



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2025 – 10:35 PM EDT

PDB ID : 3H1H  
Title : Cytochrome bc1 complex from chicken  
Authors : Zhang, Z.; Huang, L.; Shulmeister, V.M.; Chi, Y.I.; Kim, K.K.; Hung, L.W.;  
Crofts, A.R.; Berry, E.A.; Kim, S.H.  
Deposited on : 2009-04-12  
Resolution : 3.16 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

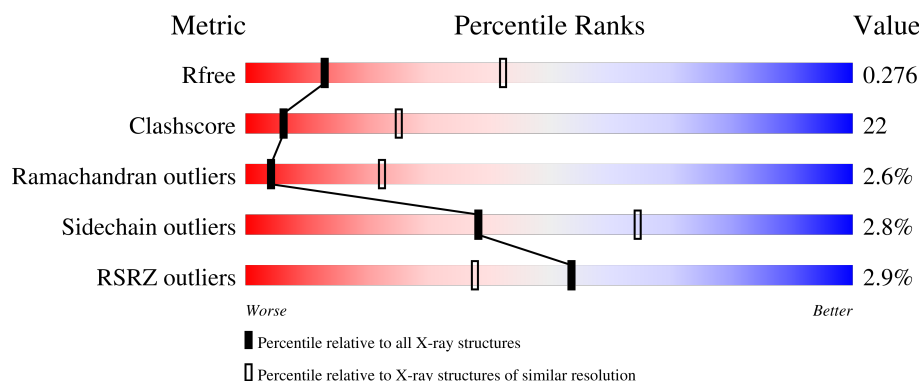
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*






The reported resolution of this entry is 3.16 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))
$R_{free}$	164625	2168 (3.20-3.12)
Clashscore	180529	2333 (3.20-3.12)
Ramachandran outliers	177936	2266 (3.20-3.12)
Sidechain outliers	177891	2265 (3.20-3.12)
RSRZ outliers	164620	2169 (3.20-3.12)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	446	 61% 35% 2% 2%
1	N	446	 59% 37% 2% 2%
2	B	441	 49% 42% 5% 2%
2	O	441	 49% 41% 5% 2%
3	C	380	 68% 31% 1% 0%

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Mol	Chain	Length	Quality of chain
3	P	380	
4	D	241	
4	Q	241	
5	E	196	
5	R	196	
6	F	110	
6	S	110	
7	G	81	
7	T	81	
8	H	77	
8	U	77	
9	I	47	
9	V	47	
10	J	61	
10	W	61	

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
15	PEE	N	3008	-	X	-	-
19	FES	E	501	-	-	X	-
19	FES	R	501	-	-	X	-

## 2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 32608 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 UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN I, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	443	Total	C	N	O	S	0	0	0
			3442	2157	606	658	21			
1	N	442	Total	C	N	O	S	0	0	0
			3437	2154	605	657	21			

- Molecule 2 is a protein called UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 2, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	421	Total	C	N	O	S	0	0	0
			3141	1974	545	613	9			
2	O	422	Total	C	N	O	S	0	0	0
			3147	1977	546	614	10			

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	380	Total	C	N	O	S	0	0	0
			3017	2022	478	505	12			
3	P	379	Total	C	N	O	S	0	0	0
			3012	2019	477	504	12			

- Molecule 4 is a protein called CYTOCHROME C1, HEME PROTEIN, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	241	Total	C	N	O	S	0	0	0
			1898	1212	327	347	12			
4	Q	241	Total	C	N	O	S	0	0	0
			1898	1212	327	347	12			

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	196	Total	C	N	O	S	0	0	0
			1513	952	263	292	6			
5	R	196	Total	C	N	O	S	0	0	0
			1509	950	263	290	6			

- Molecule 6 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KDA PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	101	Total	C	N	O	S	0	0	0
			891	570	159	159	3			
6	S	101	Total	C	N	O	S	0	0	0
			891	570	159	159	3			

- Molecule 7 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	G	80	Total	C	N	O	0	0	0
			672	437	119	116			
7	T	79	Total	C	N	O	0	0	0
			662	432	117	113			

