wwPDB X-ray Structure Validation Summary Report (i)

Aug 22, 2026 – 05:41 am BST

PDB ID	:	2UXM / pdb_00002uxm
Title	:	X-ray high resolution structure of the photosynthetic reaction center from Rb. sphaeroides at pH 10 in the charge-separated state, 2nd dataset
Authors	:	Koepke, J.; Diehm, R.; Fritzsch, G.
Deposited on	:	2007-03-28
Resolution	:	2.70 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:

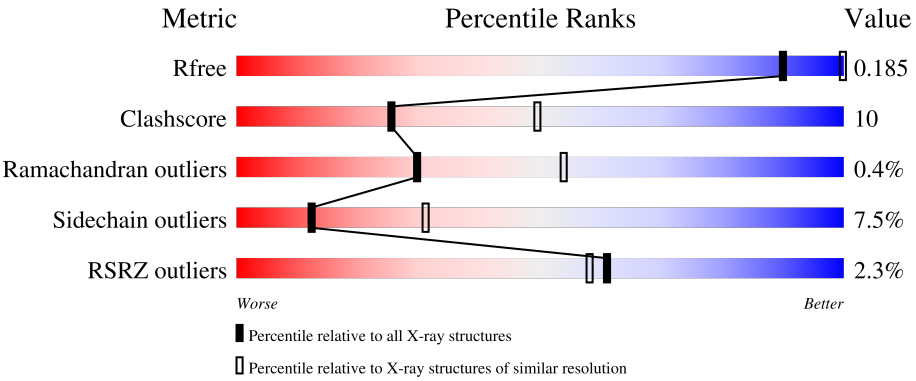
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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% 73% 18% 7%
2	L	281	% 86% 14%
3	M	307	3% 77% 20%

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	BCL	L	301	X	-	-	-
5	BCL	L	302	X	-	-	-
5	BCL	M	401	X	-	-	-
5	BCL	M	402	X	-	-	-
6	LDA	M	405	-	-	X	-

2 Entry composition (i)

There are 14 unique types of molecules in this entry. The entry contains 7442 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	241	1846	1181	319	337	9	0	3	1

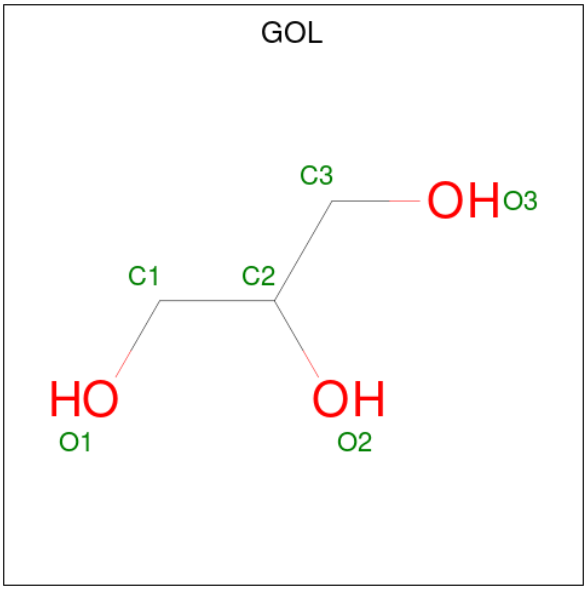
- Molecule 2 is a protein called REACTION CENTER PROTEIN L CHAIN.

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

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

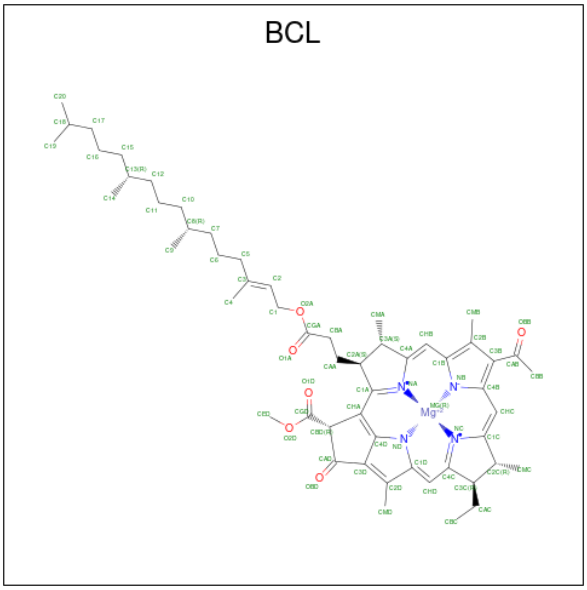
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	M	303	2409	1607	395	397	10	0	0	1

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



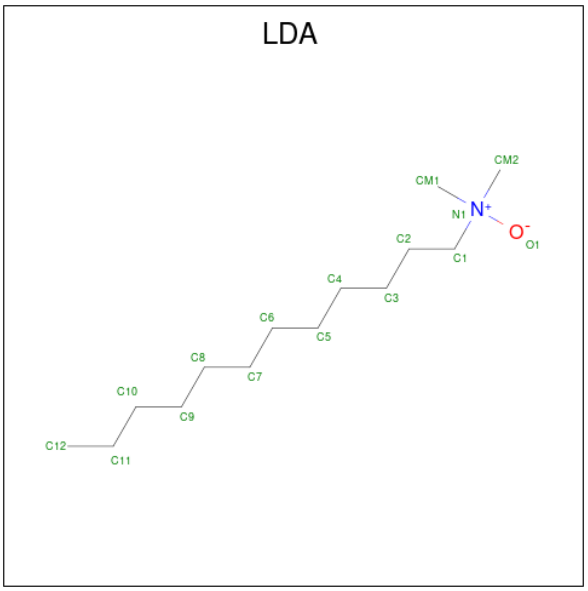
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total C O 6 3 3	0	0
4	L	1	Total C O 6 3 3	0	0
4	L	1	Total C O 6 3 3	0	0
4	L	1	Total C O 6 3 3	0	0

- Molecule 5 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $C_{55}H_{74}MgN_4O_6$).



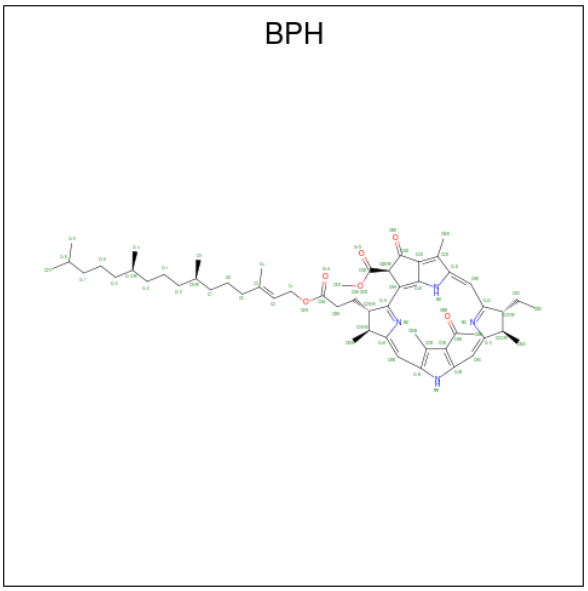
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	L	1	Total C Mg N O 66 55 1 4 6	0	0
5	L	1	Total C Mg N O 66 55 1 4 6	0	0
5	M	1	Total C Mg N O 66 55 1 4 6	0	0
5	M	1	Total C Mg N O 66 55 1 4 6	0	0

- Molecule 6 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: $C_{14}H_{31}NO$).



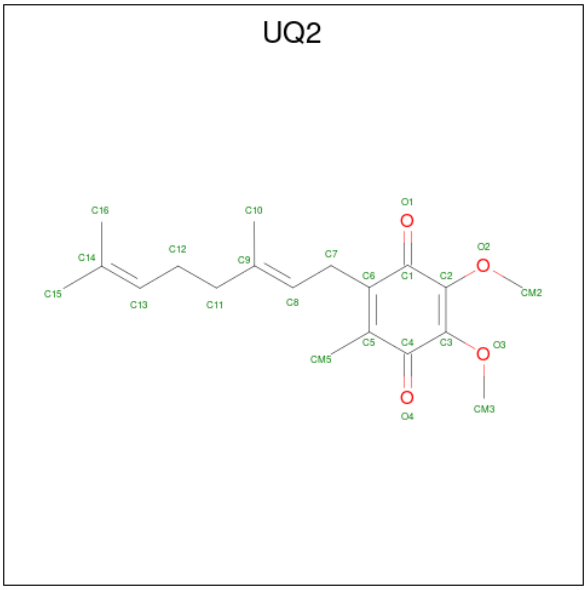
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	L	1	Total C N O 16 14 1 1	0	0
6	L	1	Total C N O 16 14 1 1	0	0
6	L	1	Total C N O 16 14 1 1	0	0
6	L	1	Total C N O 16 14 1 1	0	0
6	L	1	Total C N O 16 14 1 1	0	0
6	M	1	Total C N O 16 14 1 1	0	0
6	M	1	Total C N O 16 14 1 1	0	0
6	M	1	Total C N O 16 14 1 1	0	0
6	M	1	Total C N O 16 14 1 1	0	0

- Molecule 7 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$).



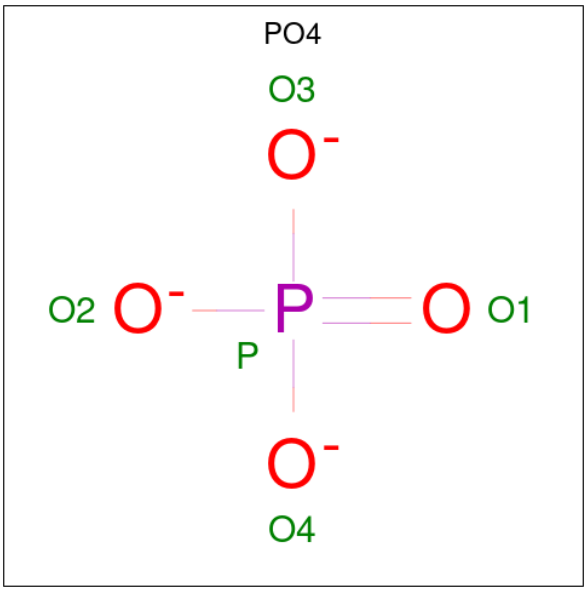
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	L	1	Total C N O 65 55 4 6	0	0
7	L	1	Total C N O 65 55 4 6	0	0

- Molecule 8 is UBIQUINONE-2 (CCD ID: UQ2) (formula: $C_{19}H_{26}O_4$).



