



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 09:04 AM EDT

PDB ID : 1PRC / pdb_00001prc
Title : CRYSTALLOGRAPHIC REFINEMENT AT 2.3 ANGSTROMS RESOLUTION AND REFINED MODEL OF THE PHOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS
Authors : Deisenhofer, J.; Epp, O.; Miki, K.; Huber, R.; Michel, H.
Deposited on : 1988-02-04
Resolution : 2.30 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) 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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

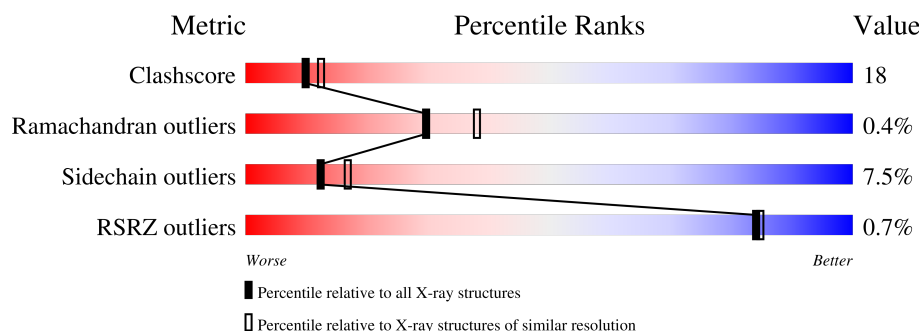
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	C	336	
2	L	273	
3	M	323	
4	H	258	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	HEC	C	609	X	-	-	-
5	HEC	C	610	X	-	-	-
5	HEC	C	611	X	-	-	-
5	HEC	C	612	X	-	-	-
6	BCB	L	602	X	-	-	-
6	BCB	L	604	X	-	-	-
6	BCB	M	601	X	-	-	-
6	BCB	M	603	X	-	-	-
8	UQ1	L	614	-	-	X	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 10288 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 PHOTOSYNTHETIC REACTION CENTER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	333	Total	C	N	O	S	54	0	1
			2603	1640	467	478	18			

- Molecule 2 is a protein called PHOTOSYNTHETIC REACTION CENTER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	273	Total	C	N	O	S	13	0	0
			2171	1459	350	355	7			

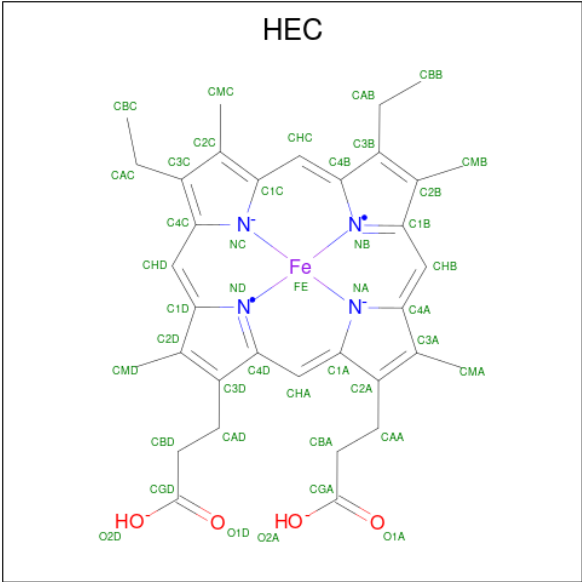
- Molecule 3 is a protein called PHOTOSYNTHETIC REACTION CENTER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	323	Total	C	N	O	S	26	0	0
			2555	1702	419	423	11			

- Molecule 4 is a protein called PHOTOSYNTHETIC REACTION CENTER.

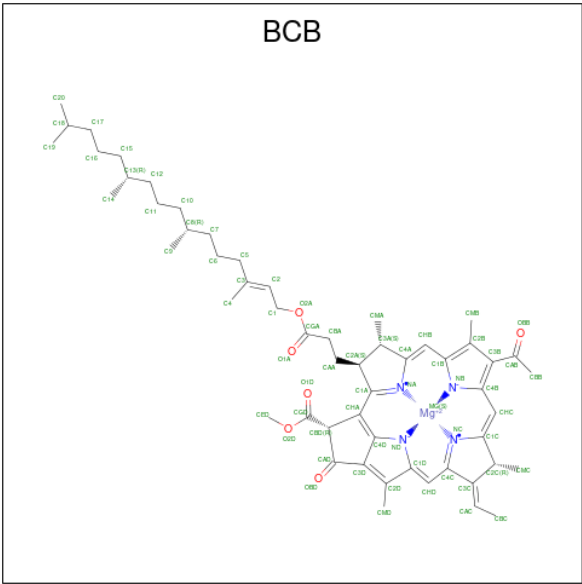
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	258	Total	C	N	O	S	106	0	0
			2018	1292	344	380	2			

- Molecule 5 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



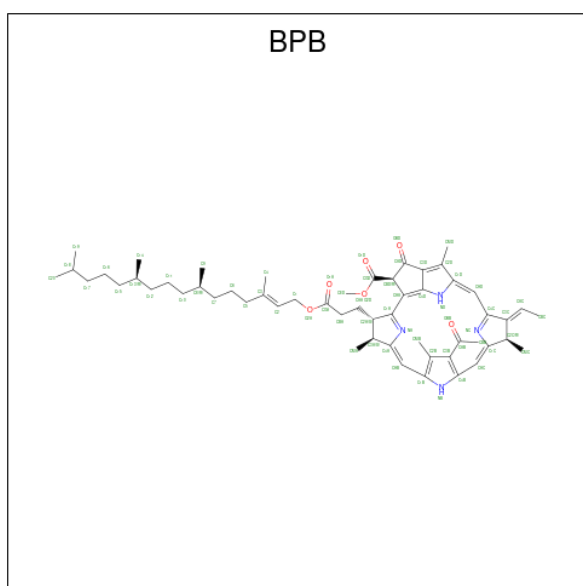
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
5	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 6 is BACTERIOCHLOROPHYLL B (CCD ID: BCB) (formula: C₅₅H₇₂MgN₄O₆).



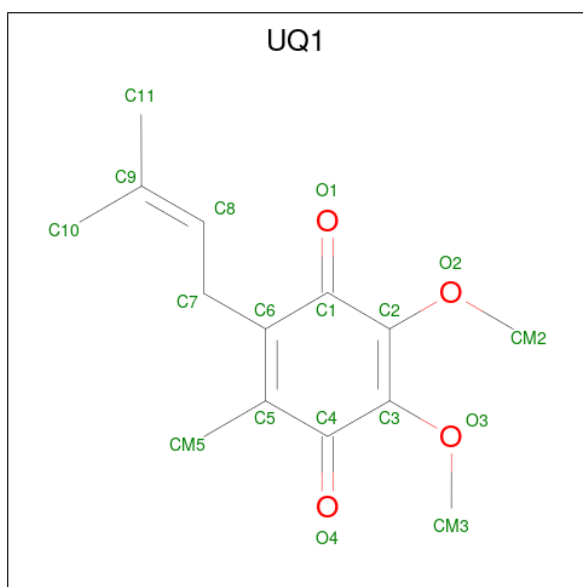
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
6	L	1	Total 66	C 55	Mg 1	N 4	O 6	0	0
6	M	1	Total 66	C 55	Mg 1	N 4	O 6	13	0
6	M	1	Total 66	C 55	Mg 1	N 4	O 6	0	0

- Molecule 7 is BACTERIOPHEOPHYTIN B (CCD ID: BPB) (formula: $C_{55}H_{74}N_4O_6$).



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

- Molecule 8 is UBIQUINONE-1 (CCD ID: UQ1) (formula: $C_{14}H_{18}O_4$).

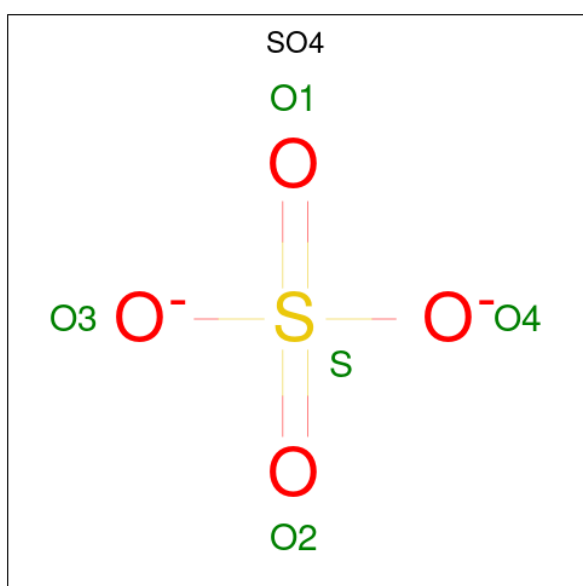


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	L	1	Total	C	O	0	0
			18	14	4		

- Molecule 9 is FE (III) ION (CCD ID: FE) (formula: Fe).

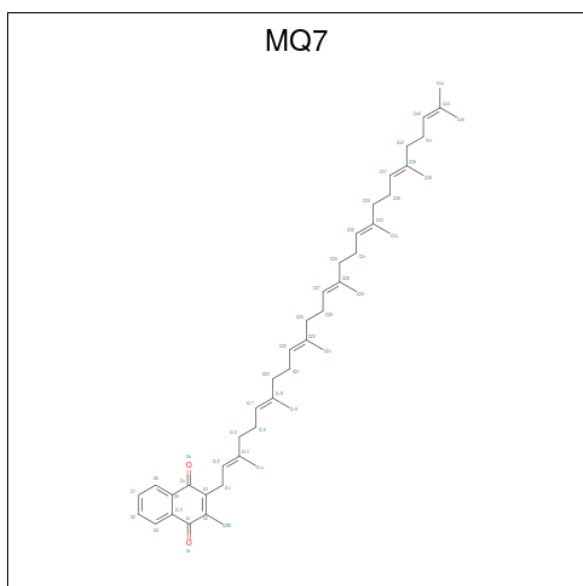
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	M	1	Total	Fe	0	0
			1	1		

- Molecule 10 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



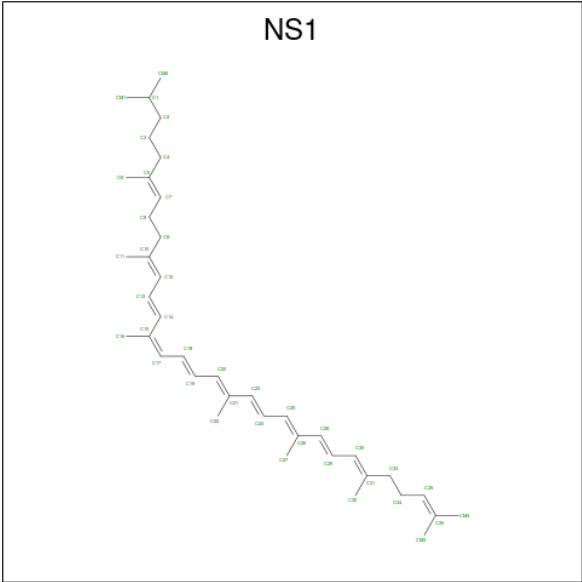
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	M	1	Total	O	S	0	0
			5	4	1		
10	M	1	Total	O	S	0	0
			5	4	1		
10	M	1	Total	O	S	0	0
			5	4	1		
10	M	1	Total	O	S	0	0
			5	4	1		
10	H	1	Total	O	S	0	0
			5	4	1		
10	H	1	Total	O	S	0	0
			5	4	1		
10	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 11 is MENAQUINONE-7 (CCD ID: MQ7) (formula: $C_{46}H_{64}O_2$).



