wwPDB X-ray Structure Validation Summary Report (i)

Aug 4, 2026 – 11:50 AM EDT

PDB ID	:	1RY5 / pdb_00001ry5
Title	:	PHOTOSYNTHETIC REACTION CENTER MUTANT FROM RHODOBACTER SPHAEROIDES WITH ASP L213 REPLACED WITH ASN
Authors	:	Xu, Q.; Axelrod, H.L.; Abresch, E.C.; Paddock, M.L.; Okamura, M.Y.; Feher, G.
Deposited on	:	2003-12-19
Resolution	:	2.10 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 (i) 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 (i)) were used in the production of this report:

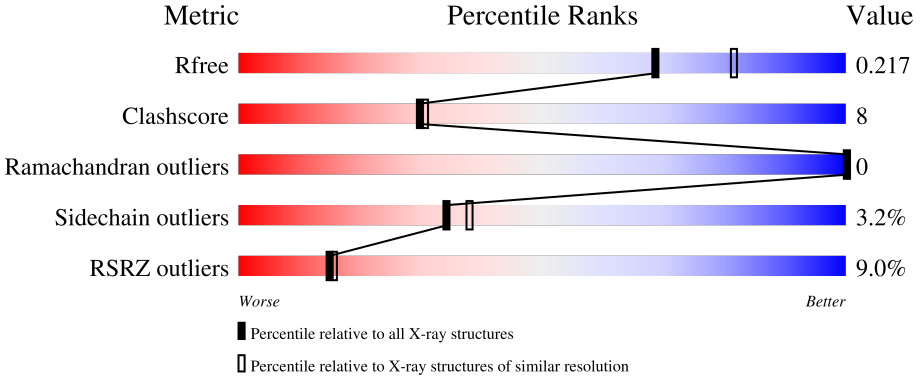
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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 <=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	11% 83% 15% •
2	M	307	9% 79% 19% • •
3	H	260	6% 72% 18% • 8%

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
5	BPH	L	856	X	-	-	-
7	GOL	L	866	-	X	-	-

2 Entry composition (i)

There are 14 unique types of molecules in this entry. The entry contains 7504 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Reaction center protein L chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	281	2232	1507	356	361	8	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	213	ASN	ASP	engineered mutation	UNP P02954

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

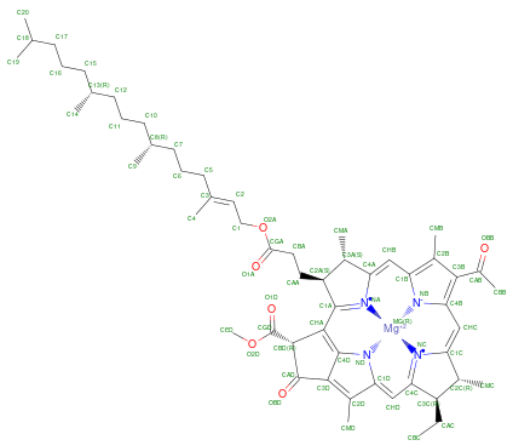
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	M	301	2404	1605	393	396	10	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	239	1832	1171	314	338	9	0	1	0

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

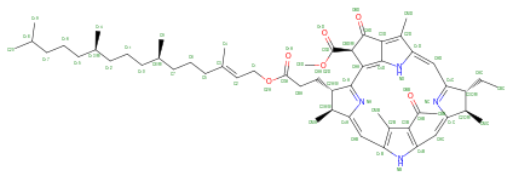
BCL



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Mg	N	O		
4	L	1	51	40	1	4	6	0	0
			Total	C	Mg	N	O		
4	L	1	66	55	1	4	6	0	0
			Total	C	Mg	N	O		
4	L	1	66	55	1	4	6	0	0
			Total	C	Mg	N	O		
4	M	1	66	55	1	4	6	0	0

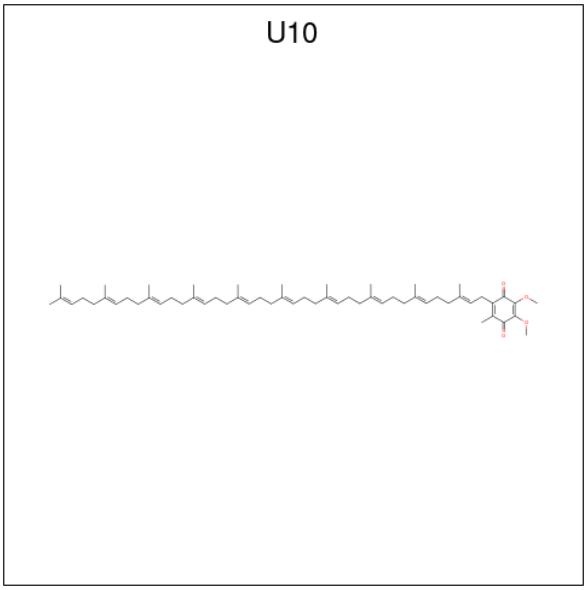
- Molecule 5 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$).

BPH



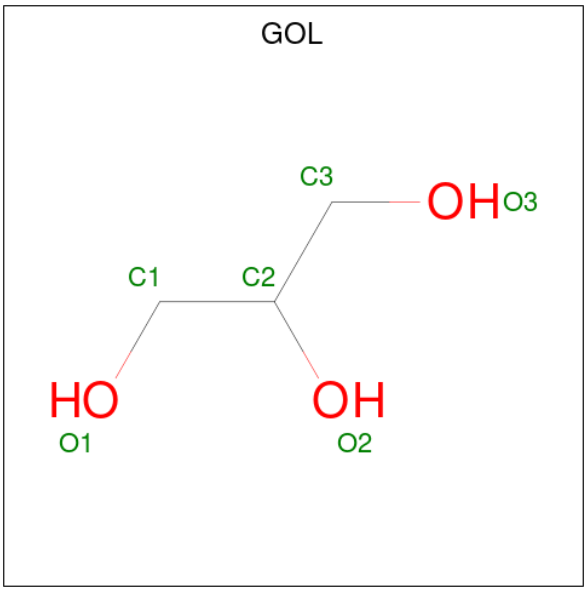
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	L	1	65	55	4	6	0	0
			Total	C	N	O		
5	M	1	51	41	4	6	0	0

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
6	L	1	24	20	4		0	0
			Total	C	O			
6	M	1	48	44	4		0	0

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).

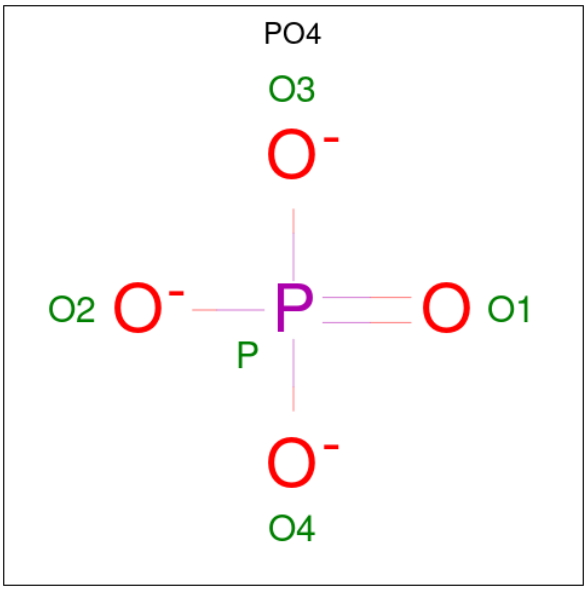


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	L	1	Total C O 6 3 3	0	0

- Molecule 8 is FE (II) ION (CCD ID: FE2) (formula: Fe).