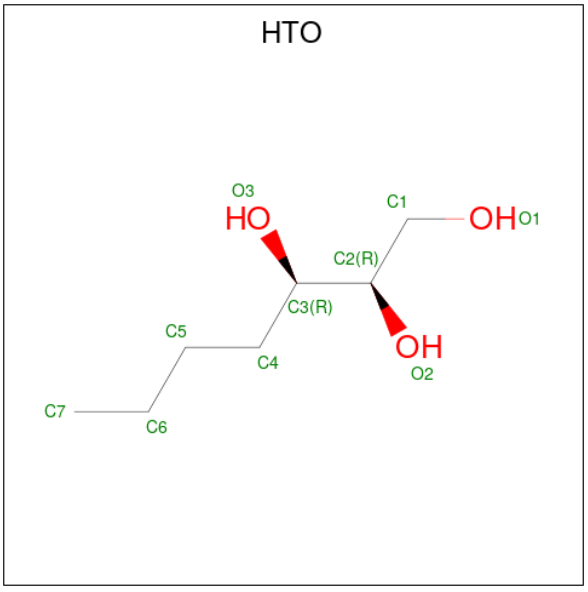
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	L	1	Total C O 46 38 8	0	1

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



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

- Molecule 10 is HEPTANE-1,2,3-TRIOL (CCD ID: HTO) (formula: $C_7H_{16}O_3$).

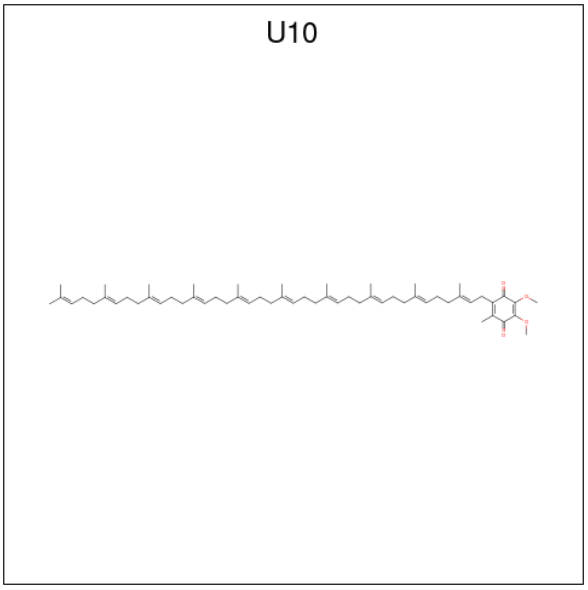


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	L	1	Total C O 10 7 3	0	0

- Molecule 11 is FE (III) ION (CCD ID: FE) (formula: Fe).

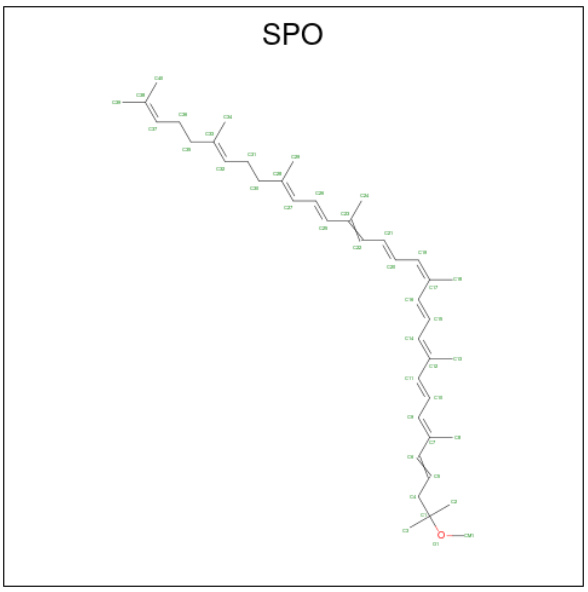
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	M	1	Total Fe 1 1	0	0

- Molecule 12 is UBIQUINONE-10 (CCD ID: U10) (formula: $C_{59}H_{90}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	M	1	Total C O 48 44 4	0	0

- Molecule 13 is SPHEROIDENE (CCD ID: SPO) (formula: $C_{41}H_{60}O$).



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

- Molecule 14 is water.

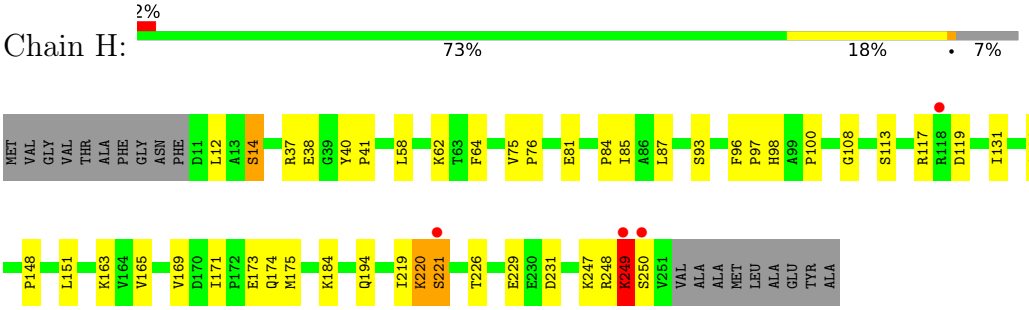
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	H	79	Total	O	0	0
			79	79		
14	L	91	Total	O	0	0
			91	91		
14	M	71	Total	O	0	0
			71	71		

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.

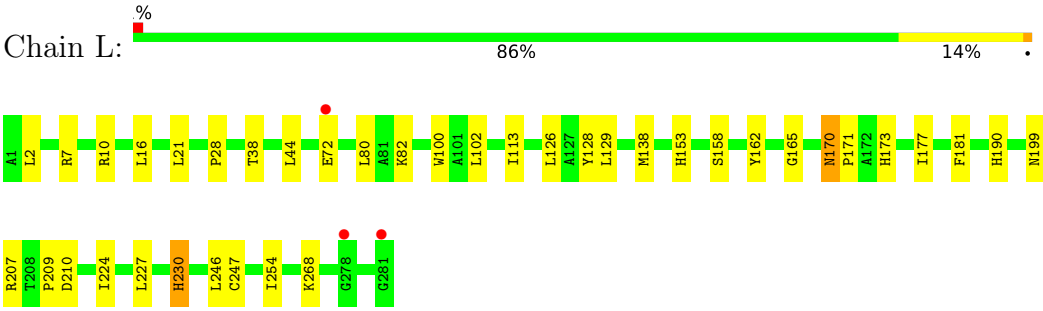
• Molecule 1: REACTION CENTER PROTEIN H CHAIN

Chain H:



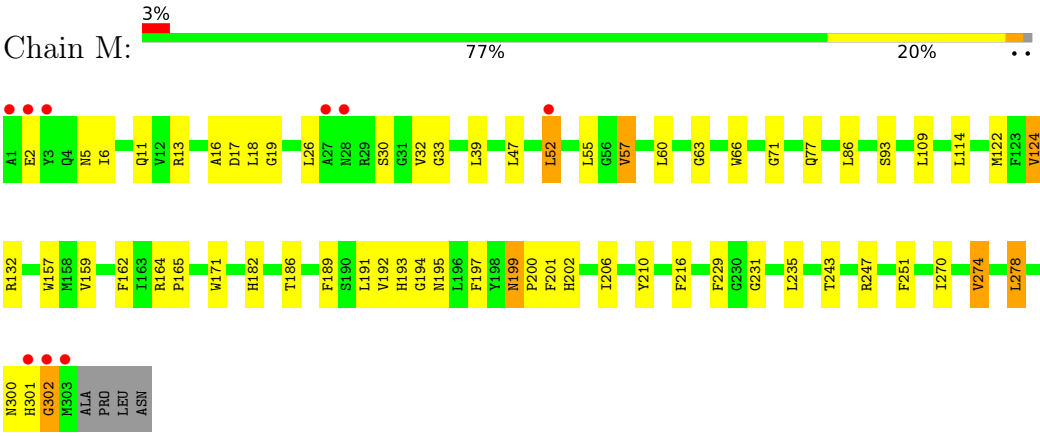
• Molecule 2: REACTION CENTER PROTEIN L CHAIN

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	139.45Å 139.45Å 185.11Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	119.52 – 2.70 119.52 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.4 (119.52-2.70) 90.4 (119.52-2.70)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.37 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.186 , 0.221 0.182 , 0.185	Depositor DCC
R_{free} test set	3339 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	41.9	Xtriage
Anisotropy	0.226	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 49.9	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	7442	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCL, GOL, BPH, FE, PO4, UQ2, U10, HTO, SPO, LDA

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	0.83	1/1906 (0.1%)	0.98	4/2591 (0.2%)
2	L	0.84	1/2320 (0.0%)	0.95	1/3175 (0.0%)
3	M	0.82	3/2501 (0.1%)	1.00	2/3415 (0.1%)
All	All	0.83	5/6727 (0.1%)	0.98	7/9181 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	250	SER	C-N	-6.28	1.24	1.33
3	M	302	GLY	C-N	-5.63	1.25	1.33
2	L	138	MET	SD-CE	5.62	1.93	1.79
3	M	57	VAL	CA-CB	5.56	1.60	1.54
3	M	124	VAL	CA-CB	5.52	1.61	1.54

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	M	19	GLY	N-CA-C	5.65	119.17	112.33
1	H	250	SER	O-C-N	-5.28	114.55	123.00
2	L	230	HIS	N-CA-C	-5.17	105.33	111.69
1	H	248	ARG	CA-C-N	5.10	130.88	121.70
1	H	248	ARG	C-N-CA	5.10	130.88	121.70

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	H	1846	0	1861	30	0
2	L	2232	0	2187	26	0
3	M	2409	0	2321	51	0
4	H	6	0	8	0	0
4	L	18	0	24	2	0
5	L	132	0	148	10	0
5	M	132	0	148	20	0
6	L	80	0	155	11	0
6	M	64	0	124	11	0
7	L	130	0	152	14	0
8	L	46	0	52	13	0
9	L	5	0	0	0	0
10	L	10	0	16	0	0
11	M	1	0	0	0	0
12	M	48	0	63	4	0
13	M	42	0	60	6	0
14	H	79	0	0	1	1
14	L	91	0	0	2	0
14	M	71	0	0	0	0
All	All	7442	0	7319	140	1

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 10.