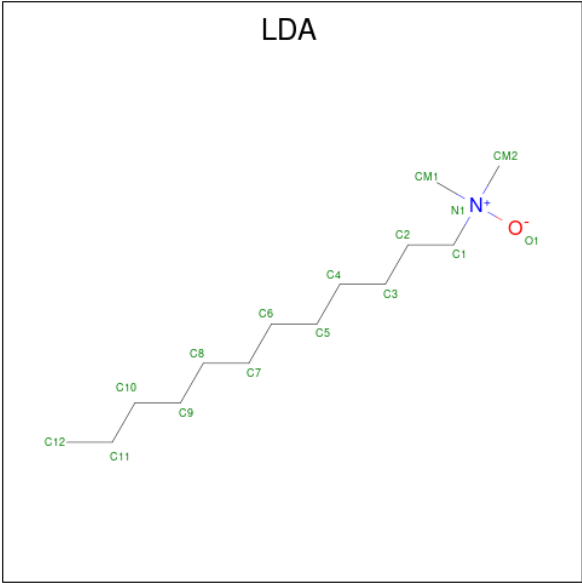
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	M	1	Total	C	O	4	0
			48	46	2		

- Molecule 12 is 15-trans-1,2-dihydroneurosporene (CCD ID: NS1) (formula: $C_{40}H_{60}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	M	1	Total	C		14	0
			40	40			

- Molecule 13 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: $C_{14}H_{31}NO$).



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

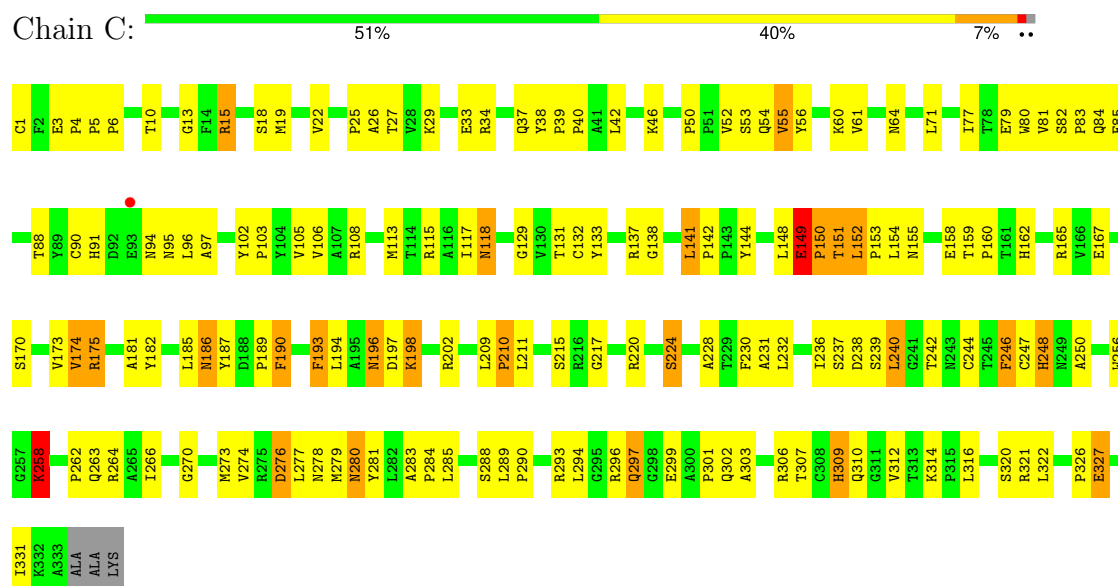
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	C	66	Total 66	O 66	0	0
14	L	39	Total 39	O 39	0	0
14	M	55	Total 55	O 55	0	0
14	H	41	Total 41	O 41	0	0

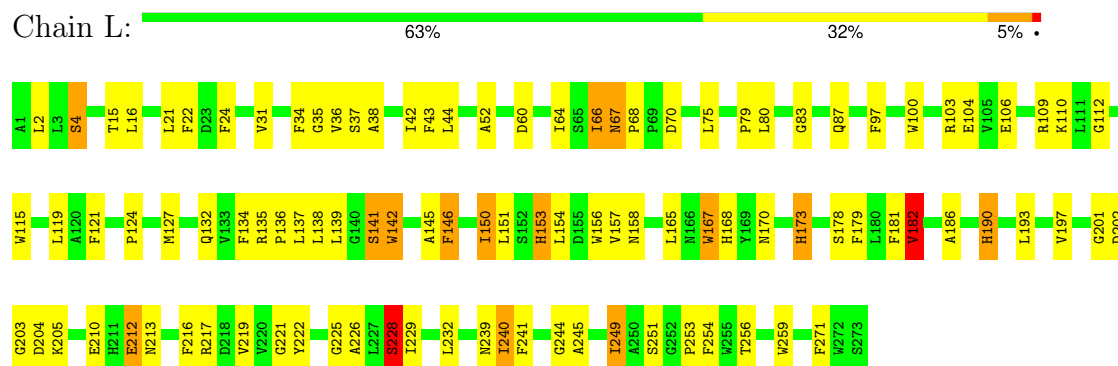
3 Residue-property plots

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.

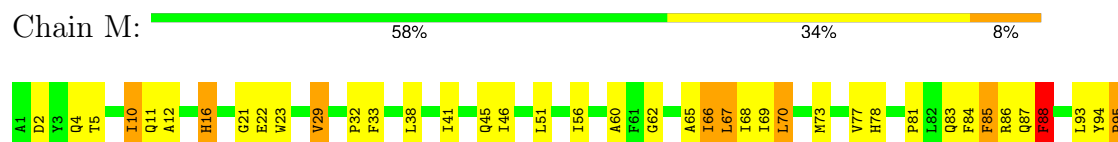
• Molecule 1: PHOTOSYNTHETIC REACTION CENTER

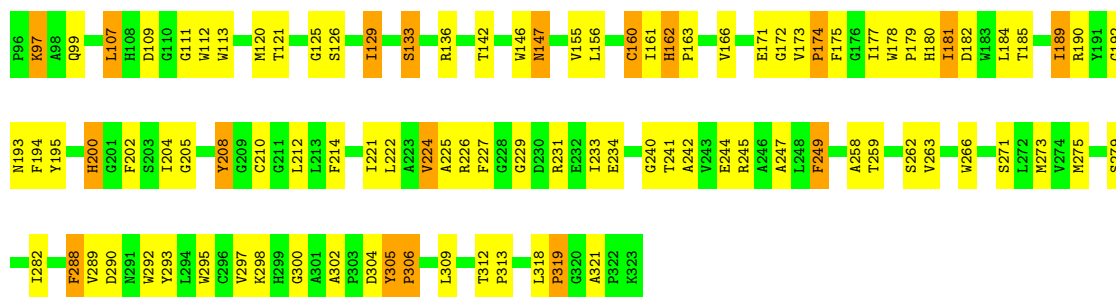


• Molecule 2: PHOTOSYNTHETIC REACTION CENTER

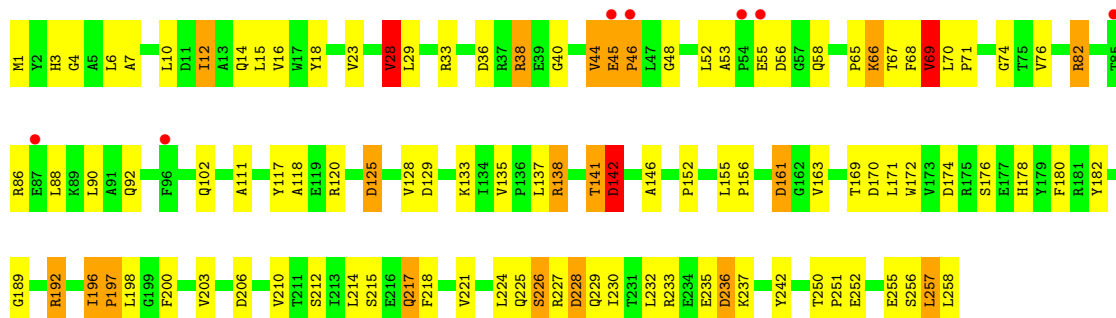


• Molecule 3: PHOTOSYNTHETIC REACTION CENTER





● Molecule 4: PHOTOSYNTHETIC REACTION CENTER



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	223.50Å 223.50Å 113.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.30 19.99 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (19.99-2.30) 75.3 (19.99-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.193 , (Not available) 0.186 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	22.4	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 60.8	EDS
L-test for twinning ¹	$\langle L \rangle = 0.32$, $\langle L^2 \rangle = 0.15$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10288	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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: FE, UQ1, MQ7, BCB, LDA, NS1, BPB, FME, SO4, HEC

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	C	1.28	3/2670 (0.1%)	1.91	67/3639 (1.8%)
2	L	1.32	2/2259 (0.1%)	1.77	36/3084 (1.2%)
3	M	1.28	2/2659 (0.1%)	1.82	65/3637 (1.8%)
4	H	1.32	3/2055 (0.1%)	1.97	59/2807 (2.1%)
All	All	1.30	10/9643 (0.1%)	1.87	227/13167 (1.7%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	167	TRP	N-CA	-6.09	1.38	1.46
3	M	208	TYR	N-CA	-5.79	1.39	1.46
3	M	180	HIS	CE1-NE2	5.55	1.38	1.32
4	H	118	ALA	N-CA	-5.50	1.39	1.45
4	H	255	GLU	CD-OE2	5.40	1.35	1.25

The worst 5 of 227 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	129	ASP	CA-CB-CG	-11.46	101.14	112.60
1	C	81	VAL	N-CA-C	10.65	120.44	110.74
3	M	161	ILE	N-CA-C	10.20	121.07	110.36
2	L	254	PHE	CA-CB-CG	-9.98	103.82	113.80
3	M	290	ASP	CA-CB-CG	9.95	122.55	112.60

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	C	2603	0	2579	92	0
2	L	2171	0	2098	82	0
3	M	2555	0	2452	88	0
4	H	2018	0	2020	58	0
5	C	172	0	122	19	0
6	L	132	0	144	22	0
6	M	132	0	144	21	0
7	L	65	0	74	8	0
7	M	65	0	74	11	0
8	L	18	0	18	8	0
9	M	1	0	0	0	0
10	H	15	0	0	0	0
10	M	20	0	0	0	0
11	M	48	0	64	1	0
12	M	40	0	59	4	0
13	H	16	0	31	2	0
13	M	16	0	31	1	0
14	C	66	0	0	5	0
14	H	41	0	0	1	0
14	L	39	0	0	3	0
14	M	55	0	0	3	0
All	All	10288	0	9910	340	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 18.