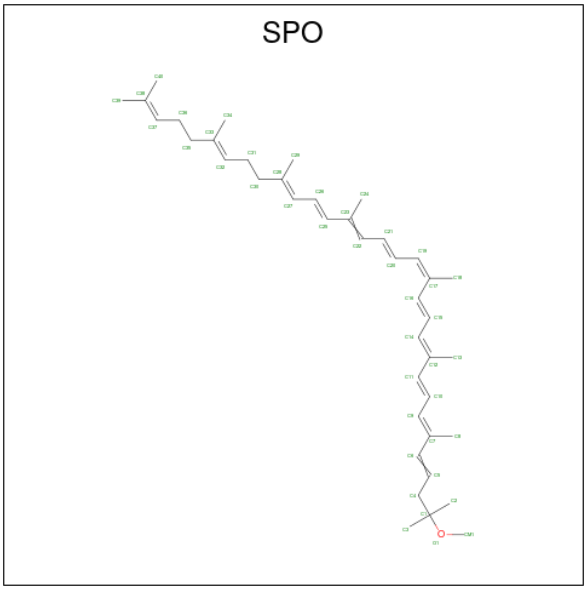
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	M	1	Total Fe 1 1	0	0

- Molecule 9 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



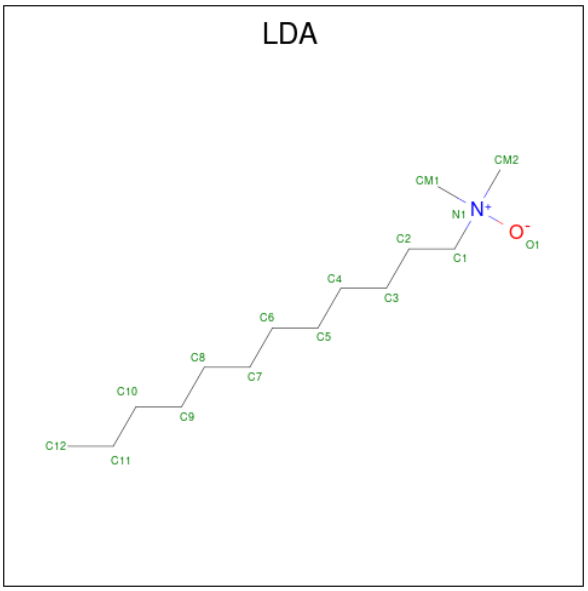
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
9	M	1	5	4	1	0	0
			Total	O	P		
9	M	1	5	4	1	0	0

- Molecule 10 is SPHEROIDENE (CCD ID: SPO) (formula: $C_{41}H_{60}O$).



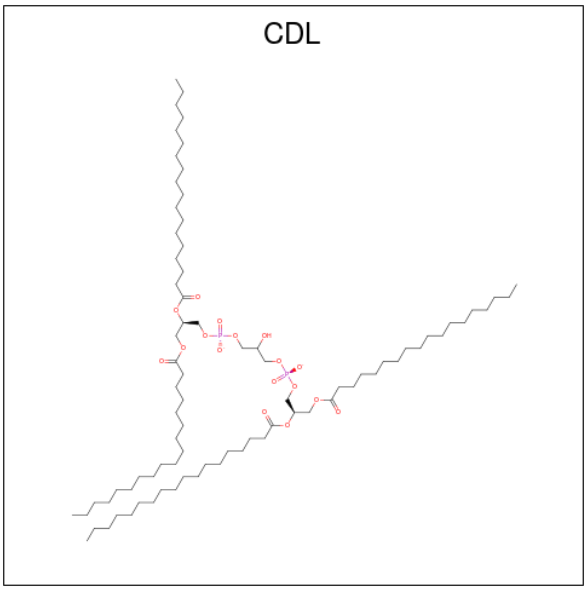
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
10	M	1	42	41	1	0	0

- Molecule 11 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: $C_{14}H_{31}NO$).



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

- Molecule 12 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



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

- Molecule 13 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	K		
13	H	1	1	1	0	0

- Molecule 14 is water.

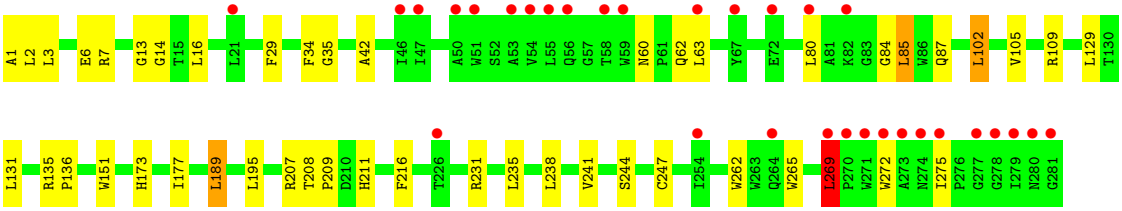
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
14	L	107	107	107	0	0
			Total	O		
14	M	130	130	130	0	1
			Total	O		
14	H	173	173	173	0	1

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.

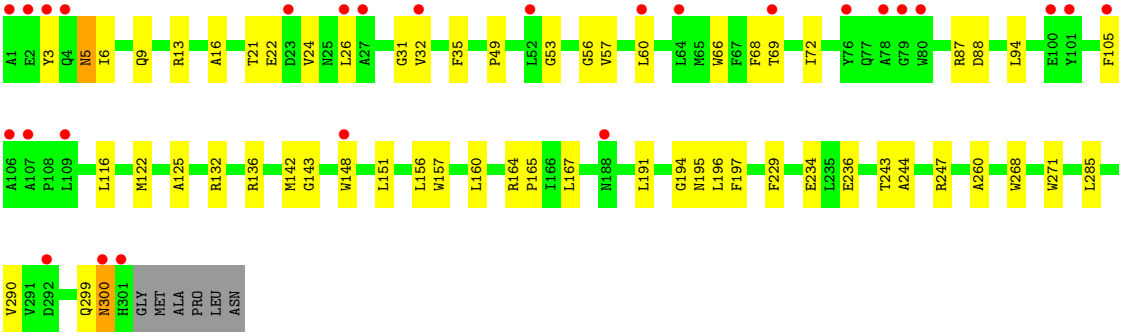
- Molecule 1: Reaction center protein L chain

Chain L:



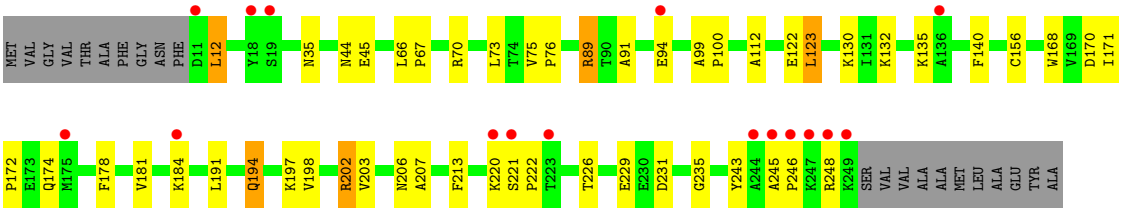
- Molecule 2: Reaction center protein M chain

Chain M:



- Molecule 3: Reaction center protein H chain

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	139.07Å 139.07Å 184.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.23 – 2.10 39.23 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.7 (39.23-2.10) 98.8 (39.23-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	3.03 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.211 , 0.226 0.203 , 0.217	Depositor DCC
R_{free} test set	6001 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	30.4	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 52.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7504	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.66% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: K, FE2, PO4, LDA, BPH, U10, BCL, CDL, GOL, SPO

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	L	0.41	0/2320	0.91	9/3175 (0.3%)
2	M	0.40	0/2496	0.88	5/3408 (0.1%)
3	H	0.39	0/1880	0.87	3/2557 (0.1%)
All	All	0.40	0/6696	0.89	17/9140 (0.2%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	6	GLU	N-CA-C	10.71	123.03	111.36
1	L	13	GLY	N-CA-C	6.98	118.58	111.95
2	M	234	GLU	N-CA-C	6.65	118.53	111.28
1	L	3	LEU	N-CA-C	-6.25	102.28	110.53
1	L	7	ARG	N-CA-C	6.23	118.87	111.33

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	2189	29	0
2	M	2404	0	2318	49	0
3	H	1832	0	1836	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	183	0	189	13	0
4	M	66	0	74	4	0
5	L	65	0	74	6	0
5	M	51	0	45	2	0
6	L	24	0	25	1	0
6	M	48	0	62	0	0
7	L	6	0	4	0	0
8	M	1	0	0	0	0
9	M	10	0	0	0	0
10	M	42	0	60	0	0
11	H	16	0	31	0	0
11	M	32	0	62	0	0
12	M	81	0	106	1	0
13	H	1	0	0	0	0
14	H	173	0	0	3	0
14	L	107	0	0	1	0
14	M	130	0	0	2	0
All	All	7504	0	7075	120	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 8.

