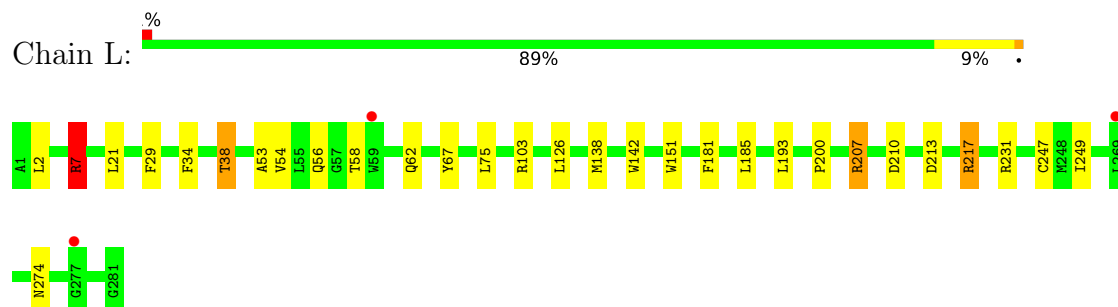
3 Residue-property plots [i](#)

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.

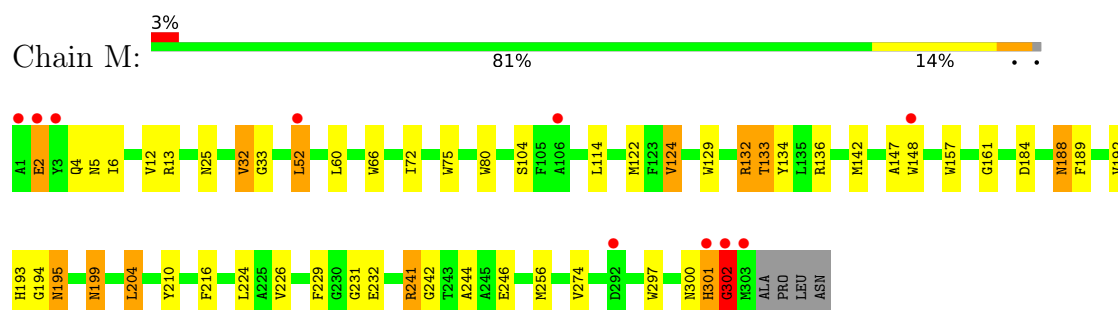
- Molecule 1: REACTION CENTER PROTEIN H CHAIN



- Molecule 2: REACTION CENTER PROTEIN L CHAIN



- Molecule 3: REACTION CENTER PROTEIN M CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	138.61Å 138.61Å 185.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	17.96 – 2.40 17.96 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.5 (17.96-2.40) 99.2 (17.96-2.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 2.40Å)	Xtriage
Refinement program	REFMAC 5.2.0000	Depositor
R, R_{free}	0.174 , 0.198 0.167 , 0.191	Depositor DCC
R_{free} test set	3991 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	35.5	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 67.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7475	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: D10, PO4, FE, BPH, SPN, U10, LDA, BCL

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	1.02	2/1878 (0.1%)	1.14	12/2555 (0.5%)
2	L	1.01	0/2320	1.00	3/3175 (0.1%)
3	M	0.96	2/2505 (0.1%)	1.01	2/3421 (0.1%)
All	All	1.00	4/6703 (0.1%)	1.04	17/9151 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	M	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	68	HIS	N-CA	7.91	1.56	1.46
1	H	250	SER	C-N	-6.28	1.24	1.33
3	M	302	GLY	C-N	-6.20	1.24	1.33
3	M	124	VAL	CA-CB	5.21	1.61	1.54

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	67	PRO	CA-C-N	-9.67	103.07	121.54
1	H	67	PRO	C-N-CA	-9.67	103.07	121.54
1	H	37	ARG	CG-CD-NE	-7.62	95.23	112.00
1	H	37	ARG	NE-CZ-NH2	-6.77	113.10	119.20
1	H	67	PRO	N-CA-C	6.70	122.84	113.53

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	M	300	ASN	Peptide

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	1830	0	1836	36	0
2	L	2232	0	2187	24	0
3	M	2413	0	2329	46	0
4	H	16	0	31	4	0
4	M	48	0	93	6	0
5	H	24	0	45	0	0
6	L	132	0	148	3	0
6	M	132	0	148	13	0
7	L	65	0	75	5	0
7	M	65	0	76	11	0
8	L	48	0	60	1	0
8	M	48	0	63	3	0
9	M	1	0	0	0	0
10	M	10	0	0	0	0
11	M	43	0	69	6	0
12	H	174	0	0	4	0
12	L	95	0	0	4	0
12	M	99	0	0	1	0
All	All	7475	0	7160	125	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 9.

The worst 5 of 125 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:220:LYS:HE2	12:H:2104:HOH:O	1.30	1.25
7:M:1311:BPH:H111	7:M:1311:BPH:H171	1.22	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:1251:LDA:H121	4:M:1307:LDA:H91	1.40	0.98
3:M:2:GLU:HG2	3:M:4:GLN:HE22	1.29	0.96
7:M:1311:BPH:HHC	7:M:1311:BPH:HBB3	1.45	0.95

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	239/260 (92%)	234 (98%)	4 (2%)	1 (0%)	30	43
2	L	279/281 (99%)	273 (98%)	6 (2%)	0	100	100
3	M	301/307 (98%)	293 (97%)	5 (2%)	3 (1%)	12	20
All	All	819/848 (97%)	800 (98%)	15 (2%)	4 (0%)	24	37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	245	ALA
3	M	301	HIS
3	M	195	ASN
3	M	302	GLY

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%)	182 (93%)	13 (7%)	15	26
2	L	220/220 (100%)	209 (95%)	11 (5%)	22	38
3	M	237/241 (98%)	222 (94%)	15 (6%)	16	29
All	All	652/669 (98%)	613 (94%)	39 (6%)	17	31

