



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:10 AM UTC

PDB ID : 1S00 / pdb_00001s00
Title : PHOTOSYNTHETIC REACTION CENTER DOUBLE MUTANT FROM RHODOBACTER SPHAEROIDES WITH ASP L213 REPLACED WITH ASN AND ARG M233 REPLACED WITH CYS IN THE CHARGE-SEPARATED D+QAQB- STATE
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Deposited on : 2003-12-29
Resolution : 2.60 Å(reported)

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

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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

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

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

MolProbity	: 4-5-2 with Phenix2.0
Mogul	: 2022.3.0, CSD as543be (2022)
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	: 9.0.010 (Gargrove)
Density-Fitness	: 1.0.12
Ideal geometry (proteins)	: Engh & Huber (2001)

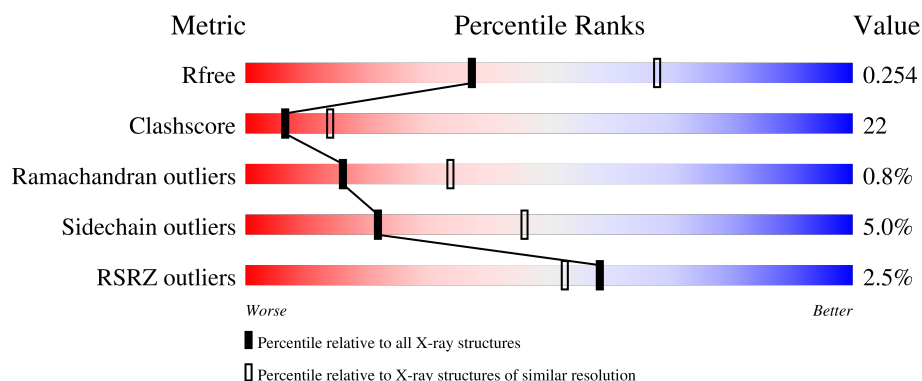
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 $\leq 5\%$. 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	% 58% 37% • •
1	R	281	2% 53% 42% 5% •
2	M	307	% 66% 27% • •

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
2	S	307	
3	H	260	
3	T	260	

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
4	BCL	M	1003	-	-	X	-
5	BPH	L	1006	X	-	-	-
5	BPH	M	1005	X	-	-	-
5	BPH	R	2006	X	-	-	-
6	U10	L	1009[A]	-	-	-	X
6	U10	L	1009[B]	-	-	-	X
6	U10	R	2009[A]	-	-	-	X
6	U10	R	2009[B]	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 14144 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
1	L	281	Total	C	N	O	S	0	0	0
			2232	1507	356	361	8			
1	R	281	Total	C	N	O	S	0	0	0
			2232	1507	356	361	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	213	ASN	ASP	engineered mutation	UNP P02954
R	213	ASN	ASP	engineered mutation	UNP P02954

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	301	Total	C	N	O	S	0	0	0
			2399	1602	390	396	11			
2	S	299	Total	C	N	O	S	0	0	0
			2385	1594	388	392	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	233	CYS	ARG	engineered mutation	UNP P02953
S	233	CYS	ARG	engineered mutation	UNP P02953

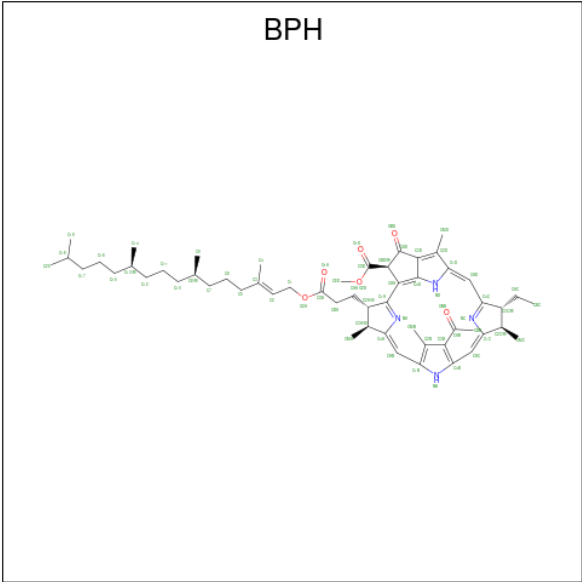
- Molecule 3 is a protein called Reaction center protein H chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	246	Total	C	N	O	S	0	0	0
			1869	1196	320	343	10			
3	T	246	Total	C	N	O	S	0	0	0
			1869	1196	320	343	10			

- # BCL

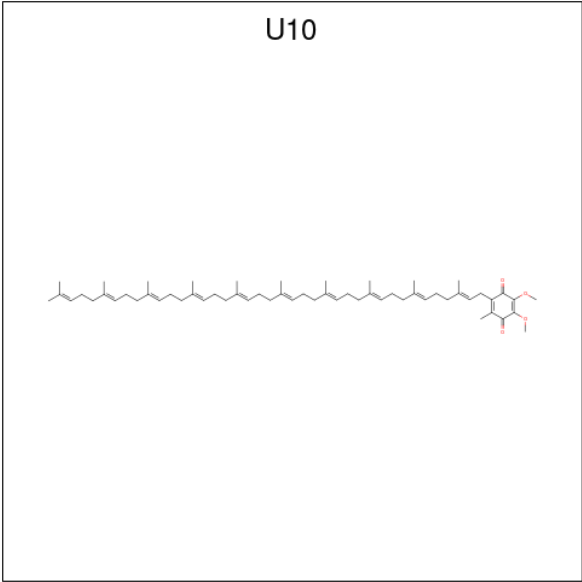
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	L	1	Total 51	C 40	Mg 1	N 4	O 6	0	0
4	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	M	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	R	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	S	1	Total 51	C 40	Mg 1	N 4	O 6	0	0
4	S	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
4	S	1	Total 66	C 55	Mg 1	N 4	O 6	0	0

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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		
5	R	1	Total	C	N	O	0	0
			65	55	4	6		
5	S	1	Total	C	N	O	0	0
			51	41	4	6		

- Molecule 6 is UBIQUINONE-10 (CCD ID: U10) (formula: C₅₉H₉₀O₄).

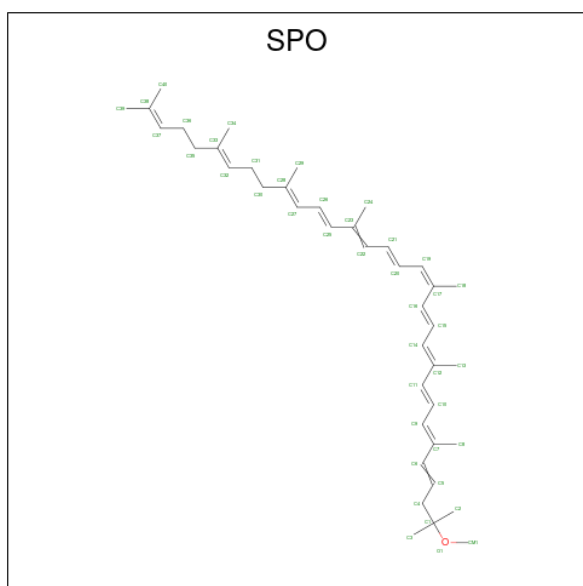


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	L	1	Total	C	O	0	1
			60	52	8		
6	M	1	Total	C	O	0	0
			38	34	4		
6	R	1	Total	C	O	0	1
			36	28	8		
6	S	1	Total	C	O	0	0
			32	28	4		

- Molecule 7 is FE (II) ION (CCD ID: FE2) (formula: Fe).

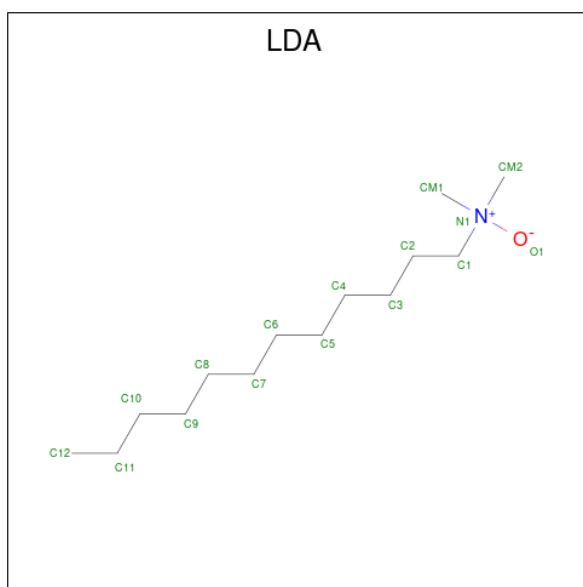
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	M	1	Total	Fe	0	0
			1	1		
7	S	1	Total	Fe	0	0
			1	1		

- Molecule 8 is SPHEROIDENE (CCD ID: SPO) (formula: C₄₁H₆₀O).



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

- Molecule 9 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: C₁₄H₃₁NO).



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

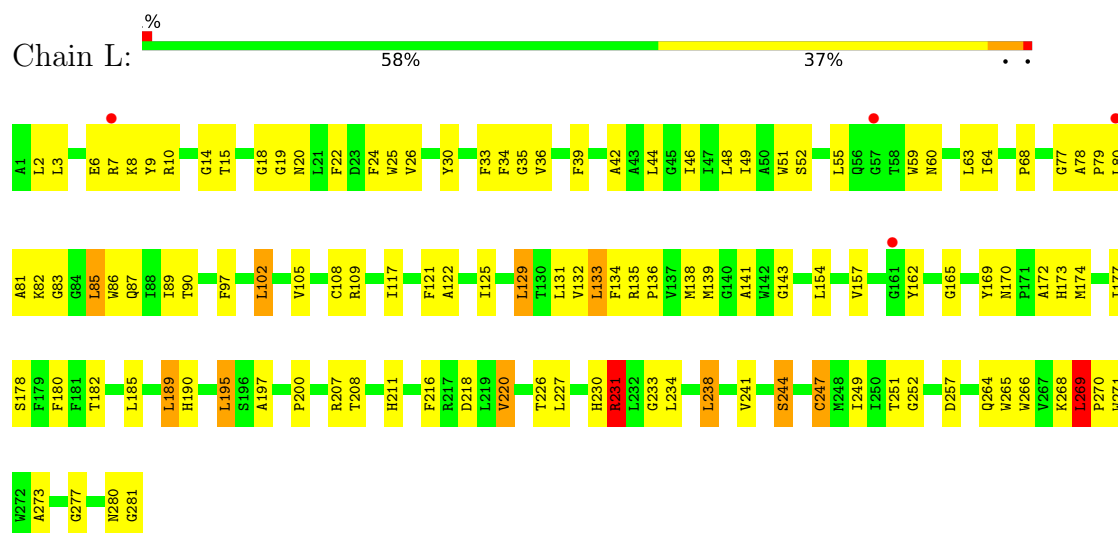
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	L	26	Total	O	0	0
			26	26		
10	M	42	Total	O	0	0
			42	42		
10	H	39	Total	O	0	0
			39	39		
10	R	13	Total	O	0	0
			13	13		
10	S	24	Total	O	0	0
			24	24		
10	T	12	Total	O	0	0
			12	12		

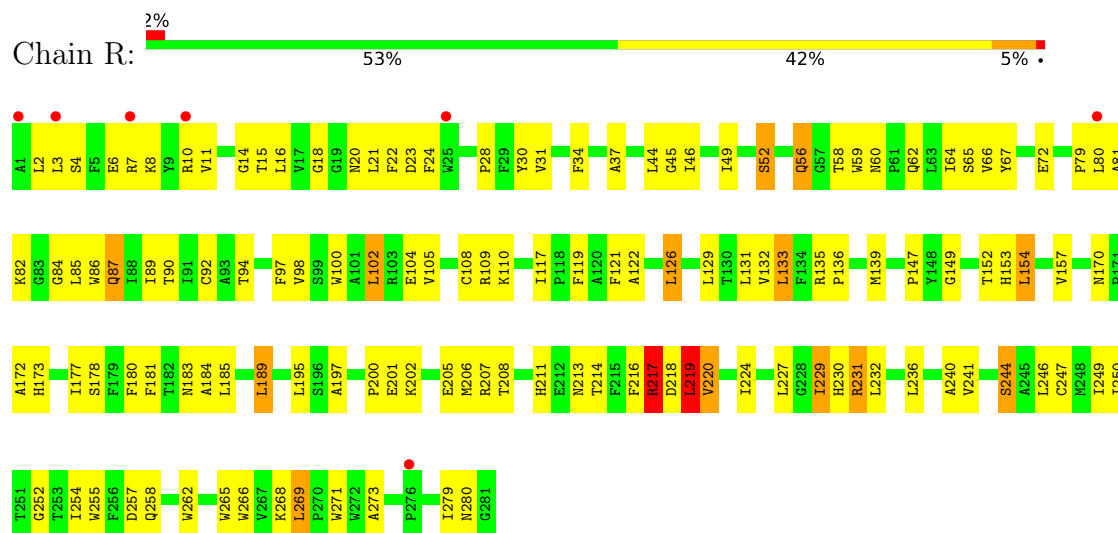
3 Residue-property plots [i](#)