The worst 5 of 120 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:L:241:VAL:HG21	5:L:856:BPH:HAC2	1.35	1.03
2:M:157:TRP:HB2	4:M:853:BCL:H62	1.54	0.90
2:M:236:GLU:HG3	3:H:122:GLU:CD	1.98	0.89
2:M:21:THR:HG23	2:M:26:LEU:HD11	1.65	0.78
2:M:13:ARG:HD2	2:M:35:PHE:CD2	2.23	0.74

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%)	270 (97%)	9 (3%)	0	100	100
2	M	299/307 (97%)	292 (98%)	7 (2%)	0	100	100
3	H	238/260 (92%)	234 (98%)	4 (2%)	0	100	100
All	All	816/848 (96%)	796 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	L	220/220 (100%)	213 (97%)	7 (3%)	34	38
2	M	236/240 (98%)	229 (97%)	7 (3%)	36	41
3	H	195/208 (94%)	188 (96%)	7 (4%)	31	34
All	All	651/668 (98%)	630 (97%)	21 (3%)	34	38

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	12	LEU
3	H	123	LEU
3	H	231	ASP
3	H	194	GLN
3	H	89	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	M	138	GLN
2	M	195	ASN
3	H	206	ASN

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Mol	Chain	Res	Type
3	H	68	HIS
3	H	194	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 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	$\#\|Z\| > 2$
10	SPO	M	860	-	41,41,41	3.19	22 (53%)	47,50,50	2.39	17 (36%)
11	LDA	H	861	-	13,15,15	1.93	1 (7%)	14,17,17	1.75	4 (28%)
9	PO4	M	864	-	4,4,4	1.71	0	6,6,6	0.46	0
4	BCL	L	851	2	54,59,74	1.88	15 (27%)	61,97,115	2.10	17 (27%)
6	U10	L	859	-	24,24,63	2.14	8 (33%)	30,32,79	2.08	10 (33%)
7	GOL	L	866	-	5,5,5	4.78	5 (100%)	5,5,5	6.07	3 (60%)
11	LDA	M	862	-	13,15,15	1.94	1 (7%)	14,17,17	1.72	4 (28%)
6	U10	M	858	-	48,48,63	2.03	16 (33%)	60,61,79	2.76	13 (21%)
5	BPH	L	856	-	59,70,70	2.17	14 (23%)	59,101,101	2.73	20 (33%)
5	BPH	M	855	-	45,56,70	2.36	14 (31%)	41,84,101	3.18	19 (46%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	BCL	L	852	1	69,74,74	1.75	11 (15%)	79,115,115	1.79	20 (25%)
11	LDA	M	863	-	13,15,15	1.97	1 (7%)	14,17,17	1.69	4 (28%)
12	CDL	M	900	-	80,80,99	0.82	2 (2%)	86,92,111	0.97	4 (4%)
4	BCL	M	853	2	69,74,74	1.74	10 (14%)	79,115,115	1.96	20 (25%)
9	PO4	M	865	-	4,4,4	1.74	1 (25%)	6,6,6	0.46	0
4	BCL	L	854	1	69,74,74	1.84	14 (20%)	79,115,115	1.76	17 (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
10	SPO	M	860	-	-	12/47/47/47	-
11	LDA	H	861	-	-	5/13/13/13	-
4	BCL	L	851	2	-	0/23/119/137	-
6	U10	L	859	-	-	4/17/41/87	0/1/1/1
7	GOL	L	866	-	-	3/4/4/4	-
11	LDA	M	862	-	-	6/13/13/13	-
6	U10	M	858	-	-	5/45/69/87	0/1/1/1
5	BPH	L	856	-	2/2/18/22	10/37/105/105	0/5/6/6
5	BPH	M	855	-	-	3/21/89/105	0/5/6/6
4	BCL	L	852	1	-	3/41/137/137	-
11	LDA	M	863	-	-	7/13/13/13	-
12	CDL	M	900	-	-	26/91/91/110	-
4	BCL	M	853	2	-	11/41/137/137	-
4	BCL	L	854	1	-	13/41/137/137	-

The worst 5 of 135 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	860	SPO	C6-C5	8.53	1.55	1.32
10	M	860	SPO	C10-C11	8.11	1.55	1.34
7	L	866	GOL	C3-C2	-8.05	1.21	1.51
10	M	860	SPO	C15-C16	7.66	1.54	1.34
5	M	855	BPH	C2C-C3C	-7.15	1.48	1.54

The worst 5 of 172 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	M	858	U10	C32-C33-C34	15.75	163.67	127.62
5	M	855	BPH	O2D-CGD-CBD	13.52	125.80	110.95
5	L	856	BPH	O2D-CGD-CBD	12.97	125.20	110.95
7	L	866	GOL	O3-C3-C2	10.92	159.56	110.38
7	L	866	GOL	O2-C2-C3	7.24	139.13	109.18

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	L	856	BPH	C13
5	L	856	BPH	C8

5 of 108 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	854	BCL	C2C-C3C-CAC-CBC
4	L	854	BCL	CHA-CBD-CGD-O1D
4	L	854	BCL	CHA-CBD-CGD-O2D
5	L	856	BPH	C2C-C3C-CAC-CBC
5	M	855	BPH	O2A-C1-C2-C3

There are no ring outliers.

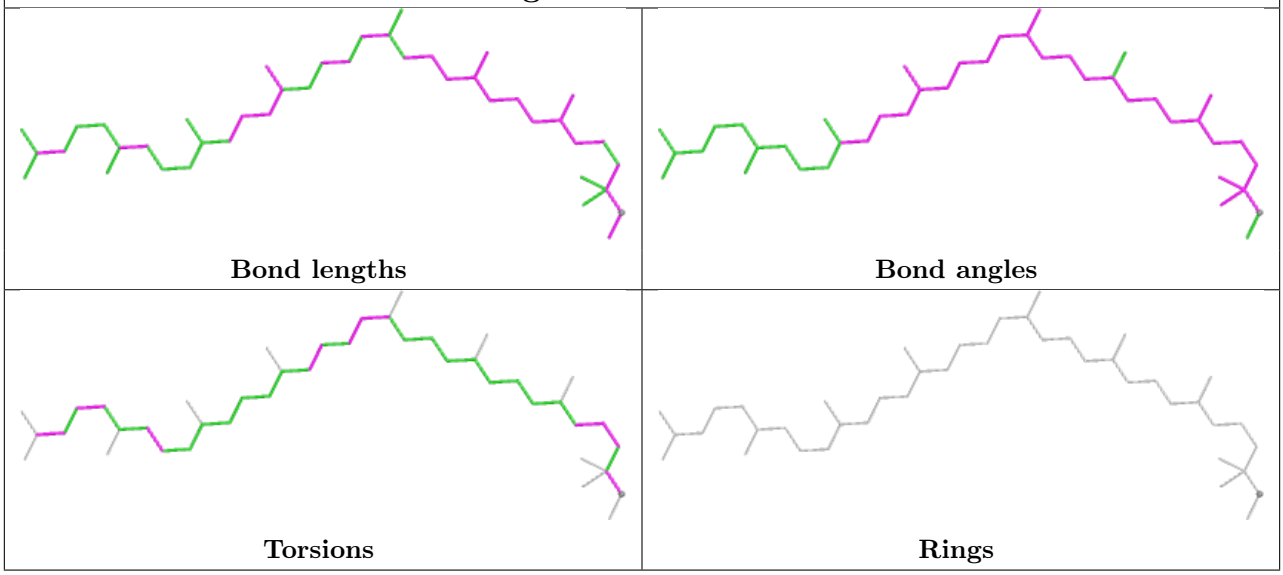
8 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	851	BCL	4	0
6	L	859	U10	1	0
5	L	856	BPH	6	0
5	M	855	BPH	2	0
4	L	852	BCL	4	0
12	M	900	CDL	1	0
4	M	853	BCL	4	0
4	L	854	BCL	8	0