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	M	60	LEU
3	M	199	ASN
3	M	104	SER
3	M	133	THR
3	M	216	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	M	199	ASN
3	M	301	HIS
3	M	4	GLN
3	M	25	ASN
3	M	44	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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 19 ligands modelled in this entry, 1 is monoatomic - leaving 18 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$
4	LDA	M	1307	-	13,15,15	2.30	1 (7%)	14,17,17	2.66	3 (21%)
8	U10	M	1313	-	48,48,63	1.95	5 (10%)	60,61,79	1.43	9 (15%)
4	LDA	M	1305	-	13,15,15	2.11	1 (7%)	14,17,17	3.72	3 (21%)
11	SPN	M	1312	-	42,42,42	3.67	16 (38%)	50,52,52	2.09	20 (40%)
4	LDA	M	1306	-	13,15,15	1.91	1 (7%)	14,17,17	3.57	3 (21%)
4	LDA	H	1251	-	13,15,15	2.15	1 (7%)	14,17,17	3.71	3 (21%)
6	BCL	M	1303	3	69,74,74	1.01	3 (4%)	79,115,115	1.63	15 (18%)
7	BPH	M	1311	-	59,70,70	1.27	5 (8%)	59,101,101	2.32	22 (37%)
5	D10	H	1252	-	8,8,9	0.27	0	7,7,8	0.47	0
5	D10	H	1253	-	7,7,9	0.25	0	6,6,8	0.69	0
7	BPH	L	1284	-	59,70,70	1.36	5 (8%)	59,101,101	1.47	10 (16%)
8	U10	L	1285	-	48,48,63	2.52	5 (10%)	60,61,79	2.10	14 (23%)
10	PO4	M	1309	-	4,4,4	1.50	0	6,6,6	1.09	1 (16%)
10	PO4	M	1310	-	4,4,4	0.73	0	6,6,6	0.56	0
6	BCL	L	1282	2	69,74,74	1.35	4 (5%)	79,115,115	1.68	18 (22%)
6	BCL	L	1283	2	69,74,74	1.15	4 (5%)	79,115,115	1.58	18 (22%)
5	D10	H	1254	-	6,6,9	0.81	0	5,5,8	0.59	0
6	BCL	M	1304	3	69,74,74	1.46	3 (4%)	79,115,115	1.59	15 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	LDA	M	1307	-	-	5/13/13/13	-
8	U10	M	1313	-	-	10/45/69/87	0/1/1/1
4	LDA	M	1305	-	-	7/13/13/13	-
11	SPN	M	1312	-	-	16/50/51/51	-
4	LDA	M	1306	-	-	5/13/13/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	LDA	H	1251	-	-	2/13/13/13	-
6	BCL	M	1303	3	-	14/41/137/137	-
7	BPH	M	1311	-	-	16/37/105/105	0/5/6/6
5	D10	H	1252	-	-	2/6/6/7	-
5	D10	H	1253	-	-	4/5/5/7	-
7	BPH	L	1284	-	-	5/37/105/105	0/5/6/6
8	U10	L	1285	-	-	16/45/69/87	0/1/1/1
6	BCL	L	1282	2	-	4/41/137/137	-
6	BCL	L	1283	2	-	5/41/137/137	-
5	D10	H	1254	-	-	1/4/4/7	-
6	BCL	M	1304	3	-	2/41/137/137	-

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	L	1285	U10	C27-C28	-12.44	1.12	1.50
11	M	1312	SPN	C3-C4	-9.44	1.35	1.50
6	M	1304	BCL	MG-NA	9.00	2.27	2.06
8	M	1313	U10	C6-C1	8.93	1.51	1.35
6	L	1282	BCL	MG-NA	8.06	2.25	2.06

The worst 5 of 154 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	1305	LDA	CM1-N1-C1	-10.25	88.69	110.23
4	M	1306	LDA	CM2-N1-C1	-9.07	91.19	110.23
4	H	1251	LDA	CM1-N1-C1	-8.73	91.89	110.23
4	H	1251	LDA	CM2-N1-C1	-8.21	92.98	110.23
4	M	1306	LDA	CM1-N1-C1	-7.92	93.59	110.23

There are no chirality outliers.

5 of 114 torsion outliers are listed below:

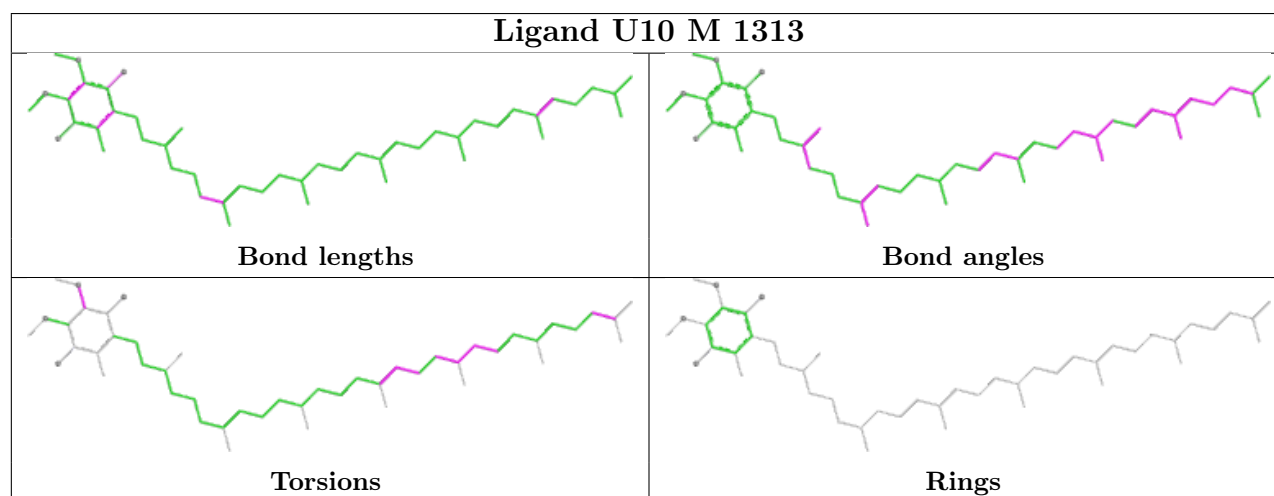
Mol	Chain	Res	Type	Atoms
4	M	1306	LDA	C2-C1-N1-O1
4	M	1306	LDA	C2-C1-N1-CM1
4	M	1306	LDA	C2-C1-N1-CM2
4	M	1307	LDA	C2-C1-N1-CM1
4	M	1307	LDA	C2-C1-N1-CM2

