

wwPDB X-ray Structure Validation Summary Report (i)

Dec 23, 2021 – 12:12 PM EST

PDB ID	:	7MH8
Title	:	Crystal structure of R. sphaeroides Photosynthetic Reaction Center variant;
		Y(M210)3-methyltyrosine
Authors	:	Mathews, I.; Weaver, J.; Boxer, S.G.
Deposited on	:	2021-04-14
Resolution	:	2.75 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 following versions of software and data (see references (1)) were used in the production of this report:

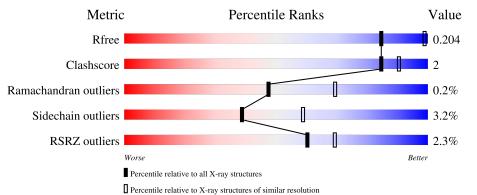
MolProbity		
		1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.25
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.25

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.75 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	Н	266	2% 8 4%	6% 10%
2	L	282	93%	7%
3	М	308	% 90%	7% •

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	BPH	М	407	Х	-	-	-



2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 7221 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

• Molecule 1 is a protein called Reaction center protein H chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Н	239	Total 1823	C 1166	N 313	O 335	S 9	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Н	260	VAL	-	expression tag	UNP P0C0Y7
Н	261	HIS	-	expression tag	UNP P0C0Y7
Н	262	HIS	-	expression tag	UNP P0C0Y7
Н	263	HIS	-	expression tag	UNP P0C0Y7
Н	264	HIS	-	expression tag	UNP P0C0Y7
Н	265	HIS	-	expression tag	UNP P0C0Y7
Н	266	HIS	-	expression tag	UNP P0C0Y7

• Molecule 2 is a protein called Reaction center protein L chain.

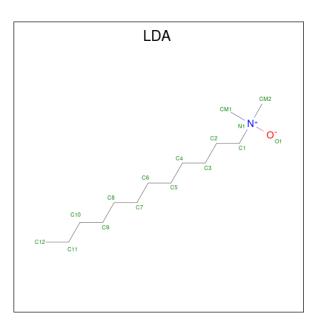
Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	L	281	Total 2232	C 1507	N 355	O 362	S 8	0	0	0

• Molecule 3 is a protein called Reaction center protein M chain.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
3	М	301	Total 2404	C 1605	N 393	O 396	S 10	0	0	0

• Molecule 4 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).

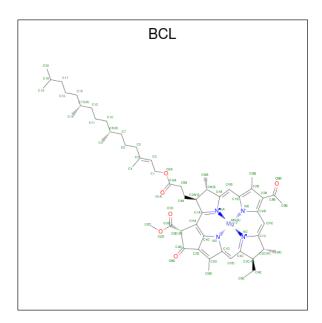




Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
4	Н	1	Total C N O	0	0	
-			16 14 1 1			
4	М	1	Total C N O	0	0	
T	111	1	16 14 1 1	0	0	
4	М	1	Total C N O	0	0	
4	101	1	16 14 1 1	0	0	
4	М	1	Total C N O	0	0	
4	1/1	1	16 14 1 1	0	0	
4	М	1	Total C N O	0	0	
4	М	1	16 14 1 1	U	U	

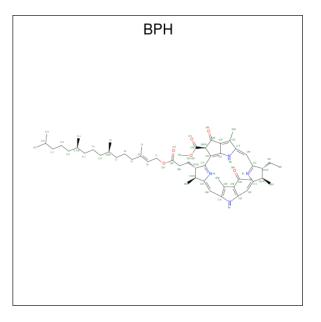
• Molecule 5 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: $C_{55}H_{74}MgN_4O_6$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	
5	т	1	Total	С	Mg	Ν	Ο	0	0	
5	L	1	66	55	1	4	6	0	0	
5	Т	1	Total	С	Mg	Ν	Ο	0	0	
5	L	1	66	55	1	4	6	0	0	
5	т	1	Total	С	Mg	Ν	Ο	0	0	
5	L	1	51	40	1	4	6	0	0	
5	М	1	Total	С	Mg	Ν	Ο	0	0	
5	IVI	1	66	55	1	4	6	0	U	

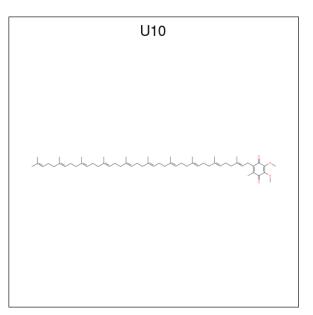
• Molecule 6 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: $C_{55}H_{76}N_4O_6$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Α	ton	ns		ZeroOcc	AltConf
6	L	1	Total 65	-		-	0	0
6	М	1	Total 55		N 4		0	0

• Molecule 7 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$) (labeled as "Ligand of Interest" by depositor).



