



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:49 AM UTC

PDB ID : 7Q7M / pdb_00007q7m
Title : Room temperature structure of the Rhodobacter Sphaeroides Photosynthetic Reaction Center F(M197)H mutant at 100 MPa helium gas pressure in a sapphire capillary
Authors : Lieske, J.; Guenther, S.; Saouane, S.; Selikhanov, G.K.; Gabdulkhakov, A.G.; Meents, A.
Deposited on : 2021-11-09
Resolution : 2.55 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 types of validation reports are described at

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

The following versions of software and data (see [references](#) ①) 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)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

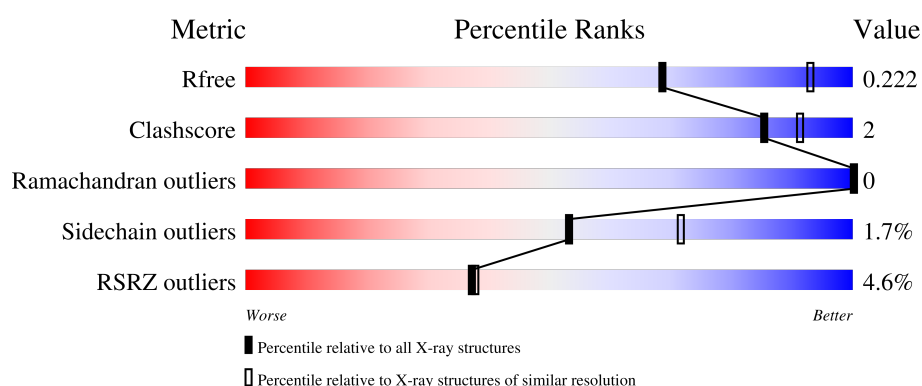
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	H	241	5% 94% 5%
2	L	281	6% 96% .
3	M	302	3% 94% 6%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 14861 atoms, of which 7386 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	H	N	O	S	0	6	0
			3770	1202	1894	322	342	10			

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	281	Total	C	H	N	O	S	0	3	0
			4467	1528	2209	358	364	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	178	THR	SER	engineered mutation	UNP P0C0Y8

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	M	300	Total	C	H	N	O	S	0	6	0
			4799	1635	2353	402	399	10			

There are 2 discrepancies between the modelled and reference sequences:

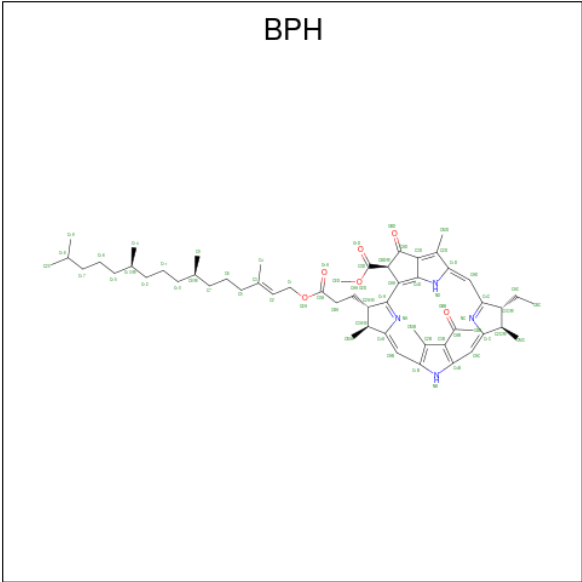
Chain	Residue	Modelled	Actual	Comment	Reference
M	8	THR	SER	engineered mutation	UNP P0C0Y9
M	197	HIS	PHE	engineered mutation	UNP P0C0Y9

- Molecule 4 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: C₁₄H₃₁NO) (labeled as "Ligand of Interest" by depositor).



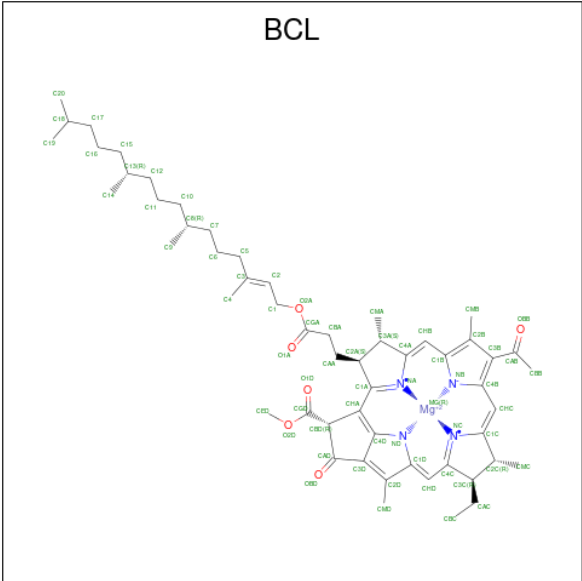
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	H	1	Total	C	H	N	O	0	0
			47	14	31	1	1		
4	H	1	Total	C	H	N	O	0	0
			47	14	31	1	1		
4	H	1	Total	C	H	N	O	0	0
			47	14	31	1	1		
4	L	1	Total	C	H	N	O	0	0
			47	14	31	1	1		
4	L	1	Total	C	H	N	O	0	0
			47	14	31	1	1		
4	L	1	Total	C	H	N	O	0	0
			47	14	31	1	1		
4	M	1	Total	C	H	N	O	0	0
			47	14	31	1	1		
4	M	1	Total	C	H	N	O	0	0
			47	14	31	1	1		
4	M	1	Total	C	H	N	O	0	0
			47	14	31	1	1		

- Molecule 5 is BACTERIOPHEOPHYTIN A (CCD ID: BPH) (formula: $C_{55}H_{76}N_4O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	L	1	Total	C	H	N	O	0	0
			141	55	76	4	6		
5	M	1	Total	C	H	N	O	0	0
			95	40	45	4	6		

- Molecule 6 is BACTERIOCHLOROPHYLL A (CCD ID: BCL) (formula: $C_{55}H_{74}MgN_4O_6$) (labeled as "Ligand of Interest" by depositor).



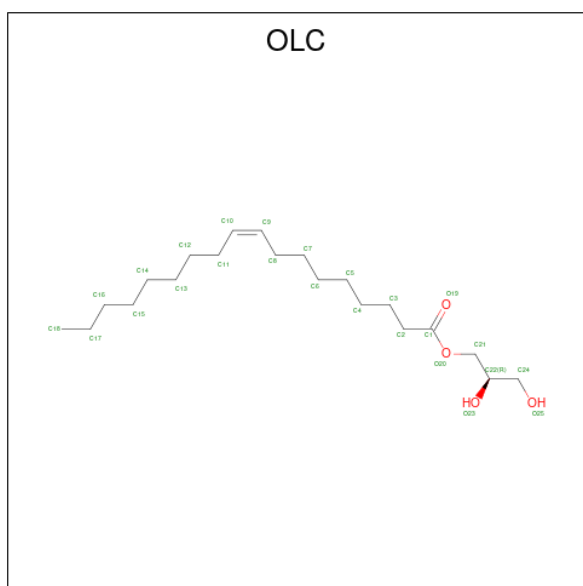
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	L	1	Total	C	H	Mg	N	O	0	0
			140	55	74	1	4	6		

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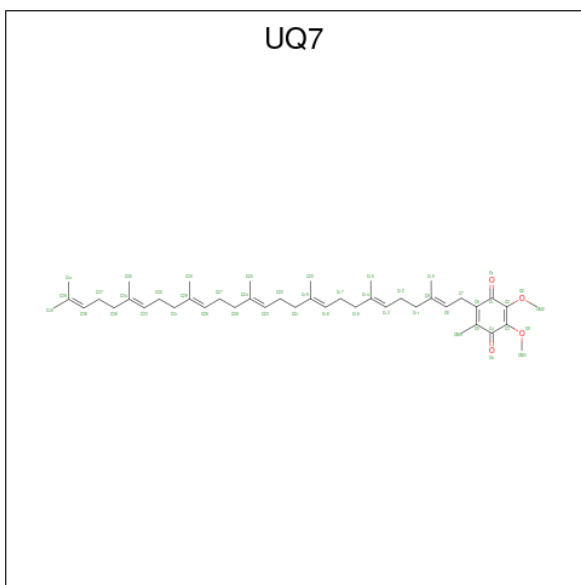
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	L	1	Total	C	H	Mg	N	O	0	0
			140	55	74	1	4	6		
6	M	1	Total	C	H	Mg	N	O	0	0
			140	55	74	1	4	6		
6	M	1	Total	C	H	Mg	N	O	0	0
			97	41	45	1	4	6		

- Molecule 7 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (CCD ID: OLC) (formula: C₂₁H₄₀O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	L	1	Total	C	H	O	0	1
			130	42	80	8		
7	M	1	Total	C	H	O	0	1
			65	21	40	4		

- Molecule 8 is UBIQUINONE-7 (CCD ID: UQ7) (formula: C₄₄H₆₆O₄) (labeled as "Ligand of Interest" by depositor).

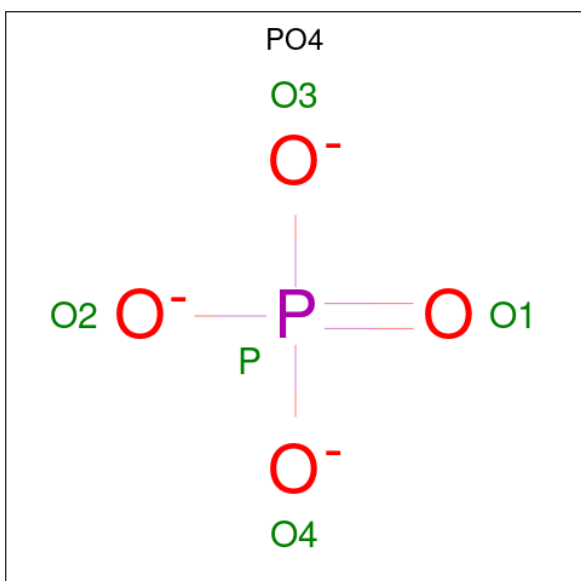


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	M	1	Total	C	H	O	0	0
			113	44	65	4		

- Molecule 9 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

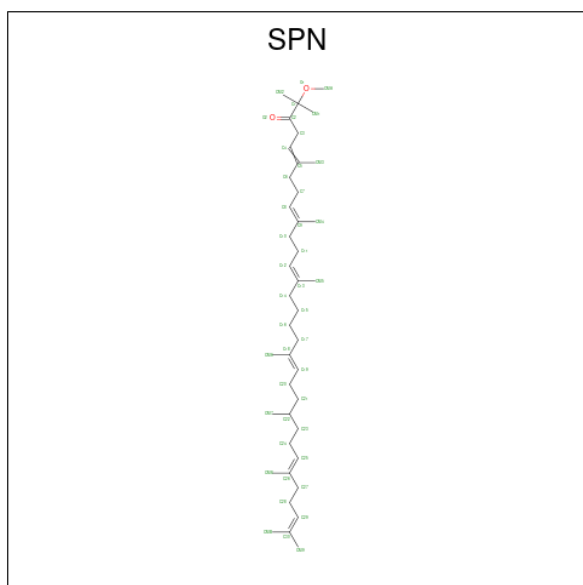
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	M	1	Total	Fe	0	0
			1	1		

- Molecule 10 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P) (labeled as "Ligand of Interest" by depositor).



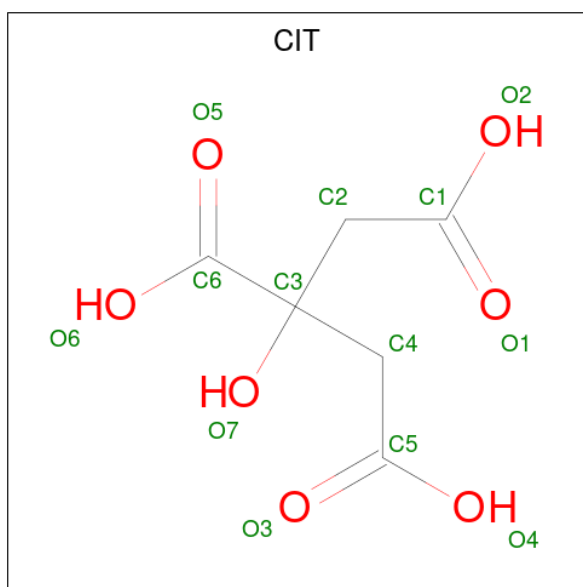
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	M	1	Total	O	P	0	0
			5	4	1		
10	M	1	Total	O	P	0	0
			5	4	1		

- Molecule 11 is SPEROIDENONE (CCD ID: SPN) (formula: $C_{41}H_{70}O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	M	1	Total	C	H	O	0	1
			113	41	70	2		

- Molecule 12 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	M	1	Total	C	H	O	0	0
			21	6	8	7		

- Molecule 13 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

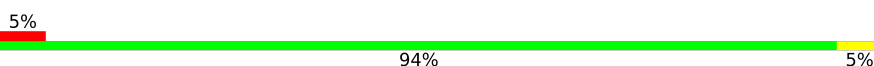
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	H	87	Total	O	0	1
			88	88		
14	L	50	Total	O	0	0
			50	50		
14	M	57	Total	O	0	0
			57	57		

3 Residue-property plots [i](#)

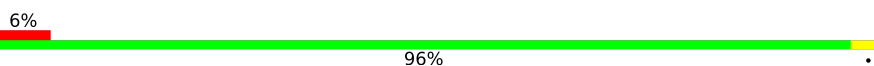
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: Reaction center protein H chain

Chain H: 

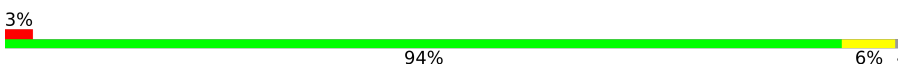


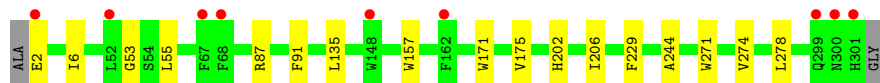
- Molecule 2: Reaction center protein L chain

Chain L: 



- Molecule 3: Reaction center protein M chain

Chain M: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	102.21 Å 102.21 Å 237.71 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.95 – 2.55 46.95 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.95-2.55) 89.1 (46.95-2.55)	Depositor EDS
R_{merge}	0.51	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.85 (at 2.54 Å)	Xtriage
Refinement program	PHENIX 1.13-2998_9999	Depositor
R, R_{free}	0.183 , 0.223 0.181 , 0.222	Depositor DCC
R_{free} test set	1686 reflections (4.01%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 69.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14861	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, OLC, SPN, CL, UQ7, BPH, BCL, FE, LDA, CIT

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	0.11	0/1936	0.27	0/2630
2	L	0.10	0/2355	0.26	0/3224
3	M	0.10	0/2553	0.27	0/3486
All	All	0.11	0/6844	0.27	0/9340