The worst 5 of 340 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)
3:M:120:MET:HE2	6:M:603:BCB:H172	1.40	1.02
3:M:136:ARG:HE	3:M:136:ARG:HA	1.31	0.93
1:C:152:LEU:HD22	1:C:175:ARG:HA	1.53	0.90
7:L:606:BPB:HBBB	7:L:606:BPB:HHC	1.52	0.90
6:L:602:BCB:H61	6:L:604:BCB:HBB3	1.55	0.88

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	331/336 (98%)	306 (92%)	24 (7%)	1 (0%)	36	46
2	L	271/273 (99%)	252 (93%)	18 (7%)	1 (0%)	30	38
3	M	321/323 (99%)	300 (94%)	19 (6%)	2 (1%)	21	27
4	H	256/258 (99%)	239 (93%)	16 (6%)	1 (0%)	30	38
All	All	1179/1190 (99%)	1097 (93%)	77 (6%)	5 (0%)	30	38

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	M	22	GLU
4	H	53	ALA
3	M	88	PHE
1	C	250	ALA
2	L	31	VAL

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	C	281/282 (100%)	258 (92%)	23 (8%)	10	14
2	L	218/218 (100%)	207 (95%)	11 (5%)	22	33
3	M	249/249 (100%)	231 (93%)	18 (7%)	13	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	H	212/212 (100%)	192 (91%)	20 (9%)	8 11
All	All	960/961 (100%)	888 (92%)	72 (8%)	12 17

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	56	ASP
4	H	258	LEU
4	H	82	ARG
4	H	196	ILE
2	L	4	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	214	GLN
2	L	239	ASN
4	H	229	GLN
4	H	3	HIS
2	L	144	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	FME	H	1	4	8,9,10	0.96	1 (12%)	8,9,11	2.54	3 (37%)

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	FME	H	1	4	-	2/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1	FME	CA-N	-2.45	1.43	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	1	FME	CA-N-CN	-4.40	116.05	122.82
4	H	1	FME	O1-CN-N	-4.10	114.72	125.32
4	H	1	FME	C-CA-N	3.01	115.31	109.50

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	1	FME	O1-CN-N-CA
4	H	1	FME	CB-CG-SD-CE

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 1 is monoatomic - leaving 22 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	HEC	C	611	1	50,50,50	1.65	15 (30%)	68,82,82	1.67	10 (14%)
5	HEC	C	610	1	50,50,50	2.01	15 (30%)	68,82,82	1.43	12 (17%)
6	BCB	L	602	2	68,74,74	1.36	7 (10%)	77,115,115	1.84	24 (31%)
6	BCB	M	603	3	68,74,74	1.72	15 (22%)	77,115,115	1.91	19 (24%)
5	HEC	C	609	1	50,50,50	1.90	12 (24%)	68,82,82	1.52	16 (23%)
7	BPB	M	605	-	57,70,70	1.81	15 (26%)	55,101,101	1.68	8 (14%)
10	SO4	M	621	-	4,4,4	1.06	0	6,6,6	0.20	0
10	SO4	H	617	-	4,4,4	0.94	0	6,6,6	0.18	0
10	SO4	M	619	-	4,4,4	0.87	0	6,6,6	0.21	0
13	LDA	M	615	-	13,15,15	2.61	2 (15%)	14,17,17	1.77	5 (35%)
10	SO4	M	620	-	4,4,4	0.71	0	6,6,6	0.17	0
8	UQ1	L	614	-	18,18,18	0.80	1 (5%)	24,25,25	1.33	3 (12%)
6	BCB	M	601	3	68,74,74	1.50	11 (16%)	77,115,115	1.54	15 (19%)
10	SO4	H	622	-	4,4,4	0.97	0	6,6,6	0.25	0
11	MQ7	M	608	-	49,49,49	1.44	5 (10%)	61,63,63	2.37	21 (34%)
7	BPB	L	606	-	57,70,70	1.91	13 (22%)	55,101,101	2.32	19 (34%)
10	SO4	M	618	-	4,4,4	0.87	0	6,6,6	0.24	0
13	LDA	H	616	-	13,15,15	2.84	2 (15%)	14,17,17	0.77	0
6	BCB	L	604	2	68,74,74	1.73	12 (17%)	77,115,115	1.59	14 (18%)
5	HEC	C	612	1	50,50,50	1.76	13 (26%)	68,82,82	1.47	10 (14%)
10	SO4	H	623	-	4,4,4	0.97	0	6,6,6	0.45	0
12	NS1	M	613	-	39,39,39	2.09	11 (28%)	46,46,46	2.27	17 (36%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	HEC	C	611	1	1/1/3/7	7/14/54/54	-
5	HEC	C	610	1	1/1/3/7	6/14/54/54	-
13	LDA	M	615	-	-	7/13/13/13	-
6	BCB	L	602	2	3/3/21/26	11/41/137/137	-
8	UQ1	L	614	-	-	0/9/33/33	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	LDA	H	616	-	-	1/13/13/13	-
6	BCB	M	601	3	1/1/21/26	2/41/137/137	-
6	BCB	L	604	2	3/3/21/26	6/41/137/137	-
5	HEC	C	609	1	1/1/3/7	8/14/54/54	-
5	HEC	C	612	1	1/1/3/7	4/14/54/54	-
6	BCB	M	603	3	3/3/21/26	7/41/137/137	-
7	BPB	M	605	-	-	10/37/105/105	0/5/6/6
7	BPB	L	606	-	-	9/37/105/105	0/5/6/6
11	MQ7	M	608	-	-	4/41/61/61	0/2/2/2
12	NS1	M	613	-	-	15/43/43/43	-

The worst 5 of 149 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	M	615	LDA	O1-N1	-8.31	1.21	1.42
13	H	616	LDA	O1-N1	-7.91	1.22	1.42
12	M	613	NS1	C35-C36	7.46	1.54	1.32
5	C	610	HEC	C4C-C3C	-6.15	1.32	1.44
13	H	616	LDA	C1-N1	-6.11	1.45	1.51

The worst 5 of 193 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	M	608	MQ7	C11-C3-C4	-9.46	108.61	118.58
7	L	606	BPB	C4D-CHA-CBD	-6.64	105.27	108.45
7	L	606	BPB	OBD-CAD-CBD	-5.90	117.17	125.82
5	C	611	HEC	CAA-C2A-C3A	-5.72	117.16	127.87
6	M	603	BCB	CAA-C2A-C1A	-5.69	93.32	111.97

5 of 14 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	C	609	HEC	NA
5	C	610	HEC	NA
5	C	611	HEC	NA
5	C	612	HEC	NA
6	L	602	BCB	NC

5 of 97 torsion outliers are listed below:

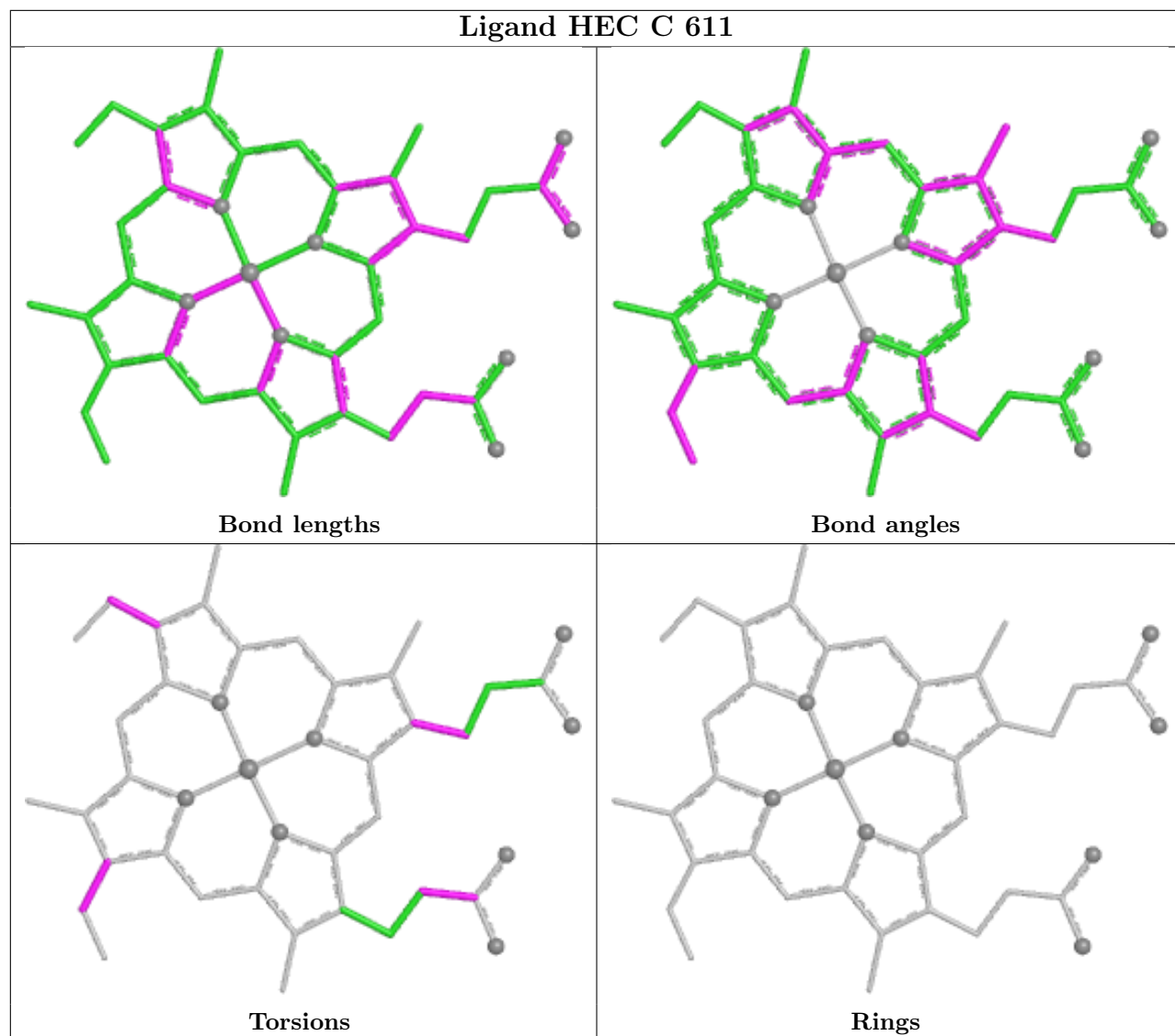
Mol	Chain	Res	Type	Atoms
5	C	611	HEC	C1A-C2A-CAA-CBA
5	C	611	HEC	C3A-C2A-CAA-CBA
6	M	601	BCB	C2C-C3C-CAC-CBC
6	M	603	BCB	CAD-CBD-CGD-O1D
6	M	603	BCB	CAD-CBD-CGD-O2D

