



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2023 – 08:51 PM EDT

PDB ID : 3DU3  
Title : E(L212)A, D(L213)A, A(M249)Y triple mutant structure of photosynthetic reaction center  
Authors : Pokkuluri, P.R.; Schiffer, M.  
Deposited on : 2008-07-16  
Resolution : 2.80 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.35  
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) : 2.35

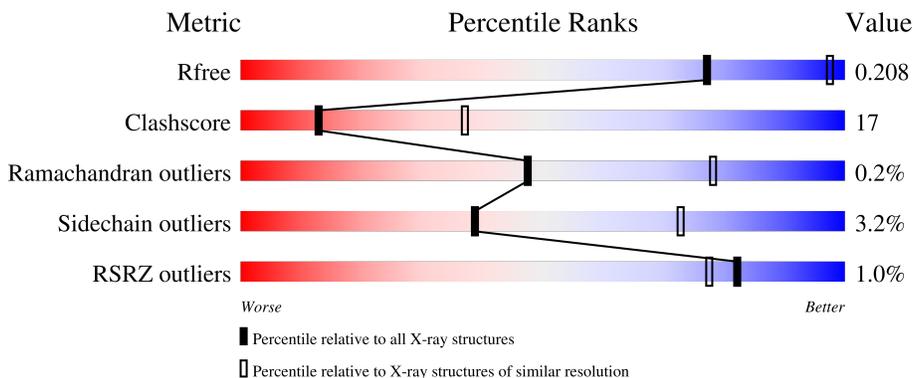
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

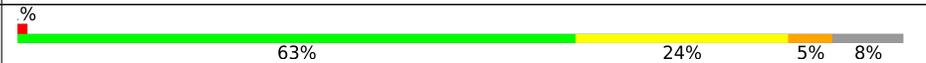
The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L	281	 72% 25%
2	M	314	 61% 30%
3	H	260	 63% 24% 5% 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	LDA	H	703	-	-	X	-
10	LDA	M	704	-	-	-	X
4	BCL	L	501	X	-	-	-
4	BCL	M	501	X	-	-	-
5	BPH	M	503	X	-	-	-
6	U10	L	504	-	-	-	X

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 7288 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	281	2225	1504	355	358	8	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	212	ALA	GLU	engineered mutation	UNP P0C0Y8
L	213	ALA	ASP	engineered mutation	UNP P0C0Y8

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	M	302	2415	1613	394	398	10	0	0	0

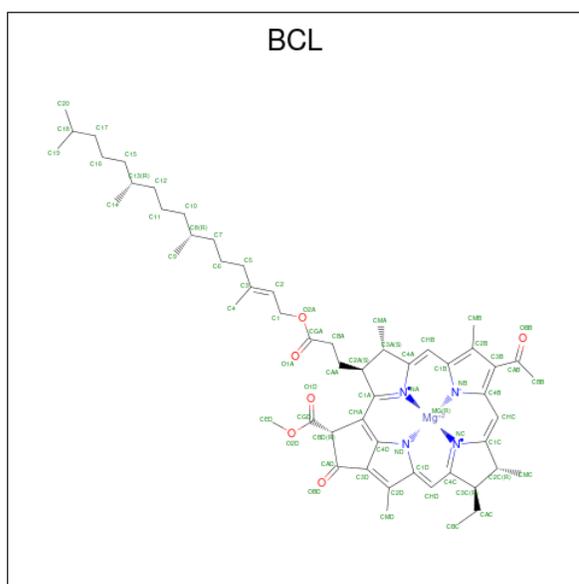
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	249	TYR	ALA	engineered mutation	UNP P0C0Y9
M	308	HIS	-	expression tag	UNP P0C0Y9
M	309	HIS	-	expression tag	UNP P0C0Y9
M	310	HIS	-	expression tag	UNP P0C0Y9
M	311	HIS	-	expression tag	UNP P0C0Y9
M	312	HIS	-	expression tag	UNP P0C0Y9
M	313	HIS	-	expression tag	UNP P0C0Y9
M	314	HIS	-	expression tag	UNP P0C0Y9

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

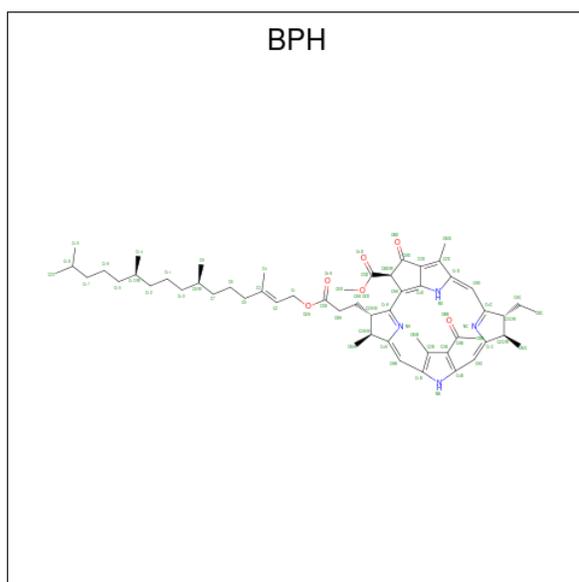
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	240	1829	1169	314	337	9	0	0	0

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



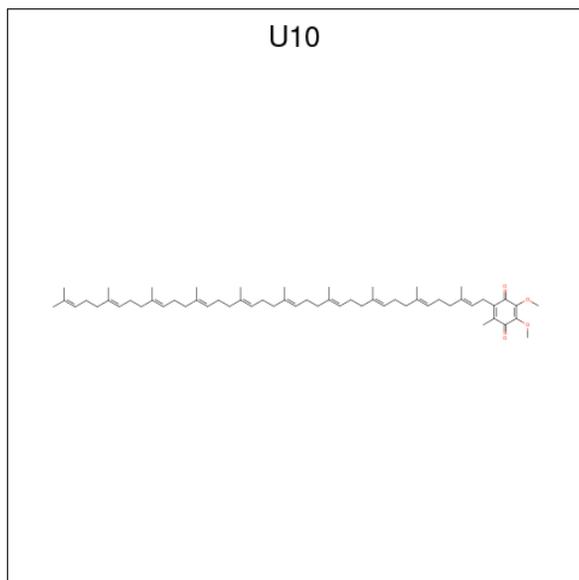
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
			Total	C	Mg	N			O	
4	L	1	Total	66	55	1	4	6	0	0
4	L	1	Total	66	55	1	4	6	0	0
4	M	1	Total	66	55	1	4	6	0	0
4	M	1	Total	66	55	1	4	6	0	0

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	L	1	Total	C	N	O	0	0
			65	55	4	6		
5	M	1	Total	C	N	O	0	0
			55	45	4	6		

- Molecule 6 is UBIQUINONE-10 (three-letter code: U10) (formula: C<sub>59</sub>H<sub>90</sub>O<sub>4</sub>).

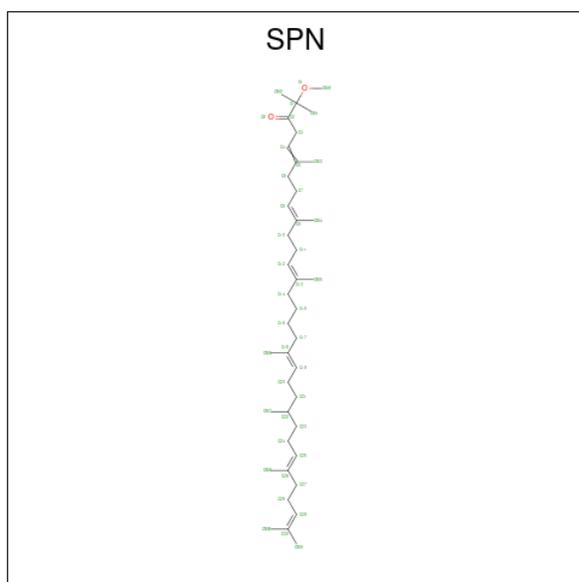


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	L	1	Total	C	O	0	0
			48	44	4		
6	M	1	Total	C	O	0	0
			48	44	4		

- Molecule 7 is FE (III) ION (three-letter code: FE) (formula: Fe).