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1876	1894	1885	7	0
2	L	2258	2209	2202	5	0
3	M	2446	2353	2338	12	0
4	H	48	93	93	1	0
4	L	48	93	93	0	0
4	M	48	93	93	2	0
5	L	65	76	76	1	0
5	M	50	45	43	4	0
6	L	132	148	148	1	0
6	M	118	119	117	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	L	50	80	80	0	0
7	M	25	40	40	0	0
8	M	48	65	66	0	0
9	M	1	0	0	0	0
10	M	10	0	0	0	0
11	M	43	70	70	3	0
12	M	13	8	5	2	0
13	M	1	0	0	0	0
14	H	88	0	0	0	0
14	L	50	0	0	0	0
14	M	57	0	0	0	0
All	All	7475	7386	7349	32	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (32) 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:H:181:VAL:HG21	1:H:191:LEU:HD12	1.74	0.68
4:M:411:LDA:HM21	4:M:411:LDA:H32	1.74	0.67
1:H:122:GLU:HB2	1:H:227:LEU:HD21	1.84	0.60
2:L:173:HIS:CE1	2:L:177:ILE:HD11	2.37	0.60
5:L:301:BPH:HMB1	5:L:301:BPH:HBB3	1.90	0.53
3:M:55:LEU:HD12	3:M:135:LEU:HD12	1.93	0.51
6:L:302:BCL:HMB3	6:L:302:BCL:HBB2	1.94	0.50
5:M:404:BPH:HBC2	5:M:404:BPH:HHH	1.93	0.50
3:M:175:VAL:HB	11:M:410[A]:SPN:HM63	1.96	0.48
12:M:413:CIT:H41	12:M:413:CIT:O2	2.16	0.46
3:M:53:GLY:HA3	12:M:413:CIT:C4	2.47	0.45
2:L:272:TRP:O	3:M:87:ARG:NH1	2.48	0.45
2:L:269:LEU:O	2:L:271:TRP:N	2.50	0.44
3:M:157:TRP:CD1	6:M:403:BCL:HBB1	2.53	0.44
1:H:181:VAL:HG21	1:H:191:LEU:CD1	2.46	0.44
3:M:157:TRP:HD1	6:M:403:BCL:HBB1	1.83	0.44
3:M:171:TRP:CZ3	11:M:410[A]:SPN:HM83	2.53	0.44
3:M:229:PHE:HB2	3:M:244:ALA:HB2	2.00	0.43
1:H:245:ALA:N	1:H:246:PRO:CD	2.83	0.42
4:H:303:LDA:HM11	3:M:278:LEU:HD21	2.01	0.42
2:L:185:LEU:HD13	5:M:404:BPH:ND	2.34	0.42
6:M:403:BCL:HHC	6:M:403:BCL:OBB	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:191:LEU:HD11	1:H:213:PHE:HE2	1.85	0.41
2:L:279:ILE:HG21	3:M:91:PHE:HB3	2.01	0.41
3:M:271:TRP:HA	3:M:274:VAL:HG22	2.02	0.41
4:M:411:LDA:HM21	4:M:411:LDA:C3	2.46	0.41
11:M:410[A]:SPN:H72	11:M:410[A]:SPN:HM31	1.96	0.41
3:M:202:HIS:CE1	3:M:206:ILE:HD11	2.56	0.40
1:H:211:ASP:OD1	1:H:211:ASP:N	2.55	0.40
5:M:404:BPH:CHD	5:M:404:BPH:CBC	2.99	0.40
1:H:87:LEU:HD23	1:H:100:PRO:HA	2.02	0.40
5:M:404:BPH:HBB3	5:M:404:BPH:HMB1	2.03	0.40

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	H	244/241 (101%)	239 (98%)	5 (2%)	0	100	100
2	L	282/281 (100%)	275 (98%)	7 (2%)	0	100	100
3	M	304/302 (101%)	298 (98%)	6 (2%)	0	100	100
All	All	830/824 (101%)	812 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	201/196 (103%)	198 (98%)	3 (2%)	57	74
2	L	223/220 (101%)	217 (97%)	6 (3%)	39	58
3	M	241/236 (102%)	239 (99%)	2 (1%)	73	84
All	All	665/652 (102%)	654 (98%)	11 (2%)	53	72

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	197	LYS
1	H	220	LYS
1	H	231	ASP
2	L	82	LYS
2	L	158	SER
2	L	216	PHE
2	L	235	LEU
2	L	265	TRP
2	L	271	TRP
3	M	2	GLU
3	M	6	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	199	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 25 ligands modelled in this entry, 2 are monoatomic - leaving 23 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	LDA	M	411	-	13,15,15	0.36	0	14,17,17	0.33	0
4	LDA	M	406	-	13,15,15	0.34	0	14,17,17	0.67	0
7	OLC	L	304[B]	-	24,24,24	0.22	0	25,25,25	0.23	0
12	CIT	M	413	-	12,12,12	0.18	0	17,17,17	0.60	0
7	OLC	M	409[B]	-	24,24,24	0.17	0	25,25,25	0.18	0
4	LDA	L	306	-	13,15,15	0.33	0	14,17,17	0.46	0
6	BCL	M	403	-	55,60,74	1.19	3 (5%)	61,98,115	1.43	8 (13%)
10	PO4	M	412	-	4,4,4	0.96	0	6,6,6	0.45	0
8	UQ7	M	401	-	48,48,48	0.22	0	60,61,61	0.45	1 (1%)
10	PO4	M	408	-	4,4,4	0.95	0	6,6,6	0.48	0
6	BCL	L	303	-	69,74,74	1.11	4 (5%)	79,115,115	1.20	6 (7%)
5	BPH	M	404	-	44,55,70	1.27	2 (4%)	41,83,101	1.70	5 (12%)
11	SPN	M	410[A]	-	42,42,42	0.15	0	50,52,52	0.52	1 (2%)
4	LDA	M	407	-	13,15,15	0.30	0	14,17,17	0.24	0
5	BPH	L	301	-	59,70,70	1.00	1 (1%)	59,101,101	1.38	5 (8%)
4	LDA	L	305	-	13,15,15	0.33	0	14,17,17	0.34	0
4	LDA	L	307	-	13,15,15	0.34	0	14,17,17	0.57	0
4	LDA	H	301	-	13,15,15	0.34	0	14,17,17	0.22	0
6	BCL	M	402	-	69,74,74	1.08	4 (5%)	79,115,115	1.32	7 (8%)
6	BCL	L	302	-	69,74,74	1.06	3 (4%)	79,115,115	1.21	6 (7%)
4	LDA	H	302	-	13,15,15	0.34	0	14,17,17	0.99	2 (14%)
7	OLC	L	304[A]	-	24,24,24	0.21	0	25,25,25	0.20	0
4	LDA	H	303	-	13,15,15	0.37	0	14,17,17	0.59	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
4	LDA	M	411	-	-	6/13/13/13	-
4	LDA	M	406	-	-	5/13/13/13	-
7	OLC	L	304[B]	-	-	13/24/24/24	-
12	CIT	M	413	-	-	5/16/16/16	-
7	OLC	M	409[B]	-	-	8/24/24/24	-
4	LDA	L	306	-	-	8/13/13/13	-
6	BCL	M	403	-	-	4/25/121/137	-
8	UQ7	M	401	-	-	4/45/69/69	0/1/1/1
6	BCL	L	303	-	-	1/41/137/137	-
5	BPH	M	404	-	-	3/19/87/105	0/5/6/6
11	SPN	M	410[A]	-	-	22/50/51/51	-
4	LDA	M	407	-	-	5/13/13/13	-
5	BPH	L	301	-	-	8/37/105/105	0/5/6/6
4	LDA	L	305	-	-	6/13/13/13	-
4	LDA	L	307	-	-	7/13/13/13	-
4	LDA	H	301	-	-	4/13/13/13	-
6	BCL	M	402	-	-	11/41/137/137	-
6	BCL	L	302	-	-	4/41/137/137	-
4	LDA	H	302	-	-	10/13/13/13	-
7	OLC	L	304[A]	-	-	18/24/24/24	-
4	LDA	H	303	-	-	10/13/13/13	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	301	BPH	C1B-C2B	5.57	1.45	1.39
5	M	404	BPH	C1B-C2B	5.30	1.45	1.39
6	M	402	BCL	MG-NA	4.71	2.17	2.06
6	L	303	BCL	MG-NA	4.70	2.17	2.06
6	L	302	BCL	MG-NA	4.43	2.16	2.06
6	M	403	BCL	MG-NA	4.39	2.16	2.06
5	M	404	BPH	C2C-C3C	4.21	1.58	1.54
6	L	303	BCL	MG-NC	3.10	2.13	2.06
6	M	403	BCL	MG-NC	2.86	2.13	2.06
6	L	302	BCL	MG-NC	2.85	2.13	2.06
6	M	402	BCL	MG-NC	2.72	2.12	2.06
6	L	302	BCL	CHD-C1D	2.66	1.43	1.38
6	M	403	BCL	CHD-C1D	2.50	1.43	1.38
6	L	303	BCL	CHD-C1D	2.41	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	L	303	BCL	C3B-C4B	2.41	1.45	1.41
6	M	402	BCL	CHD-C1D	2.34	1.43	1.38
6	M	402	BCL	C3B-C4B	2.08	1.45	1.41

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	404	BPH	C4D-CHA-CBD	-7.78	104.72	108.45
5	L	301	BPH	C4D-CHA-CBD	-7.41	104.90	108.45
6	M	402	BCL	C4D-CHA-C1A	5.37	127.65	121.24
6	L	302	BCL	C4D-CHA-C1A	5.11	127.34	121.24
6	L	303	BCL	C4D-CHA-C1A	4.92	127.12	121.24
6	M	403	BCL	C4D-CHA-C1A	4.92	127.11	121.24
6	M	402	BCL	C4A-NA-C1A	4.21	108.60	106.68
6	L	302	BCL	C1D-ND-C4D	-3.71	103.71	106.31
6	M	403	BCL	CHD-C1D-ND	-3.66	119.65	124.80
5	L	301	BPH	C2B-C1B-NB	-3.64	106.80	109.43
6	L	302	BCL	CHD-C1D-ND	-3.56	119.80	124.80
6	M	403	BCL	C1D-ND-C4D	-3.54	103.83	106.31
5	M	404	BPH	C2B-C1B-NB	-3.53	106.88	109.43
6	L	303	BCL	CHD-C1D-ND	-3.45	119.95	124.80
6	M	402	BCL	C1D-ND-C4D	-3.43	103.90	106.31
6	M	402	BCL	CHD-C1D-ND	-3.40	120.02	124.80
6	L	303	BCL	C1D-ND-C4D	-3.35	103.97	106.31
6	M	402	BCL	CHA-C1A-NA	-3.12	119.33	126.39
5	L	301	BPH	C1-C2-C3	-3.05	121.20	126.20
6	L	302	BCL	CHA-C1A-NA	-2.98	119.64	126.39
5	M	404	BPH	CMA-C3A-C4A	-2.98	108.20	114.61
6	M	403	BCL	CHA-C1A-NA	-2.91	119.79	126.39
6	M	403	BCL	C1-O2A-CGA	2.91	123.69	116.65
6	L	303	BCL	CHA-C1A-NA	-2.80	120.05	126.39
4	H	302	LDA	CM2-N1-C1	-2.77	104.41	110.23
5	L	301	BPH	C2D-C1D-ND	-2.72	107.46	109.43
6	L	302	BCL	C2A-C1A-CHA	2.71	128.57	123.87
6	L	303	BCL	C4A-NA-C1A	2.71	107.92	106.68
6	L	303	BCL	C2A-C1A-CHA	2.71	128.57	123.87
5	L	301	BPH	CMA-C3A-C4A	-2.70	108.79	114.61
5	M	404	BPH	C2D-C1D-ND	-2.67	107.50	109.43
6	M	402	BCL	C2A-C1A-CHA	2.67	128.50	123.87
6	M	403	BCL	C2A-C1A-CHA	2.65	128.47	123.87
5	M	404	BPH	C1-C2-C3	-2.53	122.67	126.76
11	M	410[A]	SPN	O1-C1-C2	-2.46	103.87	108.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	403	BCL	C1C-NC-C4C	2.45	107.80	106.68
6	M	403	BCL	C4A-NA-C1A	2.37	107.76	106.68
4	H	302	LDA	CM1-N1-C1	2.35	115.17	110.23
6	L	302	BCL	C4A-NA-C1A	2.25	107.71	106.68
6	M	402	BCL	C1-C2-C3	-2.25	122.52	126.20
8	M	401	UQ7	C7-C6-C1	-2.04	116.15	118.52

There are no chirality outliers.

All (162) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	302	LDA	C2-C1-N1-CM1
4	H	302	LDA	N1-C1-C2-C3
4	H	303	LDA	C2-C1-N1-O1
4	H	303	LDA	C2-C1-N1-CM1
4	H	303	LDA	N1-C1-C2-C3
4	L	305	LDA	C2-C1-N1-CM1
4	L	305	LDA	C2-C1-N1-CM2
4	L	306	LDA	C2-C1-N1-O1
4	L	306	LDA	C2-C1-N1-CM1
4	L	306	LDA	C2-C1-N1-CM2
4	L	307	LDA	C2-C1-N1-O1
4	L	307	LDA	C2-C1-N1-CM1
4	L	307	LDA	C2-C1-N1-CM2
4	M	406	LDA	C2-C1-N1-O1
4	M	406	LDA	C2-C1-N1-CM1
4	M	411	LDA	C2-C1-N1-O1
4	M	411	LDA	C2-C1-N1-CM1
5	M	404	BPH	C4C-C3C-CAC-CBC
6	M	403	BCL	C1A-C2A-CAA-CBA
6	M	403	BCL	C2-C3-C5-C6
6	M	403	BCL	C4-C3-C5-C6
7	L	304[A]	OLC	C21-C22-C24-O25
7	M	409[B]	OLC	C21-C22-C24-O25
7	M	409[B]	OLC	O23-C22-C24-O25
7	M	409[B]	OLC	O20-C21-C22-C24
8	M	401	UQ7	C24-C26-C27-C28
8	M	401	UQ7	C29-C31-C32-C33
11	M	410[A]	SPN	CM1-C1-O1-CMA
11	M	410[A]	SPN	C2-C1-O1-CMA
11	M	410[A]	SPN	C15-C16-C17-C18
6	M	402	BCL	C3-C5-C6-C7

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Mol	Chain	Res	Type	Atoms
7	L	304[B]	OLC	O20-C21-C22-O23
11	M	410[A]	SPN	C11-C10-C9-CM4
11	M	410[A]	SPN	C11-C10-C9-C8
11	M	410[A]	SPN	C26-C27-C28-C29
7	L	304[B]	OLC	C3-C4-C5-C6
6	M	402	BCL	C14-C13-C15-C16
7	M	409[B]	OLC	O20-C21-C22-O23
6	M	402	BCL	C15-C16-C17-C18
7	L	304[A]	OLC	O20-C21-C22-O23
7	L	304[B]	OLC	C21-C22-C24-O25
4	L	306	LDA	C7-C8-C9-C10
7	L	304[A]	OLC	C4-C5-C6-C7
5	L	301	BPH	C13-C15-C16-C17
4	H	303	LDA	C4-C5-C6-C7
4	M	407	LDA	C7-C8-C9-C10
4	M	411	LDA	C7-C8-C9-C10
7	L	304[A]	OLC	O23-C22-C24-O25
7	L	304[B]	OLC	O23-C22-C24-O25
4	H	302	LDA	C6-C7-C8-C9
11	M	410[A]	SPN	C19-C20-C21-C22
4	H	302	LDA	C7-C8-C9-C10
7	L	304[A]	OLC	C14-C15-C16-C17
4	M	411	LDA	C5-C6-C7-C8
7	L	304[A]	OLC	C5-C6-C7-C8
8	M	401	UQ7	C34-C36-C37-C38
7	M	409[B]	OLC	C14-C15-C16-C17
4	H	301	LDA	C7-C8-C9-C10
7	L	304[A]	OLC	C11-C12-C13-C14
11	M	410[A]	SPN	C13-C14-C15-C16
11	M	410[A]	SPN	CM3-C5-C6-C7
7	L	304[A]	OLC	C3-C4-C5-C6
4	M	406	LDA	C1-C2-C3-C4
4	M	407	LDA	C11-C10-C9-C8
11	M	410[A]	SPN	CM8-C26-C27-C28
4	L	305	LDA	C7-C8-C9-C10
6	M	402	BCL	C8-C10-C11-C12
5	M	404	BPH	C2C-C3C-CAC-CBC
11	M	410[A]	SPN	C25-C26-C27-C28
4	H	301	LDA	C5-C6-C7-C8
7	L	304[A]	OLC	C13-C14-C15-C16
6	M	402	BCL	C6-C7-C8-C10
11	M	410[A]	SPN	C20-C21-C22-C23