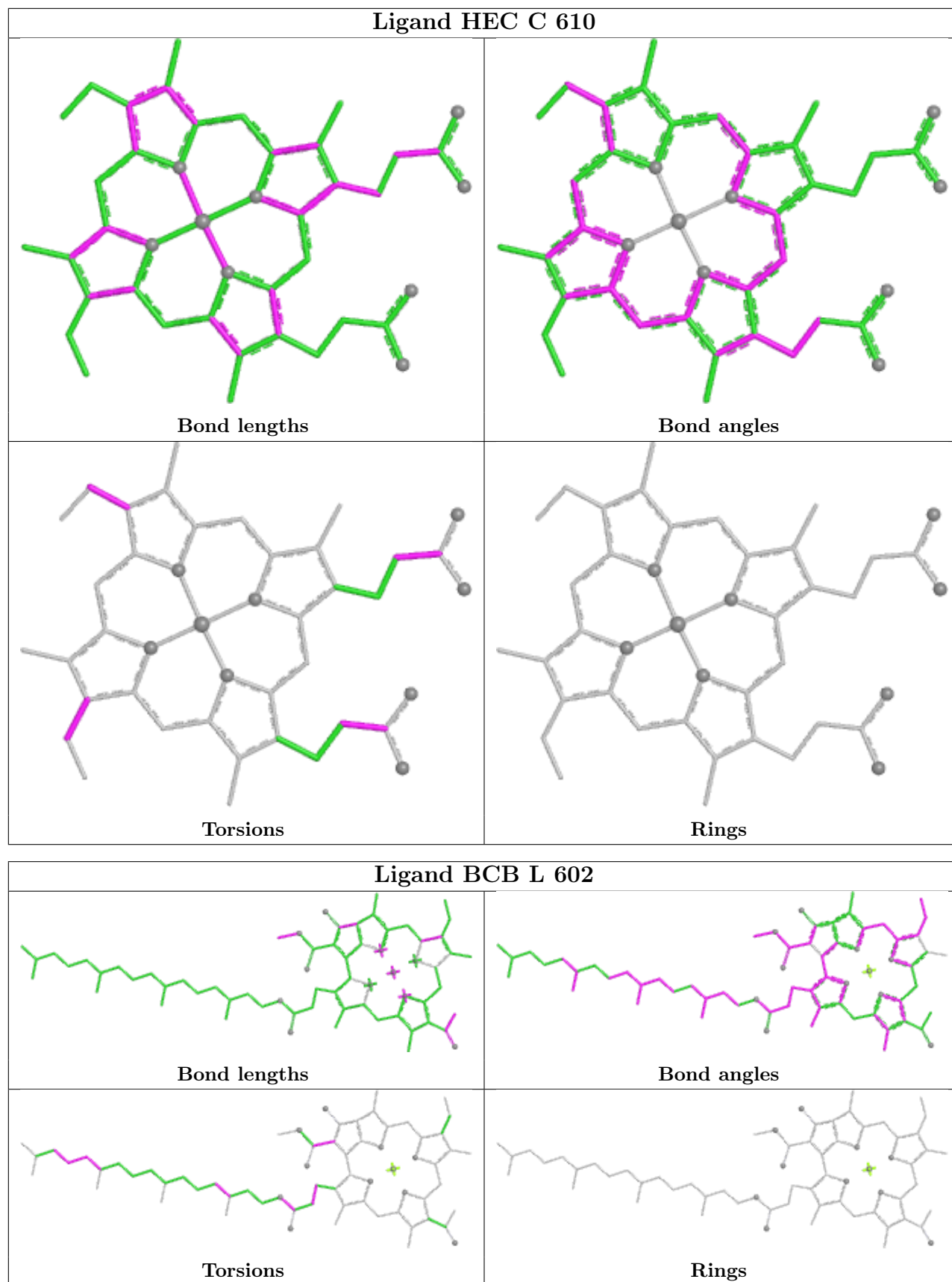
There are no ring outliers.

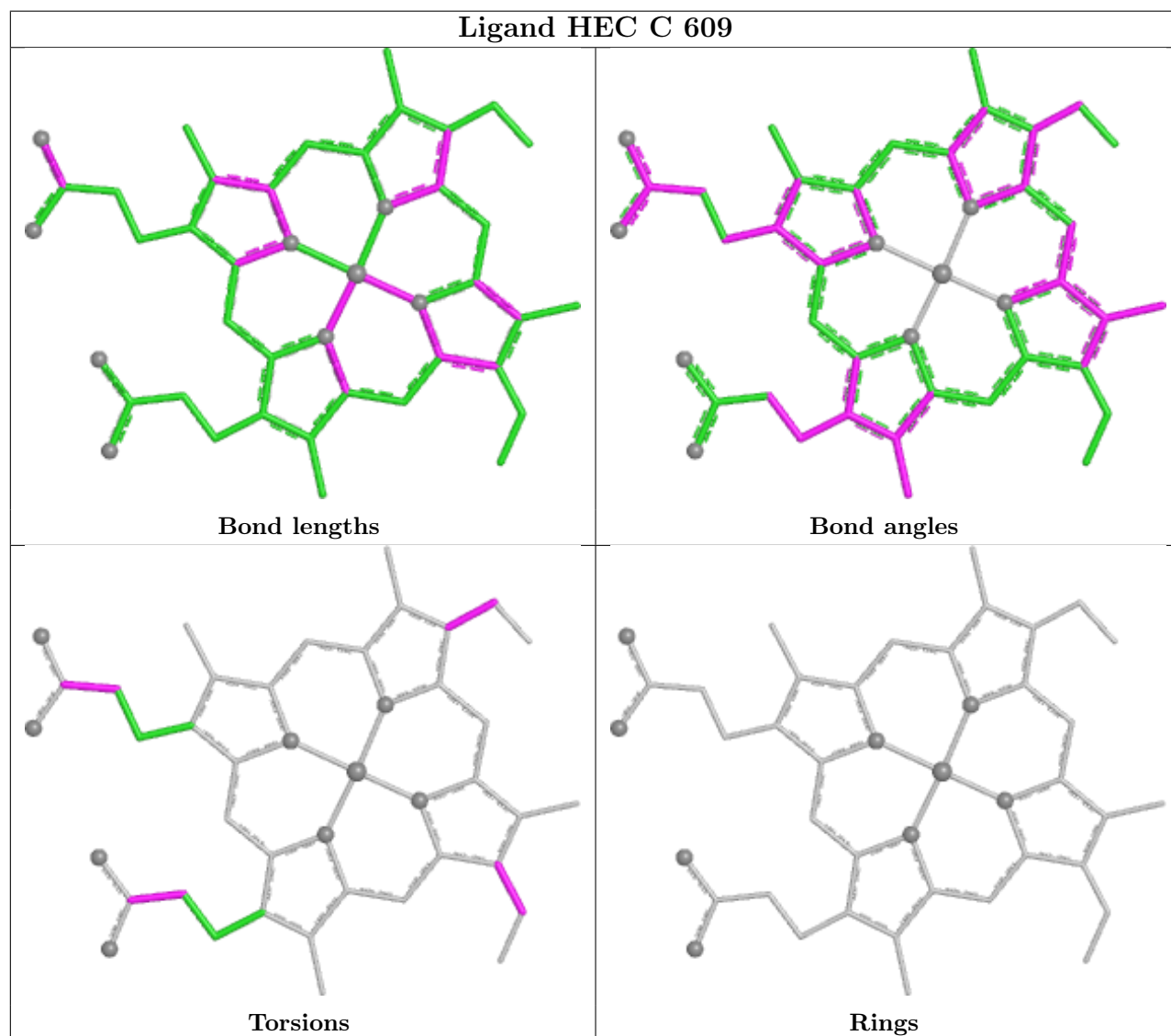
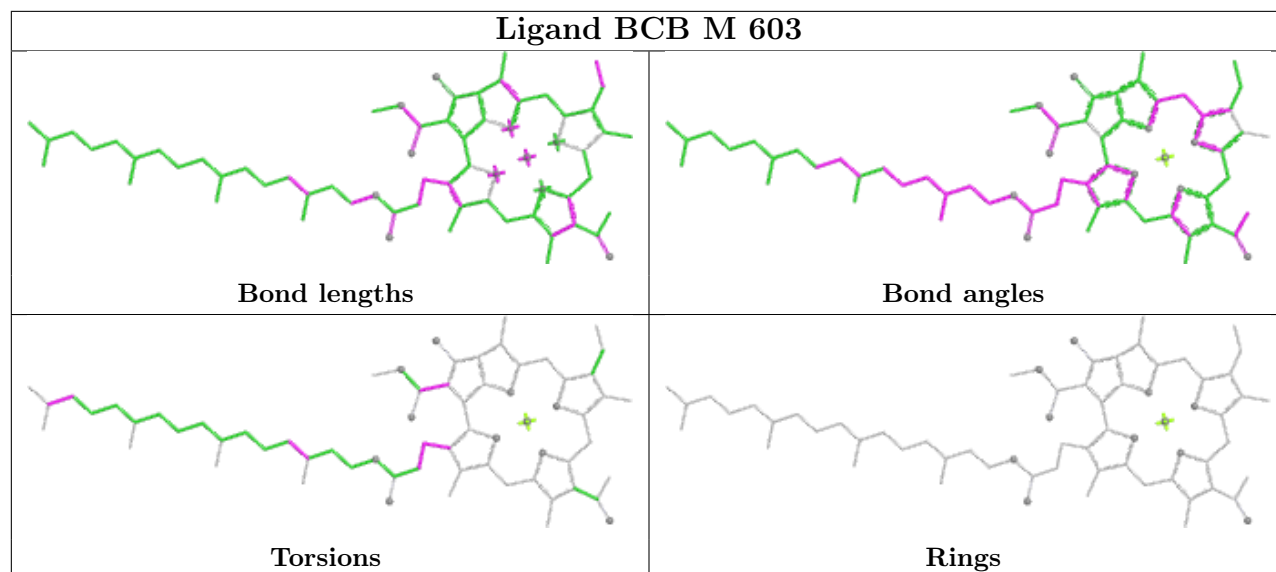
15 monomers are involved in 89 short contacts:

