wwPDB X-ray Structure Validation Summary Report (i)

Aug 22, 2026 – 04:59 am BST

PDB ID	:	2JJ0 / pdb_00002jj0
Title	:	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH ALA M248 REPLACED WITH TRP (CHAIN M, AM248W)
Authors	:	Fyfe, P.K.; Potter, J.A.; Cheng, J.; Williams, C.M.; Watson, A.J.; Jones, M.R.
Deposited on	:	2007-07-03
Resolution	:	2.80 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:

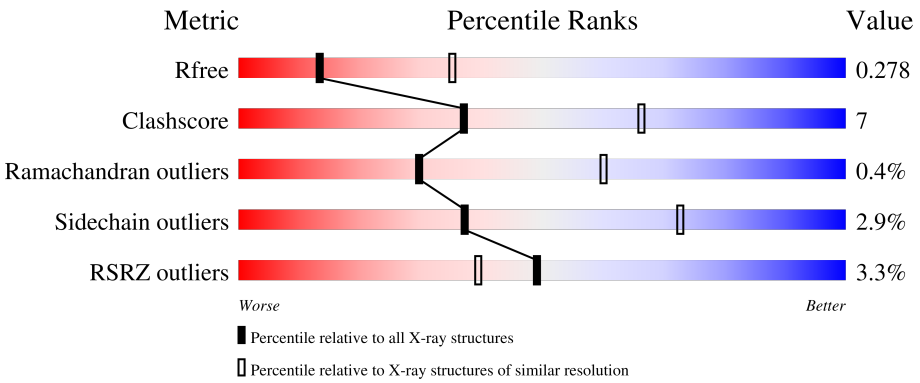
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	H	260	2%, 78%, 10%, 10%
2	L	281	6%, 84%, 15%
3	M	308	2%, 87%, 10%

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 7111 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
			Total	C	N	O	S			
1	H	235	1796	1148	305	334	9	0	1	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	281	2244	1516	356	364	8	0	1	0

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

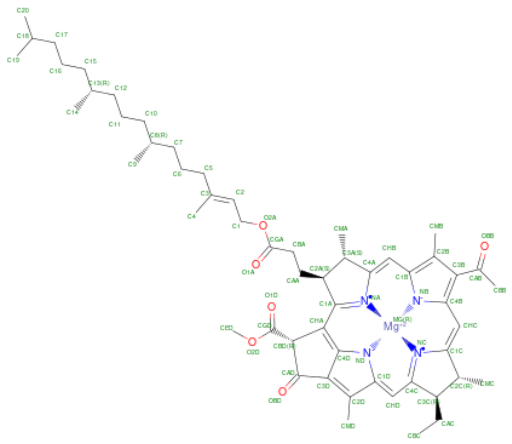
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	M	301	2412	1612	394	396	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	248	TRP	ALA	engineered mutation	UNP P0C0Y9

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

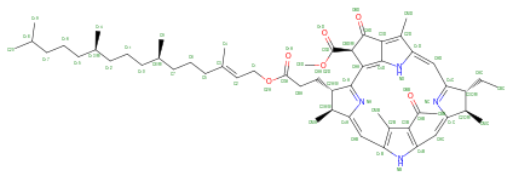
BCL



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

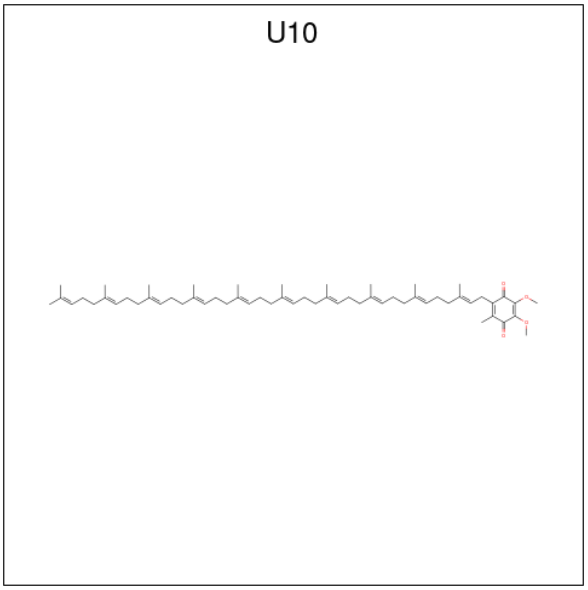
- Molecule 5 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$).

BPH



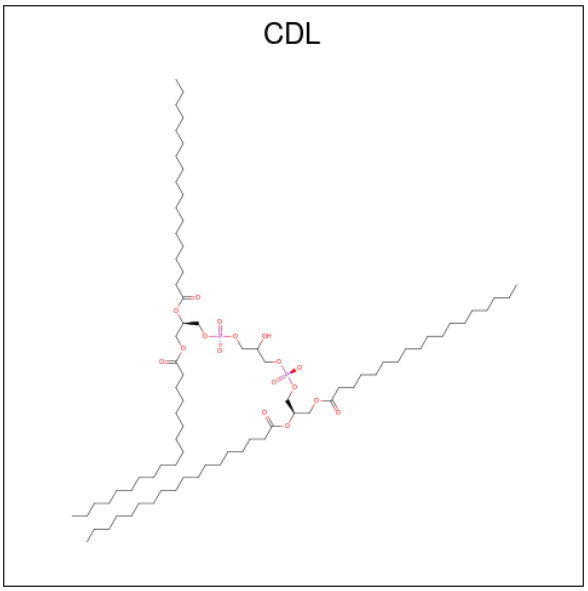
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	L	1	65	55	4	6	0	0
			Total	C	N	O		
5	M	1	65	55	4	6	0	0

- 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	17	13	4	0	0

- Molecule 7 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).

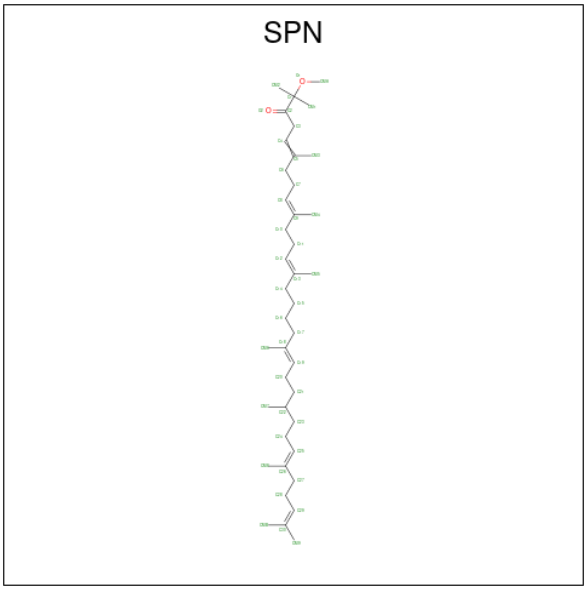


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
7	M	1	81	62	17	2	0	0

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

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

- Molecule 9 is SPEROIDENONE (CCD ID: SPN) (formula: $C_{41}H_{70}O_2$).



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

- Molecule 10 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
11	H	55	55	55	0	0

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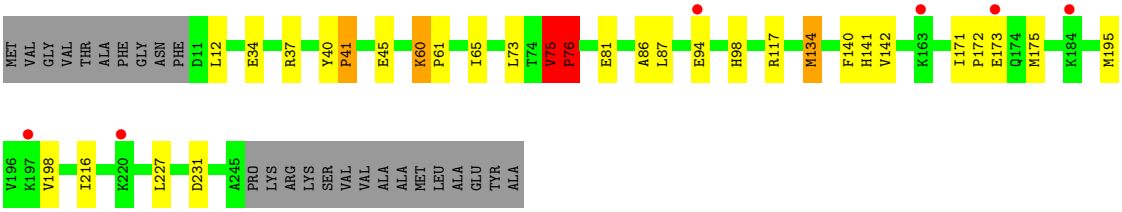
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
11	L	23	23	23	0	0
			Total	O		
11	M	44	44	44	0	0

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.