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Mol	Chain	Res	Type	Atoms
5	L	301	BPH	C4-C3-C5-C6
6	M	402	BCL	C11-C10-C8-C9
11	M	410[A]	SPN	C20-C21-C22-CM7
7	M	409[B]	OLC	C4-C5-C6-C7
7	L	304[A]	OLC	C6-C7-C8-C9
4	H	302	LDA	C1-C2-C3-C4
5	L	301	BPH	C2-C3-C5-C6
11	M	410[A]	SPN	C14-C15-C16-C17
4	M	406	LDA	C3-C4-C5-C6
4	L	307	LDA	C1-C2-C3-C4
12	M	413	CIT	C6-C3-C4-C5
11	M	410[A]	SPN	C4-C5-C6-C7
4	M	407	LDA	C2-C3-C4-C5
7	L	304[A]	OLC	C12-C13-C14-C15
4	H	301	LDA	C9-C10-C11-C12
7	L	304[A]	OLC	C15-C16-C17-C18
4	L	307	LDA	C9-C10-C11-C12
4	M	407	LDA	C4-C5-C6-C7
6	M	402	BCL	C6-C7-C8-C9
7	L	304[B]	OLC	O20-C21-C22-C24
11	M	410[A]	SPN	CM7-C22-C23-C24
4	H	302	LDA	C5-C6-C7-C8
7	L	304[A]	OLC	C2-C3-C4-C5
6	M	402	BCL	C11-C10-C8-C7
11	M	410[A]	SPN	C21-C22-C23-C24
6	M	403	BCL	C3A-C2A-CAA-CBA
7	L	304[B]	OLC	C15-C16-C17-C18
6	L	302	BCL	C16-C17-C18-C19
6	M	402	BCL	C13-C15-C16-C17
4	H	303	LDA	C7-C8-C9-C10
4	L	306	LDA	C2-C3-C4-C5
4	L	306	LDA	C11-C10-C9-C8
6	M	402	BCL	C4C-C3C-CAC-CBC
6	L	302	BCL	C16-C17-C18-C20
4	M	411	LDA	C11-C10-C9-C8
4	L	305	LDA	C4-C5-C6-C7
4	H	302	LDA	C3-C4-C5-C6
4	H	303	LDA	C2-C1-N1-CM2
4	M	406	LDA	C2-C1-N1-CM2
4	M	411	LDA	C9-C10-C11-C12
7	L	304[B]	OLC	C5-C6-C7-C8
6	M	402	BCL	C2C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
4	L	305	LDA	C2-C3-C4-C5
4	L	305	LDA	C2-C1-N1-O1
6	L	302	BCL	CHA-CBD-CGD-O1D
6	L	302	BCL	CHA-CBD-CGD-O2D
11	M	410[A]	SPN	CM2-C1-O1-CMA
4	H	302	LDA	C2-C3-C4-C5
5	L	301	BPH	C14-C13-C15-C16
5	L	301	BPH	C11-C12-C13-C15
11	M	410[A]	SPN	C27-C28-C29-C30
4	L	306	LDA	C3-C4-C5-C6
4	H	301	LDA	C4-C5-C6-C7
4	L	307	LDA	C11-C10-C9-C8
7	L	304[A]	OLC	C2-C1-O20-C21
12	M	413	CIT	O7-C3-C4-C5
7	L	304[A]	OLC	C9-C10-C11-C12
4	H	303	LDA	C5-C6-C7-C8
4	L	306	LDA	C6-C7-C8-C9
4	H	302	LDA	C9-C10-C11-C12
7	L	304[B]	OLC	C9-C10-C11-C12
11	M	410[A]	SPN	C16-C17-C18-CM6
7	L	304[A]	OLC	O20-C21-C22-C24
11	M	410[A]	SPN	CM5-C13-C14-C15
5	L	301	BPH	CHA-CBD-CGD-O1D
5	L	301	BPH	CHA-CBD-CGD-O2D
11	M	410[A]	SPN	C16-C17-C18-C19
12	M	413	CIT	C1-C2-C3-O7
7	L	304[A]	OLC	O20-C1-C2-C3
7	M	409[B]	OLC	C7-C8-C9-C10
7	L	304[B]	OLC	O20-C1-C2-C3
4	H	303	LDA	C11-C10-C9-C8
4	L	307	LDA	C2-C3-C4-C5
7	L	304[A]	OLC	O19-C1-O20-C21
7	L	304[B]	OLC	C14-C15-C16-C17
4	M	407	LDA	C6-C7-C8-C9
7	M	409[B]	OLC	C9-C10-C11-C12
5	M	404	BPH	C2-C1-O2A-CGA
4	H	303	LDA	C3-C4-C5-C6
4	H	303	LDA	C2-C3-C4-C5
4	H	302	LDA	C2-C1-N1-CM2
8	M	401	UQ7	C1-C2-O2-CM2
7	L	304[B]	OLC	C1-C2-C3-C4
6	L	303	BCL	C2A-CAA-CBA-CGA

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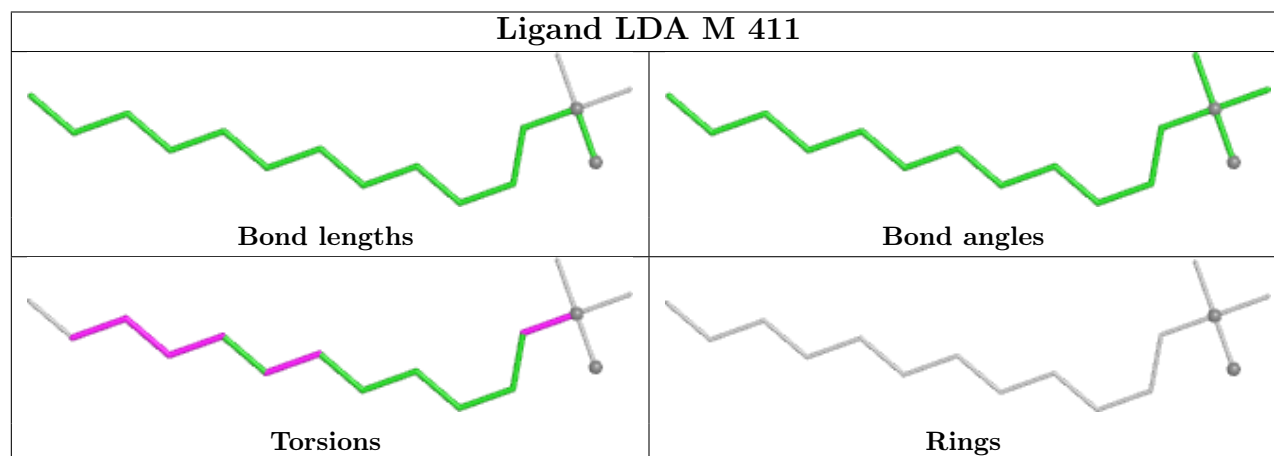
Mol	Chain	Res	Type	Atoms
7	L	304[B]	OLC	C2-C1-O20-C21
7	L	304[B]	OLC	C11-C12-C13-C14
5	L	301	BPH	C8-C10-C11-C12
12	M	413	CIT	O1-C1-C2-C3
12	M	413	CIT	O2-C1-C2-C3

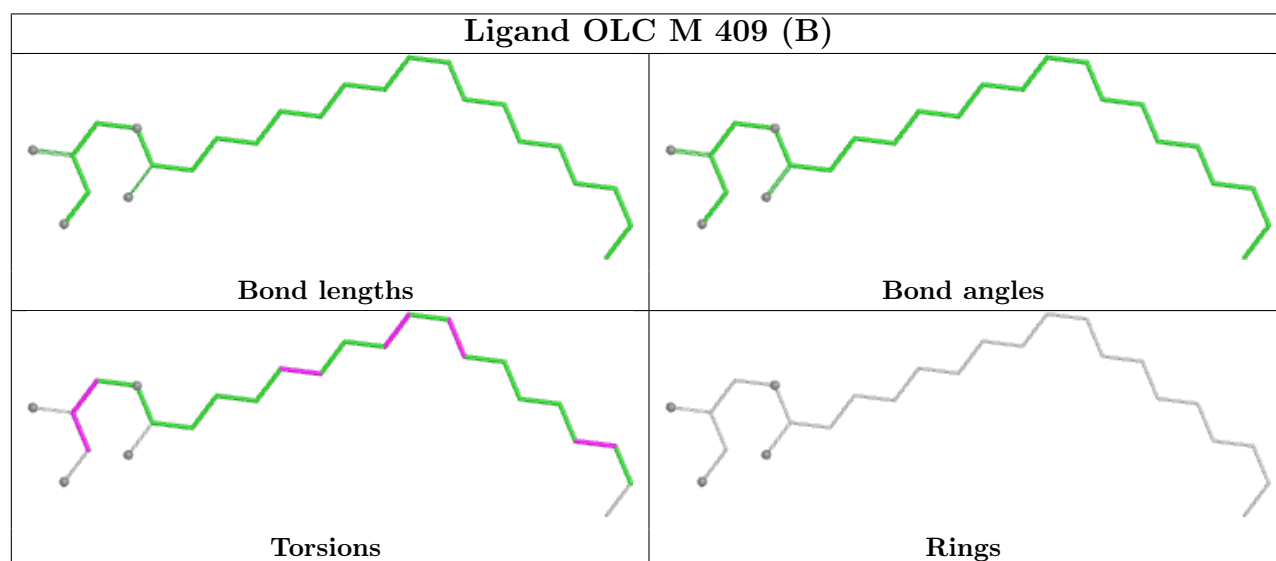
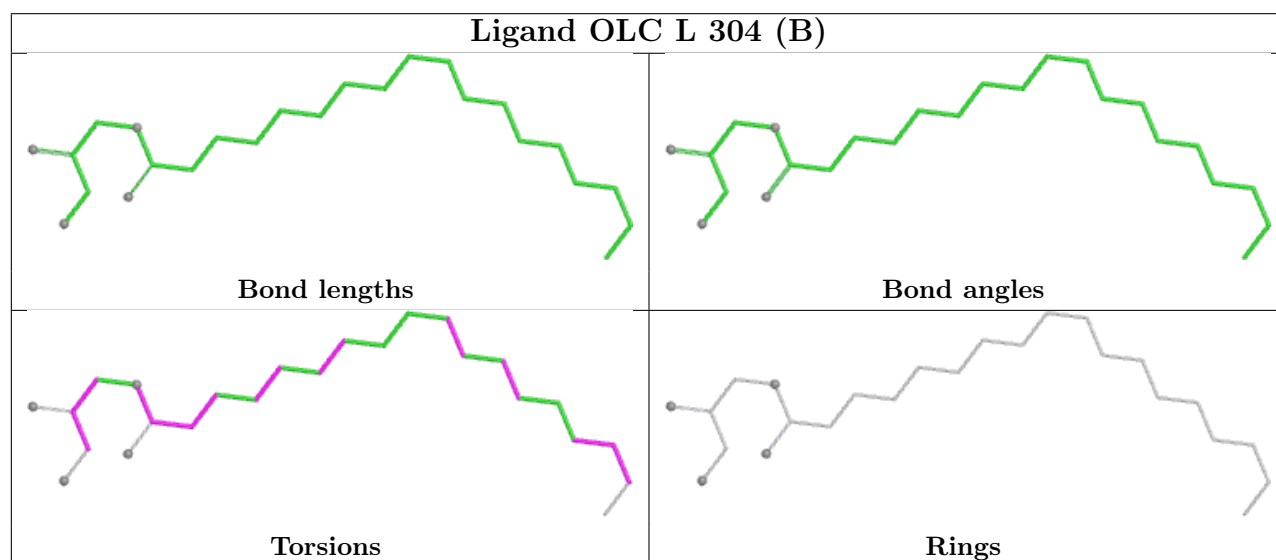
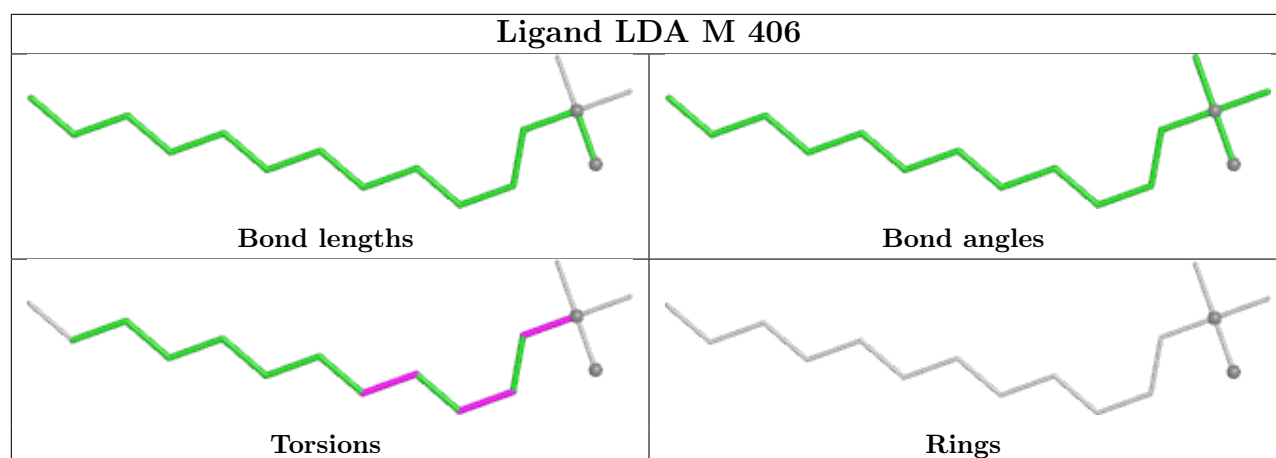
There are no ring outliers.

