



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 12:23 pm BST

PDB ID : 1M3X
Title : Photosynthetic Reaction Center From Rhodobacter Sphaeroides
Authors : Camara-Artigas, A.; Brune, D.; Allen, J.P.
Deposited on : 2002-07-01
Resolution : 2.55 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

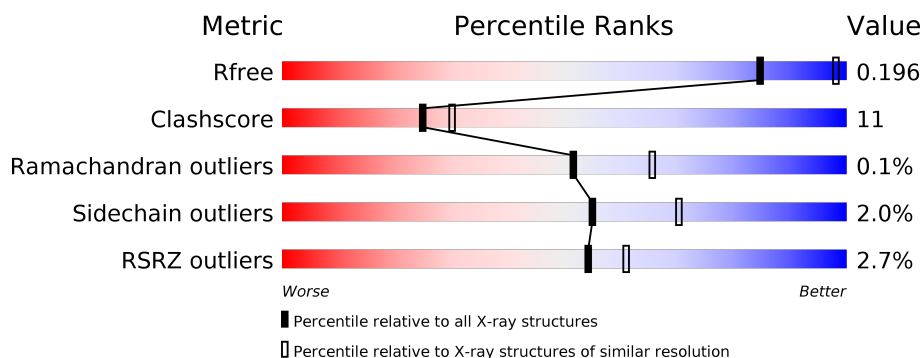
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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

Mol	Chain	Length	Quality of chain
1	L	281	<div> <div>4%</div> <div> <div></div> <div>85%</div> <div>14%</div> <div>.</div> </div> </div>
2	M	307	<div> <div>3%</div> <div> <div></div> <div>77%</div> <div>21%</div> <div>..</div> </div> </div>
3	H	260	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>13%</div> <div>8%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	U10	L	858	-	-	-	X
7	PC1	L	901	-	-	-	X

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 7323 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Photosynthetic Reaction center 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			

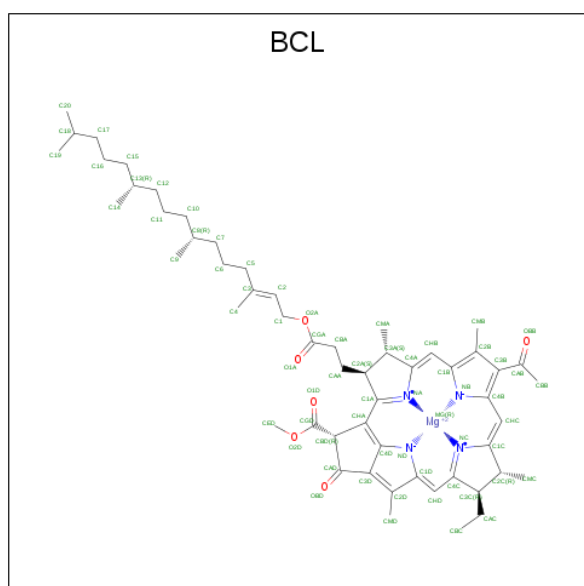
- Molecule 2 is a protein called Photosynthetic Reaction center protein M chain.

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

- Molecule 3 is a protein called Photosynthetic Reaction center protein H chain.

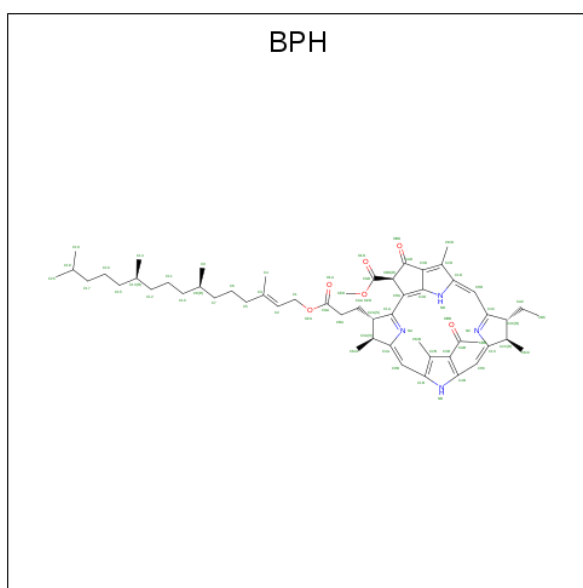
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	238	Total	C	N	O	S	0	0	0
			1814	1160	311	334	9			

- Molecule 4 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



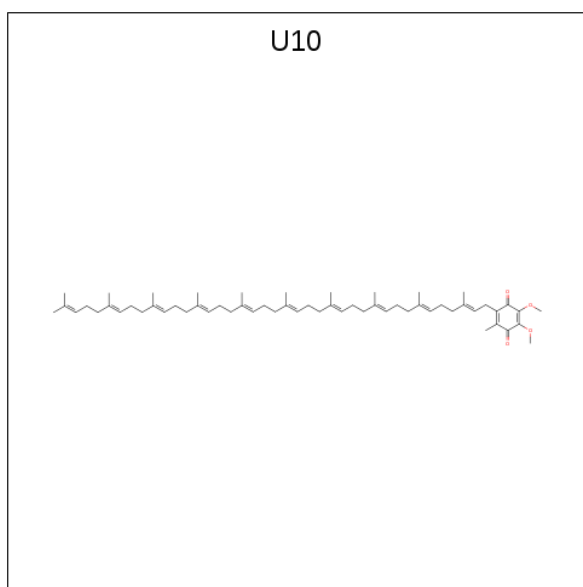
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	L	1	Total 52	C 41	Mg 1	N 4	O 6	0	0
4	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	M	1	Total 66	C 55	Mg 1	N 4	O 6	0	0

- Molecule 5 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: $C_{55}H_{76}N_4O_6$).



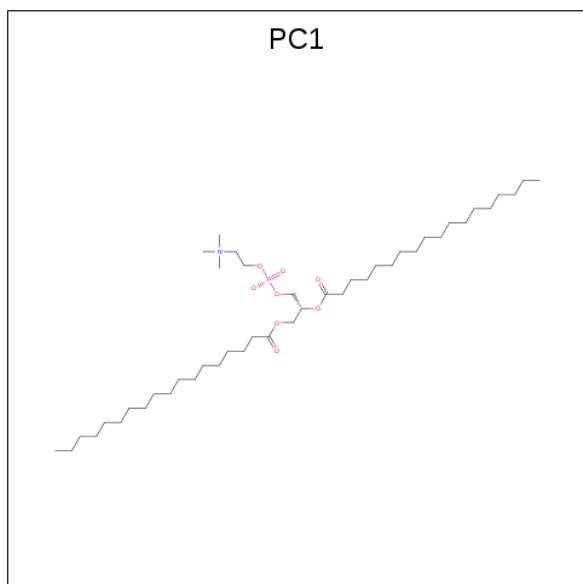
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	L	1	Total	C	N	O	0	0
			65	55	4	6		
5	M	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 6 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	L	1	Total	C	O	0	0
			13	9	4		
6	M	1	Total	C	O	0	0
			48	44	4		

- Molecule 7 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: $C_{44}H_{88}NO_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	L	1	Total	C	N	O	P	0	0
			43	33	1	8	1		

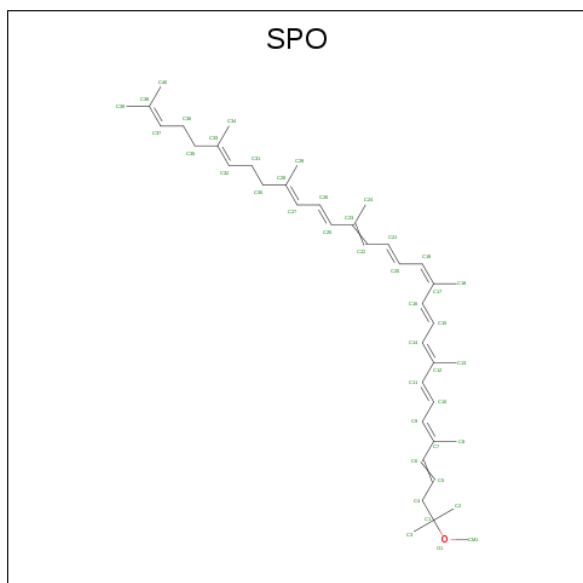
- Molecule 8 is FE (III) ION (three-letter code: FE) (formula: Fe).

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

- Molecule 9 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

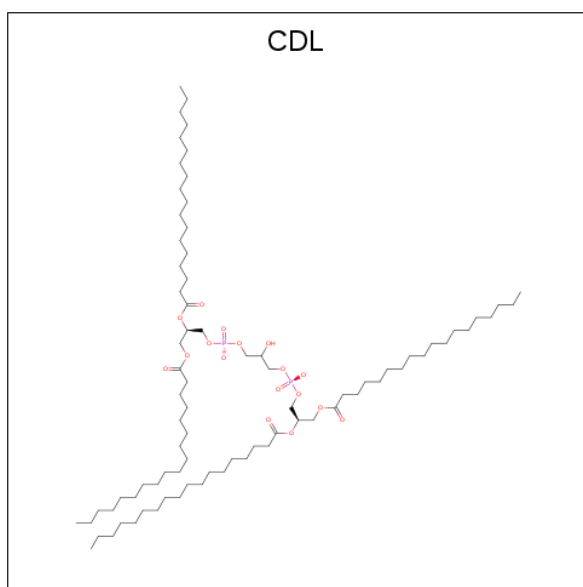
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	M	1	Total	Cl	0	0
			1	1		

- Molecule 10 is SPHEROIDENE (three-letter code: SPO) (formula: C₄₁H₆₀O).