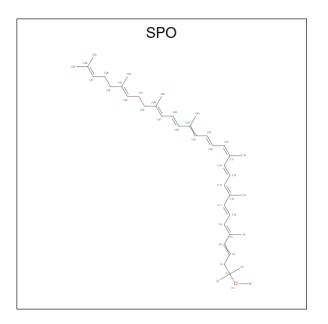
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
7	T	1	Total C O	0	0	
1	L	1	18 14 4	0	0	
7	М	1	Total C O	0	0	
	111	1	48 44 4	0	0	

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

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

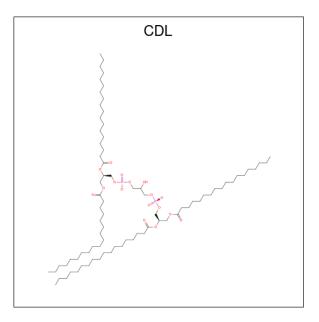
• Molecule 9 is SPHEROIDENE (three-letter code: SPO) (formula: $C_{41}H_{60}O$).





Mo	l Chain	Residues	At	oms		ZeroOcc	AltConf
9	М	1	Total 42	C 41	0 1	0	0

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



Mol	Chain	Residues			ZeroOcc	AltConf		
10	М	1	Total	С	Ο	Р	0	0
10	111	1	69	50	17	2		

• Molecule 11 is water.

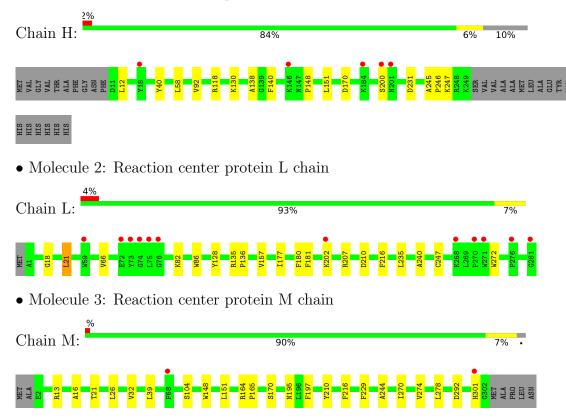


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	Н	58	$\begin{array}{cc} {\rm Total} & {\rm O} \\ 59 & 59 \end{array}$	0	1
11	L	31	Total O 31 31	0	0
11	М	43	$\begin{array}{cc} \text{Total} & \text{O} \\ 45 & 45 \end{array}$	0	2



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



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	140.96Å 140.96 Å 187.01 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.96 - 2.75	Depositor
Resolution (A)	38.96 - 2.75	EDS
% Data completeness	99.7(38.96-2.75)	Depositor
(in resolution range)	99.8(38.96-2.75)	EDS
R _{merge}	0.15	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.80 (at 2.77 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.179 , 0.201	Depositor
II, II, <i>free</i>	0.185 , 0.204	DCC
R_{free} test set	2811 reflections $(5.00%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	61.7	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.30 , 57.7	EDS
L-test for twinning ²	$< L > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7221	wwPDB-VP
Average B, all atoms $(Å^2)$	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.63% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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, ZDJ, BCL, SPO, LDA, U10, BPH, CDL

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	Н	0.62	0/1871	0.75	0/2545	
2	L	0.63	0/2320	0.69	0/3175	
3	М	0.63	0/2481	0.72	0/3385	
All	All	0.63	0/6672	0.72	0/9105	

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	Н	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Н	138	ALA	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	Н	1823	0	1831	5	0
2	L	2232	0	2187	10	0
3	М	2404	0	2304	10	0
4	Н	16	0	31	0	0
4	М	64	0	124	0	0
5	L	183	0	189	7	0
5	М	66	0	74	5	0
6	L	65	0	76	1	0
6	М	55	0	53	3	0
7	L	18	0	15	0	0
7	М	48	0	63	1	0
8	М	1	0	0	0	0
9	М	42	0	60	0	0
10	М	69	0	82	1	0
11	Н	59	0	0	0	0
11	L	31	0	0	0	0
11	М	45	0	0	0	0
All	All	7221	0	7089	33	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 2.