- Molecule 8 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KDA PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	70	Total	C	N	O	S	0	0	0
			574	350	105	114	5			
8	U	67	Total	C	N	O	S	0	0	0
			553	338	103	107	5			

- Molecule 9 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	46	Total	C	N	O	S	0	0	0
			287	171	58	56	2			
9	V	44	Total	C	N	O	S	0	0	1
			278	167	56	53	2			

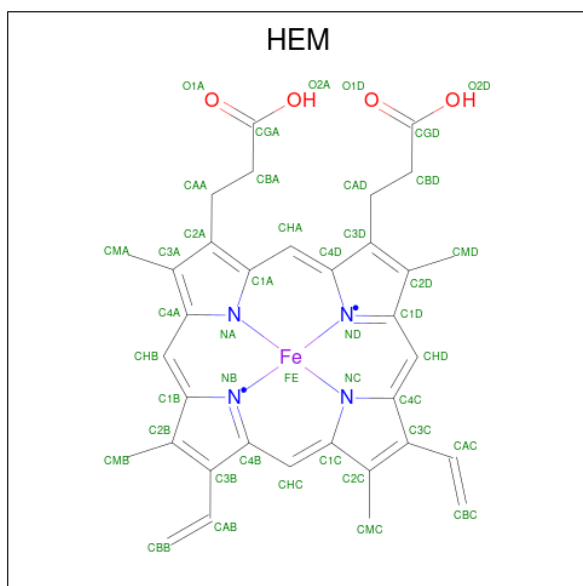
- Molecule 10 is a protein called UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2 KDA PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	J	61	Total	C	N	O	0	0	0
			497	321	87	89			
10	W	60	Total	C	N	O	0	0	1
			479	311	86	82			

- Molecule 11 is UNKNOWN LIGAND (three-letter code: UNL) (formula: ).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	3	Total	O	0	0
			3	3		
11	C	2	Total	O	0	0
			2	2		
11	N	3	Total	O	0	0
			3	3		
11	P	1	Total	O	0	0
			1	1		

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



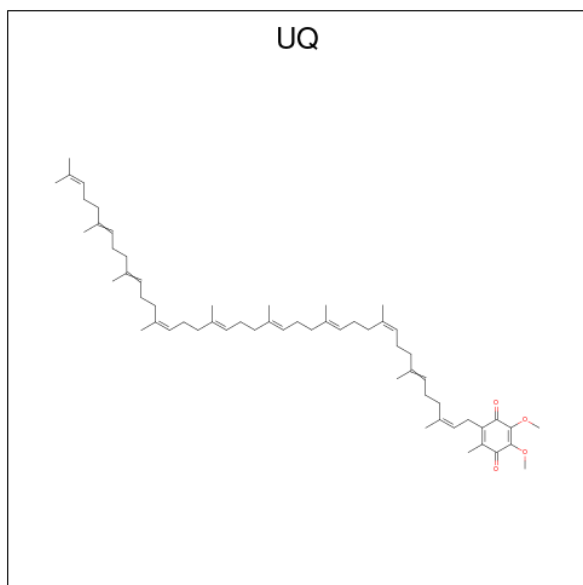
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	0
12	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	0
12	P	1	Total	C	Fe	N	O	0
			43	34	1	4	4	0

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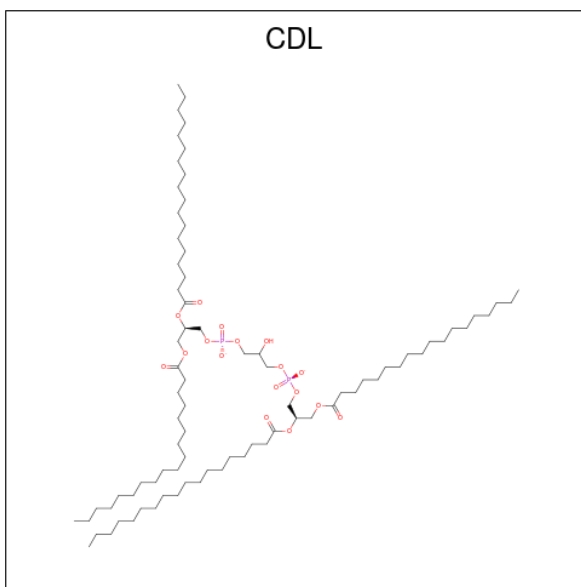
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	P	1	Total	C	Fe	N	O	
			43	34	1	4	4	
							0	0