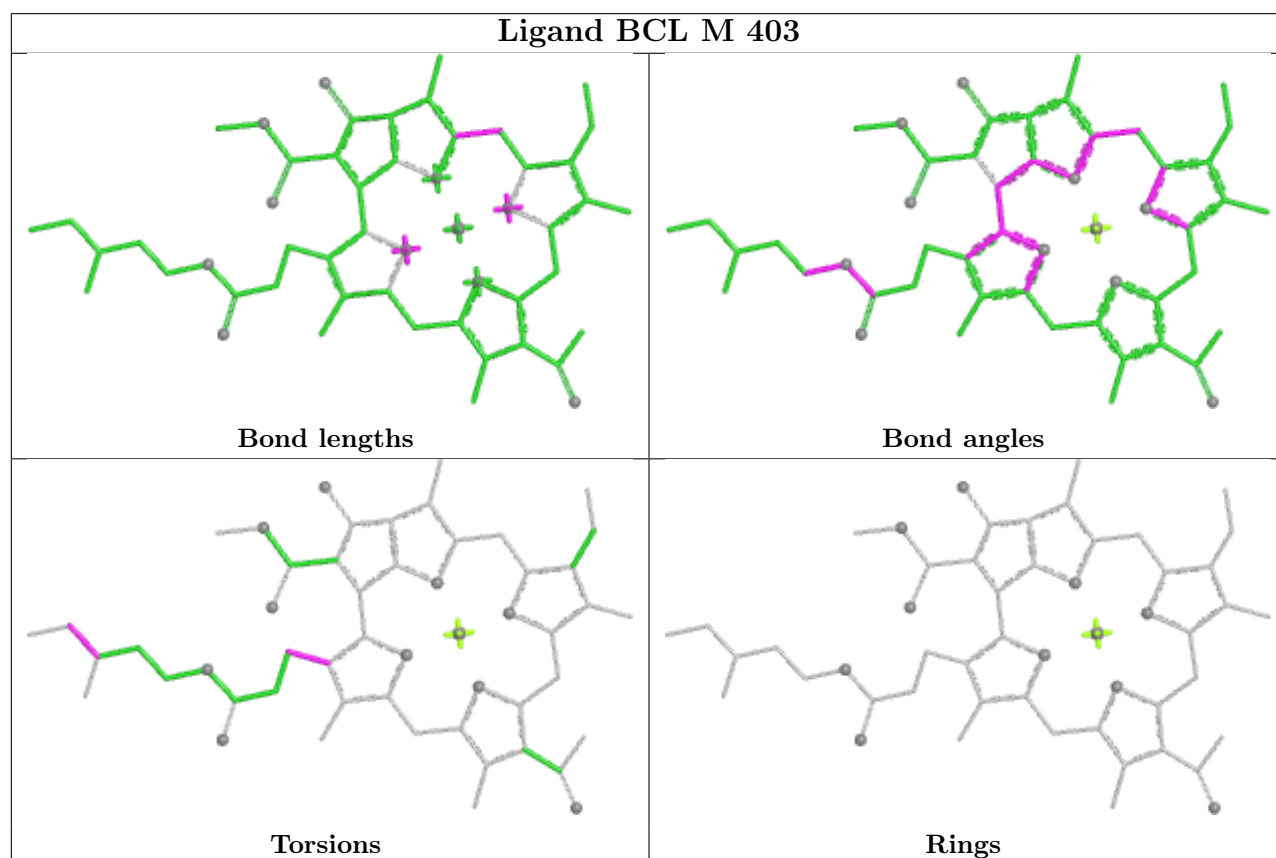
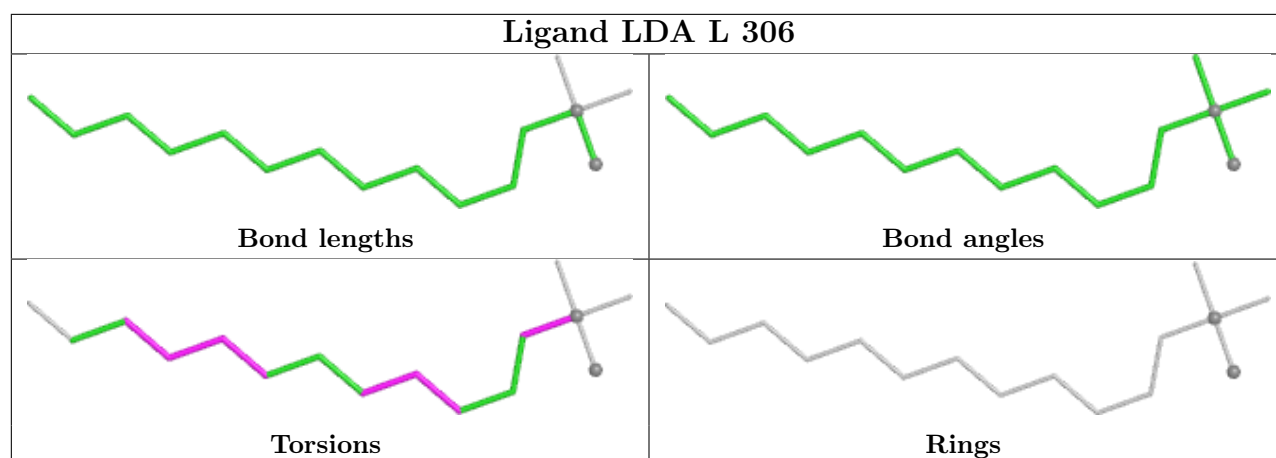
8 monomers are involved in 17 short contacts:

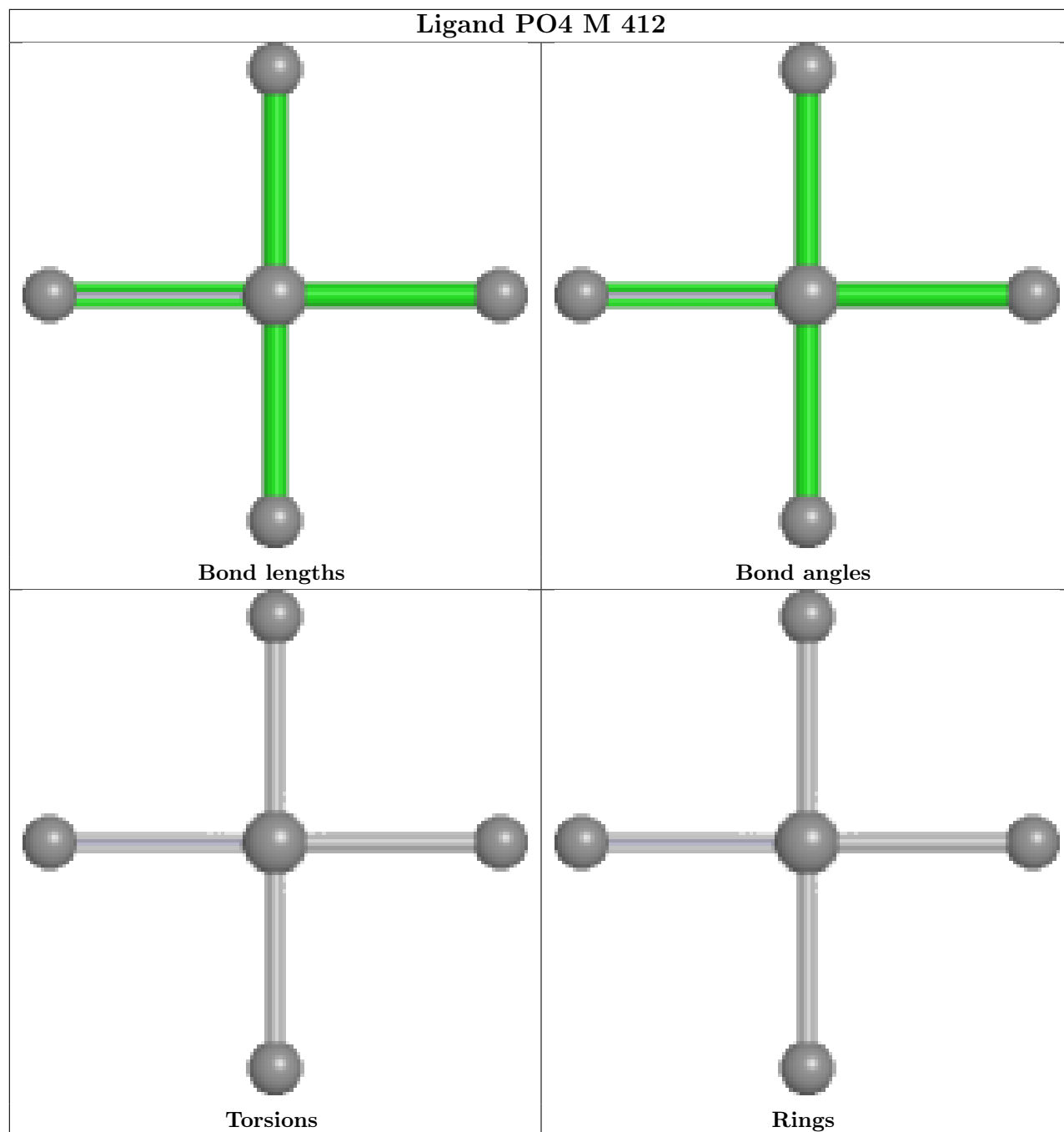
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	M	411	LDA	2	0
12	M	413	CIT	2	0
6	M	403	BCL	3	0
5	M	404	BPH	4	0
11	M	410[A]	SPN	3	0
5	L	301	BPH	1	0
6	L	302	BCL	1	0
4	H	303	LDA	1	0

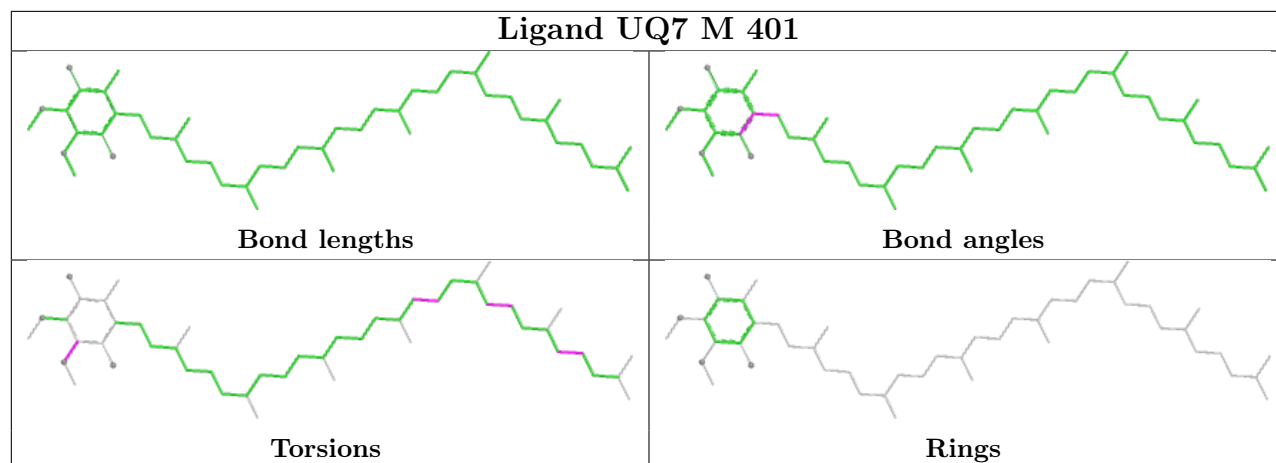
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

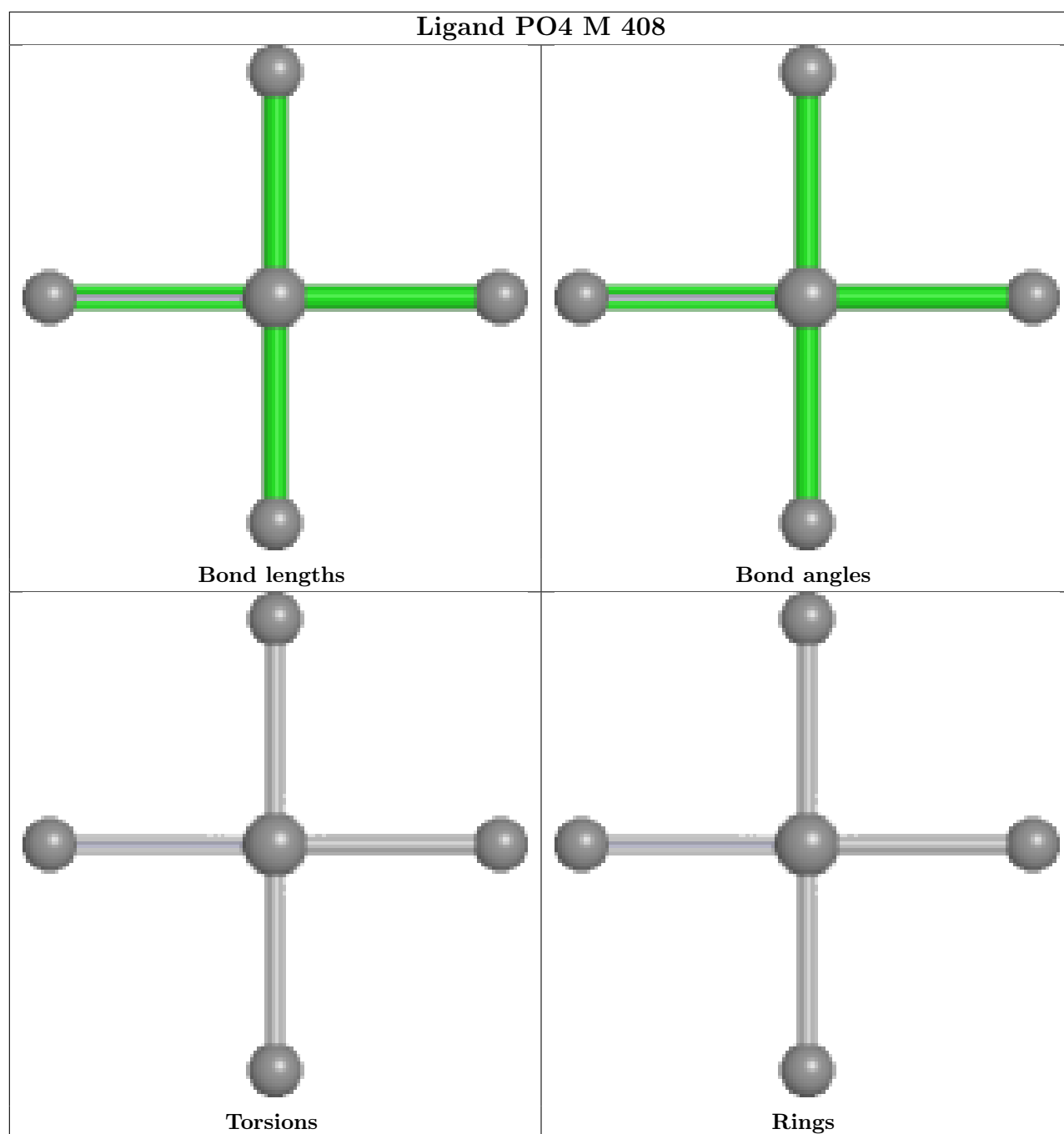


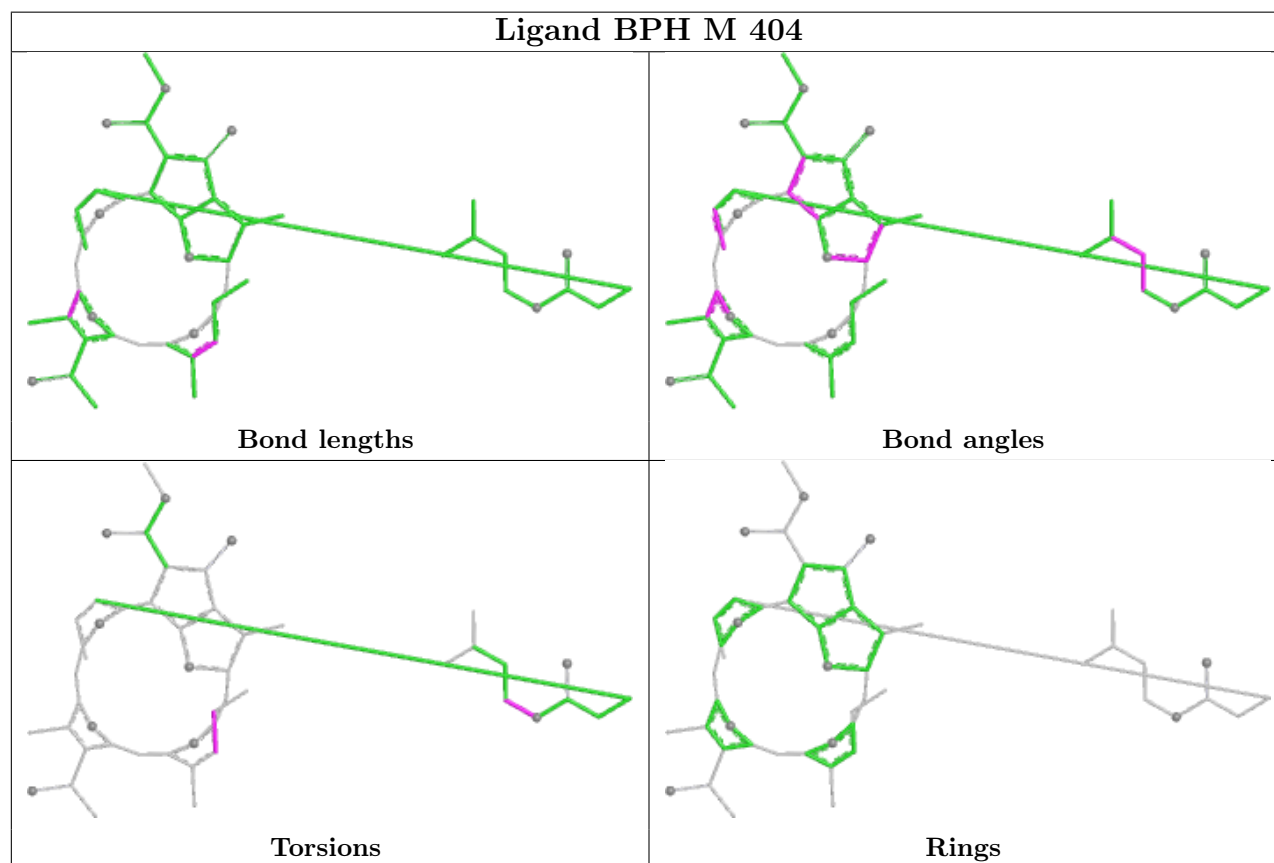
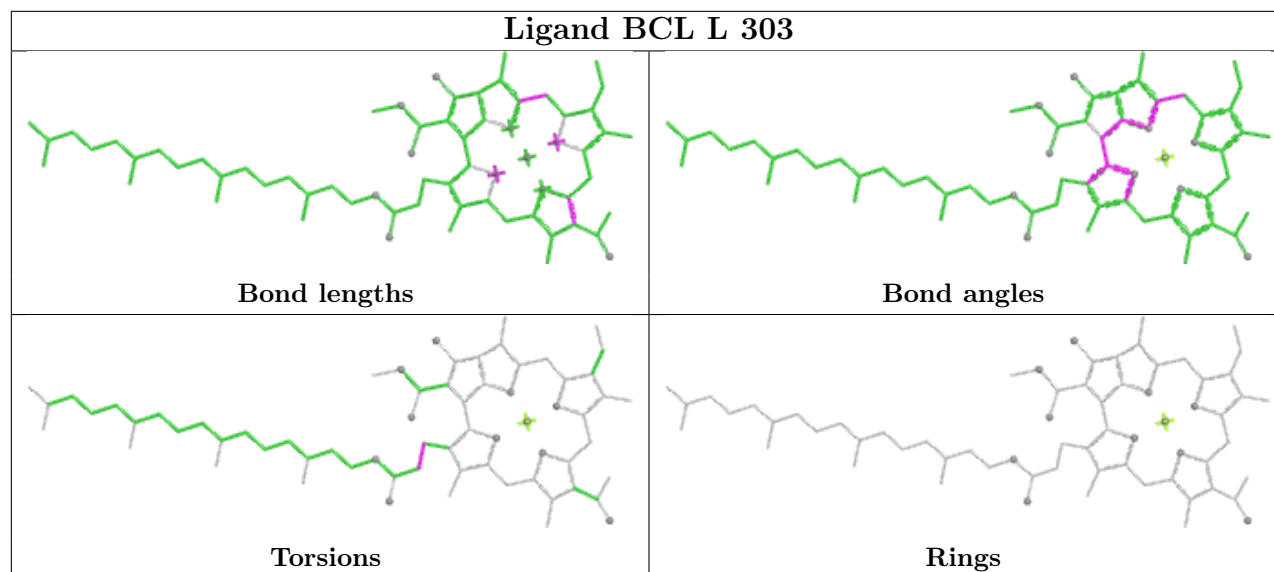