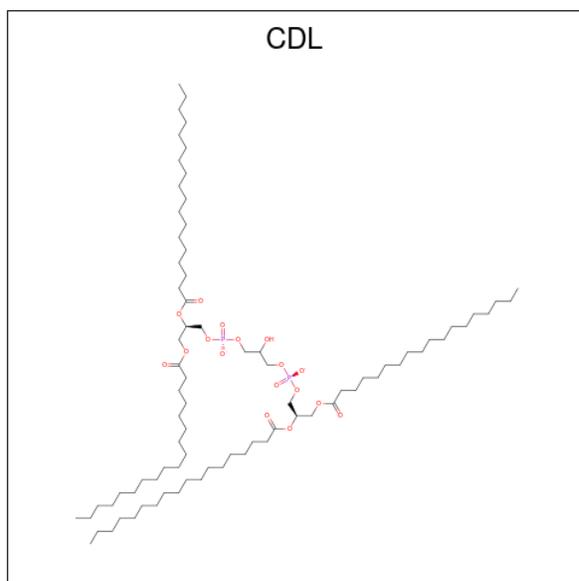
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	M	1	Total	Fe	0	0
			1	1		

- Molecule 8 is SPEROIDENONE (three-letter code: SPN) (formula: C<sub>41</sub>H<sub>70</sub>O<sub>2</sub>).



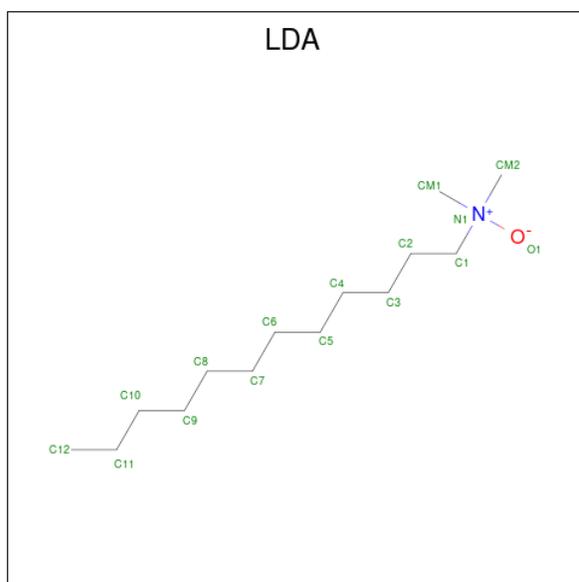
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
8	M	1	43	41	2	0	0

- Molecule 9 is CARDIOLIPIN (three-letter code: CDL) (formula:  $C_{81}H_{156}O_{17}P_2$ ).



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

- Molecule 10 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula:  $C_{14}H_{31}NO$ ).



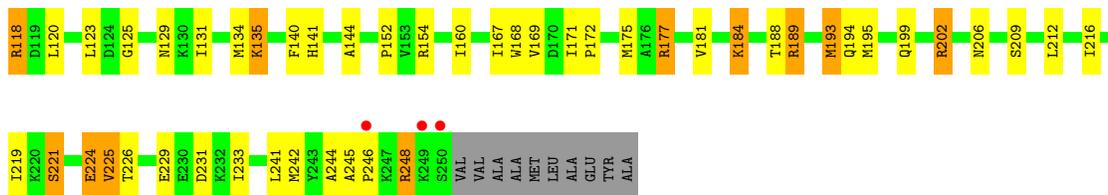
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	M	1	Total	C	N	O	0	0
			16	14	1	1		
10	M	1	Total	C	N	O	0	0
			16	14	1	1		
10	H	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	L	41	Total	O	0	0
			41	41		
11	M	55	Total	O	0	0
			55	55		
11	H	70	Total	O	0	0
			70	70		







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	141.10Å 141.10Å 187.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.80 29.14 – 2.80	Depositor EDS
% Data completeness (in resolution range)	84.0 (10.00-2.80) 92.1 (29.14-2.80)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.10 (at 2.80Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.191 , 0.201 0.200 , 0.208	Depositor DCC
$R_{free}$ test set	3488 reflections (7.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.3	Xtrriage
Anisotropy	0.022	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 62.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.020 for -h,-k,l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7288	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtrriage'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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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.

## 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, SPN, U10, BCL, CDL, LDA, BPH

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	L	1.10	2/2313 (0.1%)	1.18	16/3166 (0.5%)
2	M	1.15	2/2508 (0.1%)	1.26	29/3424 (0.8%)
3	H	1.03	2/1877 (0.1%)	1.32	22/2553 (0.9%)
All	All	1.10	6/6698 (0.1%)	1.25	67/9143 (0.7%)

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
2	M	0	1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	272	TRP	C-N	8.66	1.53	1.34
3	H	75	VAL	C-N	6.89	1.47	1.34
1	L	143	GLY	N-CA	5.42	1.54	1.46
2	M	89	LEU	N-CA	5.39	1.57	1.46
2	M	301	HIS	CA-C	-5.16	1.39	1.52

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	272	TRP	O-C-N	-7.61	110.52	122.70
3	H	37	ARG	NE-CZ-NH2	7.61	124.11	120.30
2	M	164	ARG	NE-CZ-NH2	7.46	124.03	120.30
2	M	49	PRO	O-C-N	7.42	134.58	122.70
3	H	202	ARG	NE-CZ-NH2	7.42	124.01	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	M	301	HIS	Mainchain

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	2225	0	2187	62	0
2	M	2415	0	2325	99	0
3	H	1829	0	1836	72	0
4	L	132	0	148	17	0
4	M	132	0	148	17	0
5	L	65	0	76	1	0
5	M	55	0	53	1	0
6	L	48	0	62	5	0
6	M	48	0	63	15	0
7	M	1	0	0	0	0
8	M	43	0	69	4	0
9	M	81	0	106	3	0
10	H	16	0	31	10	0
10	M	32	0	62	8	0
11	H	70	0	0	2	0
11	L	41	0	0	1	0
11	M	55	0	0	0	0
All	All	7288	0	7166	236	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 17.

The worst 5 of 236 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:M:265:ILE:HG21	6:M:504:U10:H3M3	1.17	1.12
2:M:265:ILE:HG21	6:M:504:U10:C3M	1.88	1.03
2:M:204:LEU:HB3	2:M:279:THR:HG21	1.50	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:34:PHE:O	1:L:38:THR:HG23	1.69	0.91
6:M:504:U10:H202	10:H:703:LDA:H112	1.52	0.88

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	279/281 (99%)	270 (97%)	9 (3%)	0	100	100
2	M	300/314 (96%)	290 (97%)	8 (3%)	2 (1%)	22	53
3	H	238/260 (92%)	227 (95%)	11 (5%)	0	100	100
All	All	817/855 (96%)	787 (96%)	28 (3%)	2 (0%)	47	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	M	301	HIS
2	M	22	GLU

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	218/218 (100%)	209 (96%)	9 (4%)	30	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	M	237/248 (96%)	230 (97%)	7 (3%)	41	75
3	H	195/208 (94%)	190 (97%)	5 (3%)	46	79
All	All	650/674 (96%)	629 (97%)	21 (3%)	39	73

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

Mol	Chain	Res	Type
2	M	216	PHE
3	H	184	LYS
3	H	231	ASP
3	H	221	SER
3	H	135	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	68	HIS
3	H	199	GLN
3	H	206	ASN
2	M	44	ASN
2	M	4	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 1 is monoatomic - leaving 13 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	U10	M	504	-	48,48,63	2.49	20 (41%)	58,61,79	1.76	12 (20%)
4	BCL	L	502	1	58,74,74	1.61	10 (17%)	69,115,115	2.62	14 (20%)
4	BCL	M	501	2	58,74,74	1.58	10 (17%)	69,115,115	2.54	28 (40%)
4	BCL	M	502	2	58,74,74	1.32	8 (13%)	69,115,115	1.94	13 (18%)
6	U10	L	504	-	48,48,63	1.80	12 (25%)	58,61,79	2.79	17 (29%)
8	SPN	M	600	-	40,42,42	3.77	17 (42%)	50,52,52	2.58	16 (32%)
10	LDA	M	701	-	12,15,15	2.58	1 (8%)	14,17,17	0.41	0
10	LDA	H	703	-	12,15,15	2.43	1 (8%)	14,17,17	0.65	0
4	BCL	L	501	1	58,74,74	1.38	8 (13%)	69,115,115	2.25	14 (20%)
9	CDL	M	800	-	80,80,99	0.52	0	86,92,111	1.08	6 (6%)
5	BPH	M	503	-	41,60,70	1.88	9 (21%)	40,89,101	3.00	18 (45%)
5	BPH	L	503	-	51,70,70	1.76	11 (21%)	52,101,101	2.49	15 (28%)
10	LDA	M	704	-	12,15,15	2.07	1 (8%)	14,17,17	0.52	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	U10	M	504	-	-	10/45/69/87	0/1/1/1
4	BCL	L	502	1	-	6/37/137/137	-
4	BCL	M	501	2	2/2/21/25	15/37/137/137	-
4	BCL	M	502	2	-	9/37/137/137	-
6	U10	L	504	-	-	11/45/69/87	0/1/1/1
8	SPN	M	600	-	-	18/50/51/51	-
10	LDA	M	701	-	-	8/13/13/13	-
10	LDA	H	703	-	-	5/13/13/13	-
4	BCL	L	501	1	1/1/21/25	10/37/137/137	-
9	CDL	M	800	-	-	29/91/91/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BPH	M	503	-	1/1/16/22	8/25/93/105	0/5/6/6
5	BPH	L	503	-	-	5/37/105/105	0/5/6/6
10	LDA	M	704	-	-	4/13/13/13	-