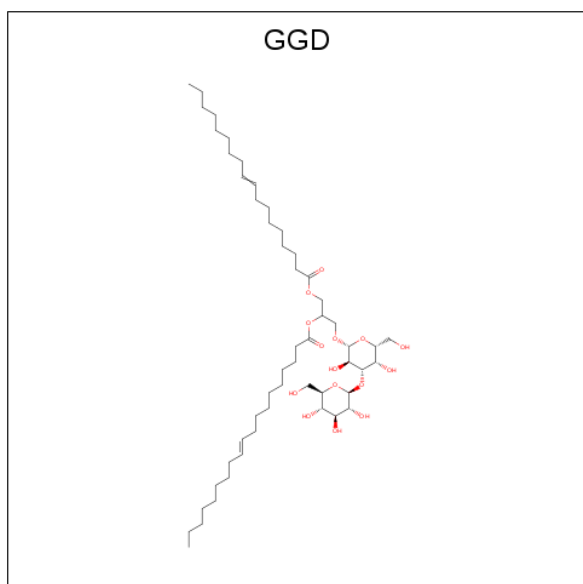
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	M	1	Total	C	O	0	0
			42	41	1		

- Molecule 11 is CARDIOLIPIN (three-letter code: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



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

- Molecule 12 is NONADEC-10-ENOIC ACID 2-[3,4-DIHYDROXY-6-HYDROXYMETHYL-L-5-(3,4,5-TRIHYDROXY-6-HYDROXYMETHYL-TETRAHYDRO-PYRAN-2-YLOXY)-TETRAHYDRO-PYRAN-2-YLOXY]-1-OCTADEC-9-ENOYLOXYMETHYL-ETHYL ESTER (three-letter code: GGD) (formula: $C_{52}H_{94}O_{15}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	M	1	Total	C	O		0	0
			57	42	15			

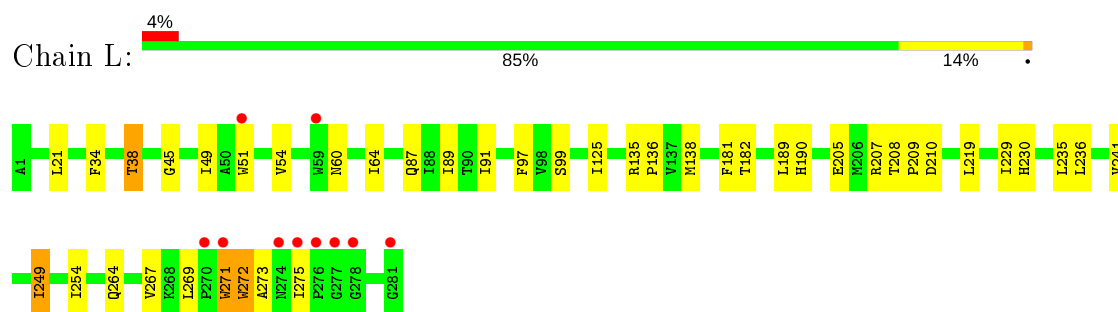
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	L	63	Total 63	O 63	0	0
13	M	68	Total 68	O 68	0	0
13	H	72	Total 72	O 72	0	0

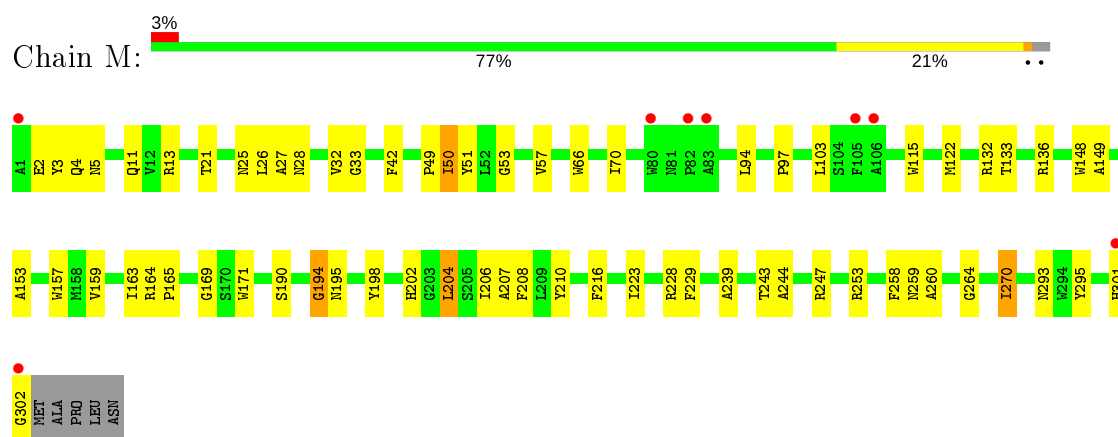
3 Residue-property plots [i](#)

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

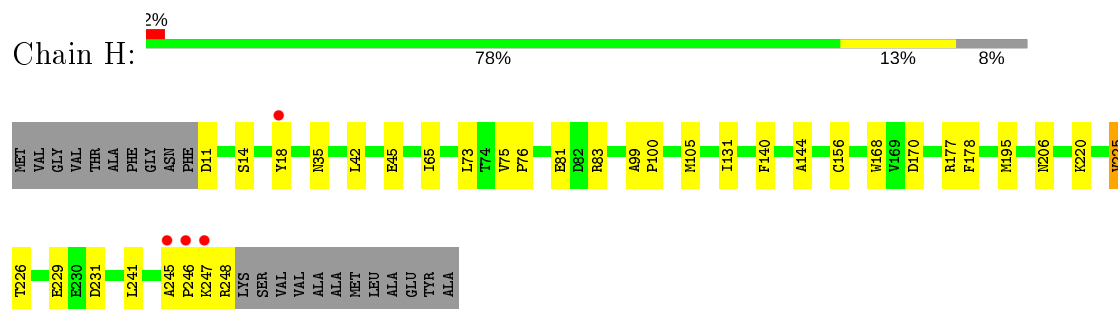
- Molecule 1: Photosynthetic Reaction center protein L chain



- Molecule 2: Photosynthetic Reaction center protein M chain



- Molecule 3: Photosynthetic Reaction center protein H chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	141.80Å 141.80Å 187.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.91 – 2.55 30.84 – 2.55	Depositor EDS
% Data completeness (in resolution range)	96.2 (29.91-2.55) 96.9 (30.84-2.55)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.54Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.185 , 0.209 0.181 , 0.196	Depositor DCC
R_{free} test set	6974 reflections (10.12%)	wwPDB-VP
Wilson B-factor (Å ²)	33.4	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 72.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7323	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 2.67% 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: BCL, CL, CDL, BPH, PC1, GGD, FE, SPO, U10

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L	0.40	0/2320	0.56	0/3175
2	M	0.40	0/2500	0.55	1/3413 (0.0%)
3	H	0.35	0/1862	0.61	0/2534
All	All	0.38	0/6682	0.57	1/9122 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	194	GLY	N-CA-C	-5.64	99.00	113.10

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	46	0
2	M	2408	0	2321	62	0
3	H	1814	0	1818	34	0
4	L	184	0	191	14	0
4	M	66	0	74	5	0
5	L	65	0	76	6	0
5	M	65	0	76	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	L	13	0	9	2	0
6	M	48	0	63	4	0
7	L	43	0	60	8	0
8	M	1	0	0	0	0
9	M	1	0	0	0	0
10	M	42	0	60	0	0
11	M	81	0	106	0	0
12	M	57	0	65	16	0
13	H	72	0	0	3	0
13	L	63	0	0	1	0
13	M	68	0	0	2	0
All	All	7323	0	7106	154	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 11.

The worst 5 of 154 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)
7:L:901:PC1:C1	7:L:901:PC1:C2	1.74	1.64
7:L:901:PC1:O11	7:L:901:PC1:C1	1.74	1.35
2:M:202:HIS:O	2:M:206:ILE:HD13	1.78	0.84
7:L:901:PC1:C1	7:L:901:PC1:P	2.76	0.74
2:M:253:ARG:HH22	12:M:902:GGD:C24	2.01	0.73

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	L	279/281 (99%)	267 (96%)	12 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	M	300/307 (98%)	289 (96%)	10 (3%)	1 (0%)	41	51
3	H	236/260 (91%)	227 (96%)	9 (4%)	0	100	100
All	All	815/848 (96%)	783 (96%)	31 (4%)	1 (0%)	51	65

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	M	301	HIS

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%)	213 (97%)	7 (3%)	39	53
2	M	236/240 (98%)	232 (98%)	4 (2%)	60	75
3	H	193/208 (93%)	191 (99%)	2 (1%)	76	84
All	All	649/668 (97%)	636 (98%)	13 (2%)	55	70

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	271	TRP
1	L	272	TRP
2	M	270	ILE
1	L	249	ILE
2	M	216	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	M	4	GLN
2	M	28	ASN
2	M	188	ASN

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Mol	Chain	Res	Type
2	M	259	ASN
2	M	299	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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	BCL	L	850	-	44,60,74	1.76	9 (20%)	52,98,115	2.18	16 (30%)
11	CDL	M	900	-	80,80,99	0.67	2 (2%)	86,92,111	0.91	4 (4%)
5	BPH	M	854	-	64,70,70	1.41	9 (14%)	76,101,101	1.80	17 (22%)
4	BCL	L	851	-	58,74,74	1.63	12 (20%)	69,115,115	1.85	14 (20%)
7	PC1	L	901	-	42,42,53	2.41	12 (28%)	48,50,61	1.67	11 (22%)
6	U10	M	857	-	48,48,63	2.39	13 (27%)	58,61,79	2.13	20 (34%)
10	SPO	M	859	-	40,41,41	3.62	25 (62%)	47,50,50	2.73	14 (29%)
5	BPH	L	855	-	64,70,70	1.32	10 (15%)	76,101,101	1.82	20 (26%)
4	BCL	L	853	-	58,74,74	1.67	10 (17%)	69,115,115	2.22	19 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	U10	L	858	-	13,13,63	3.04	6 (46%)	16,18,79	1.59	5 (31%)
12	GGD	M	902	-	58,58,68	2.92	20 (34%)	72,72,82	4.32	33 (45%)
4	BCL	M	852	-	58,74,74	1.53	8 (13%)	69,115,115	1.90	15 (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
4	BCL	L	850	-	-	3/21/121/137	-
11	CDL	M	900	-	-	29/91/91/110	-
5	BPH	M	854	-	-	10/54/105/105	0/5/6/6
4	BCL	L	851	-	-	5/37/137/137	-
7	PC1	L	901	-	-	16/46/46/57	-
6	U10	M	857	-	-	14/45/69/87	0/1/1/1
10	SPO	M	859	-	-	13/47/47/47	-
5	BPH	L	855	-	-	9/54/105/105	0/5/6/6
4	BCL	L	853	-	-	5/37/137/137	-
6	U10	L	858	-	-	2/4/24/87	0/1/1/1
12	GGD	M	902	-	-	27/47/87/97	0/2/2/2
4	BCL	M	852	-	-	9/37/137/137	-

The worst 5 of 136 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	M	902	GGD	OC6-CC4	-12.19	1.16	1.46
6	M	857	U10	C6-C1	9.71	1.52	1.35
10	M	859	SPO	C15-C16	9.39	1.58	1.34
6	L	858	U10	C6-C1	8.49	1.52	1.35
12	M	902	GGD	OA1-CC3	8.01	1.58	1.43

The worst 5 of 188 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	M	902	GGD	CB1-OB1-CA3	19.32	165.77	117.96
12	M	902	GGD	OA1-CC3-CC4	16.46	150.62	110.90
10	M	859	SPO	C25-C23-C22	-11.39	101.47	118.94
12	M	902	GGD	CC4-OC6-CC5	9.32	140.74	117.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	M	902	GGD	C32-C31-CC7	7.97	142.59	113.62

There are no chirality outliers.