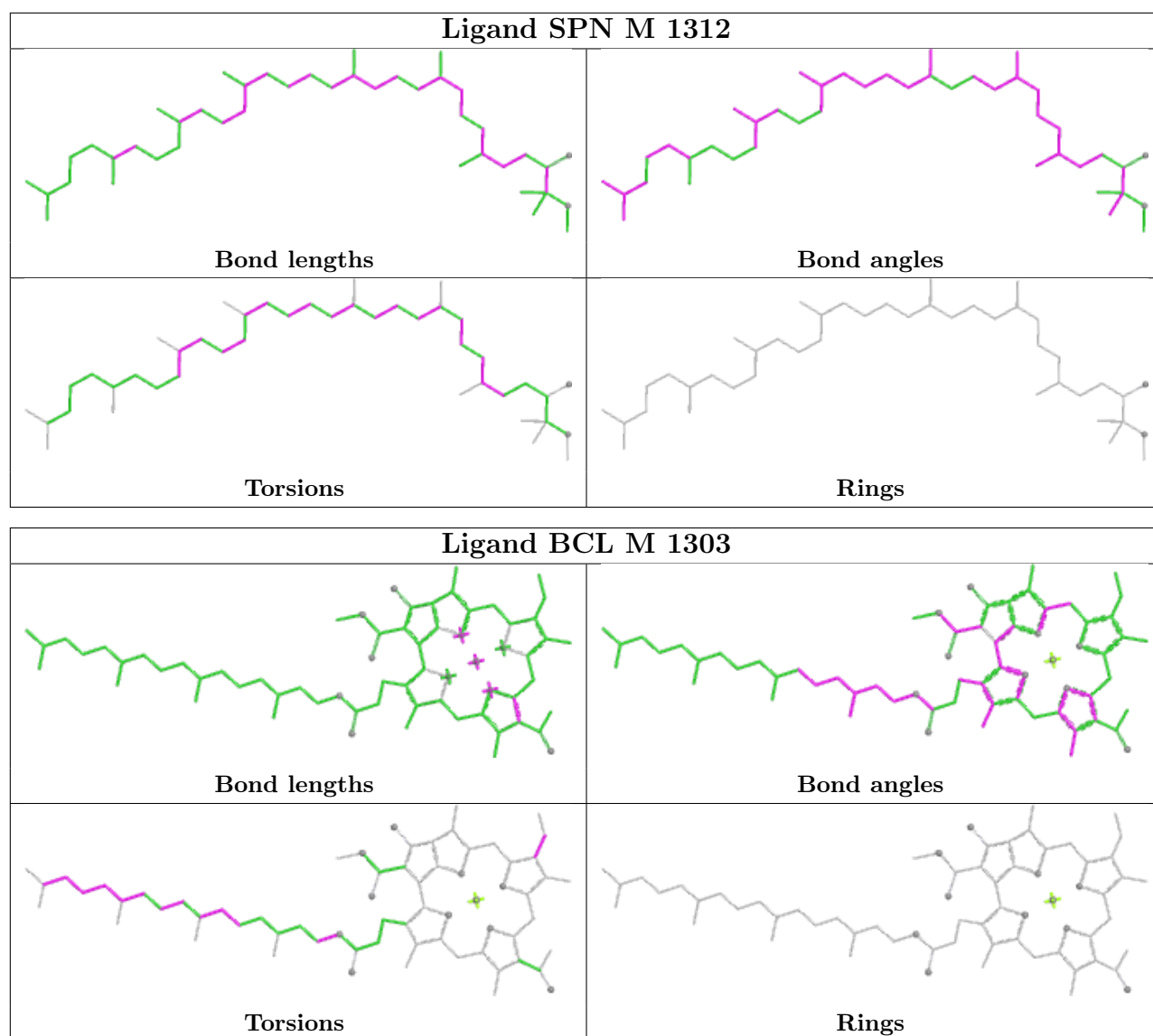
There are no ring outliers.

11 monomers are involved in 44 short contacts:

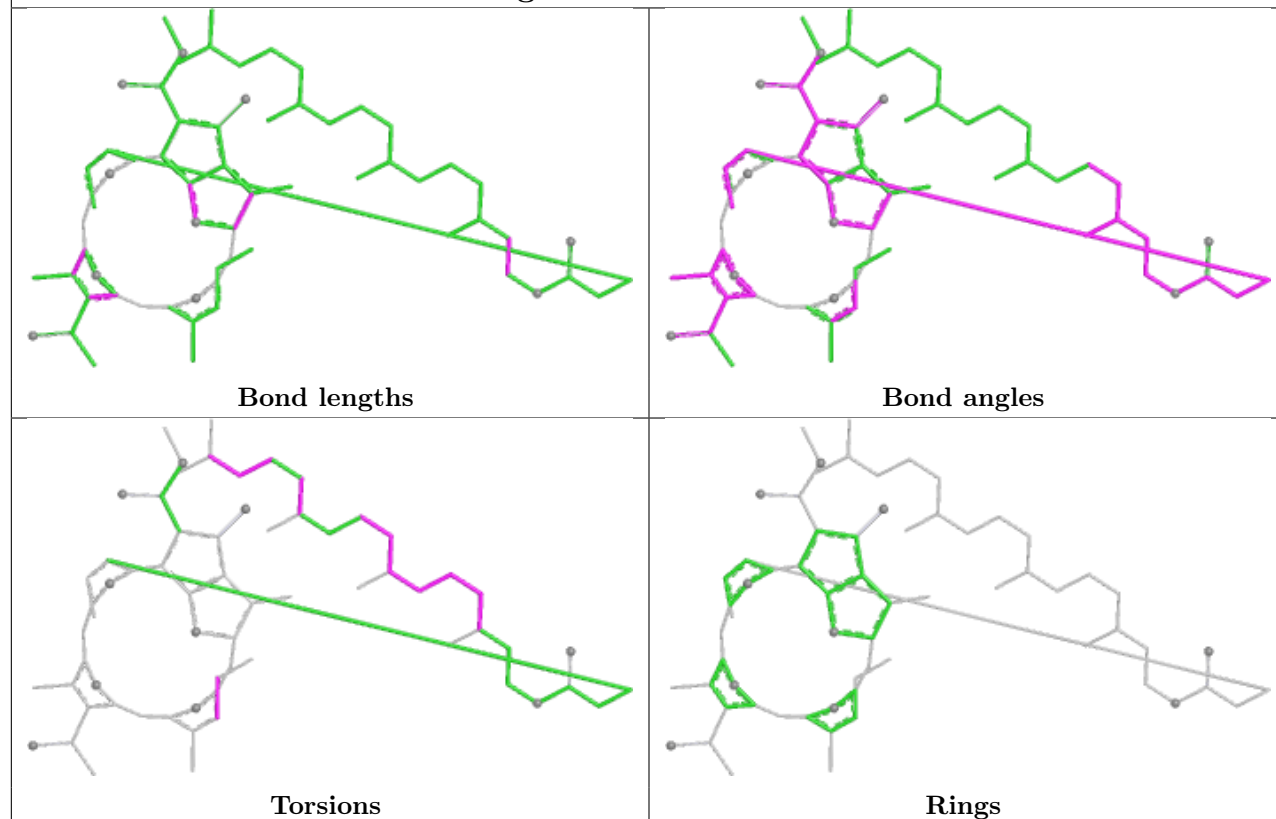
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	M	1307	LDA	6	0
8	M	1313	U10	3	0
11	M	1312	SPN	6	0
4	H	1251	LDA	4	0
6	M	1303	BCL	9	0
7	M	1311	BPH	11	0
7	L	1284	BPH	5	0
8	L	1285	U10	1	0
6	L	1282	BCL	2	0
6	L	1283	BCL	1	0
6	M	1304	BCL	5	0

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.