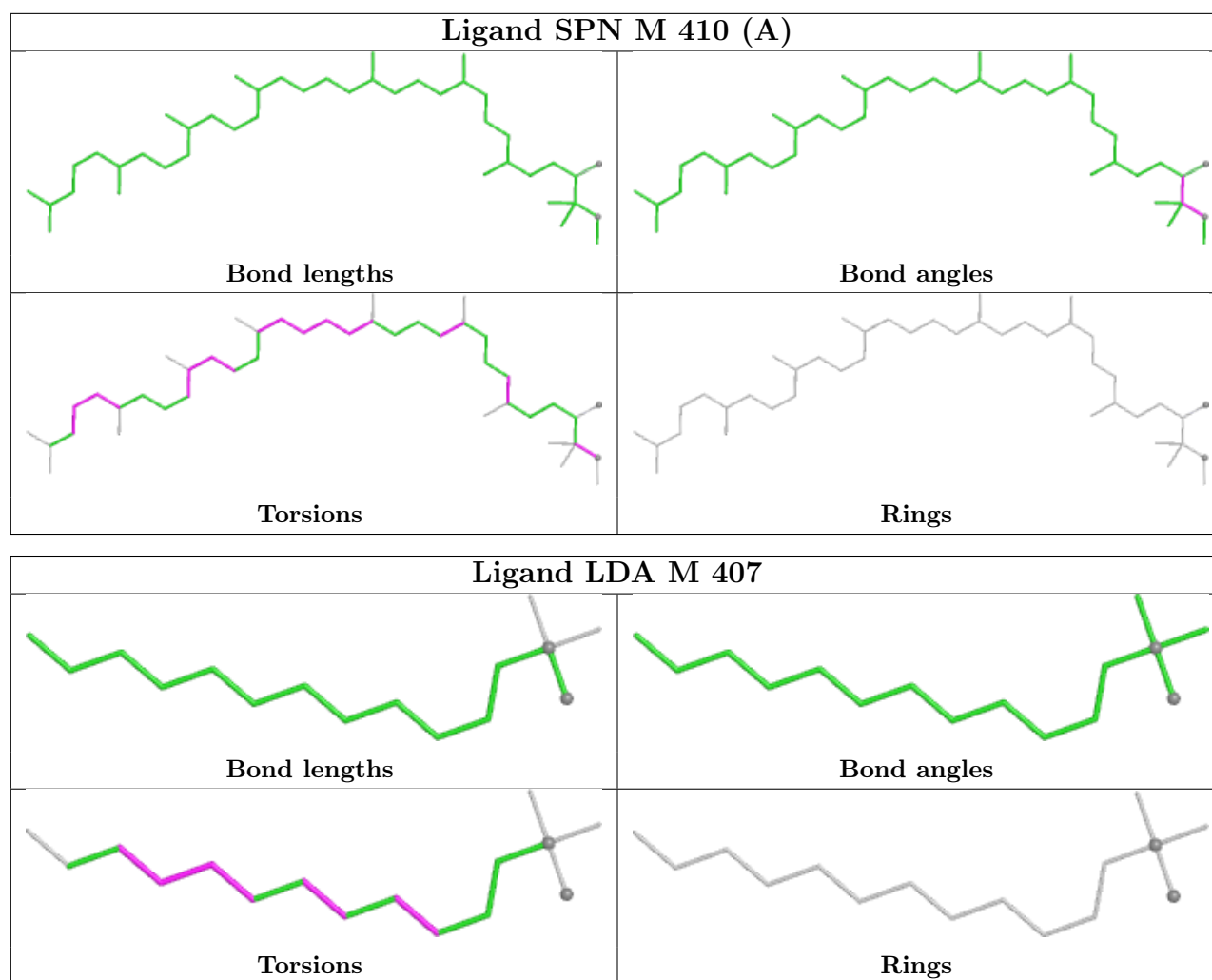




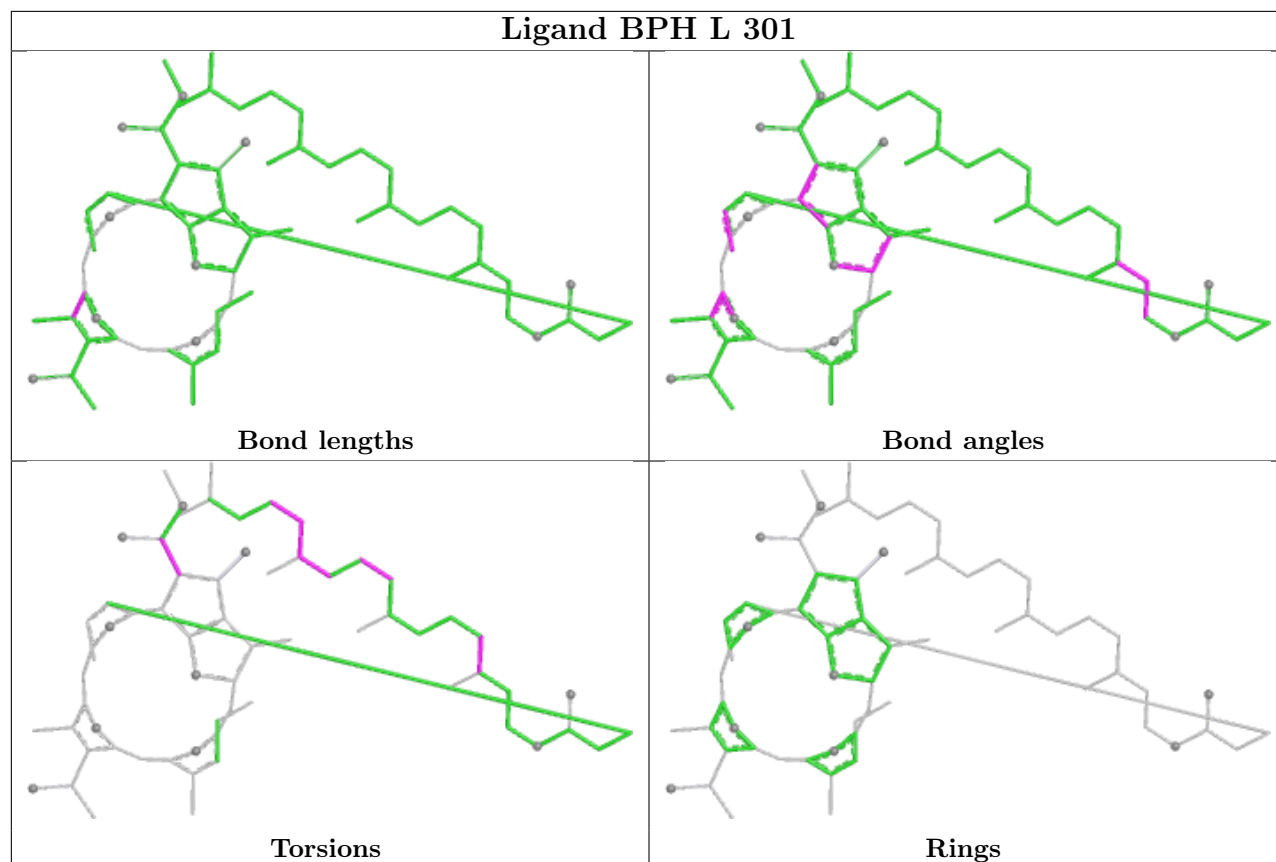




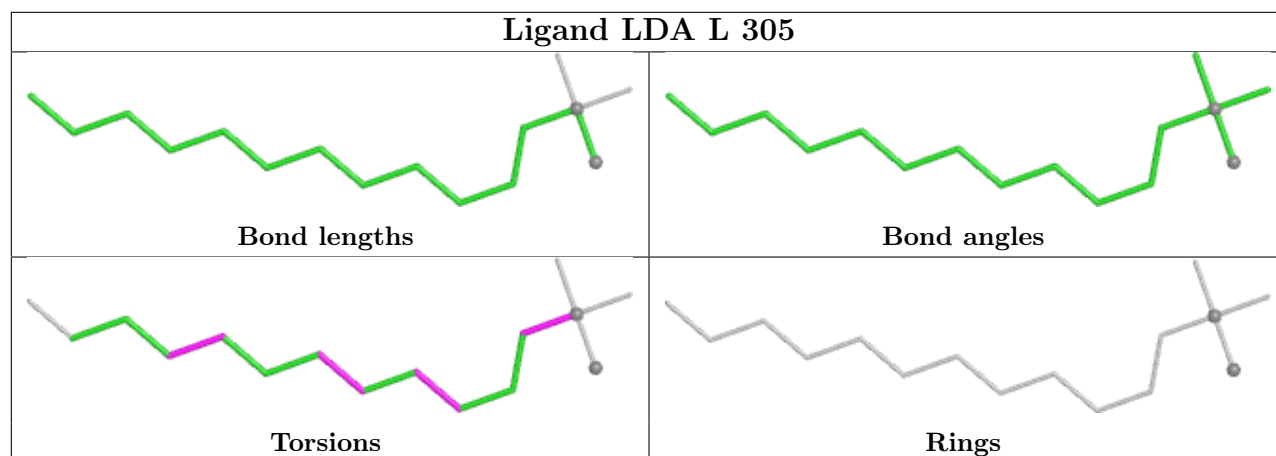




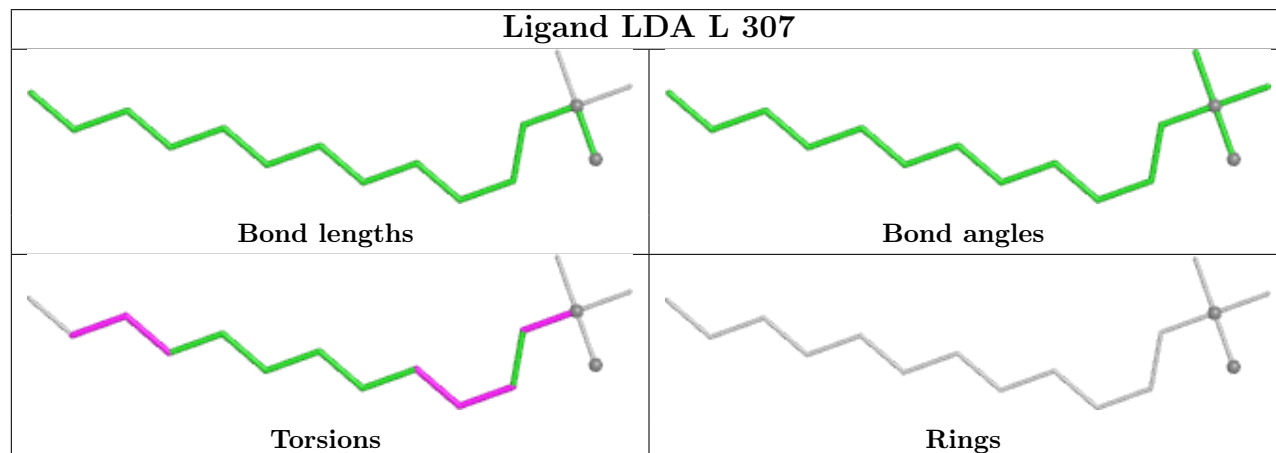
Ligand BPH L 301

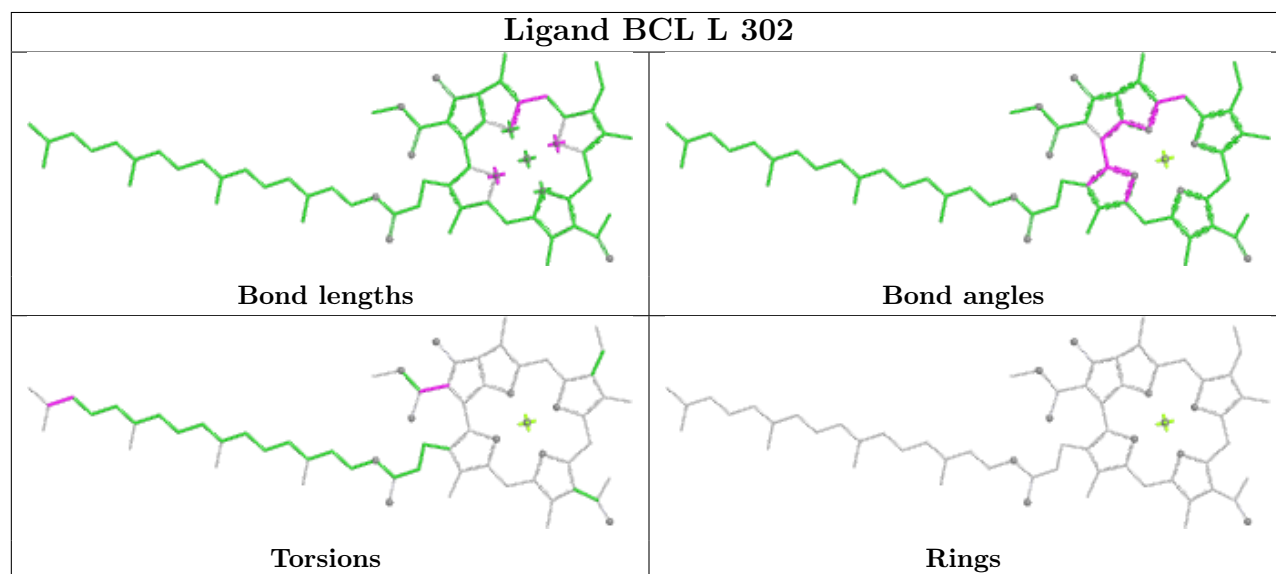
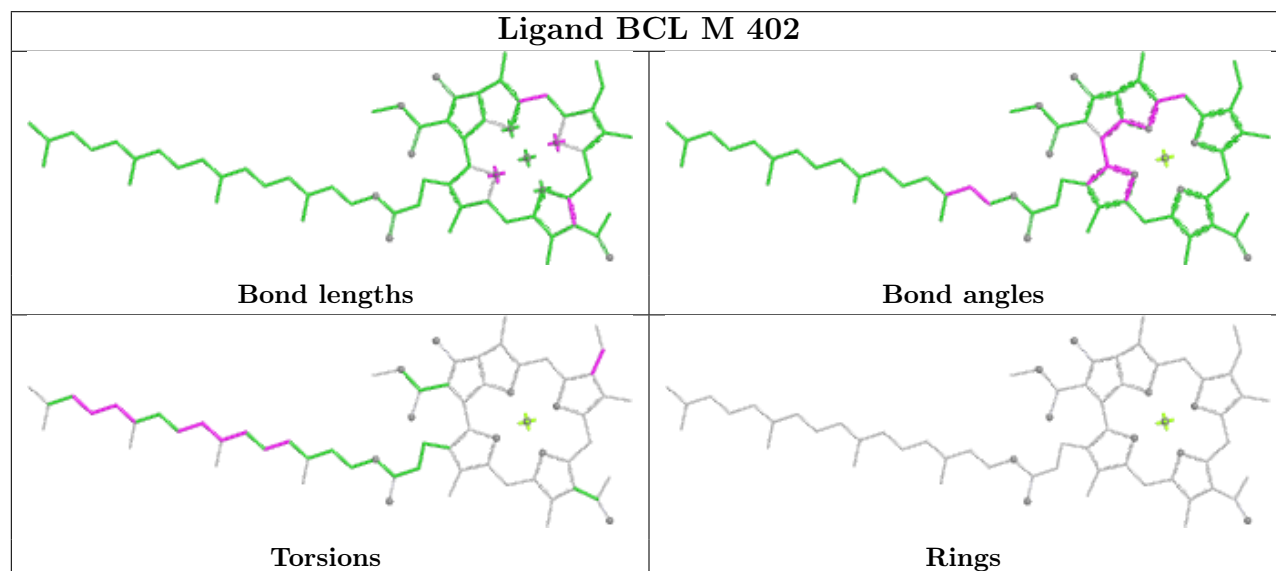
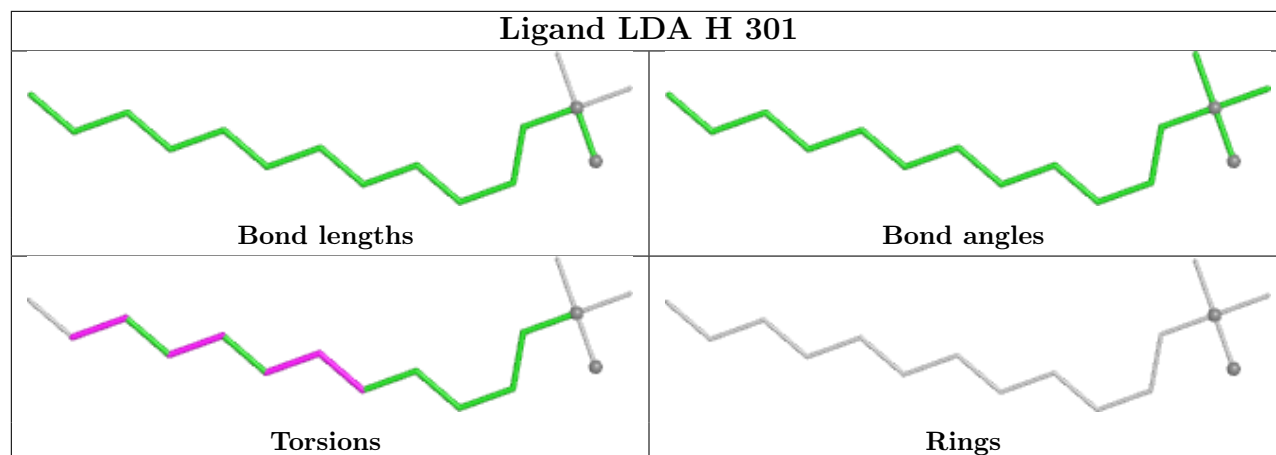


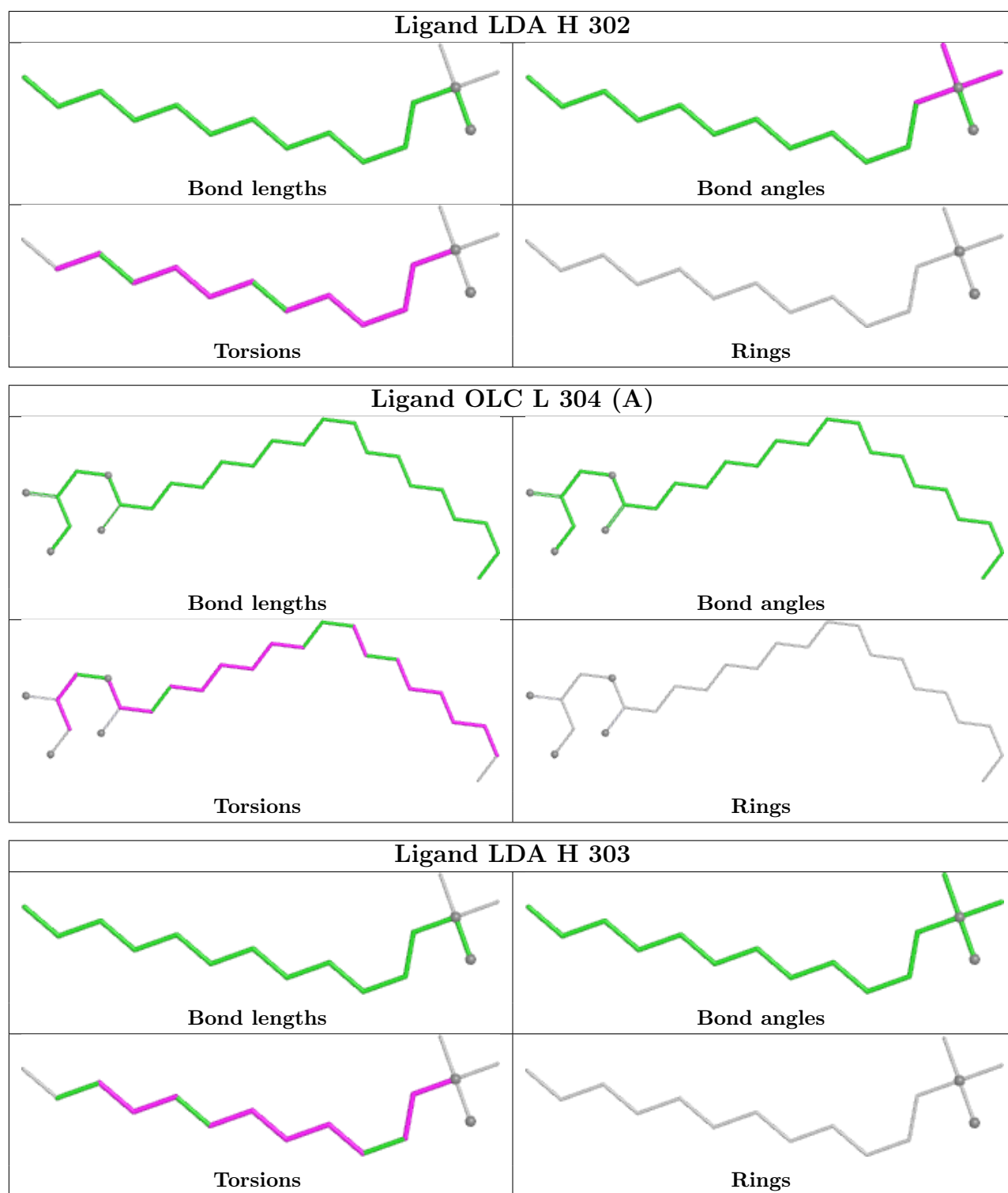
Ligand LDA L 305



Ligand LDA L 307







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, 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	H	240/241 (99%)	0.05	12 (5%) 34 33	20, 44, 79, 158	5 (2%)
2	L	281/281 (100%)	0.03	17 (6%) 27 27	23, 43, 102, 128	2 (0%)
3	M	300/302 (99%)	-0.07	9 (3%) 52 54	22, 42, 77, 100	4 (1%)
All	All	821/824 (99%)	-0.00	38 (4%) 37 38	20, 43, 83, 158	11 (1%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	51[A]	TRP	6.3
3	M	68[A]	PHE	5.9
3	M	148[A]	TRP	5.1
2	L	59	TRP	4.8
2	L	265	TRP	4.6
1	H	10	PHE	4.5
2	L	270	PRO	4.2
3	M	162[A]	PHE	4.1
1	H	249	LYS	4.0
1	H	184[A]	LYS	4.0
2	L	277	GLY	3.6
2	L	278	GLY	3.4
1	H	15[A]	LEU	3.3
2	L	271	TRP	3.2
1	H	247	LYS	3.1
2	L	40[A]	PHE	3.0
2	L	57	GLY	3.0
2	L	273	ALA	3.0
3	M	301	HIS	3.0
1	H	246	PRO	3.0
2	L	276	PRO	2.9
1	H	244	ALA	2.8
1	H	11	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
2	L	267	VAL	2.6
1	H	245	ALA	2.6
2	L	281	GLY	2.5
2	L	61	PRO	2.5
3	M	299	GLN	2.3
1	H	91	ALA	2.3
2	L	264	GLN	2.2
3	M	52	LEU	2.2
1	H	248	ARG	2.2
2	L	274	ASN	2.2
3	M	300	ASN	2.2
3	M	2	GLU	2.1
2	L	58	THR	2.1
3	M	67	PHE	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 oligosaccharides 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, 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
4	LDA	L	307	16/16	0.70	0.28	84,103,137,137	0
4	LDA	H	302	16/16	0.74	0.27	79,96,105,107	0
4	LDA	H	303	16/16	0.76	0.22	75,97,120,120	0