- Molecule 13 is Coenzyme Q10, (2Z,6E,10Z,14E,18E,22E,26Z)-isomer (three-letter code: UQ) (formula: C<sub>59</sub>H<sub>90</sub>O<sub>4</sub>).



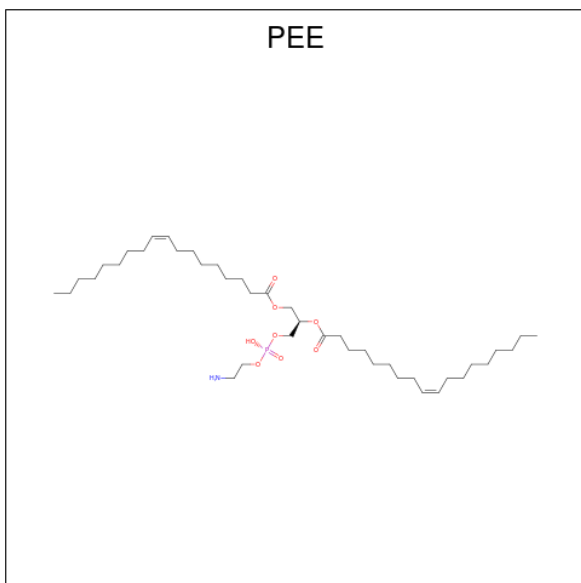
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	C	1	Total	C	O		
			19	15	4	0	0
13	P	1	Total	C	O		
			19	15	4	0	0

- Molecule 14 is CARDIOLIPIN (three-letter code: CDL) (formula: C<sub>81</sub>H<sub>156</sub>O<sub>17</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
14	C	1	Total	C	O	P	0	0
			40	21	17	2		
14	D	1	Total	C	O	P	0	0
			42	23	17	2		
14	P	1	Total	C	O	P	0	0
			40	21	17	2		
14	Q	1	Total	C	O	P	0	0
			42	23	17	2		

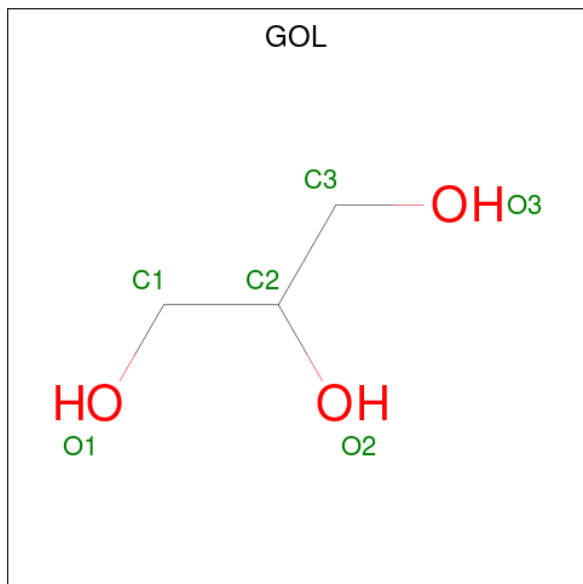
- Molecule 15 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (three-letter code: PEE) (formula:  $C_{41}H_{78}NO_8P$ ).





