Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 07:34 am BST

PDB ID	:	2JIY
Title	:	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH ALA M149 REPLACED WITH TRP (CHAIN M, AM149W)
Authors	:	Fyfe, P.K.; Potter, J.A.; Cheng, J.; Williams, C.M.; Watson, A.J.; Jones, M.R.
Deposited on	:	2007-07-03
Resolution	:	2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ⓘ) were used in the production of this report:

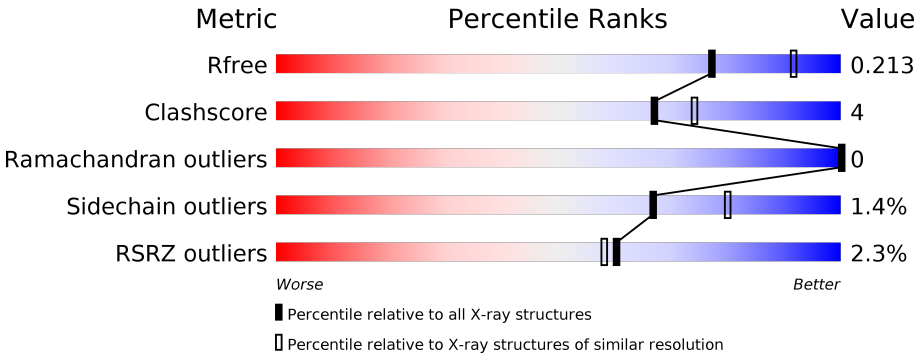
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	3% 86% 6% 8%
2	L	281	2% 94% 6%
3	M	308	2% 87% 10%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 7600 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	H	240	Total	C	N	O	S	0	6	0
			1877	1198	322	347	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	281	Total	C	N	O	S	0	3	0
			2252	1520	358	366	8			

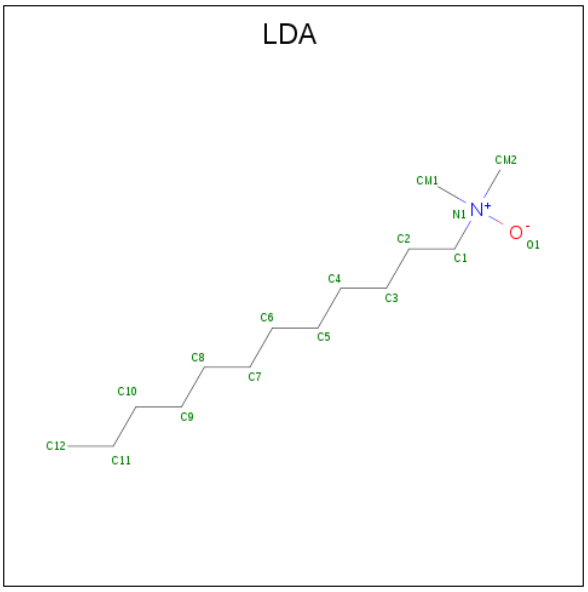
- Molecule 3 is a protein called REACTION CENTER PROTEIN M CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	301	Total	C	N	O	S	0	6	0
			2451	1635	404	401	11			

There is a discrepancy between the modelled and reference sequences:

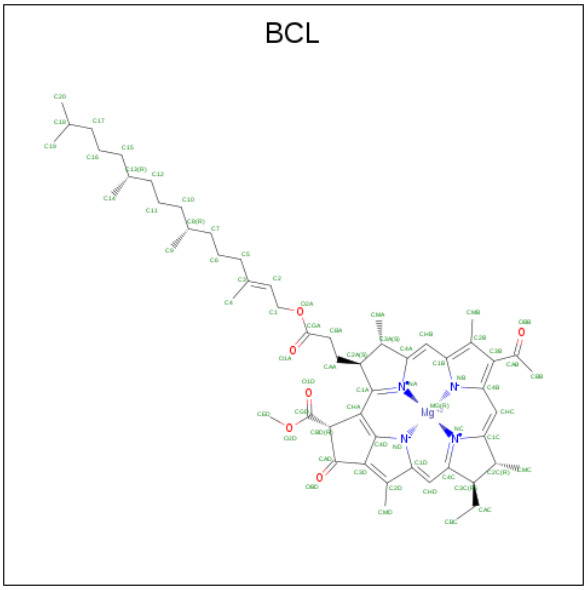
Chain	Residue	Modelled	Actual	Comment	Reference
M	149	TRP	ALA	engineered mutation	UNP P0C0Y9

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



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

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



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

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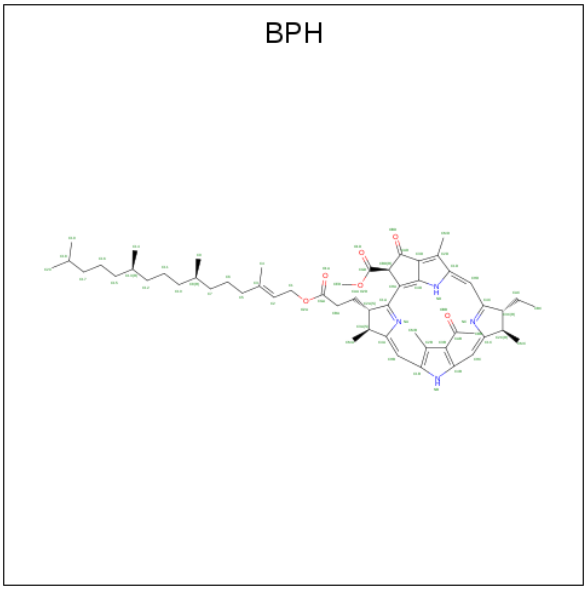
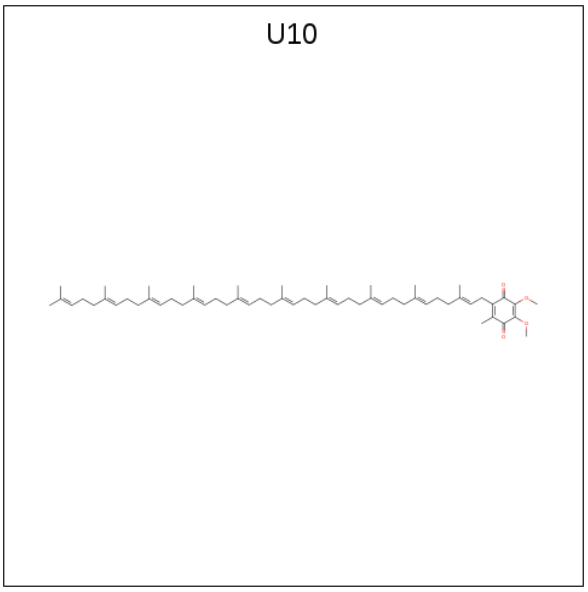
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	M	1	Total	C	Mg	N	O	0	1
			132	110	2	8	12		

- Molecule 6 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: $C_{55}H_{76}N_4O_6$).



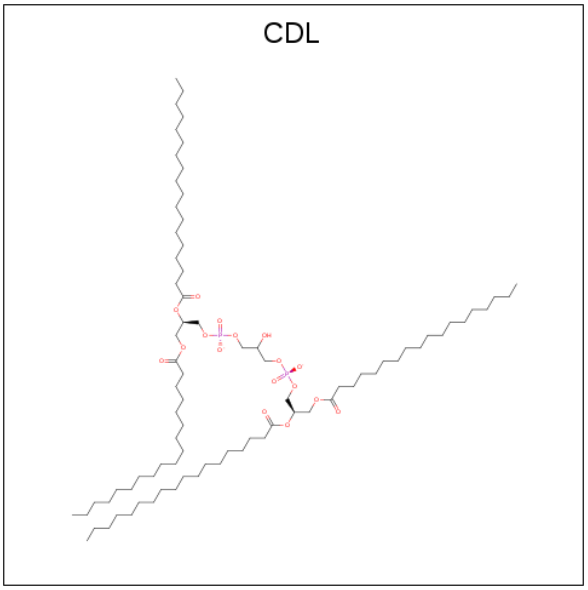
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	L	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 7 is UBIQUINONE-10 (three-letter code: U10) (formula: $C_{59}H_{90}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	L	1	Total C O 27 23 4	0	0
7	M	1	Total C O 48 44 4	0	0

- Molecule 8 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).

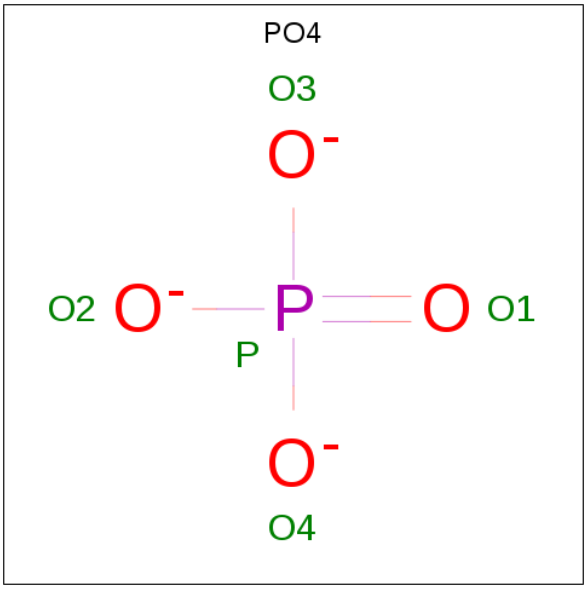


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	M	1	Total C O P 73 54 17 2	0	0

- Molecule 9 is FE (III) ION (three-letter code: FE) (formula: Fe).

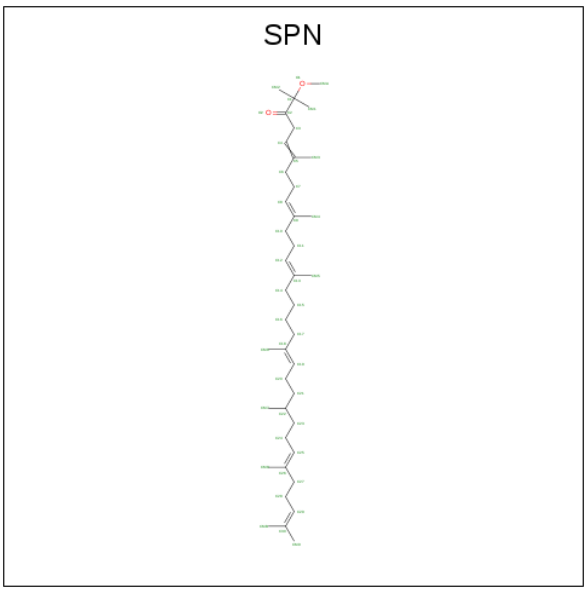
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	M	1	Total Fe 1 1	0	0

- Molecule 10 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

- Molecule 11 is SPEROIDENONE (three-letter code: SPN) (formula: $C_{41}H_{70}O_2$).

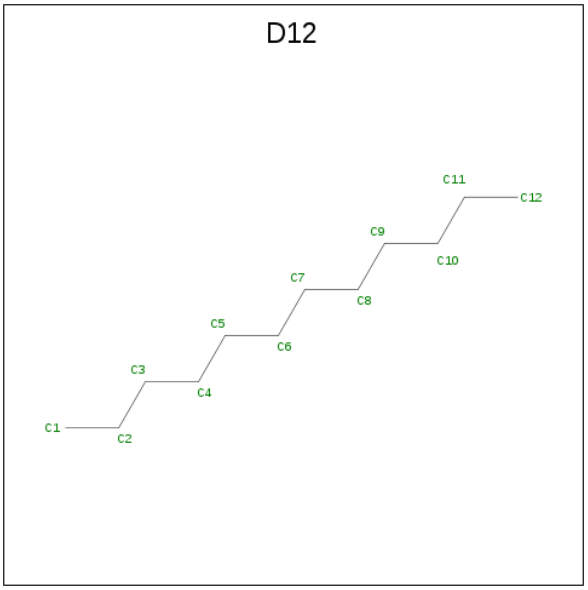


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	M	1	Total C O 43 41 2	0	0

- Molecule 12 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 13 is DODECANE (three-letter code: D12) (formula: $C_{12}H_{26}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	M	1	Total C 12 12	0	0

- Molecule 14 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	H	178	Total O 178 178	0	0
14	L	82	Total O 82 82	0	0
14	M	123	Total O 123 123	0	0

3 Residue-property plots (i)

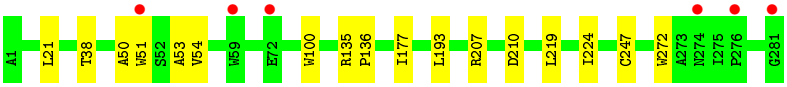
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

- Molecule 1: REACTION CENTER PROTEIN H CHAIN

Chain H:

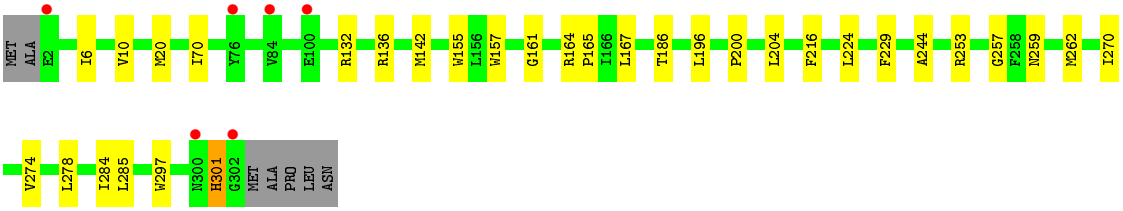
- Molecule 2: REACTION CENTER PROTEIN L CHAIN

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	139.78Å 139.78Å 185.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	15.97 – 2.20 15.97 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.7 (15.97-2.20) 96.7 (15.97-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.75 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.181 , 0.207 0.189 , 0.213	Depositor DCC
R_{free} test set	5088 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	40.3	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 64.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7600	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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, LDA, D12, CL, CDL, BPH, PO4, FE, SPN, U10

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	H	0.52	0/1928	0.65	1/2621 (0.0%)
2	L	0.48	0/2343	0.54	0/3206
3	M	0.47	0/2557	0.59	1/3489 (0.0%)
All	All	0.49	0/6828	0.59	2/9316 (0.0%)

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	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	M	262	MET	CG-SD-CE	6.54	110.67	100.20
1	H	83	ARG	NE-CZ-NH2	-5.32	117.64	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	167	ILE	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	1877	0	1882	10	0
2	L	2252	0	2209	9	0
3	M	2451	0	2362	25	0
4	H	16	0	31	2	0
4	M	16	0	31	4	0
5	L	198	0	222	9	0
5	M	132	0	148	8	0
6	L	65	0	76	0	0
7	L	27	0	31	2	0
7	M	48	0	63	0	0
8	M	73	0	90	1	0
9	M	1	0	0	0	0
10	M	5	0	0	0	0
11	M	43	0	69	7	0
12	M	1	0	0	0	0
13	M	12	0	26	1	0
14	H	178	0	0	2	0
14	L	82	0	0	0	0
14	M	123	0	0	0	0
All	All	7600	0	7240	56	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 4.