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 L chain

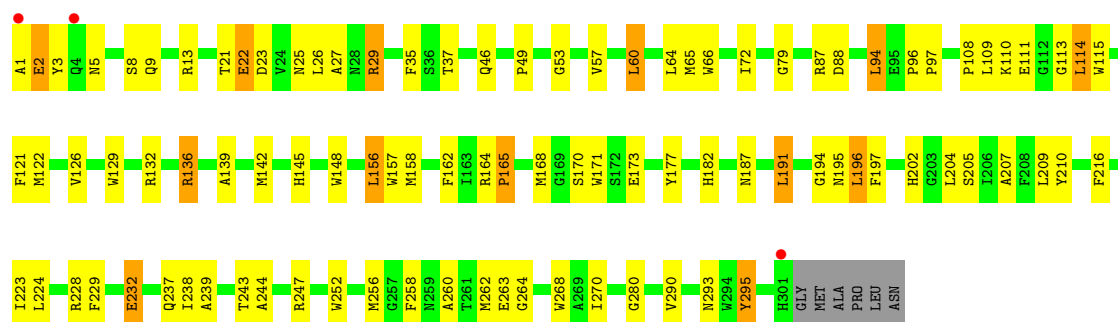


- Molecule 1: Reaction center protein L chain

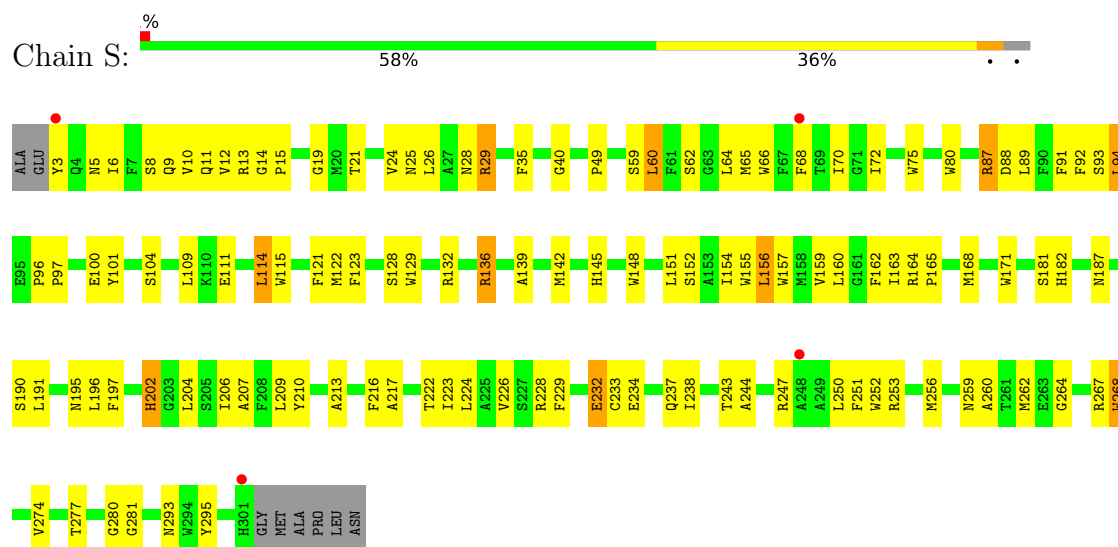


- Molecule 2: Reaction center protein M chain

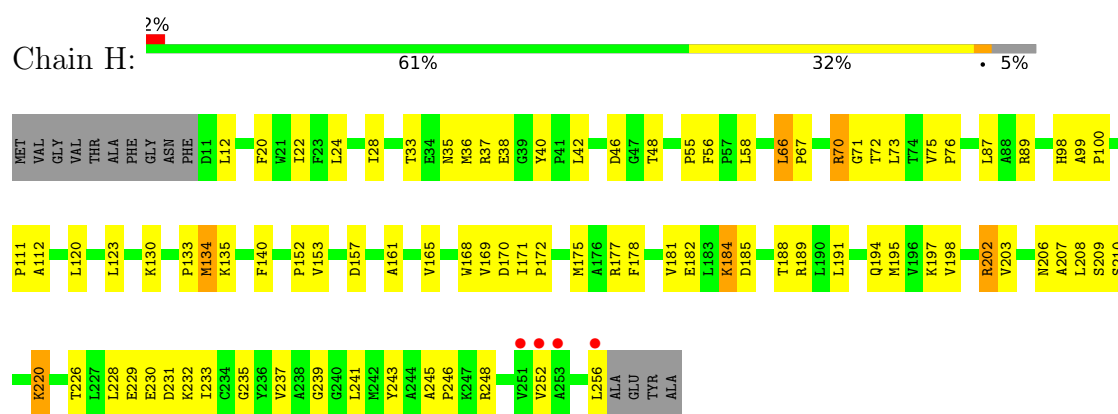




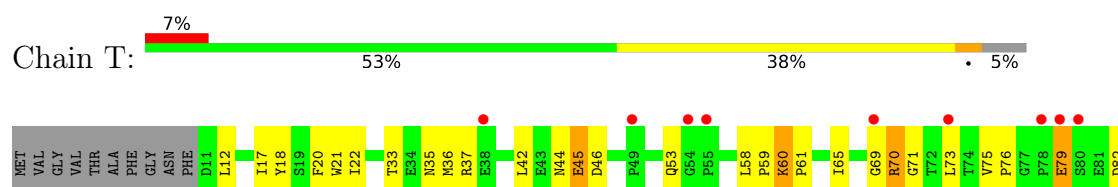
• Molecule 2: Reaction center protein M chain

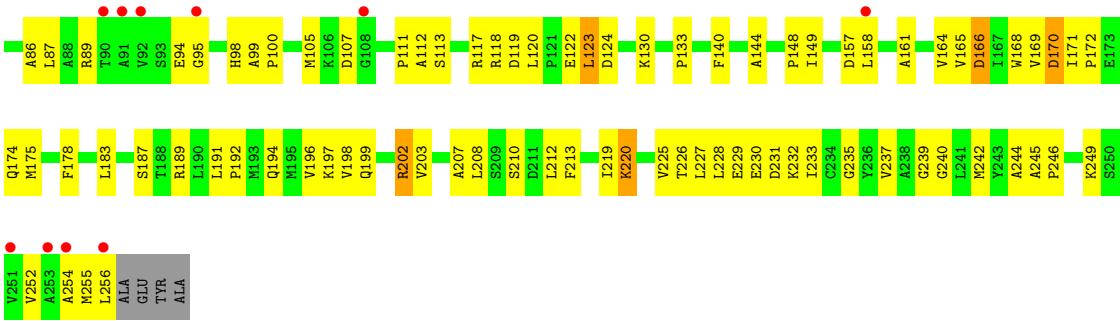


• Molecule 3: Reaction center protein H chain



• Molecule 3: Reaction center protein H chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	137.73Å 137.73Å 277.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.84 – 2.60 39.84 – 2.60	Depositor EDS
% Data completeness (in resolution range)	94.8 (39.84-2.60) 94.8 (39.84-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.226 , 0.268 0.210 , 0.254	Depositor DCC
R_{free} test set	3965 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	51.1	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 58.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14144	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.32% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCL, U10, FE2, SPO, BPH, 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	L	0.51	0/2320	0.92	8/3175 (0.3%)
1	R	0.43	0/2320	0.96	7/3175 (0.2%)
2	M	0.51	0/2491	0.94	8/3402 (0.2%)
2	S	0.44	0/2477	0.91	6/3383 (0.2%)
3	H	0.47	0/1917	0.92	5/2608 (0.2%)
3	T	0.39	0/1917	0.90	3/2608 (0.1%)
All	All	0.46	0/13442	0.93	37/18351 (0.2%)

There are no bond length outliers.

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	22	ILE	N-CA-C	-7.55	102.98	110.30
2	M	46	GLN	N-CA-C	7.31	120.43	109.25
1	R	244	SER	N-CA-C	-7.03	103.31	110.97
1	R	229	ILE	CB-CA-C	-6.77	103.15	112.02
1	R	217	ARG	N-CA-C	-6.76	103.84	111.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2232	0	2189	111	0
1	R	2232	0	2189	131	0
2	M	2399	0	2310	91	0
2	S	2385	0	2296	121	0
3	H	1869	0	1884	78	0
3	T	1869	0	1884	107	0
4	L	183	0	189	27	0
4	M	66	0	74	21	0
4	R	66	0	74	10	0
4	S	183	0	189	29	0
5	L	65	0	74	5	0
5	M	55	0	53	1	0
5	R	65	0	74	9	0
5	S	51	0	45	6	0
6	L	60	0	70	3	0
6	M	38	0	47	0	0
6	R	36	0	30	3	0
6	S	32	0	39	1	0
7	M	1	0	0	0	0
7	S	1	0	0	0	0
8	M	42	0	60	6	0
8	S	42	0	60	2	0
9	M	16	0	31	2	0
10	H	39	0	0	2	0
10	L	26	0	0	4	0
10	M	42	0	0	1	0
10	R	13	0	0	0	0
10	S	24	0	0	2	0
10	T	12	0	0	1	0
All	All	14144	0	13861	606	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 22.

The worst 5 of 606 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)
1:R:200:PRO:HB3	1:R:207:ARG:HD3	1.42	1.02
2:S:157:TRP:HB2	4:S:2003:BCL:H62	1.44	0.99
1:R:219:LEU:HD13	1:R:220:VAL:HG23	1.48	0.95
3:T:226:THR:OG1	3:T:229:GLU:HG3	1.68	0.93
3:H:33:THR:HA	3:H:36:MET:HE2	1.52	0.92

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%)	262 (94%)	16 (6%)	1 (0%)	30	51
1	R	279/281 (99%)	264 (95%)	12 (4%)	3 (1%)	11	25
2	M	299/307 (97%)	280 (94%)	18 (6%)	1 (0%)	36	58
2	S	297/307 (97%)	284 (96%)	11 (4%)	2 (1%)	18	38
3	H	244/260 (94%)	233 (96%)	11 (4%)	0	100	100
3	T	244/260 (94%)	223 (91%)	15 (6%)	6 (2%)	4	8
All	All	1642/1696 (97%)	1546 (94%)	83 (5%)	13 (1%)	16	34

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	M	2	GLU
3	T	45	GLU
3	T	220	LYS
1	R	80	LEU
1	R	257	ASP

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	220/220 (100%)	208 (94%)	12 (6%)	19	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	220/220 (100%)	208 (94%)	12 (6%)	19	41
2	M	236/240 (98%)	225 (95%)	11 (5%)	23	48
2	S	235/240 (98%)	222 (94%)	13 (6%)	19	41
3	H	199/208 (96%)	189 (95%)	10 (5%)	22	46
3	T	199/208 (96%)	192 (96%)	7 (4%)	32	59
All	All	1309/1336 (98%)	1244 (95%)	65 (5%)	22	46

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	S	232	GLU
3	T	79	GLU
3	H	73	LEU
3	H	70	ARG
3	T	82	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
2	S	5	ASN
2	S	44	ASN
2	S	28	ASN
2	S	195	ASN
2	M	195	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 23 ligands modelled in this entry, 2 are monoatomic - leaving 21 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$
4	BCL	L	1001	-	54,59,74	2.04	15 (27%)	61,97,115	2.02	15 (24%)
4	BCL	M	1003	-	69,74,74	1.74	14 (20%)	79,115,115	1.91	25 (31%)
6	U10	M	1008	-	38,38,63	2.05	13 (34%)	48,49,79	1.80	13 (27%)
6	U10	L	1009[B]	-	30,30,63	2.02	9 (30%)	37,39,79	2.01	11 (29%)
8	SPO	M	1010	-	41,41,41	3.09	21 (51%)	47,50,50	2.44	15 (31%)
6	U10	R	2009[B]	-	18,18,63	2.14	6 (33%)	24,25,79	2.15	7 (29%)
6	U10	S	2008	-	32,32,63	1.96	10 (31%)	40,41,79	1.90	10 (25%)
9	LDA	M	1011	-	13,15,15	1.85	1 (7%)	14,17,17	1.62	4 (28%)
4	BCL	S	2004	-	69,74,74	1.83	17 (24%)	79,115,115	1.87	19 (24%)
5	BPH	M	1005	-	49,60,70	2.20	15 (30%)	47,89,101	3.06	21 (44%)
4	BCL	L	1004	-	69,74,74	1.79	13 (18%)	79,115,115	1.77	18 (22%)
8	SPO	S	2010	-	41,41,41	3.08	22 (53%)	47,50,50	2.47	17 (36%)
5	BPH	R	2006	-	59,70,70	2.11	14 (23%)	59,101,101	2.85	21 (35%)
6	U10	L	1009[A]	-	30,30,63	2.12	11 (36%)	37,39,79	2.08	11 (29%)
6	U10	R	2009[A]	-	18,18,63	2.17	6 (33%)	24,25,79	2.20	7 (29%)
5	BPH	L	1006	-	59,70,70	2.16	14 (23%)	59,101,101	2.82	22 (37%)
4	BCL	S	2003	-	69,74,74	1.79	12 (17%)	79,115,115	1.88	23 (29%)
4	BCL	L	1002	-	69,74,74	1.79	12 (17%)	79,115,115	1.90	22 (27%)
4	BCL	R	2002	-	69,74,74	1.81	11 (15%)	79,115,115	1.88	20 (25%)
4	BCL	S	2001	-	54,59,74	2.09	16 (29%)	61,97,115	1.95	17 (27%)
5	BPH	S	2005	-	45,56,70	2.32	15 (33%)	41,84,101	3.29	19 (46%)

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
4	BCL	L	1001	-	-	0/23/119/137	-
4	BCL	M	1003	-	-	9/41/137/137	-
6	U10	M	1008	-	-	4/33/57/87	0/1/1/1
6	U10	L	1009[B]	-	-	5/24/48/87	0/1/1/1
8	SPO	M	1010	-	-	13/47/47/47	-
6	U10	R	2009[B]	-	-	0/9/33/87	0/1/1/1
6	U10	S	2008	-	-	4/26/50/87	0/1/1/1
9	LDA	M	1011	-	-	7/13/13/13	-
4	BCL	S	2004	-	-	9/41/137/137	-
5	BPH	M	1005	-	1/1/16/22	6/25/93/105	0/5/6/6
4	BCL	L	1004	-	-	9/41/137/137	-
8	SPO	S	2010	-	-	12/47/47/47	-
5	BPH	R	2006	-	2/2/18/22	9/37/105/105	0/5/6/6
6	U10	L	1009[A]	-	-	9/24/48/87	0/1/1/1
6	U10	R	2009[A]	-	-	1/9/33/87	0/1/1/1
5	BPH	L	1006	-	2/2/18/22	8/37/105/105	0/5/6/6
4	BCL	S	2003	-	-	10/41/137/137	-
4	BCL	L	1002	-	-	4/41/137/137	-
4	BCL	R	2002	-	-	7/41/137/137	-
4	BCL	S	2001	-	-	8/23/119/137	-
5	BPH	S	2005	-	-	9/21/89/105	0/5/6/6

The worst 5 of 267 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	M	1010	SPO	C15-C16	7.96	1.55	1.34
8	S	2010	SPO	C6-C5	7.91	1.54	1.32
8	S	2010	SPO	C10-C11	7.73	1.54	1.34
8	M	1010	SPO	C6-C5	7.73	1.53	1.32
8	M	1010	SPO	C10-C11	7.58	1.54	1.34

The worst 5 of 337 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	S	2005	BPH	O2D-CGD-CBD	14.28	126.64	110.95
5	R	2006	BPH	O2D-CGD-CBD	13.97	126.30	110.95
5	L	1006	BPH	O2D-CGD-CBD	13.54	125.83	110.95
5	M	1005	BPH	O2D-CGD-CBD	13.51	125.80	110.95
8	S	2010	SPO	C15-C14-C12	-6.63	117.98	127.28

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	L	1006	BPH	C13
5	L	1006	BPH	C8
5	M	1005	BPH	C8
5	R	2006	BPH	C13
5	R	2006	BPH	C8

5 of 143 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	L	1004	BCL	C1A-C2A-CAA-CBA
4	L	1004	BCL	C3A-C2A-CAA-CBA
4	S	2001	BCL	C1A-C2A-CAA-CBA
5	L	1006	BPH	C4C-C3C-CAC-CBC
5	R	2006	BPH	CBD-CGD-O2D-CED