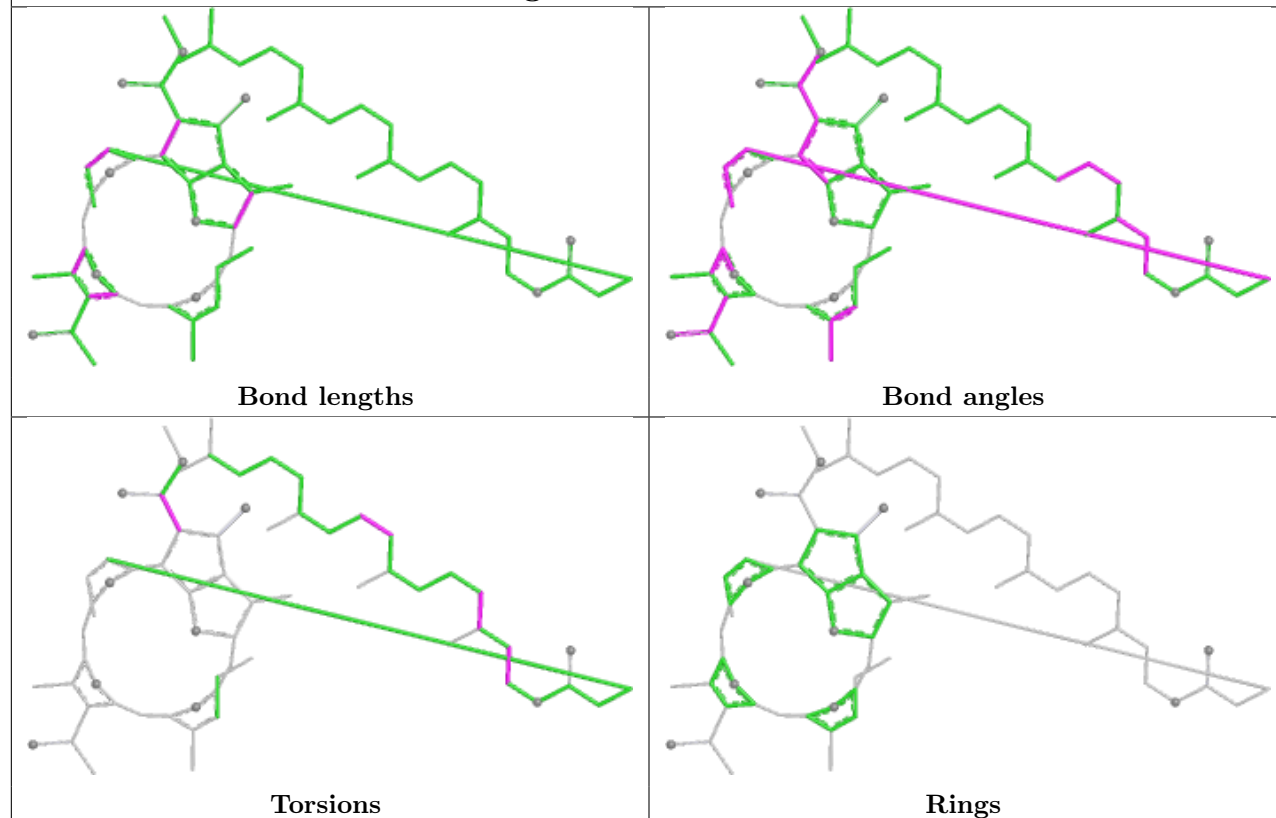


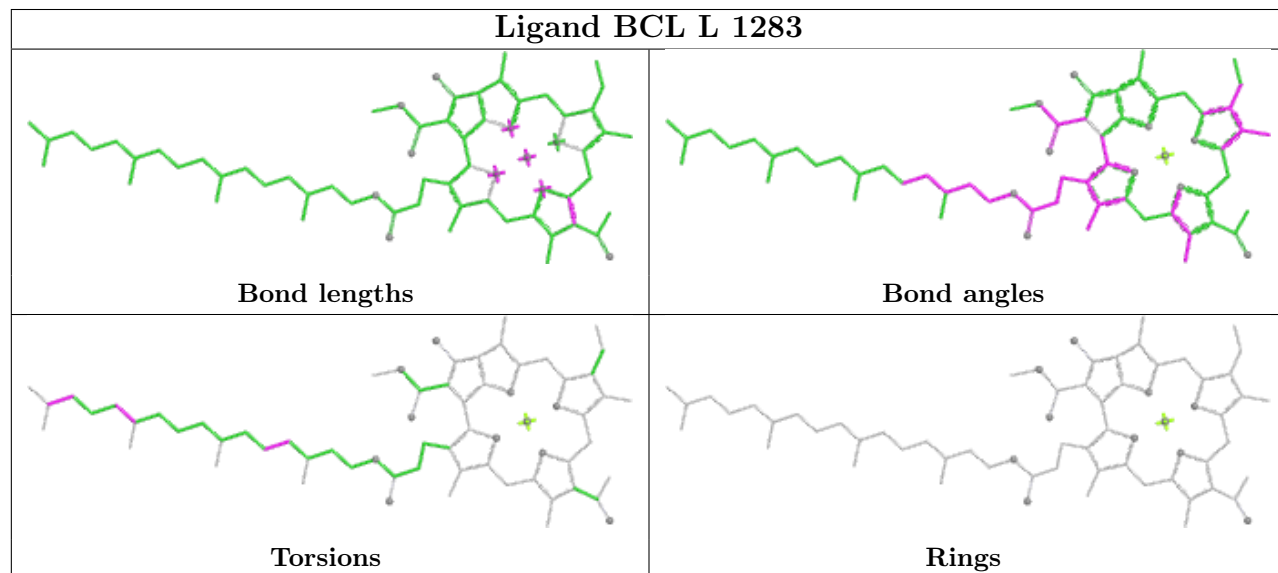