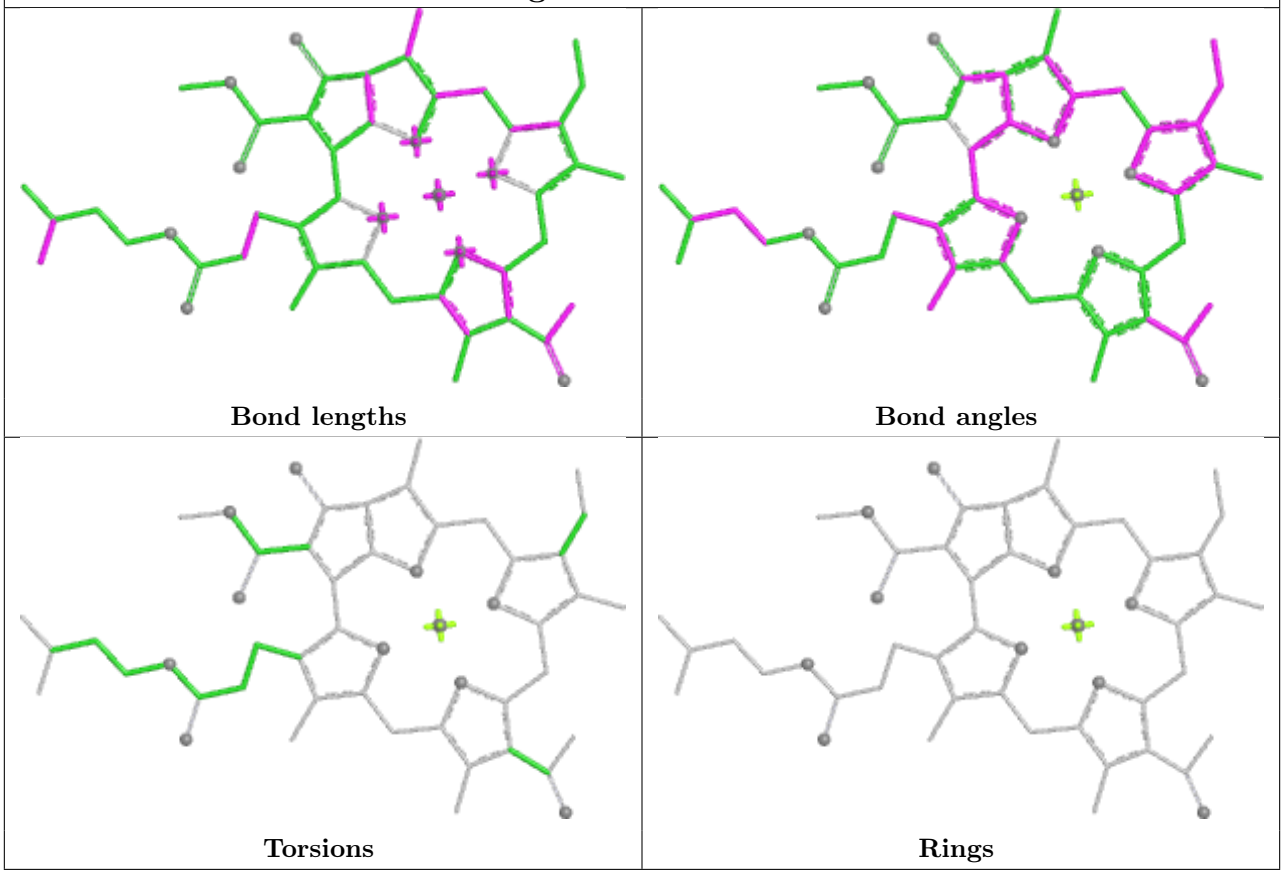
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