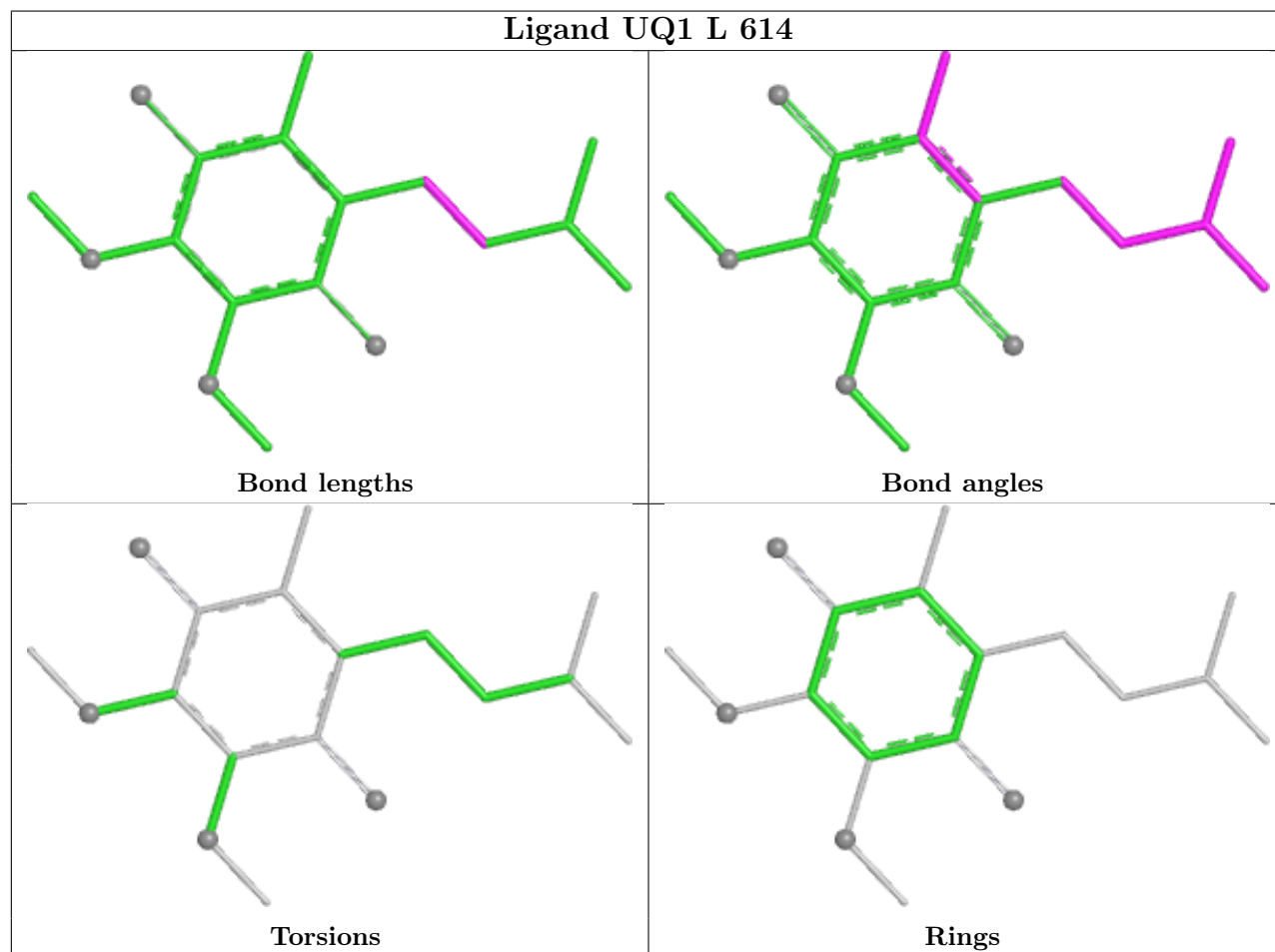
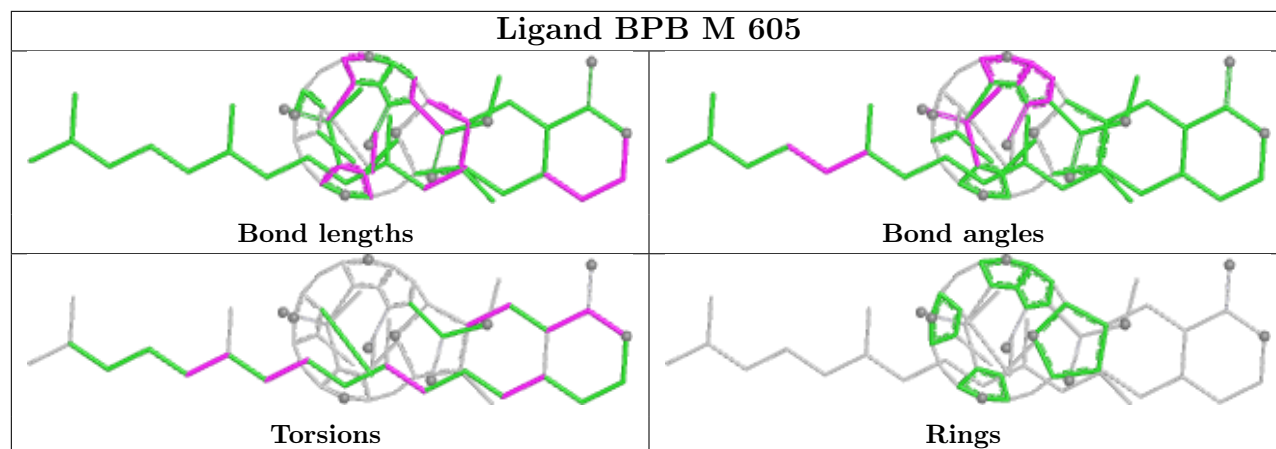
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	611	HEC	7	0
5	C	610	HEC	4	0
6	L	602	BCB	16	0
6	M	603	BCB	15	0
5	C	609	HEC	6	0
7	M	605	BPB	11	0
13	M	615	LDA	1	0
8	L	614	UQ1	8	0
6	M	601	BCB	6	0
11	M	608	MQ7	1	0
7	L	606	BPB	8	0
13	H	616	LDA	2	0
6	L	604	BCB	11	0
5	C	612	HEC	2	0
12	M	613	NS1	4	0

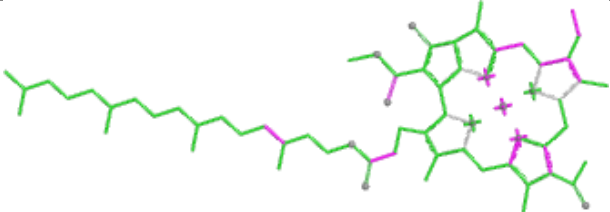
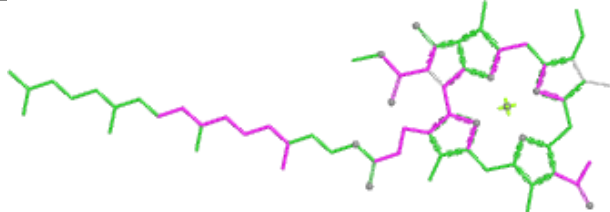
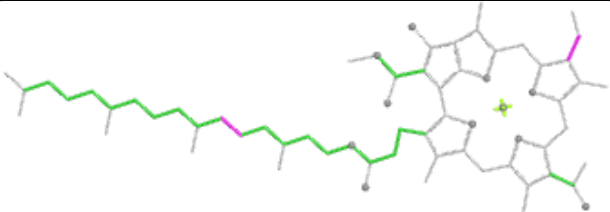
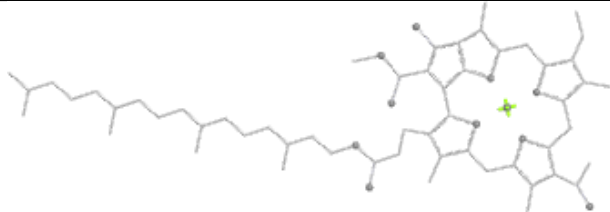
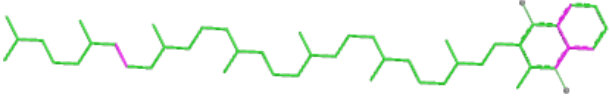
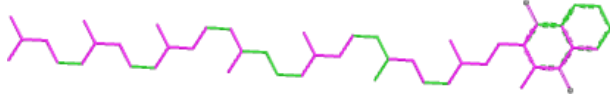
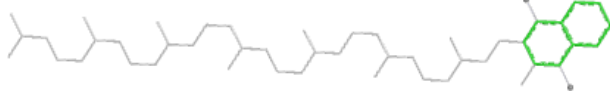
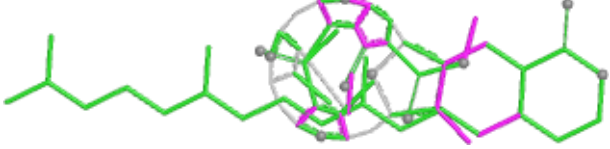
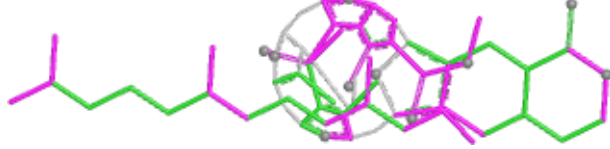
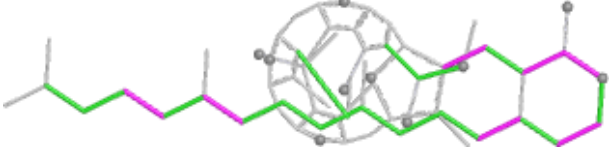
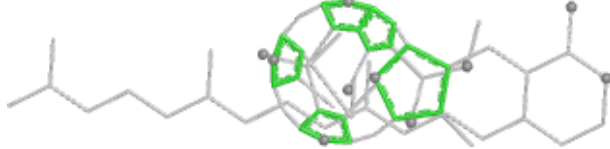
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