All (56) 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)
2:L:51:TRP:O	2:L:54:VAL:HG22	1.82	0.79
1:H:175:MET:HE3	14:H:2137:HOH:O	1.83	0.77
14:H:2125:HOH:O	3:M:10[A]:VAL:HG22	1.87	0.73
5:L:1284:BCL:HBB2	5:L:1284:BCL:HMB1	1.78	0.66
5:M:1303[B]:BCL:CBB	5:M:1303[B]:BCL:HMB1	2.27	0.65
2:L:207:ARG:HG3	3:M:142:MET:HG2	1.80	0.64
3:M:297:TRP:O	3:M:301:HIS:HA	1.99	0.63
3:M:204:LEU:HG	4:M:1305:LDA:CM2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:1251:LDA:H123	4:M:1305:LDA:H101	1.81	0.62
5:L:1282:BCL:CBB	5:L:1282:BCL:HMB1	2.31	0.61
3:M:157:TRP:CD1	11:M:1309:SPN:H202	2.36	0.60
2:L:224:ILE:HG22	7:L:1286:U10:H8	1.86	0.57
3:M:253[B]:ARG:HH11	3:M:259:ASN:ND2	2.02	0.56
5:M:1303[A]:BCL:CBB	5:M:1303[A]:BCL:HMB1	2.35	0.56
4:H:1251:LDA:H123	4:M:1305:LDA:C10	2.36	0.55
5:L:1282:BCL:HMB1	5:L:1282:BCL:HBB2	1.88	0.55
2:L:135:ARG:HB3	2:L:136:PRO:HD3	1.88	0.55
5:L:1283:BCL:CBB	5:L:1283:BCL:HMB1	2.37	0.54
2:L:193:LEU:HD23	7:L:1286:U10:C2	2.37	0.54
1:H:206:ASN:HD21	1:H:248:ARG:HD2	1.72	0.54
5:M:1303[B]:BCL:HBB3	5:M:1303[B]:BCL:HMB1	1.90	0.54
3:M:157:TRP:NE1	11:M:1309:SPN:H202	2.23	0.54
1:H:241:LEU:O	1:H:248:ARG:NH2	2.42	0.53
5:L:1283:BCL:HBB3	5:L:1283:BCL:HMB1	1.92	0.52
3:M:167:LEU:HD12	3:M:285:LEU:HD11	1.92	0.51
5:M:1303[A]:BCL:H191	11:M:1309:SPN:H101	1.92	0.51
1:H:122:GLU:HB2	1:H:227:LEU:HD21	1.93	0.51
5:L:1284:BCL:CBB	5:L:1284:BCL:HMB1	2.41	0.51
1:H:168:TRP:CD1	1:H:168:TRP:N	2.80	0.50
2:L:177:ILE:HG12	5:L:1283:BCL:HMB3	1.95	0.49
3:M:284:ILE:HG12	5:M:1303[B]:BCL:HED3	1.95	0.48
5:M:1303[A]:BCL:HBB3	5:M:1303[A]:BCL:HMB1	1.94	0.48
3:M:301:HIS:ND1	3:M:301:HIS:N	2.63	0.46
2:L:219:LEU:HD12	3:M:132[B]:ARG:NH1	2.31	0.45
3:M:70:ILE:HD13	11:M:1309:SPN:H102	1.99	0.45
2:L:38:THR:HG21	2:L:100:TRP:HE3	1.82	0.45
3:M:200:PRO:O	4:M:1305:LDA:HM23	2.18	0.44
1:H:126:HIS:CE1	3:M:20[B]:MET:CE	3.01	0.44
3:M:229:PHE:HB2	3:M:244:ALA:HB2	1.99	0.43
3:M:164:ARG:HB3	3:M:165:PRO:HD3	2.00	0.43
3:M:270:ILE:O	3:M:274:VAL:HG23	2.19	0.43
1:H:168:TRP:HB2	1:H:178:PHE:HB2	2.00	0.43
1:H:126:HIS:ND1	3:M:20[B]:MET:HE1	2.34	0.42
5:L:1282:BCL:CAB	11:M:1309:SPN:H162	2.50	0.42
5:L:1282:BCL:C3B	11:M:1309:SPN:H152	2.50	0.42
3:M:161:GLY:HA3	11:M:1309:SPN:H201	2.02	0.41
2:L:50:ALA:O	2:L:53:ALA:HB3	2.21	0.41
5:M:1303[B]:BCL:HBB2	5:M:1303[B]:BCL:HMB1	2.02	0.41
3:M:257:GLY:O	13:M:1314:D12:H122	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:245:ALA:N	1:H:246:PRO:HD2	2.36	0.41
1:H:181:VAL:HG21	1:H:191:LEU:HD13	2.03	0.41
3:M:186:THR:HG23	5:M:1303[A]:BCL:HMD2	2.03	0.41
3:M:278:LEU:HD21	8:M:1304:CDL:H771	2.03	0.41
3:M:6:ILE:HD13	3:M:224:LEU:HD13	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	244/260 (94%)	244 (100%)	0	0	100	100
2	L	282/281 (100%)	278 (99%)	4 (1%)	0	100	100
3	M	305/308 (99%)	297 (97%)	8 (3%)	0	100	100
All	All	831/849 (98%)	819 (99%)	12 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	201/208 (97%)	199 (99%)	2 (1%)	76	86
2	L	223/220 (101%)	219 (98%)	4 (2%)	59	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	M	243/242 (100%)	240 (99%)	3 (1%)	71 83
All	All	667/670 (100%)	658 (99%)	9 (1%)	67 81

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	191	LEU
1	H	231	ASP
2	L	21	LEU
2	L	210	ASP
2	L	247	CYS
2	L	272	TRP
3	M	196	LEU
3	M	216	PHE
3	M	301	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	199	GLN
1	H	206	ASN
2	L	183	ASN
3	M	44	ASN
3	M	187	ASN
3	M	259	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 2 are monoatomic - leaving 14 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	$\#\|Z\| > 2$
5	BCL	M	1303[A]	3	58,74,74	1.16	3 (5%)	69,115,115	1.54	13 (18%)
5	BCL	M	1303[B]	3	58,74,74	1.14	3 (5%)	69,115,115	1.30	8 (11%)
10	PO4	M	1307	-	4,4,4	1.00	0	6,6,6	0.58	0
5	BCL	L	1282	3	58,74,74	1.14	3 (5%)	69,115,115	1.33	9 (13%)
4	LDA	H	1251	-	12,15,15	2.20	1 (8%)	14,17,17	3.48	3 (21%)
4	LDA	M	1305	-	12,15,15	2.20	1 (8%)	14,17,17	3.28	3 (21%)
8	CDL	M	1304	-	72,72,99	1.16	4 (5%)	78,84,111	1.18	6 (7%)
5	BCL	L	1283	2	58,74,74	1.15	3 (5%)	69,115,115	1.27	8 (11%)
11	SPN	M	1309	-	40,42,42	3.65	14 (35%)	50,52,52	2.18	19 (38%)
6	BPH	L	1285	-	64,70,70	0.74	1 (1%)	76,101,101	1.27	9 (11%)
7	U10	M	1310	-	48,48,63	1.73	3 (6%)	58,61,79	1.28	10 (17%)
13	D12	M	1314	-	11,11,11	0.26	0	10,10,10	0.52	0
7	U10	L	1286	-	27,27,63	1.74	2 (7%)	32,35,79	1.66	7 (21%)
5	BCL	L	1284	2	58,74,74	0.96	3 (5%)	69,115,115	1.51	17 (24%)

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
5	BCL	M	1303[A]	3	-	13/37/137/137	-
5	BCL	M	1303[B]	3	-	4/37/137/137	-
5	BCL	L	1282	3	-	15/37/137/137	-
4	LDA	H	1251	-	-	8/13/13/13	-
4	LDA	M	1305	-	-	3/13/13/13	-
8	CDL	M	1304	-	-	28/83/83/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BCL	L	1283	2	-	6/37/137/137	-
11	SPN	M	1309	-	-	16/50/51/51	-
6	BPH	L	1285	-	-	4/54/105/105	0/5/6/6
7	U10	M	1310	-	-	11/45/69/87	0/1/1/1
13	D12	M	1314	-	-	2/9/9/9	-
7	U10	L	1286	-	-	9/20/44/87	0/1/1/1
5	BCL	L	1284	2	-	1/37/137/137	-

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	M	1309	SPN	C3-C4	-9.77	1.36	1.50
7	L	1286	U10	C6-C1	8.04	1.49	1.35
4	H	1251	LDA	O1-N1	-7.56	1.24	1.42
7	M	1310	U10	C6-C1	7.55	1.49	1.35
4	M	1305	LDA	O1-N1	-7.39	1.24	1.42
7	M	1310	U10	C36-C34	-7.37	1.36	1.51
11	M	1309	SPN	C6-C5	-7.30	1.36	1.51
11	M	1309	SPN	C10-C9	-7.28	1.36	1.51
11	M	1309	SPN	C17-C18	-6.81	1.37	1.51
11	M	1309	SPN	C14-C13	-6.59	1.37	1.51
11	M	1309	SPN	C4-C5	6.15	1.47	1.33
5	M	1303[B]	BCL	MG-NA	6.04	2.20	2.06
11	M	1309	SPN	C8-C9	5.87	1.47	1.33
11	M	1309	SPN	C19-C18	5.83	1.47	1.33
5	L	1283	BCL	MG-NA	5.59	2.19	2.06
11	M	1309	SPN	C12-C13	5.54	1.46	1.33
5	L	1282	BCL	MG-NA	5.37	2.19	2.06
5	M	1303[A]	BCL	MG-NA	5.32	2.18	2.06
8	M	1304	CDL	OA6-CA5	4.60	1.47	1.34
11	M	1309	SPN	C20-C19	-4.58	1.35	1.50
8	M	1304	CDL	OB6-CB5	4.55	1.47	1.34
8	M	1304	CDL	OB8-CB7	4.49	1.46	1.33
11	M	1309	SPN	C11-C12	-4.48	1.35	1.50
11	M	1309	SPN	C7-C8	-4.45	1.35	1.50
8	M	1304	CDL	OA8-CA7	4.18	1.45	1.33
5	M	1303[A]	BCL	C1B-NB	3.64	1.38	1.35
5	L	1282	BCL	C1B-NB	3.48	1.38	1.35
11	M	1309	SPN	C21-C22	-3.23	1.35	1.52
5	M	1303[B]	BCL	C1B-NB	3.21	1.38	1.35
5	L	1284	BCL	C1B-NB	3.16	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	M	1310	U10	C4-C3	3.16	1.49	1.36
5	M	1303[B]	BCL	C4B-NB	3.05	1.37	1.35
5	L	1283	BCL	C1B-NB	3.05	1.37	1.35
5	L	1283	BCL	C4B-NB	3.00	1.37	1.35
5	M	1303[A]	BCL	C4B-NB	2.97	1.37	1.35
7	L	1286	U10	C4-C3	2.96	1.48	1.36
5	L	1284	BCL	C4B-NB	2.87	1.37	1.35
5	L	1282	BCL	C4B-NB	2.85	1.37	1.35
11	M	1309	SPN	C16-C15	-2.60	1.37	1.51
5	L	1284	BCL	MG-NA	2.25	2.11	2.06
6	L	1285	BPH	CHC-C1C	2.05	1.40	1.36