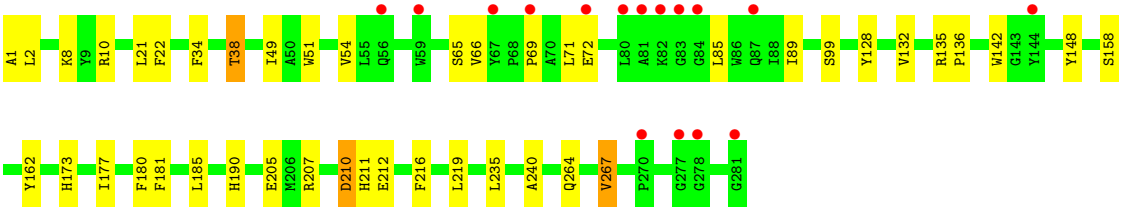
• Molecule 1: REACTION CENTER PROTEIN H CHAIN

Chain H:



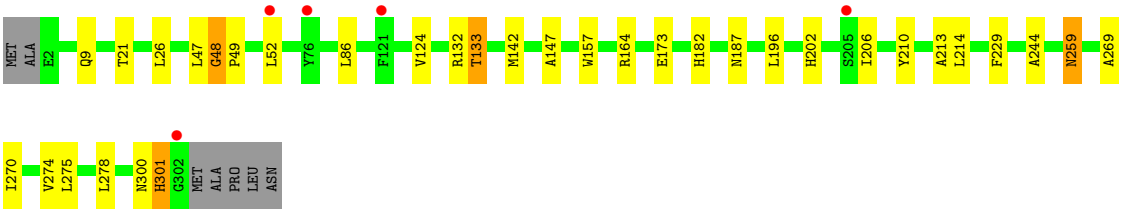
• Molecule 2: REACTION CENTER PROTEIN L CHAIN

Chain L:



• Molecule 3: REACTION CENTER PROTEIN M CHAIN

Chain M:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	139.81Å 139.81Å 185.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	27.90 – 2.80 27.90 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (27.90-2.80) 98.8 (27.90-2.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.10 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.203 , 0.245 0.237 , 0.278	Depositor DCC
R_{free} test set	2573 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	60.5	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 34.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7111	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% 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: FE, CL, U10, CDL, BPH, SPN, 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	0.82	0/1843	0.97	6/2509 (0.2%)
2	L	0.77	0/2333	0.87	1/3194 (0.0%)
3	M	0.75	0/2506	0.93	4/3422 (0.1%)
All	All	0.78	0/6682	0.92	11/9125 (0.1%)

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
1	H	0	2
3	M	0	2
All	All	0	4

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	M	48	GLY	CA-C-N	9.89	132.20	119.84
3	M	48	GLY	C-N-CA	9.89	132.20	119.84
1	H	75	VAL	CA-C-N	9.21	131.35	119.84
1	H	75	VAL	C-N-CA	9.21	131.35	119.84
1	H	76	PRO	N-CA-C	-6.08	99.95	112.47

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	40	TYR	Peptide
1	H	75	VAL	Peptide
3	M	300	ASN	Peptide
3	M	48	GLY	Peptide

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	H	1796	0	1790	23	0
2	L	2244	0	2196	32	0
3	M	2412	0	2318	27	0
4	L	198	0	222	15	0
4	M	66	0	74	4	0
5	L	65	0	76	8	0
5	M	65	0	76	8	0
6	L	17	0	15	2	0
7	M	81	0	106	2	0
8	M	1	0	0	0	0
9	M	43	0	69	9	0
10	M	1	0	0	0	0
11	H	55	0	0	1	0
11	L	23	0	0	0	0
11	M	44	0	0	1	0
All	All	7111	0	6942	98	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 7.

The worst 5 of 98 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)
3:M:275:LEU:HD23	3:M:278:LEU:HD23	1.53	0.88
1:H:173[B]:GLU:OE2	1:H:175:MET:HE3	1.77	0.82
5:L:1285:BPH:HHC	5:L:1285:BPH:HBB3	1.62	0.80
5:M:1307:BPH:HHC	5:M:1307:BPH:HBB3	1.64	0.79
2:L:181:PHE:CD2	5:M:1307:BPH:HBB1	2.20	0.77

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	234/260 (90%)	224 (96%)	9 (4%)	1 (0%)	30	60
2	L	280/281 (100%)	265 (95%)	15 (5%)	0	100	100
3	M	299/308 (97%)	284 (95%)	13 (4%)	2 (1%)	18	47
All	All	813/849 (96%)	773 (95%)	37 (5%)	3 (0%)	30	60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	M	49	PRO
3	M	301	HIS
1	H	76	PRO

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	191/208 (92%)	187 (98%)	4 (2%)	47	79
2	L	221/220 (100%)	214 (97%)	7 (3%)	34	70
3	M	237/242 (98%)	229 (97%)	8 (3%)	32	68
All	All	649/670 (97%)	630 (97%)	19 (3%)	37	73

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	M	133	THR
3	M	274	VAL
3	M	301	HIS
3	M	196	LEU
2	L	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	259	ASN
3	M	300	ASN
3	M	9	GLN
3	M	28	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 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	$\#\|Z\| > 2$
6	U10	L	1286	-	17,17,63	2.20	2 (11%)	19,23,79	1.29	3 (15%)
4	BCL	M	1304	3	69,74,74	1.16	4 (5%)	83,115,115	1.35	10 (12%)
9	SPN	M	1308	-	40,42,42	3.70	16 (40%)	50,52,52	2.14	20 (40%)
5	BPH	M	1307	-	59,70,70	1.02	4 (6%)	61,101,101	2.06	16 (26%)
5	BPH	L	1285	-	59,70,70	1.17	5 (8%)	61,101,101	1.57	10 (16%)
4	BCL	L	1282	3	69,74,74	1.22	3 (4%)	83,115,115	1.55	19 (22%)
4	BCL	L	1283	2	69,74,74	1.13	2 (2%)	83,115,115	1.30	11 (13%)
4	BCL	L	1284	2	69,74,74	1.22	5 (7%)	83,115,115	1.71	16 (19%)
7	CDL	M	1305	-	80,80,99	1.11	4 (5%)	86,92,111	1.11	7 (8%)

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
6	U10	L	1286	-	-	3/8/32/87	0/1/1/1
4	BCL	M	1304	3	-	1/41/137/137	-
9	SPN	M	1308	-	-	15/50/51/51	-
5	BPH	M	1307	-	-	15/37/105/105	0/5/6/6
5	BPH	L	1285	-	-	15/37/105/105	0/5/6/6
4	BCL	L	1282	3	-	9/41/137/137	-
4	BCL	L	1283	2	-	6/41/137/137	-
4	BCL	L	1284	2	-	5/41/137/137	-
7	CDL	M	1305	-	-	44/91/91/110	-

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	M	1308	SPN	C3-C4	-9.51	1.36	1.50
6	L	1286	U10	C6-C1	8.07	1.50	1.35
9	M	1308	SPN	C10-C9	-7.71	1.35	1.51
9	M	1308	SPN	C14-C13	-7.35	1.36	1.51
9	M	1308	SPN	C6-C5	-7.24	1.36	1.51

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	M	1307	BPH	C4D-CHA-CBD	-6.39	105.63	108.52
5	M	1307	BPH	O2D-CGD-CBD	6.38	119.08	111.00
4	L	1284	BCL	C2B-C1B-NB	-5.40	106.61	110.23
9	M	1308	SPN	CM5-C13-C14	4.98	123.64	115.27
5	M	1307	BPH	C2B-C1B-NB	-4.97	106.09	109.53

There are no chirality outliers.