The worst 5 of 140 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)
8:L:305[A]:UQ2:H152	6:L:311:LDA:H111	1.47	0.97
5:M:402:BCL:HBB3	5:M:402:BCL:HHC	1.50	0.91
8:L:305[B]:UQ2:H162	6:L:313:LDA:H121	1.56	0.87
2:L:72:GLU:HB3	14:L:416:HOH:O	1.74	0.87
1:H:249:LYS:HE3	1:H:249:LYS:HA	1.59	0.84

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:H:457:HOH:O	14:H:457:HOH:O[4_555]	1.99	0.21

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	242/260 (93%)	233 (96%)	8 (3%)	1 (0%)	30 54
2	L	279/281 (99%)	266 (95%)	13 (5%)	0	100 100
3	M	301/307 (98%)	282 (94%)	17 (6%)	2 (1%)	18 41
All	All	822/848 (97%)	781 (95%)	38 (5%)	3 (0%)	30 54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	249	LYS
3	M	52	LEU
3	M	301	HIS

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	198/208 (95%)	186 (94%)	12 (6%)	17 40
2	L	220/220 (100%)	203 (92%)	17 (8%)	12 30
3	M	236/240 (98%)	215 (91%)	21 (9%)	9 23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	654/668 (98%)	604 (92%)	50 (8%)	12 30

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	268	LYS
3	M	52	LEU
3	M	278	LEU
3	M	2	GLU
3	M	18	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
3	M	187	ASN
3	M	193	HIS
3	M	199	ASN
2	L	170	ASN
2	L	258	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 26 ligands modelled in this entry, 1 is monoatomic - leaving 25 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	LDA	M	406	-	12,15,15	1.98	1 (8%)	14,17,17	0.52	0
5	BCL	L	302	2	69,74,74	1.89	9 (13%)	83,115,115	2.59	26 (31%)
8	UQ2	L	305[A]	-	23,23,23	2.80	7 (30%)	28,31,31	1.19	1 (3%)
6	LDA	M	405	-	12,15,15	2.02	1 (8%)	14,17,17	0.58	0
7	BPH	L	304	-	59,70,70	2.71	10 (16%)	61,101,101	2.48	18 (29%)
6	LDA	L	310	-	12,15,15	2.09	1 (8%)	14,17,17	0.69	0
4	GOL	L	315	-	5,5,5	0.36	0	5,5,5	0.47	0
5	BCL	M	402	3	69,74,74	1.86	8 (11%)	83,115,115	2.43	27 (32%)
5	BCL	L	301	2	69,74,74	1.86	9 (13%)	83,115,115	2.45	24 (28%)
6	LDA	M	404	-	12,15,15	2.05	1 (8%)	14,17,17	0.51	0
13	SPO	M	409	-	40,41,41	4.25	12 (30%)	47,50,50	1.95	12 (25%)
9	PO4	L	306	-	4,4,4	0.84	0	6,6,6	0.54	0
6	LDA	L	313	-	12,15,15	2.11	1 (8%)	14,17,17	0.76	0
6	LDA	L	303	-	12,15,15	1.98	1 (8%)	14,17,17	0.73	0
10	HTO	L	307	-	9,9,9	0.56	0	10,10,10	0.69	0
6	LDA	L	312	-	12,15,15	2.03	1 (8%)	14,17,17	0.56	0
12	U10	M	408	-	48,48,63	2.76	12 (25%)	58,61,79	1.60	13 (22%)
4	GOL	L	309	-	5,5,5	0.29	0	5,5,5	0.41	0
6	LDA	M	403	-	12,15,15	2.04	1 (8%)	14,17,17	0.94	1 (7%)
4	GOL	H	301	-	5,5,5	0.38	0	5,5,5	0.36	0
6	LDA	L	311	-	12,15,15	2.11	1 (8%)	14,17,17	0.64	0
8	UQ2	L	305[B]	-	23,23,23	2.71	8 (34%)	28,31,31	1.64	6 (21%)
7	BPH	L	314	-	59,70,70	2.77	11 (18%)	61,101,101	2.58	18 (29%)
5	BCL	M	401	3	69,74,74	1.95	10 (14%)	83,115,115	2.21	24 (28%)
4	GOL	L	308	-	5,5,5	0.35	0	5,5,5	0.57	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
6	LDA	M	406	-	-	11/13/13/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BCL	L	302	2	2/2/21/25	10/41/137/137	-
8	UQ2	L	305[A]	-	-	6/15/39/39	0/1/1/1
6	LDA	M	405	-	-	4/13/13/13	-
7	BPH	L	304	-	-	9/37/105/105	0/5/6/6
6	LDA	L	310	-	-	5/13/13/13	-
4	GOL	L	315	-	-	2/4/4/4	-
5	BCL	M	402	3	2/2/21/25	4/41/137/137	-
5	BCL	L	301	2	2/2/21/25	10/41/137/137	-
6	LDA	M	404	-	-	5/13/13/13	-
13	SPO	M	409	-	-	11/47/47/47	-
6	LDA	L	313	-	-	4/13/13/13	-
6	LDA	L	303	-	-	10/13/13/13	-
10	HTO	L	307	-	-	9/10/10/10	-
6	LDA	L	312	-	-	9/13/13/13	-
12	U10	M	408	-	-	11/45/69/87	0/1/1/1
4	GOL	L	309	-	-	4/4/4/4	-
6	LDA	M	403	-	-	5/13/13/13	-
4	GOL	H	301	-	-	2/4/4/4	-
6	LDA	L	311	-	-	6/13/13/13	-
8	UQ2	L	305[B]	-	-	6/15/39/39	0/1/1/1
7	BPH	L	314	-	-	19/37/105/105	0/5/6/6
5	BCL	M	401	3	2/2/21/25	15/41/137/137	-
4	GOL	L	308	-	-	2/4/4/4	-

The worst 5 of 105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	M	409	SPO	C27-C28	13.69	1.48	1.34
7	L	314	BPH	OBD-CAD	13.59	1.41	1.22
7	L	304	BPH	OBD-CAD	12.46	1.39	1.22
5	L	302	BCL	OBD-CAD	10.83	1.41	1.22
5	M	401	BCL	OBD-CAD	10.45	1.40	1.22

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	L	314	BPH	O2D-CGD-CBD	9.28	122.75	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	L	301	BCL	C1D-ND-C4D	9.22	112.88	106.33
7	L	304	BPH	O2D-CGD-CBD	9.07	122.49	111.00
5	L	301	BCL	C2D-C1D-ND	-9.06	103.43	110.10
5	L	301	BCL	CHD-C1D-ND	-7.96	117.14	124.45

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	L	301	BCL	C13
5	L	301	BCL	C8
5	L	302	BCL	C13
5	L	302	BCL	C8
5	M	401	BCL	C13

5 of 179 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	308	GOL	C1-C2-C3-O3
4	L	309	GOL	C1-C2-C3-O3
4	L	315	GOL	C1-C2-C3-O3
5	L	301	BCL	C11-C12-C13-C14
5	M	401	BCL	C1-C2-C3-C4

There are no ring outliers.

18 monomers are involved in 73 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	302	BCL	5	0
8	L	305[A]	UQ2	5	0
6	M	405	LDA	10	0
7	L	304	BPH	8	0
6	L	310	LDA	4	0
4	L	315	GOL	1	0
5	M	402	BCL	14	0
5	L	301	BCL	6	0
13	M	409	SPO	6	0
6	L	313	LDA	4	0
6	L	303	LDA	1	0
12	M	408	U10	4	0
6	M	403	LDA	3	0
6	L	311	LDA	2	0
8	L	305[B]	UQ2	8	0

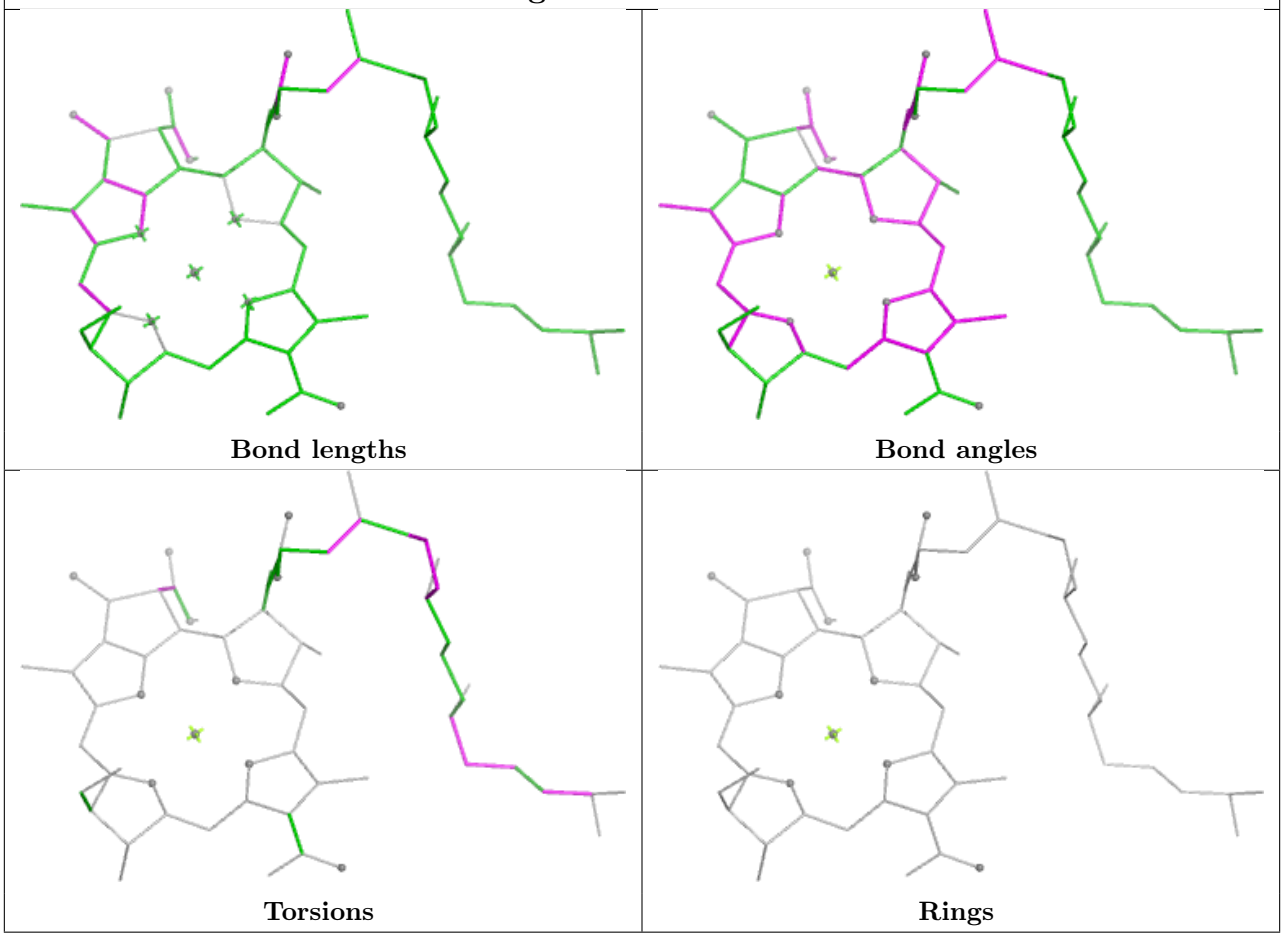
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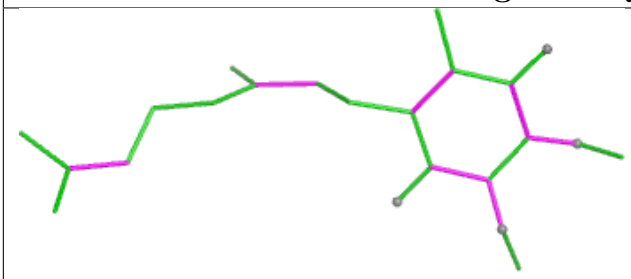
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	L	314	BPH	6	0
5	M	401	BCL	6	0
4	L	308	GOL	1	0

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.