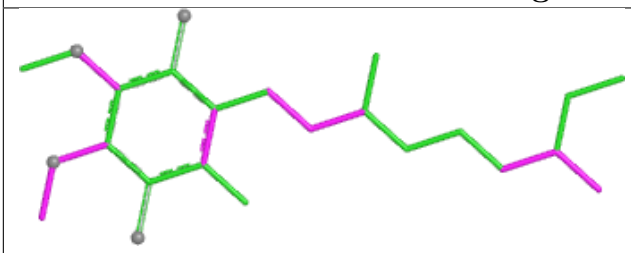
Ligand SPO M 860



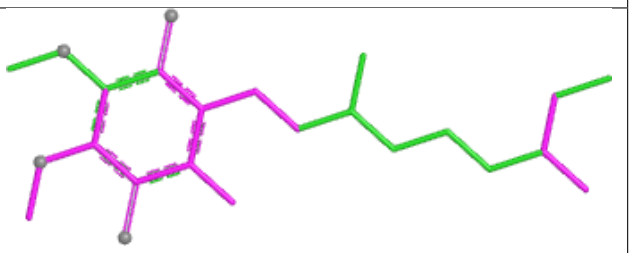
Ligand BCL L 851



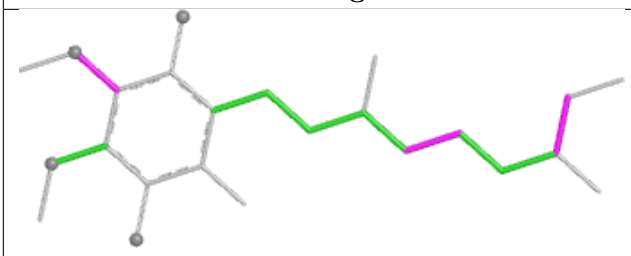
Ligand U10 L 859



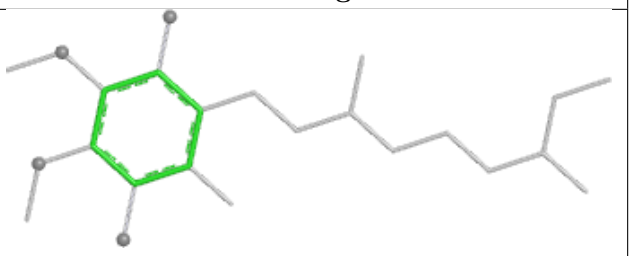
Bond lengths



Bond angles

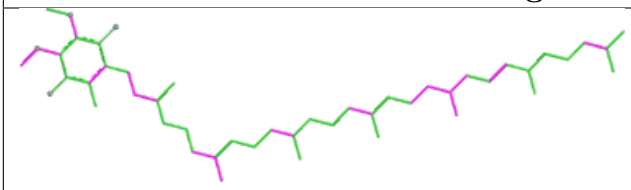


Torsions

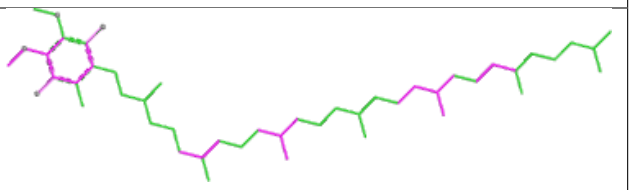


Rings

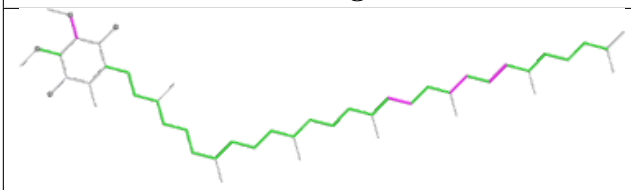
Ligand U10 M 858



Bond lengths



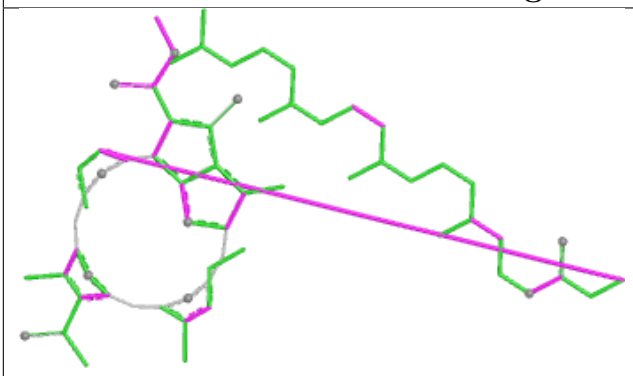
Bond angles



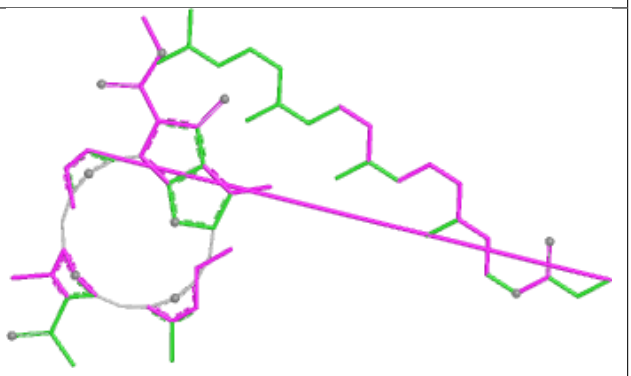
Torsions

Rings

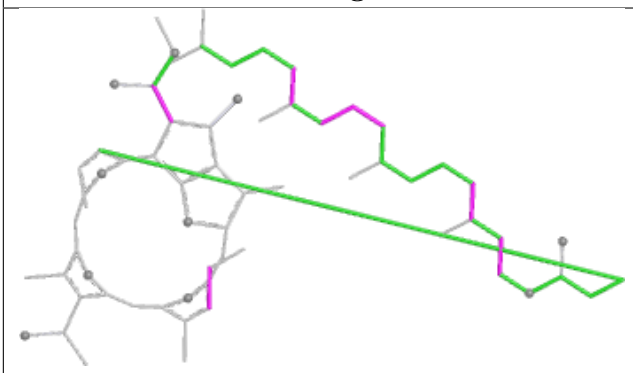
Ligand BPH L 856



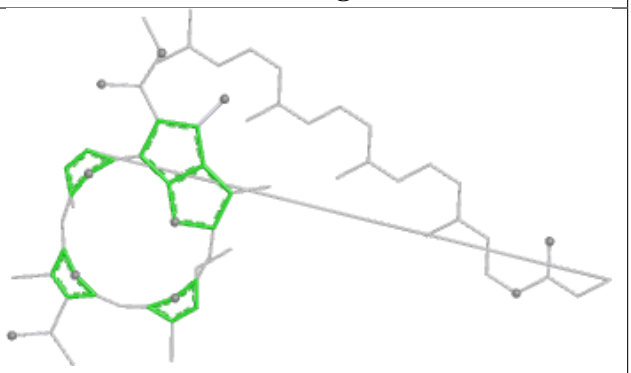
Bond lengths



Bond angles

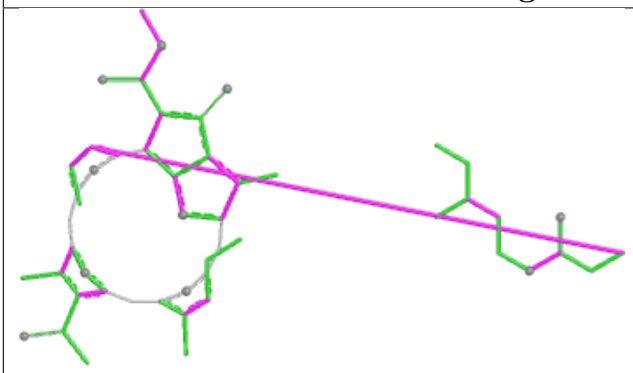


Torsions

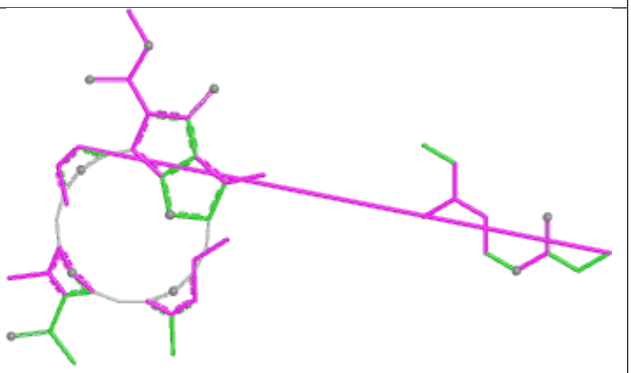


Rings

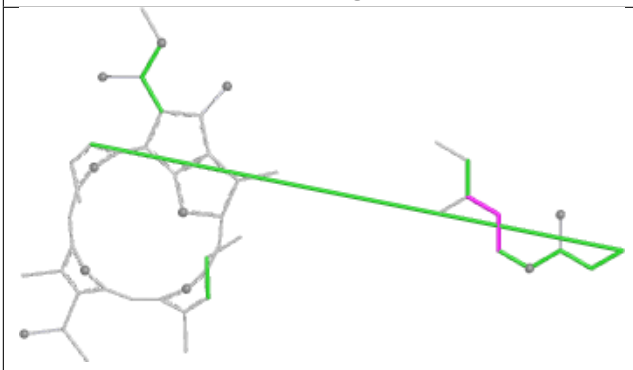
Ligand BPH M 855



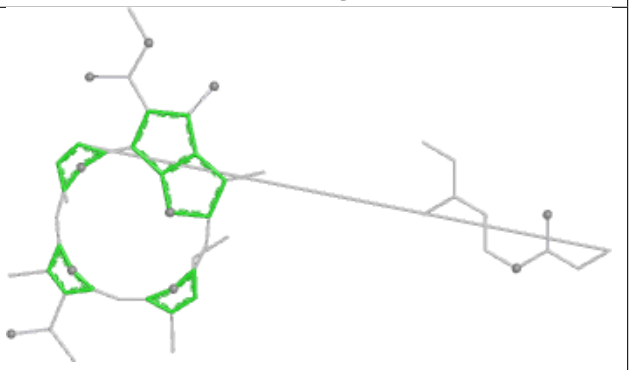
Bond lengths



Bond angles

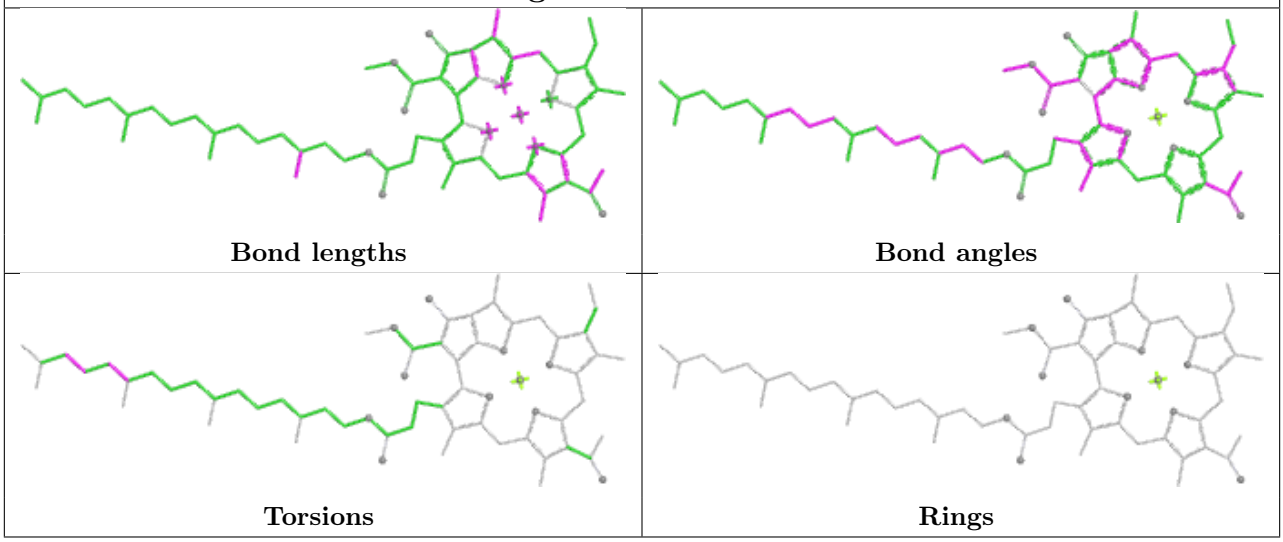


Torsions

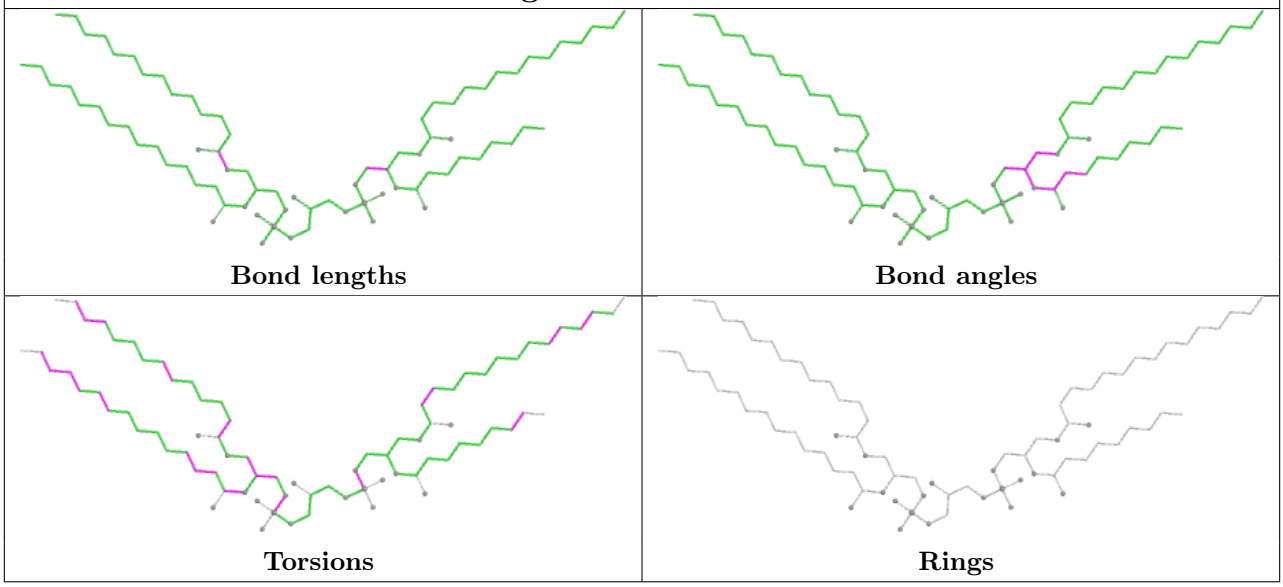


Rings

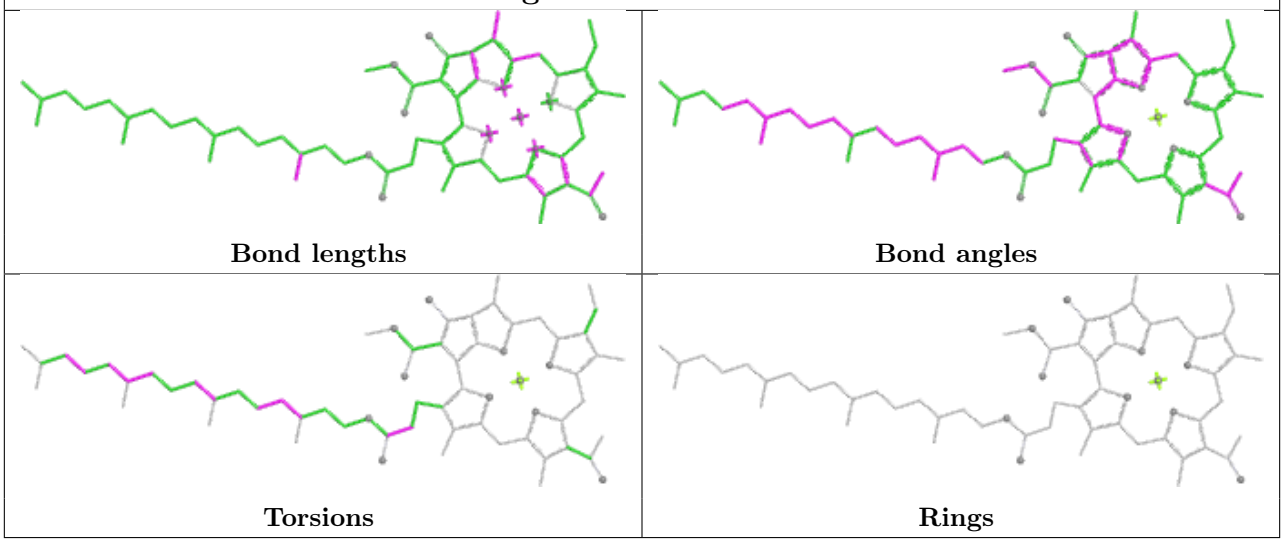
Ligand BCL L 852

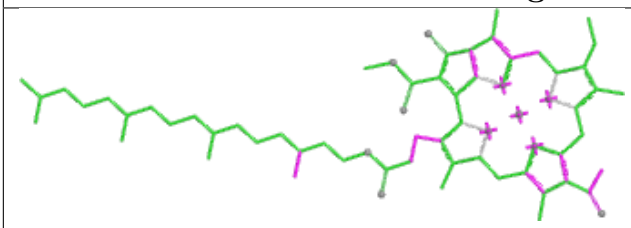
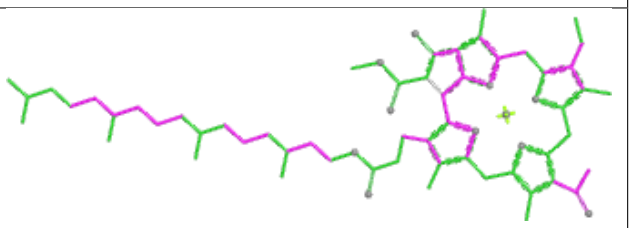
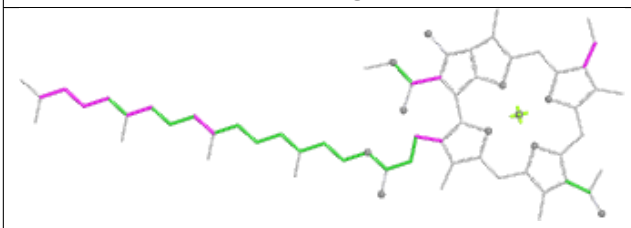
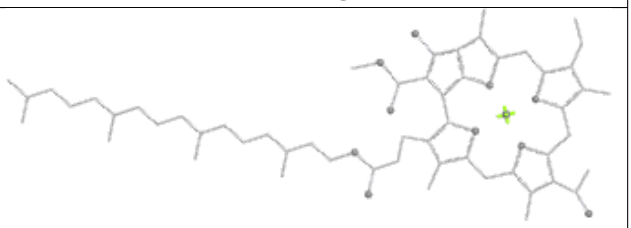


Ligand CDL M 900



Ligand BCL M 853



Ligand BCL L 854	
 Bond lengths	 Bond angles