5 of 113 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	M	1307	BPH	C4C-C3C-CAC-CBC
6	L	1286	U10	C6-C7-C8-C9
7	M	1305	CDL	CA2-OA2-PA1-OA3
7	M	1305	CDL	CB2-OB2-PB2-OB3
7	M	1305	CDL	CB2-OB2-PB2-OB4

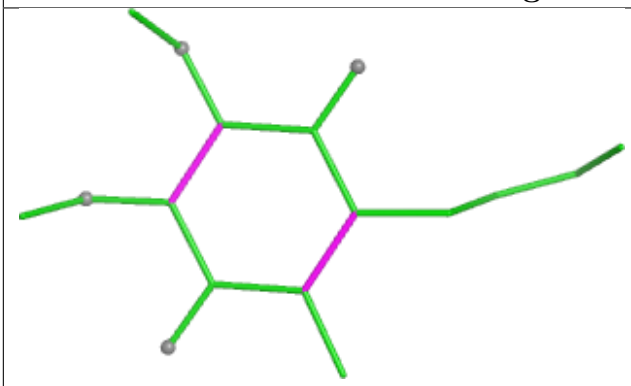
There are no ring outliers.

9 monomers are involved in 39 short contacts:

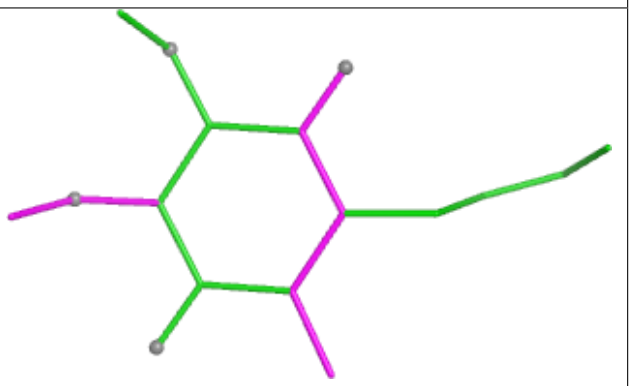
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	L	1286	U10	2	0
4	M	1304	BCL	4	0
9	M	1308	SPN	9	0
5	M	1307	BPH	8	0
5	L	1285	BPH	8	0
4	L	1282	BCL	9	0
4	L	1283	BCL	3	0
4	L	1284	BCL	3	0
7	M	1305	CDL	2	0

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.