4	LDA	L	305	16/16	0.78	0.24	66,84,125,125	0
10	PO4	M	412	5/5	0.81	0.21	136,136,136,136	0
12	CIT	M	413	13/13	0.81	0.34	147,153,183,186	0
7	OLC	L	304[A]	25/25	0.82	0.25	47,66,84,85	65
7	OLC	L	304[B]	25/25	0.82	0.25	47,67,84,85	65

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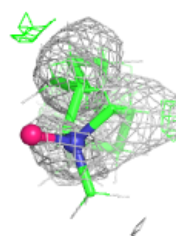
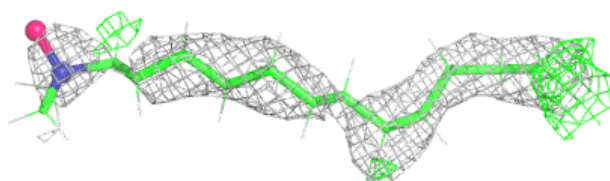
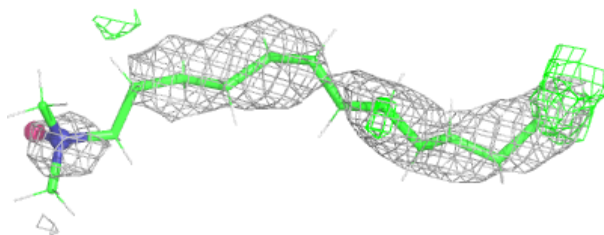
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	OLC	M	409[B]	25/25	0.82	0.29	55,72,87,89	65
4	LDA	M	406	16/16	0.82	0.26	61,84,124,127	0
4	LDA	M	407	16/16	0.82	0.20	45,66,83,85	0
4	LDA	M	411	16/16	0.84	0.22	69,100,147,148	0
4	LDA	L	306	16/16	0.85	0.22	65,84,111,112	0
11	SPN	M	410[A]	43/43	0.88	0.23	52,71,87,88	113
10	PO4	M	408	5/5	0.92	0.15	60,61,65,69	0
4	LDA	H	301	16/16	0.92	0.19	50,77,126,129	0
5	BPH	M	404	50/65	0.94	0.08	24,36,65,76	0
8	UQ7	M	401	48/48	0.94	0.14	27,61,107,112	0
6	BCL	M	403	52/66	0.94	0.09	26,36,57,62	0
6	BCL	M	402	66/66	0.95	0.09	29,39,84,87	0
6	BCL	L	302	66/66	0.96	0.09	25,39,80,82	0
6	BCL	L	303	66/66	0.96	0.09	24,36,99,119	0
5	BPH	L	301	65/65	0.96	0.08	19,36,56,61	0
13	CL	M	414	1/1	0.96	0.09	44,44,44,44	0
9	FE	M	405	1/1	0.99	0.09	36,36,36,36	0

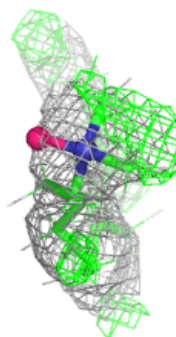
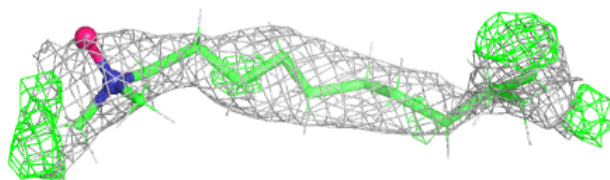
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around LDA L 307:

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

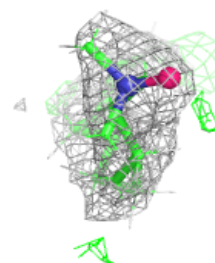
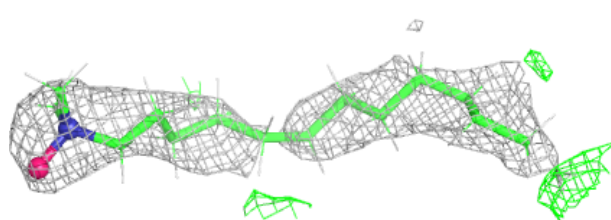
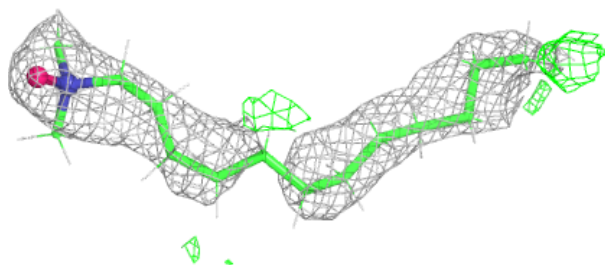
**Electron density around LDA H 302:**

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

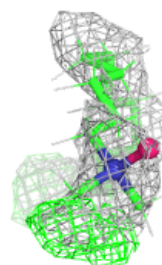
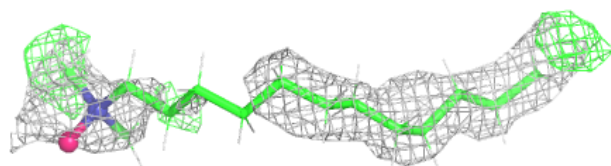
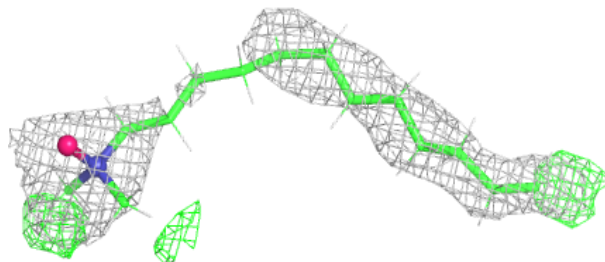