All (112) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	M	1305	LDA	CM2-N1-C1	-8.38	92.63	110.23
4	H	1251	LDA	CM1-N1-C1	-7.98	93.46	110.23
4	H	1251	LDA	O1-N1-C1	-7.13	91.77	109.27
4	H	1251	LDA	CM2-N1-C1	-7.06	95.40	110.23
4	M	1305	LDA	CM1-N1-C1	-6.35	96.88	110.23
4	M	1305	LDA	O1-N1-C1	-5.96	94.64	109.27
11	M	1309	SPN	CM6-C18-C17	4.91	123.53	115.27
11	M	1309	SPN	CM5-C13-C14	4.67	123.12	115.27
8	M	1304	CDL	OB6-CB5-C51	4.62	121.46	111.50
7	L	1286	U10	C7-C8-C9	-4.58	119.17	126.79
5	M	1303[A]	BCL	CMB-C2B-C1B	-4.51	121.54	128.46
5	L	1282	BCL	CMB-C2B-C1B	-4.48	121.58	128.46
8	M	1304	CDL	OA6-CA5-C11	4.45	121.08	111.50
5	L	1283	BCL	CMB-C2B-C1B	-4.33	121.81	128.46
11	M	1309	SPN	C16-C17-C18	3.99	123.93	113.45
5	M	1303[B]	BCL	CMB-C2B-C1B	-3.84	122.56	128.46
11	M	1309	SPN	CM4-C9-C10	3.82	121.69	115.27
11	M	1309	SPN	C16-C15-C14	3.73	126.58	113.19
11	M	1309	SPN	C11-C10-C9	3.57	124.71	112.98
5	L	1284	BCL	CAC-C3C-C2C	-3.52	105.47	114.26
11	M	1309	SPN	CM3-C5-C6	3.49	121.13	115.27
7	L	1286	U10	C12-C13-C14	-3.46	119.32	127.66
5	M	1303[B]	BCL	CHA-C1A-NA	-3.46	118.48	126.40
5	L	1284	BCL	CMB-C2B-C1B	-3.42	123.21	128.46
5	L	1284	BCL	O2D-CGD-CBD	3.39	117.30	111.27
5	M	1303[A]	BCL	C4D-C3D-CAD	-3.39	106.58	108.47
5	M	1303[A]	BCL	OBD-CAD-CBD	-3.39	121.06	125.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	L	1285	BPH	C1B-NB-C4B	3.34	112.80	106.51
11	M	1309	SPN	C7-C6-C5	3.34	123.96	112.98
5	L	1282	BCL	CMB-C2B-C3B	3.25	130.76	124.68
11	M	1309	SPN	C15-C14-C13	3.24	121.95	113.45
5	M	1303[A]	BCL	CMB-C2B-C3B	3.13	130.54	124.68
11	M	1309	SPN	C15-C16-C17	3.06	124.19	113.19
6	L	1285	BPH	C1-C2-C3	-3.03	120.80	126.04
5	M	1303[A]	BCL	OBD-CAD-C3D	2.98	132.93	127.98
7	M	1310	U10	C32-C33-C34	-2.96	120.53	127.66
7	L	1286	U10	C15-C14-C16	2.95	120.23	115.27
6	L	1285	BPH	CAC-C3C-C2C	2.94	121.61	114.26
5	M	1303[B]	BCL	C1-C2-C3	-2.91	121.01	126.04
5	M	1303[A]	BCL	CHA-C1A-NA	-2.91	119.74	126.40
5	M	1303[A]	BCL	CAC-C3C-C2C	-2.89	107.03	114.26
5	L	1283	BCL	CMB-C2B-C3B	2.89	130.09	124.68
5	M	1303[A]	BCL	CAC-C3C-C4C	-2.88	106.19	112.58
5	L	1284	BCL	CAA-C2A-C3A	-2.84	105.00	112.78
11	M	1309	SPN	CM7-C22-C21	2.84	121.56	111.29
5	L	1282	BCL	CHA-C1A-NA	-2.83	119.92	126.40
11	M	1309	SPN	C17-C18-C19	-2.77	115.51	121.12
6	L	1285	BPH	C1C-NC-C4C	-2.72	108.14	110.54
5	L	1283	BCL	CAA-C2A-C3A	-2.71	105.36	112.78
5	L	1284	BCL	CAC-C3C-C4C	-2.70	106.60	112.58
5	L	1283	BCL	CHA-C1A-NA	-2.68	120.27	126.40
5	M	1303[A]	BCL	C4-C3-C5	2.62	119.67	115.27
5	L	1282	BCL	C1-O2A-CGA	2.59	123.24	116.44
7	L	1286	U10	C10-C9-C11	2.59	119.63	115.27
7	M	1310	U10	C37-C36-C34	2.55	121.36	112.98
5	M	1303[B]	BCL	CMB-C2B-C3B	2.52	129.40	124.68
8	M	1304	CDL	OA8-CA7-C31	2.52	119.82	111.91
11	M	1309	SPN	C20-C21-C22	2.51	124.46	115.76
7	L	1286	U10	C1M-C1-C6	-2.51	120.30	124.40
5	L	1284	BCL	C6-C5-C3	-2.51	106.87	113.45
6	L	1285	BPH	CMC-C2C-C3C	2.47	123.78	113.83
8	M	1304	CDL	OB8-CB7-C71	2.46	119.61	111.91
7	M	1310	U10	C27-C28-C29	-2.45	121.75	127.66
5	L	1284	BCL	OBB-CAB-C3B	2.45	124.35	119.99
5	L	1283	BCL	C11-C12-C13	-2.45	108.00	115.92
7	M	1310	U10	C4M-O4-C4	2.45	125.14	116.47
5	L	1284	BCL	C4B-C3B-CAB	-2.43	122.44	127.13
7	M	1310	U10	C17-C18-C19	-2.42	121.82	127.66
7	L	1286	U10	C3M-O3-C3	2.42	125.05	116.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	L	1284	BCL	C2C-C3C-C4C	2.40	104.94	101.34
5	M	1303[B]	BCL	C4D-C3D-CAD	-2.39	107.14	108.47
7	M	1310	U10	C30-C29-C31	2.39	119.29	115.27
6	L	1285	BPH	CHD-C4C-NC	-2.37	122.39	125.20
11	M	1309	SPN	CM7-C22-C23	2.34	119.77	111.29
5	M	1303[B]	BCL	C4-C3-C5	2.33	119.19	115.27
5	M	1303[B]	BCL	C2A-C1A-CHA	2.31	127.90	123.86
11	M	1309	SPN	C24-C25-C26	-2.31	122.10	127.66
5	L	1282	BCL	OBB-CAB-C3B	2.31	124.09	119.99
5	L	1284	BCL	CMD-C2D-C3D	2.30	128.98	124.68
11	M	1309	SPN	C28-C29-C30	-2.29	119.92	127.75
11	M	1309	SPN	CMB-C30-CM9	2.27	119.61	114.60
5	M	1303[A]	BCL	C4-C3-C2	-2.25	117.90	123.68
6	L	1285	BPH	C2B-C1B-NB	-2.25	106.40	109.79
5	L	1283	BCL	C4B-C3B-CAB	-2.23	122.83	127.13
5	L	1284	BCL	CHA-C1A-NA	-2.21	121.34	126.40
5	M	1303[A]	BCL	O2D-CGD-O1D	-2.18	119.57	123.84
5	L	1282	BCL	OBD-CAD-CBD	-2.18	122.78	125.89
5	M	1303[A]	BCL	CMD-C2D-C3D	2.18	128.76	124.68
5	L	1282	BCL	O2D-CGD-CBD	2.18	115.14	111.27
5	L	1284	BCL	CMA-C3A-C2A	-2.18	105.05	113.83
6	L	1285	BPH	CMA-C3A-C2A	-2.18	105.05	113.83
7	M	1310	U10	C10-C9-C11	2.17	118.91	115.27
7	L	1286	U10	O2-C2-C3	-2.16	116.34	120.93
5	L	1284	BCL	C4A-NA-C1A	2.15	107.67	106.71
5	M	1303[B]	BCL	OBD-CAD-CBD	-2.15	122.83	125.89
5	L	1284	BCL	CMB-C2B-C3B	2.14	128.69	124.68
5	L	1282	BCL	C4D-C3D-CAD	-2.14	107.28	108.47
6	L	1285	BPH	O2D-CGD-CBD	2.14	115.07	111.27
7	M	1310	U10	C15-C14-C16	2.12	118.84	115.27
8	M	1304	CDL	OA8-CA7-OA9	-2.12	118.24	123.59
7	M	1310	U10	C3M-O3-C3	2.10	123.92	116.47
5	L	1283	BCL	CMA-C3A-C2A	-2.08	105.44	113.83
5	L	1284	BCL	C4D-C3D-CAD	-2.07	107.31	108.47
7	M	1310	U10	C25-C24-C26	2.07	118.75	115.27
5	M	1303[A]	BCL	C1-C2-C3	-2.06	122.47	126.04
5	L	1284	BCL	C5-C3-C2	-2.05	116.98	121.12
5	L	1282	BCL	CAA-CBA-CGA	2.04	119.23	113.25
11	M	1309	SPN	CM5-C13-C12	-2.04	118.44	123.68
8	M	1304	CDL	CA6-CA4-CA3	-2.02	107.01	111.79
5	L	1284	BCL	C1-O2A-CGA	2.02	121.73	116.44
5	L	1283	BCL	OBD-CAD-CBD	-2.02	123.02	125.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	M	1309	SPN	C10-C9-C8	-2.01	117.05	121.12

There are no chirality outliers.

All (120) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	L	1282	BCL	C1A-C2A-CAA-CBA
5	L	1282	BCL	C3A-C2A-CAA-CBA
8	M	1304	CDL	CA2-OA2-PA1-OA3
8	M	1304	CDL	CB2-OB2-PB2-OB4
8	M	1304	CDL	CB3-OB5-PB2-OB4
11	M	1309	SPN	C20-C21-C22-CM7
7	L	1286	U10	C7-C8-C9-C10
7	L	1286	U10	C7-C8-C9-C11
7	L	1286	U10	C9-C11-C12-C13
7	L	1286	U10	C12-C13-C14-C15
7	L	1286	U10	C12-C13-C14-C16
11	M	1309	SPN	C14-C15-C16-C17
11	M	1309	SPN	CM3-C5-C6-C7
11	M	1309	SPN	C11-C10-C9-CM4
11	M	1309	SPN	CM5-C13-C14-C15
11	M	1309	SPN	C16-C17-C18-CM6
11	M	1309	SPN	C4-C5-C6-C7
11	M	1309	SPN	C11-C10-C9-C8
11	M	1309	SPN	C12-C13-C14-C15
11	M	1309	SPN	C16-C17-C18-C19
7	L	1286	U10	C14-C16-C17-C18
7	M	1310	U10	C32-C33-C34-C35
5	L	1282	BCL	C11-C10-C8-C9
5	L	1282	BCL	C15-C16-C17-C18
5	L	1282	BCL	C10-C11-C12-C13
7	M	1310	U10	C37-C38-C39-C41
5	L	1282	BCL	C3-C5-C6-C7
7	M	1310	U10	C24-C26-C27-C28
5	M	1303[A]	BCL	C15-C16-C17-C18
8	M	1304	CDL	CA2-OA2-PA1-OA5
8	M	1304	CDL	CB2-OB2-PB2-OB5
8	M	1304	CDL	CB3-OB5-PB2-OB2
4	H	1251	LDA	C5-C6-C7-C8
8	M	1304	CDL	C78-C79-C80-C81
8	M	1304	CDL	C40-C41-C42-C43
8	M	1304	CDL	C75-C76-C77-C78

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Mol	Chain	Res	Type	Atoms
4	H	1251	LDA	C3-C4-C5-C6
8	M	1304	CDL	C76-C77-C78-C79
8	M	1304	CDL	C37-C38-C39-C40
4	M	1305	LDA	C11-C10-C9-C8
5	M	1303[B]	BCL	C15-C16-C17-C18
8	M	1304	CDL	C51-C52-C53-C54
7	M	1310	U10	C37-C38-C39-C40
7	M	1310	U10	C30-C29-C31-C32
7	M	1310	U10	C35-C34-C36-C37
5	L	1282	BCL	C6-C7-C8-C10
11	M	1309	SPN	C21-C22-C23-C24
7	M	1310	U10	C28-C29-C31-C32
8	M	1304	CDL	OB7-CB5-OB6-CB4
7	M	1310	U10	C27-C28-C29-C30
8	M	1304	CDL	C51-CB5-OB6-CB4
7	M	1310	U10	C33-C34-C36-C37
5	L	1282	BCL	C6-C7-C8-C9
8	M	1304	CDL	C71-C72-C73-C74
8	M	1304	CDL	OB5-CB3-CB4-CB6
4	M	1305	LDA	C9-C10-C11-C12
13	M	1314	D12	C1-C2-C3-C4
5	L	1284	BCL	C15-C16-C17-C18
5	M	1303[A]	BCL	C6-C7-C8-C9
5	M	1303[A]	BCL	C5-C6-C7-C8
4	H	1251	LDA	N1-C1-C2-C3
4	M	1305	LDA	C2-C3-C4-C5
8	M	1304	CDL	C57-C58-C59-C60
5	L	1282	BCL	C5-C6-C7-C8
6	L	1285	BPH	C8-C10-C11-C12
7	L	1286	U10	C15-C14-C16-C17
8	M	1304	CDL	CA3-OA5-PA1-OA2
4	H	1251	LDA	C4-C5-C6-C7
8	M	1304	CDL	OB5-CB3-CB4-OB6
7	L	1286	U10	C17-C18-C19-C20
5	M	1303[A]	BCL	C6-C7-C8-C10
5	L	1282	BCL	C11-C10-C8-C7
6	L	1285	BPH	CAD-CBD-CGD-O2D
5	L	1283	BCL	C13-C15-C16-C17
8	M	1304	CDL	C73-C74-C75-C76
4	H	1251	LDA	C9-C10-C11-C12
5	M	1303[A]	BCL	C10-C11-C12-C13
7	M	1310	U10	C32-C33-C34-C36