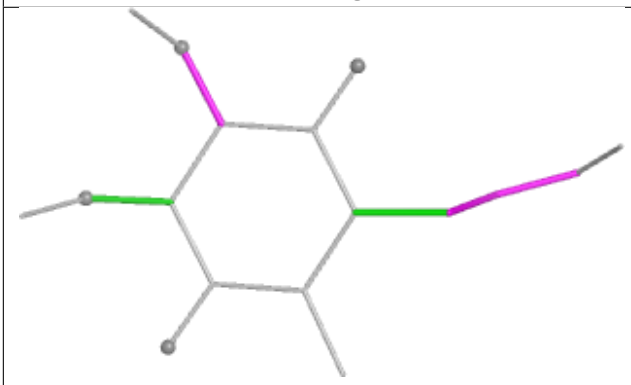
Ligand U10 L 1286



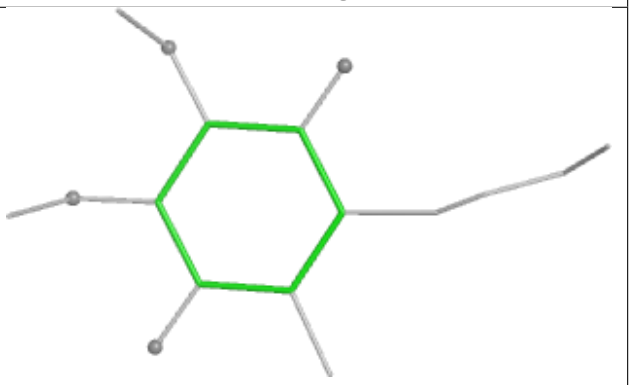
Bond lengths



Bond angles

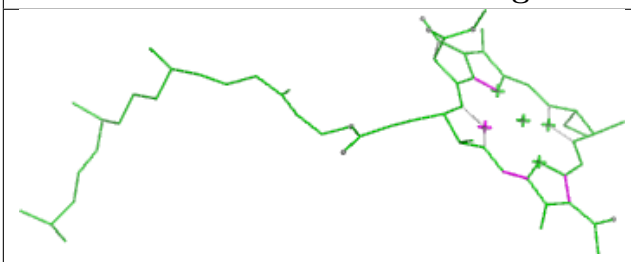


Torsions

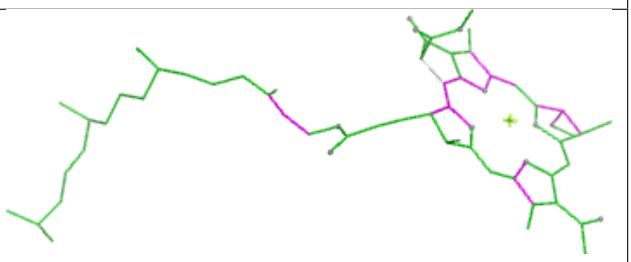


Rings

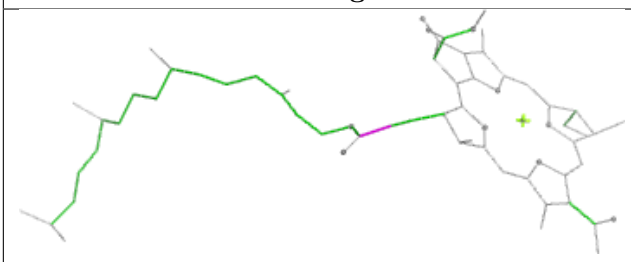
Ligand BCL M 1304



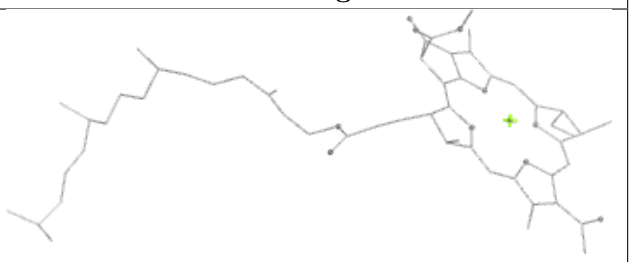
Bond lengths



Bond angles

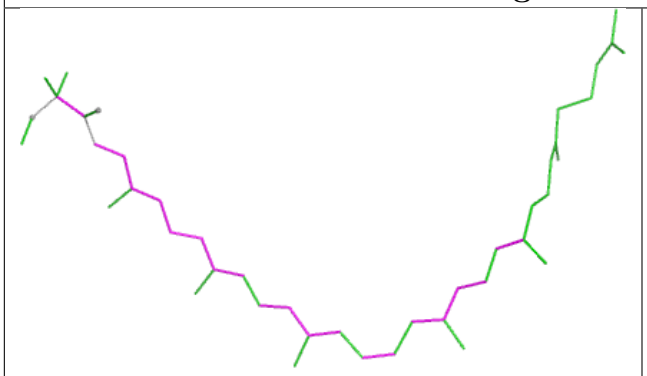


Torsions

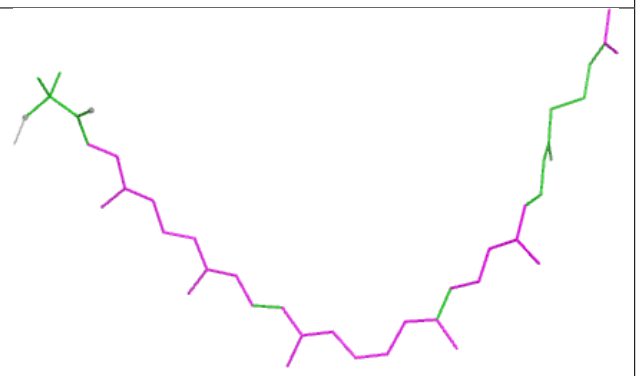


Rings

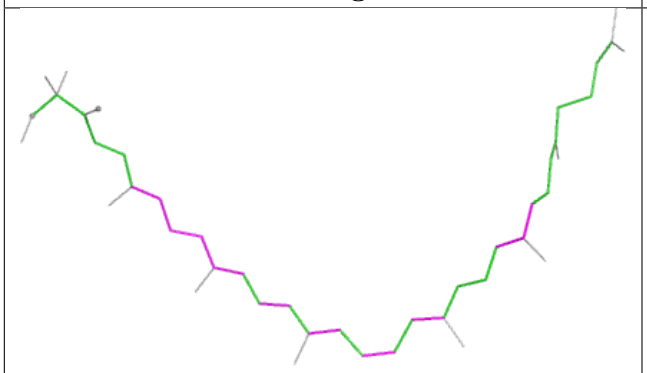
Ligand SPN M 1308



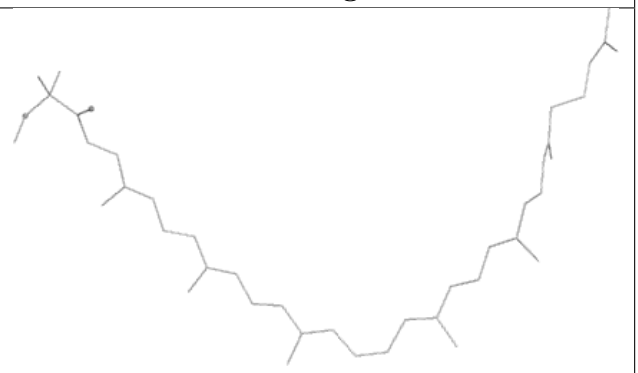
Bond lengths



Bond angles

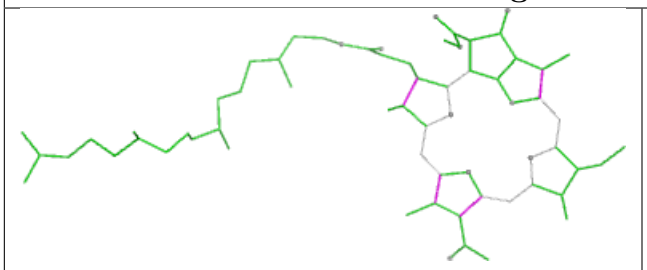


Torsions

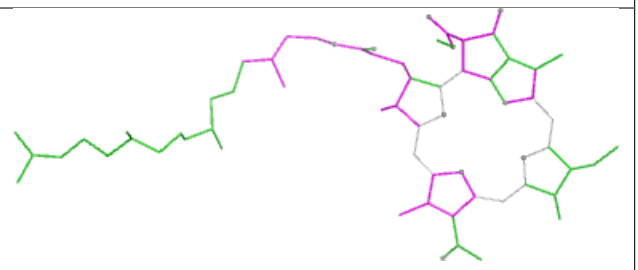


Rings

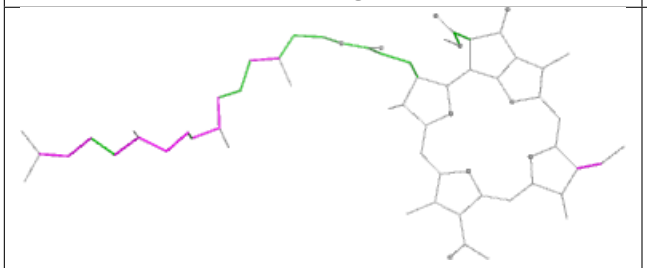
Ligand BPH M 1307



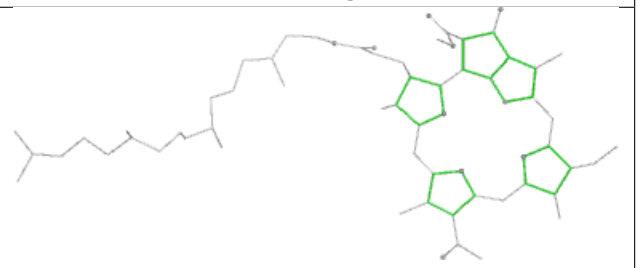