The worst 5 of 108 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	M	600	SPN	C4-C5	8.94	1.54	1.33
8	M	600	SPN	C19-C18	8.81	1.54	1.33
10	M	701	LDA	O1-N1	-8.80	1.21	1.42
8	M	600	SPN	C8-C9	8.46	1.53	1.33
10	H	703	LDA	O1-N1	-8.38	1.22	1.42

The worst 5 of 153 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	504	U10	C32-C33-C34	14.64	162.91	127.66
5	M	503	BPH	O2D-CGD-CBD	11.82	125.97	111.00
5	L	503	BPH	O2D-CGD-CBD	11.30	125.31	111.00
4	L	502	BCL	C4B-C3B-CAB	-11.06	105.77	127.13
4	L	502	BCL	OBB-CAB-C3B	9.34	136.56	119.99

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	L	501	BCL	C13
4	M	501	BCL	C8
4	M	501	BCL	C13
5	M	503	BPH	C8

5 of 138 torsion outliers are listed below:

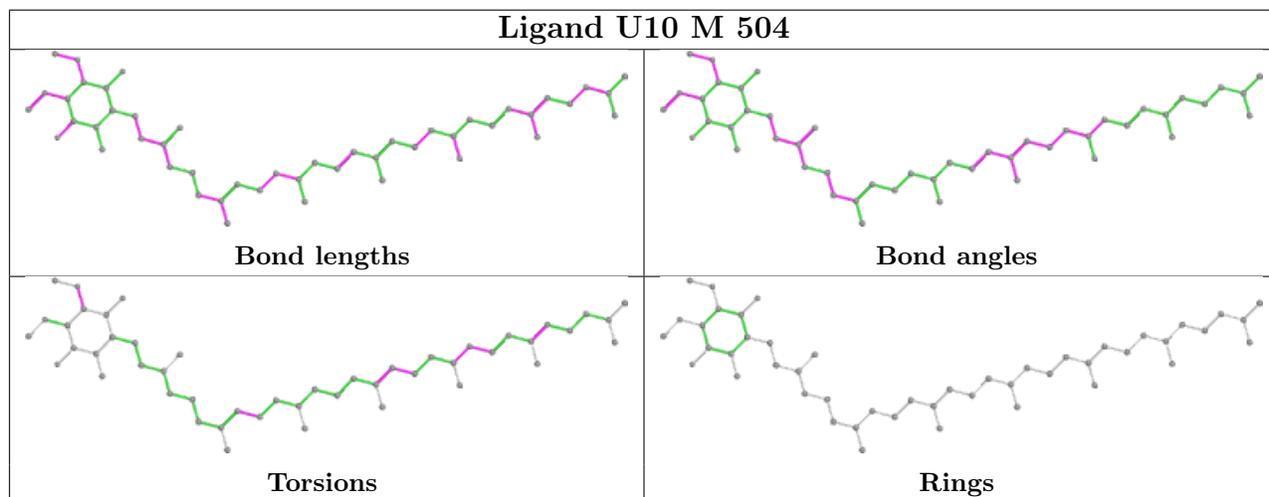
Mol	Chain	Res	Type	Atoms
4	L	501	BCL	C2C-C3C-CAC-CBC
4	L	501	BCL	C4C-C3C-CAC-CBC
4	M	501	BCL	C1-C2-C3-C4
5	M	503	BPH	O2A-C1-C2-C3
5	M	503	BPH	C1-C2-C3-C4

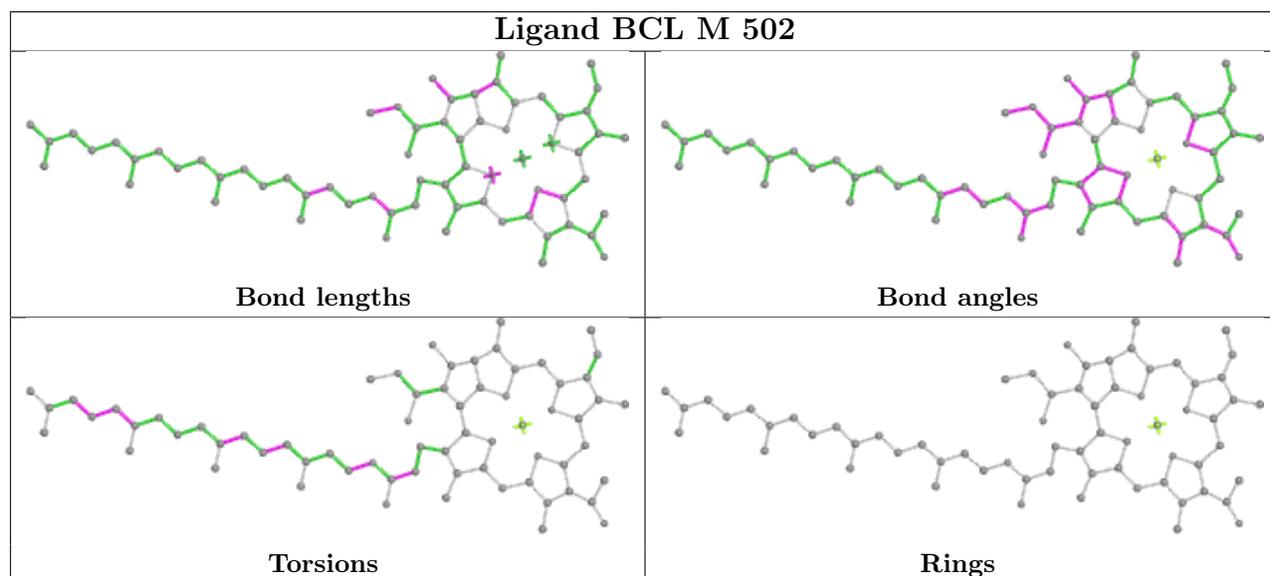
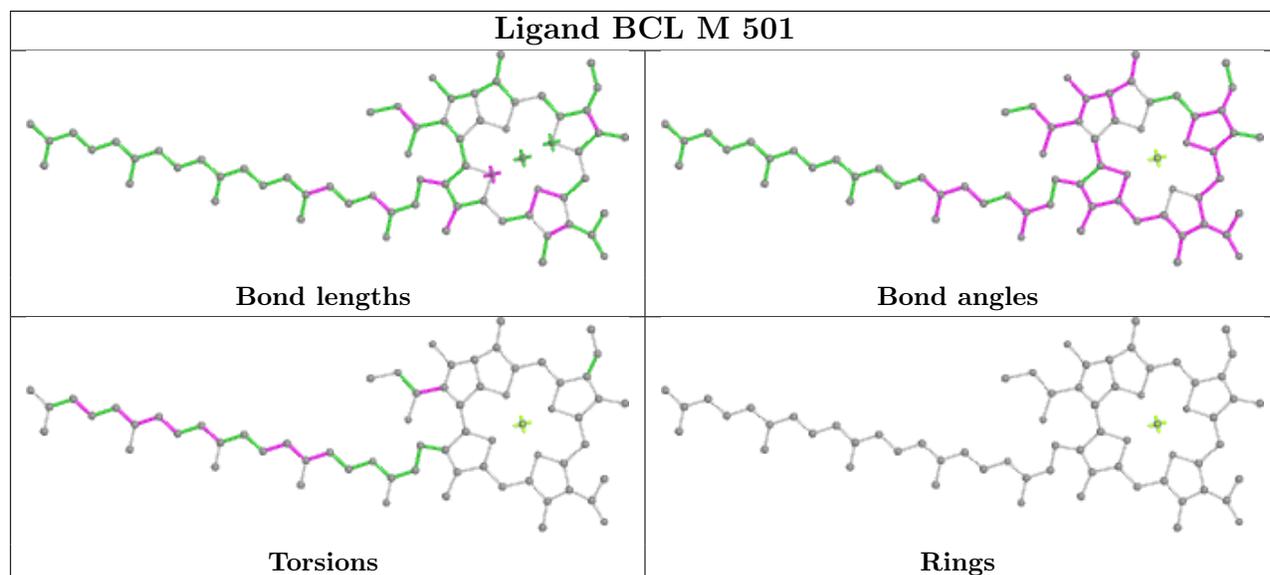
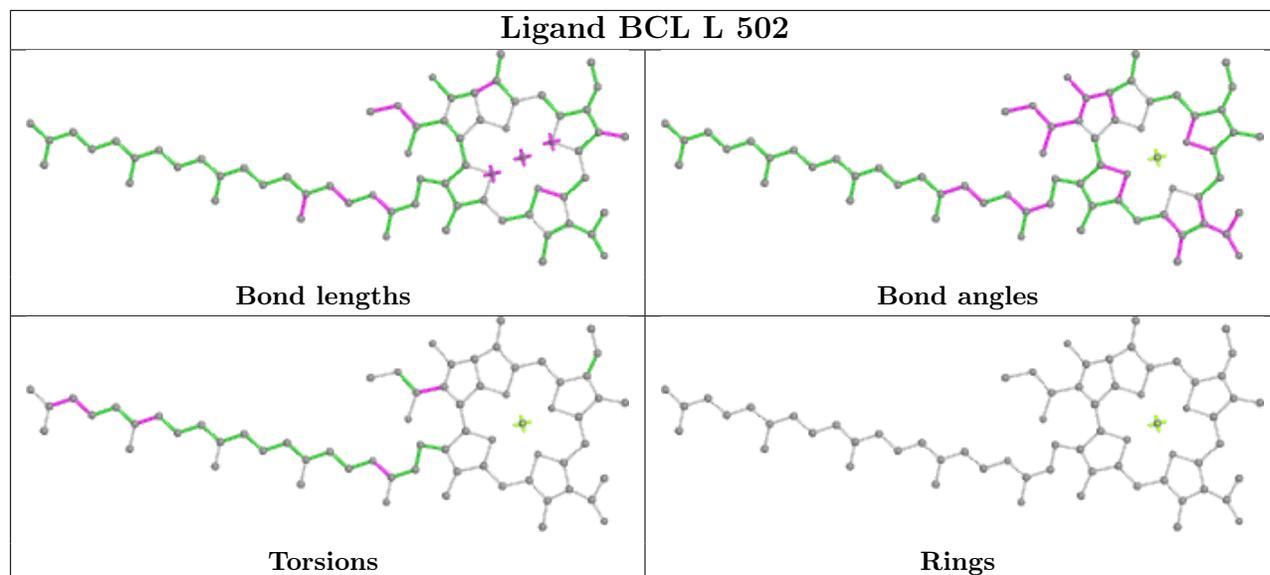
There are no ring outliers.