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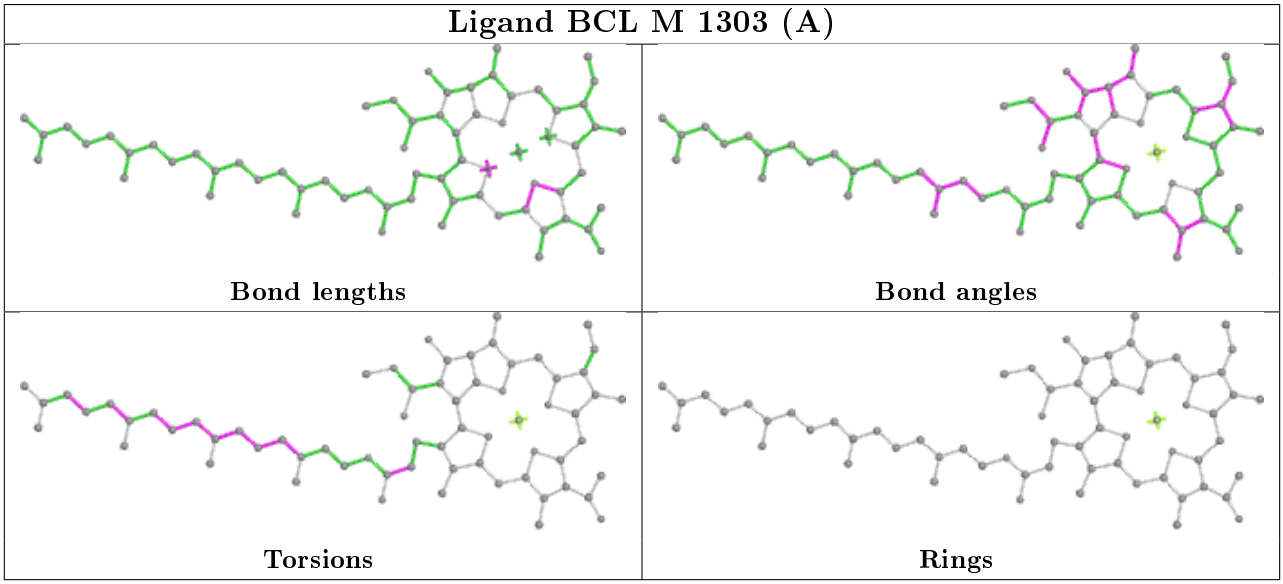
Mol	Chain	Res	Type	Atoms
11	M	1309	SPN	CM8-C26-C27-C28
7	L	1286	U10	C13-C14-C16-C17
8	M	1304	CDL	CA2-OA2-PA1-OA4
8	M	1304	CDL	CB2-OB2-PB2-OB3
8	M	1304	CDL	CB3-OB5-PB2-OB3
8	M	1304	CDL	C33-C34-C35-C36
5	L	1283	BCL	C11-C12-C13-C15
4	H	1251	LDA	C11-C10-C9-C8
11	M	1309	SPN	C25-C26-C27-C28
5	L	1282	BCL	C16-C17-C18-C20
5	L	1283	BCL	C15-C16-C17-C18
8	M	1304	CDL	OA6-CA4-CA6-OA8
5	L	1283	BCL	C2A-CAA-CBA-CGA
7	M	1310	U10	C5-C4-O4-C4M
13	M	1314	D12	C11-C10-C9-C8
5	M	1303[A]	BCL	C8-C10-C11-C12
4	H	1251	LDA	C2-C3-C4-C5
5	M	1303[A]	BCL	CAA-CBA-CGA-O2A
5	M	1303[A]	BCL	C4-C3-C5-C6
5	L	1282	BCL	C16-C17-C18-C19
5	L	1282	BCL	CAA-CBA-CGA-O2A
5	L	1282	BCL	CAD-CBD-CGD-O2D
5	L	1283	BCL	CAD-CBD-CGD-O2D
5	M	1303[B]	BCL	C13-C15-C16-C17
5	L	1283	BCL	C2-C1-O2A-CGA
5	M	1303[B]	BCL	O2A-C1-C2-C3
6	L	1285	BPH	O2A-C1-C2-C3
5	M	1303[B]	BCL	CHA-CBD-CGD-O2D
8	M	1304	CDL	CB5-C51-C52-C53
5	M	1303[A]	BCL	C11-C10-C8-C9
5	M	1303[A]	BCL	C3-C5-C6-C7
11	M	1309	SPN	C6-C7-C8-C9
11	M	1309	SPN	C18-C19-C20-C21
8	M	1304	CDL	C74-C75-C76-C77
5	M	1303[A]	BCL	C2-C3-C5-C6
5	L	1282	BCL	CAA-CBA-CGA-O1A
8	M	1304	CDL	CA3-OA5-PA1-OA3
6	L	1285	BPH	C2B-C3B-CAB-OBB
11	M	1309	SPN	C10-C11-C12-C13
4	H	1251	LDA	C7-C8-C9-C10
5	M	1303[A]	BCL	C14-C13-C15-C16
5	M	1303[A]	BCL	C12-C13-C15-C16

There are no ring outliers.

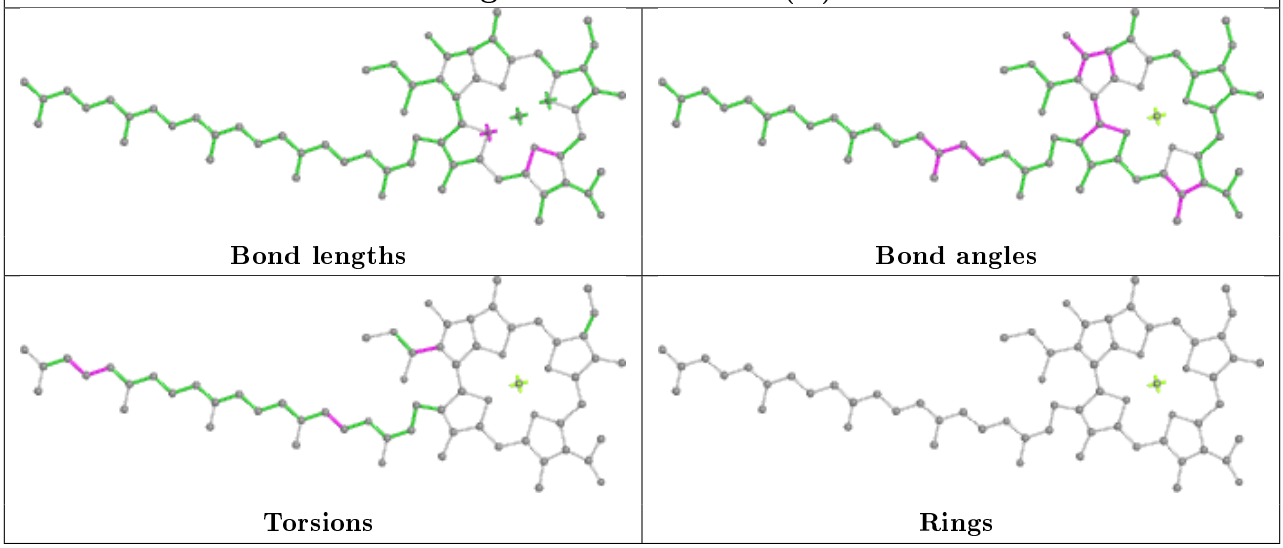
11 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	1303[A]	BCL	4	0
5	M	1303[B]	BCL	4	0
5	L	1282	BCL	4	0
4	H	1251	LDA	2	0
4	M	1305	LDA	4	0
8	M	1304	CDL	1	0
5	L	1283	BCL	3	0
11	M	1309	SPN	7	0
13	M	1314	D12	1	0
7	L	1286	U10	2	0
5	L	1284	BCL	2	0

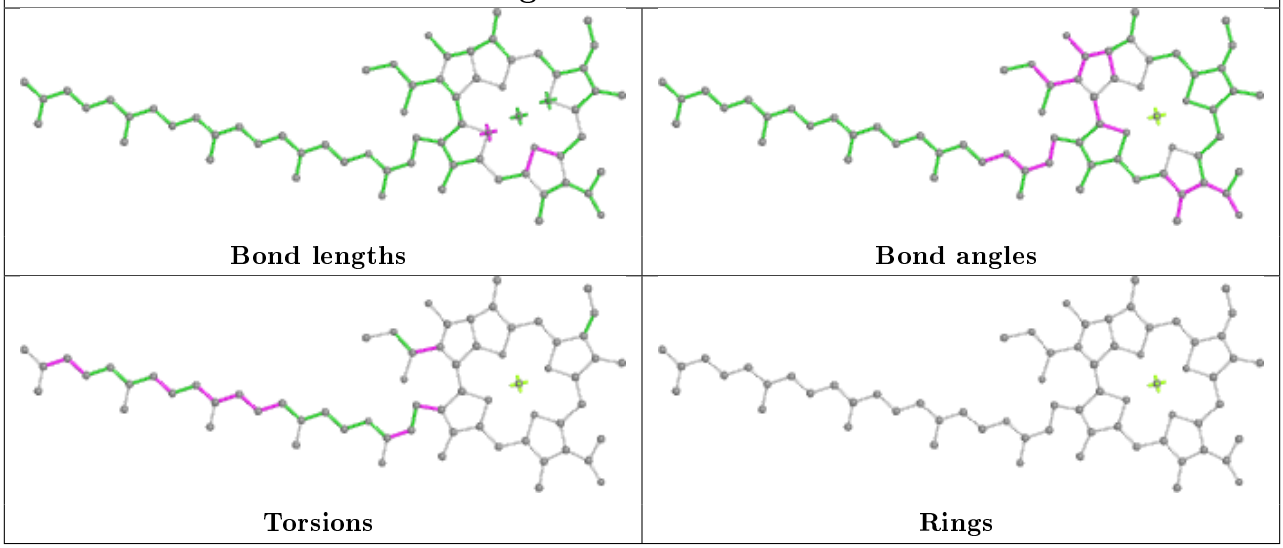
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



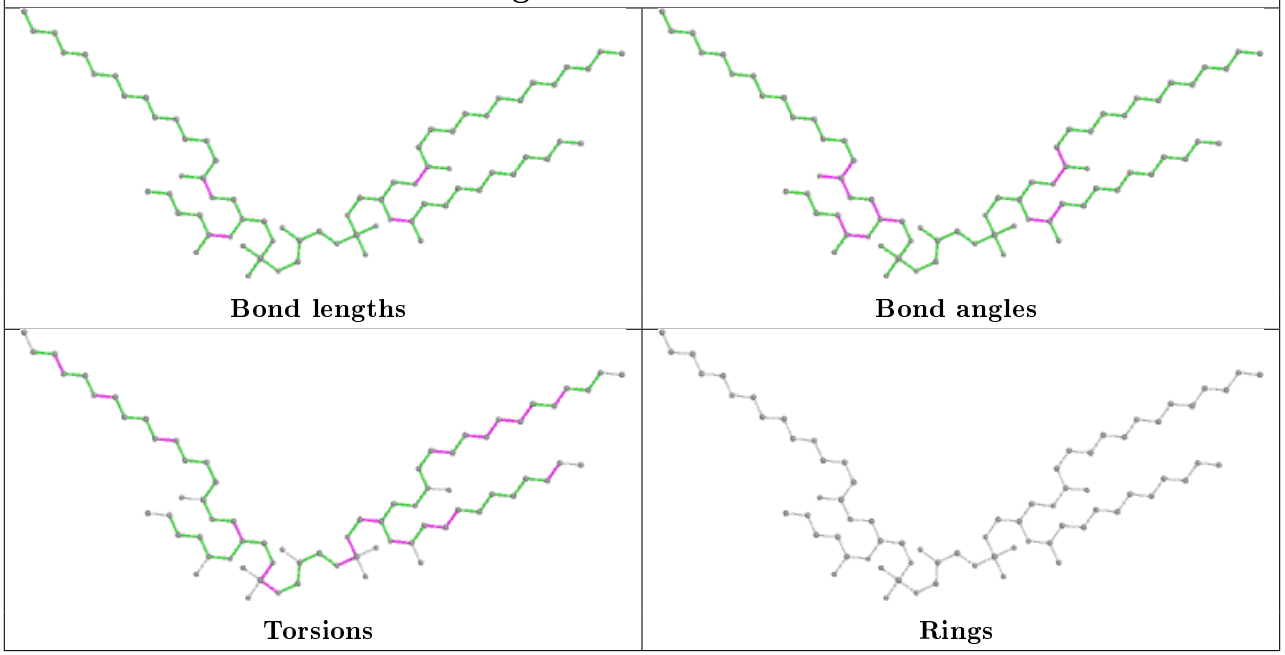
Ligand BCL M 1303 (B)