Bond lengths



Bond angles

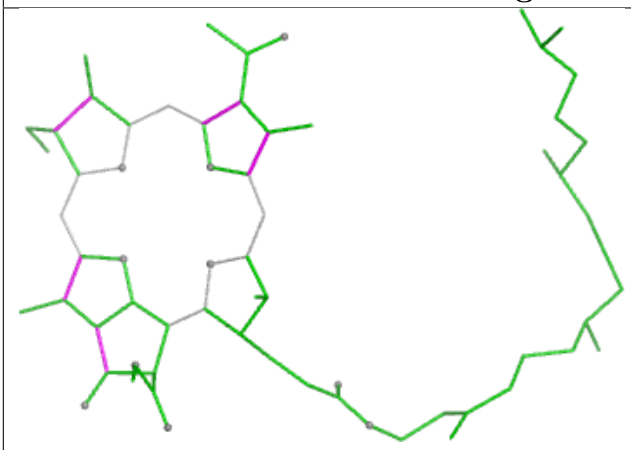


Torsions

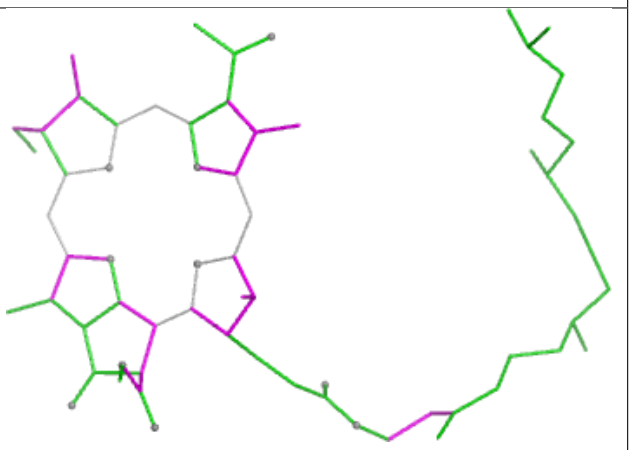


Rings

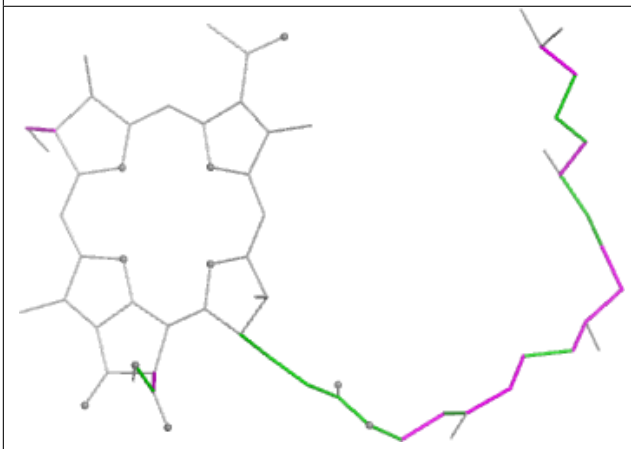
Ligand BPH L 1285



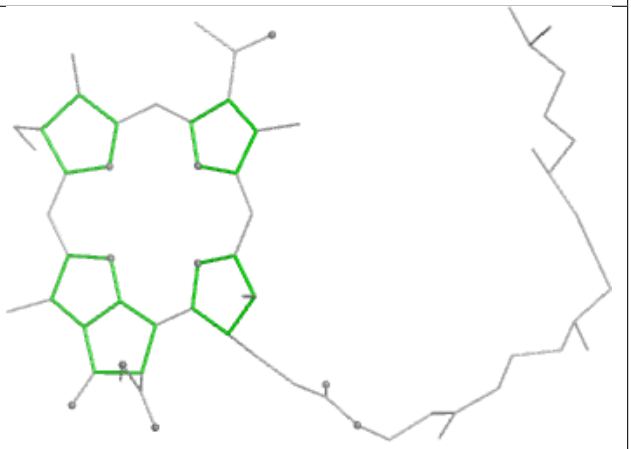
Bond lengths



Bond angles

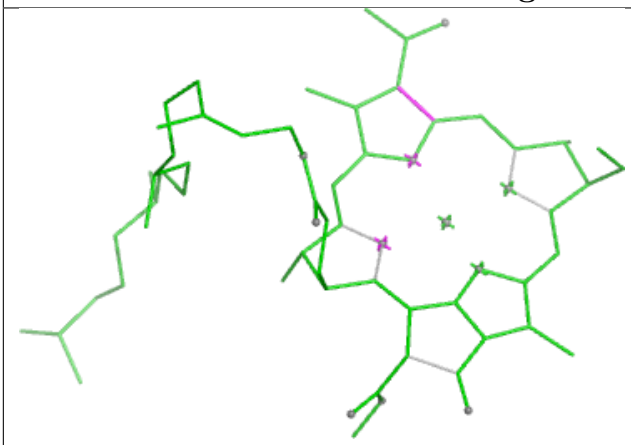


Torsions

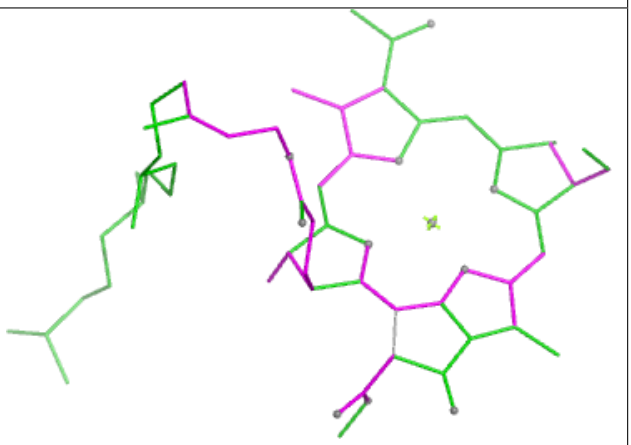


Rings

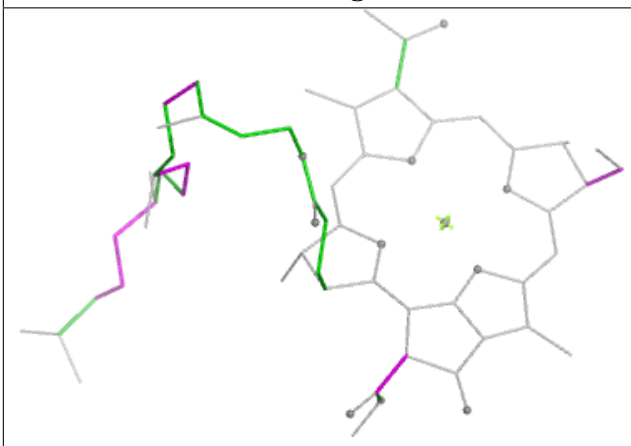
Ligand BCL L 1282



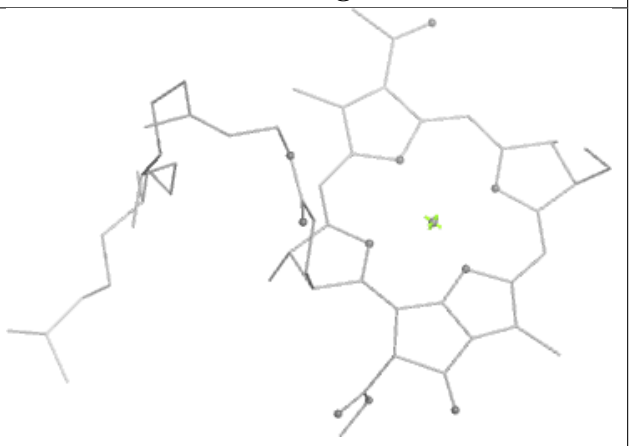
Bond lengths



Bond angles

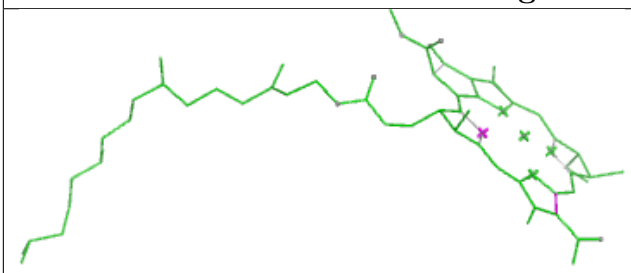


Torsions

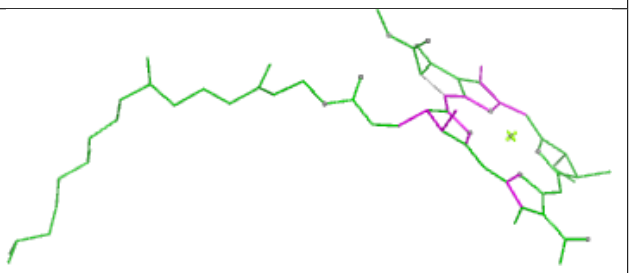


Rings

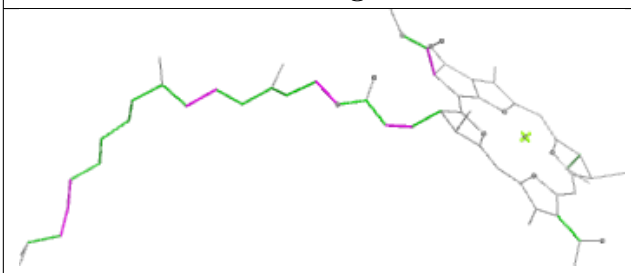
Ligand BCL L 1283



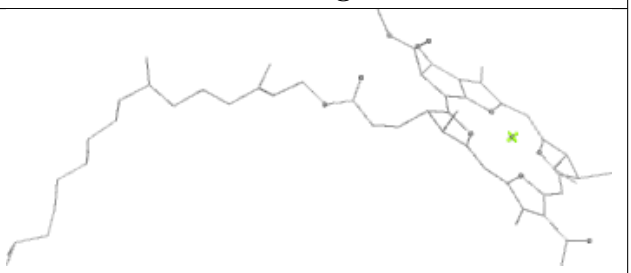
Bond lengths



Bond angles

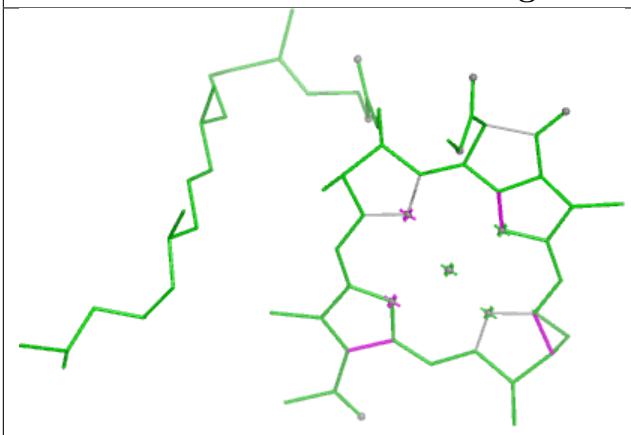


Torsions