 Torsions	 Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	L	281/281 (100%)	0.60	31 (11%)	10	11	22, 31, 55, 82	0
2	M	301/307 (98%)	0.60	27 (8%)	15	16	21, 35, 57, 78	0
3	H	239/260 (91%)	0.56	16 (6%)	24	25	21, 35, 49, 84	1 (0%)
All	All	821/848 (96%)	0.59	74 (9%)	15	16	21, 34, 54, 84	1 (0%)

The worst 5 of 74 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	M	1	ALA	8.3
2	M	3	TYR	8.1
1	L	279	ILE	6.5
2	M	301	HIS	5.9
2	M	2	GLU	5.4

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 oligosaccharides in this entry.

6.4 Ligands (i)

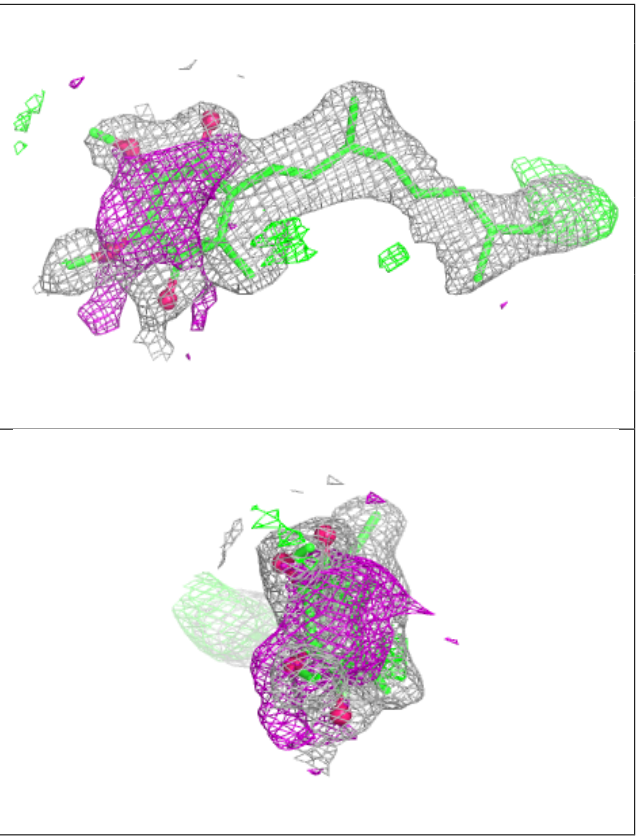
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	U10	L	859	24/63	0.75	0.27	43,53,58,58	0
11	LDA	M	863	16/16	0.78	0.31	67,72,73,73	0
11	LDA	M	862	16/16	0.79	0.32	74,75,82,82	0
12	CDL	M	900	81/100	0.83	0.27	61,75,84,86	0
7	GOL	L	866	6/6	0.85	0.17	47,52,53,54	0
11	LDA	H	861	16/16	0.86	0.27	63,65,68,69	0
10	SPO	M	860	42/42	0.86	0.21	34,46,62,64	0
9	PO4	M	864	5/5	0.87	0.11	67,68,68,69	0
9	PO4	M	865	5/5	0.88	0.12	70,71,71,71	0
4	BCL	L	854	66/66	0.90	0.15	22,29,54,57	0
4	BCL	L	851	51/66	0.91	0.14	24,29,55,57	0
6	U10	M	858	48/63	0.91	0.18	25,41,69,69	0
4	BCL	M	853	66/66	0.92	0.14	19,26,56,62	0
5	BPH	M	855	51/65	0.92	0.12	28,33,56,59	0
5	BPH	L	856	65/65	0.93	0.12	22,26,50,51	0
4	BCL	L	852	66/66	0.94	0.10	21,26,41,47	0
13	K	H	867	1/1	0.97	0.06	36,36,36,36	0
8	FE2	M	857	1/1	0.99	0.02	21,21,21,21	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.