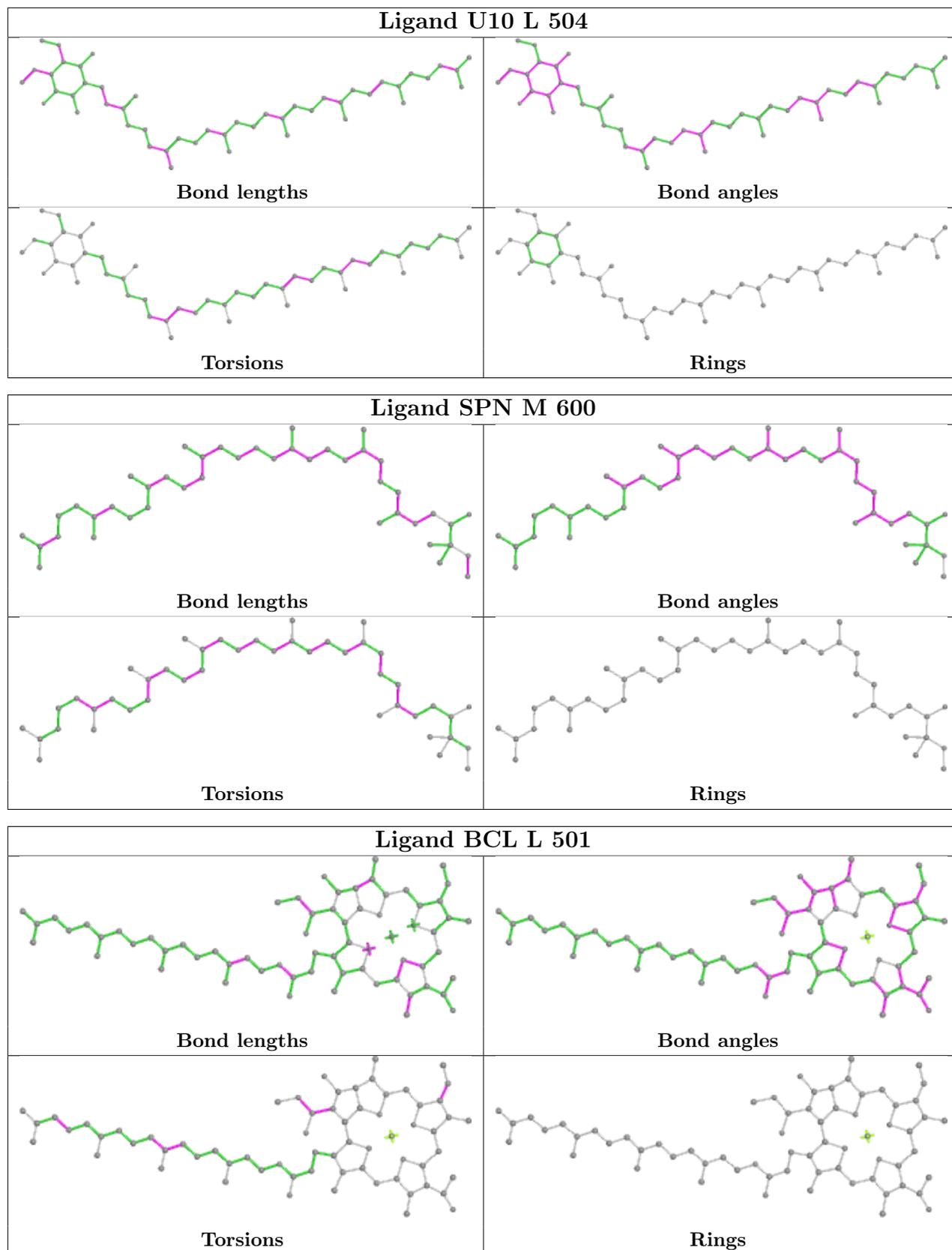
13 monomers are involved in 74 short contacts:

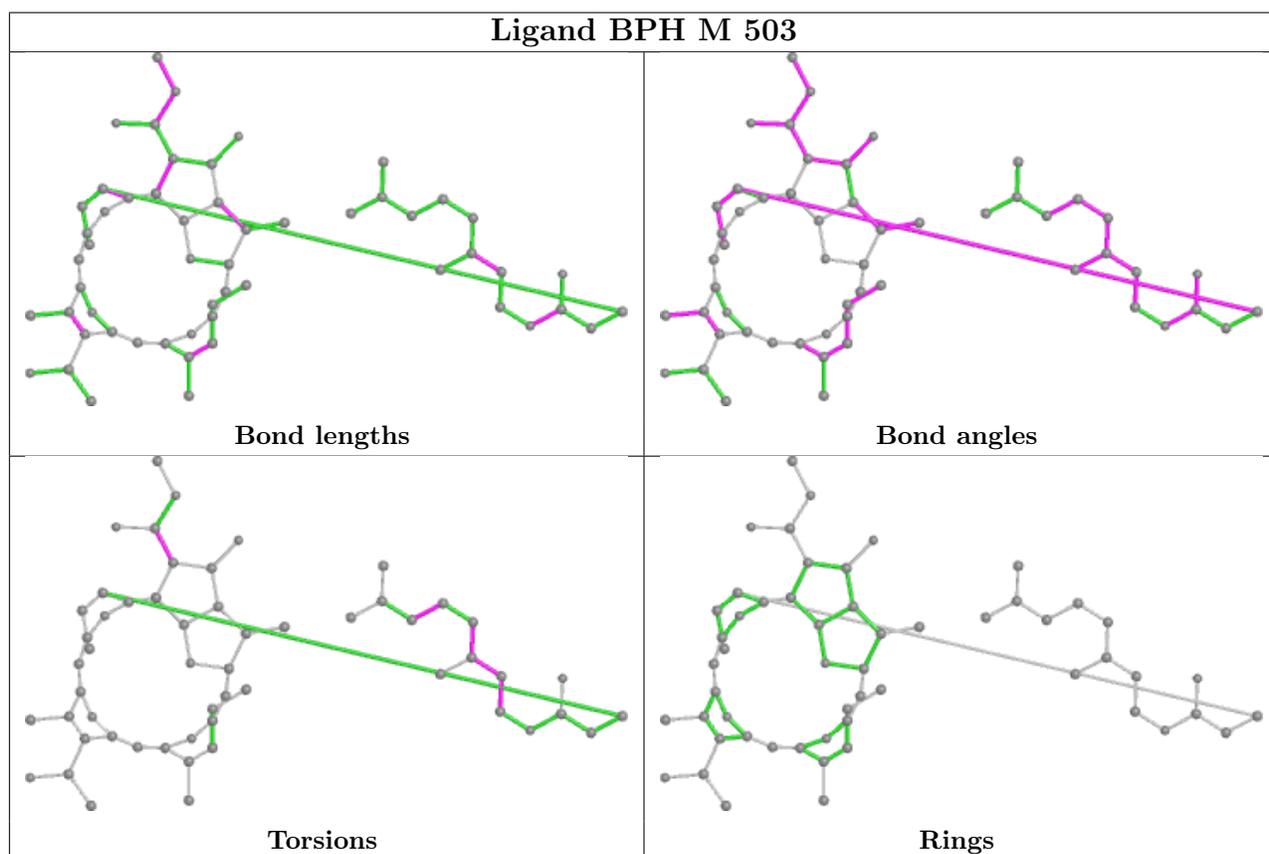
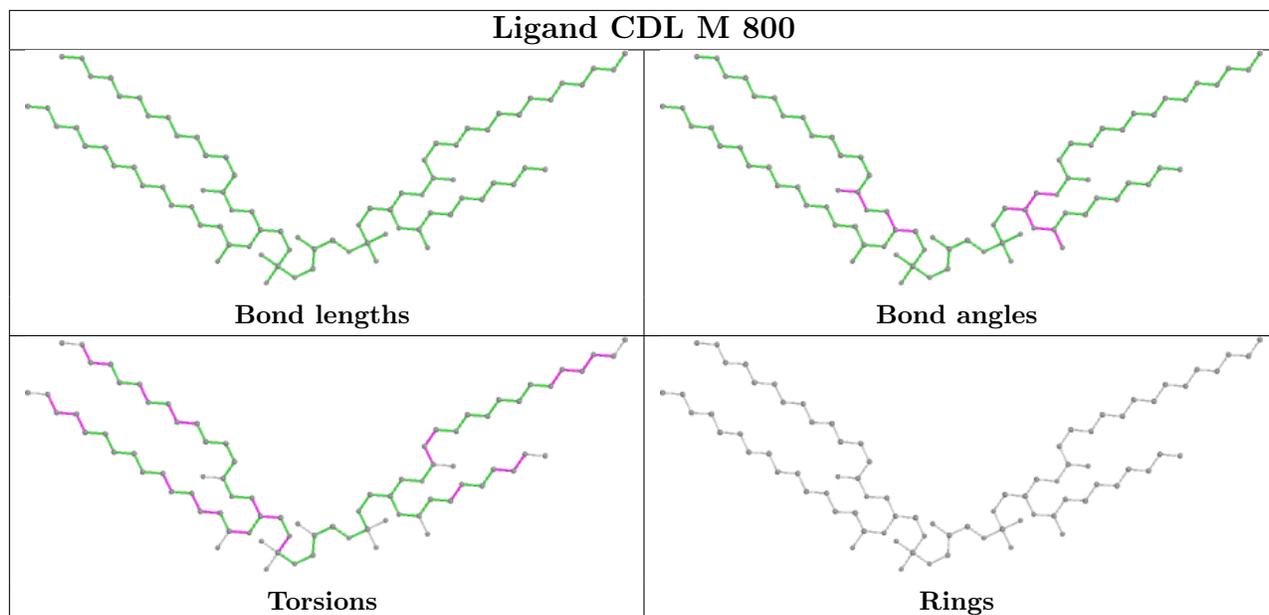
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	M	504	U10	15	0
4	L	502	BCL	12	0
4	M	501	BCL	9	0
4	M	502	BCL	12	0
6	L	504	U10	5	0
8	M	600	SPN	4	0
10	M	701	LDA	6	0
10	H	703	LDA	10	0
4	L	501	BCL	7	0
9	M	800	CDL	3	0
5	M	503	BPH	1	0
5	L	503	BPH	1	0
10	M	704	LDA	2	0

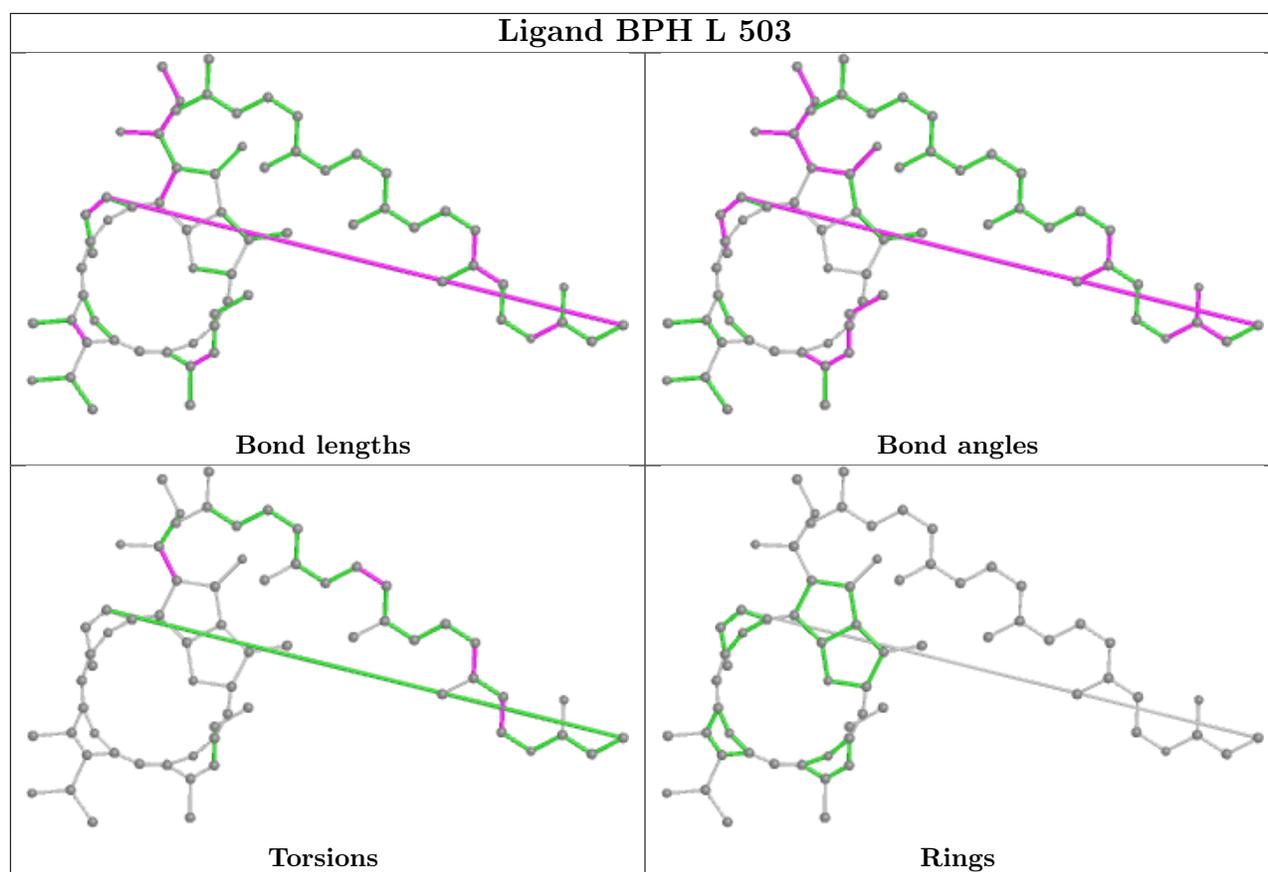
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	L	281/281 (100%)	-0.51	3 (1%) 80 75	19, 34, 76, 89	0
2	M	302/314 (96%)	-0.53	2 (0%) 87 84	16, 38, 75, 101	0
3	H	240/260 (92%)	-0.50	3 (1%) 77 72	24, 37, 62, 94	0
All	All	823/855 (96%)	-0.52	8 (0%) 82 77	16, 37, 73, 101	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	250	SER	5.4
1	L	59	TRP	4.0
1	L	281	GLY	3.9
2	M	1	ALA	3.7
3	H	249	LYS	3.0