5 of 142 torsion outliers are listed below:

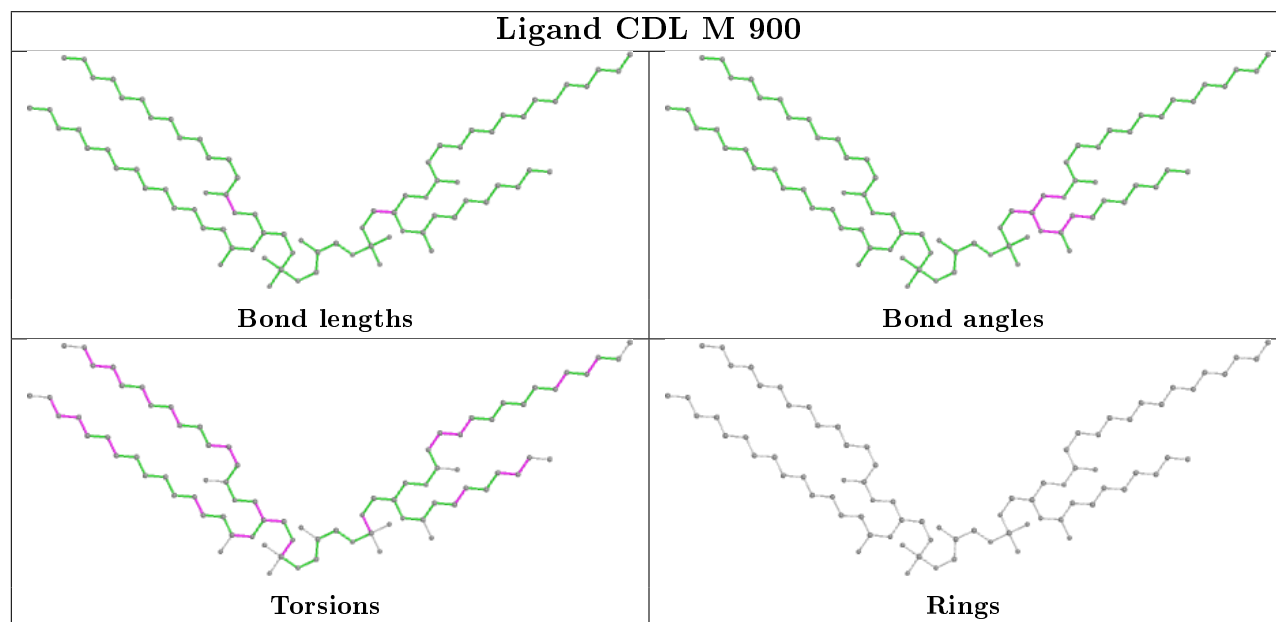
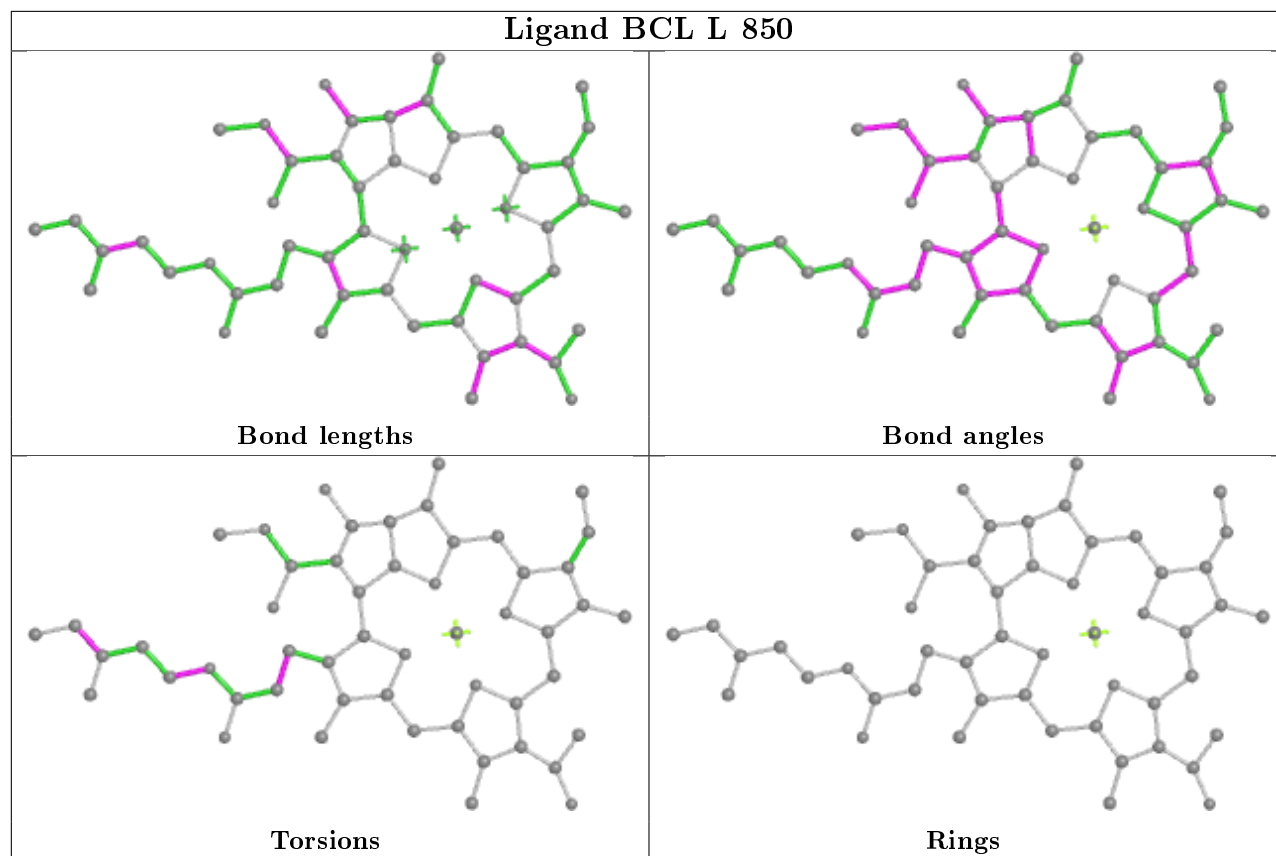
Mol	Chain	Res	Type	Atoms
11	M	900	CDL	CA3-OA5-PA1-OA2
11	M	900	CDL	CA3-OA5-PA1-OA3
11	M	900	CDL	CA3-OA5-PA1-OA4
5	M	854	BPH	C4C-C3C-CAC-CBC
5	M	854	BPH	C2C-C3C-CAC-CBC

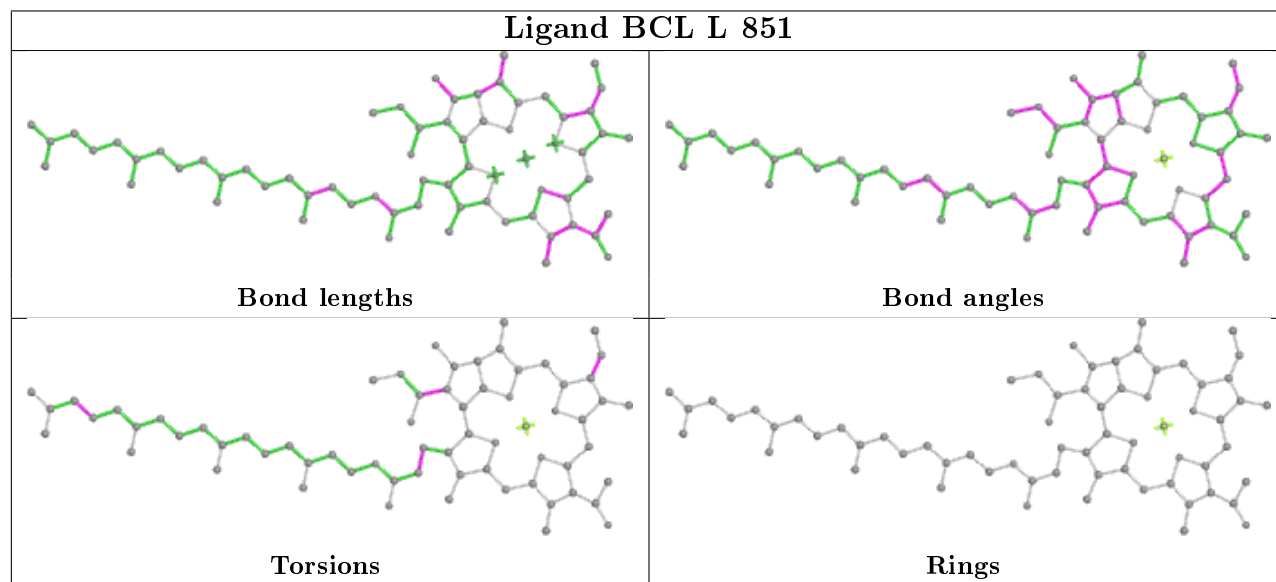
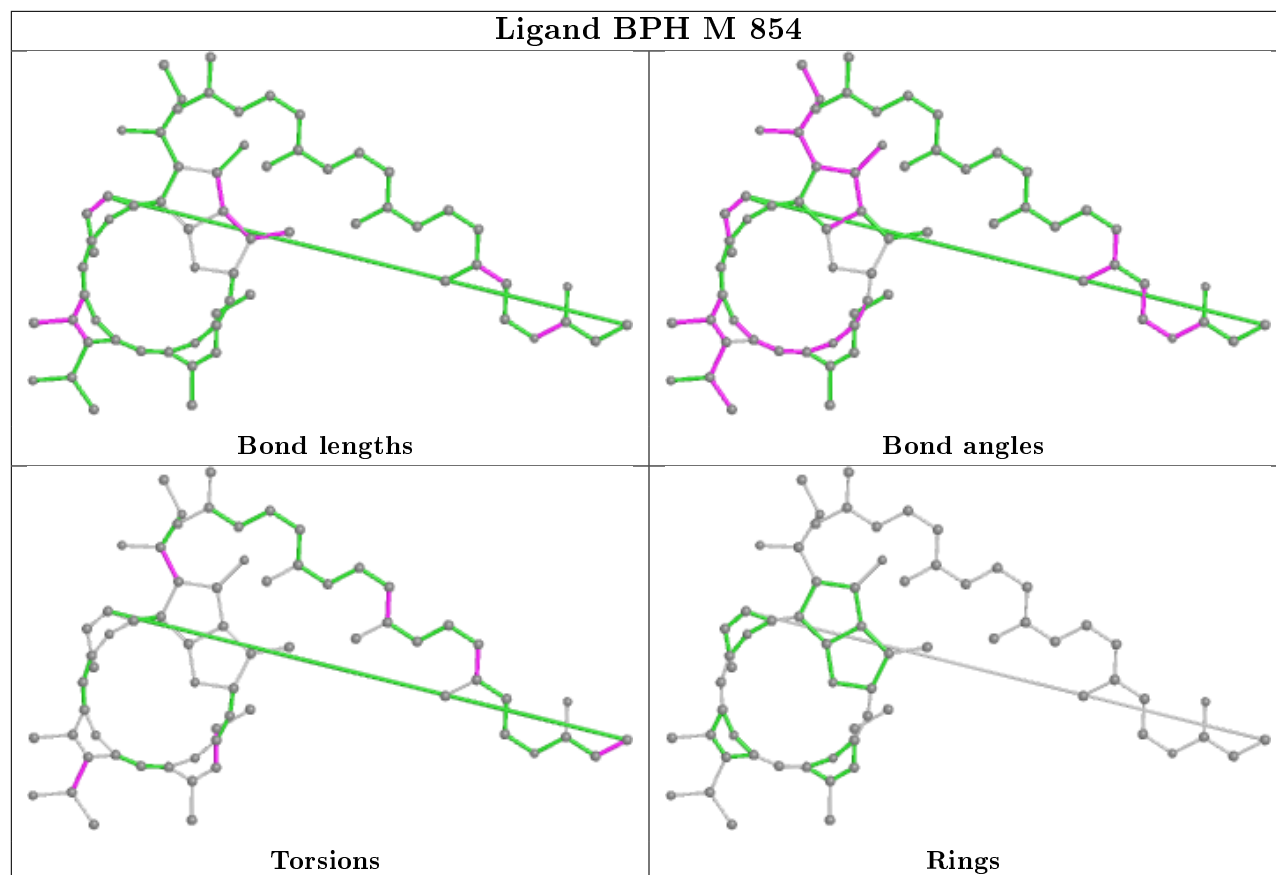
There are no ring outliers.