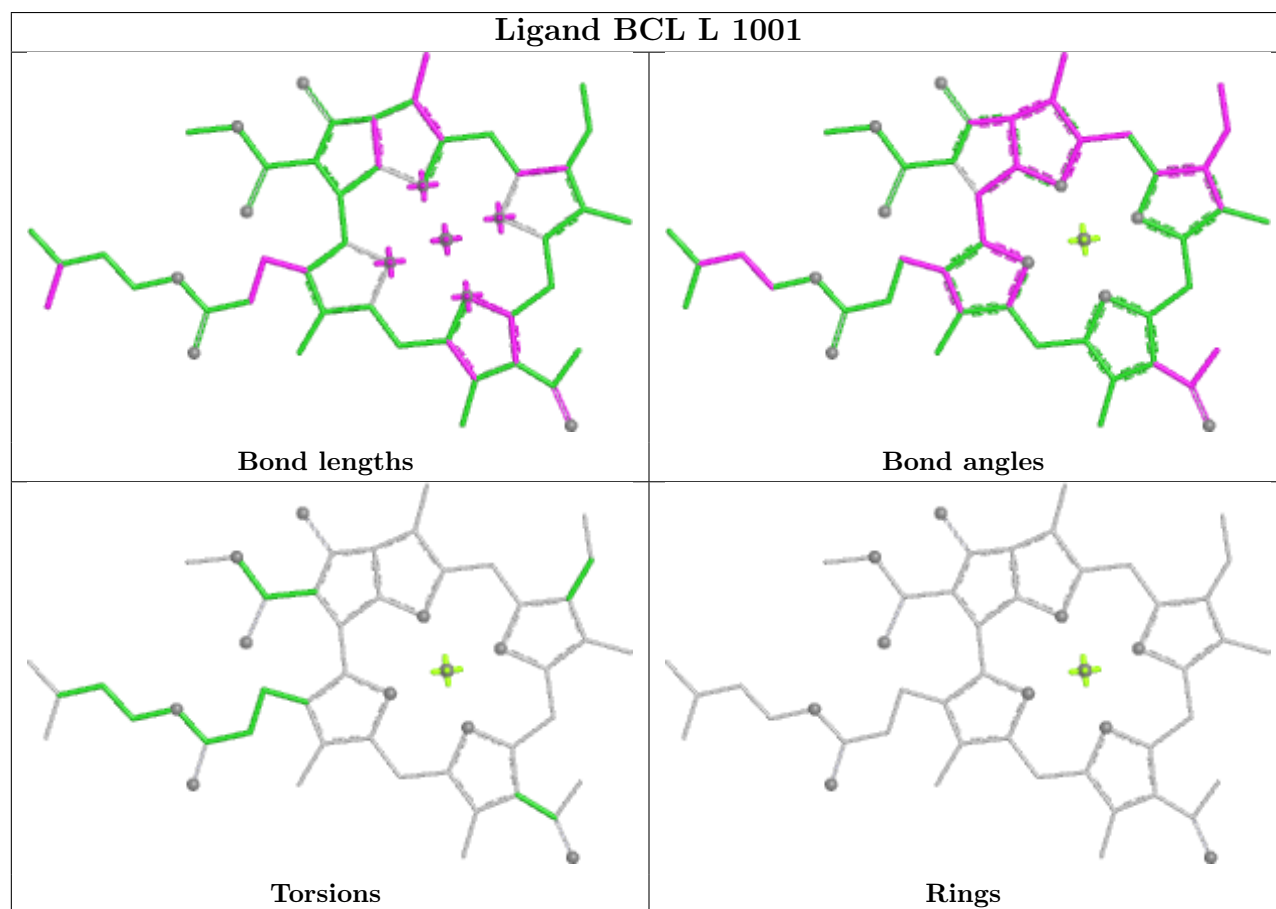
There are no ring outliers.

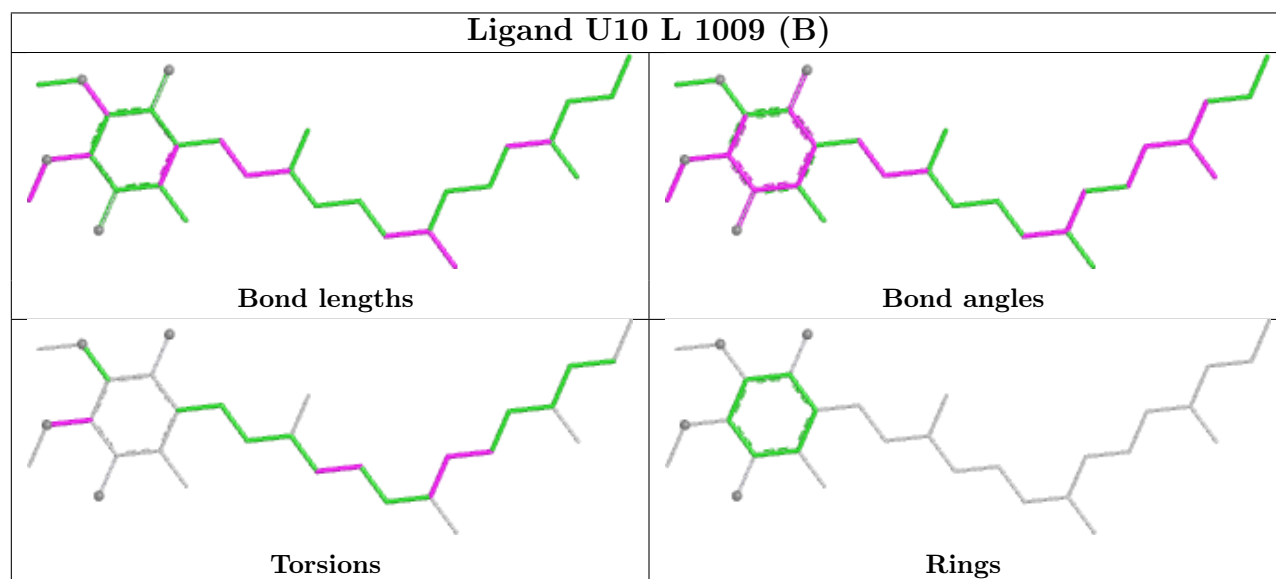
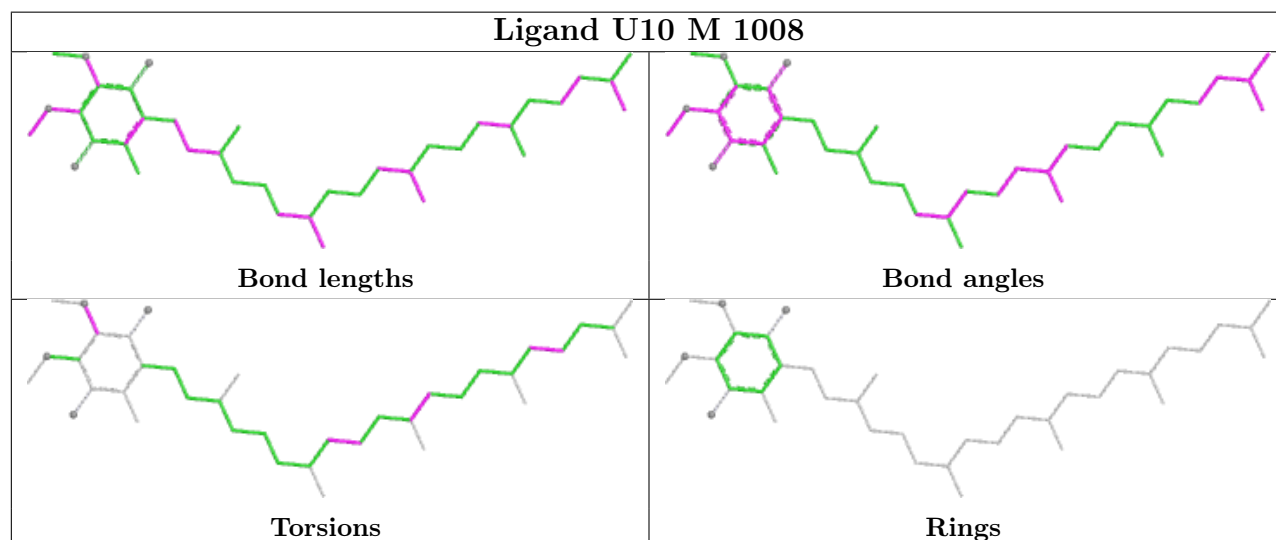
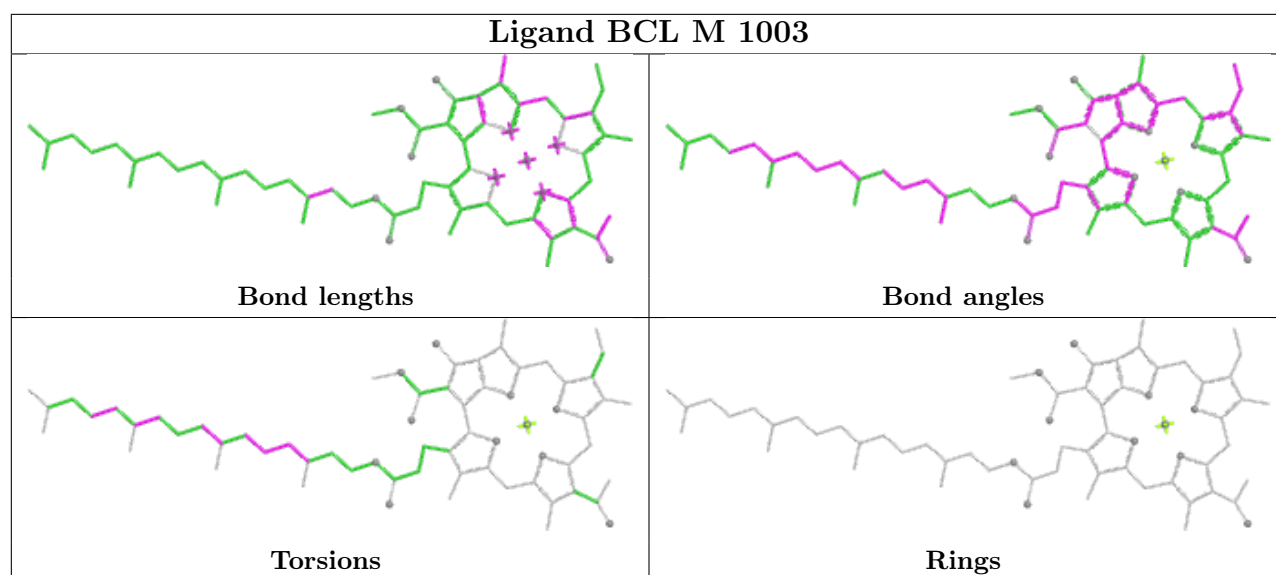
20 monomers are involved in 104 short contacts:

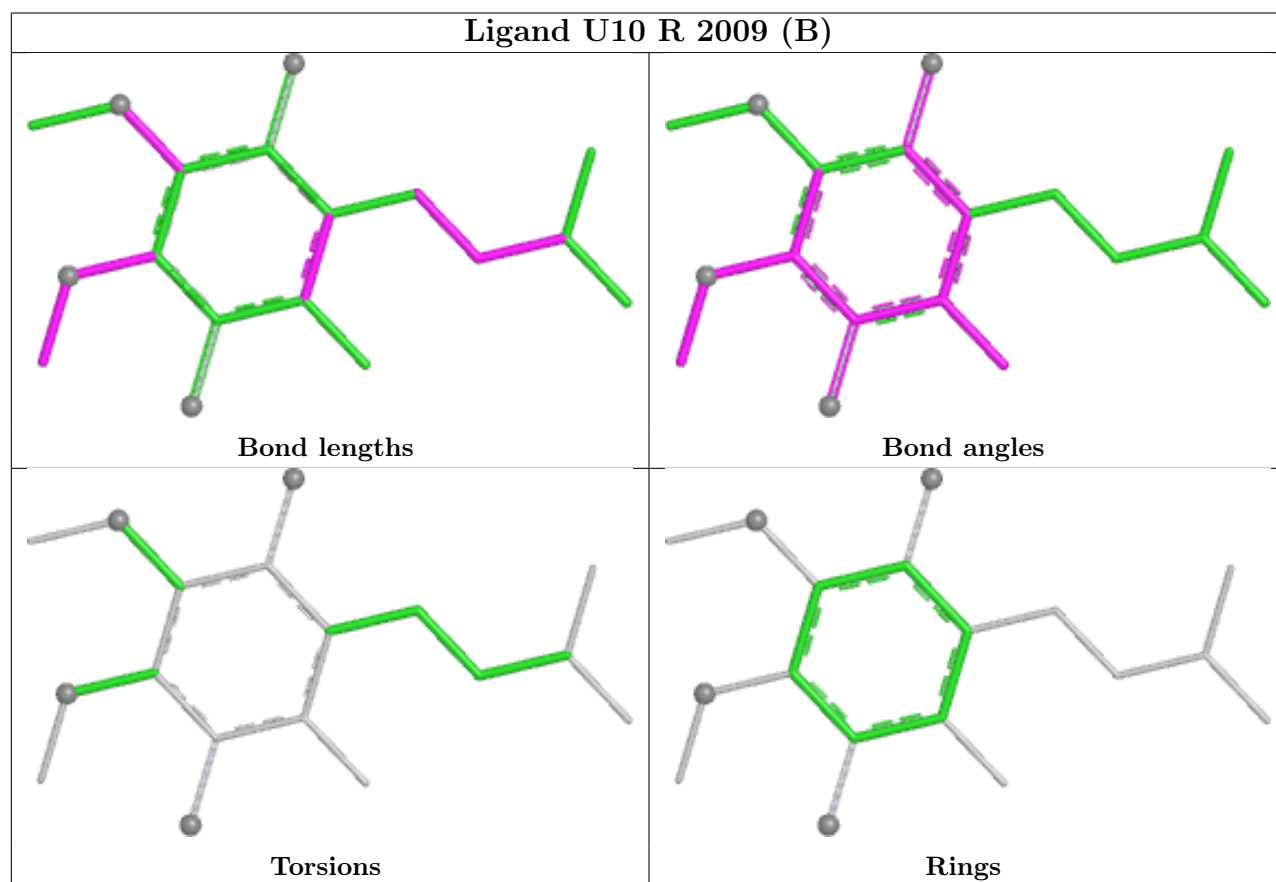
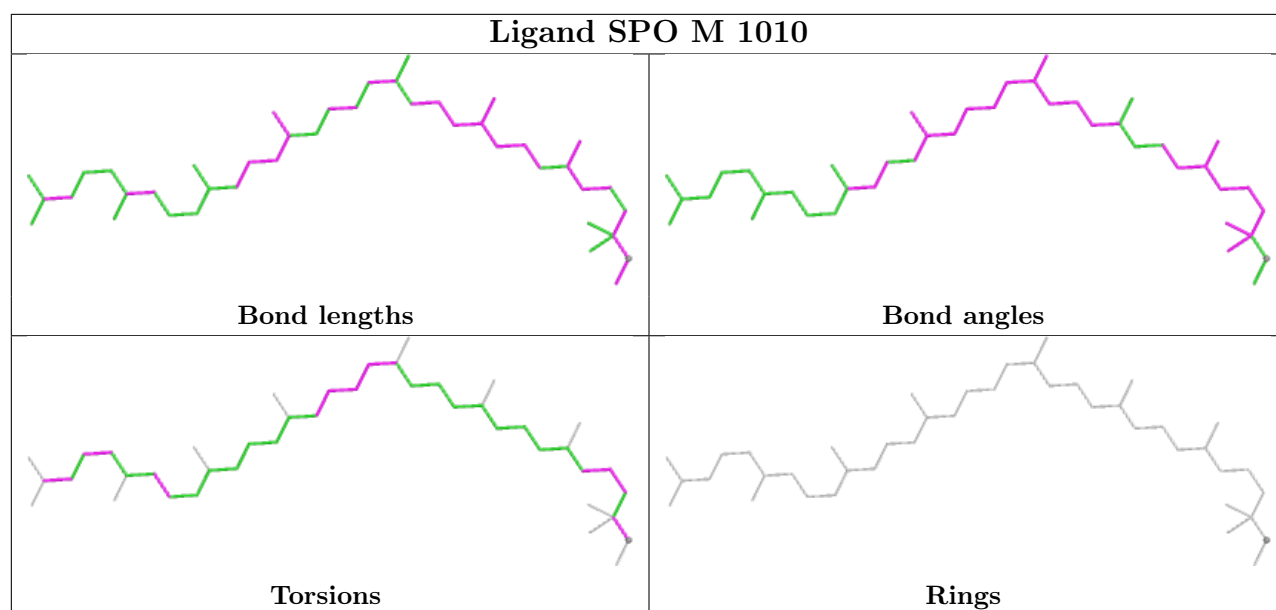
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	1001	BCL	11	0
4	M	1003	BCL	21	0
6	L	1009[B]	U10	2	0
8	M	1010	SPO	6	0
6	R	2009[B]	U10	2	0
6	S	2008	U10	1	0
9	M	1011	LDA	2	0
4	S	2004	BCL	8	0
5	M	1005	BPH	1	0
4	L	1004	BCL	9	0
8	S	2010	SPO	2	0
5	R	2006	BPH	9	0
6	L	1009[A]	U10	1	0
6	R	2009[A]	U10	1	0
5	L	1006	BPH	5	0
4	S	2003	BCL	16	0
4	L	1002	BCL	11	0
4	R	2002	BCL	10	0
4	S	2001	BCL	8	0
5	S	2005	BPH	6	0