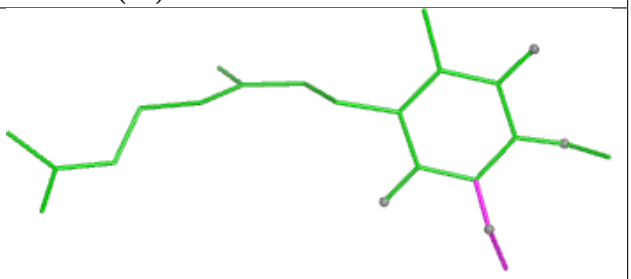
Ligand BCL L 302



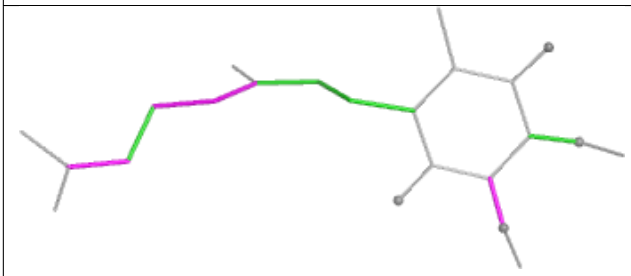
Ligand UQ2 L 305 (A)



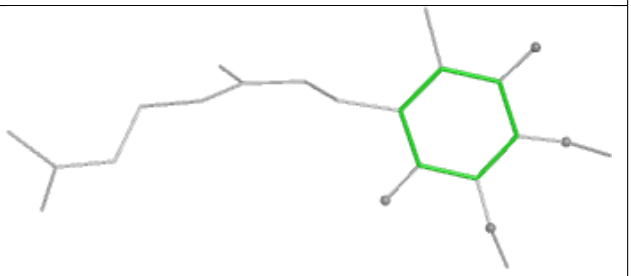
Bond lengths



Bond angles

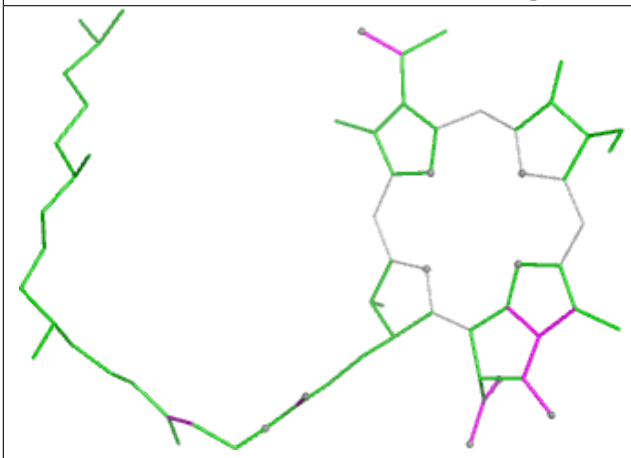


Torsions

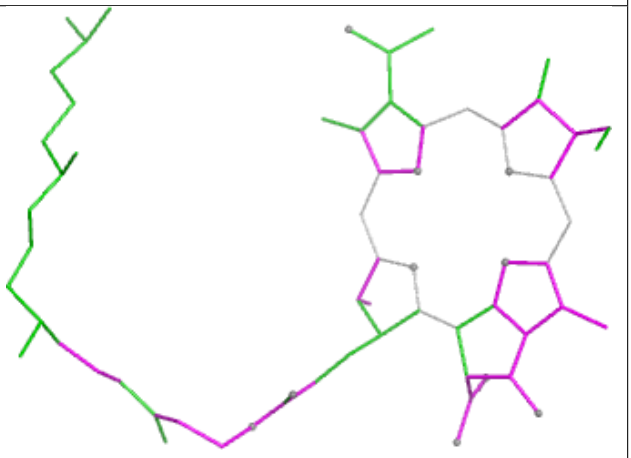


Rings

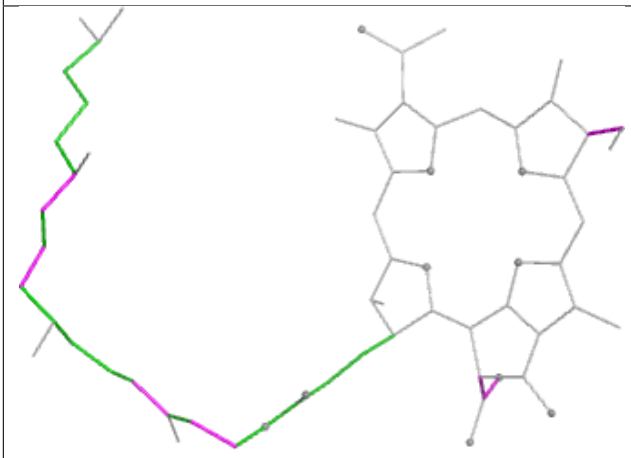
Ligand BPH L 304



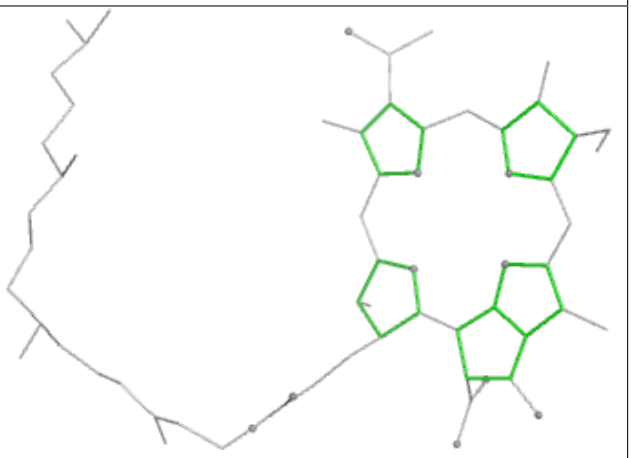
Bond lengths



Bond angles

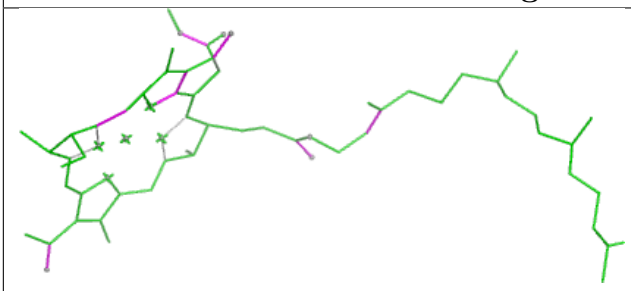


Torsions

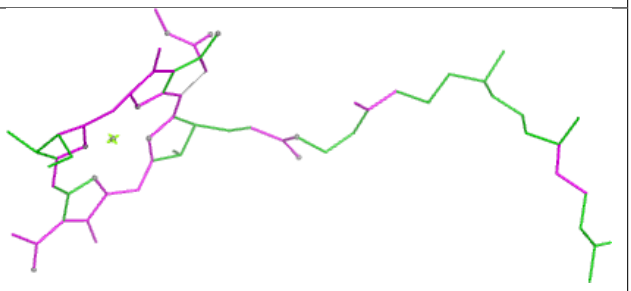


Rings

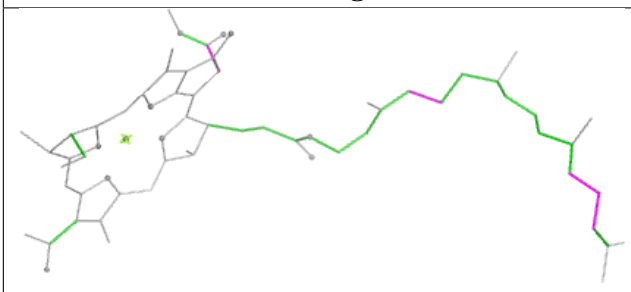
Ligand BCL M 402