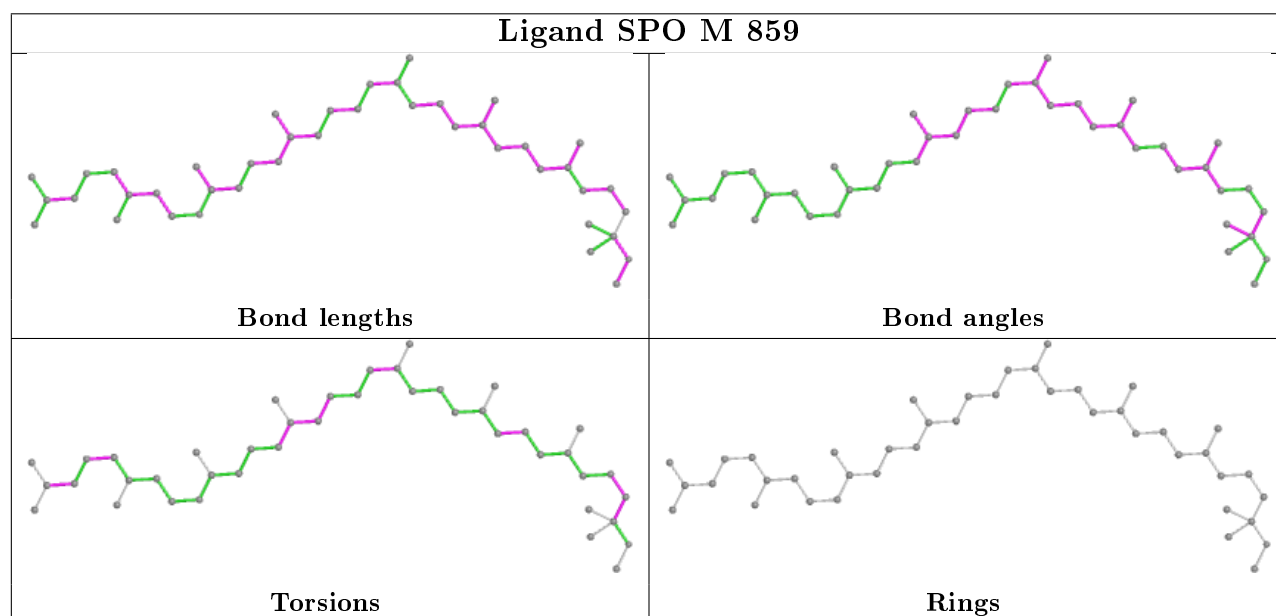
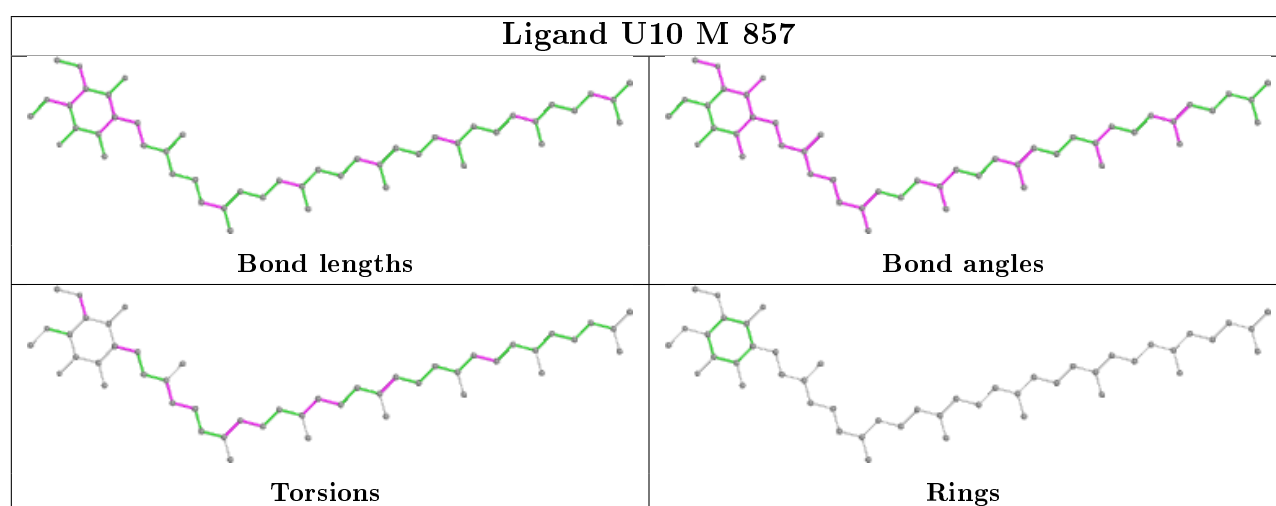
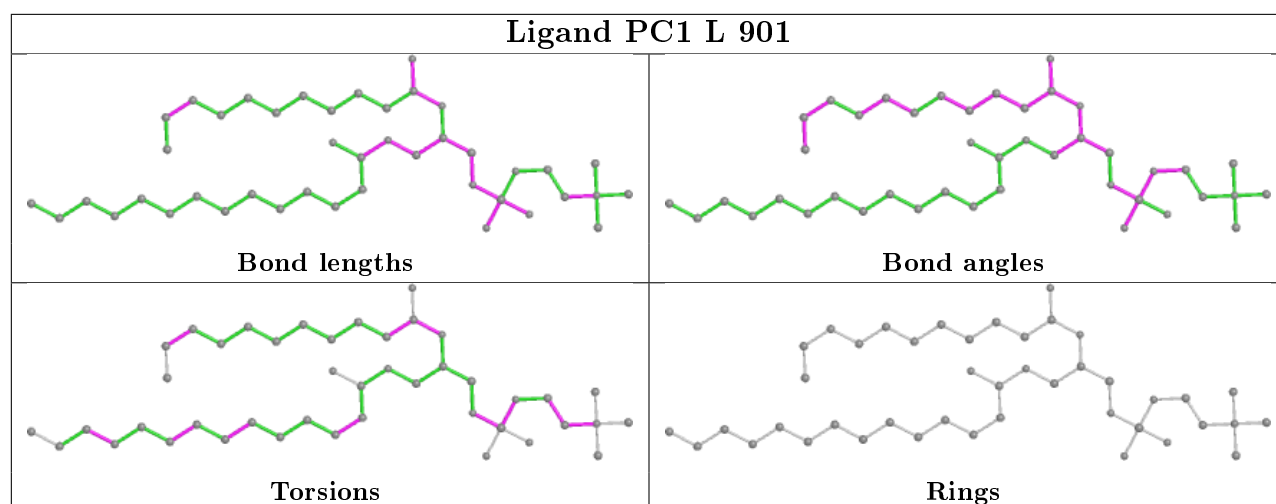
10 monomers are involved in 52 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	850	BCL	7	0
5	M	854	BPH	7	0
4	L	851	BCL	4	0
7	L	901	PC1	8	0
6	M	857	U10	4	0
5	L	855	BPH	6	0
4	L	853	BCL	6	0
6	L	858	U10	2	0
12	M	902	GGD	16	0
4	M	852	BCL	5	0