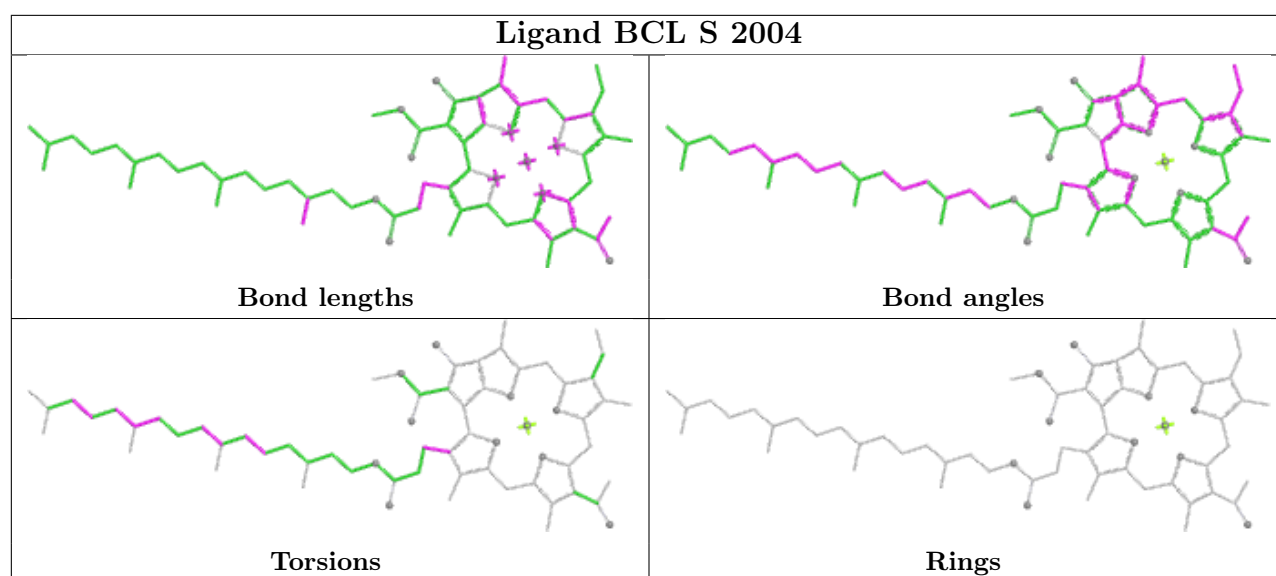
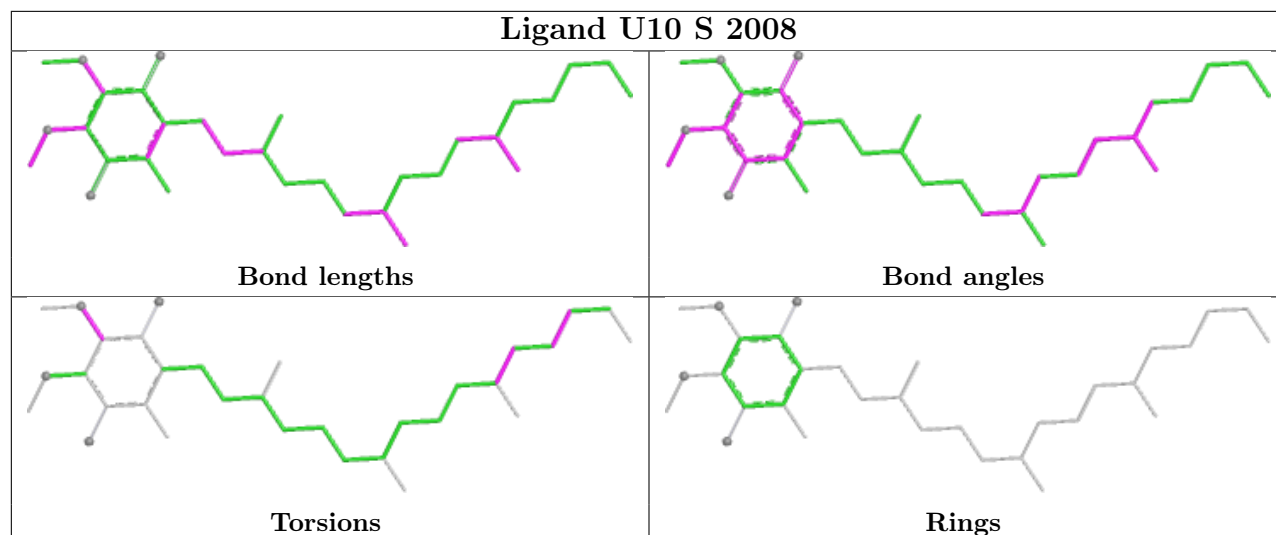
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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.