Electron density around LDA H 303:

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

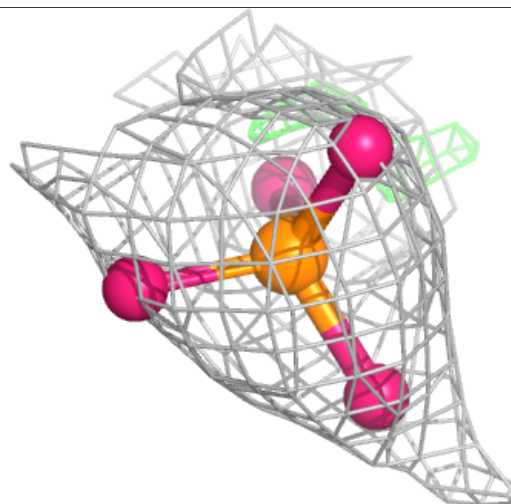
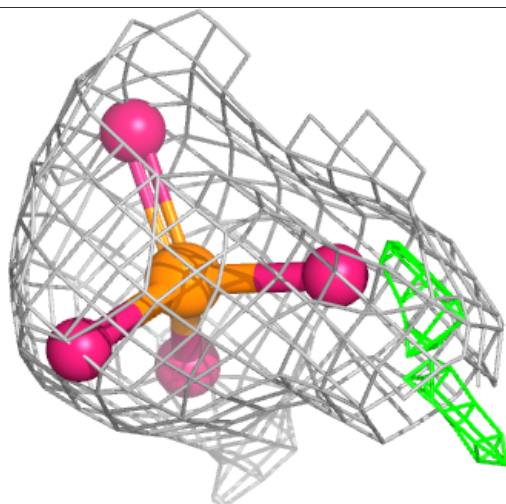
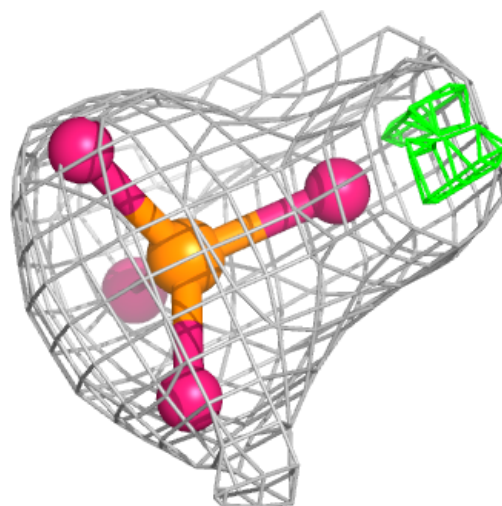
**Electron density around LDA L 305:**

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



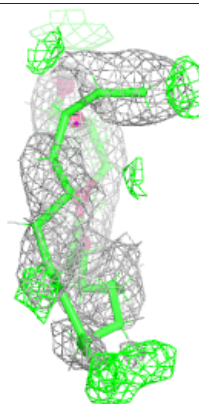
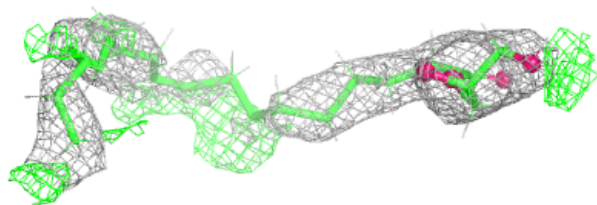
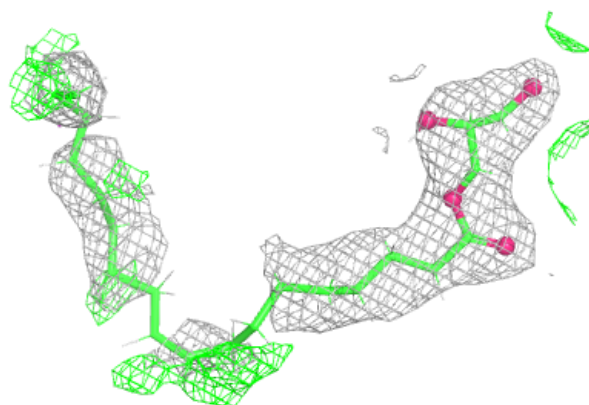
Electron density around PO4 M 412:

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

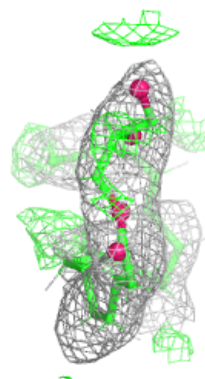
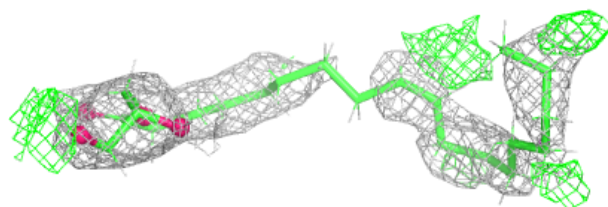
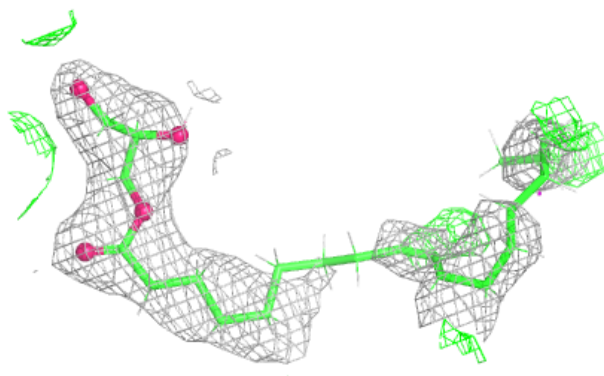


Electron density around OLC L 304 (A):

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

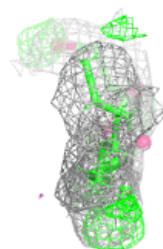
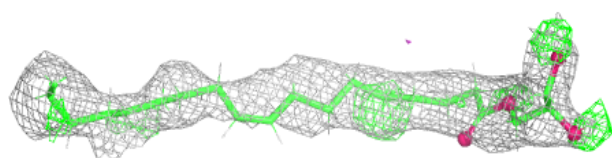
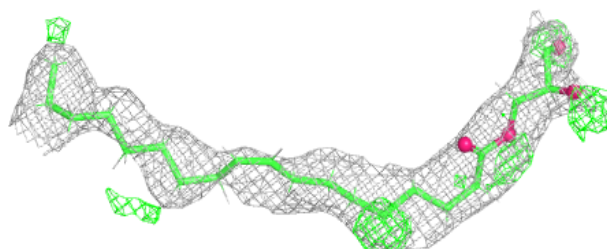
**Electron density around OLC L 304 (B):**

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

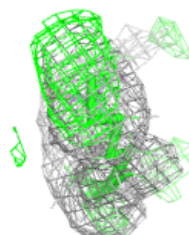
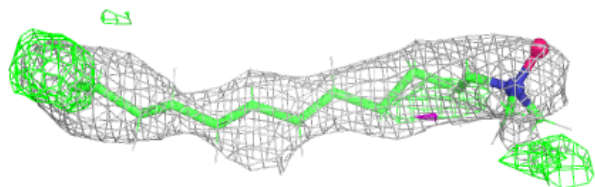
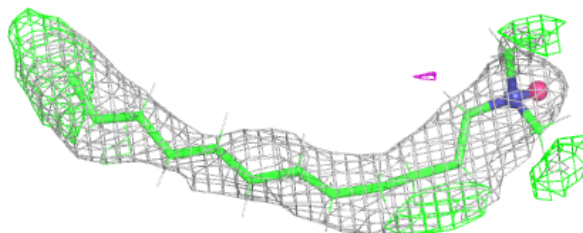


Electron density around OLC M 409 (B):

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

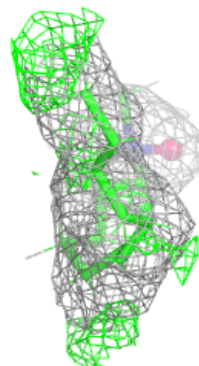
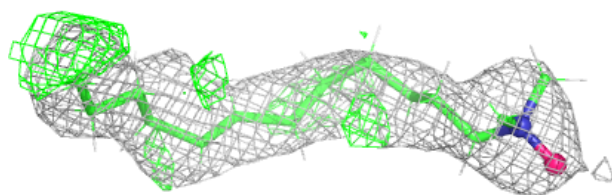
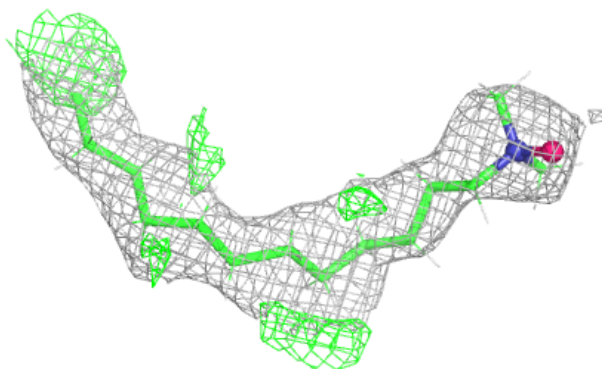
**Electron density around LDA M 406:**

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

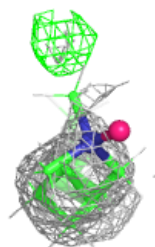
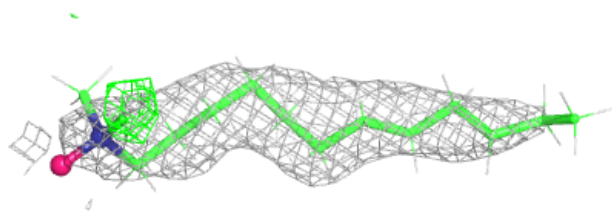
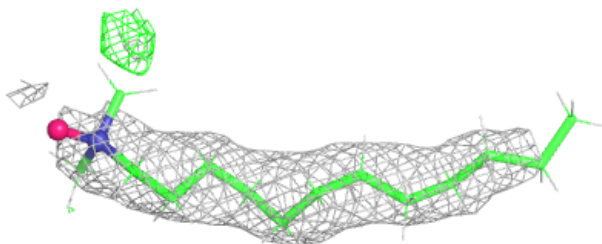


Electron density around LDA M 407:

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

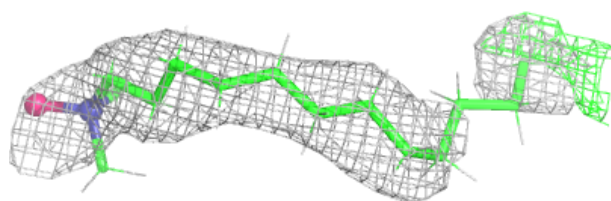
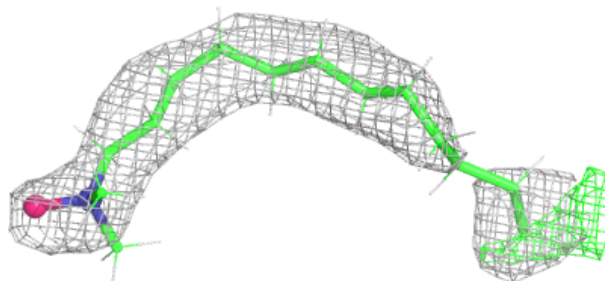
**Electron density around LDA M 411:**

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

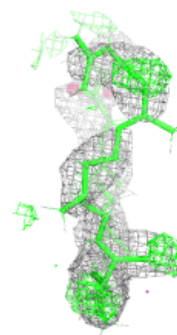
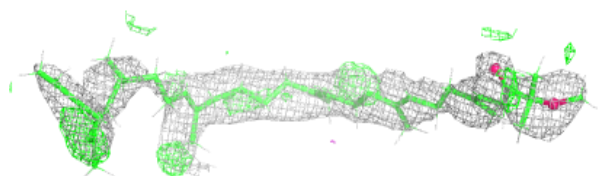
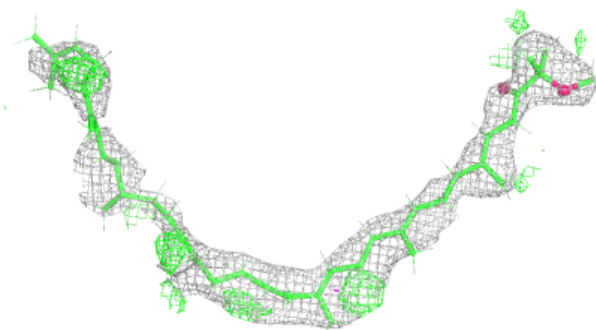


Electron density around LDA L 306:

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

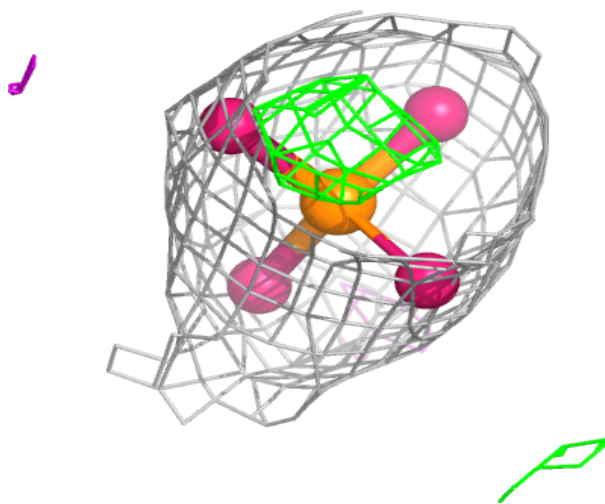
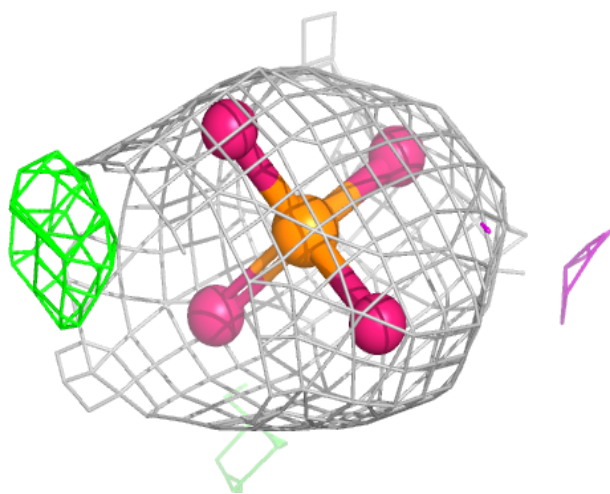
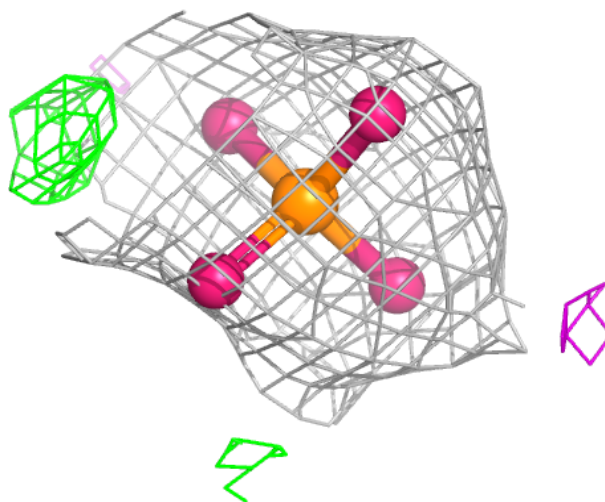
**Electron density around SPN M 410 (A):**