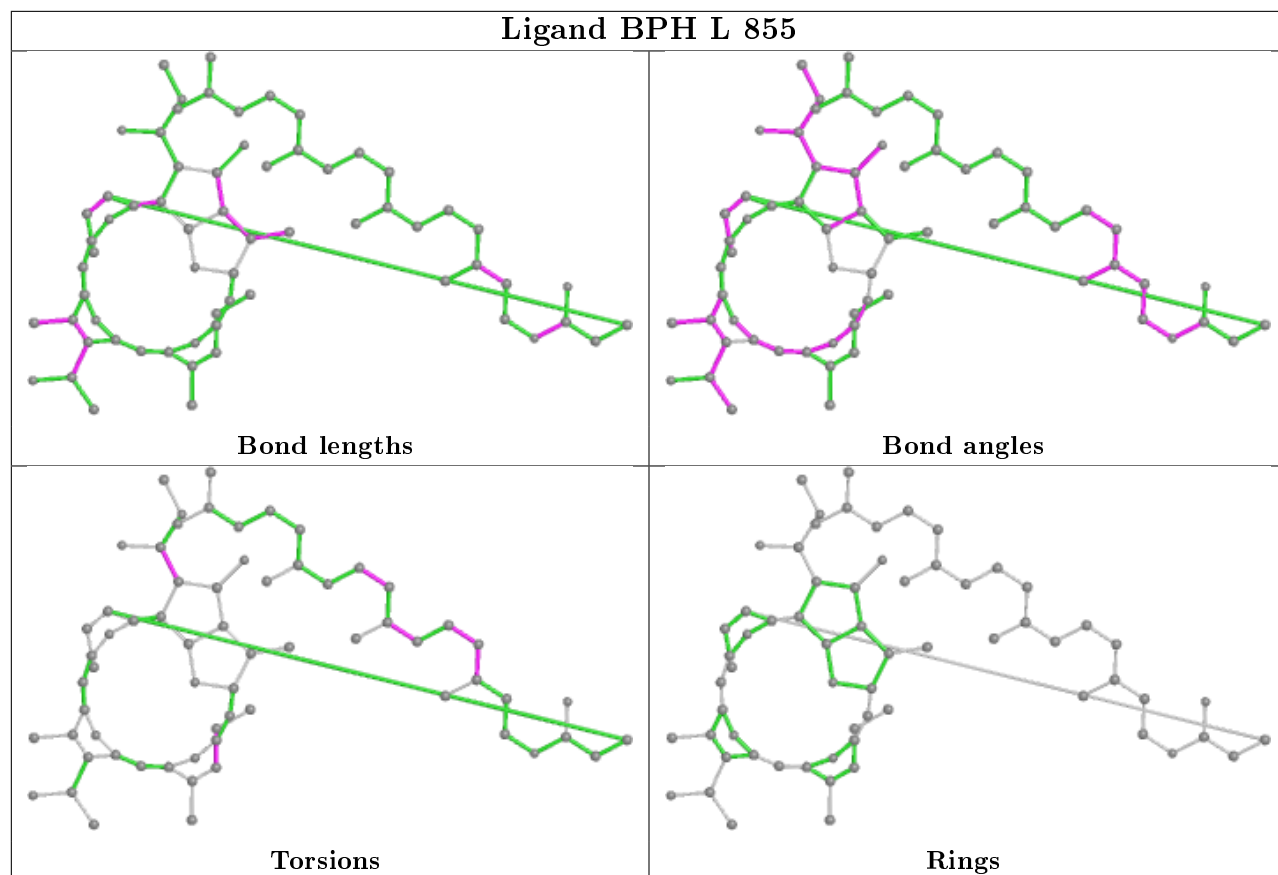
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