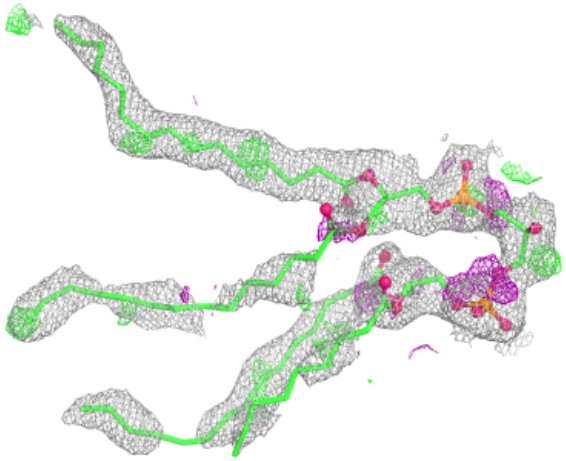
Electron density around U10 L 859:

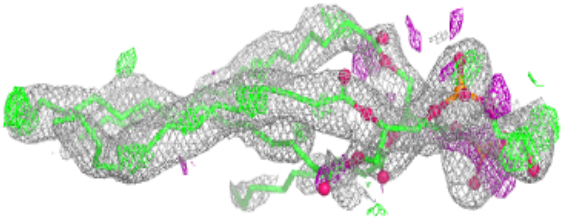
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

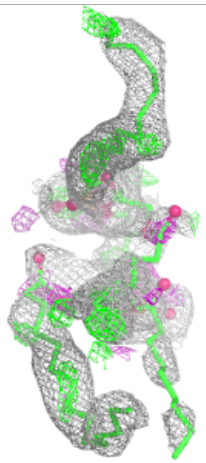


Electron density around CDL M 900:

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

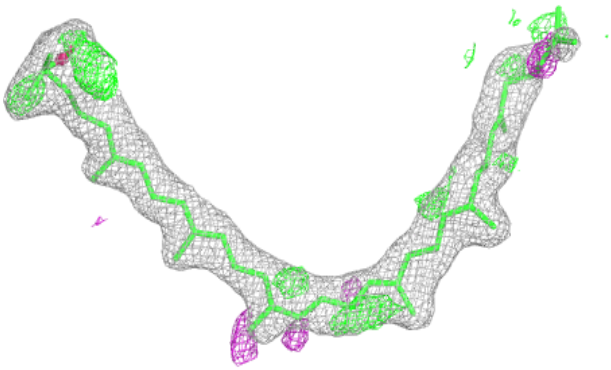


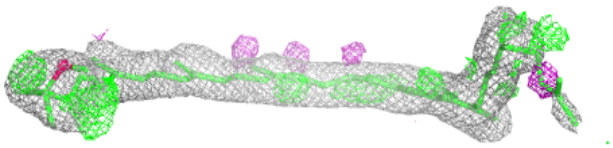


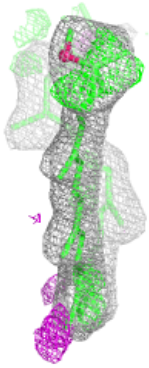


Electron density around SPO M 860:

$2mF_o$-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 854:

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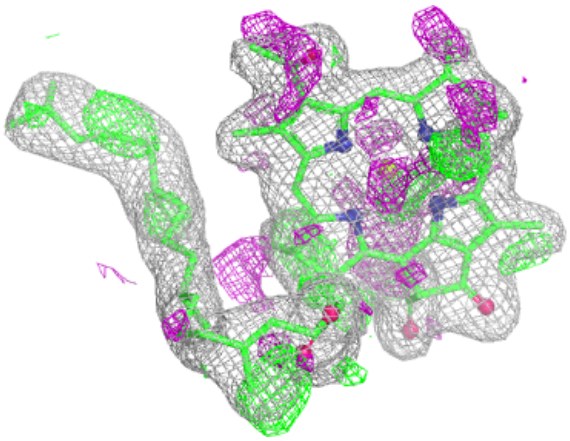
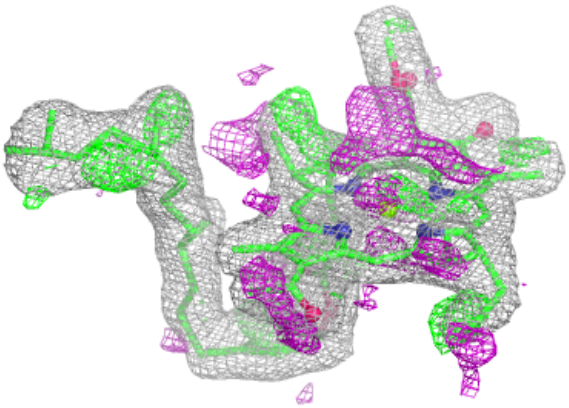
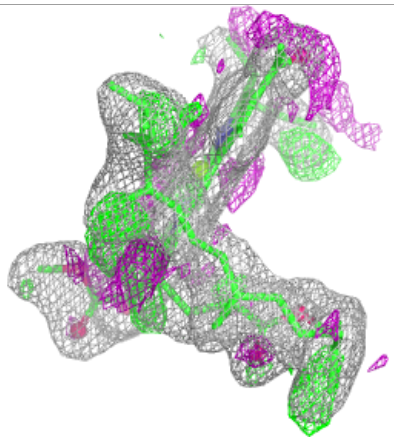
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

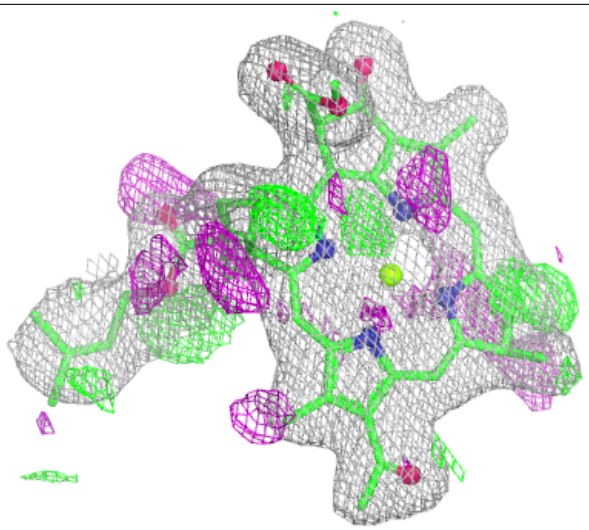


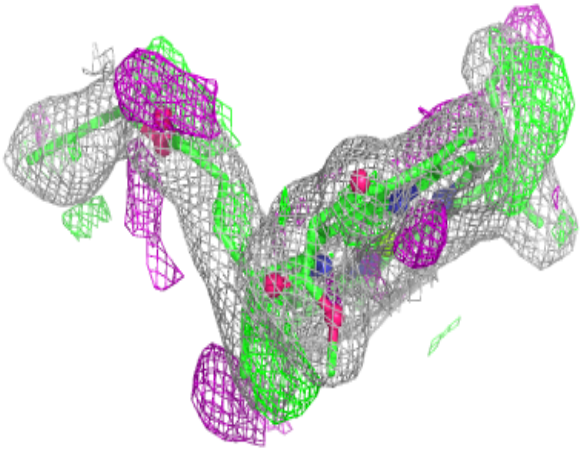


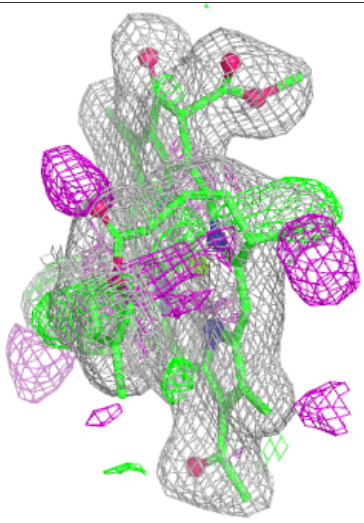


Electron density around BCL L 851:

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

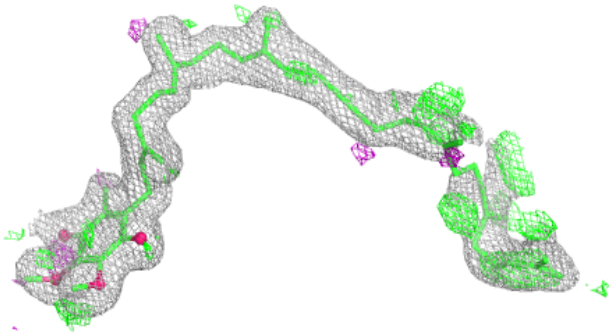


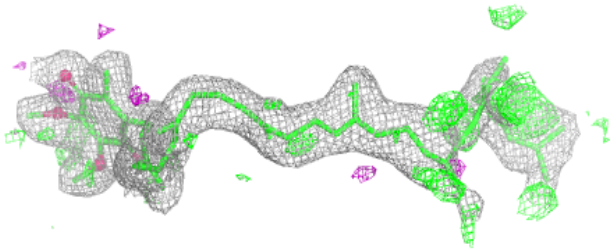


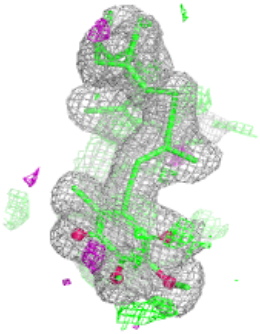


Electron density around U10 M 858:

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

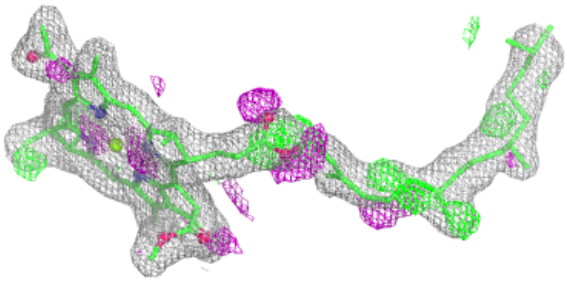


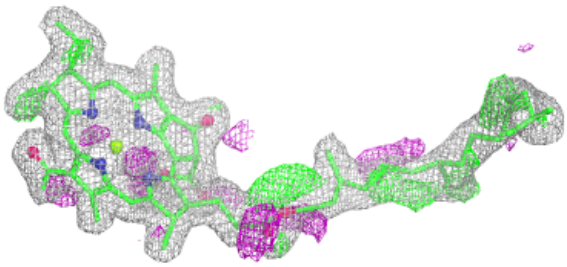


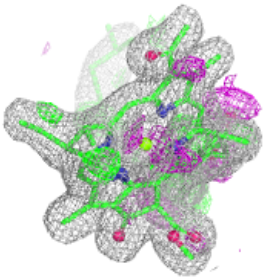


Electron density around BCL M 853:

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

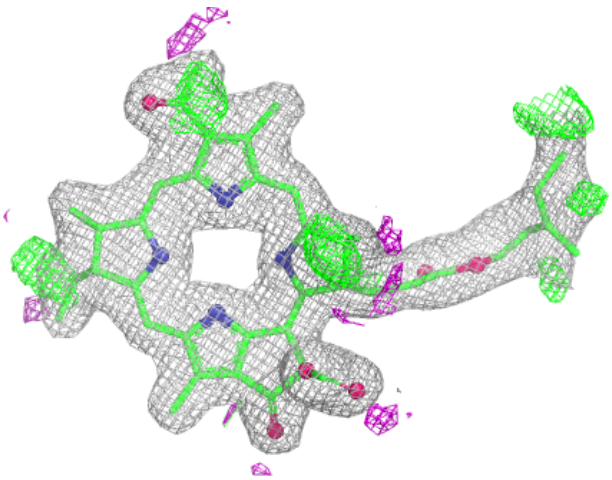


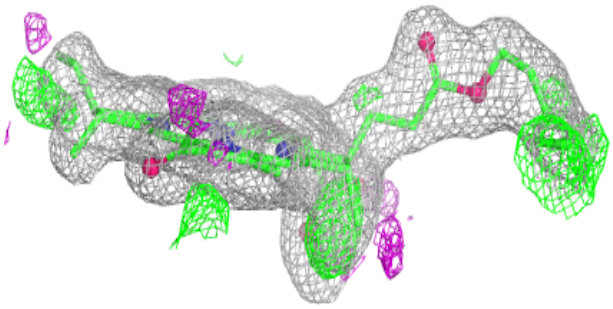


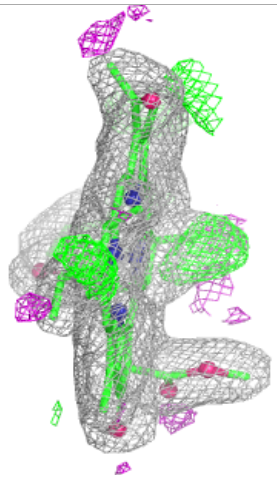


Electron density around BPH M 855:

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

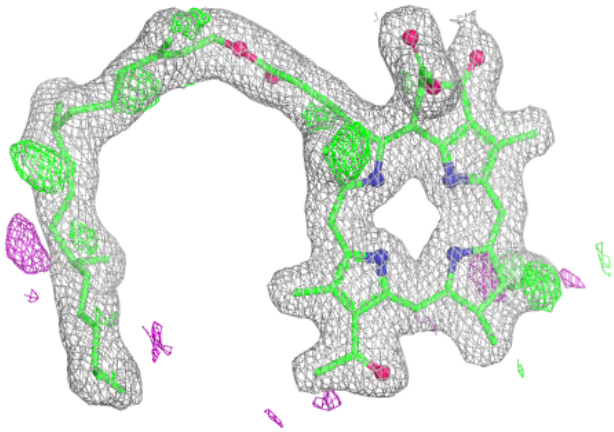


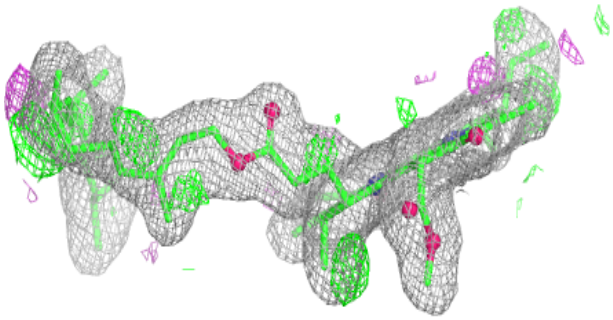


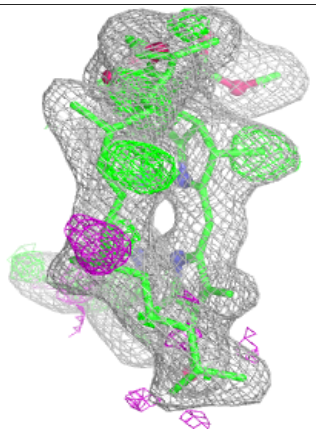


Electron density around BPH L 856:

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

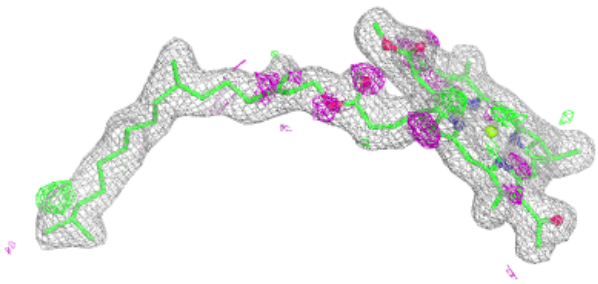


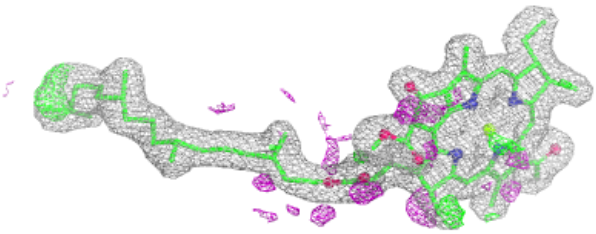


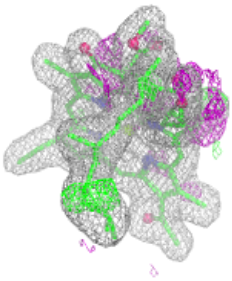


Electron density around BCL L 852:

$2mF_o$-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.