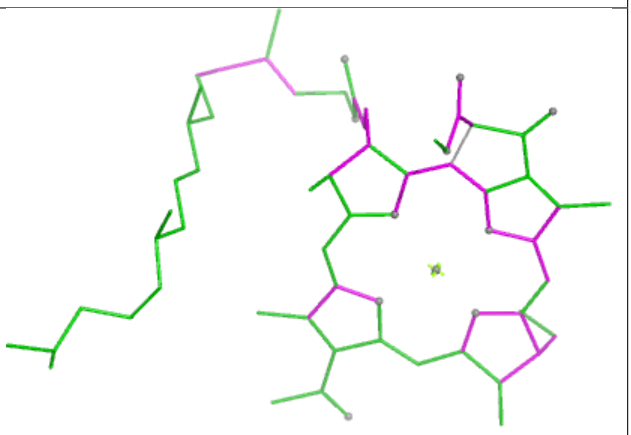


Rings

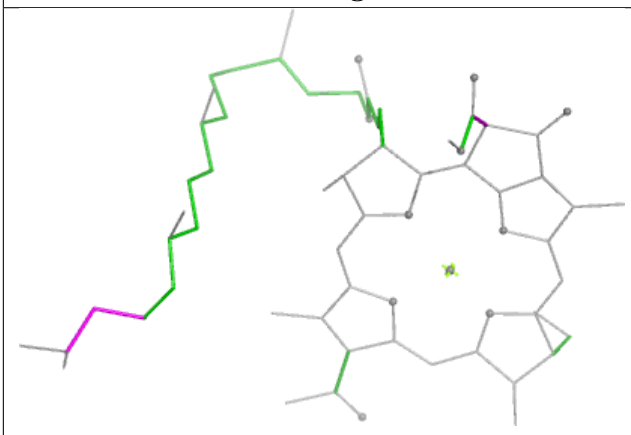
Ligand BCL L 1284



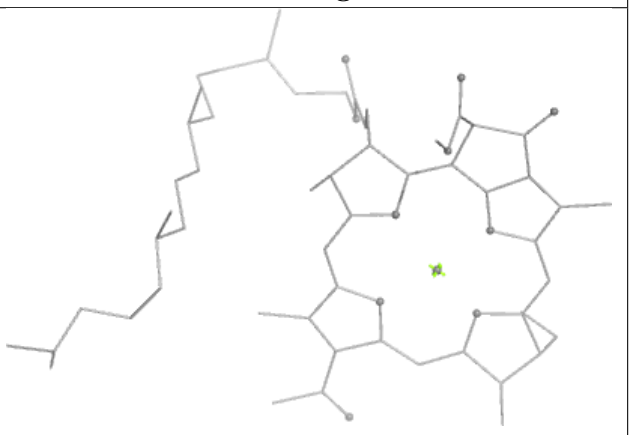
Bond lengths



Bond angles

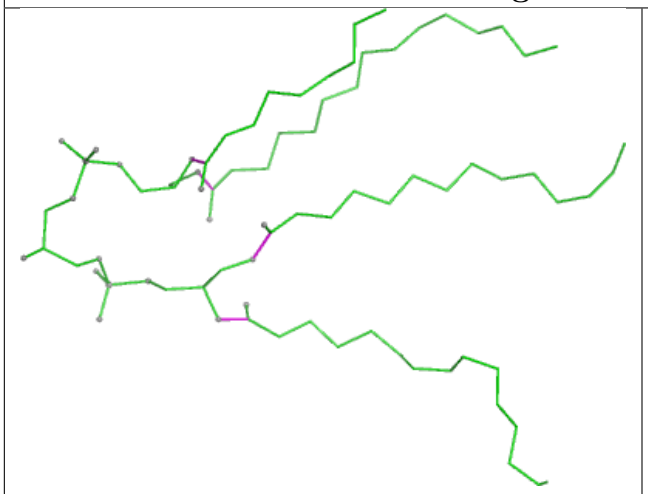


Torsions

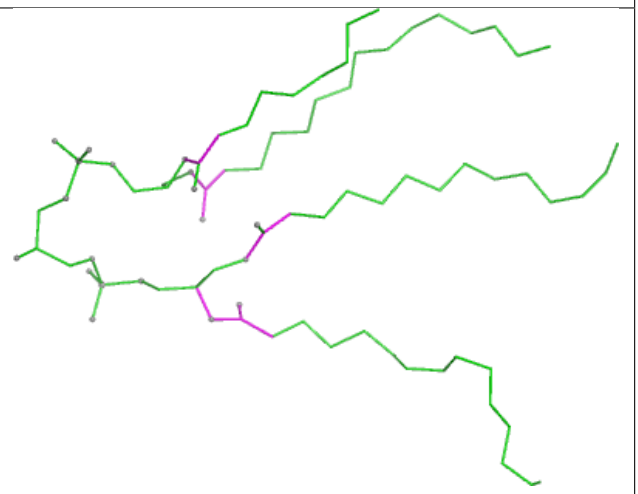


Rings

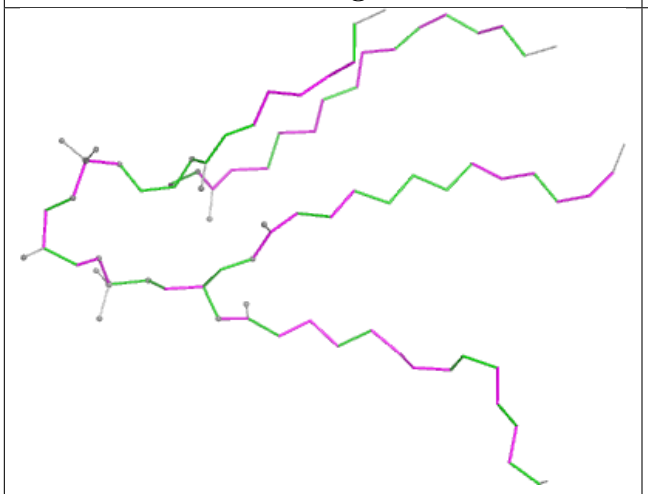
Ligand CDL M 1305



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	H	235/260 (90%)	0.20	6 (2%)	57	47	21, 43, 53, 58	5 (2%)
2	L	281/281 (100%)	0.50	16 (5%)	29	22	22, 44, 56, 63	2 (0%)
3	M	301/308 (97%)	0.41	5 (1%)	69	60	31, 44, 54, 79	1 (0%)
All	All	817/849 (96%)	0.38	27 (3%)	49	39	21, 44, 54, 79	8 (0%)

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	82	LYS	6.1
1	H	184	LYS	4.7
1	H	220	LYS	4.5
1	H	197	LYS	4.5
3	M	302	GLY	4.5

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)