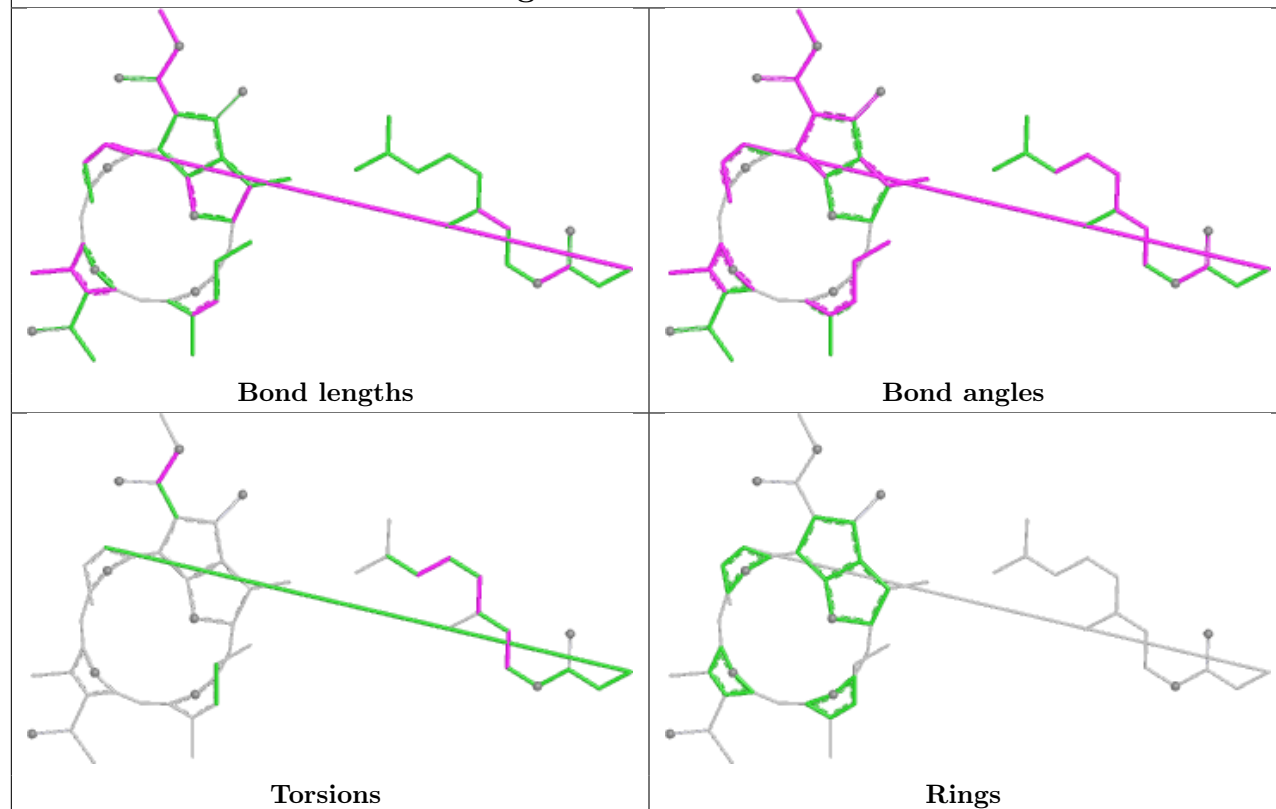




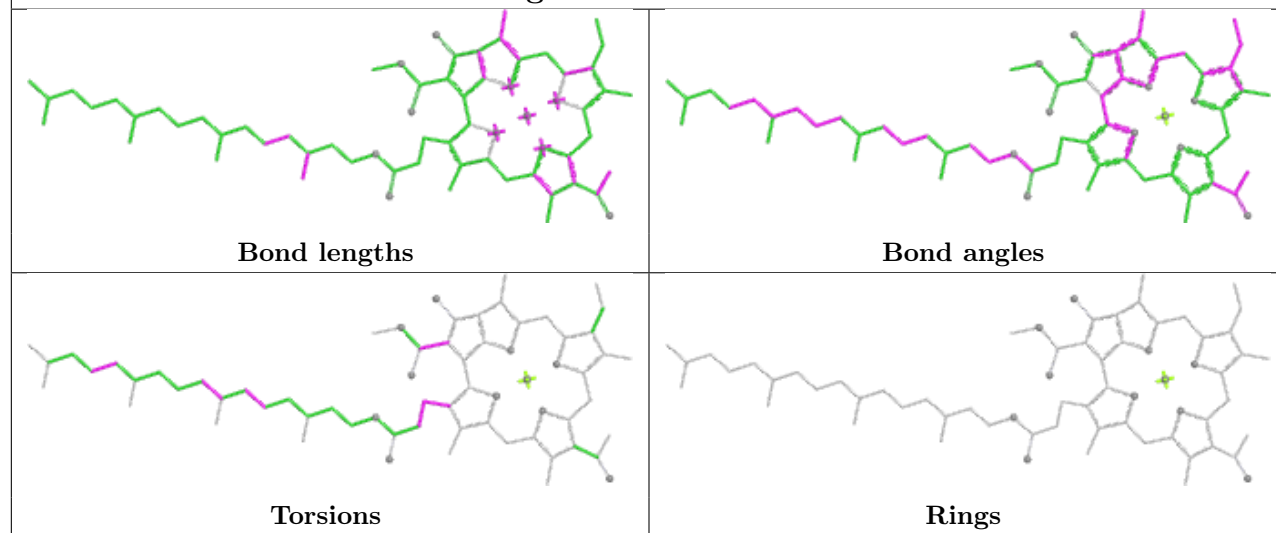


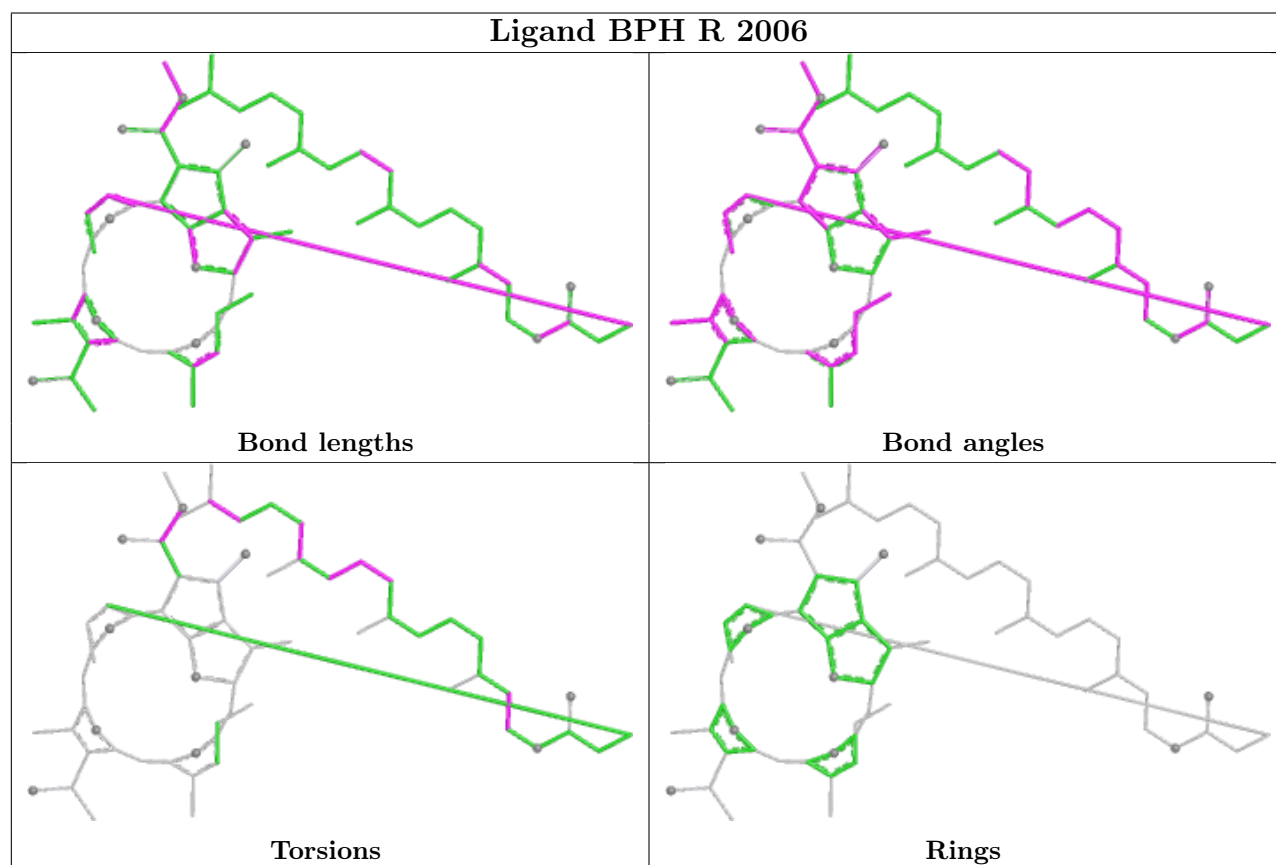
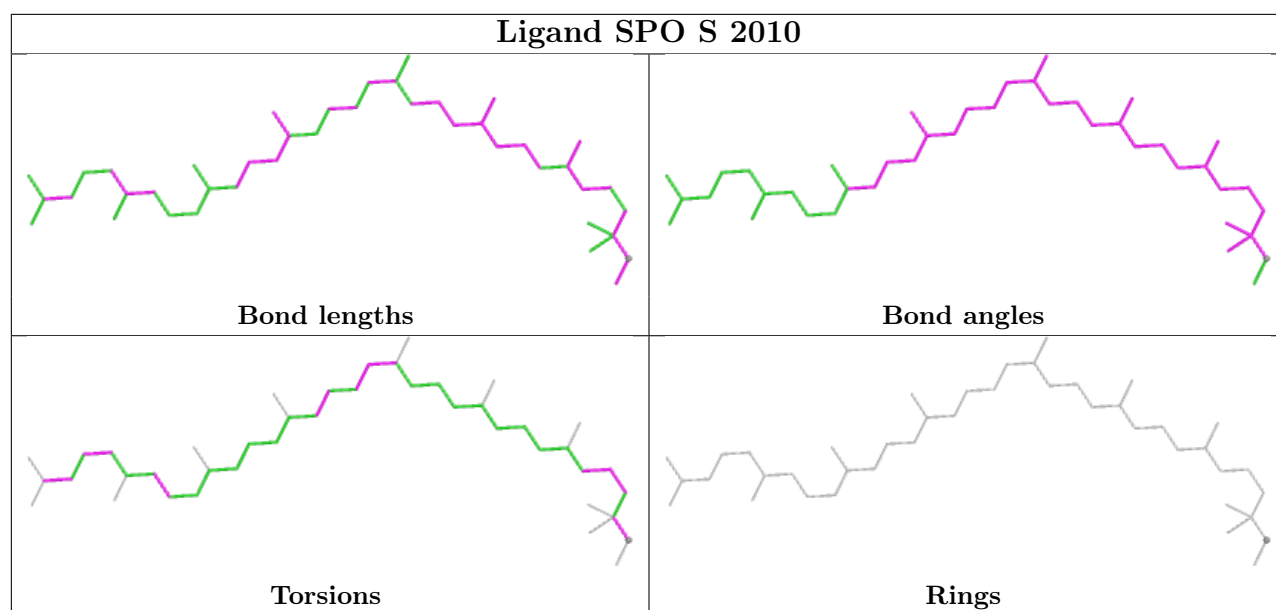


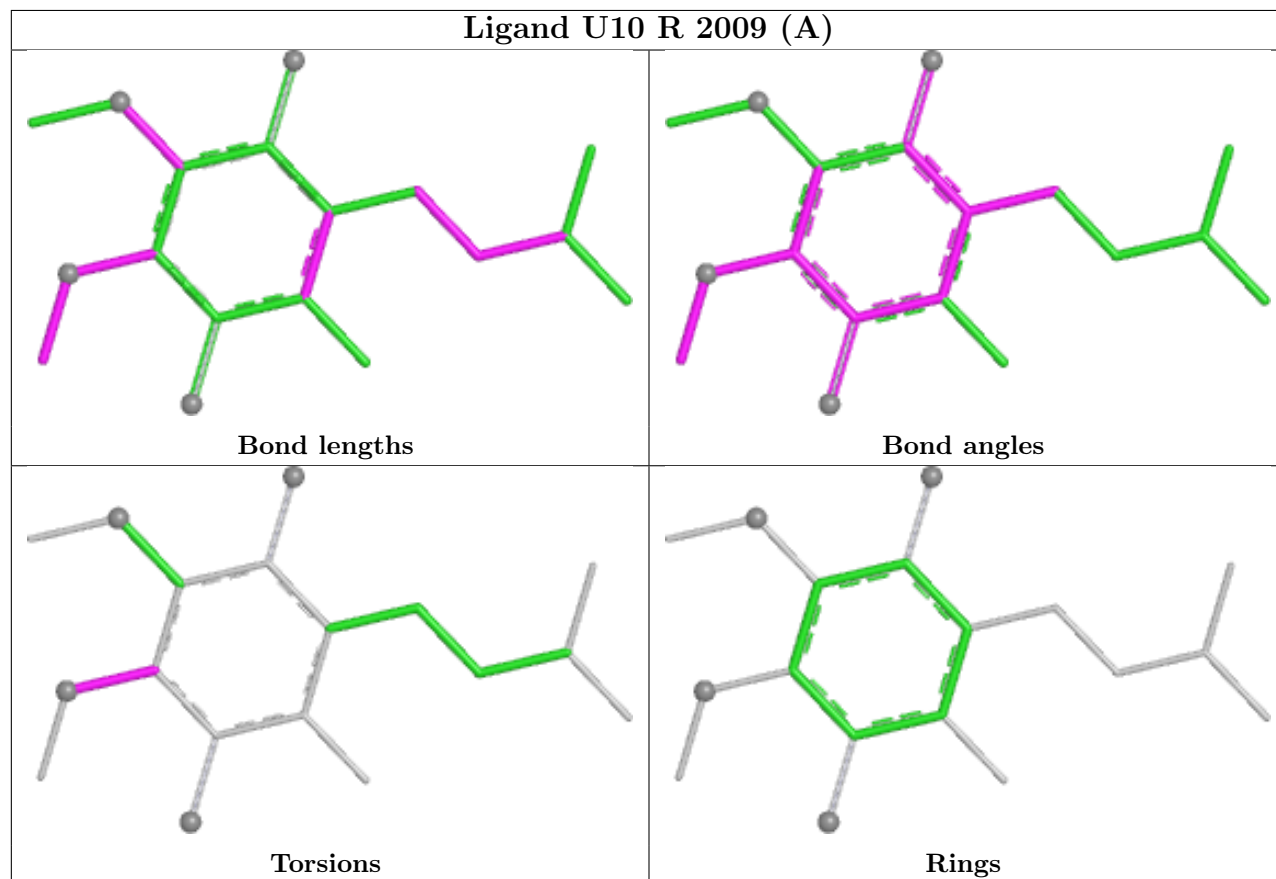
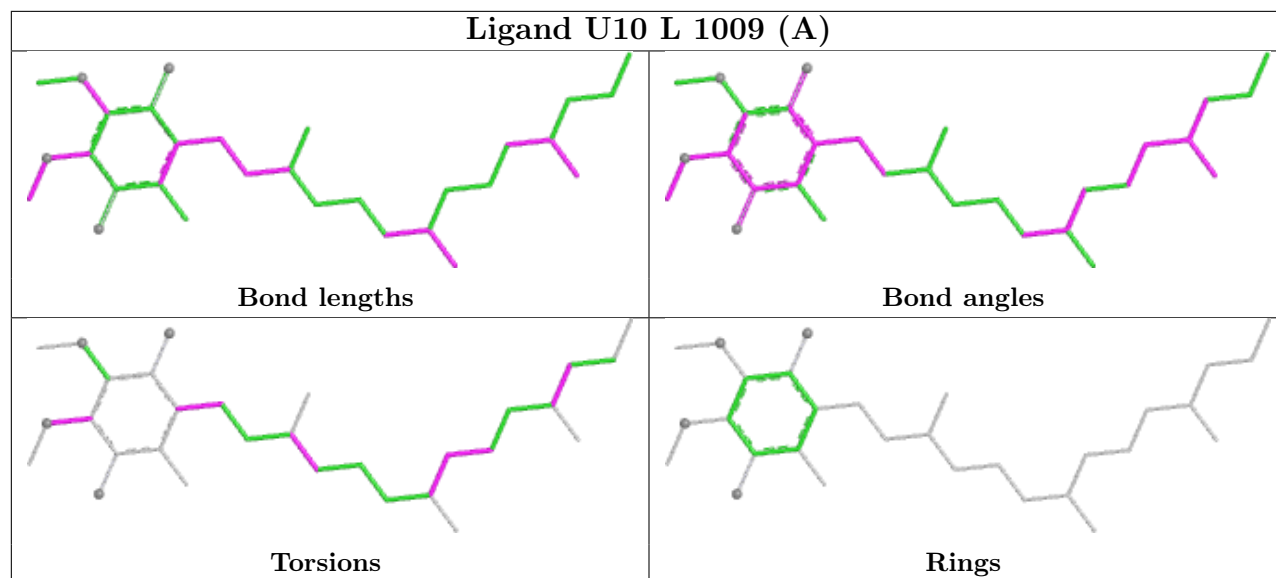
Ligand BPH M 1005

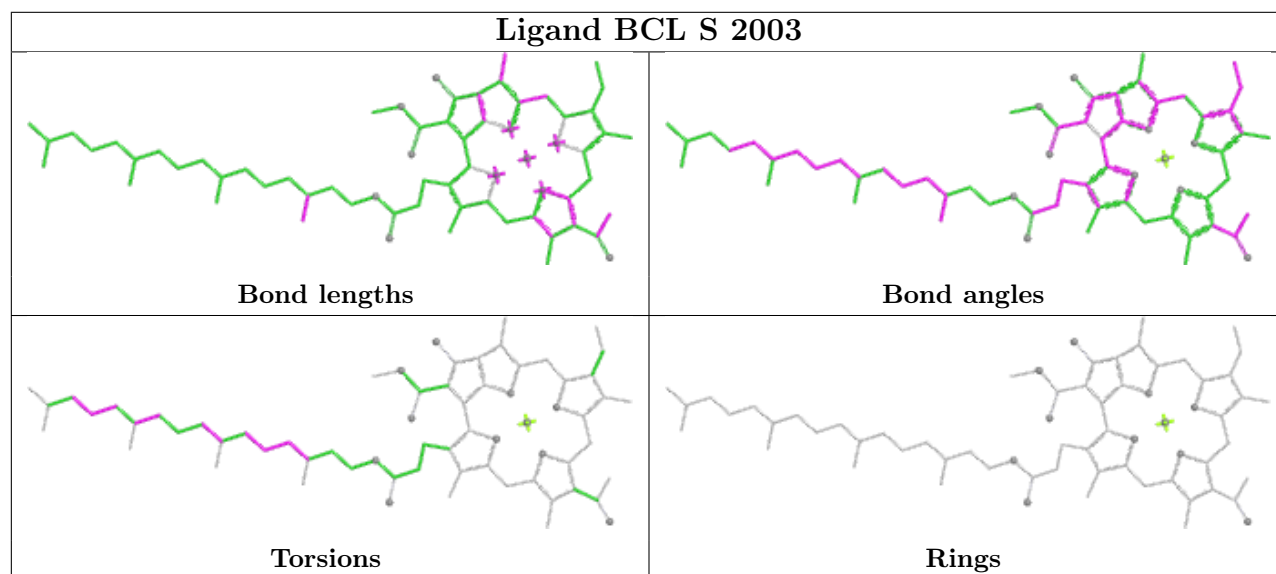
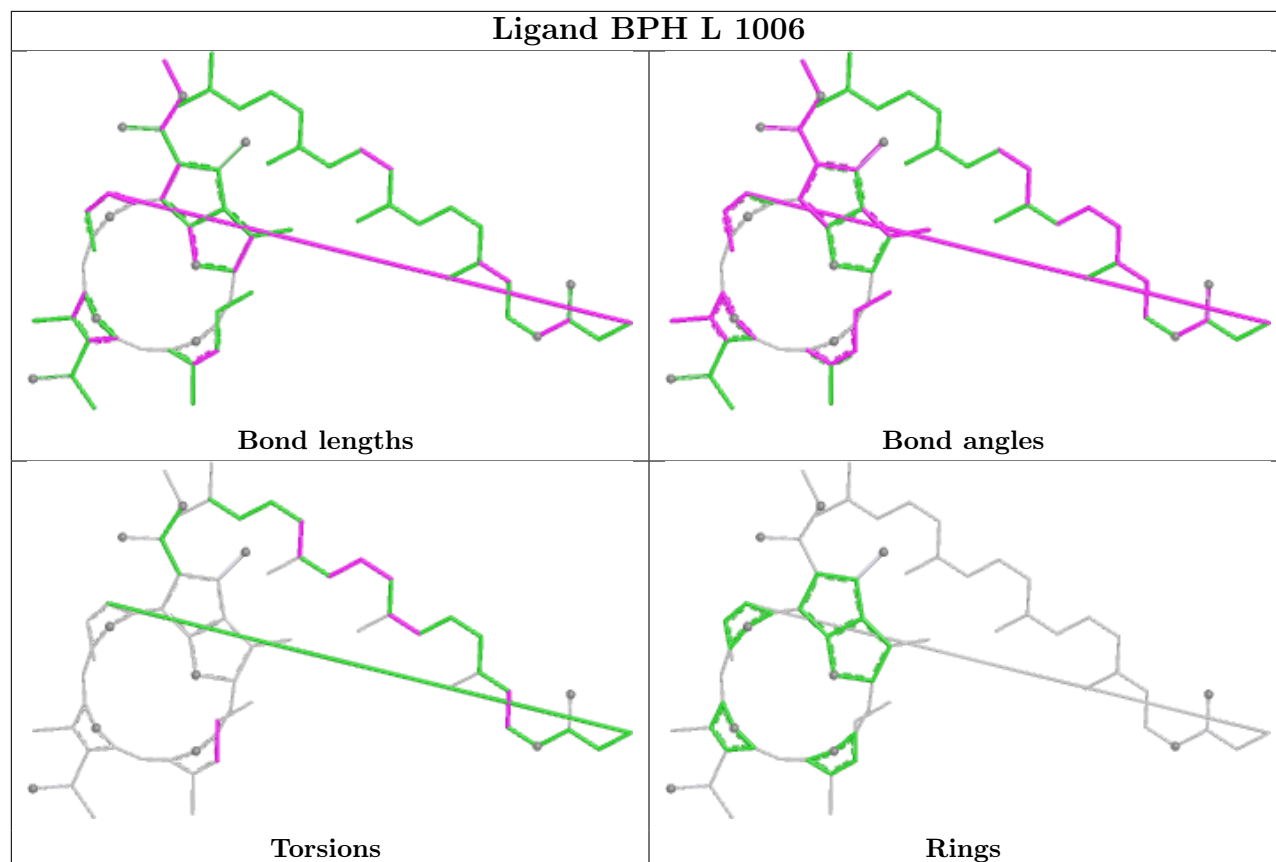