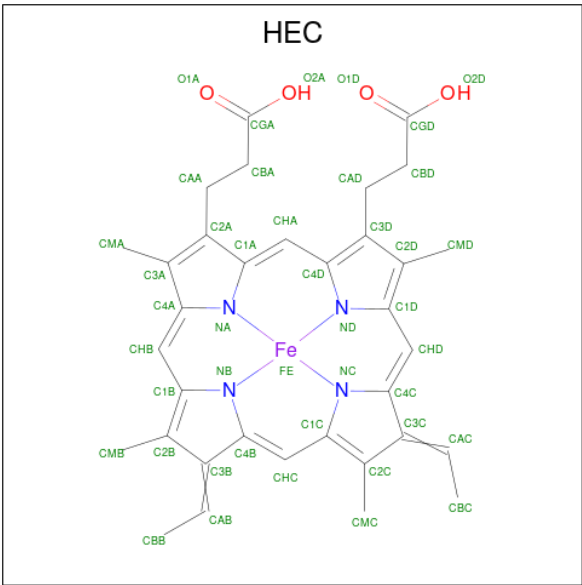
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
15	C	1	Total	C	N	O	P	0	0
			49	39	1	8	1		
15	C	1	Total	C	O	P		0	0
			21	12	8	1			
15	E	1	Total	C	N	O	P	0	0
			50	40	1	8	1		
15	N	1	Total	O	P			0	0
			5	4	1				
15	P	1	Total	C	N	O	P	0	0
			49	39	1	8	1		
15	R	1	Total	C	N	O	P	0	0
			50	40	1	8	1		

- Molecule 16 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



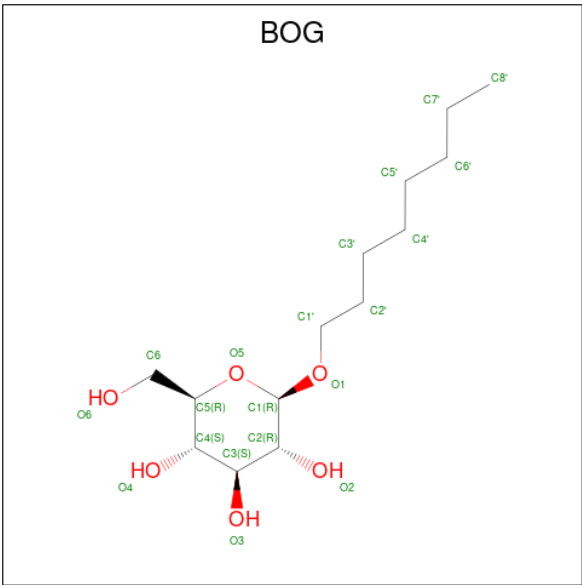
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
16	C	1	Total	C	O	0	0
			6	3	3		
16	P	1	Total	C	O	0	0
			6	3	3		

- Molecule 17 is HEME C (three-letter code: HEC) (formula:  $C_{34}H_{34}FeN_4O_4$ ).



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

- Molecule 18 is octyl beta-D-glucopyranoside (three-letter code: BOG) (formula: C<sub>14</sub>H<sub>28</sub>O<sub>6</sub>).



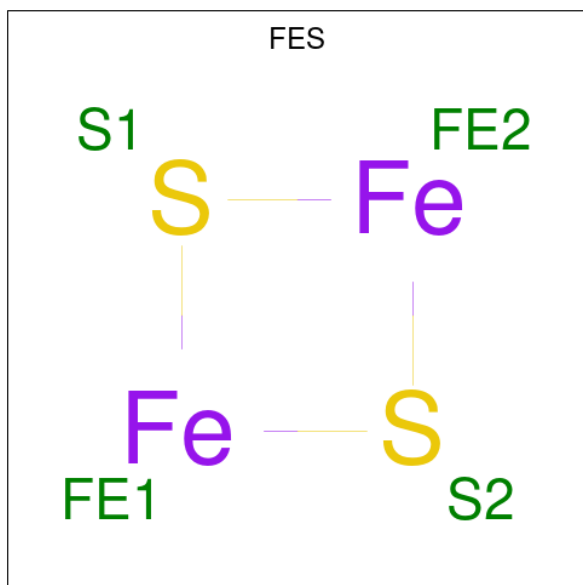
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	D	1	Total	C	O	0	0
			20	14	6		
18	D	1	Total	C	O	0	0
			13	7	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	P	1	Total	C	O	0	0
			12	6	6		
18	Q	1	Total	C	O	0	0
			20	14	6		
18	Q	1	Total	C	O	0	0
			13	7	6		