### 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](#)

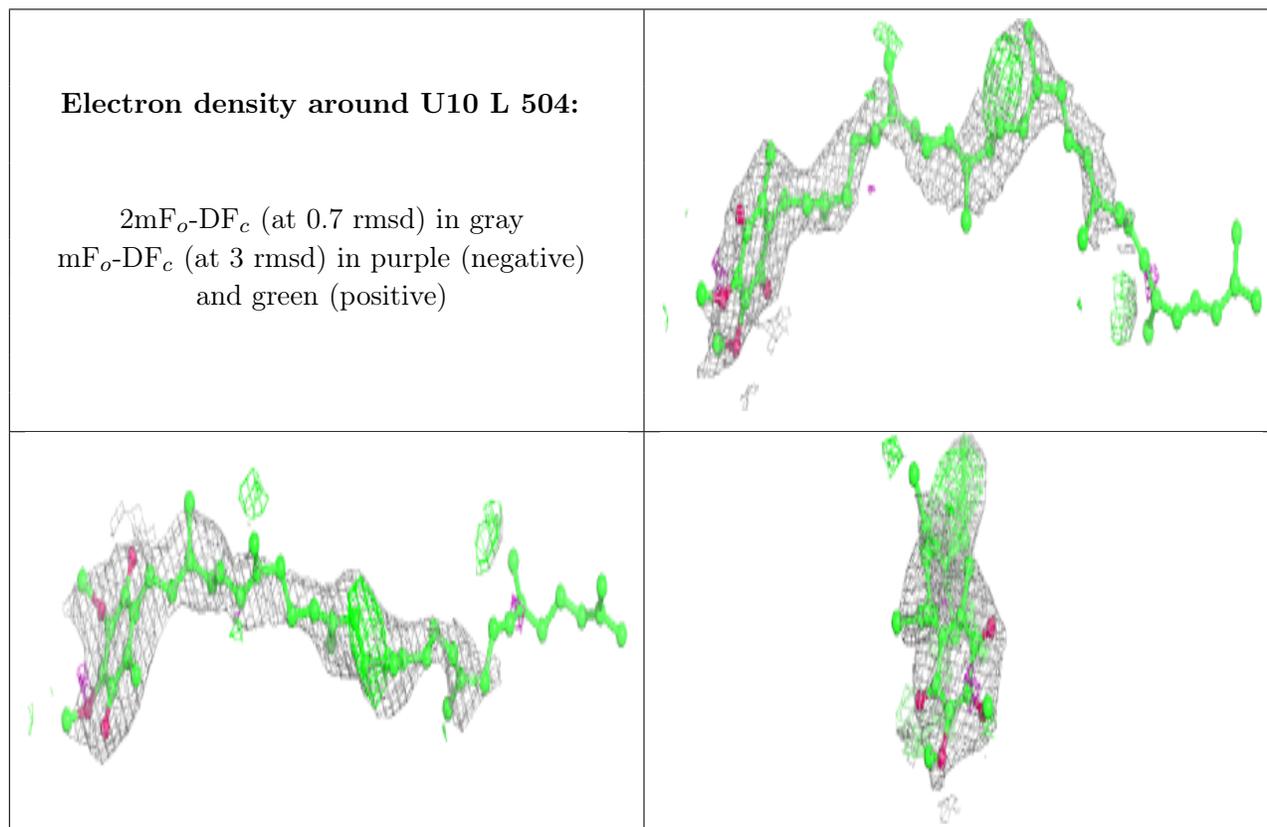
There are no monosaccharides in this entry.

### 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<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
10	LDA	M	704	16/16	0.59	0.47	81,95,110,111	0
6	U10	L	504	48/63	0.66	0.45	56,81,114,115	0
10	LDA	H	703	16/16	0.85	0.32	64,71,83,85	0
9	CDL	M	800	81/100	0.87	0.27	49,73,88,91	0
10	LDA	M	701	16/16	0.87	0.22	40,61,80,80	0
8	SPN	M	600	43/43	0.88	0.25	30,53,76,79	0
6	U10	M	504	48/63	0.91	0.21	31,48,77,80	0
4	BCL	M	502	66/66	0.96	0.17	21,31,64,66	0
4	BCL	M	501	66/66	0.96	0.16	19,25,101,104	0
5	BPH	M	503	55/65	0.97	0.14	20,35,74,82	0
4	BCL	L	502	66/66	0.97	0.16	17,30,49,58	0
4	BCL	L	501	66/66	0.97	0.14	16,25,53,61	0
5	BPH	L	503	65/65	0.97	0.12	15,24,43,47	0
7	FE	M	500	1/1	0.98	0.07	24,24,24,24	0

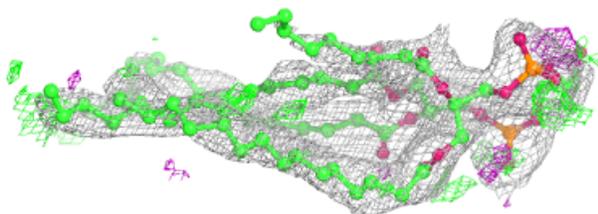
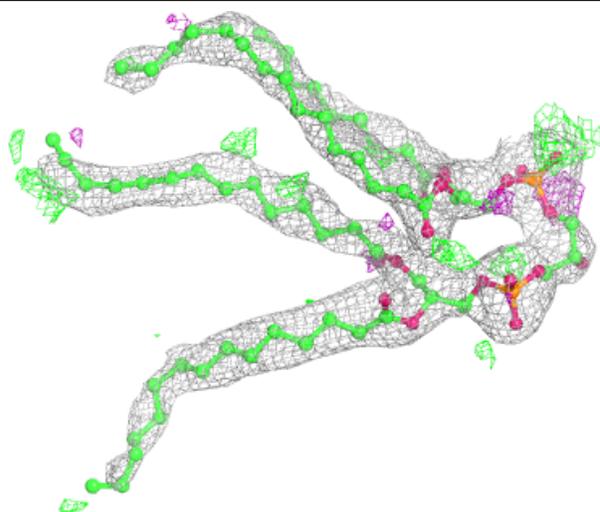
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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





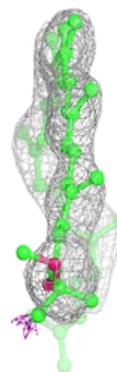
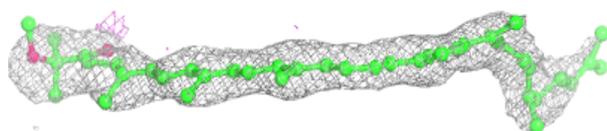
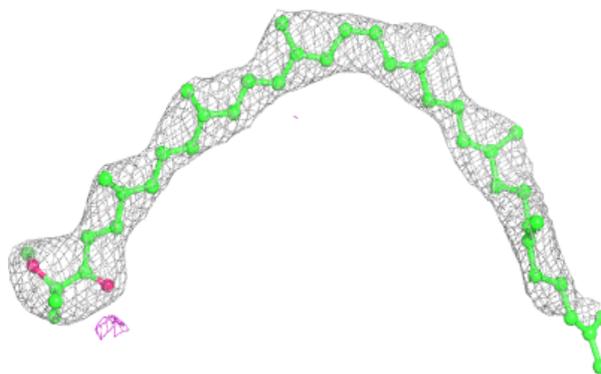
**Electron density around CDL M 800:**