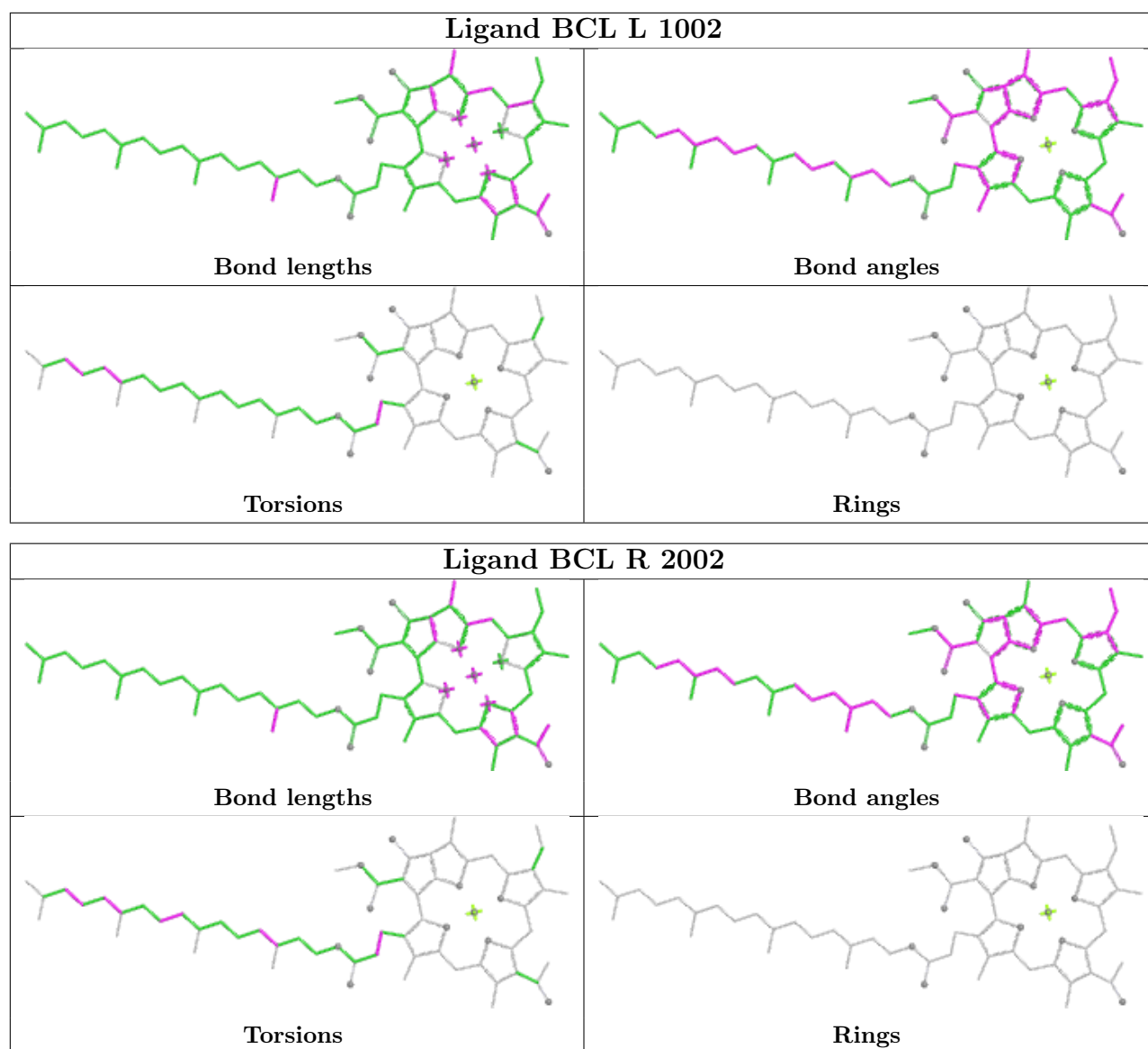
Ligand BCL L 1004

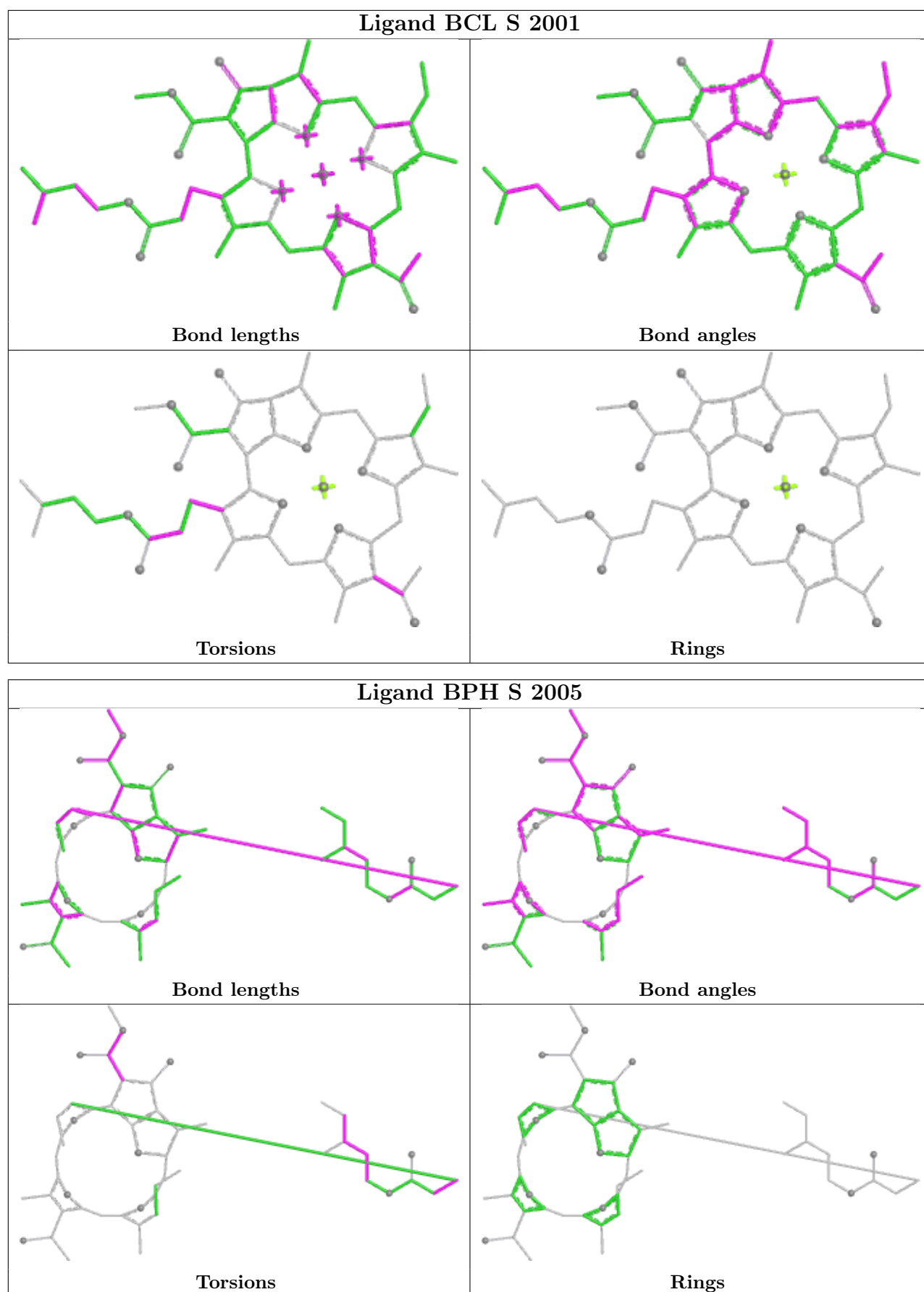












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	L	281/281 (100%)	0.01	4 (1%) 73 69	23, 42, 61, 77	0
1	R	281/281 (100%)	0.42	7 (2%) 58 52	35, 56, 73, 82	0
2	M	301/307 (98%)	-0.18	3 (0%) 79 76	26, 38, 53, 85	0
2	S	299/307 (97%)	0.10	4 (1%) 75 71	37, 50, 59, 89	0
3	H	246/260 (94%)	0.02	4 (1%) 70 66	28, 44, 65, 97	0
3	T	246/260 (94%)	0.68	19 (7%) 19 15	47, 62, 84, 99	0
All	All	1654/1696 (97%)	0.16	41 (2%) 58 52	23, 49, 74, 99	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	R	1	ALA	5.1
2	M	1	ALA	4.0
2	M	301	HIS	3.9
3	H	256	LEU	3.6
3	T	254	ALA	3.6

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

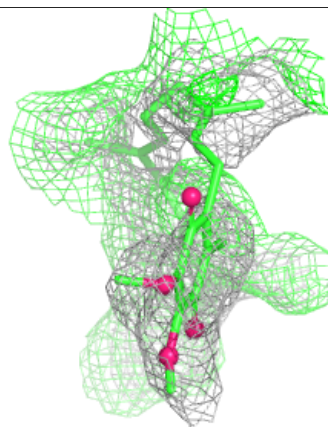
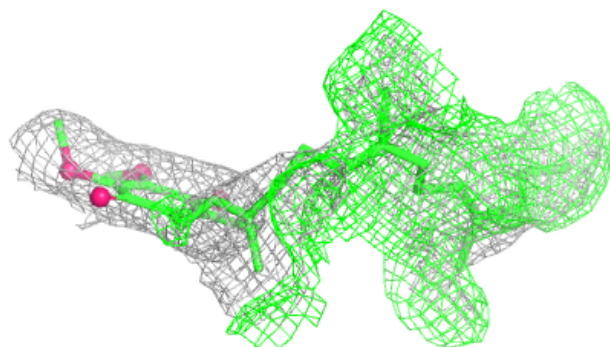
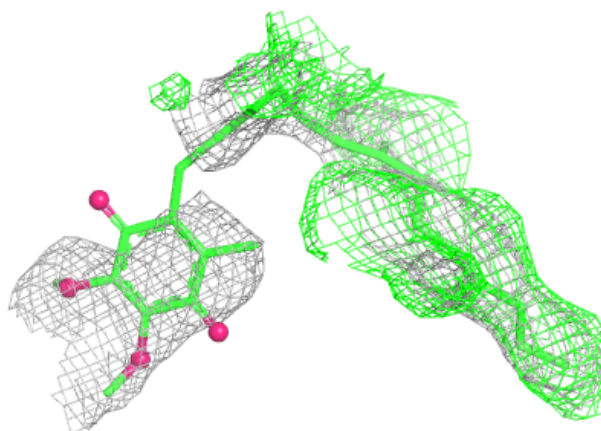
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	U10	L	1009[A]	30/63	0.68	0.50	54,67,69,70	30
6	U10	L	1009[B]	30/63	0.68	0.50	44,54,65,66	30
6	U10	R	2009[A]	18/63	0.68	0.51	94,96,97,98	18
6	U10	R	2009[B]	18/63	0.68	0.51	95,96,97,97	18
9	LDA	M	1011	16/16	0.81	0.22	49,61,78,78	0
6	U10	S	2008	32/63	0.87	0.16	56,58,64,66	0
4	BCL	S	2001	51/66	0.87	0.15	38,45,58,61	0
4	BCL	S	2004	66/66	0.88	0.16	44,52,74,75	0
8	SPO	S	2010	42/42	0.89	0.16	38,49,64,66	0
4	BCL	R	2002	66/66	0.90	0.14	42,53,56,56	0
4	BCL	L	1001	51/66	0.90	0.12	26,32,45,48	0
4	BCL	S	2003	66/66	0.91	0.14	44,49,62,71	0
4	BCL	L	1002	66/66	0.91	0.13	31,36,44,52	0
8	SPO	M	1010	42/42	0.91	0.14	31,36,59,61	0
6	U10	M	1008	38/63	0.91	0.14	36,42,63,64	0
5	BPH	R	2006	65/65	0.91	0.13	47,56,61,62	0
4	BCL	L	1004	66/66	0.92	0.12	28,34,57,59	0
4	BCL	M	1003	66/66	0.92	0.12	24,38,47,49	0
5	BPH	M	1005	55/65	0.94	0.09	26,32,43,46	0
5	BPH	L	1006	65/65	0.94	0.10	24,35,41,43	0
5	BPH	S	2005	51/65	0.94	0.09	35,42,51,52	0
7	FE2	S	2007	1/1	0.99	0.02	51,51,51,51	0
7	FE2	M	1007	1/1	0.99	0.02	33,33,33,33	0

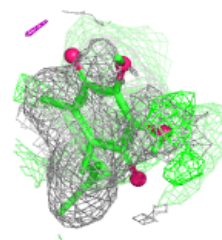
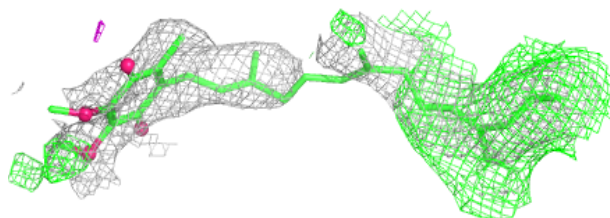
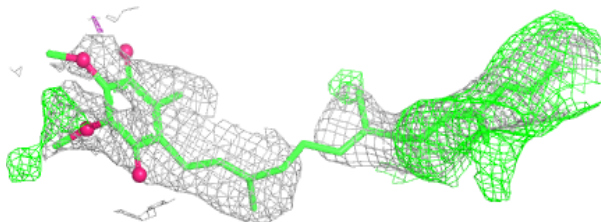
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around U10 L 1009 (A):