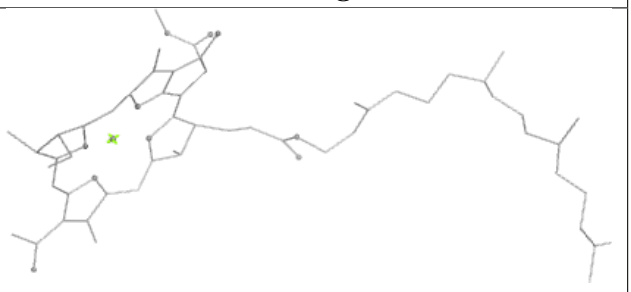
Bond lengths



Bond angles

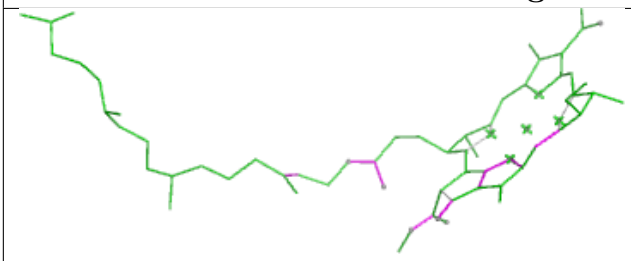


Torsions

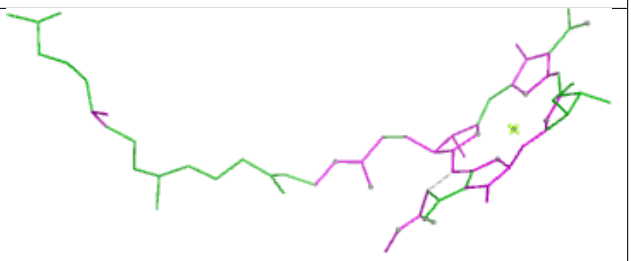


Rings

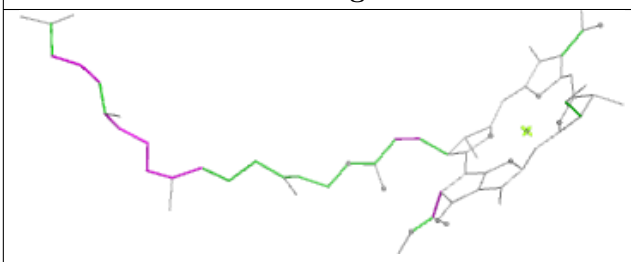
Ligand BCL L 301



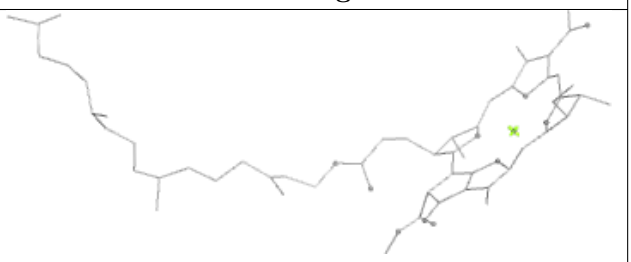
Bond lengths



Bond angles

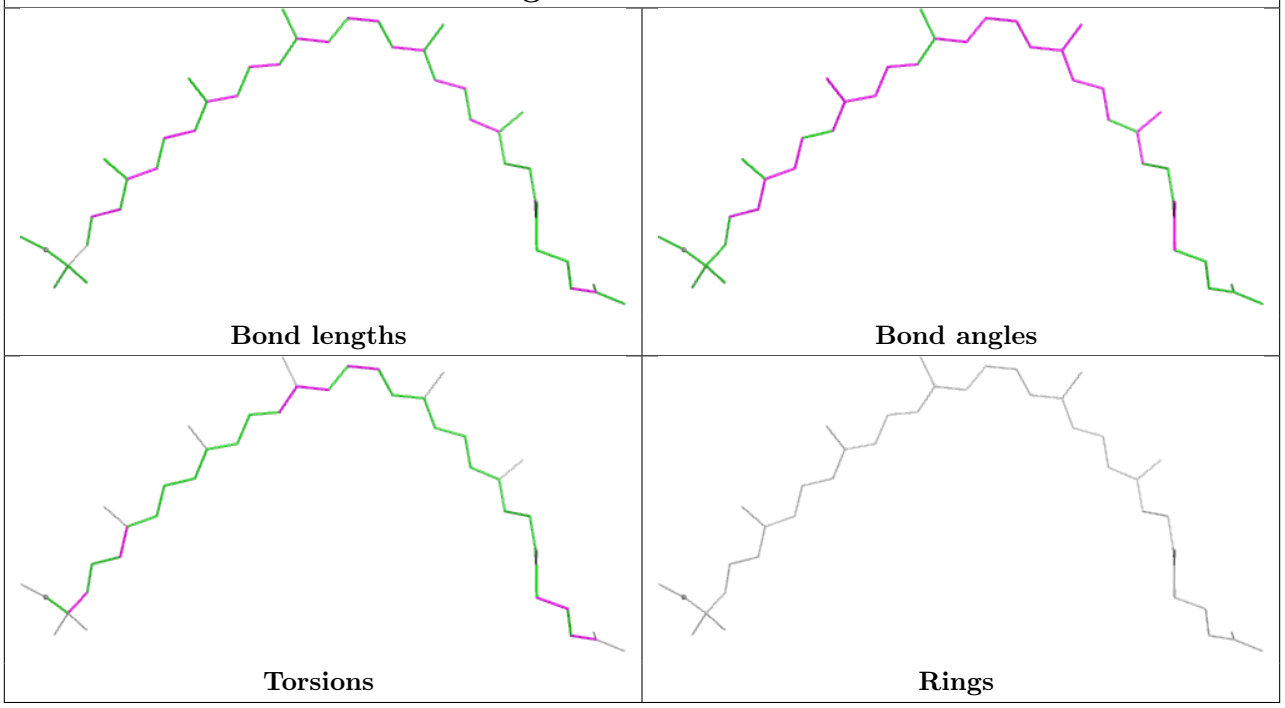


Torsions

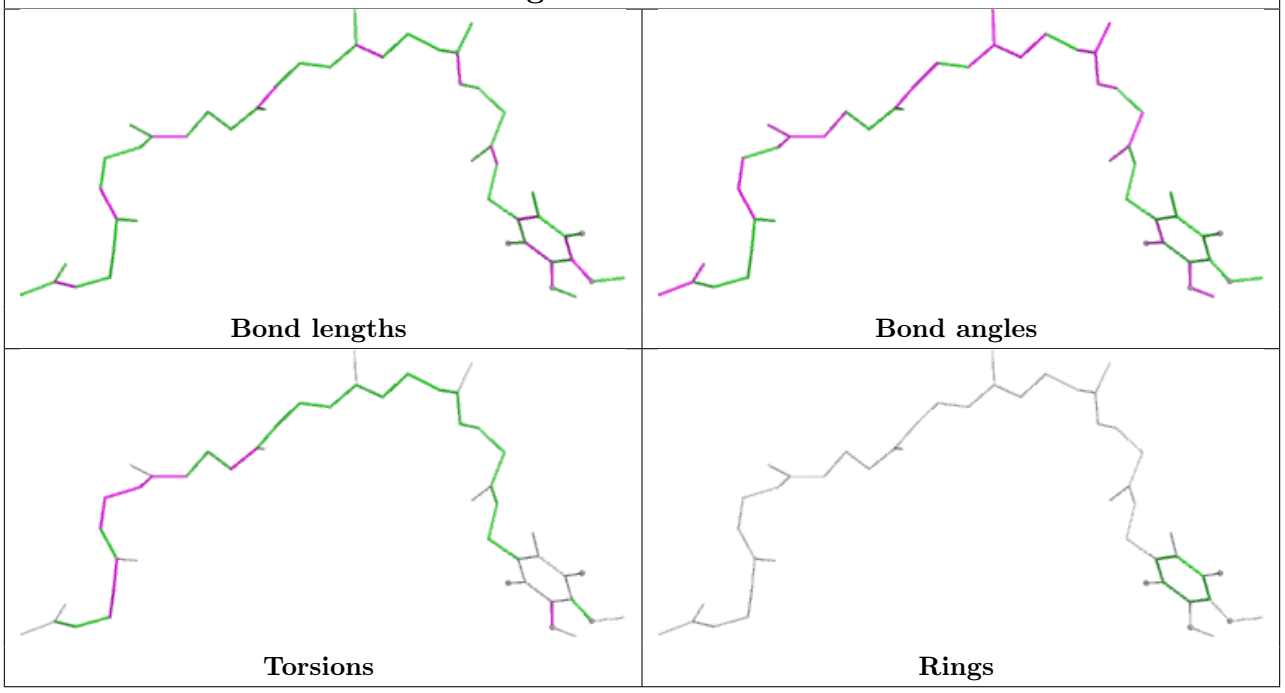


Rings

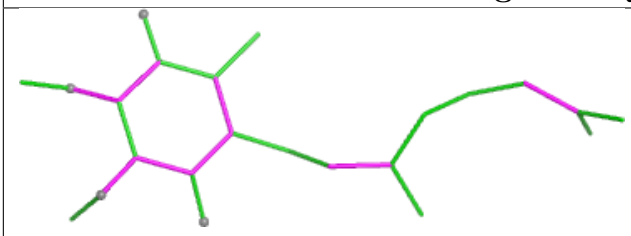
Ligand SPO M 409



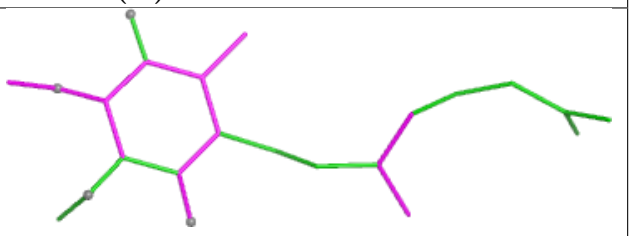
Ligand U10 M 408



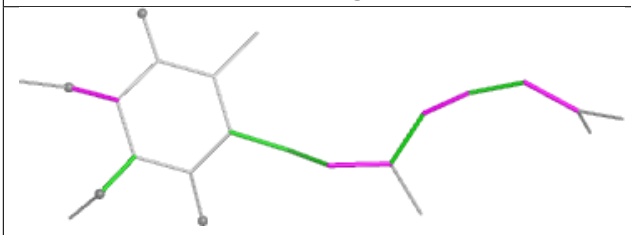
Ligand UQ2 L 305 (B)