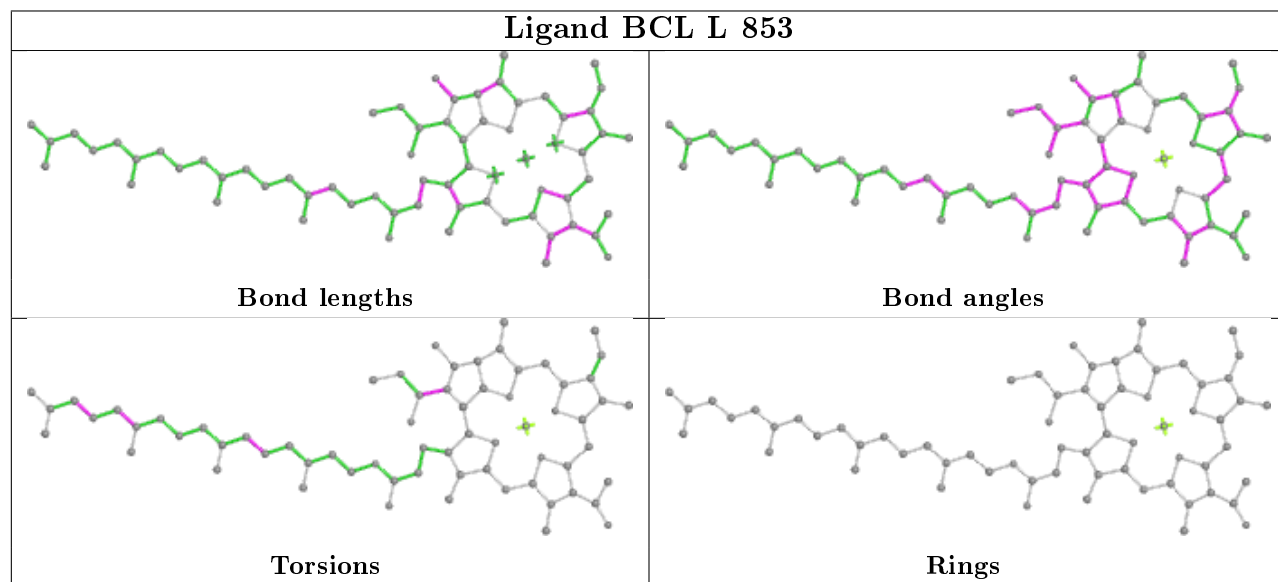




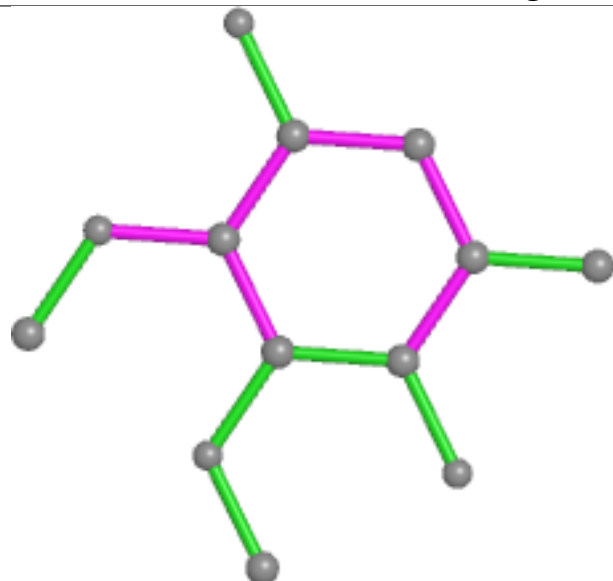
Ligand BPH L 855



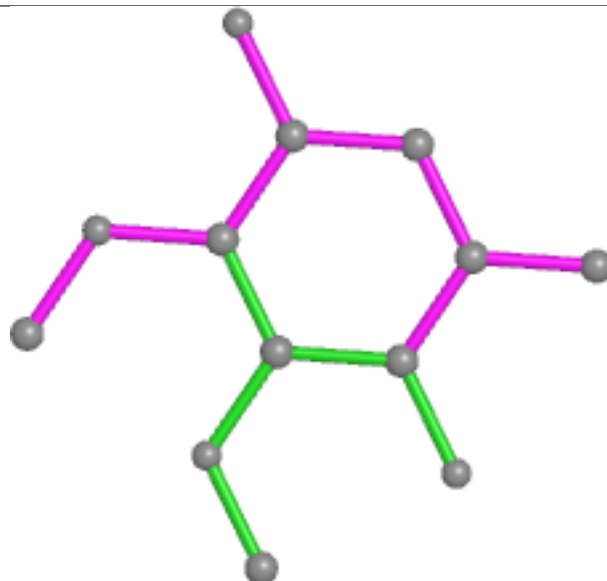
Ligand BCL L 853



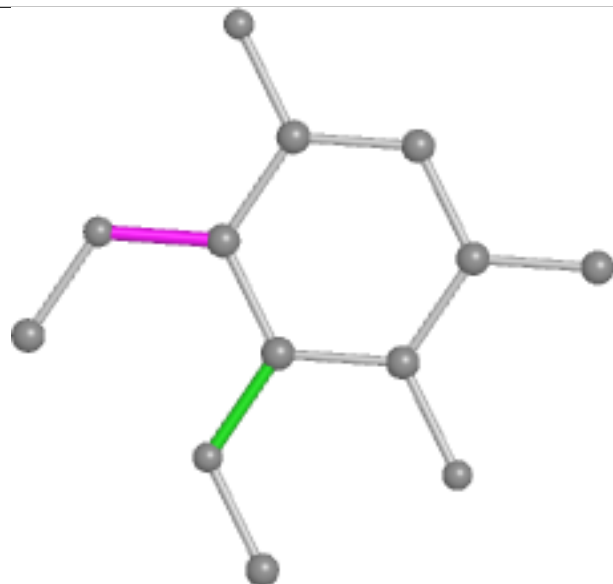
Ligand U10 L 858



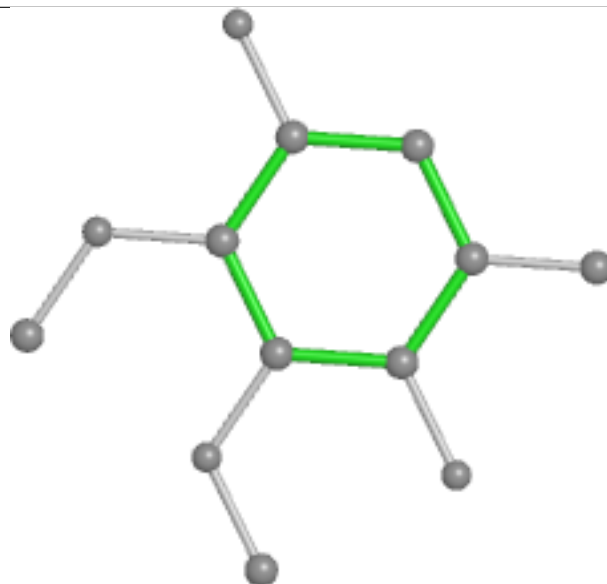
Bond lengths



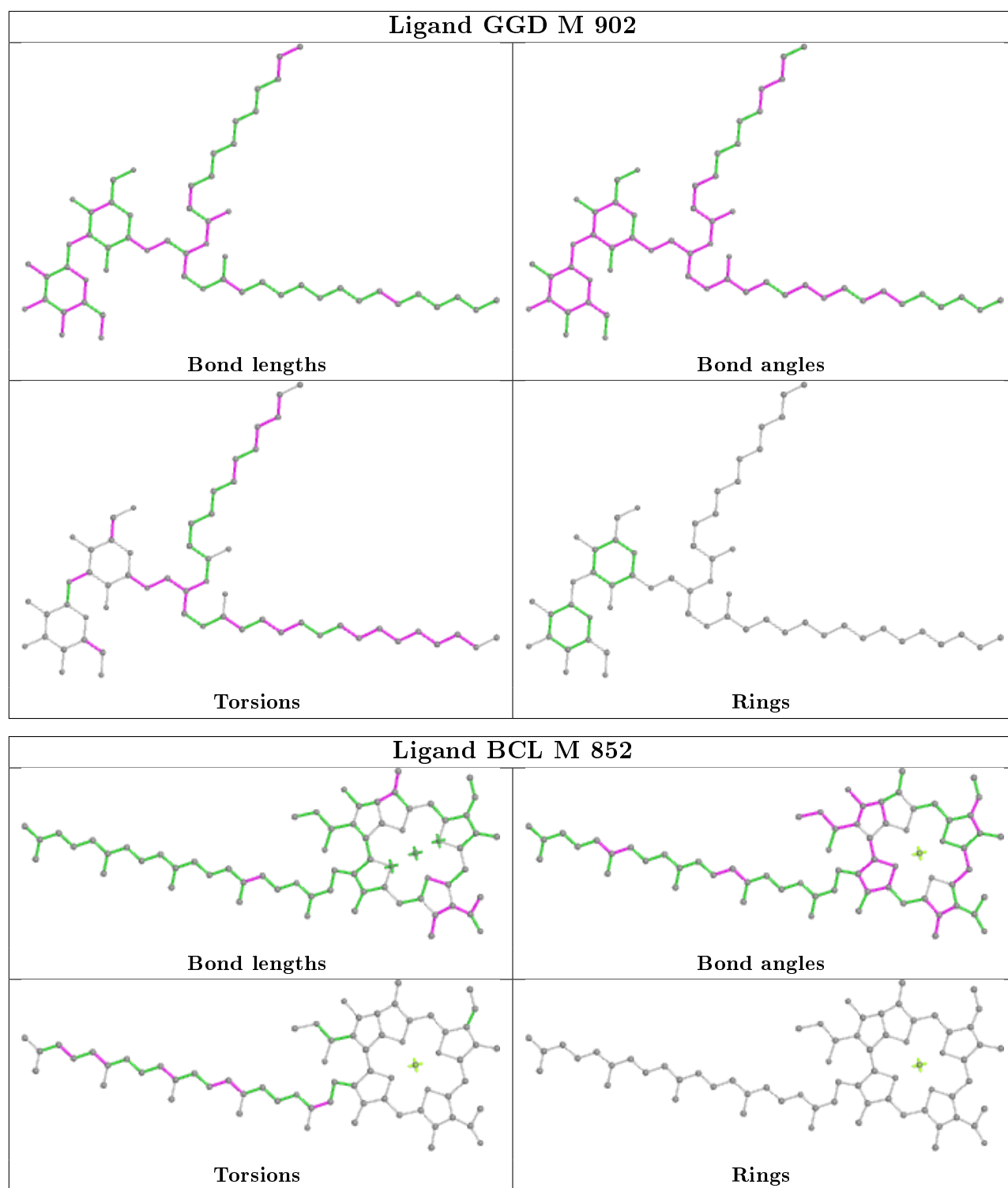
Bond angles



Torsions



Rings



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [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%)	-0.51	10 (3%) 42 49	15, 29, 64, 80	0
2	M	302/307 (98%)	-0.36	8 (2%) 56 62	13, 34, 67, 79	0
3	H	238/260 (91%)	-0.50	4 (1%) 70 76	20, 33, 53, 80	0
All	All	821/848 (96%)	-0.45	22 (2%) 54 61	13, 32, 64, 80	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	18	TYR	5.0
1	L	281	GLY	4.9
2	M	1	ALA	4.7
2	M	302	GLY	4.7
1	L	59	TRP	4.4

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](#)

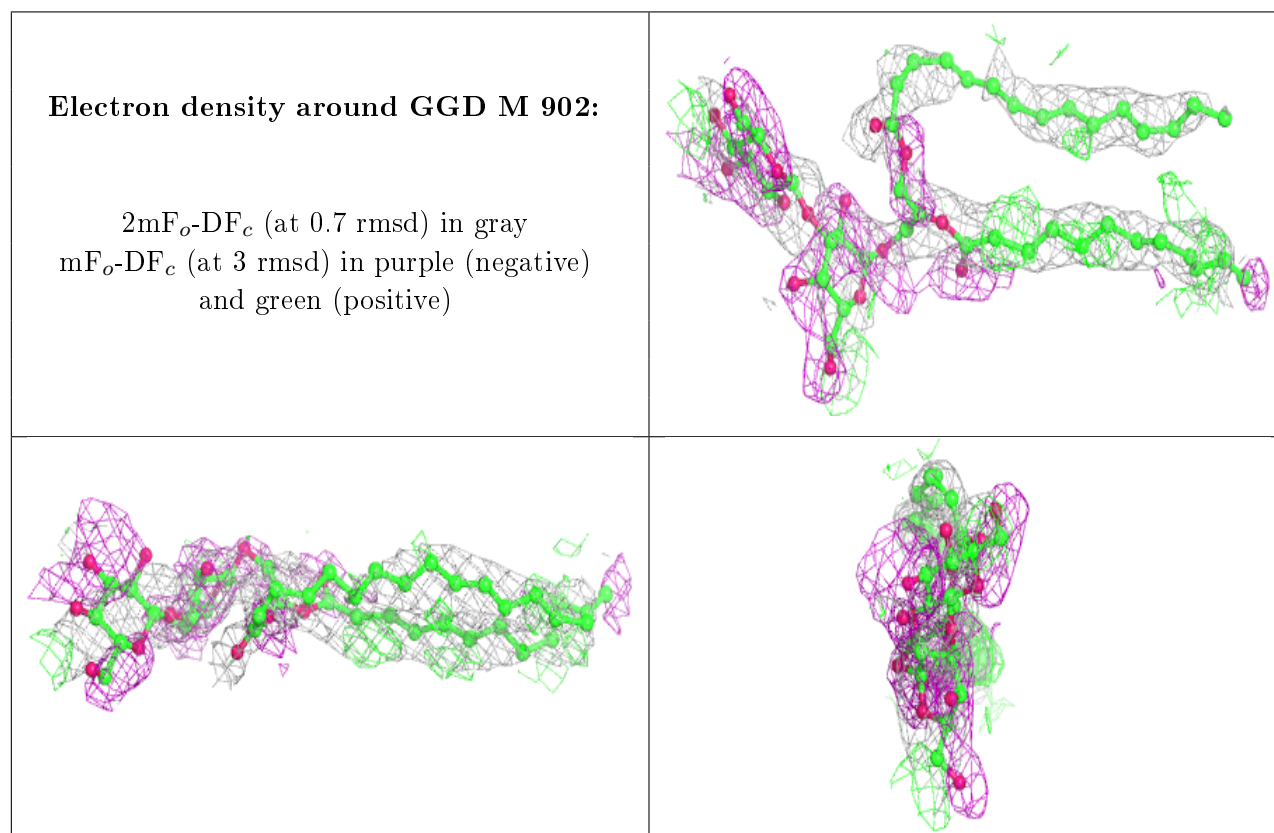
There are no carbohydrates in this entry.

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.

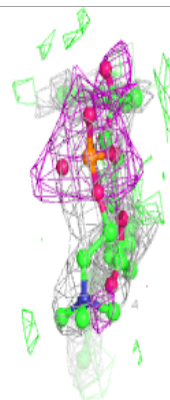
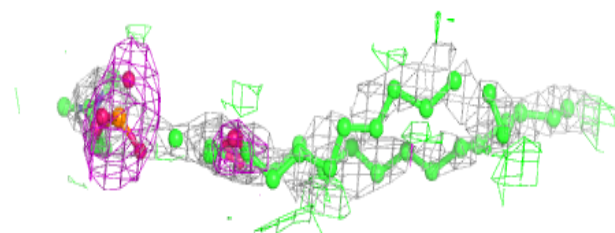
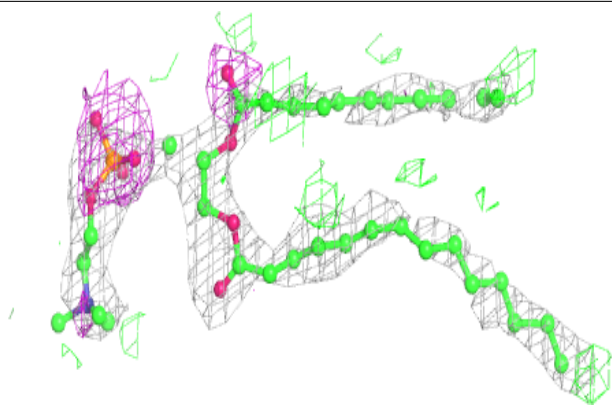
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
12	GGD	M	902	57/67	0.66	0.36	66,79,80,80	0
7	PC1	L	901	43/54	0.77	0.43	65,79,80,80	0
6	U10	L	858	13/63	0.78	0.46	55,56,57,59	13
10	SPO	M	859	42/42	0.84	0.24	34,47,65,68	0
5	BPH	M	854	65/65	0.88	0.21	30,35,80,80	0
9	CL	M	2000	1/1	0.88	0.26	80,80,80,80	0
11	CDL	M	900	81/100	0.89	0.19	55,67,78,80	0
6	U10	M	857	48/63	0.90	0.23	27,39,67,68	0
4	BCL	L	853	66/66	0.94	0.19	11,17,52,59	0
4	BCL	L	850	52/66	0.94	0.18	23,28,54,56	0
4	BCL	L	851	66/66	0.95	0.17	16,23,36,44	0
5	BPH	L	855	65/65	0.95	0.17	18,23,33,43	0
4	BCL	M	852	66/66	0.95	0.17	19,24,56,69	0
8	FE	M	856	1/1	1.00	0.06	18,18,18,18	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.