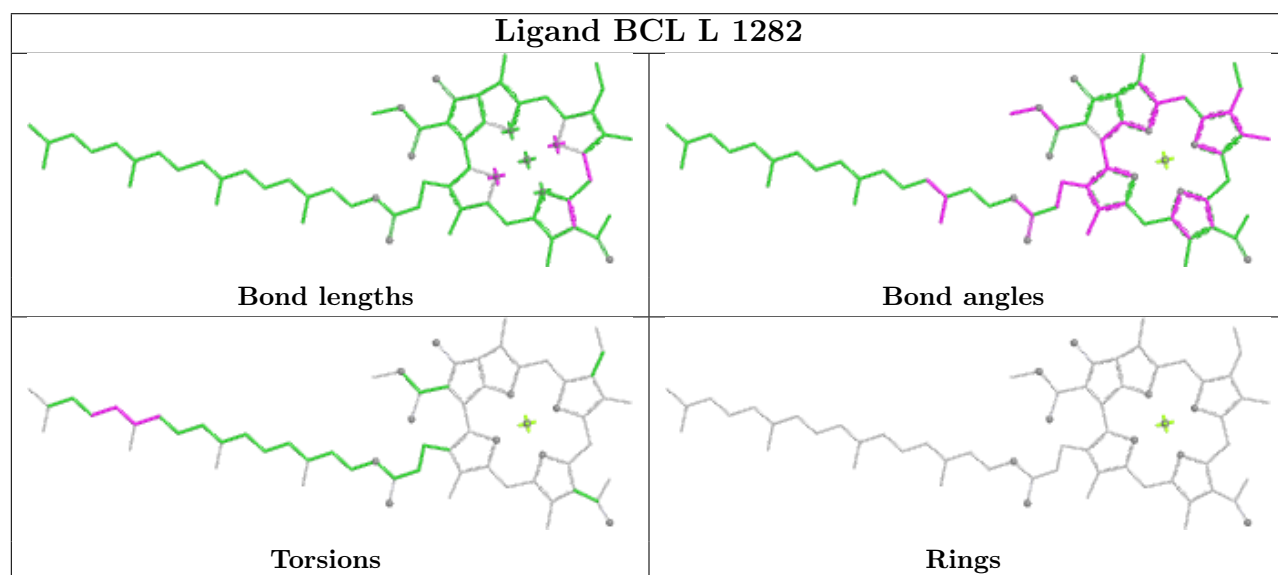
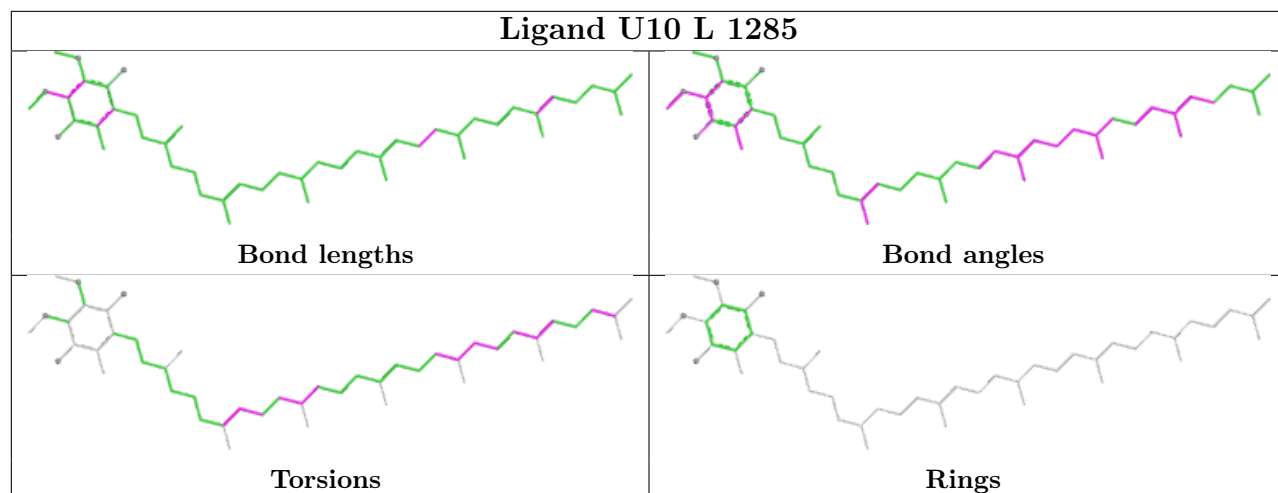