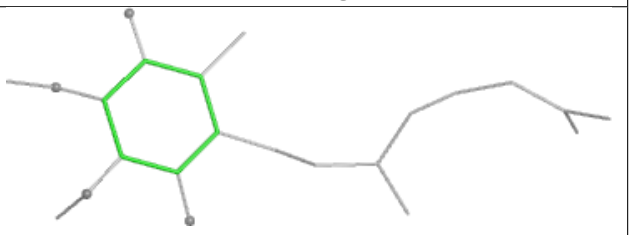
Bond lengths



Bond angles

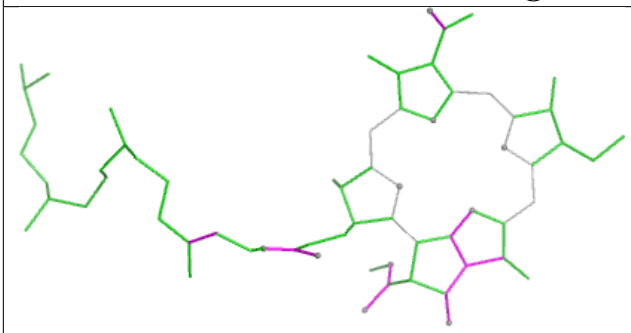


Torsions

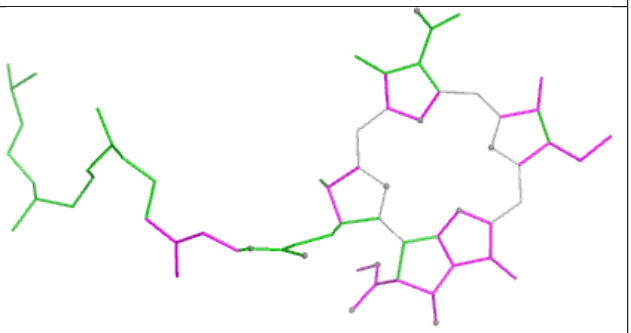


Rings

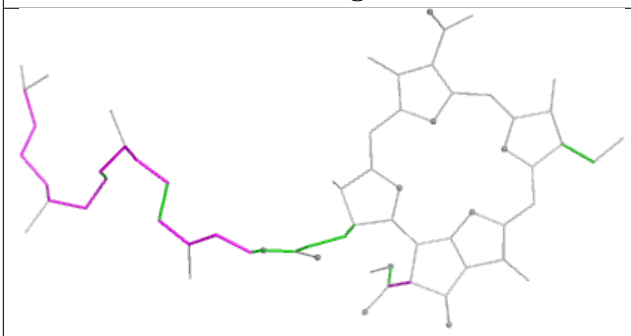
Ligand BPH L 314



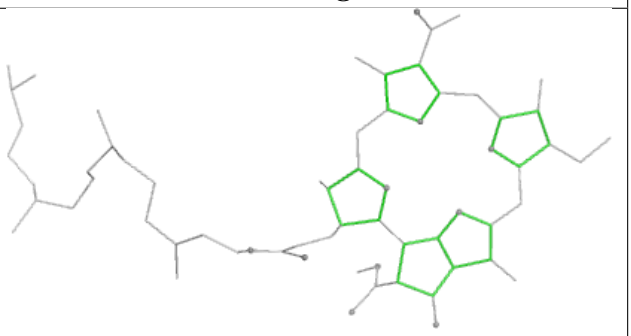
Bond lengths



Bond angles

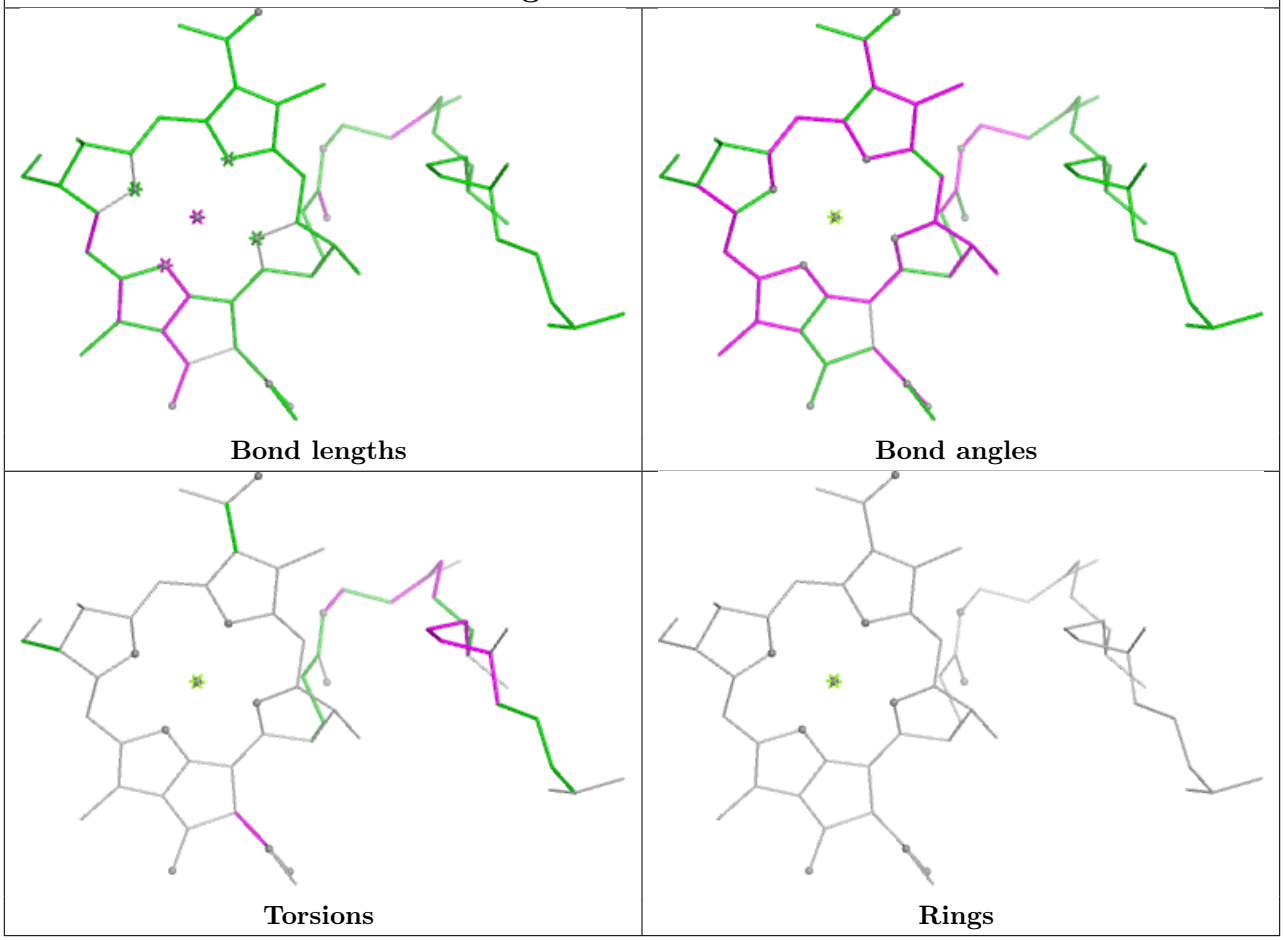


Torsions



Rings

Ligand BCL M 401



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

6.1 Protein, DNA and RNA chains

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	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	H	241/260 (92%)	-0.14	5 (2%)	63	61	27, 50, 63, 104	3 (1%)
2	L	281/281 (100%)	-0.36	4 (1%)	73	72	32, 43, 69, 77	0
3	M	303/307 (98%)	-0.08	10 (3%)	49	45	31, 50, 75, 96	0
All	All	825/848 (97%)	-0.19	19 (2%)	61	58	27, 48, 71, 104	3 (0%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	249	LYS	7.5
3	M	1	ALA	5.7
1	H	250	SER	4.7
3	M	302	GLY	4.6
3	M	2	GLU	3.8

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

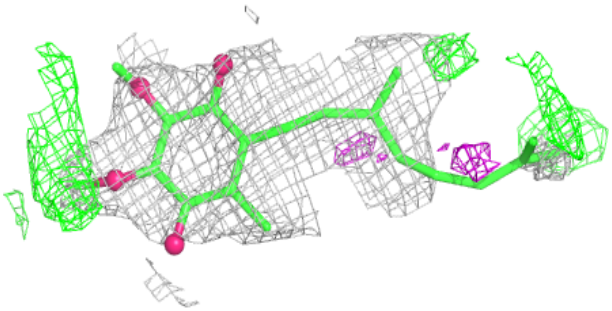
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

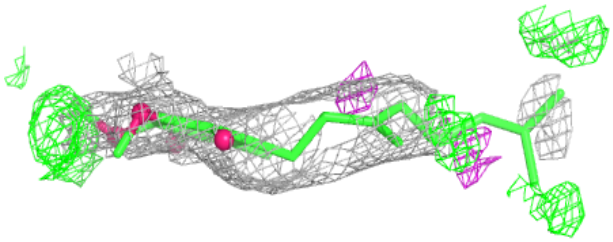
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	LDA	L	311	16/16	0.63	0.39	111,117,128,129	0
4	GOL	L	315	6/6	0.72	0.21	98,101,101,103	0
6	LDA	L	312	16/16	0.75	0.39	87,101,112,113	0
9	PO4	L	306	5/5	0.75	0.20	156,156,157,157	0
6	LDA	M	406	16/16	0.76	0.37	100,116,126,126	0
6	LDA	L	310	16/16	0.78	0.35	91,99,110,110	0
6	LDA	L	303	16/16	0.79	0.24	61,96,114,115	0
6	LDA	L	313	16/16	0.80	0.29	101,109,116,116	0
8	UQ2	L	305[B]	23/23	0.81	0.24	43,49,55,55	23
8	UQ2	L	305[A]	23/23	0.81	0.24	51,53,54,55	23
6	LDA	M	404	16/16	0.82	0.22	76,79,86,86	0
6	LDA	M	403	16/16	0.84	0.21	45,71,82,82	0
4	GOL	H	301	6/6	0.85	0.17	96,97,98,98	0
10	HTO	L	307	10/10	0.88	0.21	77,81,82,82	0
6	LDA	M	405	16/16	0.90	0.18	65,67,78,79	0
7	BPH	L	314	65/65	0.92	0.14	42,50,111,113	0
4	GOL	L	309	6/6	0.93	0.11	81,81,82,82	0
4	GOL	L	308	6/6	0.93	0.14	71,74,74,76	0
12	U10	M	408	48/63	0.94	0.13	37,48,78,80	0
5	BCL	M	401	66/66	0.95	0.10	30,34,81,82	0
5	BCL	L	302	66/66	0.95	0.08	30,37,58,62	0
13	SPO	M	409	42/42	0.95	0.12	44,60,78,81	0
5	BCL	L	301	66/66	0.97	0.07	30,36,47,52	0
7	BPH	L	304	65/65	0.97	0.07	26,32,41,43	0
5	BCL	M	402	66/66	0.97	0.08	29,39,60,70	0
11	FE	M	407	1/1	1.00	0.05	37,37,37,37	0

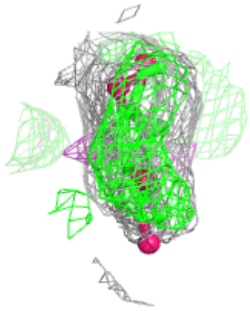
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around UQ2 L 305 (B):

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

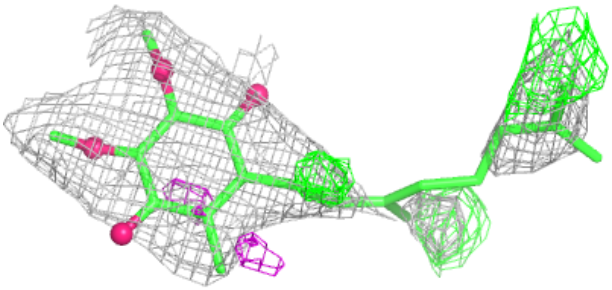


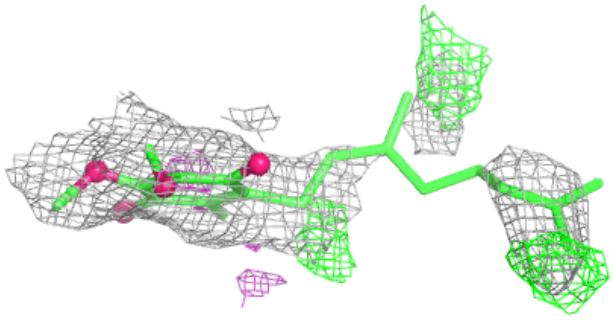


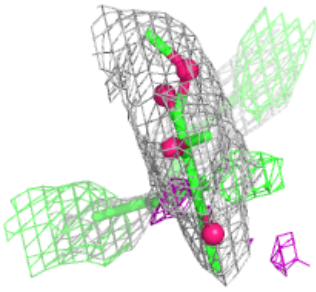


Electron density around UQ2 L 305 (A):