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



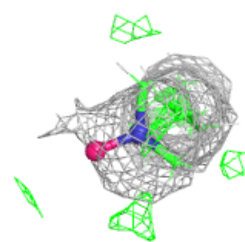
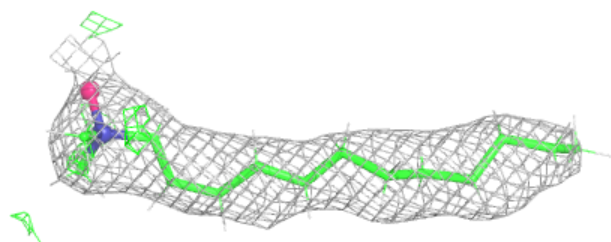
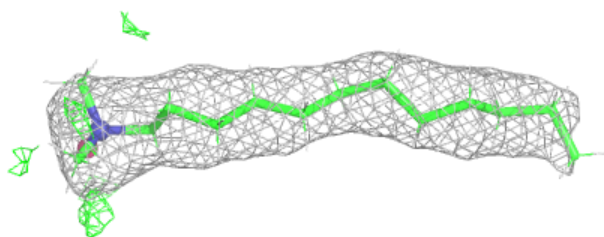
Electron density around PO4 M 408:

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

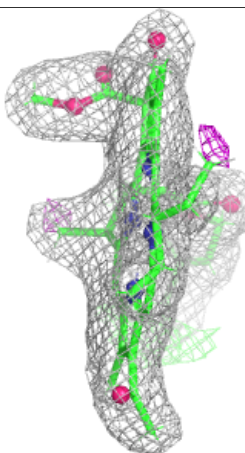
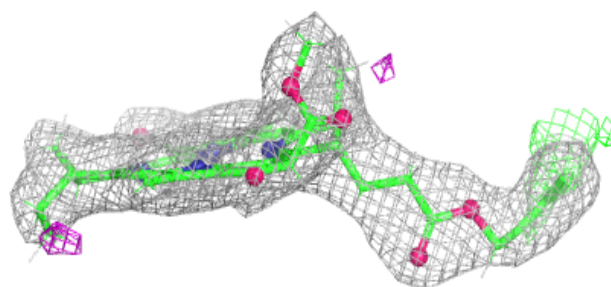
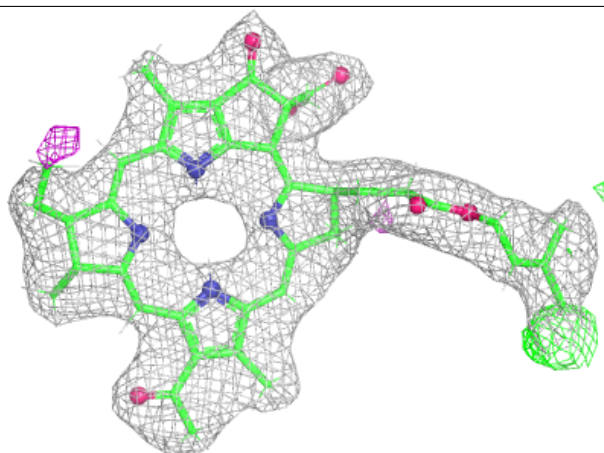


Electron density around LDA H 301:

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

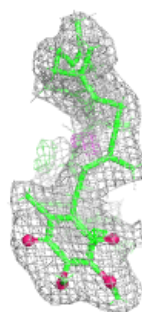
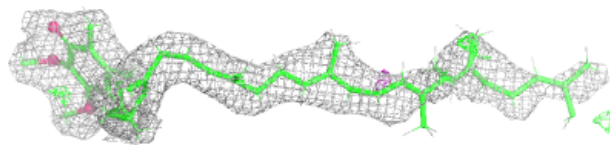
**Electron density around BPH M 404:**

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



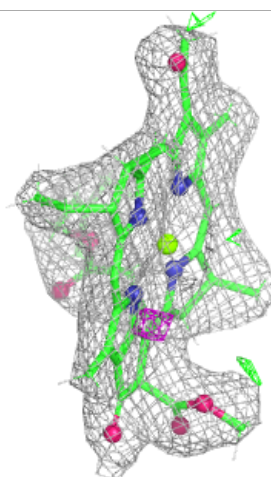
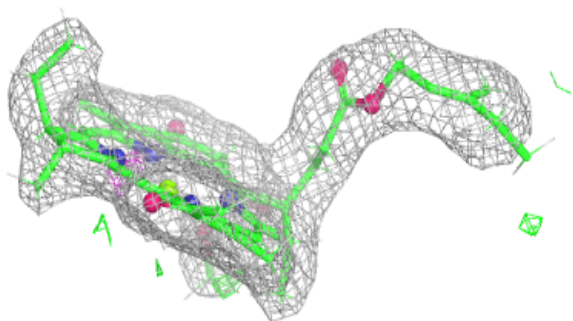
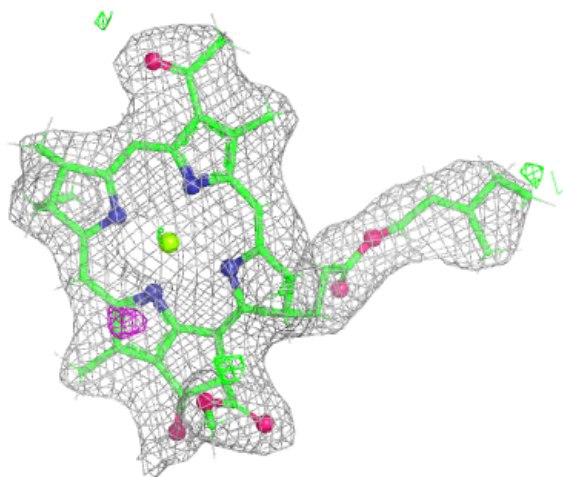
Electron density around UQ7 M 401:

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



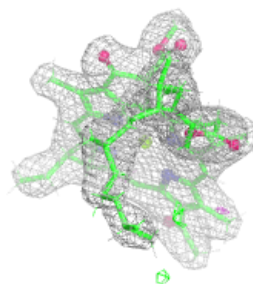
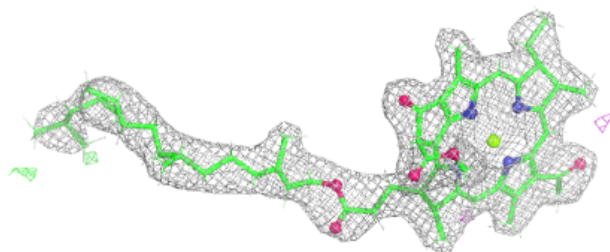
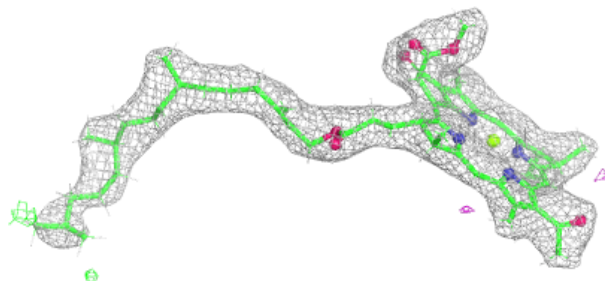
Electron density around BCL M 403:

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

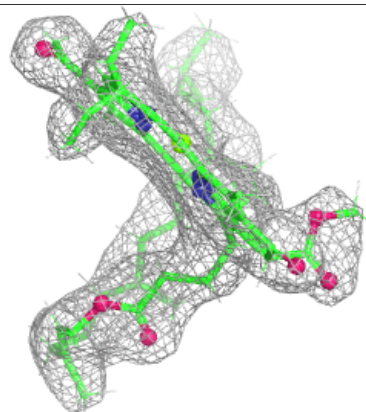
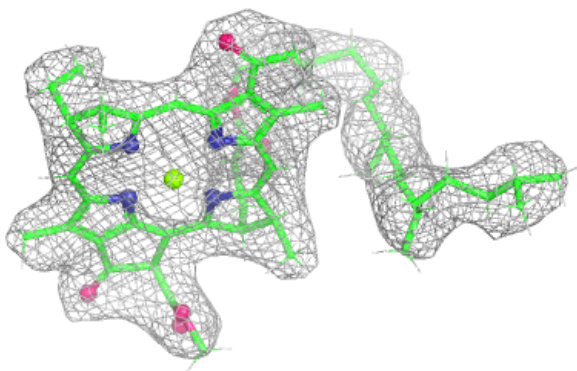
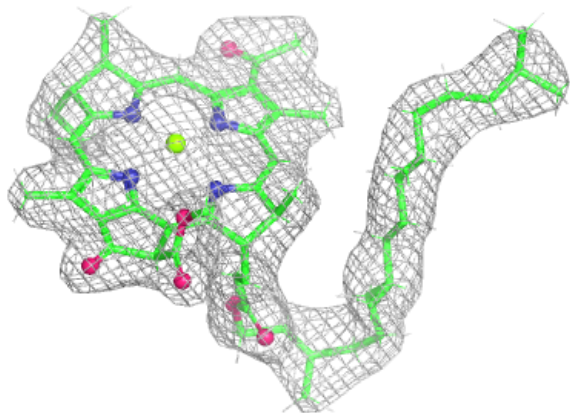


Electron density around BCL M 402:

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

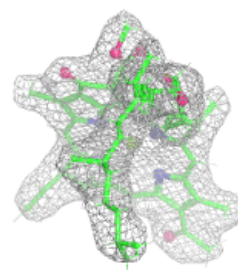
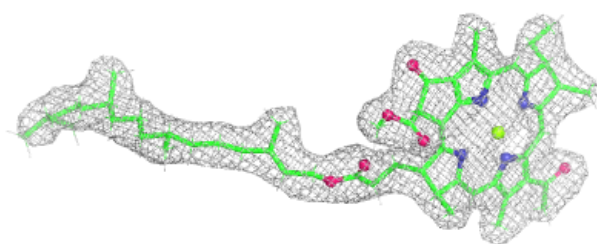
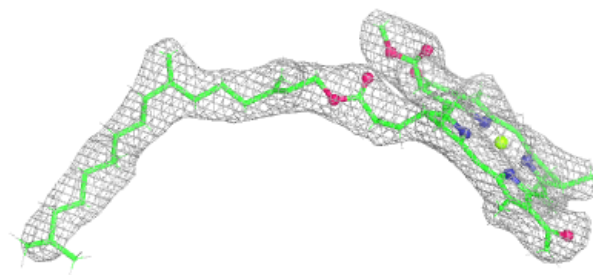
**Electron density around BCL L 302:**

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



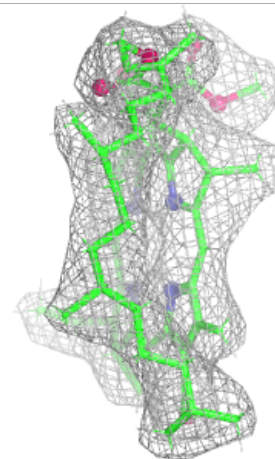
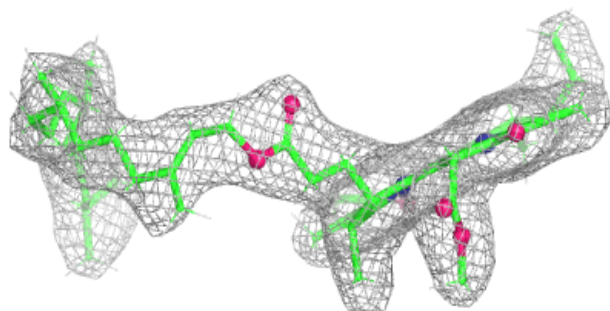
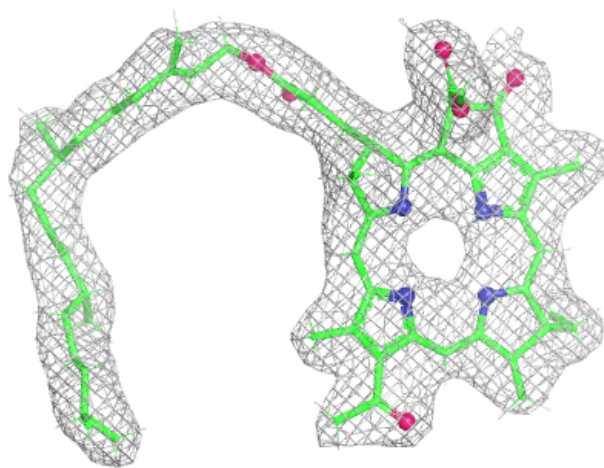
Electron density around BCL L 303:

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



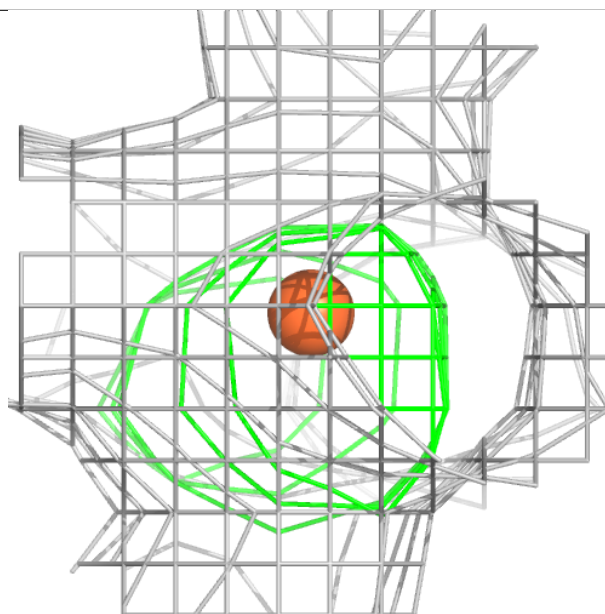
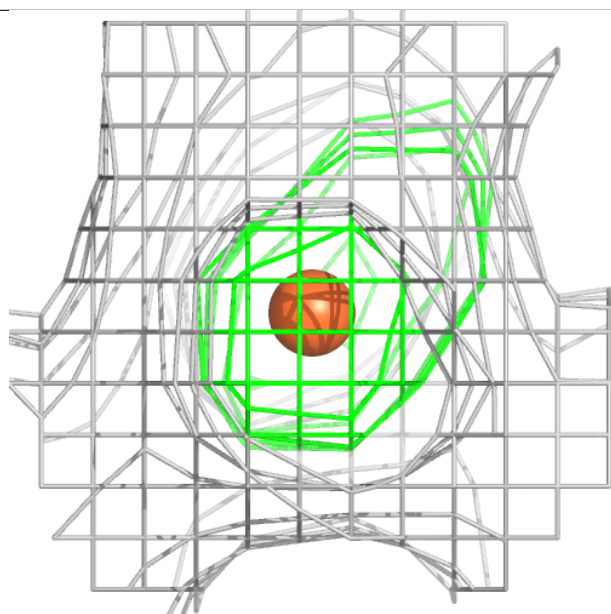
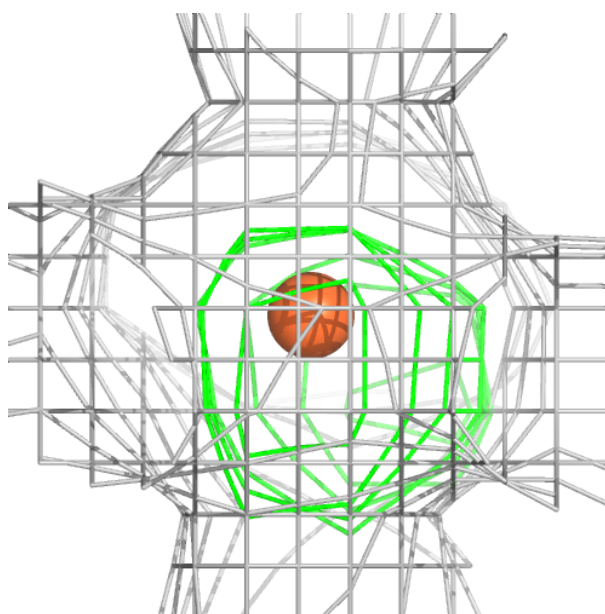
Electron density around BPH L 301:

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



Electron density around FE M 405:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.