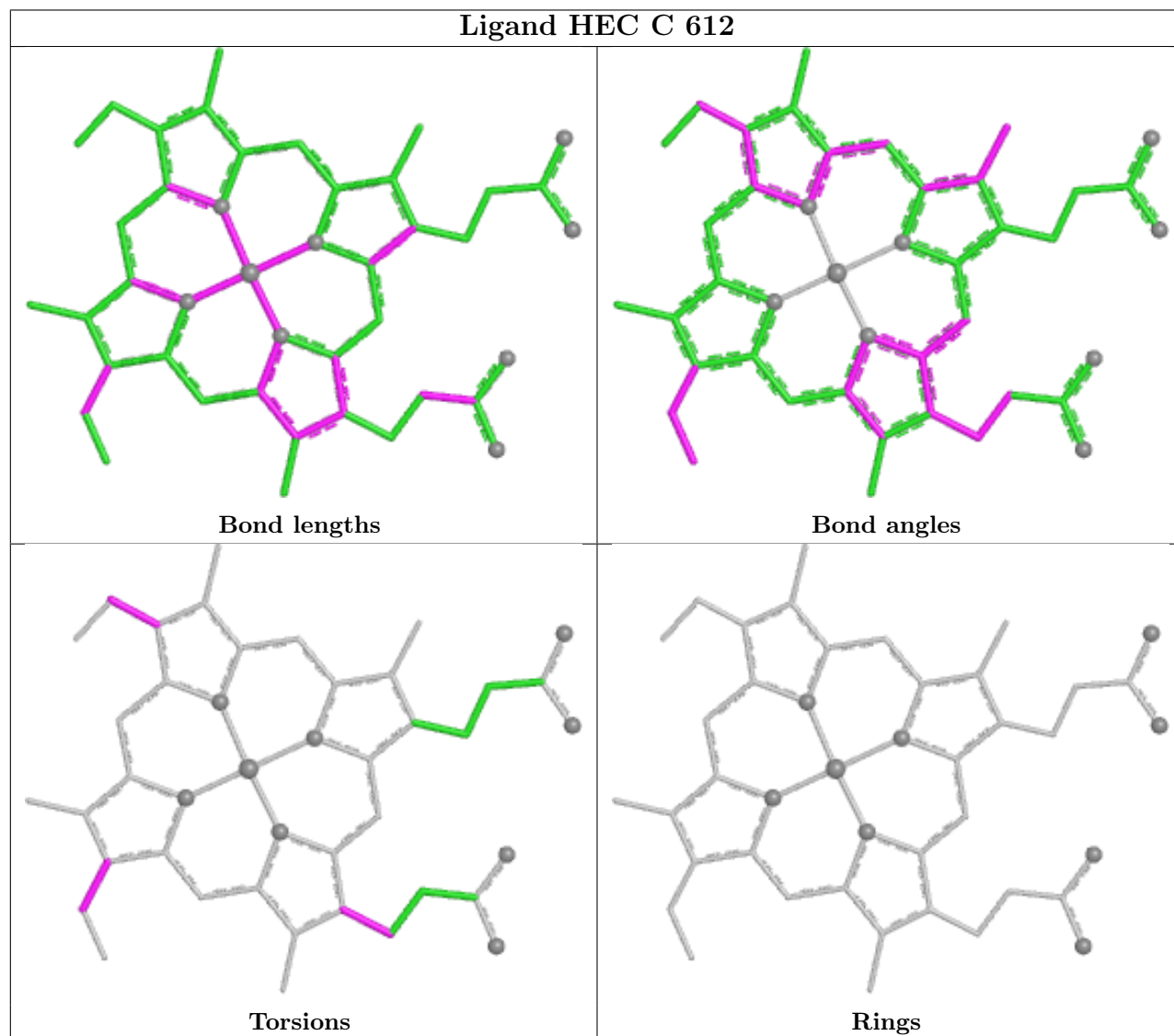
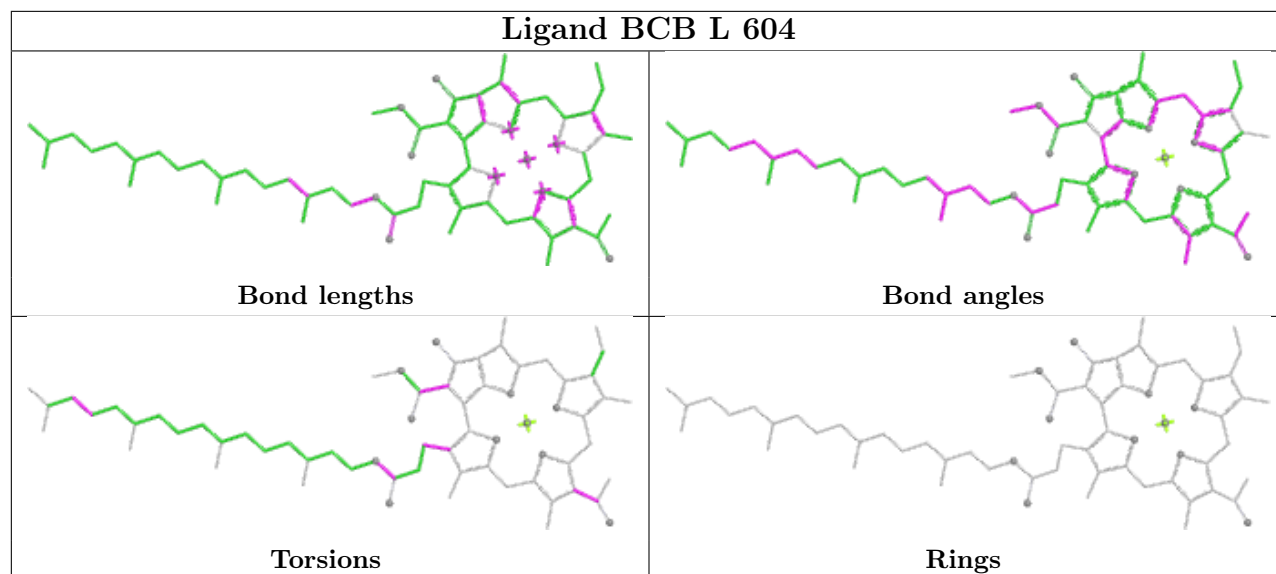


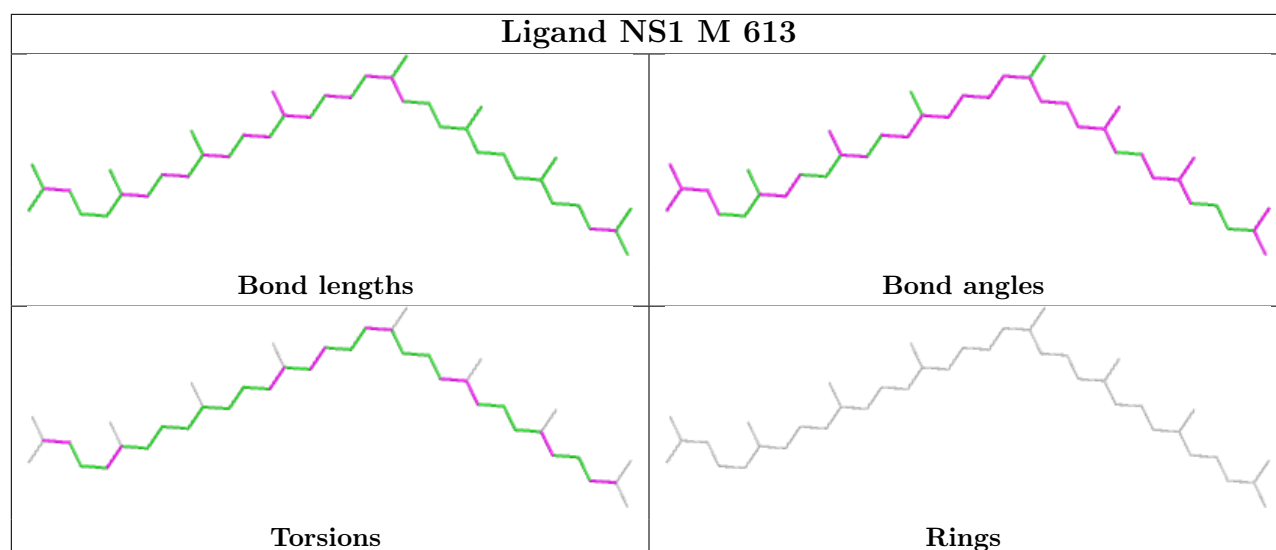






Ligand BCB M 601	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand MQ7 M 608	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BPB L 606	
 Bond lengths	 Bond angles
 Torsions	 Rings





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	C	333/336 (99%)	-0.68	1 (0%) 90 90	7, 21, 42, 73	17 (5%)
2	L	273/273 (100%)	-0.86	0 100 100	6, 16, 35, 47	6 (2%)
3	M	323/323 (100%)	-0.77	0 100 100	4, 18, 41, 58	8 (2%)
4	H	250/258 (96%)	-0.56	7 (2%) 55 57	8, 23, 46, 78	17 (6%)
All	All	1179/1190 (99%)	-0.72	8 (0%) 84 85	4, 19, 42, 78	48 (4%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	H	54	PRO	3.2
4	H	45	GLU	2.8
4	H	55	GLU	2.8
4	H	46	PRO	2.8
4	H	96	PHE	2.5

6.2 Non-standard residues in protein, DNA, RNA chains [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	FME	H	1	10/11	0.96	0.07	21,32,41,45	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

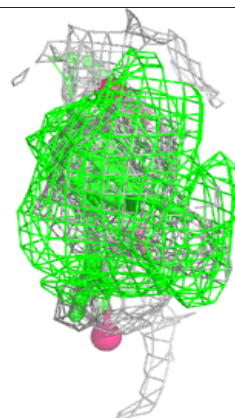
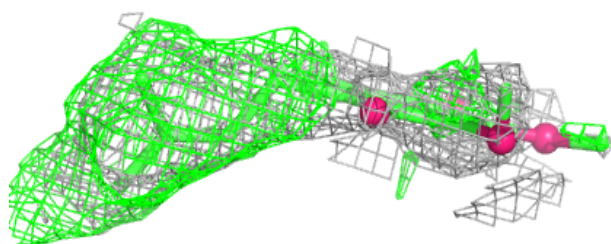
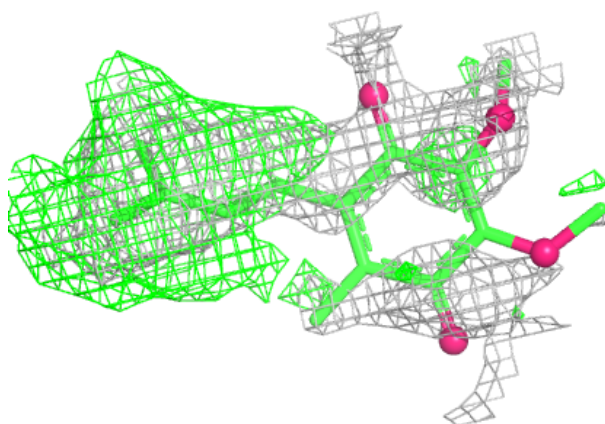
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	UQ1	L	614	18/18	0.81	0.37	19,26,29,30	18
10	SO4	H	622	5/5	0.84	0.17	73,74,85,89	0
13	LDA	H	616	16/16	0.85	0.14	0,27,42,46	6
10	SO4	H	623	5/5	0.89	0.12	58,59,62,64	5
10	SO4	M	621	5/5	0.89	0.15	68,78,81,82	0
12	NS1	M	613	40/40	0.92	0.10	0,25,39,49	14
13	LDA	M	615	16/16	0.94	0.07	17,25,36,37	0
10	SO4	H	617	5/5	0.94	0.09	47,50,59,61	0
11	MQ7	M	608	48/48	0.97	0.05	0,10,20,32	4
6	BCB	M	601	66/66	0.97	0.06	0,12,40,61	13
10	SO4	M	619	5/5	0.97	0.10	39,43,50,59	0
7	BPB	M	605	65/65	0.97	0.07	0,21,62,71	7
7	BPB	L	606	65/65	0.98	0.04	3,10,19,22	0
6	BCB	L	604	66/66	0.98	0.04	3,10,27,35	0
6	BCB	L	602	66/66	0.98	0.04	3,10,19,21	0
6	BCB	M	603	66/66	0.98	0.05	3,10,20,21	0
5	HEC	C	611	43/43	0.99	0.04	5,16,25,38	0
10	SO4	M	618	5/5	0.99	0.04	22,23,35,37	0
5	HEC	C	612	43/43	0.99	0.05	3,22,31,46	0
10	SO4	M	620	5/5	0.99	0.04	31,34,40,41	0
5	HEC	C	609	43/43	0.99	0.06	7,22,32,36	0
5	HEC	C	610	43/43	0.99	0.05	3,21,29,37	0
9	FE	M	607	1/1	1.00	0.01	19,19,19,19	0