The worst 5 of 33 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:16:ALA:HB1	3:M:32:VAL:HG11	1.64	0.78
5:L:305:BCL:HHC	5:L:305:BCL:HBB2	1.73	0.70
6:L:302:BPH:HBB3	6:L:302:BPH:HHC	1.74	0.68
5:L:301:BCL:HBB2	5:L:301:BCL:HHC	1.77	0.65
2:L:181:PHE:CD2	6:M:407:BPH:HBB1	2.37	0.59

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.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	Н	237/266~(89%)	231~(98%)	6~(2%)	0	100	100
2	L	279/282~(99%)	$270 \ (97\%)$	9~(3%)	0	100	100
3	М	298/308~(97%)	289~(97%)	7 (2%)	2(1%)	22	39
All	All	814/856~(95%)	790 (97%)	22 (3%)	2(0%)	47	69

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

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	М	301	HIS
3	М	195	ASN

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Н	194/215~(90%)	188~(97%)	6 (3%)	40	60	
2	L	$220/221 \ (100\%)$	211 (96%)	9 (4%)	30	50	
3	М	235/240~(98%)	229~(97%)	6 (3%)	46	66	
All	All	649/676~(96%)	628~(97%)	21 (3%)	39	59	

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

Mol	Chain	Res	Type
2	L	272	TRP
3	М	170	SER
3	М	292	ASP
3	М	216	PHE
3	М	104	SER

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such side chains are listed below:



Mol	Chain	Res	Type
1	Н	98	HIS
2	L	183	ASN
3	М	77	GLN
3	М	300	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	Dec	Link	Bond lengths			Bond angles		
	туре		nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	ZDJ	М	210	3	12,13,14	0.55	0	$14,\!17,\!19$	1.62	3 (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
3	ZDJ	М	210	3	-	2/5/6/8	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	М	210	ZDJ	CME-CE1-CZ	3.56	123.98	120.73
3	М	210	ZDJ	CD1-CE1-CZ	2.76	119.77	117.56
3	М	210	ZDJ	OH-CZ-CE1	2.39	122.59	117.63

There are no chirality outliers.



Mol	Chain	Res	Type	Atoms
3	М	210	ZDJ	CA-CB-CG-CD1
3	М	210	ZDJ	CA-CB-CG-CD2

All (2) torsion outliers are listed below:

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 1 is monoatomic - leaving 15 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).

Mal	T	Chain	Dag	Link	B	ond leng	gths	Bo	ond angl	es
Mol	Type	Chain	Res	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
7	U10	М	408	-	48,48,63	0.62	2 (4%)	58,61,79	0.46	0
4	LDA	М	402	-	12,15,15	0.20	0	14,17,17	0.40	0
5	BCL	L	301	-	58,74,74	1.57	9 (15%)	69,115,115	1.75	15 (21%)
4	LDA	М	404	-	12,15,15	0.17	0	14,17,17	0.22	0
6	BPH	L	302	-	64,70,70	0.56	0	76,101,101	0.79	4 (5%)
4	LDA	Н	301	-	12,15,15	0.14	0	14,17,17	0.34	0
5	BCL	М	401	-	58,74,74	1.61	10 (17%)	69,115,115	1.68	15 (21%)
9	SPO	М	409	-	40,41,41	1.63	8 (20%)	47,50,50	1.24	7 (14%)
10	CDL	М	410	-	68,68,99	0.35	0	74,80,111	0.39	0
4	LDA	М	405	-	12,15,15	0.15	0	14,17,17	0.16	0
4	LDA	М	403	-	12,15,15	0.13	0	14,17,17	0.30	0
5	BCL	L	304	-	58,74,74	1.61	8 (13%)	69,115,115	1.56	16 (23%)
6	BPH	М	407	-	54,60,70	0.62	0	64,89,101	0.91	4 (6%)
5	BCL	L	305	-	43,59,74	1.87	9 (20%)	51,97,115	1.81	14 (27%)
7	U10	L	303	-	18,18,63	1.02	2 (11%)	22,25,79	0.63	0



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
7	U10	М	408	-	-	6/45/69/87	0/1/1/1
4	LDA	М	402	-	-	6/13/13/13	-
5	BCL	L	301	-	-	7/37/137/137	-
4	LDA	М	404	-	-	4/13/13/13	-
6	BPH	L	302	-	-	10/54/105/105	0/5/6/6
4	LDA	Н	301	-	-	8/13/13/13	-
5	BCL	М	401	-	-	7/37/137/137	-
9	SPO	М	409	-	-	3/47/47/47	-
10	CDL	М	410	-	-	28/79/79/110	-
4	LDA	М	405	-	-	4/13/13/13	-
4	LDA	М	403	-	-	5/13/13/13	-
5	BCL	L	304	-	-	3/37/137/137	-
6	BPH	М	407	-	1/1/16/22	13/42/93/105	0/5/6/6
5	BCL	L	305	-	-	0/19/119/137	-
7	U10	L	303	-	_	3/9/33/87	0/1/1/1

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
5	L	301	BCL	O2D-CGD	5.17	1.45	1.33
5	L	305	BCL	O2D-CGD	5.15	1.45	1.33
5	М	401	BCL	O2D-CGD	5.11	1.45	1.33
5	L	304	BCL	O2D-CGD	5.10	1.45	1.33
5	L	304	BCL	OBD-CAD	4.92	1.29	1.22