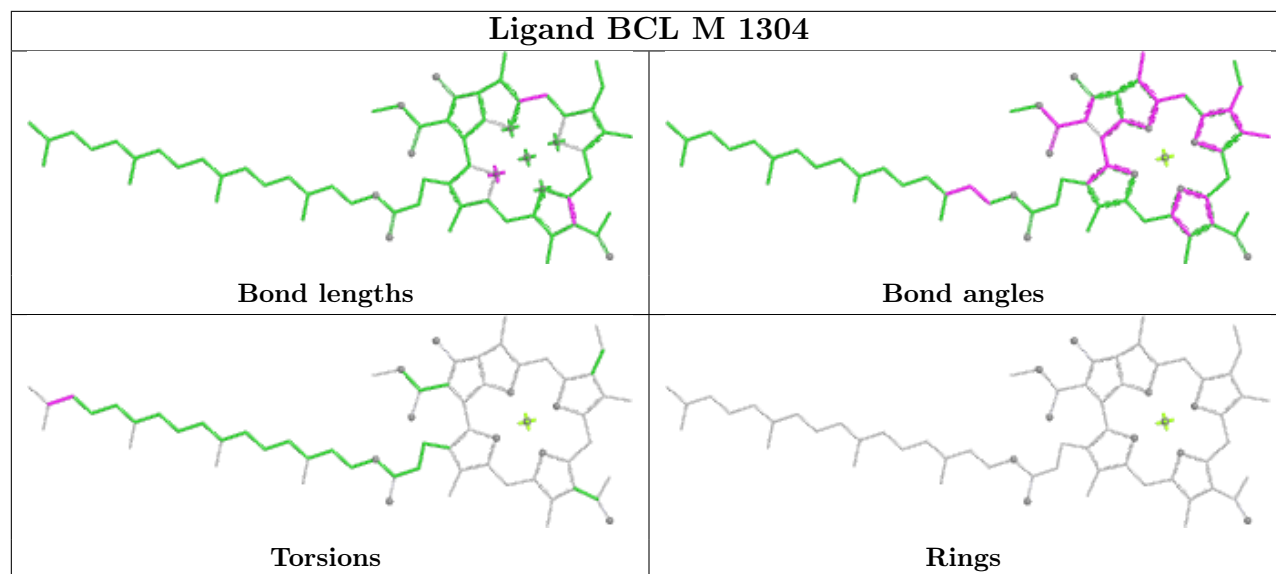
Ligand BPH M 1311



Ligand BPH L 1284







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	H	241/260 (92%)	-0.24	8 (3%) 49 45	24, 31, 42, 100	0
2	L	281/281 (100%)	-0.35	3 (1%) 78 74	27, 35, 49, 55	0
3	M	303/307 (98%)	0.28	10 (3%) 49 45	29, 36, 48, 77	0
All	All	825/848 (97%)	-0.09	21 (2%) 58 54	24, 35, 48, 100	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	M	303	MET	9.3
3	M	302	GLY	9.0
3	M	1	ALA	7.6
1	H	245	ALA	7.2
1	H	246	PRO	6.2

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](#)

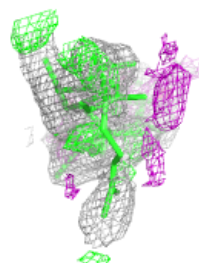
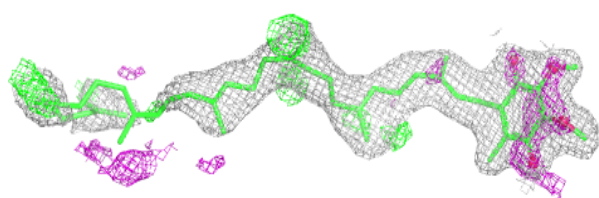
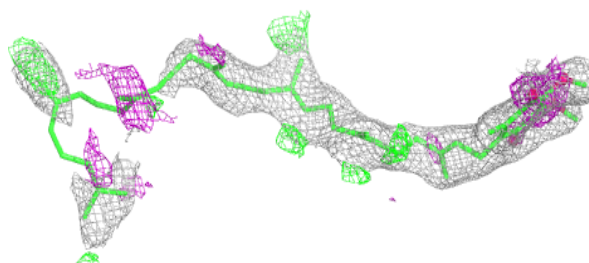
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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
4	LDA	M	1306	16/16	0.64	0.25	66,71,91,92	0
4	LDA	M	1305	16/16	0.69	0.26	78,80,85,87	0
5	D10	H	1253	8/10	0.72	0.22	66,67,71,72	0
5	D10	H	1252	9/10	0.73	0.22	74,74,76,76	0
5	D10	H	1254	7/10	0.73	0.22	77,77,77,78	0
4	LDA	M	1307	16/16	0.76	0.19	31,59,69,70	0
10	PO4	M	1310	5/5	0.85	0.18	74,75,76,77	0
8	U10	L	1285	48/63	0.86	0.14	37,51,81,82	14
4	LDA	H	1251	16/16	0.86	0.13	57,60,65,66	0
8	U10	M	1313	48/63	0.91	0.11	12,27,53,55	0
7	BPH	M	1311	65/65	0.92	0.12	22,28,81,82	0
11	SPN	M	1312	43/43	0.92	0.11	22,37,59,63	0
6	BCL	M	1303	66/66	0.94	0.10	19,23,65,67	0
6	BCL	L	1282	66/66	0.95	0.08	15,21,33,41	0
6	BCL	M	1304	66/66	0.95	0.09	17,24,38,51	0
7	BPH	L	1284	65/65	0.95	0.07	12,19,25,28	0
6	BCL	L	1283	66/66	0.95	0.09	12,17,38,41	0
10	PO4	M	1309	5/5	0.97	0.14	39,42,44,46	0
9	FE	M	1308	1/1	1.00	0.12	20,20,20,20	0

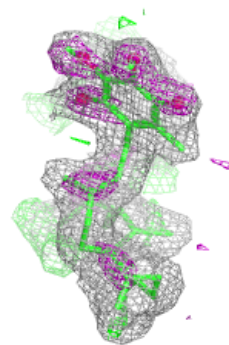
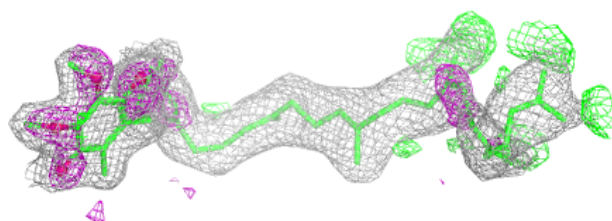
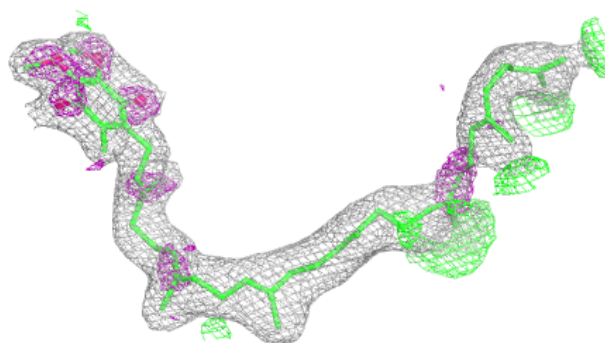
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around U10 L 1285:

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

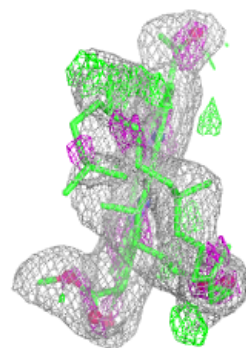
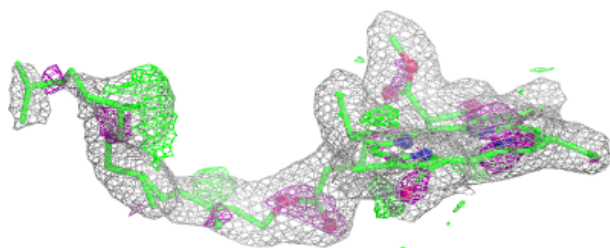
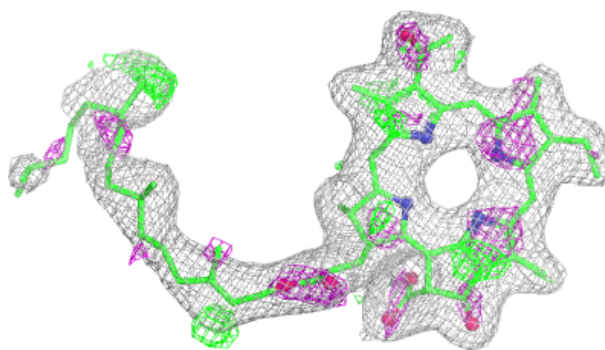
**Electron density around U10 M 1313:**