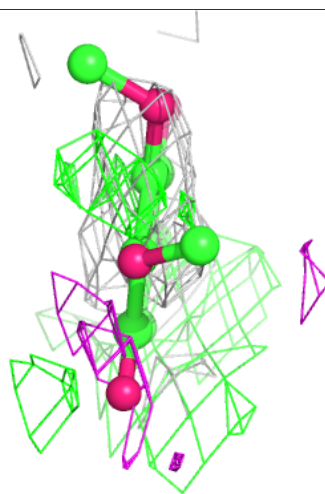
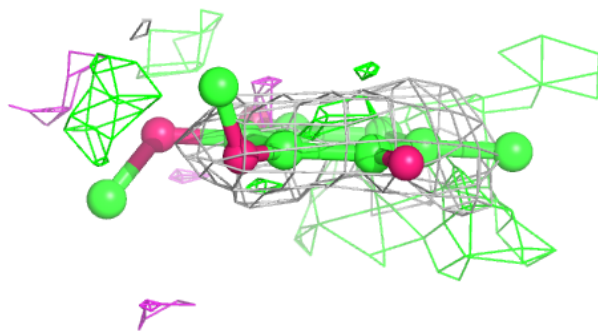
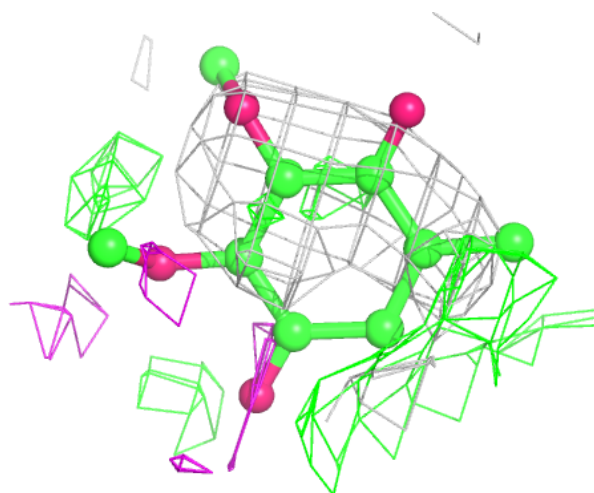
Electron density around PC1 L 901:

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



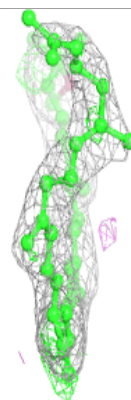
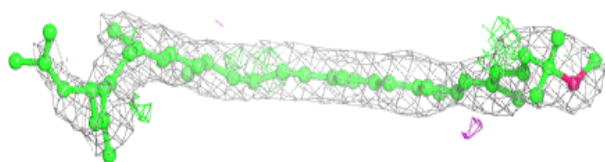
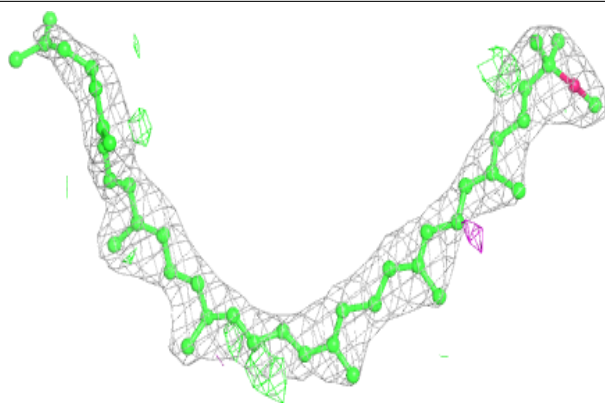
Electron density around U10 L 858:

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

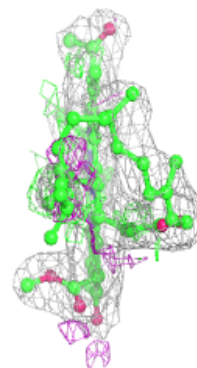
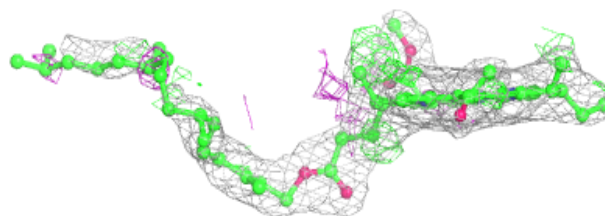
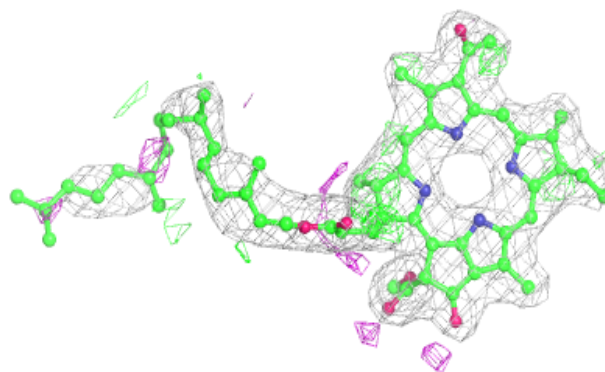


Electron density around SPO M 859:

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

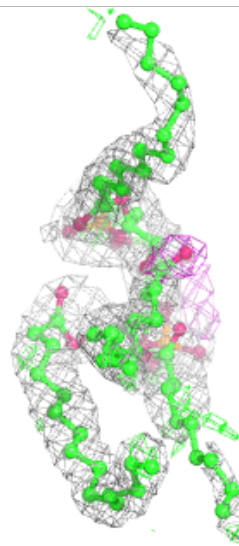
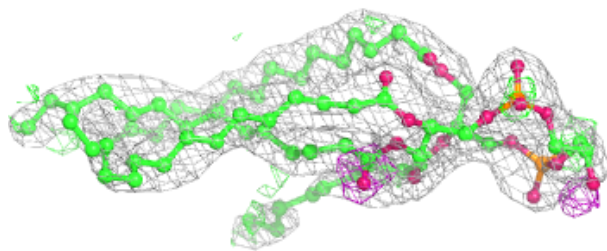
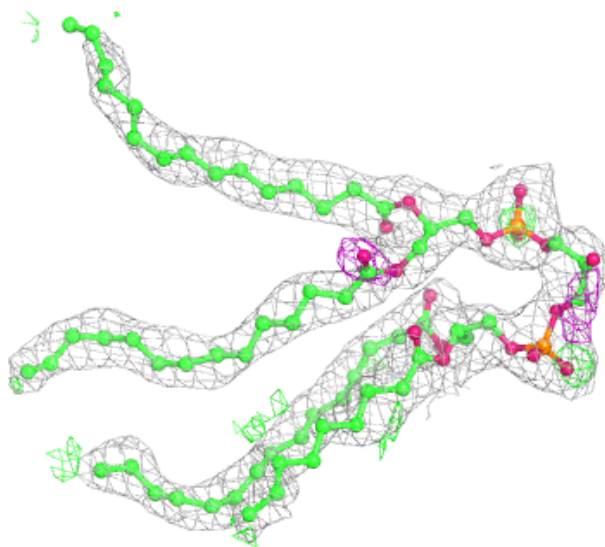
**Electron density around BPH M 854:**

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



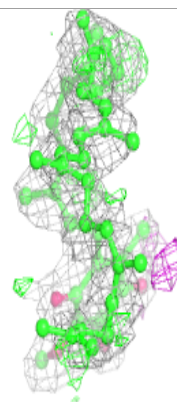
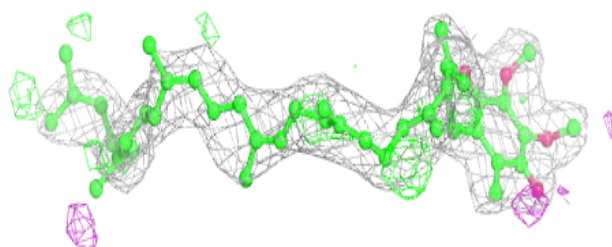
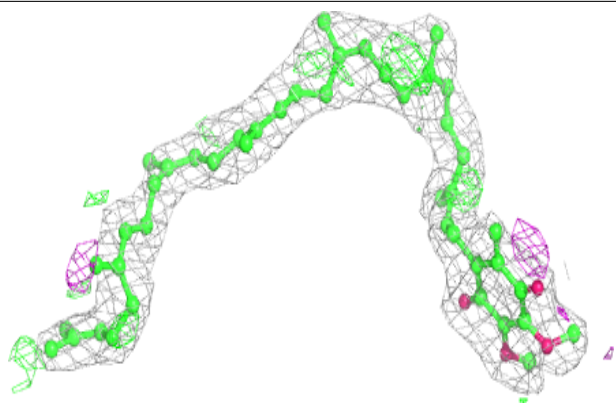
Electron density around CDL M 900:

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



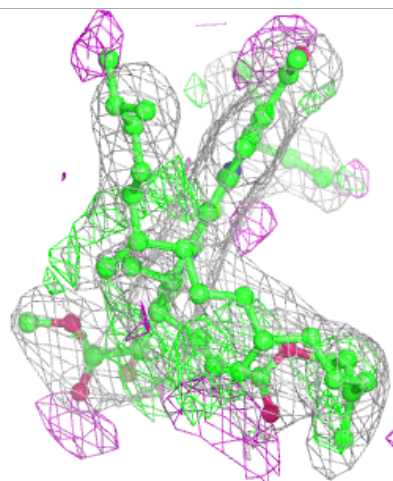
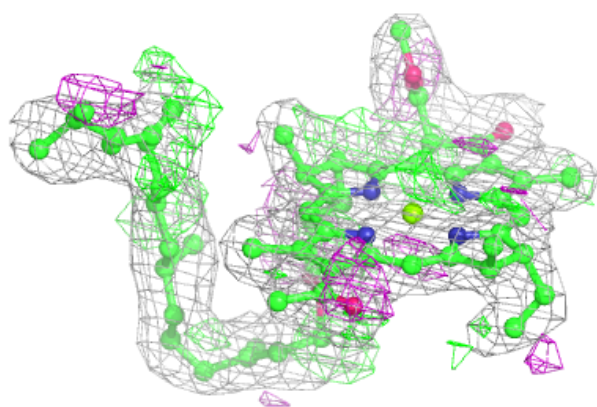
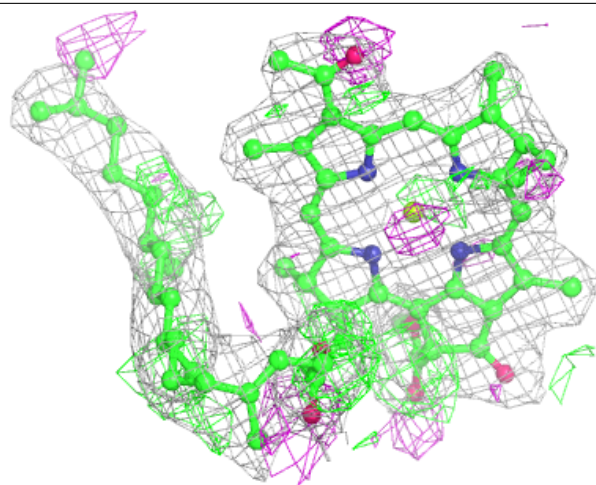
Electron density around U10 M 857:

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



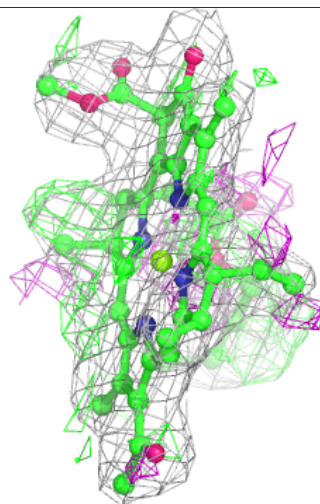
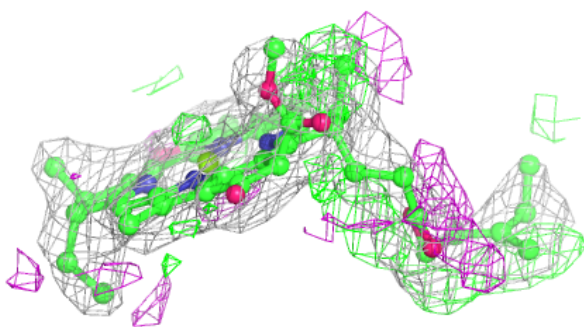
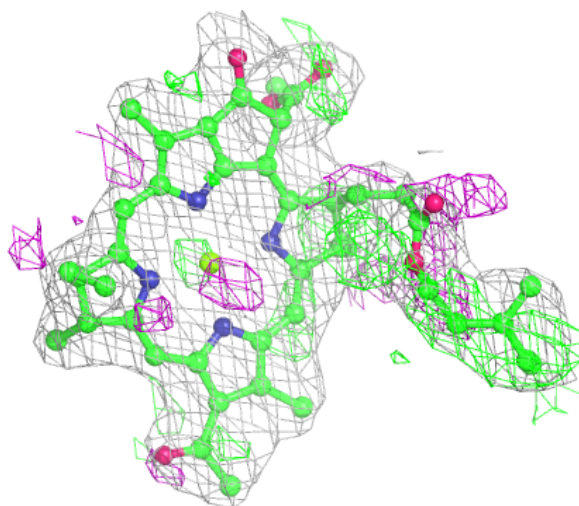
Electron density around BCL L 853:

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



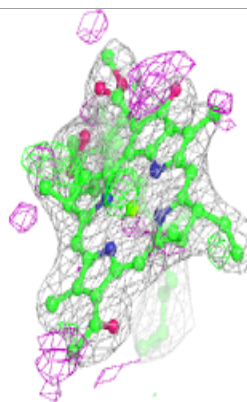
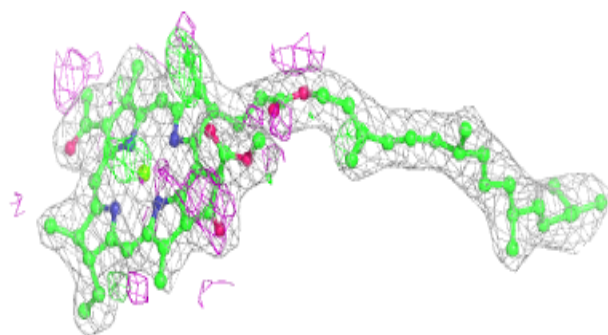
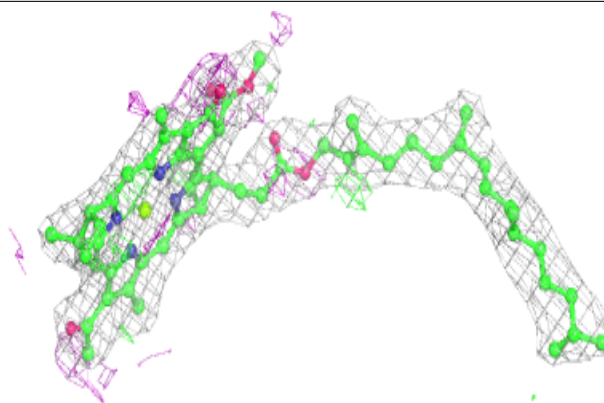
Electron density around BCL L 850:

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

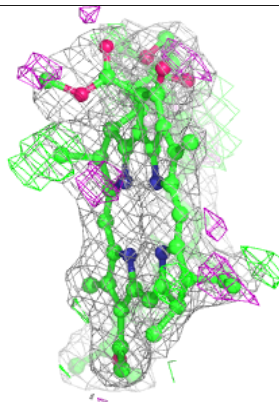
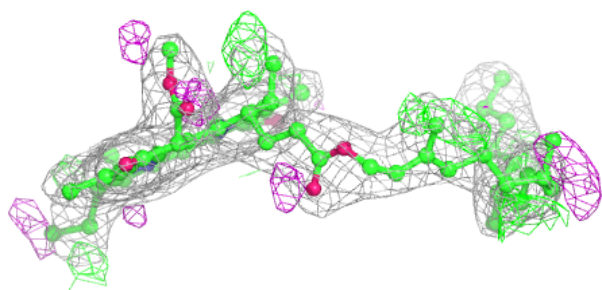
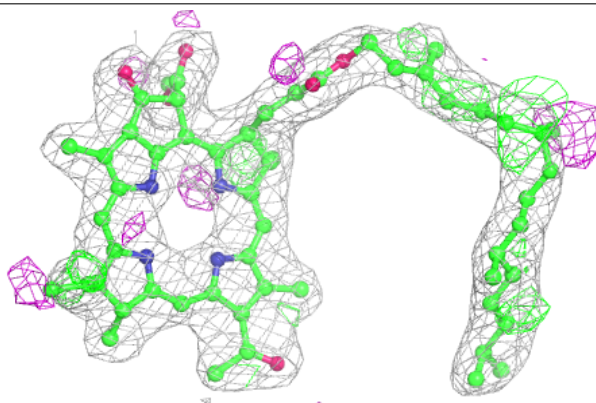


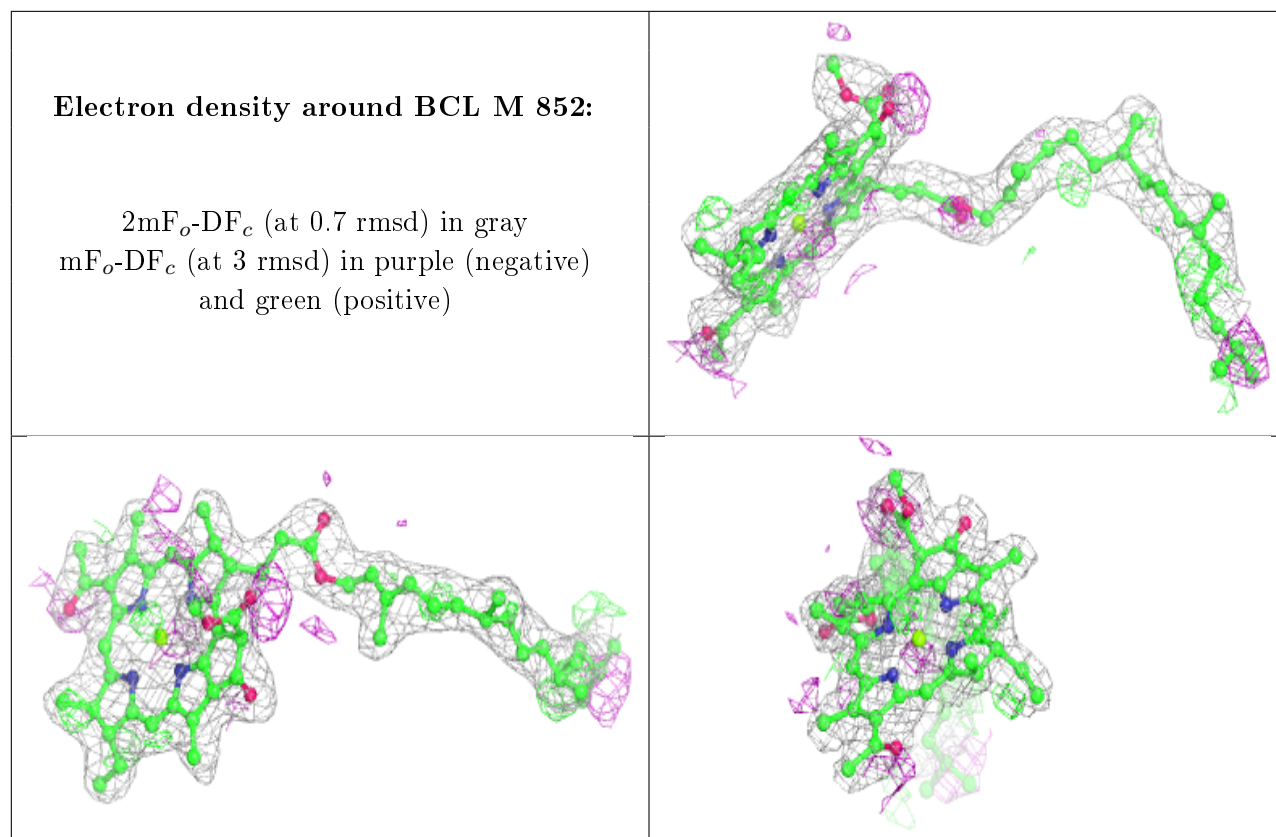
Electron density around BCL L 851:

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

**Electron density around BPH L 855:**

$2mF_o-DF_c$ (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.