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
5	L	301	BCL	O2D-CGD-CBD	5.50	121.03	111.27
5	L	305	BCL	O2D-CGD-CBD	4.91	119.99	111.27
5	L	301	BCL	CHD-C4C-NC	4.68	130.27	125.08
5	М	401	BCL	CHD-C4C-NC	4.42	129.99	125.08
5	L	305	BCL	C3C-C4C-CHD	-4.32	114.17	123.39

All (1) chirality outliers are listed below:



Mol	Chain	Res	Type	Atom
6	М	407	BPH	C8

5 of 107 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	Н	301	LDA	C2-C1-N1-O1
4	Н	301	LDA	C2-C1-N1-CM1
4	Н	301	LDA	C2-C1-N1-CM2
4	М	402	LDA	C2-C1-N1-O1
4	М	402	LDA	C2-C1-N1-CM1

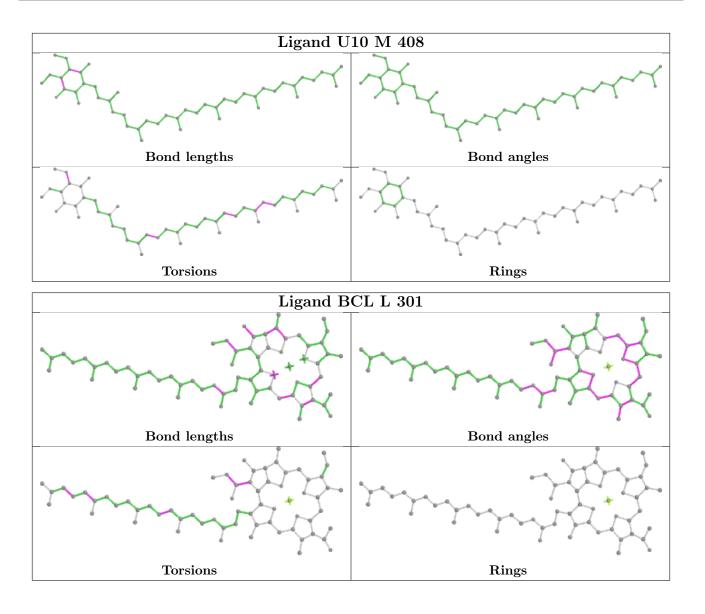
There are no ring outliers.

8 monomers are involved in 18 short contacts:

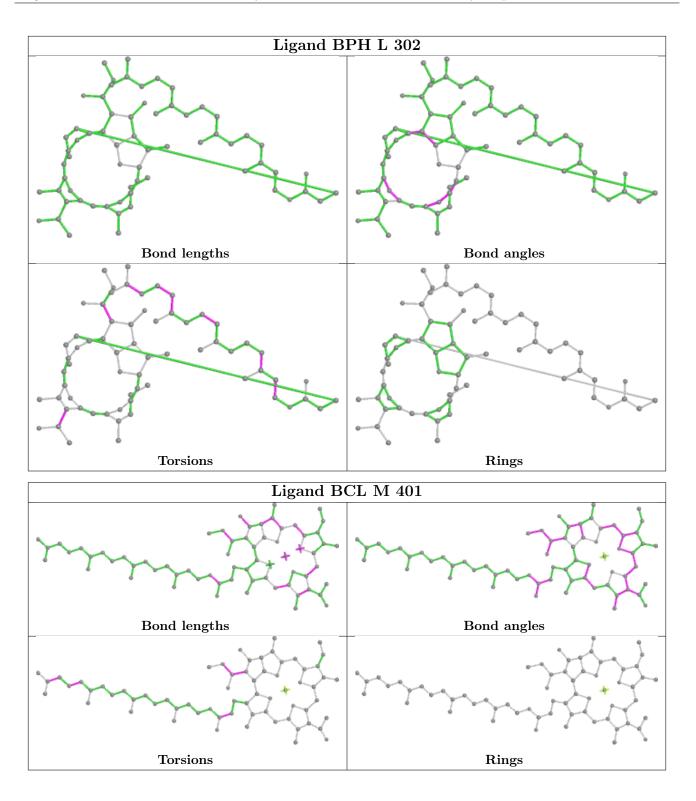
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	М	408	U10	1	0
5	L	301	BCL	2	0
6	L	302	BPH	1	0
5	М	401	BCL	5	0
10	М	410	CDL	1	0
5	L	304	BCL	3	0
6	М	407	BPH	3	0
5	L	305	BCL	2	0

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.