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

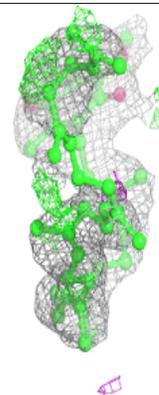
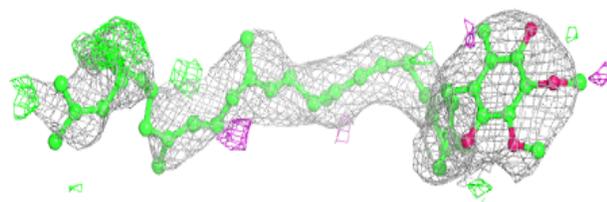
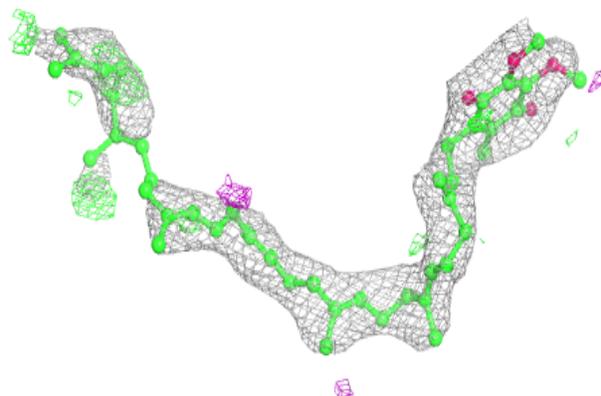


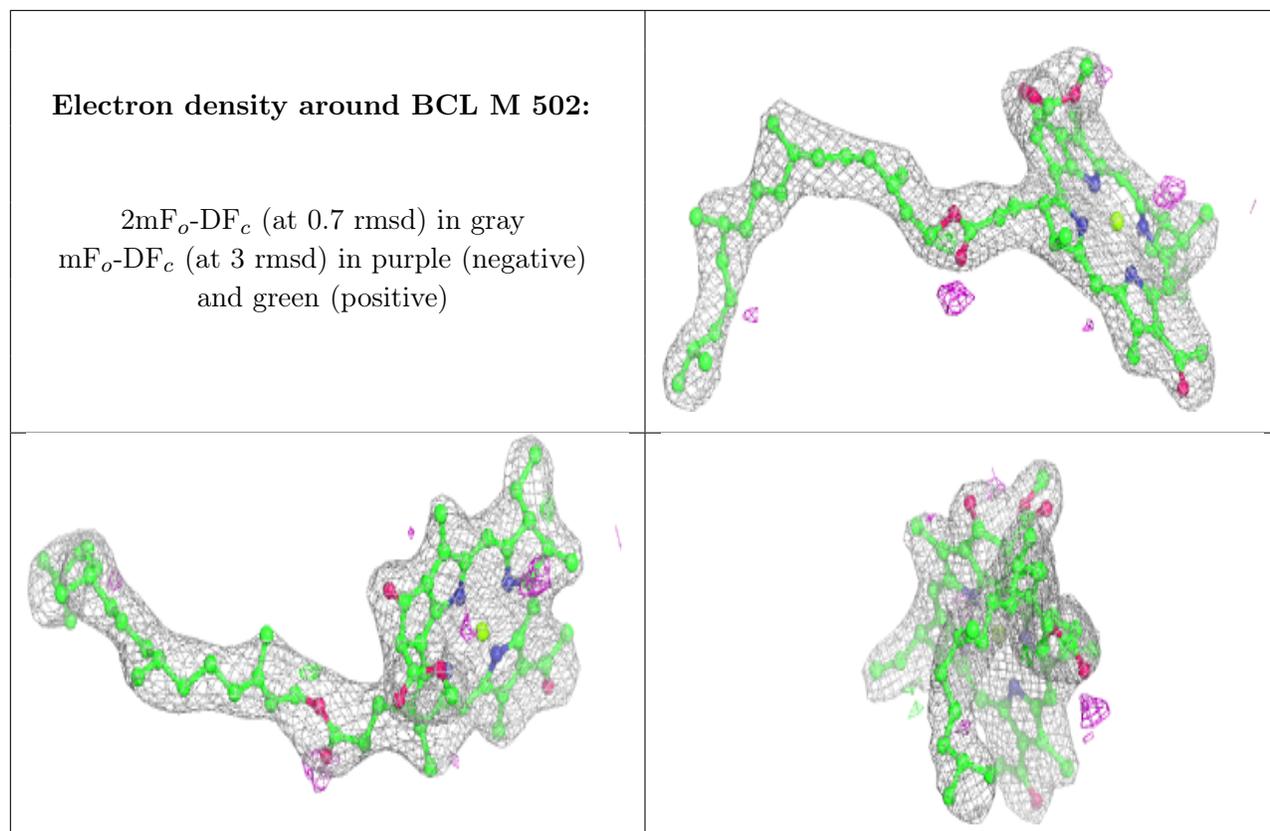
**Electron density around SPN M 600:**

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

**Electron density around U10 M 504:**

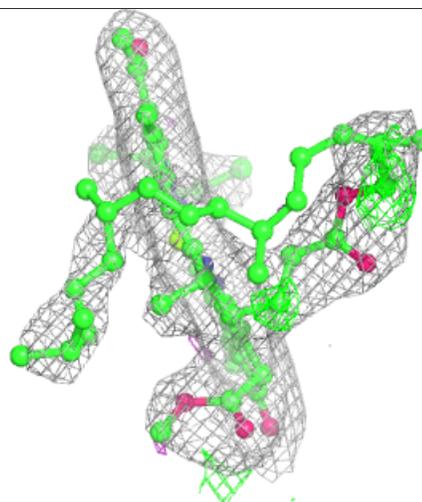
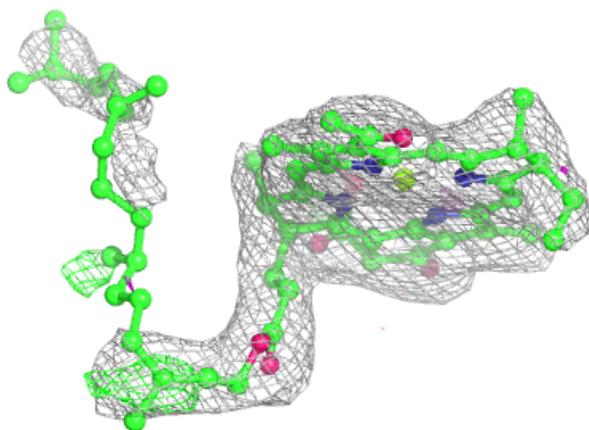
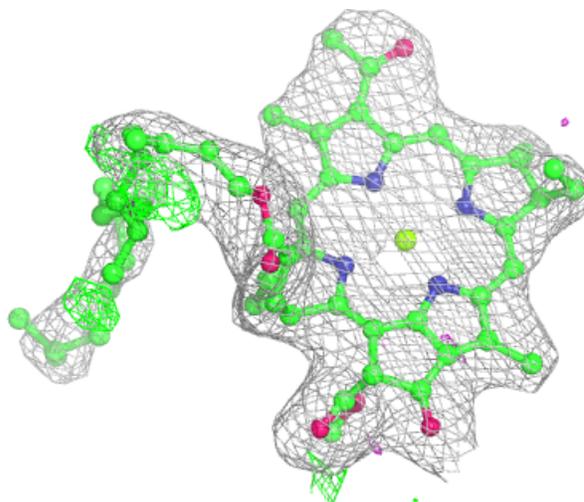
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





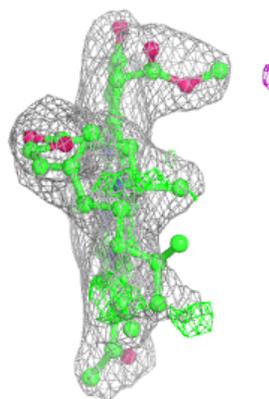
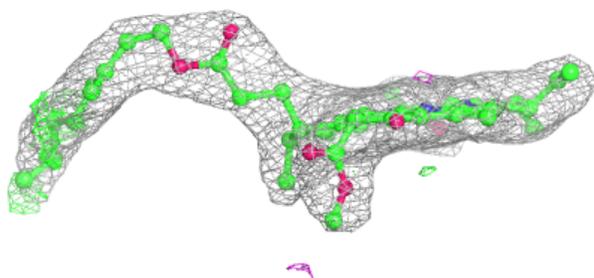
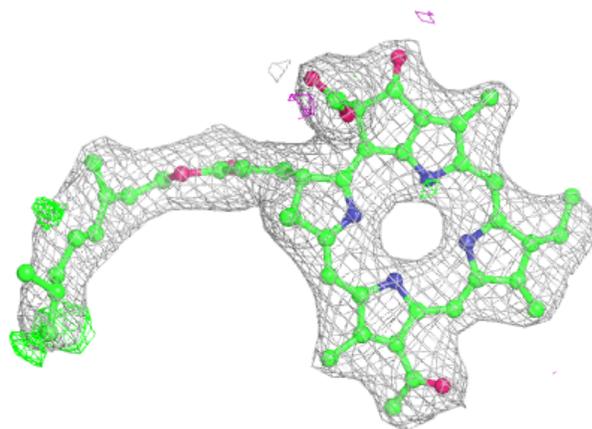
**Electron density around BCL M 501:**