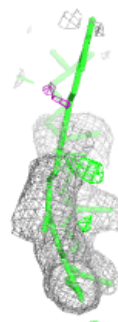
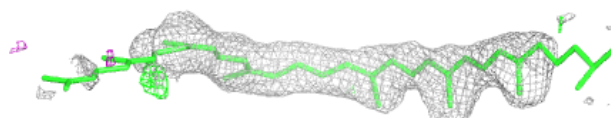
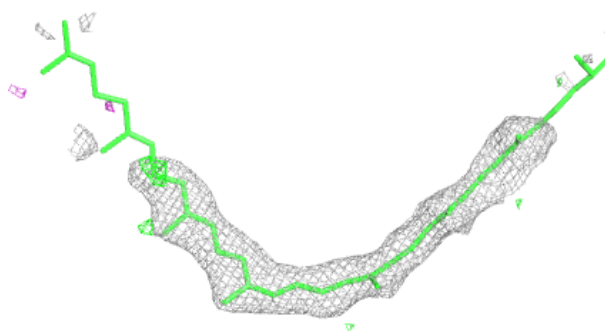
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around UQ1 L 614:

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

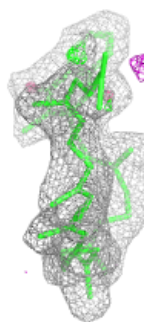
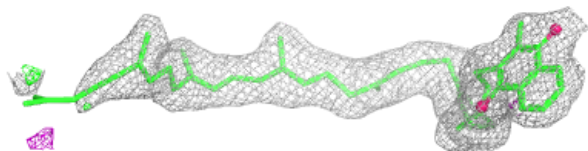
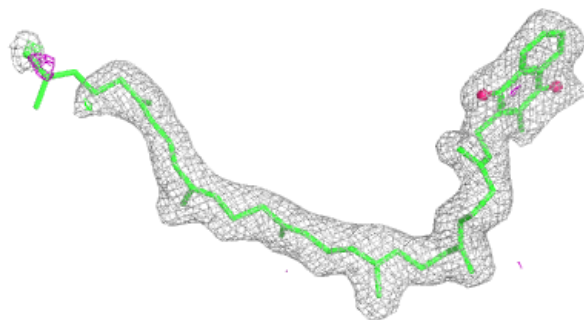
**Electron density around NS1 M 613:**

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

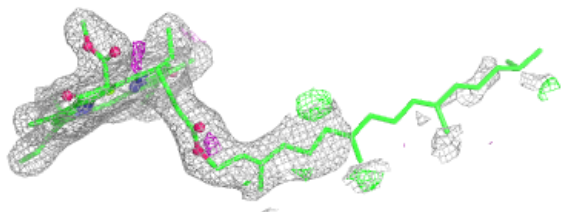
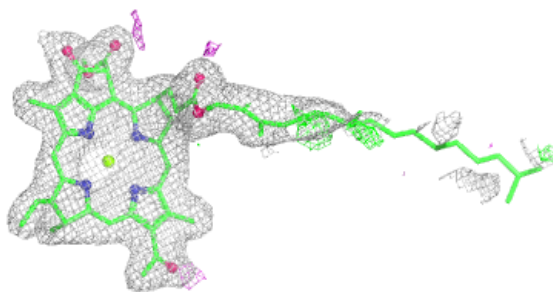


Electron density around MQ7 M 608:

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

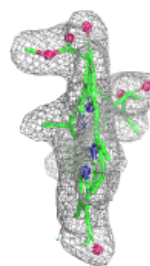
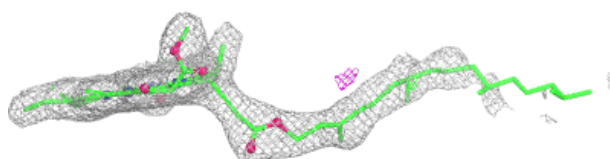
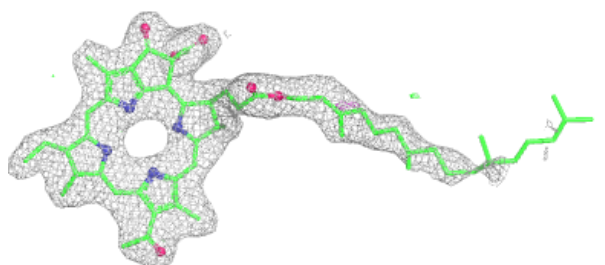
**Electron density around BCB M 601:**

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

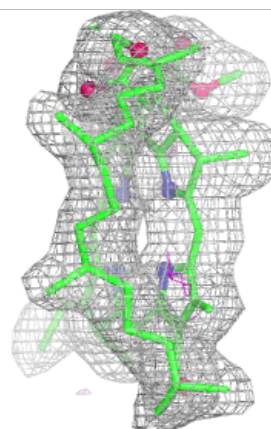
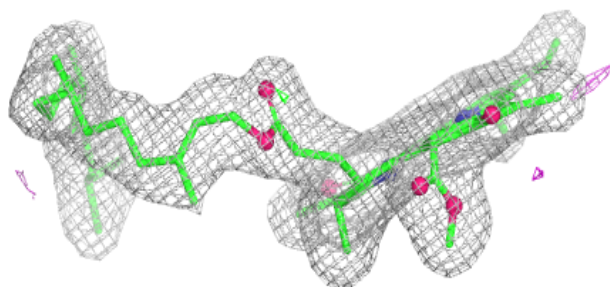
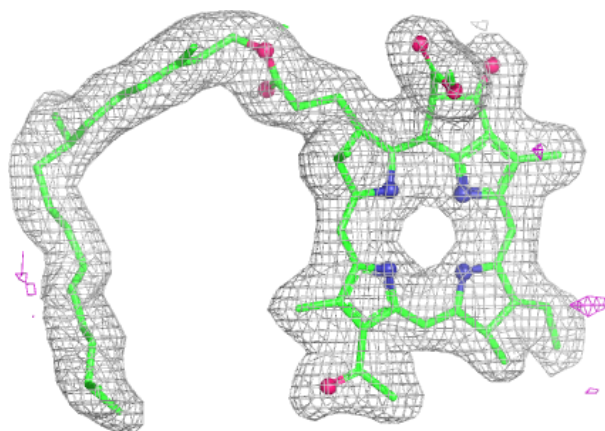


Electron density around BPB M 605:

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and green (positive)

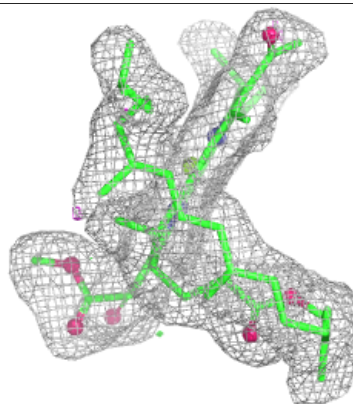
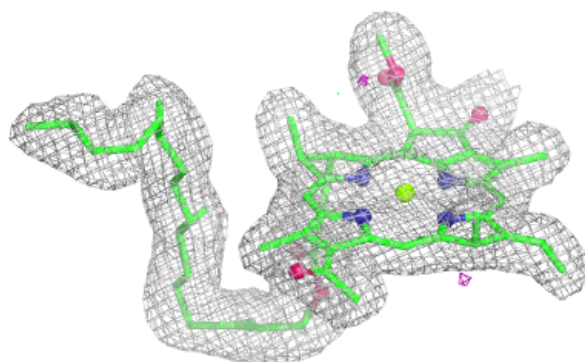
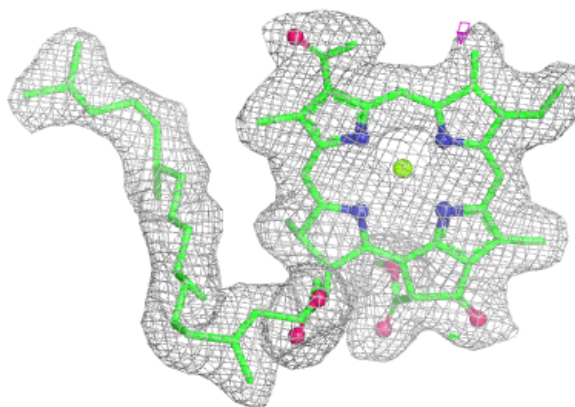
**Electron density around BPB L 606:**

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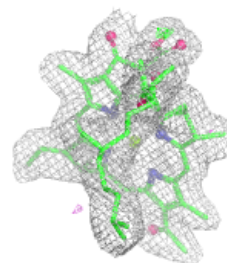
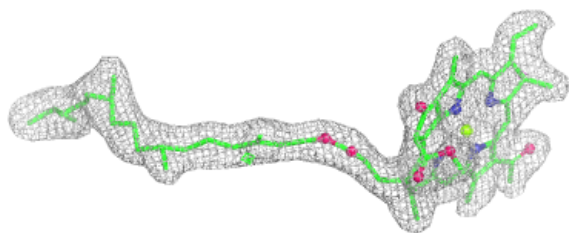
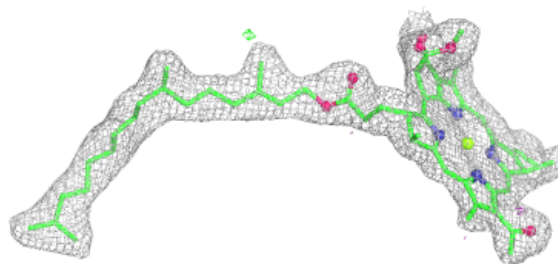


Electron density around BCB L 604:

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

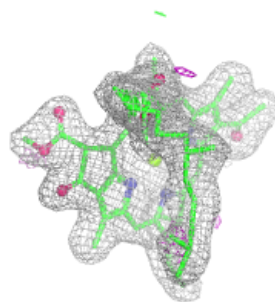
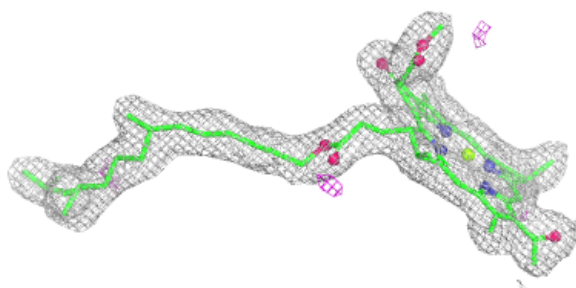
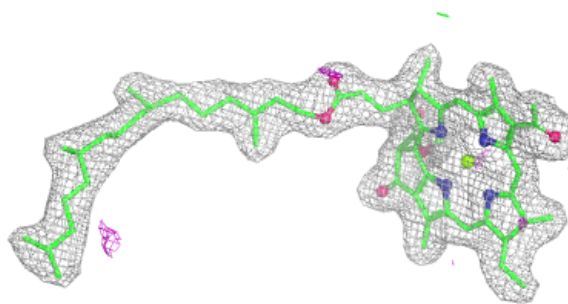
**Electron density around BCB L 602:**

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



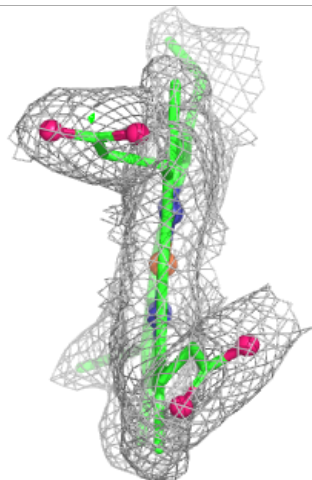
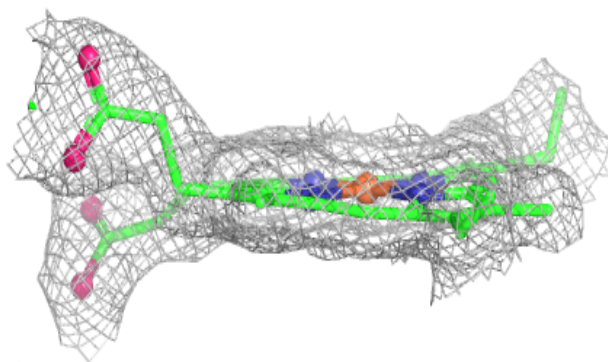
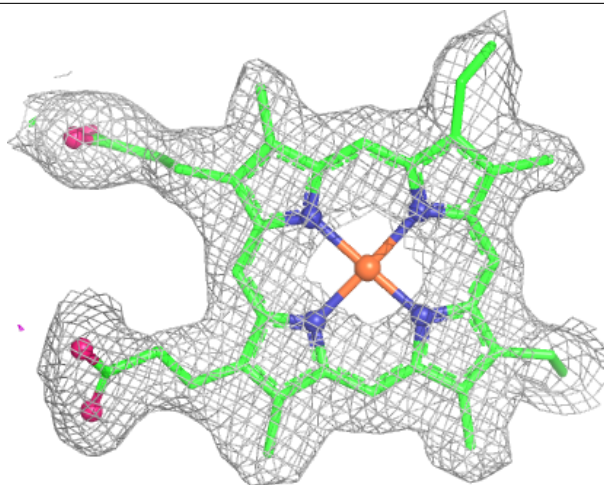
Electron density around BCB M 603:

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



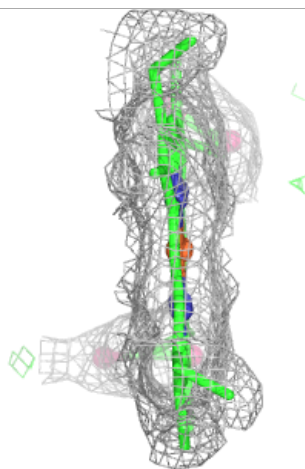
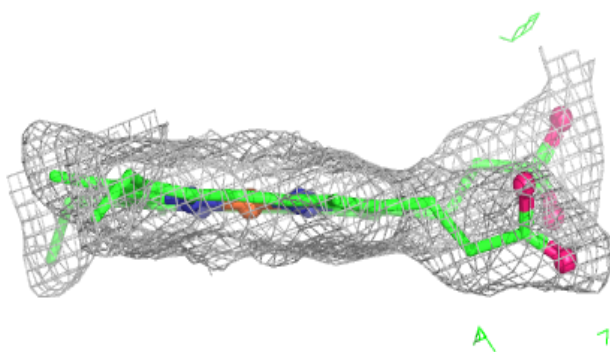
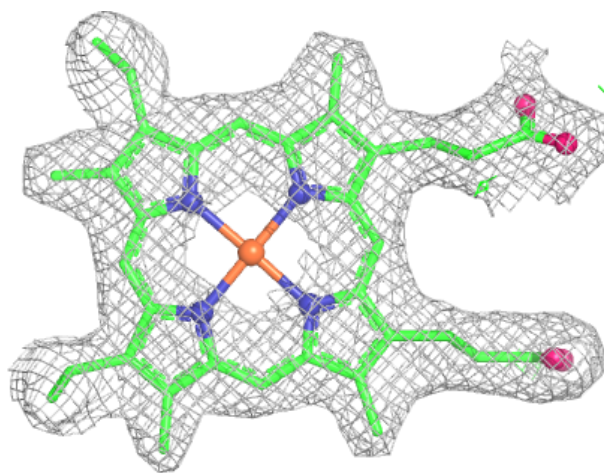
Electron density around HEC C 611:

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



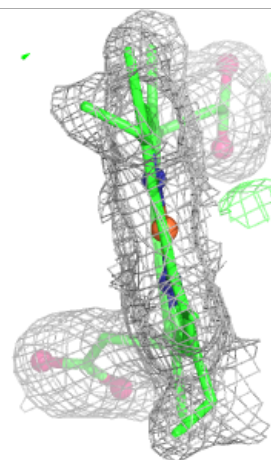
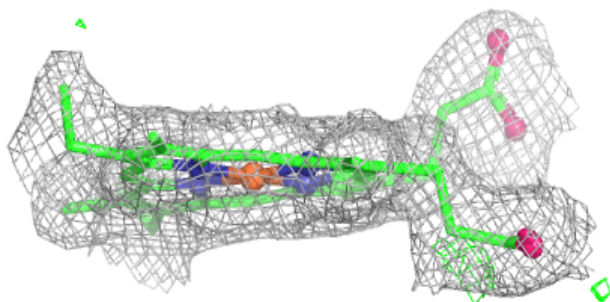
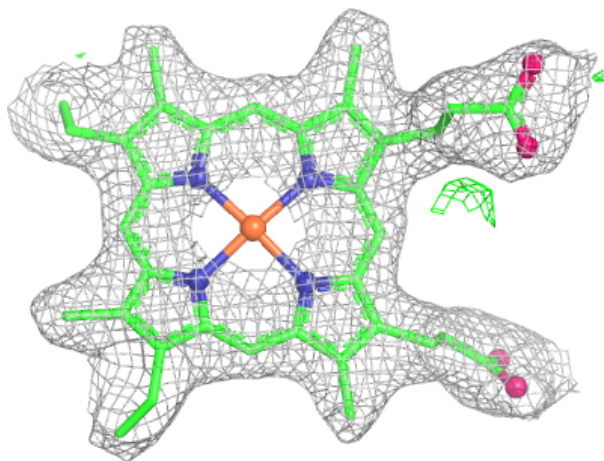
Electron density around HEC C 612:

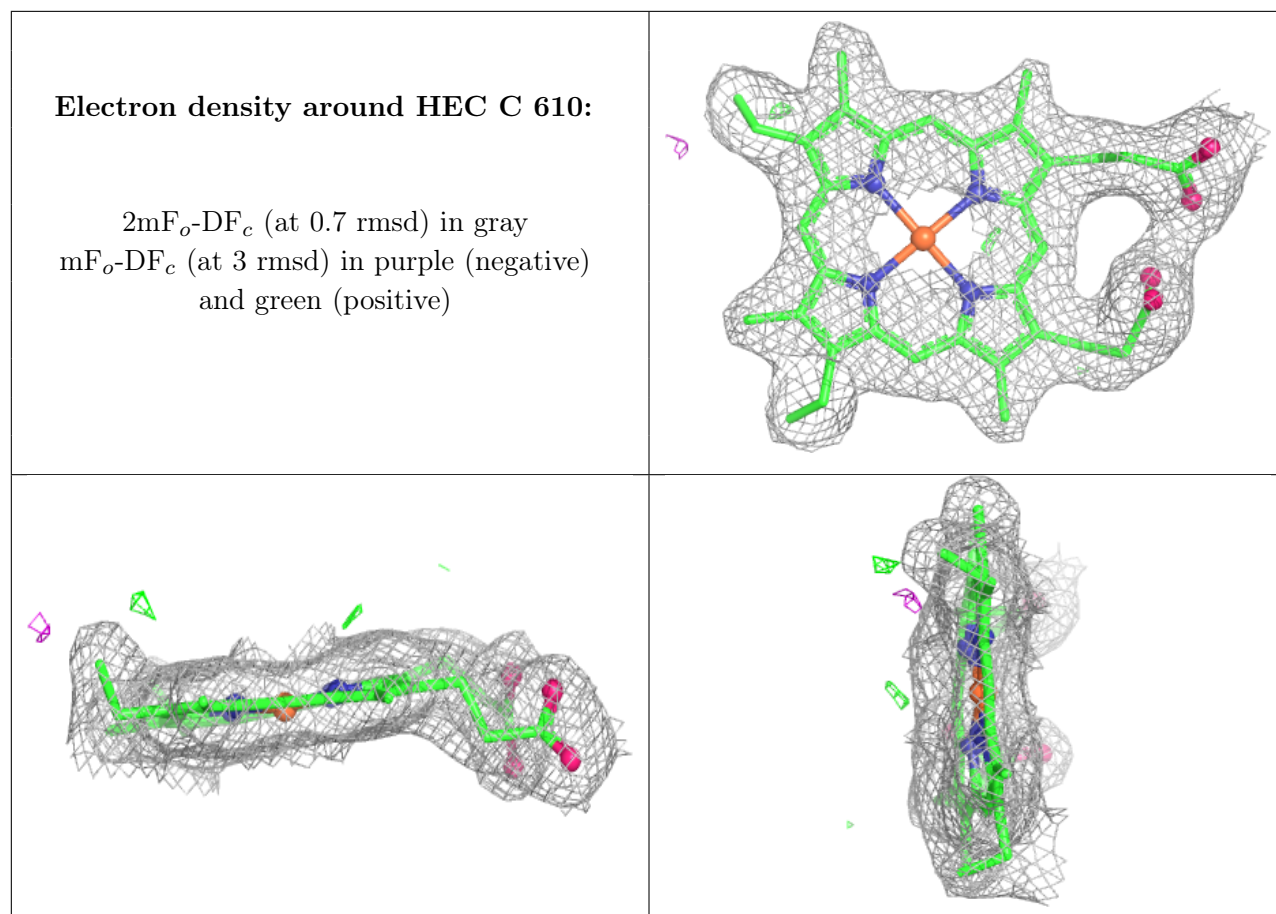
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC C 609:

$2mF_o-DF_c$ (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.