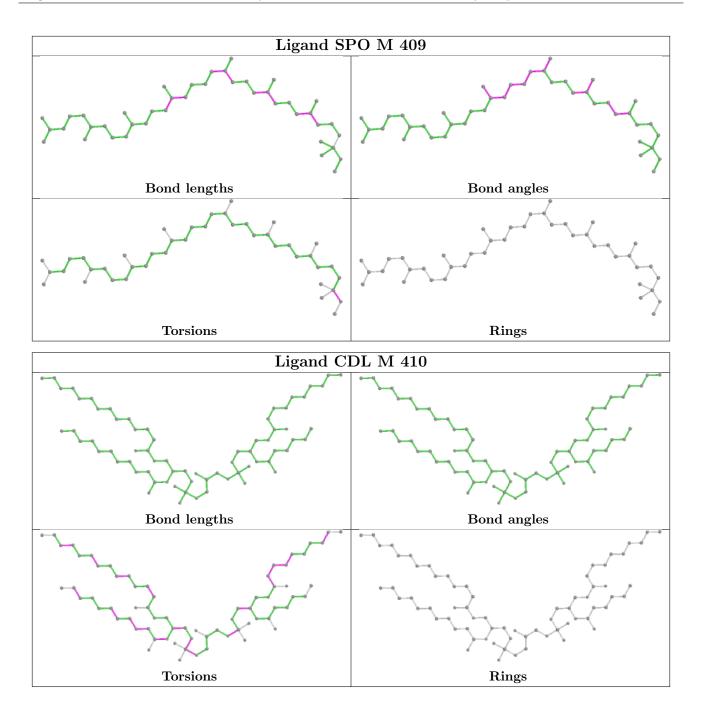




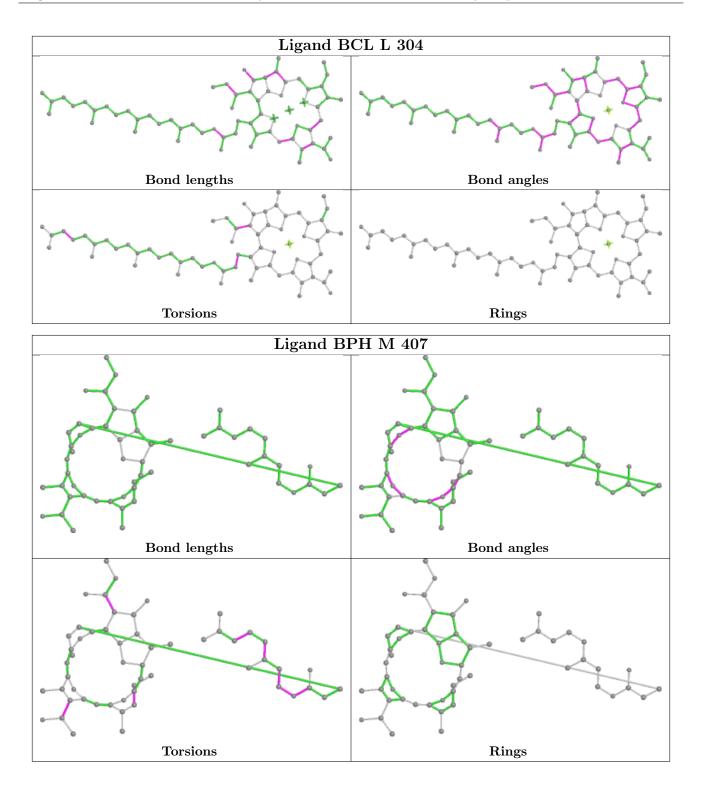




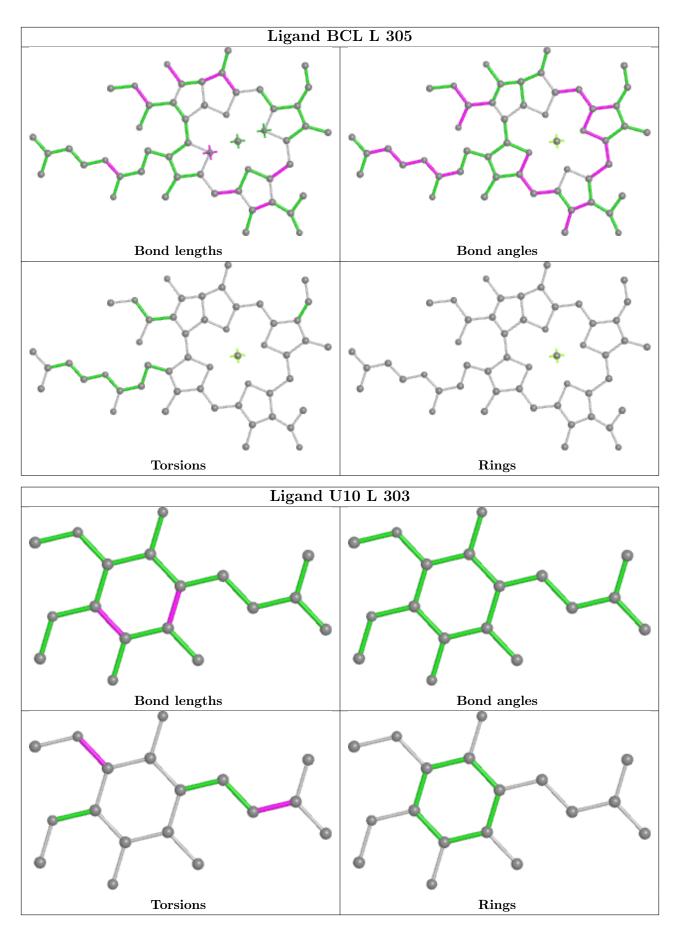














5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	$\langle RSRZ \rangle$	# RSR	2Z>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	Н	239/266~(89%)	-0.49	5 (2%) 6	3 72	47, 61, 83, 95	0
2	L	281/282 (99%)	-0.28	12 (4%) 3	35 42	47, 59, 96, 112	0
3	М	300/308~(97%)	-0.44	2 (0%) 8	7 91	43, 63, 94, 119	0
All	All	820/856~(95%)	-0.40	19 (2%) 6	60 69	43, 61, 92, 119	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	72	GLU	3.9
2	L	59	TRP	3.8
2	L	202	LYS	3.8
2	L	270	PRO	3.4
1	Н	146	LYS	2.9

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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
3	ZDJ	М	210	13/14	0.96	0.18	50,52,54,54	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.



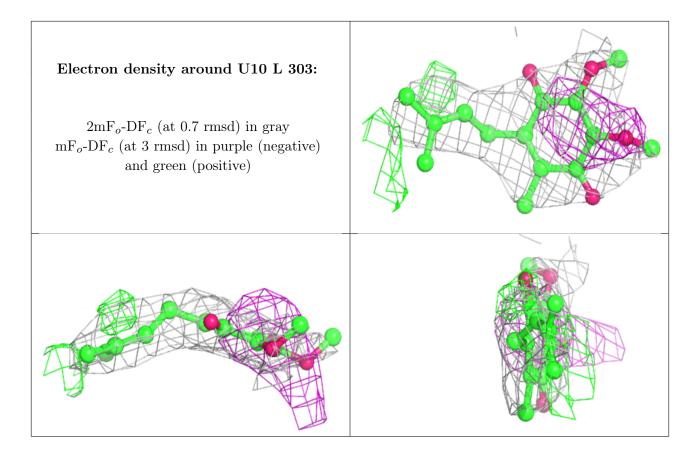