- Molecule 19 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula:  $\text{Fe}_2\text{S}_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	E	1	Total	Fe	S	0	0
			4	2	2		
19	R	1	Total	Fe	S	0	0
			4	2	2		

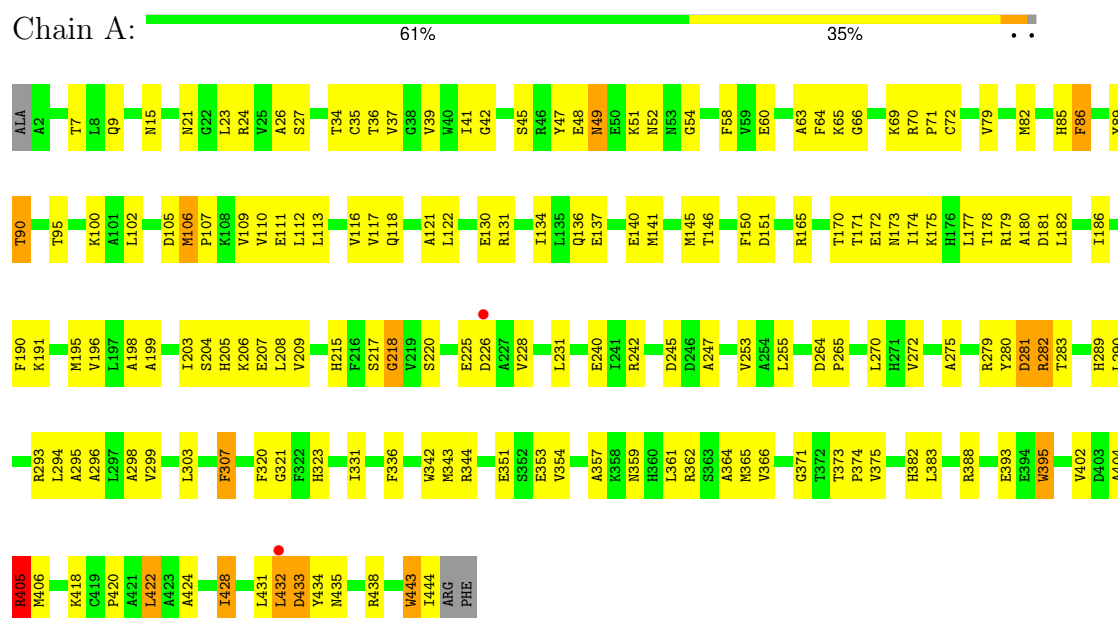
- Molecule 20 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	C	8	Total	O	0	0
			8	8		
20	E	1	Total	O	0	0
			1	1		
20	P	9	Total	O	0	0
			9	9		
20	R	1	Total	O	0	0
			1	1		