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

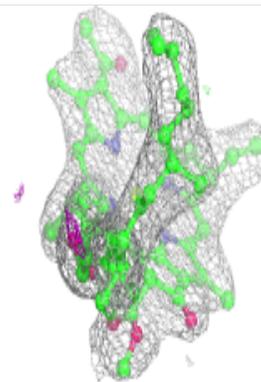
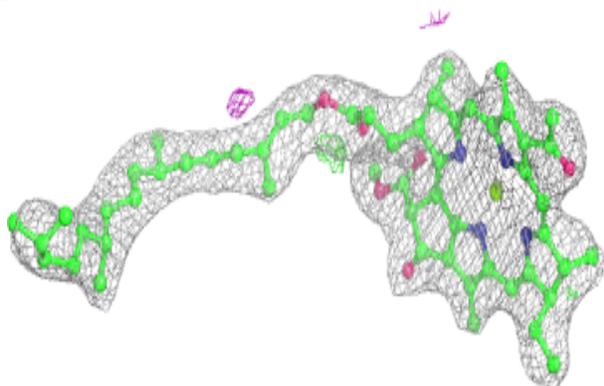
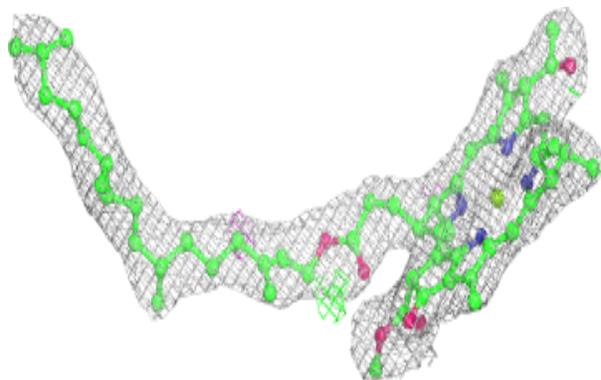


**Electron density around BPH M 503:**

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

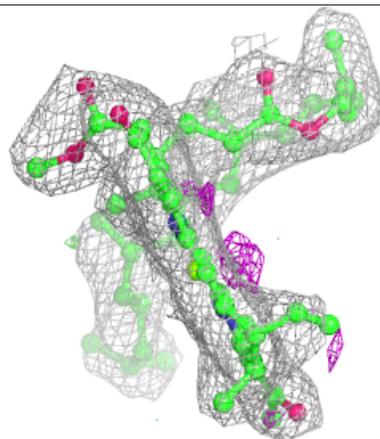
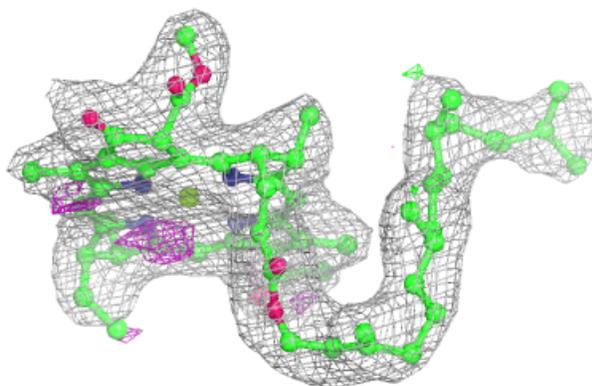
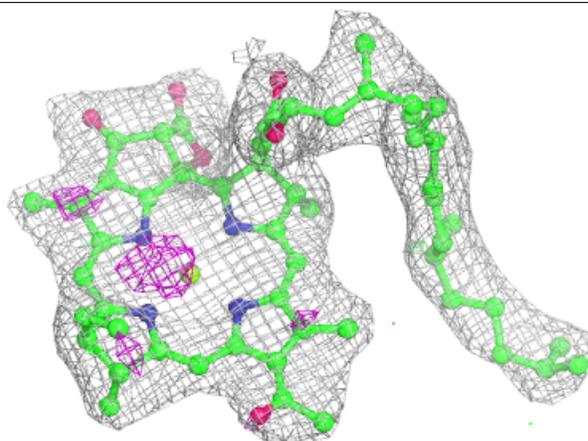
**Electron density around BCL L 502:**

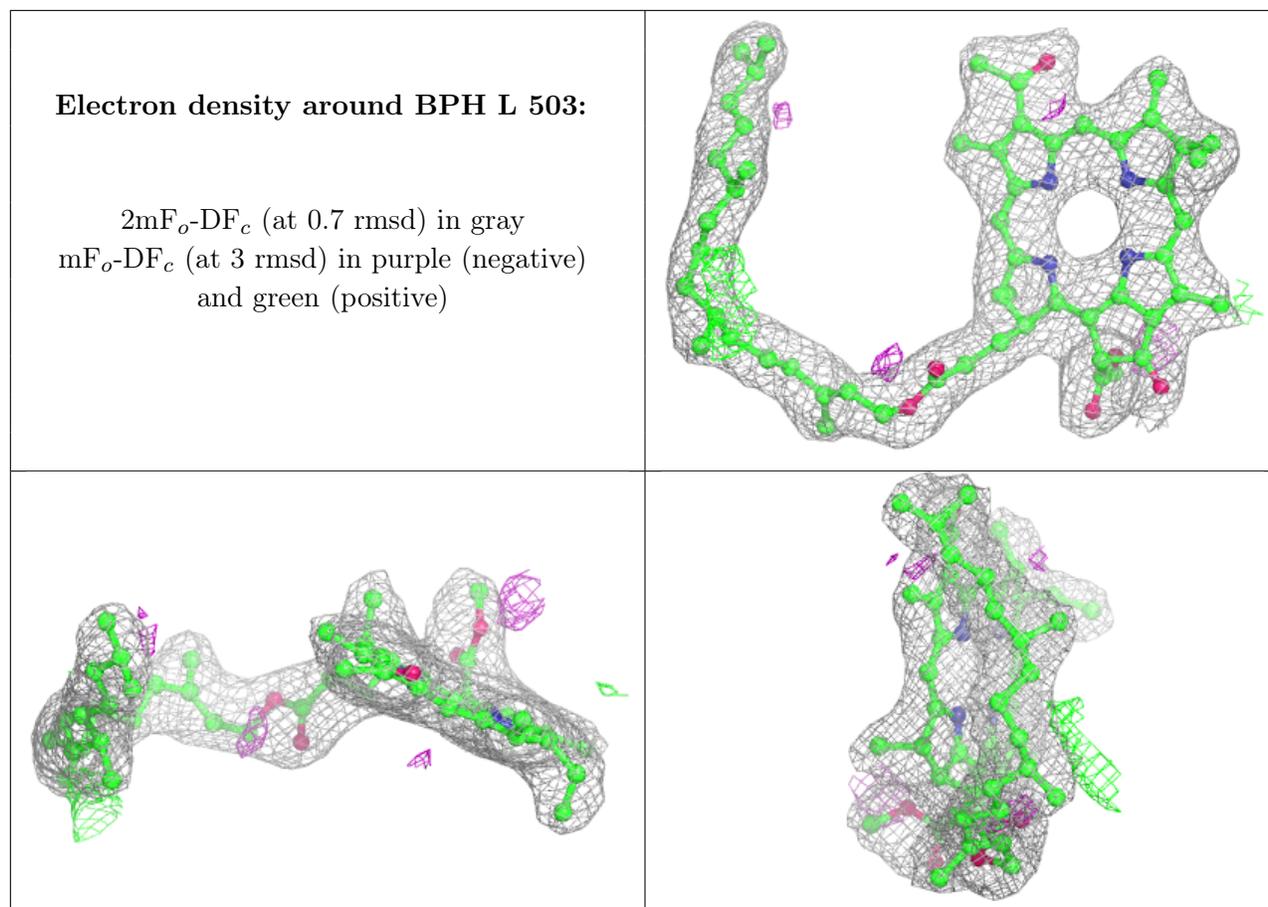
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around BCL L 501:**

$2mF_o-DF_c$  (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.