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

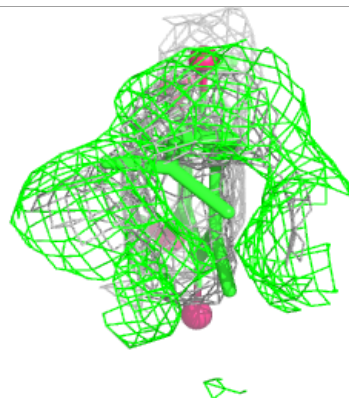
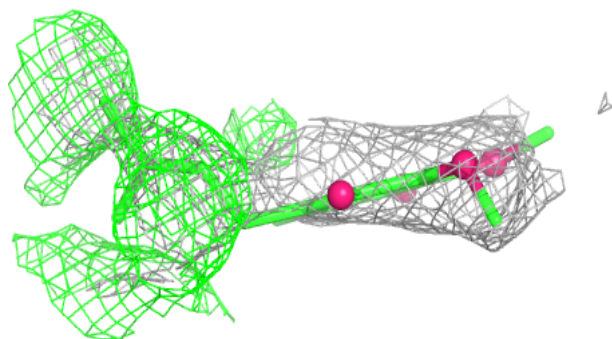
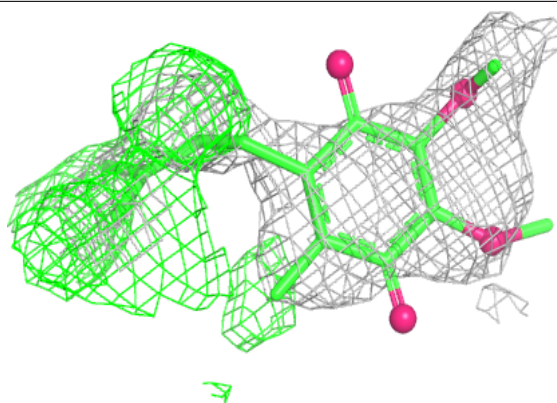
**Electron density around U10 L 1009 (B):**

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and green (positive)

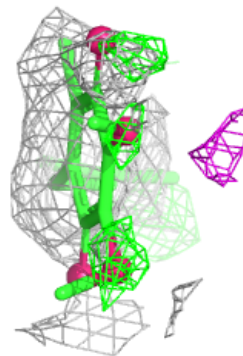
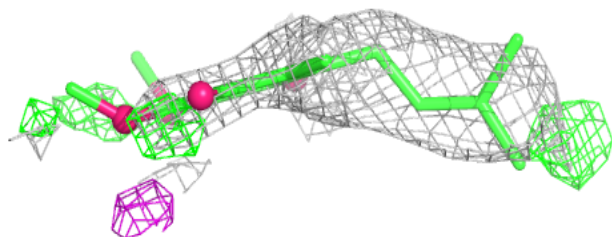
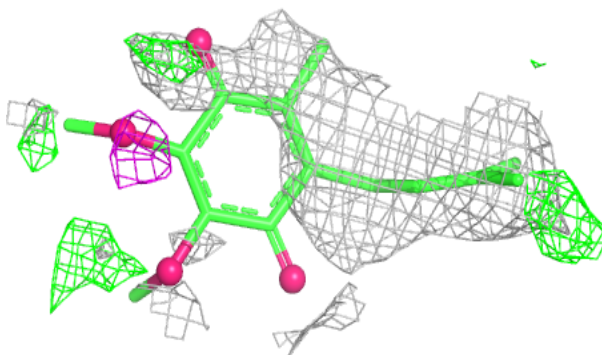


Electron density around U10 R 2009 (A):

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

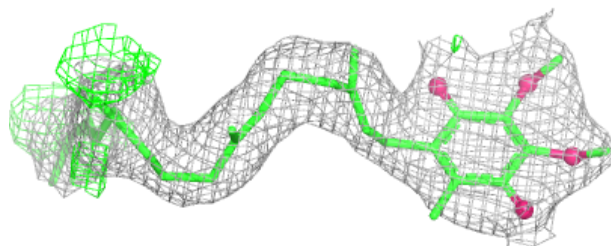
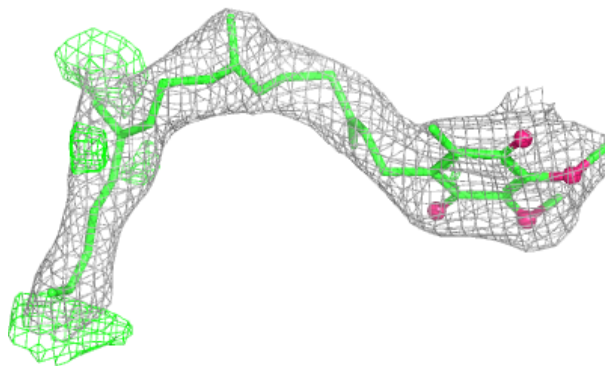
**Electron density around U10 R 2009 (B):**

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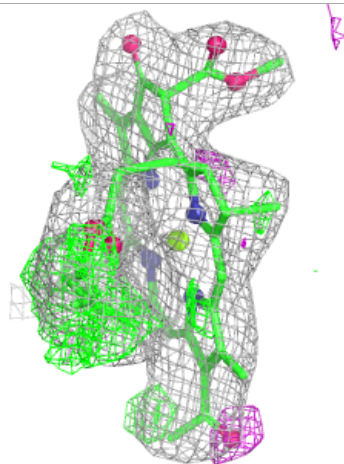
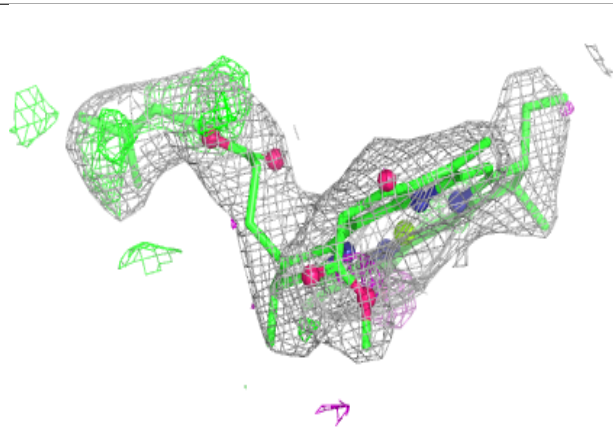
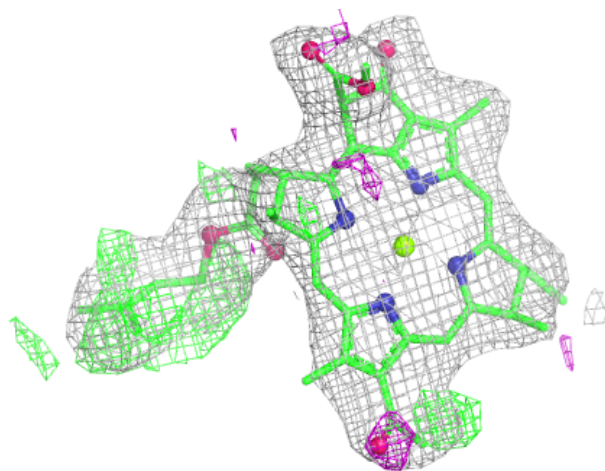
Electron density around U10 S 2008:

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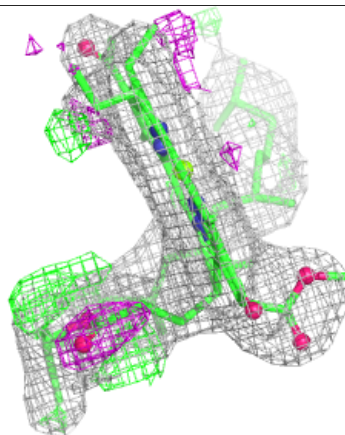
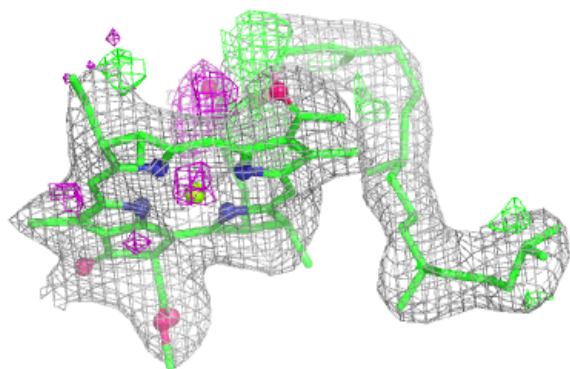
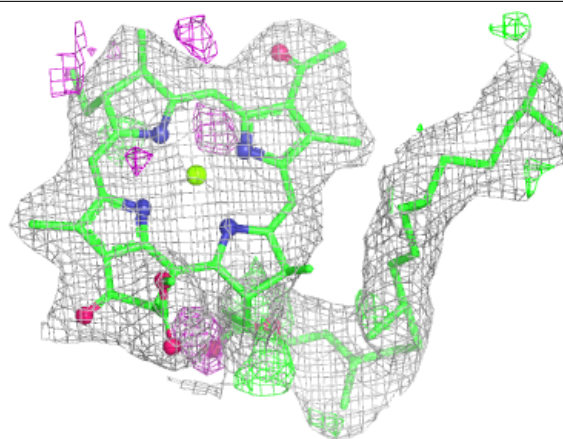
Electron density around BCL S 2001:

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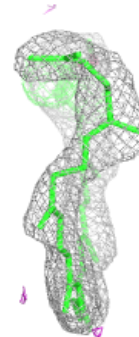
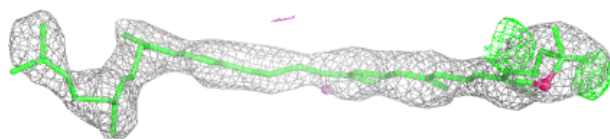
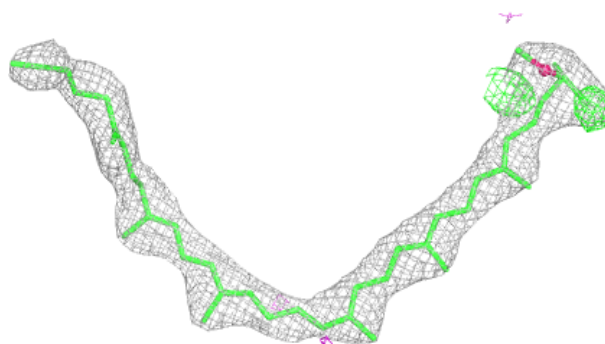


Electron density around BCL S 2004:

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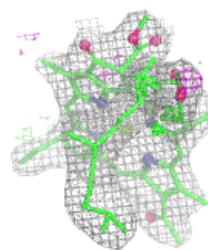
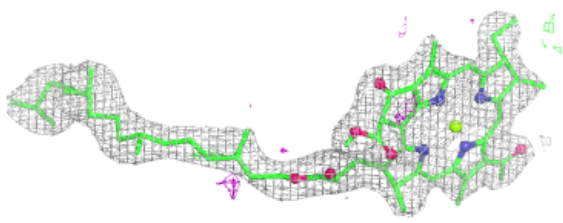
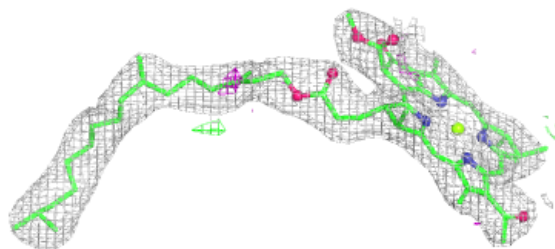
**Electron density around SPO S 2010:**

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and green (positive)



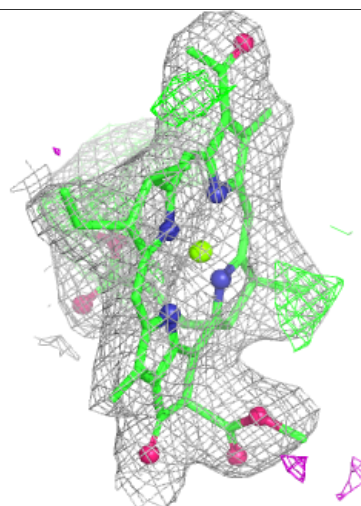
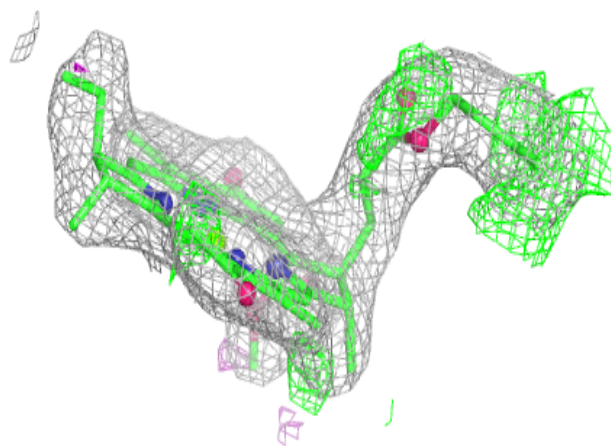
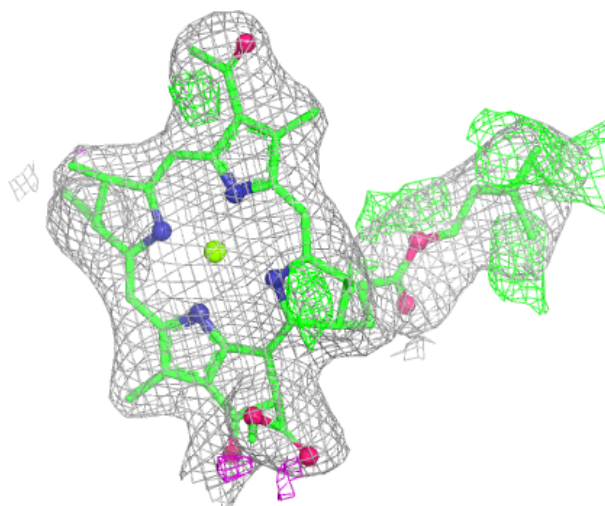
Electron density around BCL R 2002:

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



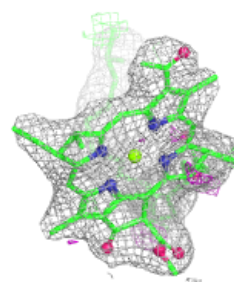
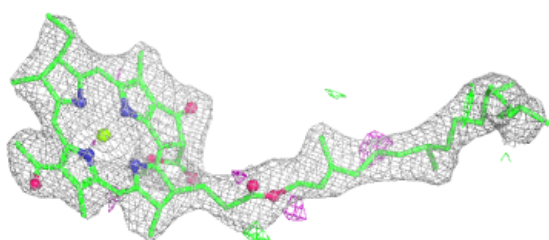
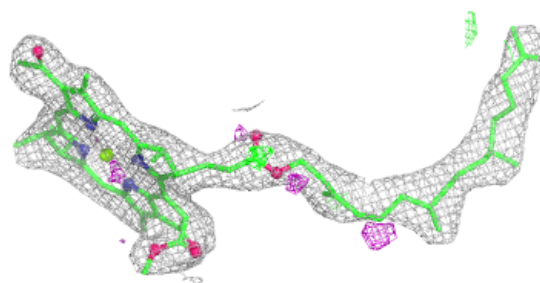
Electron density around BCL L 1001:

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

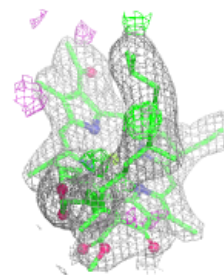
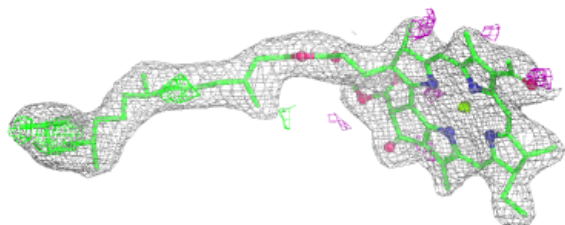
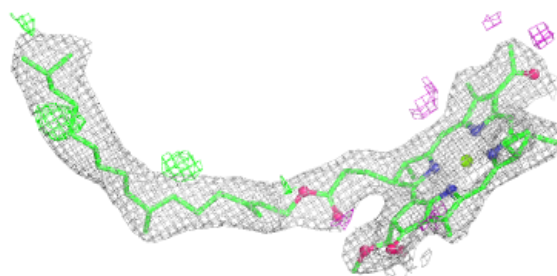


Electron density around BCL S 2003:

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

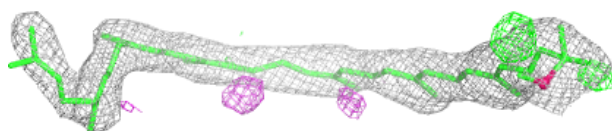
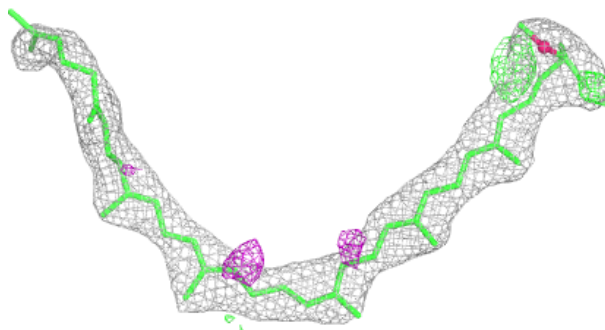
**Electron density around BCL L 1002:**

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

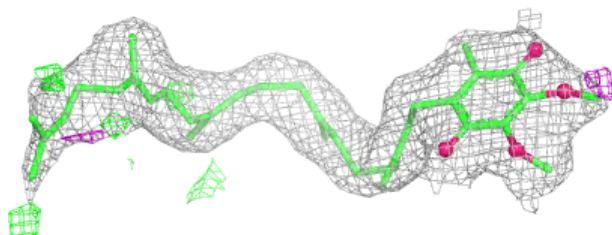
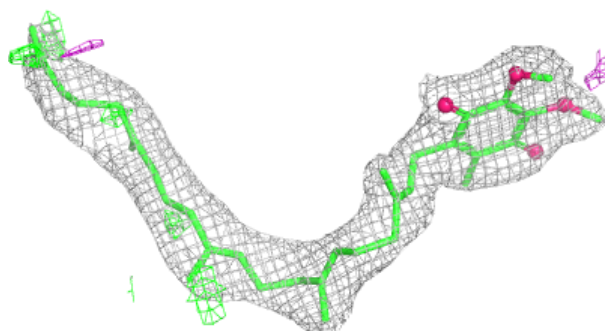


Electron density around SPO M 1010:

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

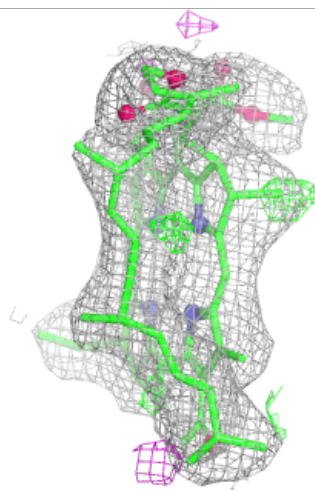
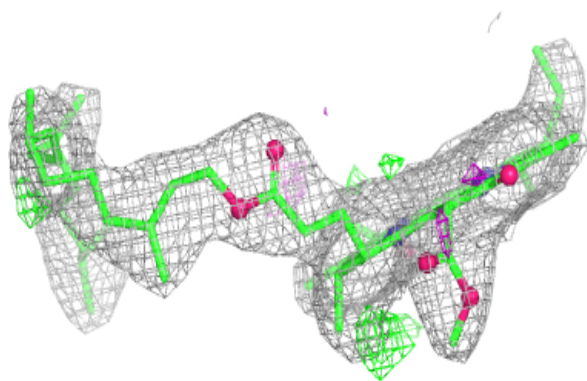
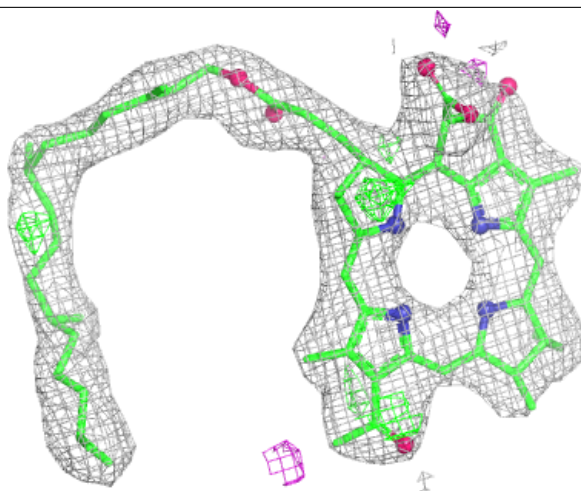
**Electron density around U10 M 1008:**

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



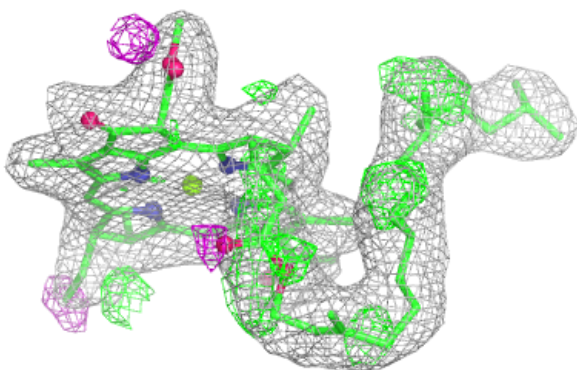
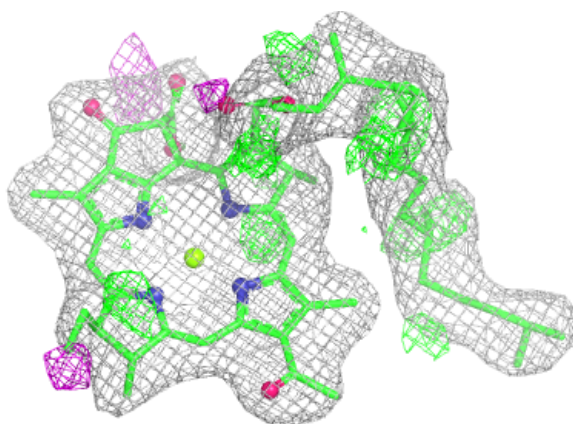
Electron density around BPH R 2006:

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

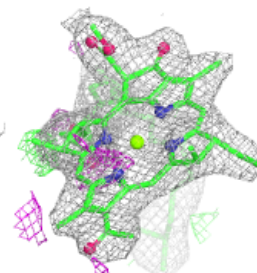
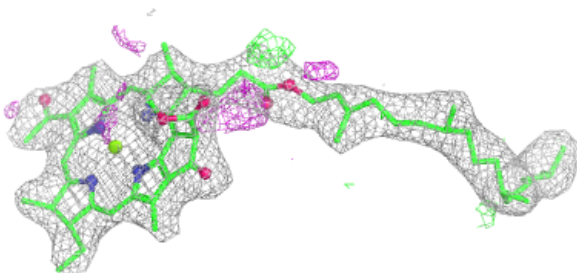
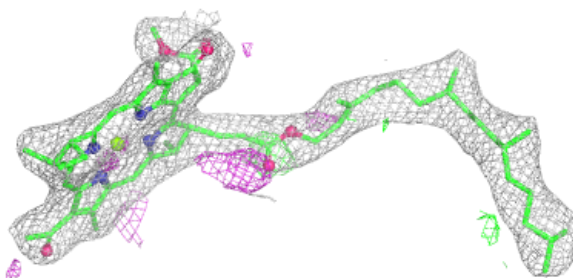


Electron density around BCL L 1004:

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

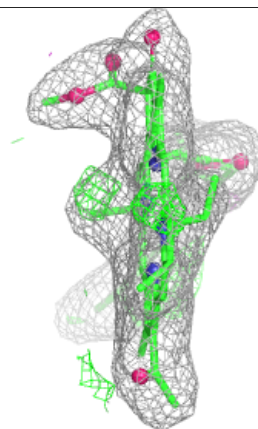
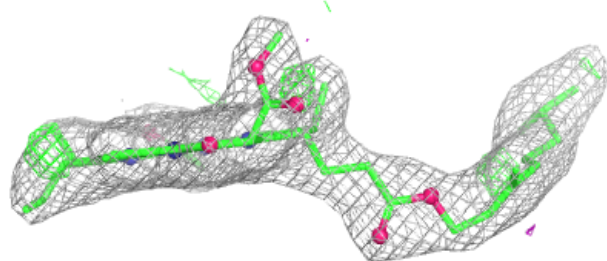
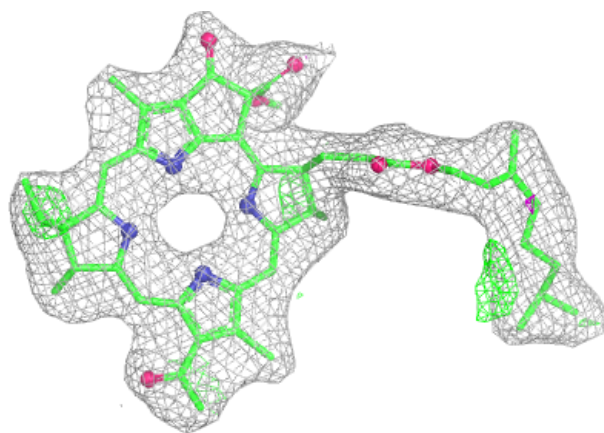
**Electron density around BCL M 1003:**

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



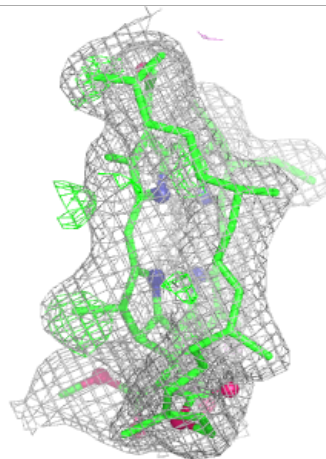
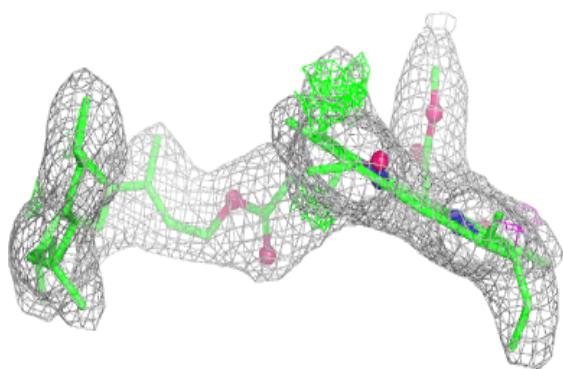
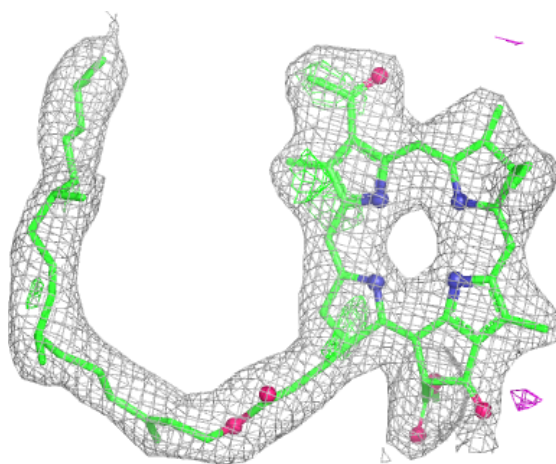
Electron density around BPH M 1005:

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



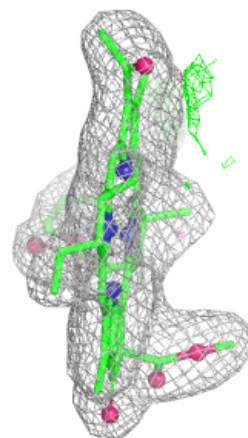
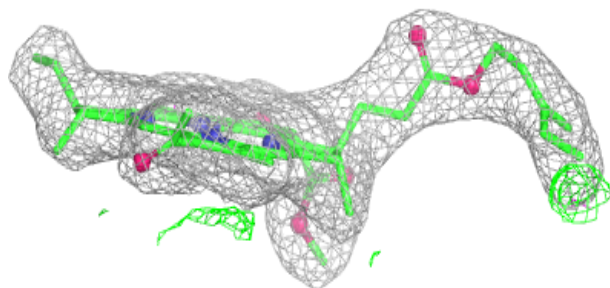
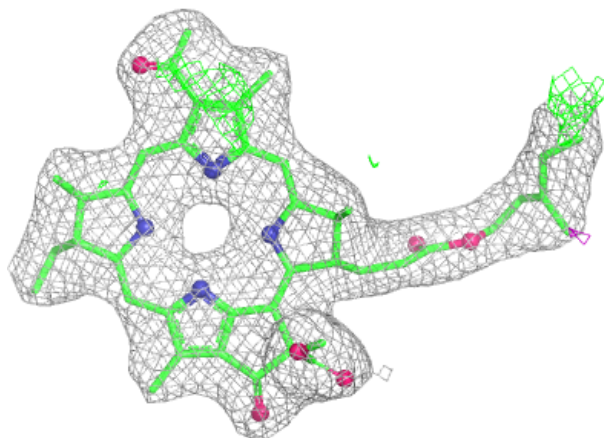
Electron density around BPH L 1006:

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



Electron density around BPH S 2005:

$2mF_o-DF_c$ (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.