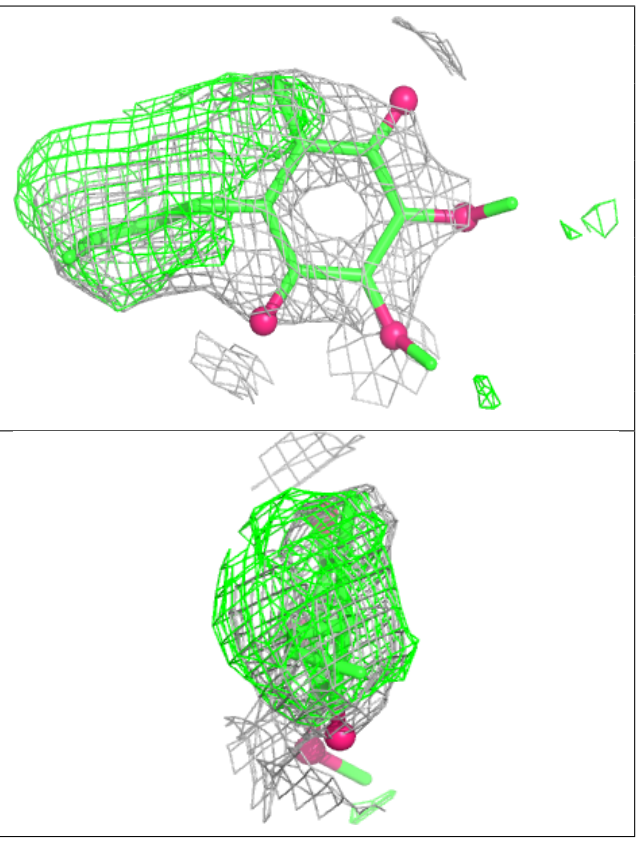
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	1286	17/63	0.83	0.36	29,32,33,33	17
7	CDL	M	1305	81/100	0.85	0.31	24,39,52,54	81
5	BPH	M	1307	65/65	0.91	0.13	38,44,85,86	0
9	SPN	M	1308	43/43	0.91	0.13	37,43,51,52	0
4	BCL	L	1284	66/66	0.93	0.12	29,36,50,54	0
4	BCL	L	1282	66/66	0.94	0.11	37,44,69,69	0
5	BPH	L	1285	65/65	0.94	0.11	33,40,43,46	0
4	BCL	M	1304	66/66	0.95	0.11	36,40,51,54	0
4	BCL	L	1283	66/66	0.95	0.11	29,39,53,56	0
10	CL	M	1309	1/1	0.98	0.05	39,39,39,39	0
8	FE	M	1306	1/1	0.99	0.05	44,44,44,44	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.

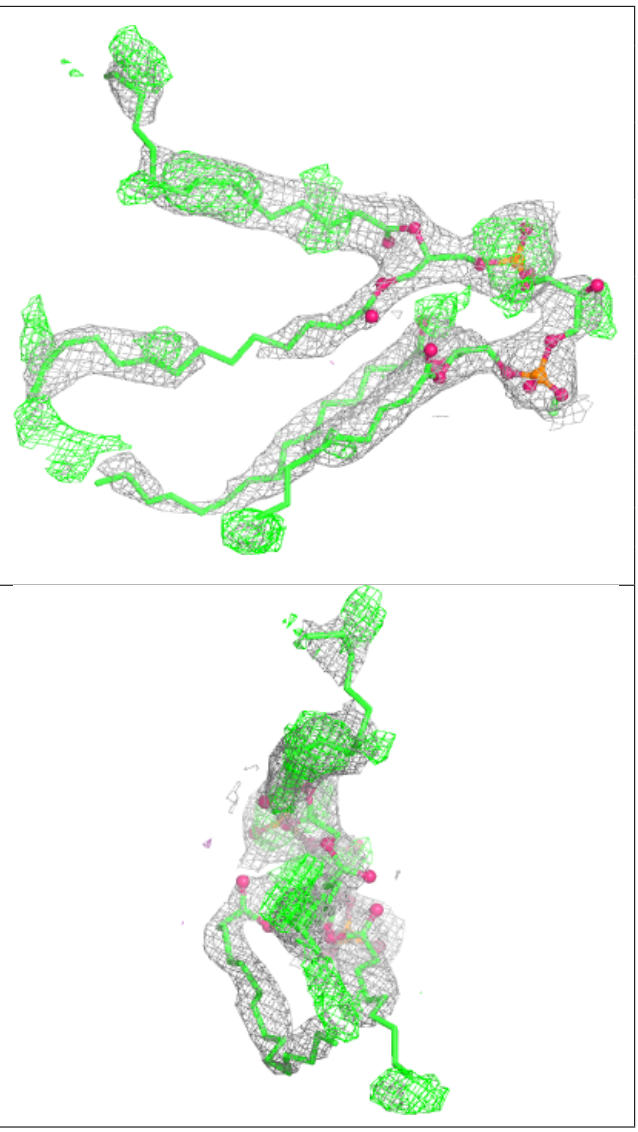
Electron density around U10 L 1286:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



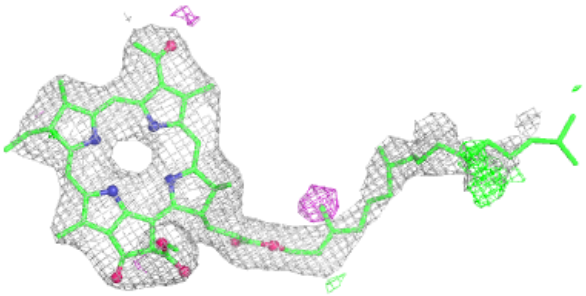
Electron density around CDL M 1305:

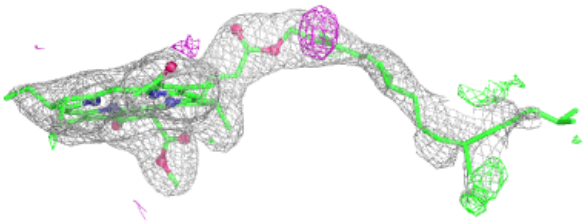
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

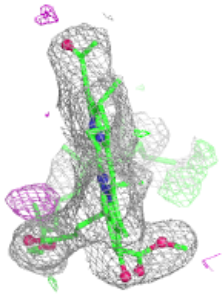


Electron density around BPH M 1307:

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

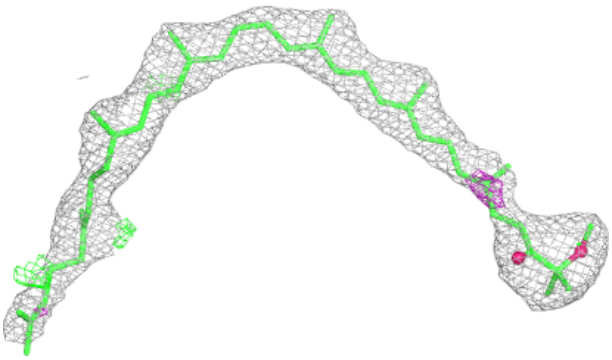


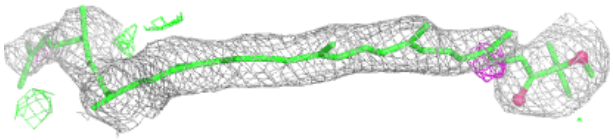


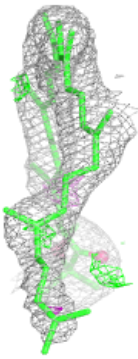


Electron density around SPN M 1308:

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

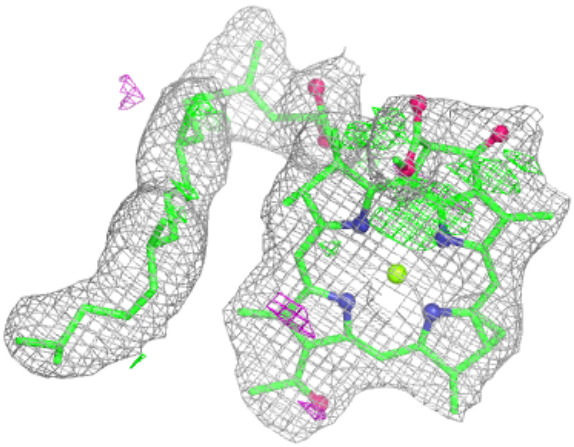


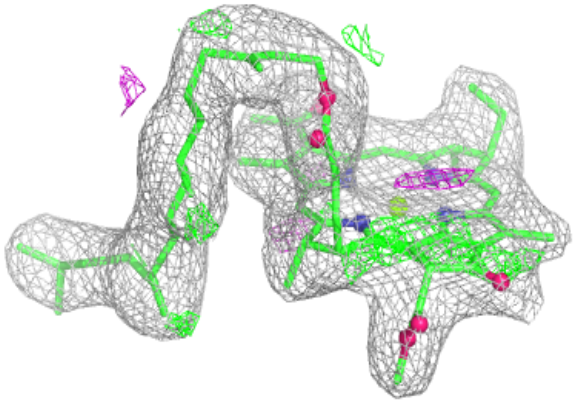




Electron density around BCL L 1284:

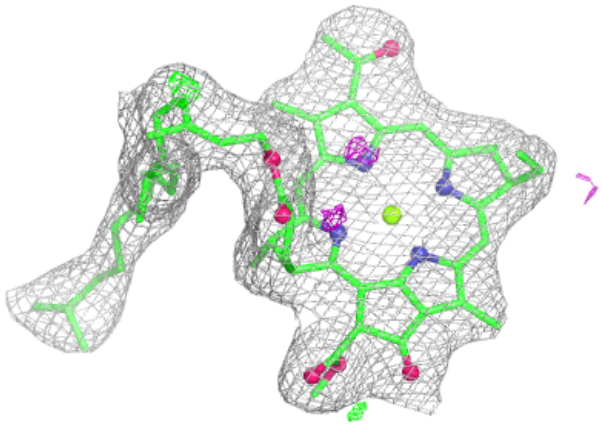
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

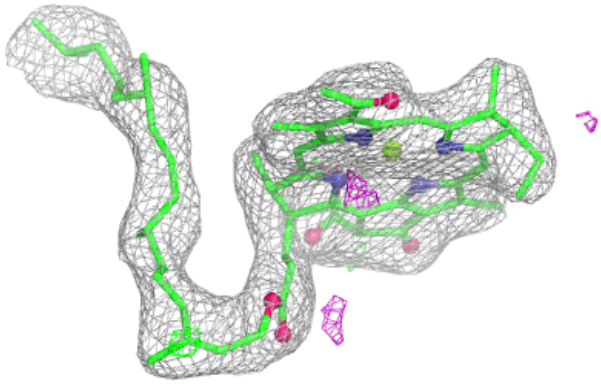


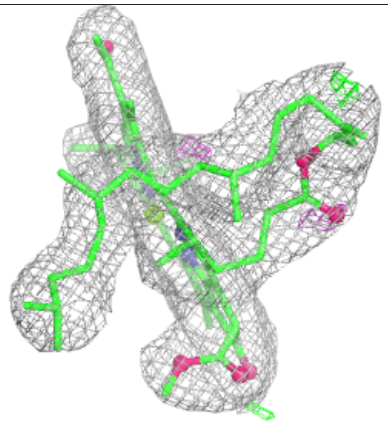


Electron density around BCL L 1282:

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

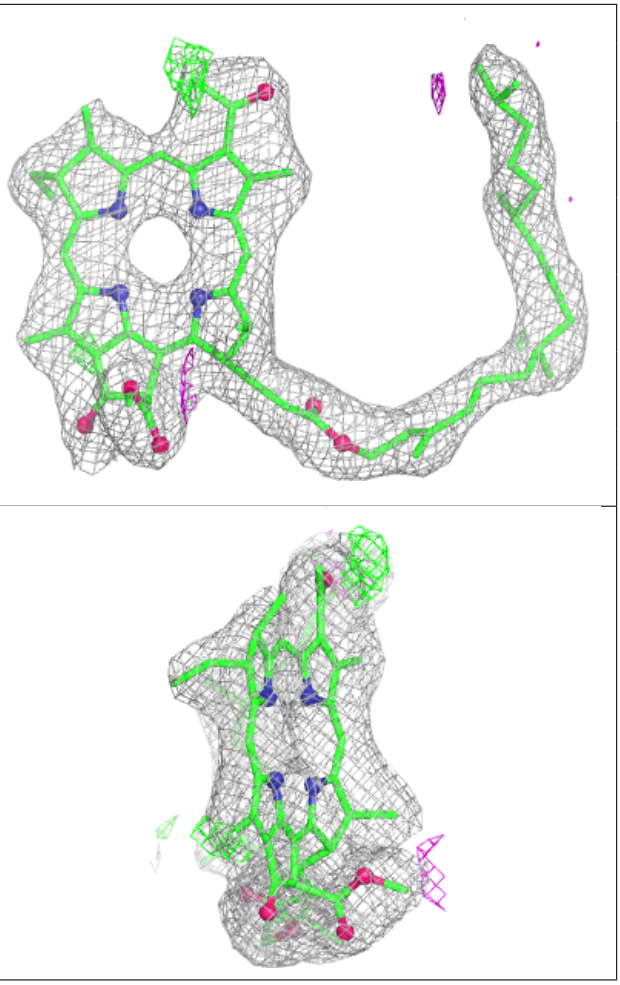


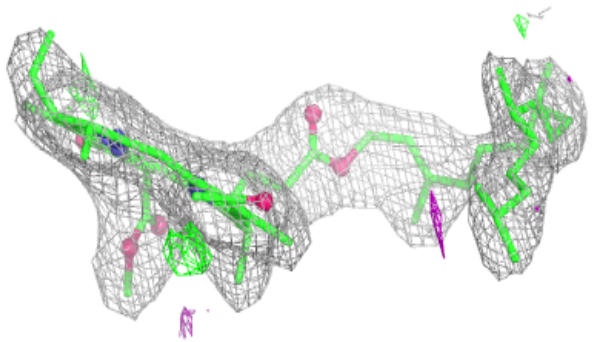




Electron density around BPH L 1285:

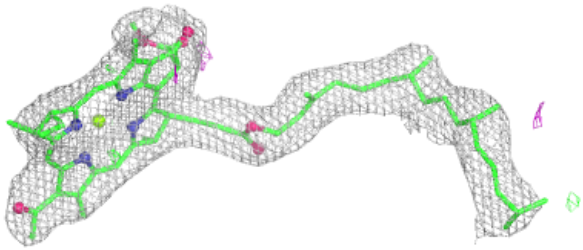
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

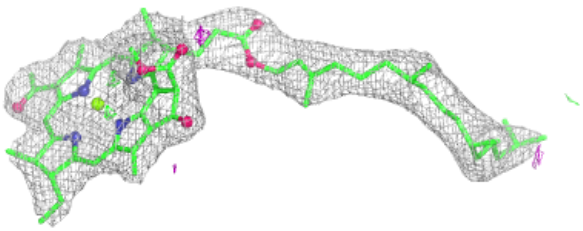


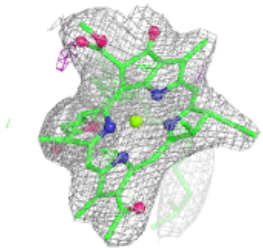


Electron density around BCL M 1304:

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

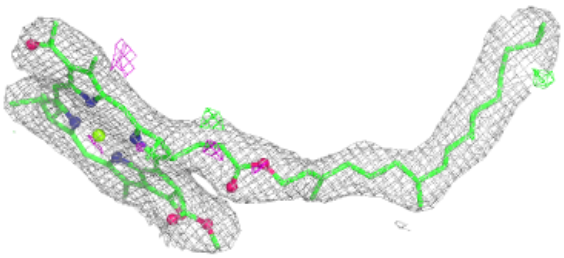


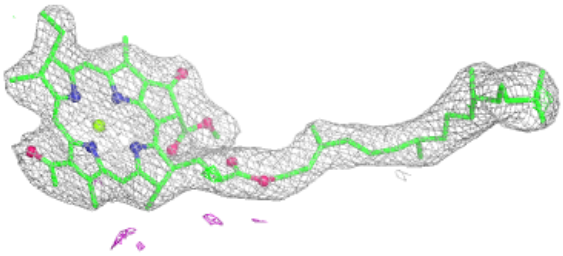


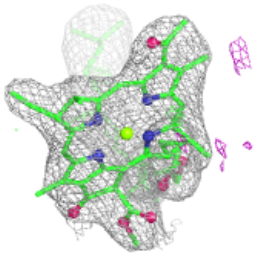


Electron density around BCL L 1283:

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







6.5 Other polymers (i)

There are no such residues in this entry.