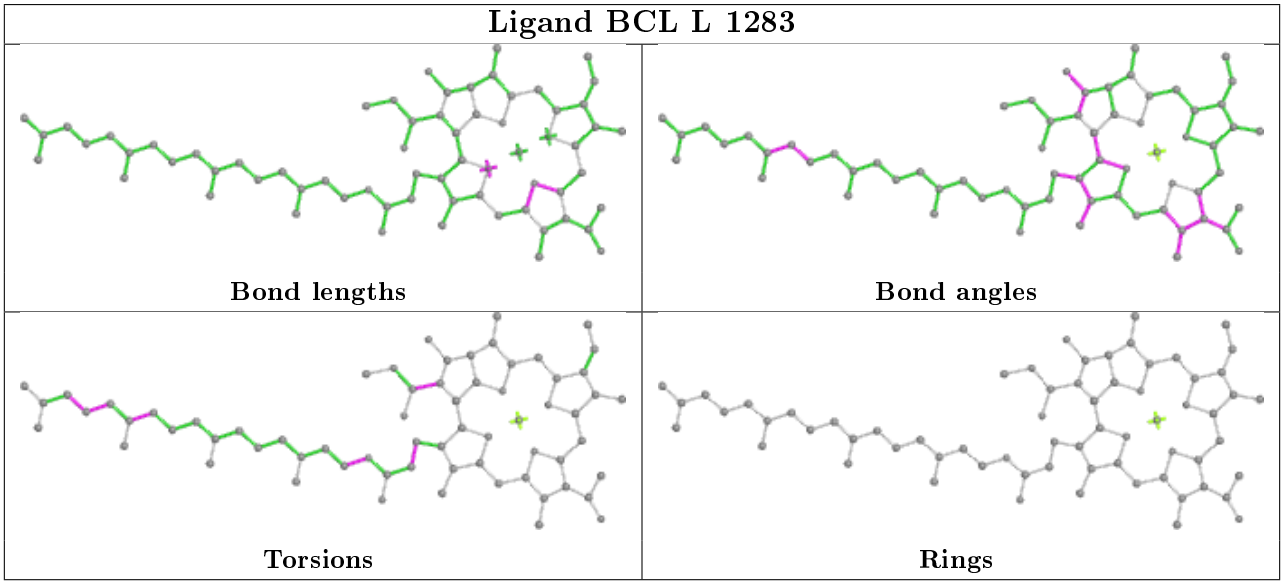
Ligand BCL L 1282



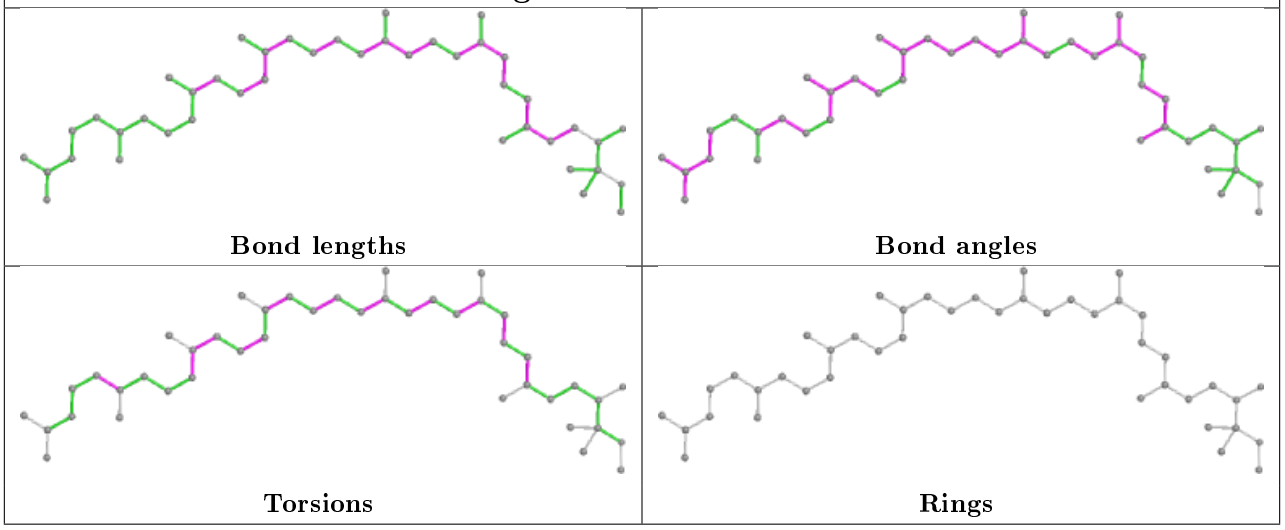
Ligand CDL M 1304



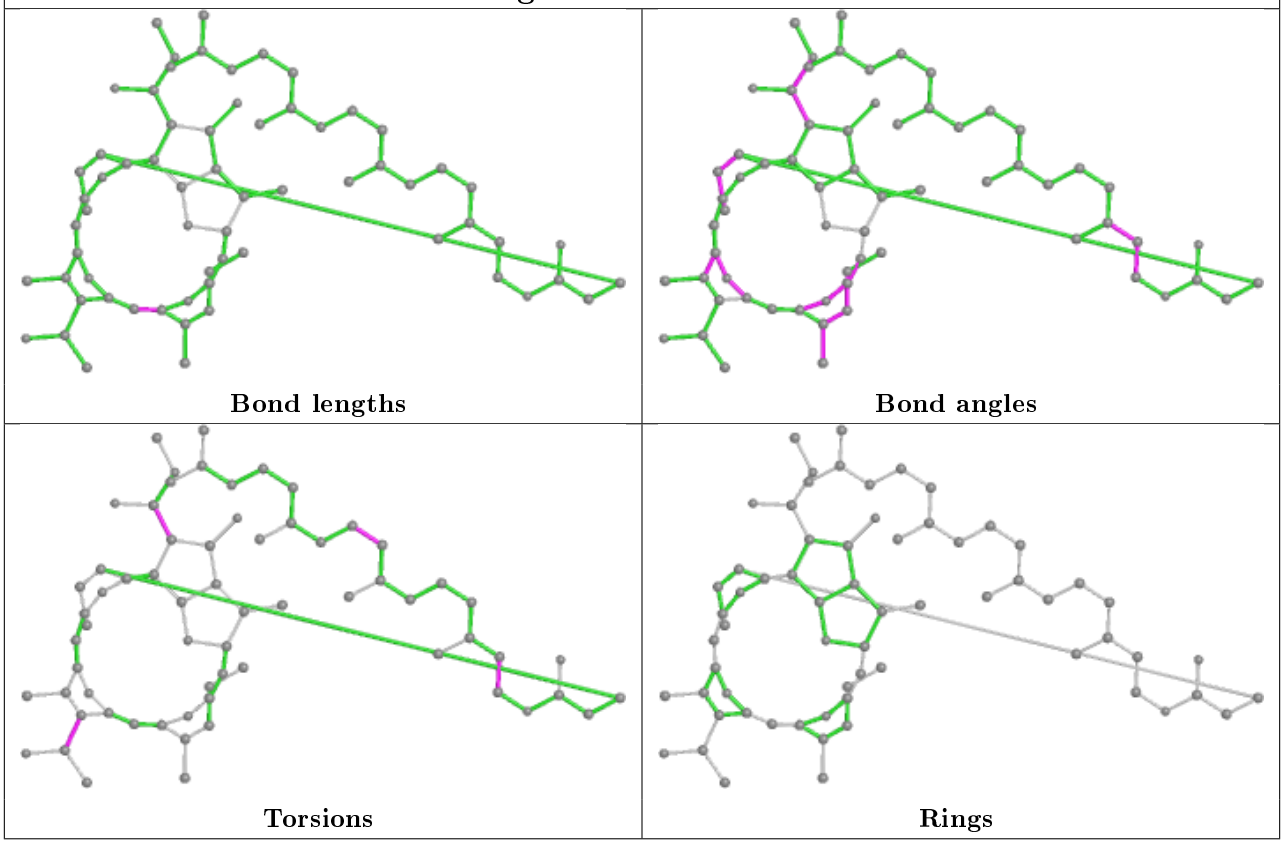
Ligand BCL L 1283



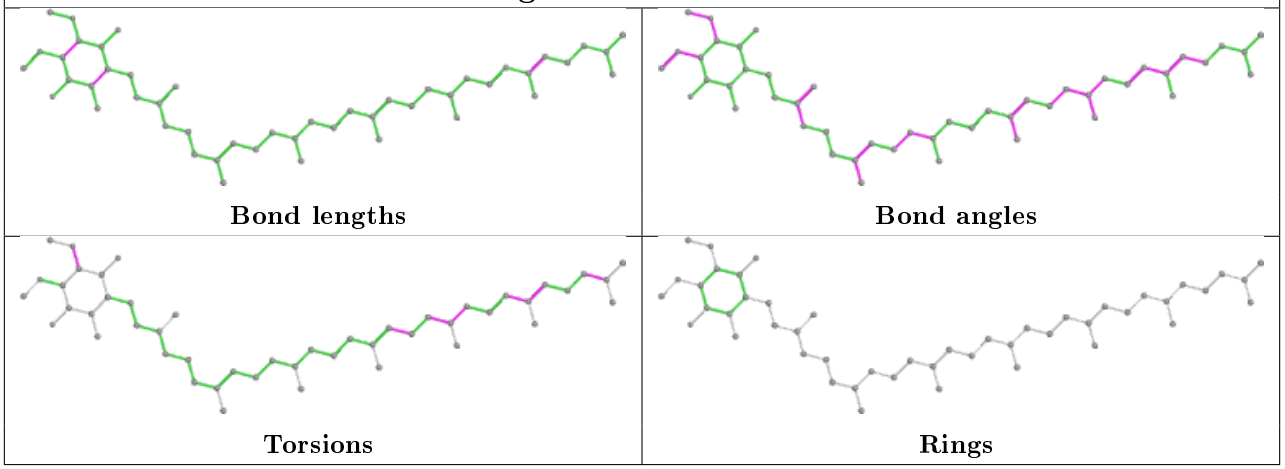
Ligand SPN M 1309



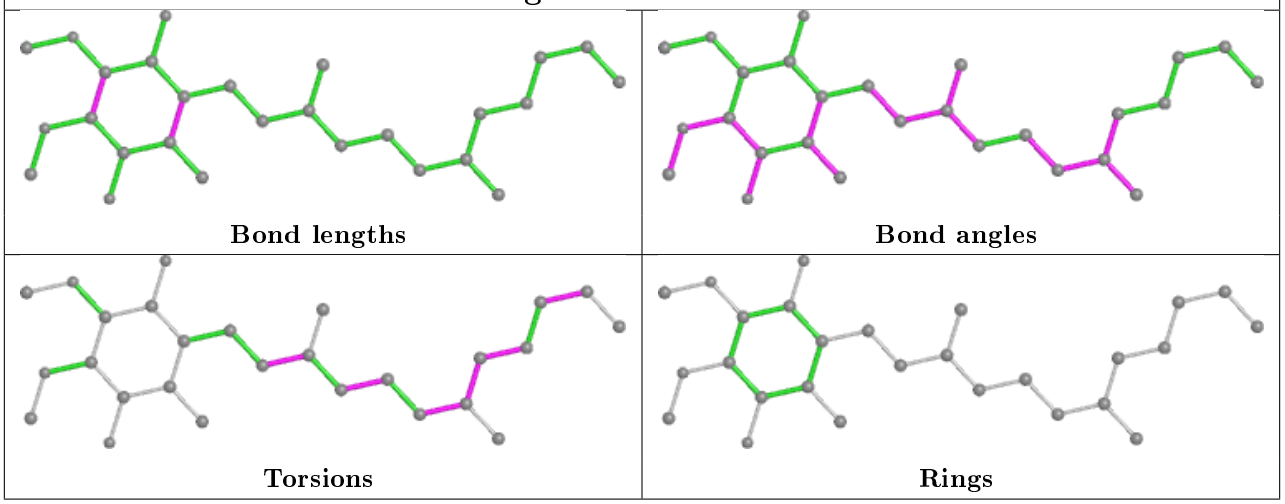
Ligand BPH L 1285



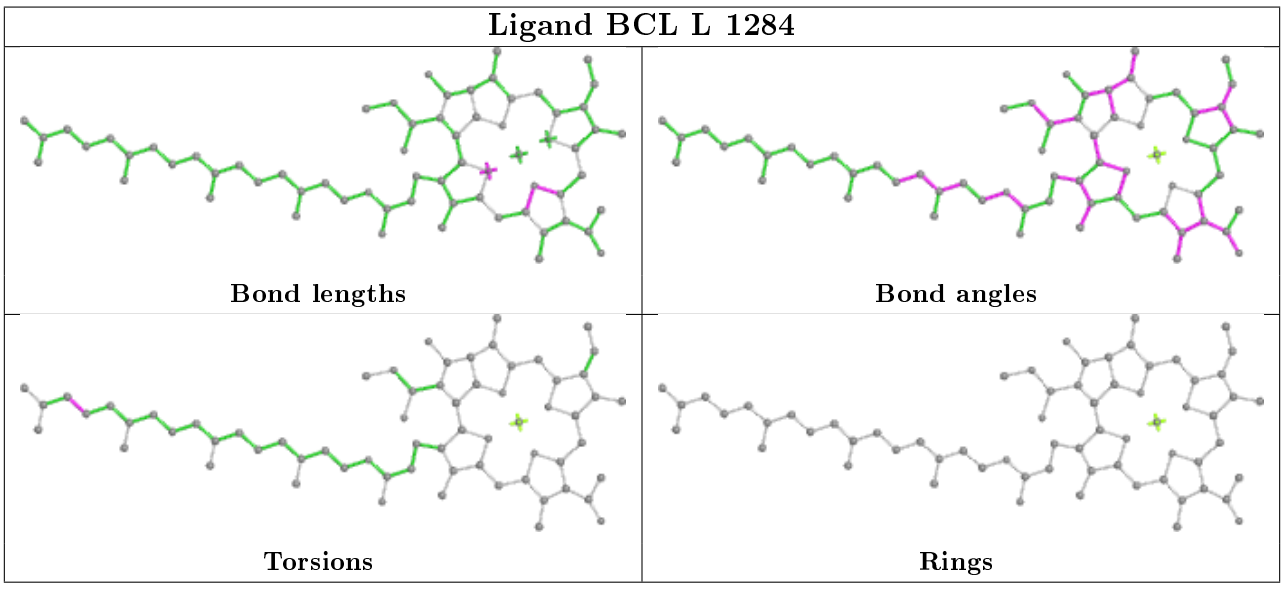
Ligand U10 M 1310



Ligand U10 L 1286



Ligand BCL L 1284



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

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	240/260 (92%)	-0.41	7 (2%)	51	49	31, 36, 46, 72	4 (1%)
2	L	281/281 (100%)	-0.42	6 (2%)	63	61	27, 35, 50, 61	4 (1%)
3	M	301/308 (97%)	-0.51	6 (1%)	65	63	30, 36, 48, 57	2 (0%)
All	All	822/849 (96%)	-0.45	19 (2%)	60	58	27, 36, 48, 72	10 (1%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	250	SER	7.2
2	L	59	TRP	6.5
3	M	302	GLY	5.5
1	H	245	ALA	4.4
2	L	281	GLY	4.4
1	H	247	LYS	4.0
1	H	246	PRO	3.8
3	M	2	GLU	3.1
3	M	84	VAL	3.0
1	H	249	LYS	2.8
1	H	201	ASN	2.4
3	M	76	TYR	2.3
2	L	51	TRP	2.3
3	M	300	ASN	2.2
2	L	72	GLU	2.2
3	M	100	GLU	2.2
2	L	274	ASN	2.1
2	L	276	PRO	2.1