6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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.

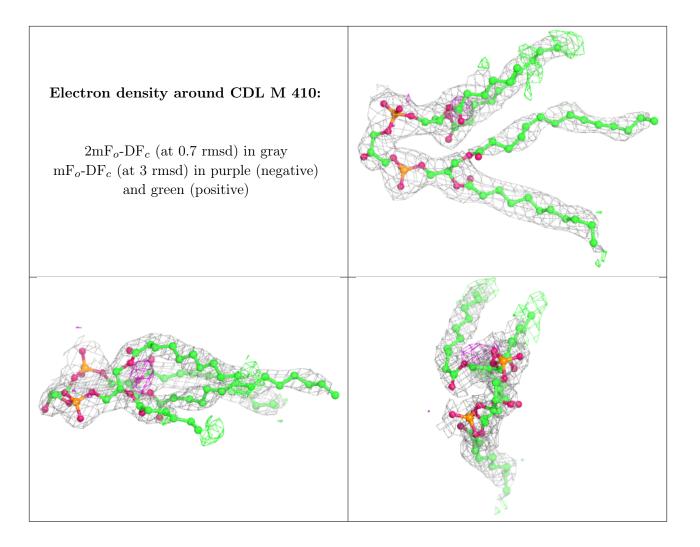
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
4	LDA	М	405	16/16	0.73	0.20	$95,\!104,\!139,\!143$	0
4	LDA	М	404	16/16	0.84	0.24	98,112,115,116	0
7	U10	L	303	18/63	0.86	0.27	86,89,94,95	0
10	CDL	М	410	69/100	0.86	0.25	79,110,130,150	0
4	LDA	М	403	16/16	0.88	0.40	90,99,121,123	0
4	LDA	М	402	16/16	0.92	0.22	80,84,87,89	0
9	SPO	М	409	42/42	0.93	0.21	61,74,104,110	0
4	LDA	Н	301	16/16	0.94	0.15	69,79,99,102	0
7	U10	М	408	48/63	0.95	0.22	47,64,112,115	0
5	BCL	L	304	66/66	0.96	0.15	48,54,71,83	0
6	BPH	М	407	55/65	0.96	0.16	52,61,88,89	0
5	BCL	L	305	51/66	0.97	0.16	49,51,73,79	0
5	BCL	М	401	66/66	0.97	0.17	49,54,81,97	0
6	BPH	L	302	65/65	0.97	0.14	41,51,65,67	0
5	BCL	L	301	66/66	0.97	0.14	43,47,81,87	0
8	\mathbf{FE}	М	406	1/1	0.99	0.12	50, 50, 50, 50	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.