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

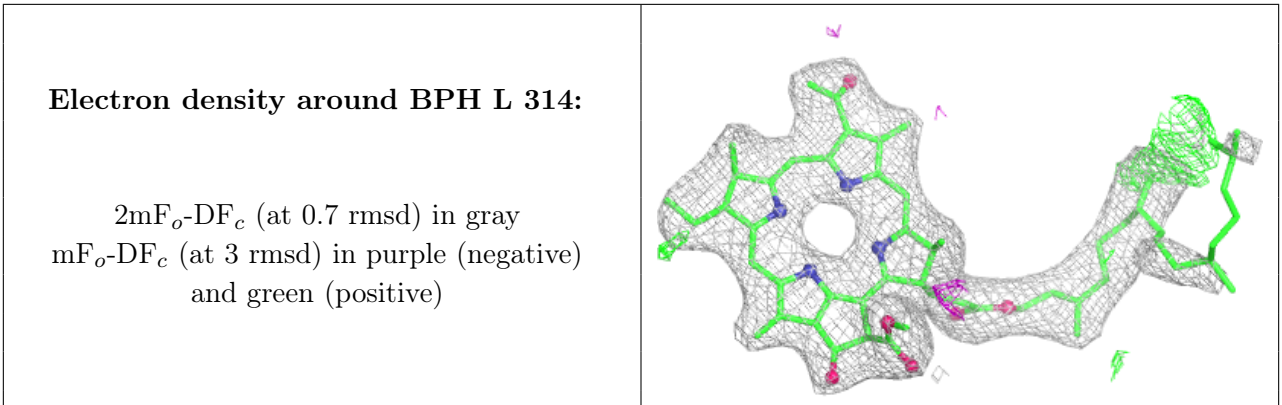


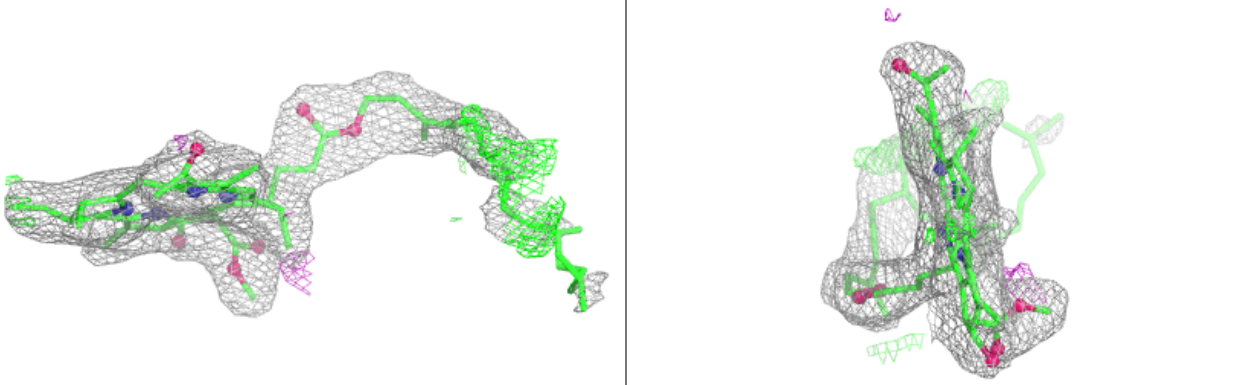




Electron density around BPH L 314:

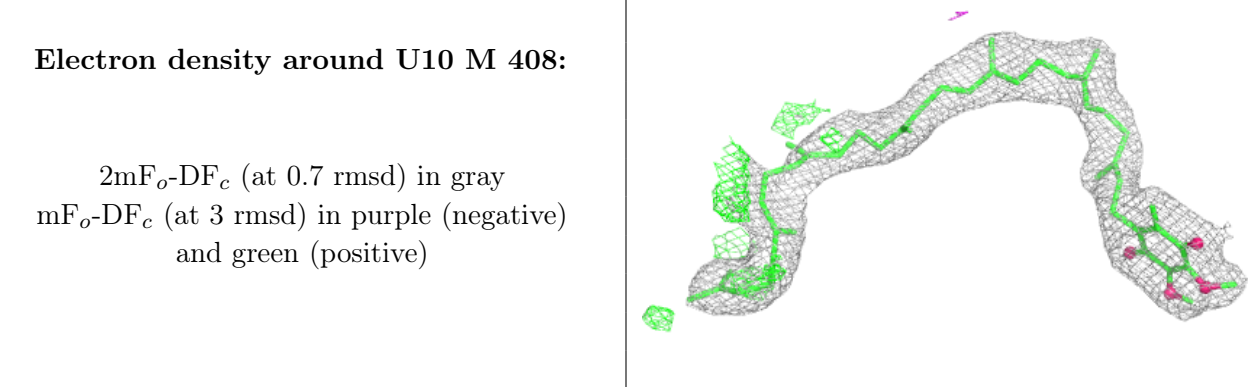
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

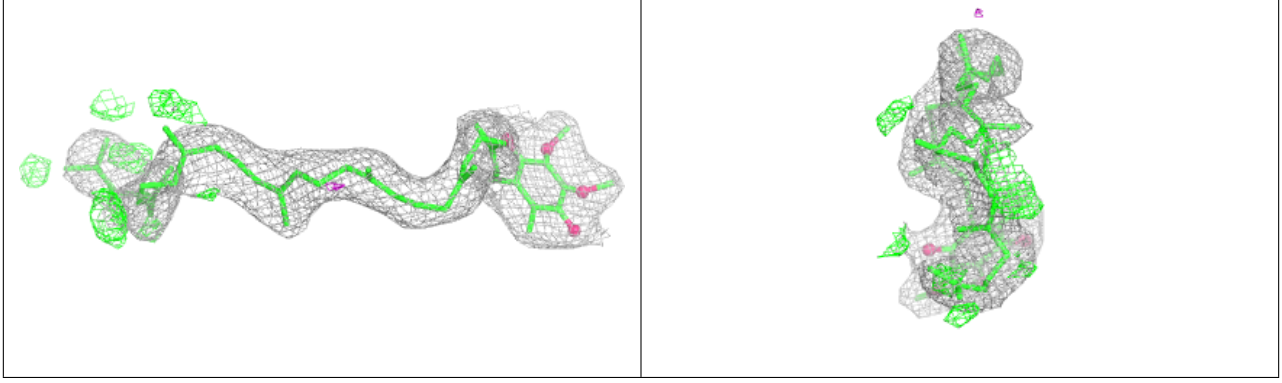




Electron density around U10 M 408:

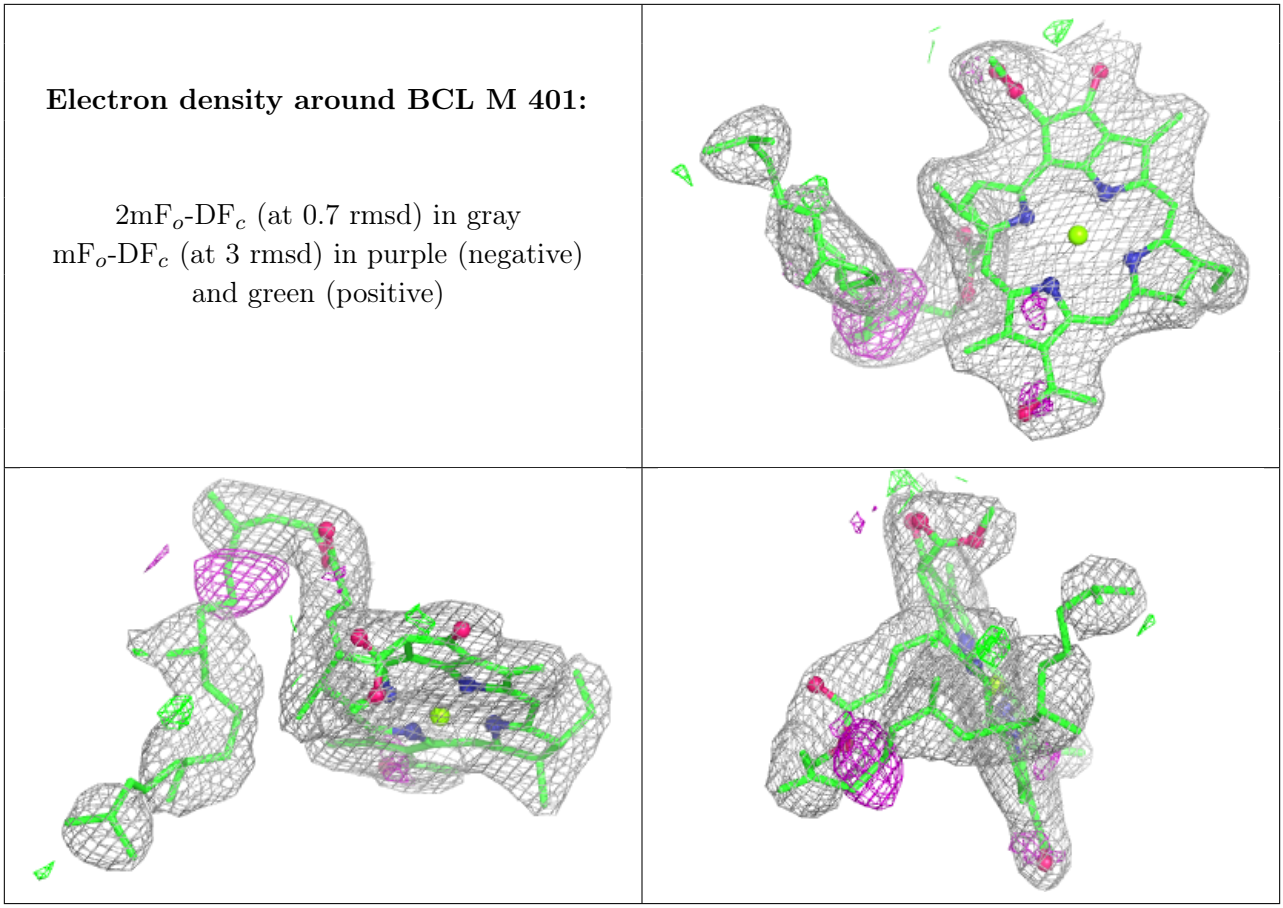
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