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

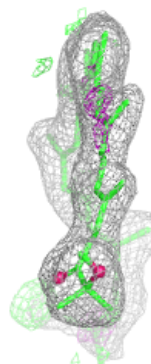
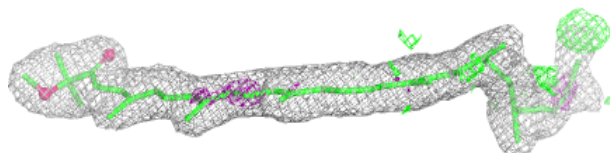
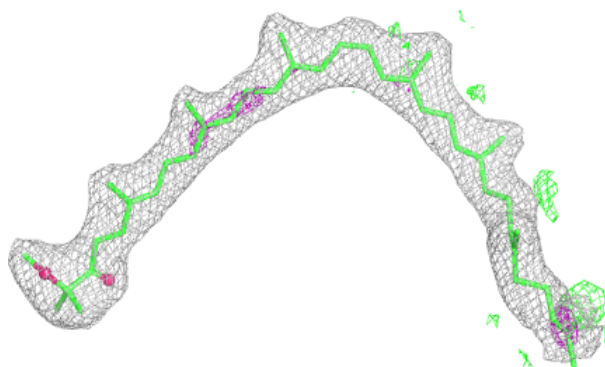


Electron density around BPH M 1311:

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

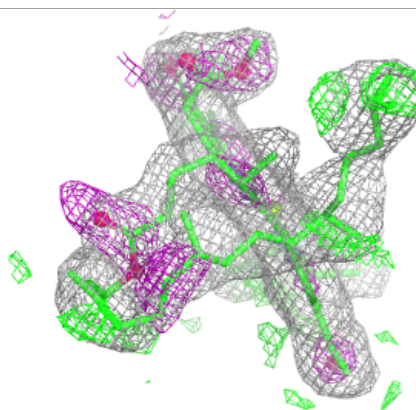
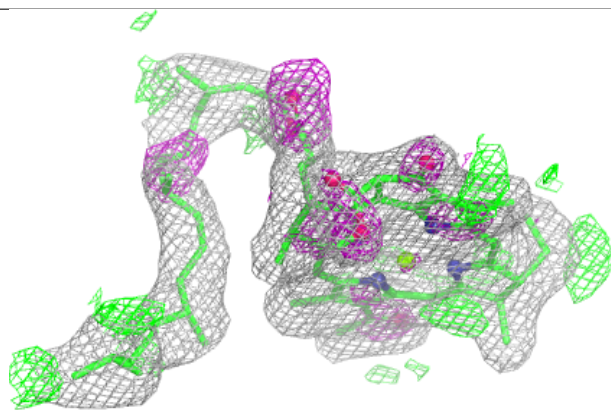
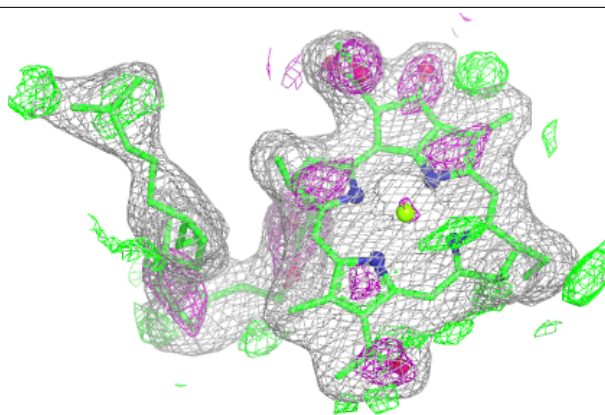
**Electron density around SPN M 1312:**

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

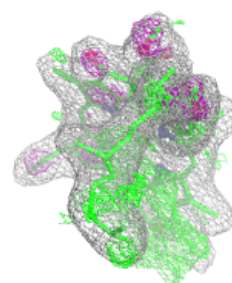
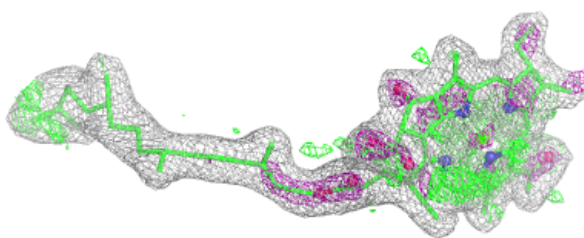
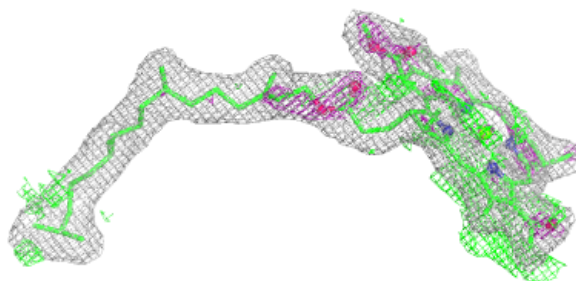


Electron density around BCL M 1303:

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

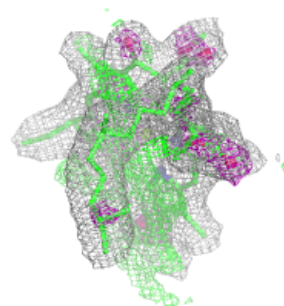
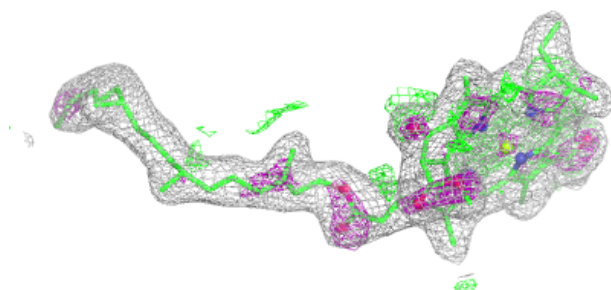
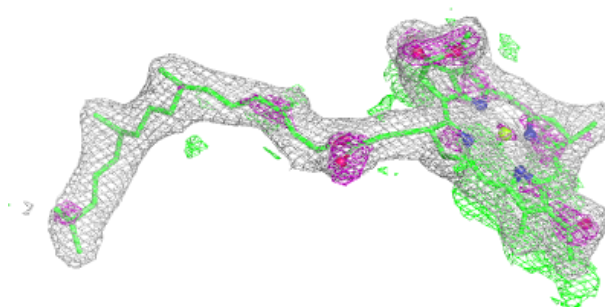
**Electron density around BCL L 1282:**