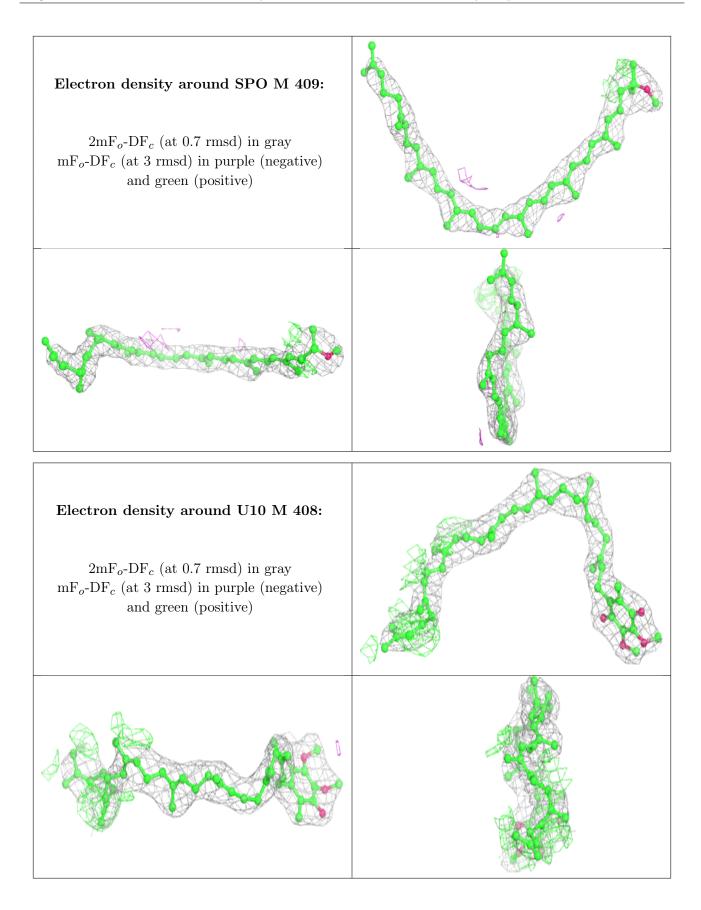




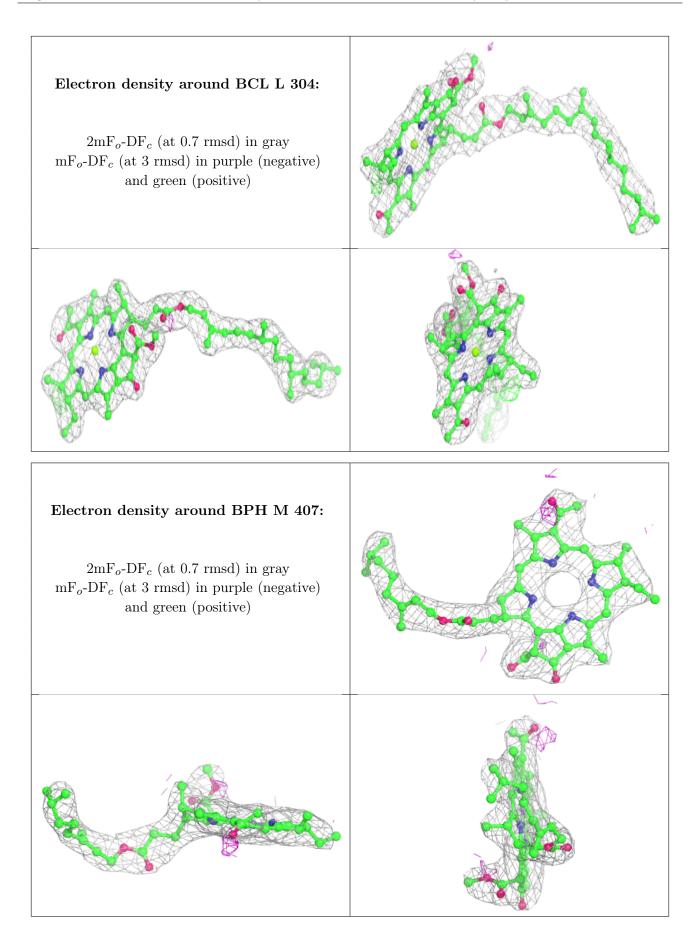




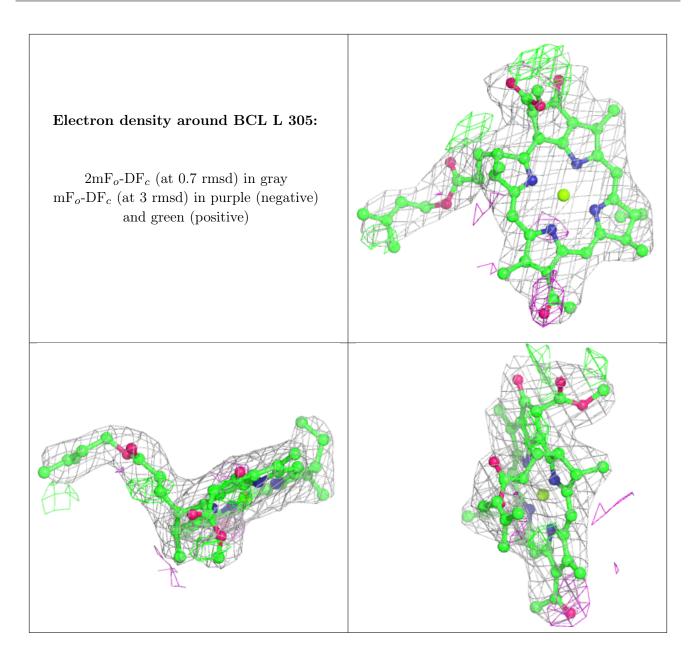