1	H	18	TYR	2.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

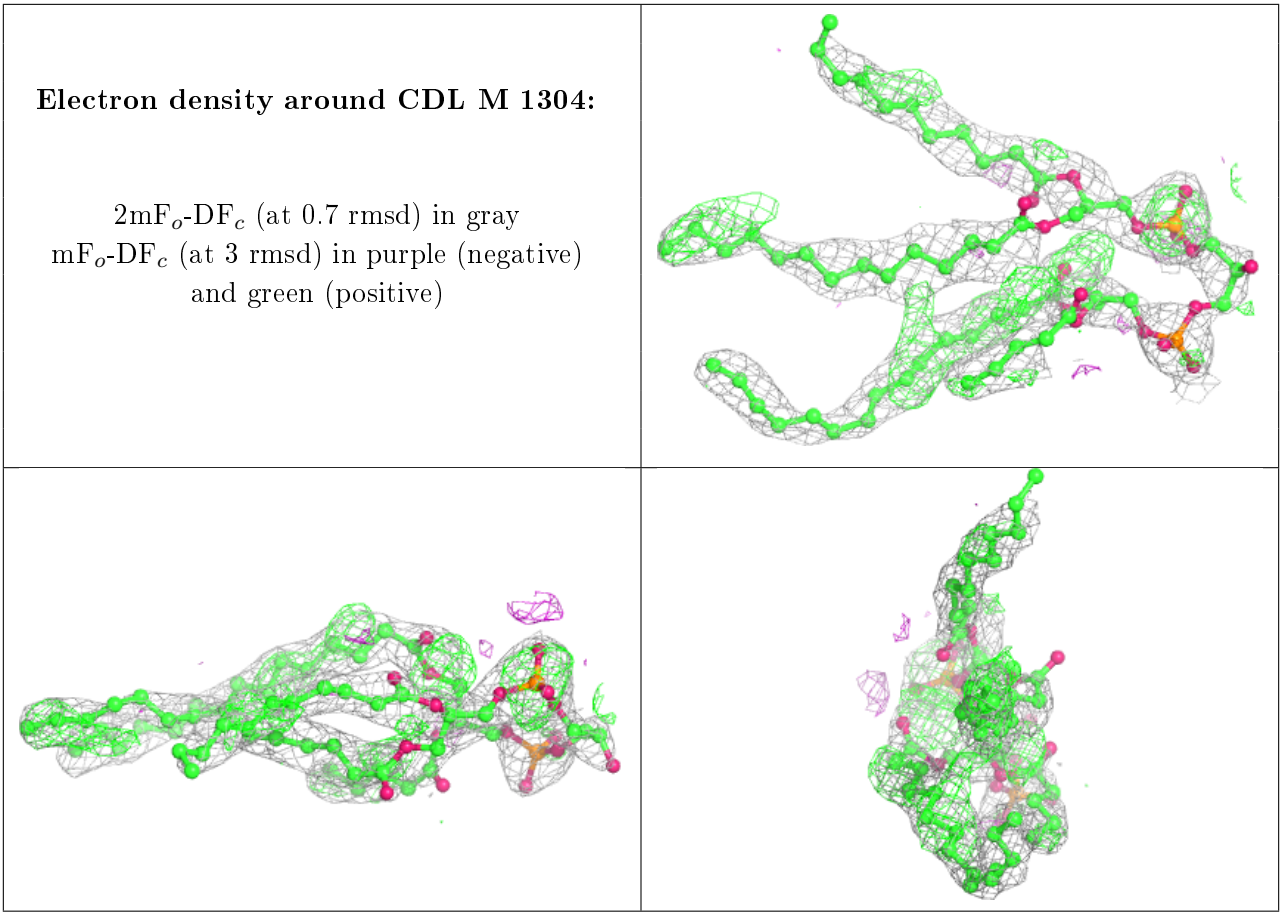
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	M	1305	16/16	0.56	0.32	66,74,77,78	0
8	CDL	M	1304	73/100	0.69	0.33	27,46,54,55	73
13	D12	M	1314	12/12	0.71	0.18	71,73,74,74	0
4	LDA	H	1251	16/16	0.74	0.24	74,79,82,82	0
12	CL	M	1311	1/1	0.83	0.17	83,83,83,83	0
7	U10	L	1286	27/63	0.84	0.14	47,52,67,70	0
11	SPN	M	1309	43/43	0.87	0.14	33,40,48,50	0
7	U10	M	1310	48/63	0.91	0.14	31,39,63,65	0
5	BCL	L	1282	66/66	0.92	0.13	31,38,79,81	0
5	BCL	M	1303[A]	66/66	0.92	0.15	16,20,52,53	66
5	BCL	M	1303[B]	66/66	0.92	0.15	31,40,45,47	66
5	BCL	L	1283	66/66	0.94	0.10	29,32,45,49	0
5	BCL	L	1284	66/66	0.96	0.10	28,32,50,53	0
6	BPH	L	1285	65/65	0.97	0.10	28,32,39,41	0
10	PO4	M	1307	5/5	0.97	0.19	53,54,54,54	0
9	FE	M	1306	1/1	1.00	0.06	34,34,34,34	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.

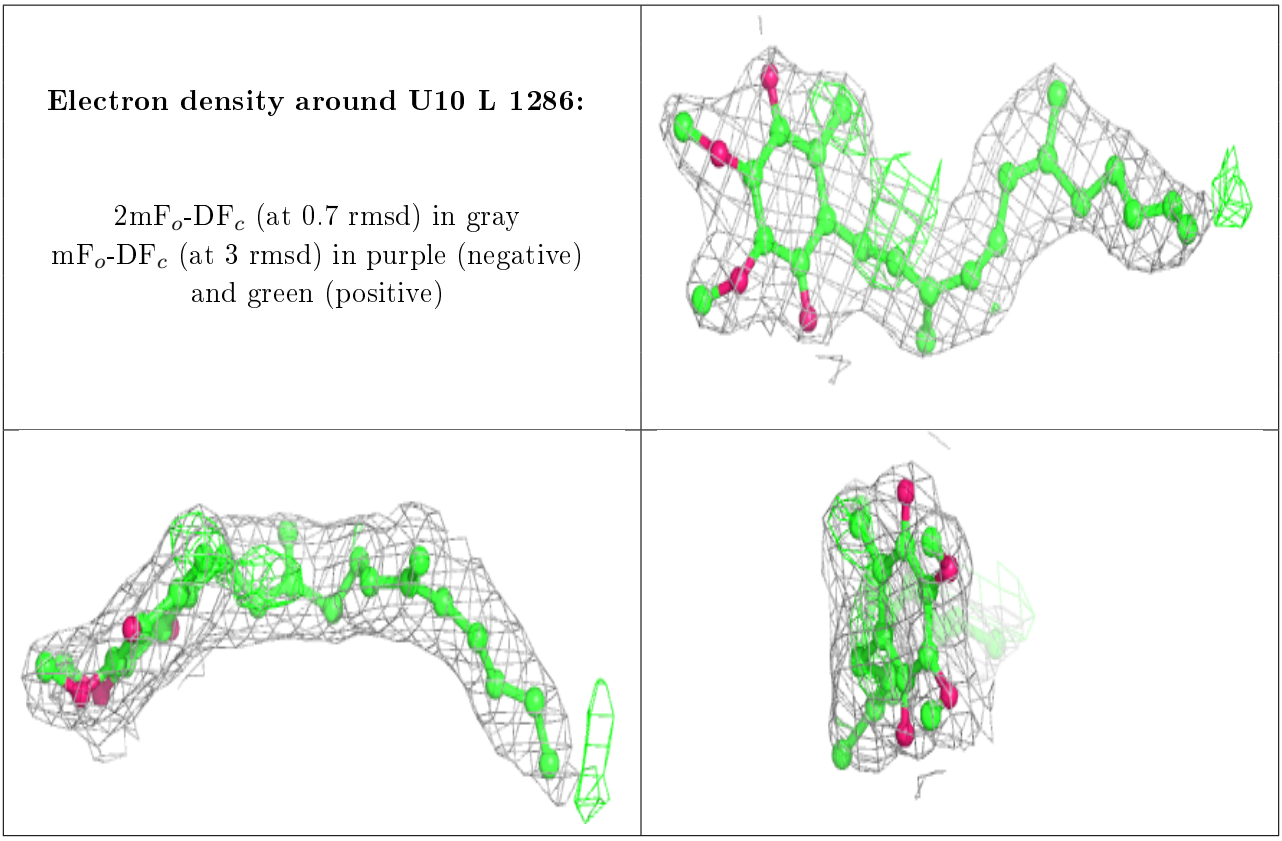
Electron density around CDL M 1304:

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



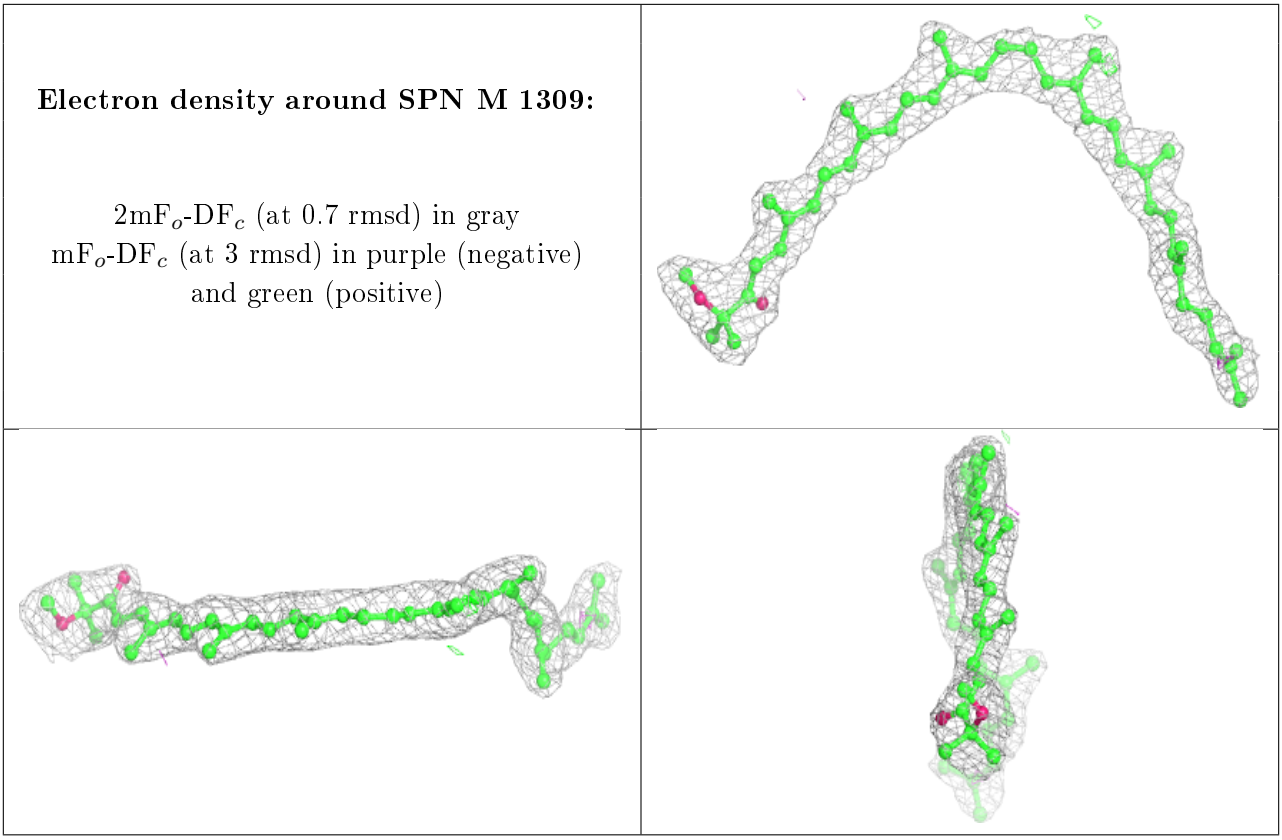
Electron density around U10 L 1286:

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



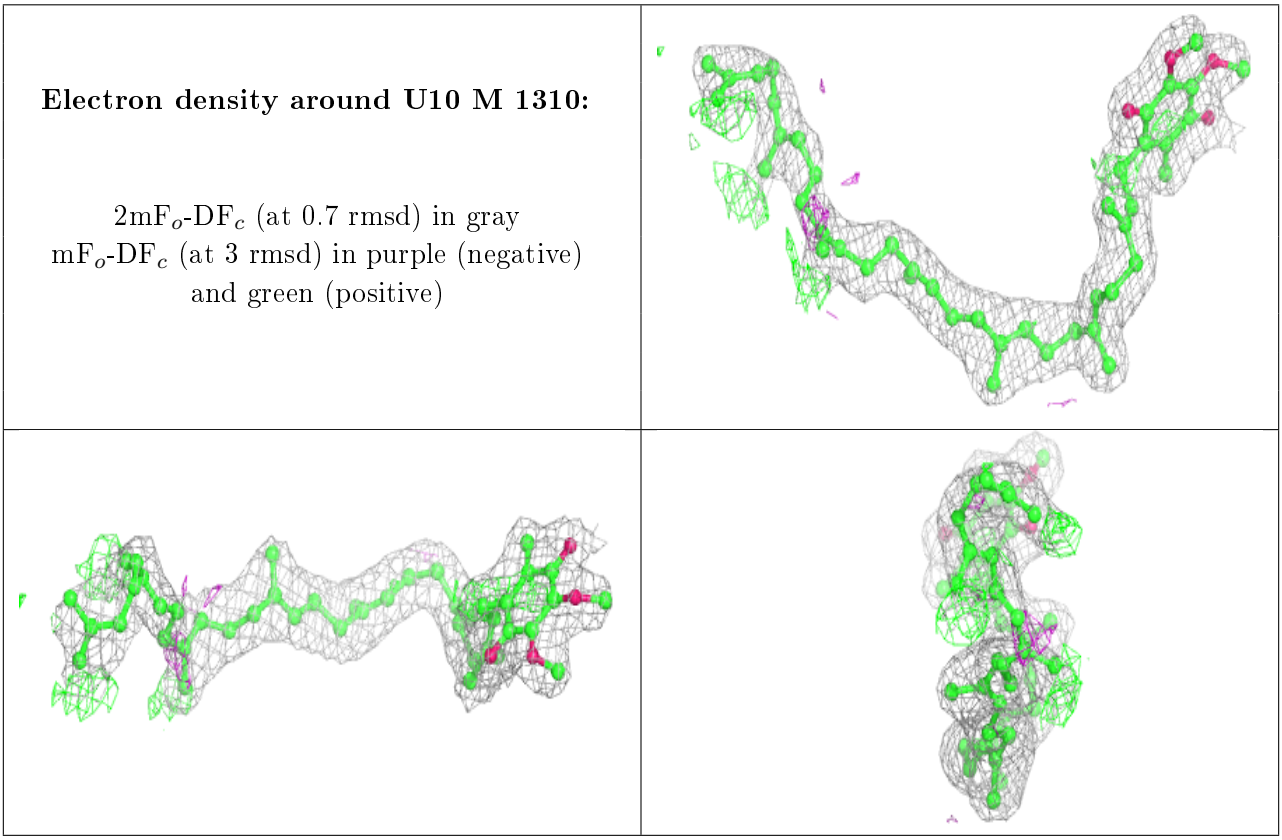
Electron density around SPN M 1309:

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



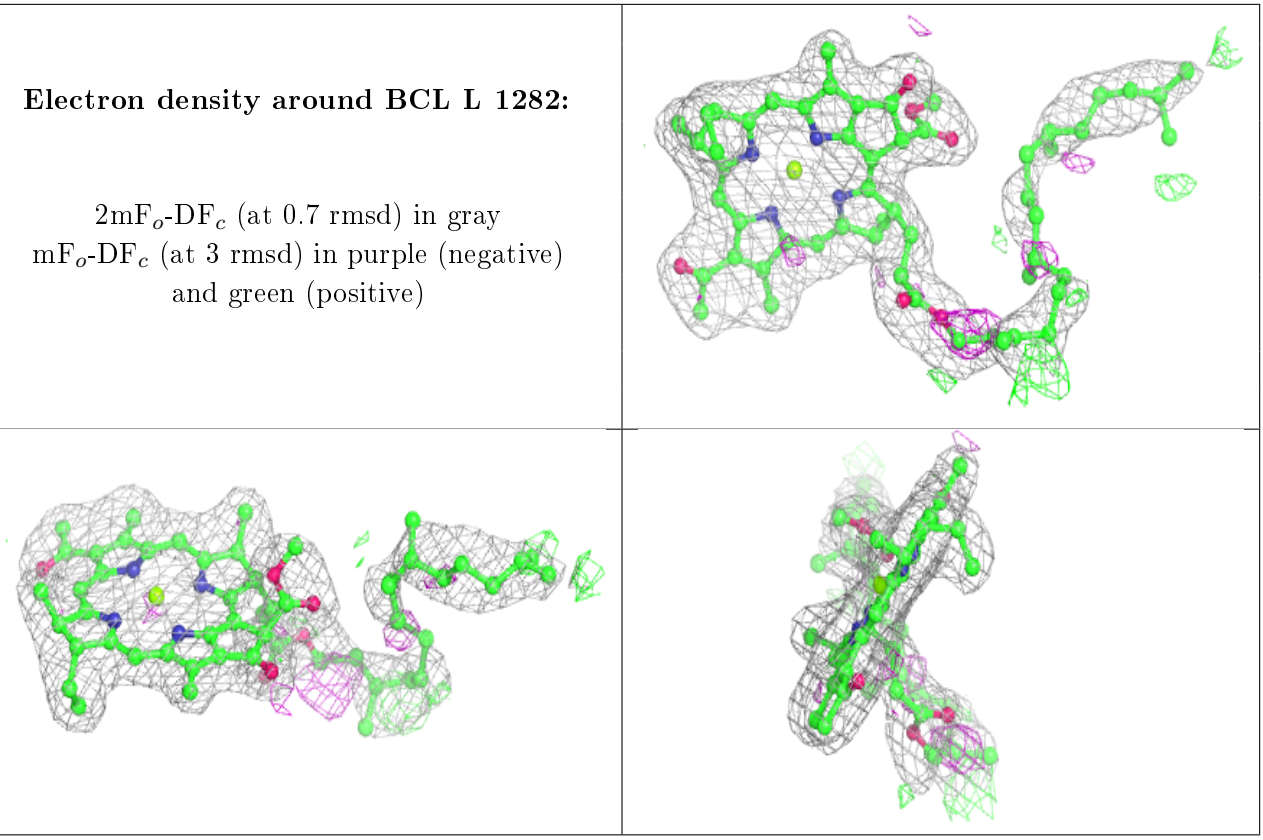
Electron density around U10 M 1310:

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



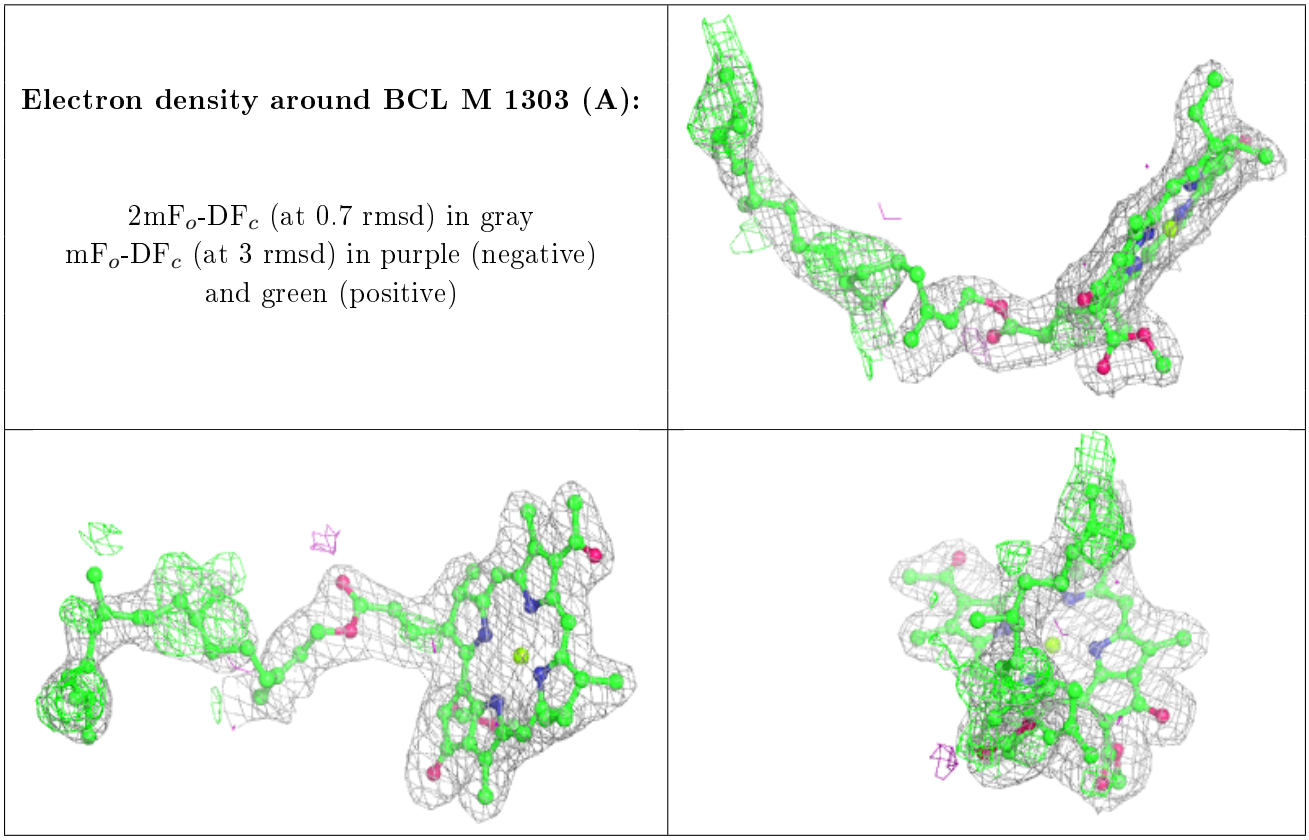
Electron density around BCL L 1282:

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



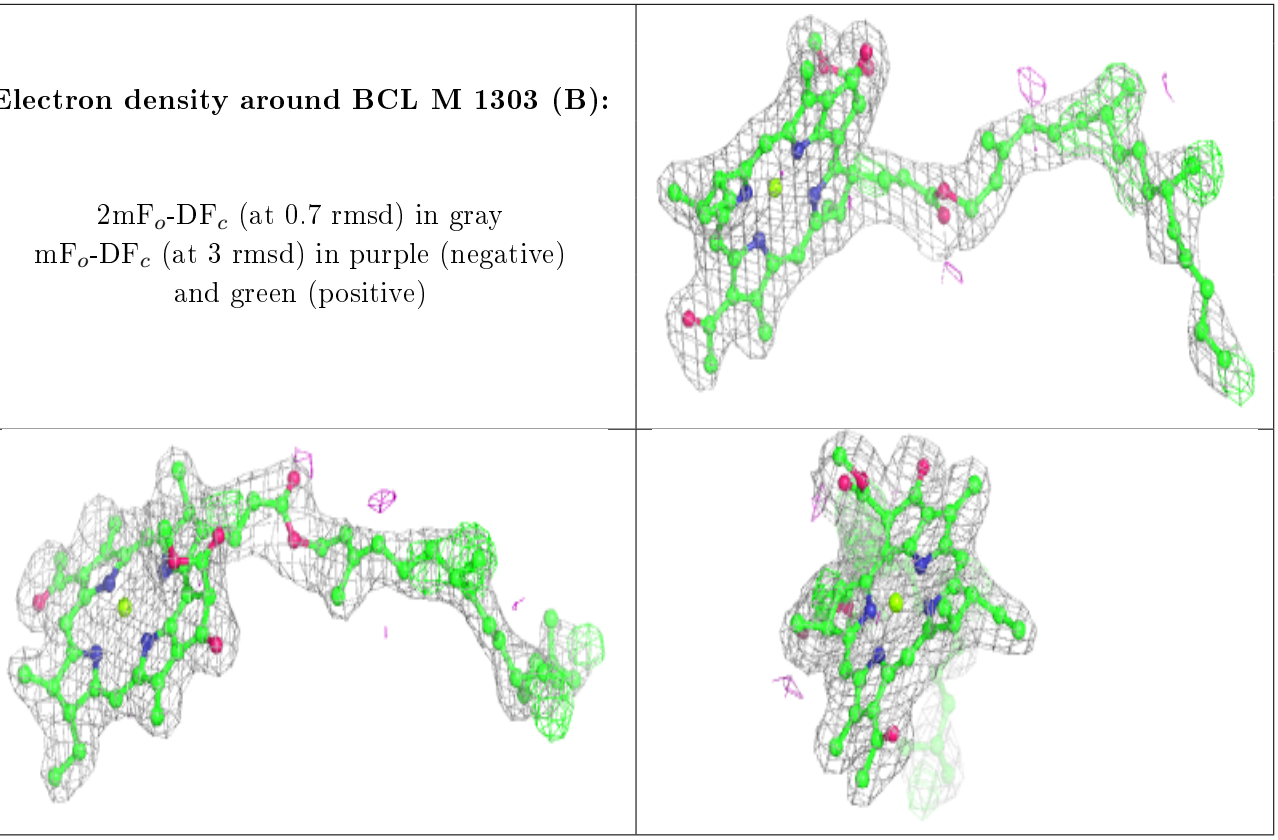
Electron density around BCL M 1303 (A):

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



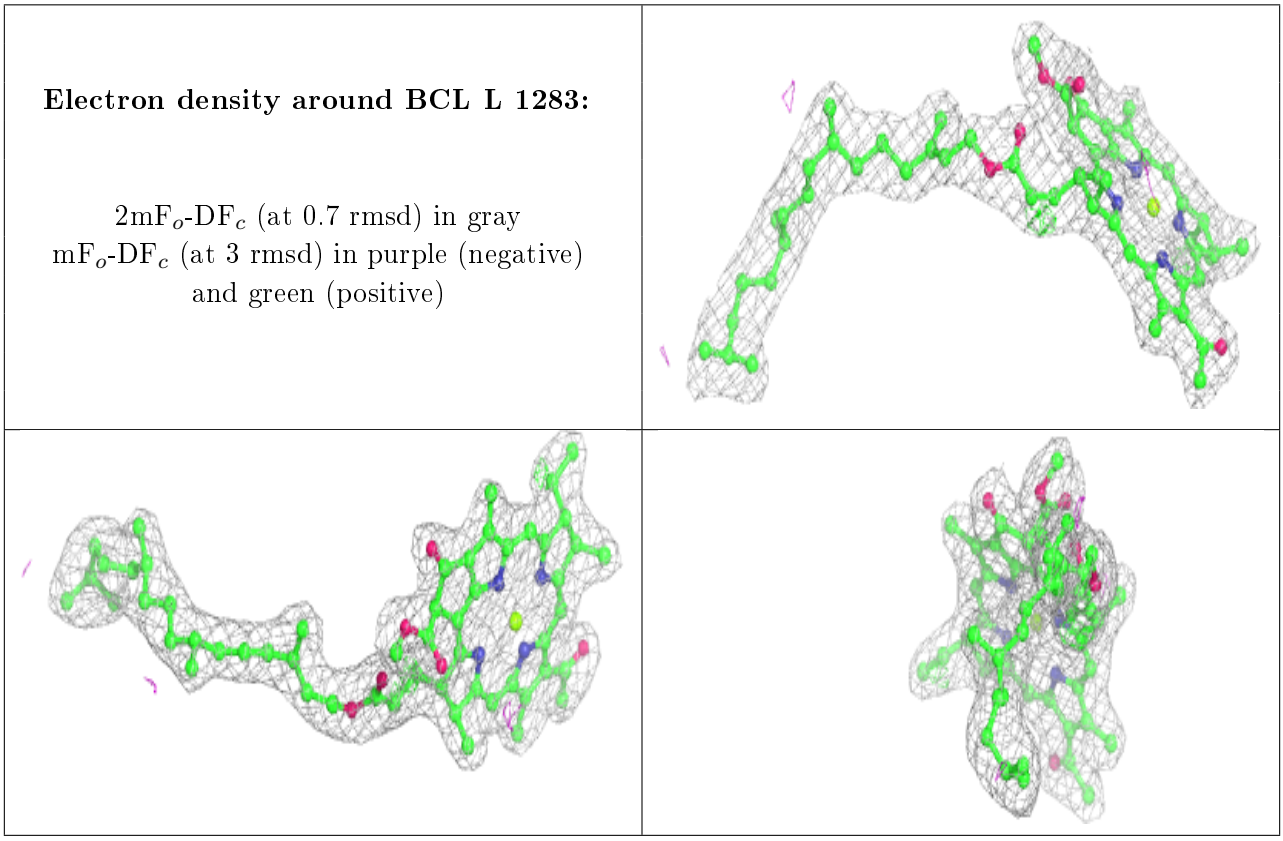
Electron density around BCL M 1303 (B):

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



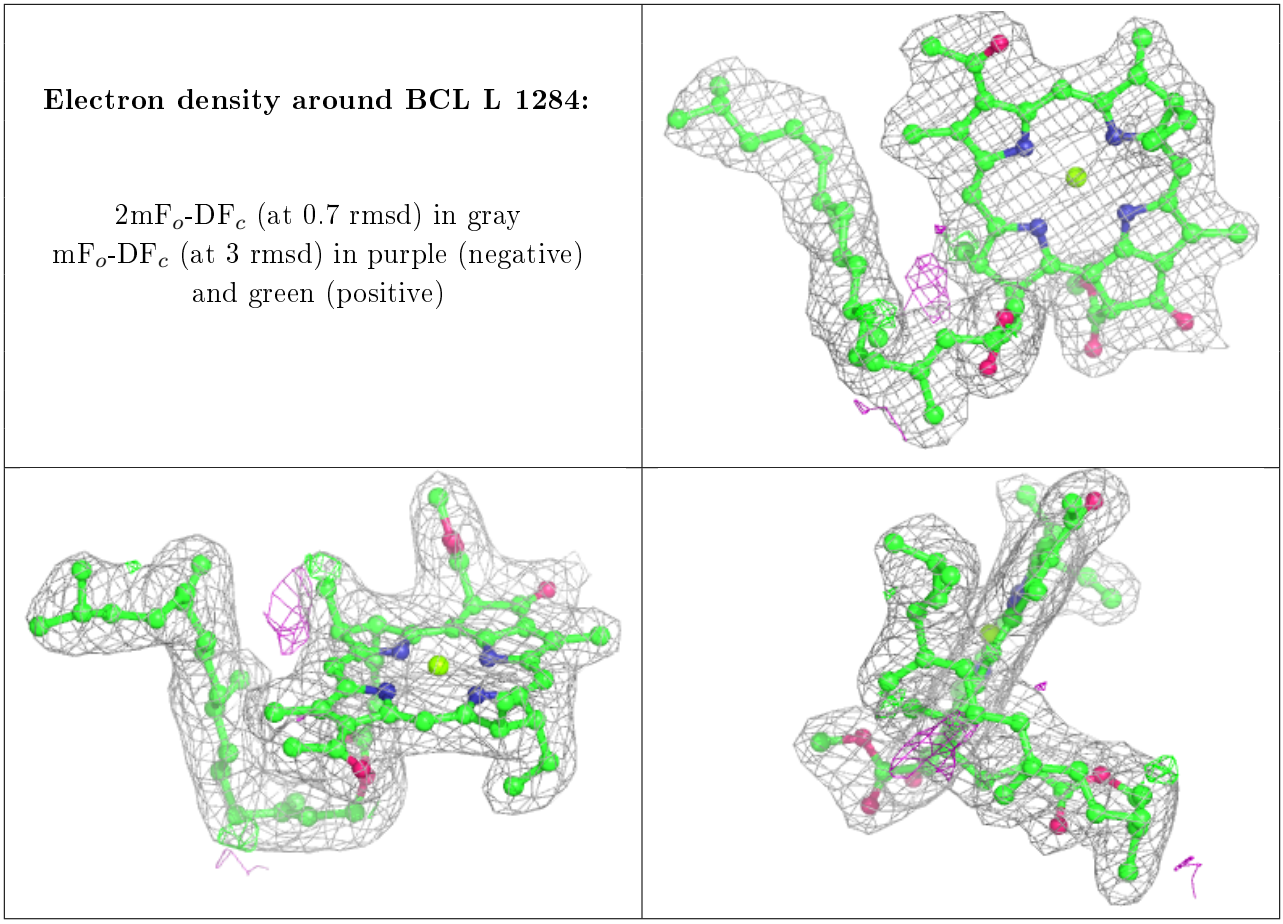
Electron density around BCL L 1283:

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



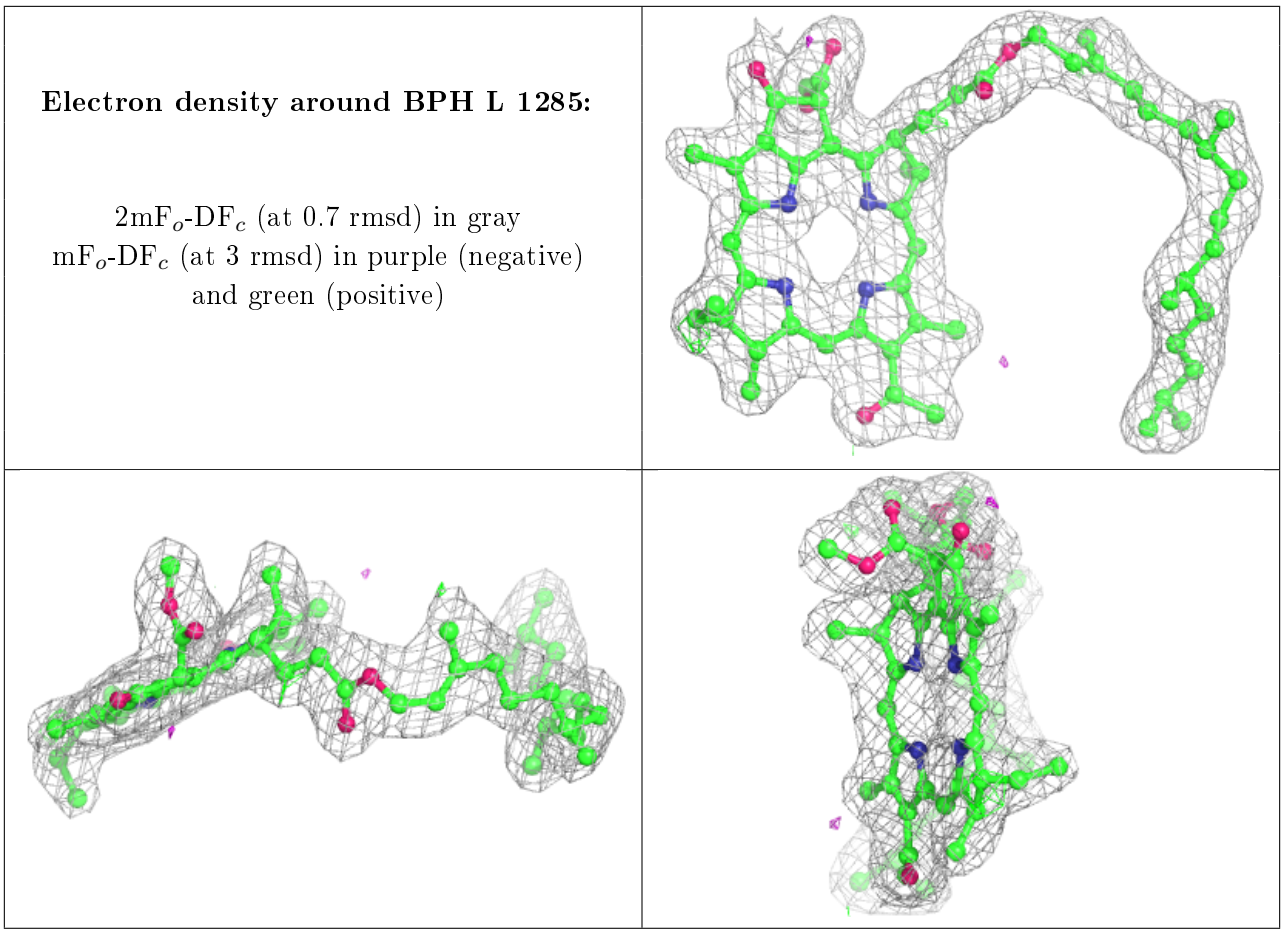
Electron density around BCL L 1284:

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



Electron density around 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)



6.5 Other polymers (i)

There are no such residues in this entry.