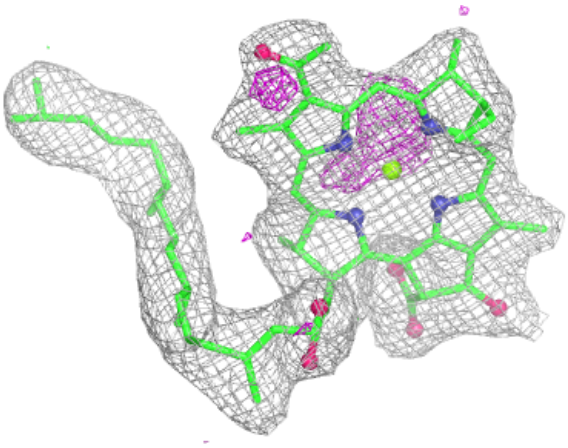
Electron density around BCL M 401:

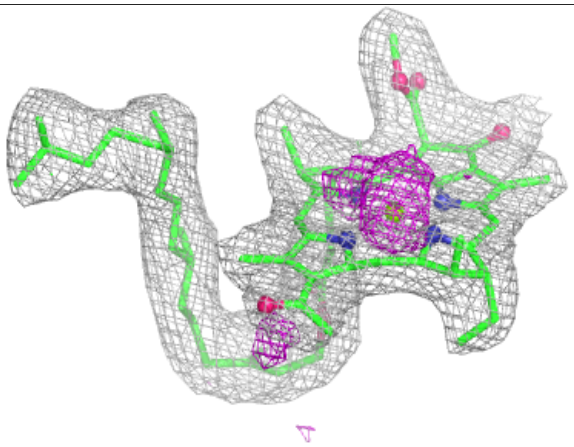
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

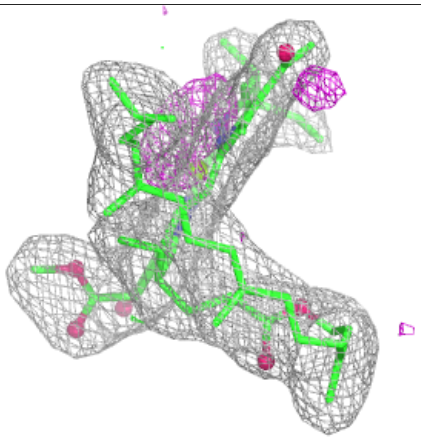


Electron density around BCL L 302:

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

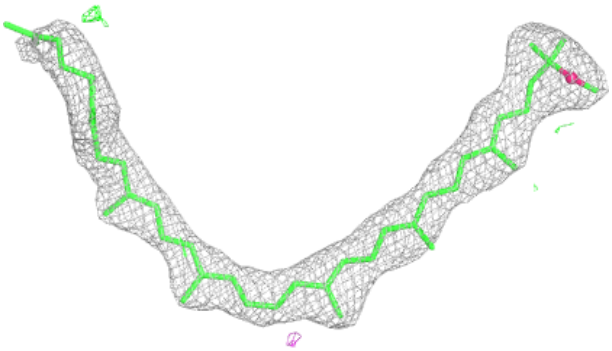


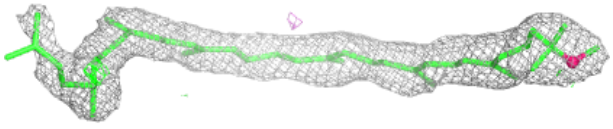


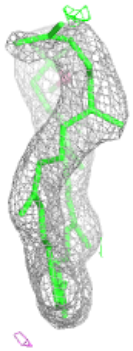


Electron density around SPO M 409:

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

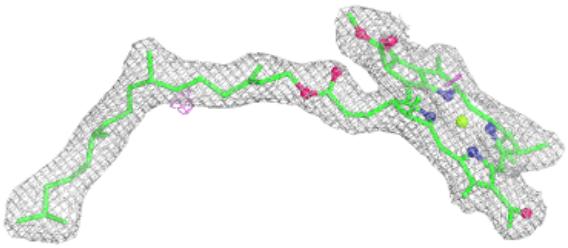


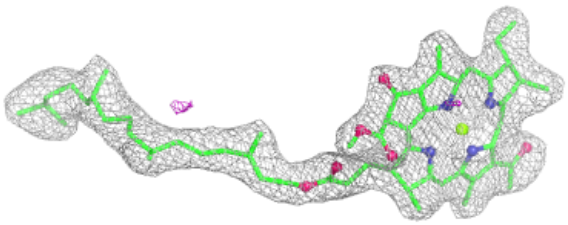


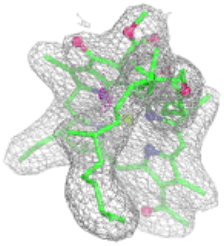


Electron density around BCL L 301:

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

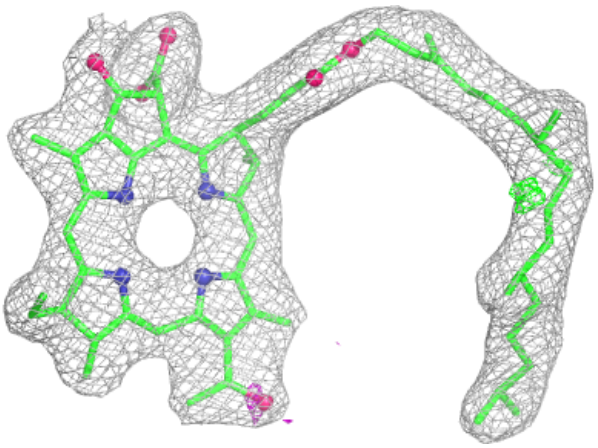


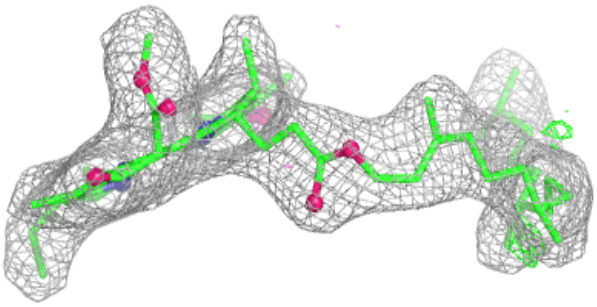


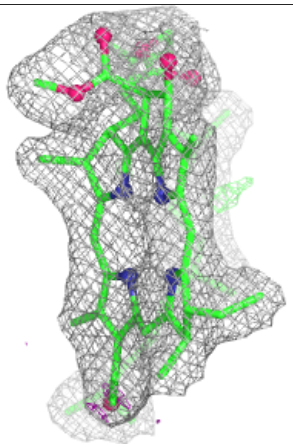


Electron density around BPH L 304:

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

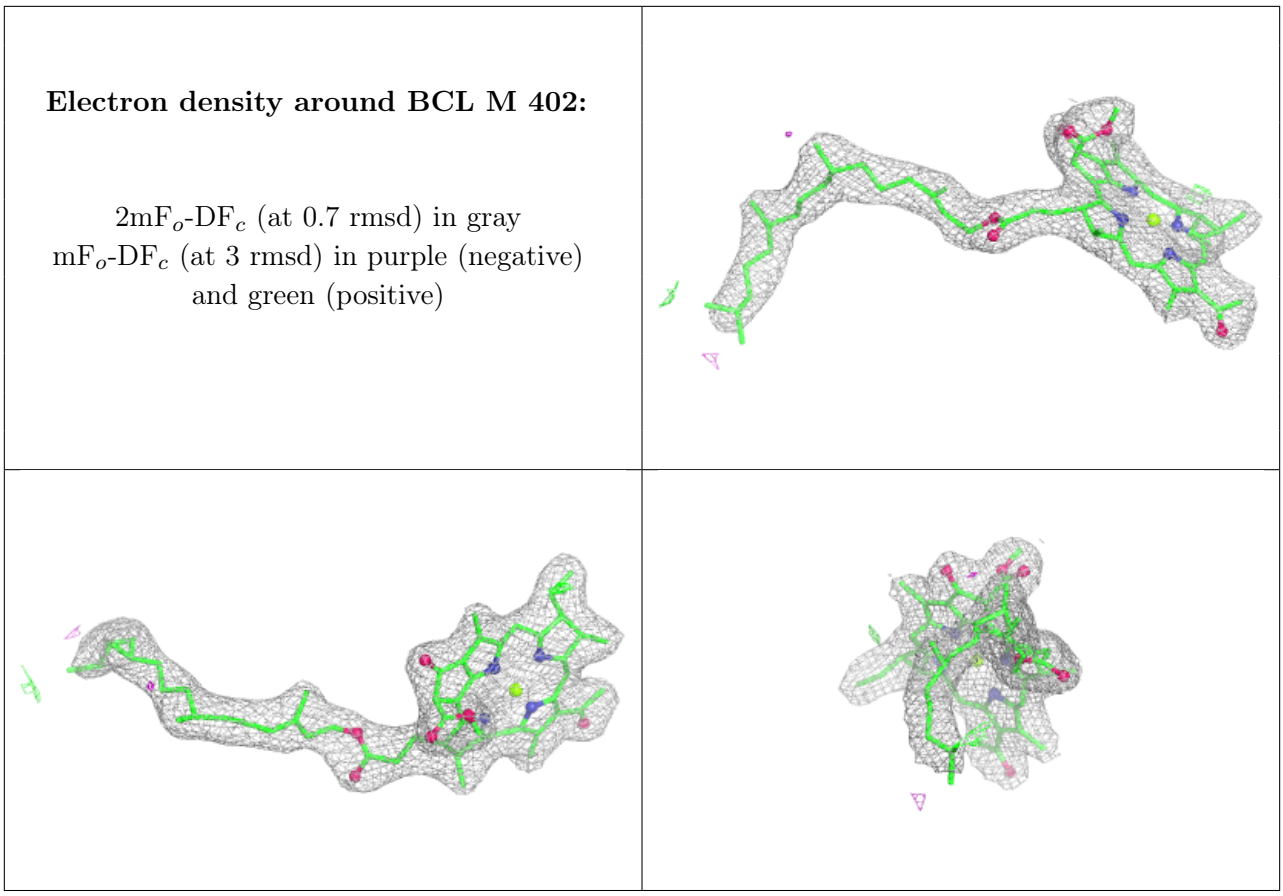






Electron density around BCL M 402:

$2mF_o$-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.