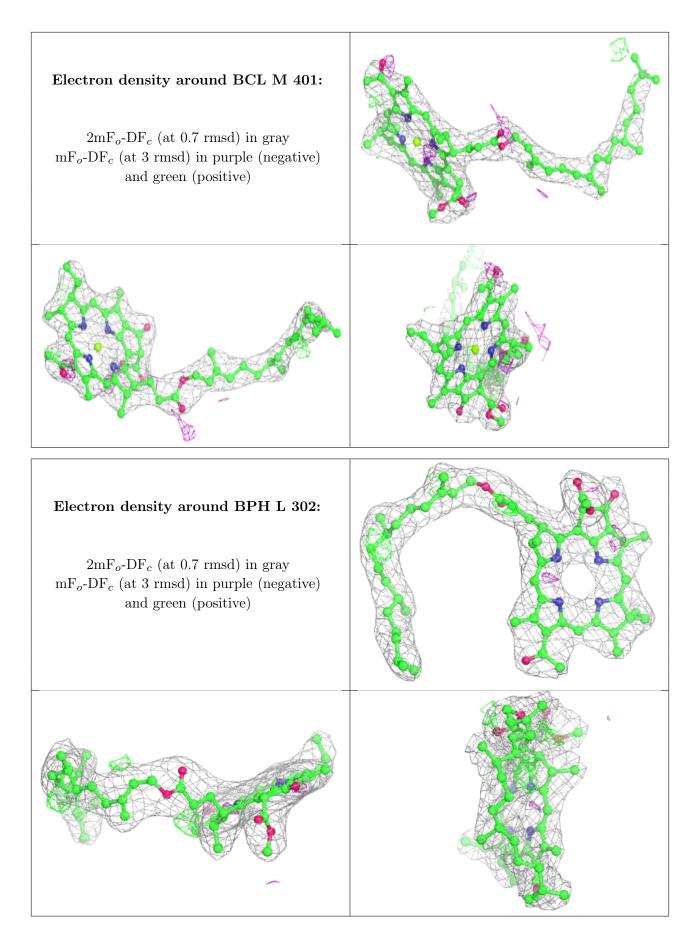




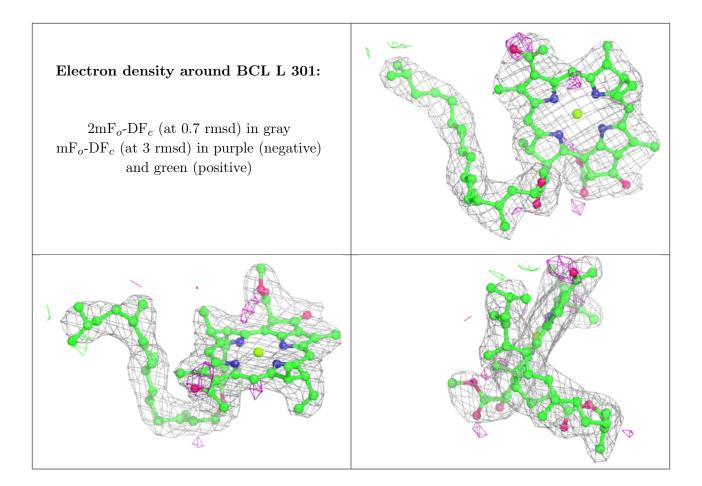












6.5 Other polymers (i)

There are no such residues in this entry.