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

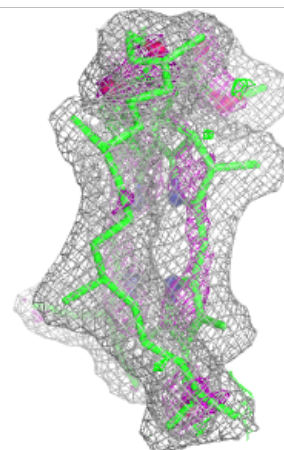
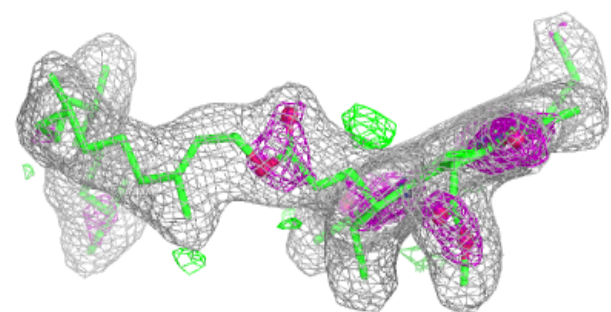
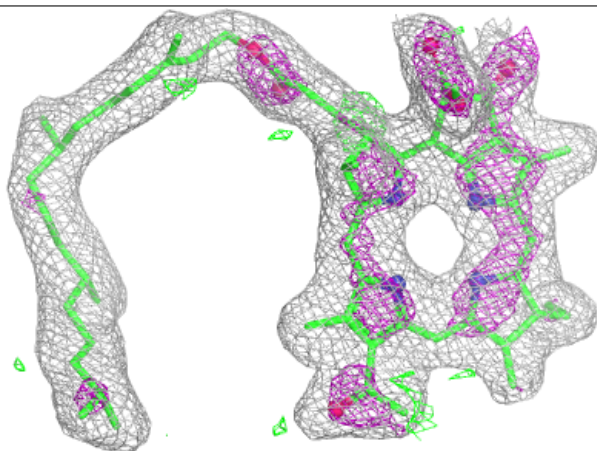


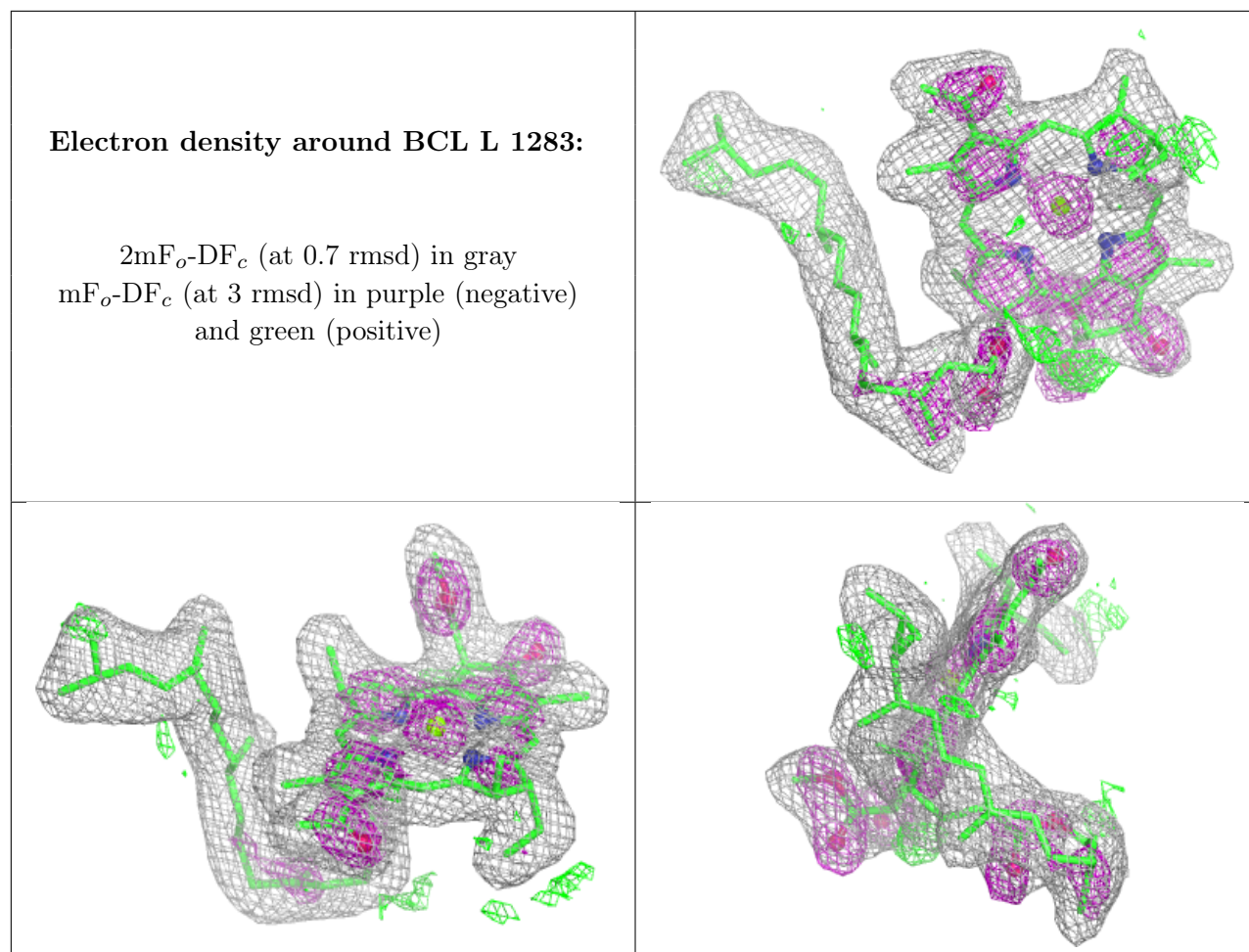
Electron density around BCL M 1304:

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

**Electron density around BPH L 1284:**

$2mF_o-DF_c$ (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.