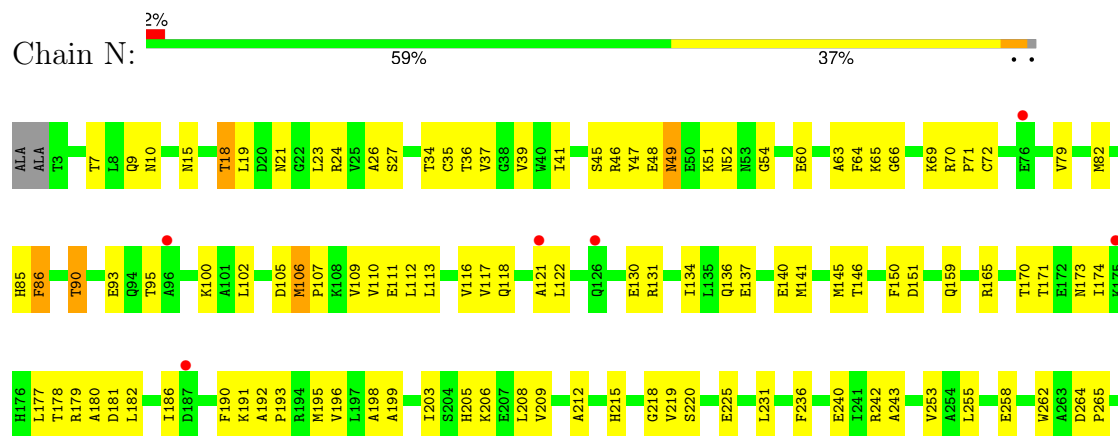
### 3 Residue-property plots

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.

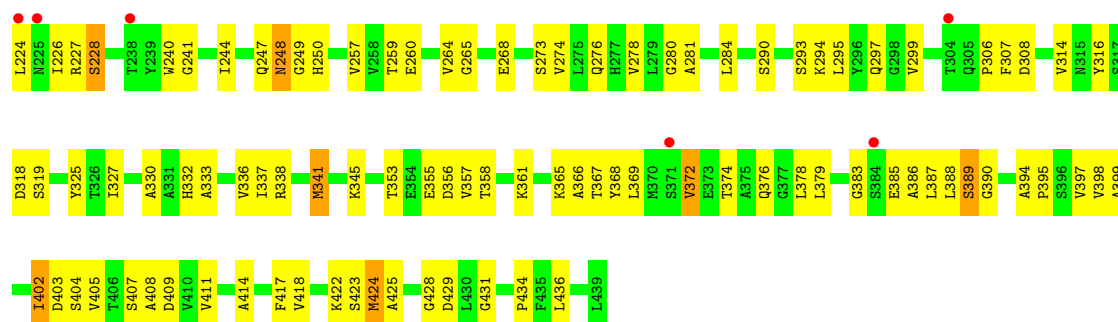
#### • Molecule 1: UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN I, MITOCHONDRIAL



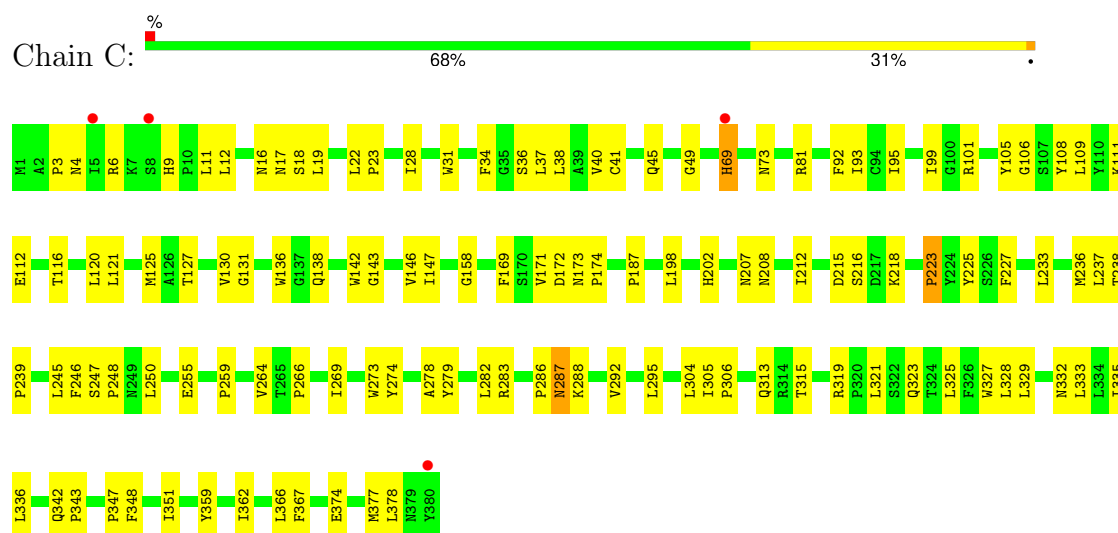
#### • Molecule 1: UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN I, MITOCHONDRIAL



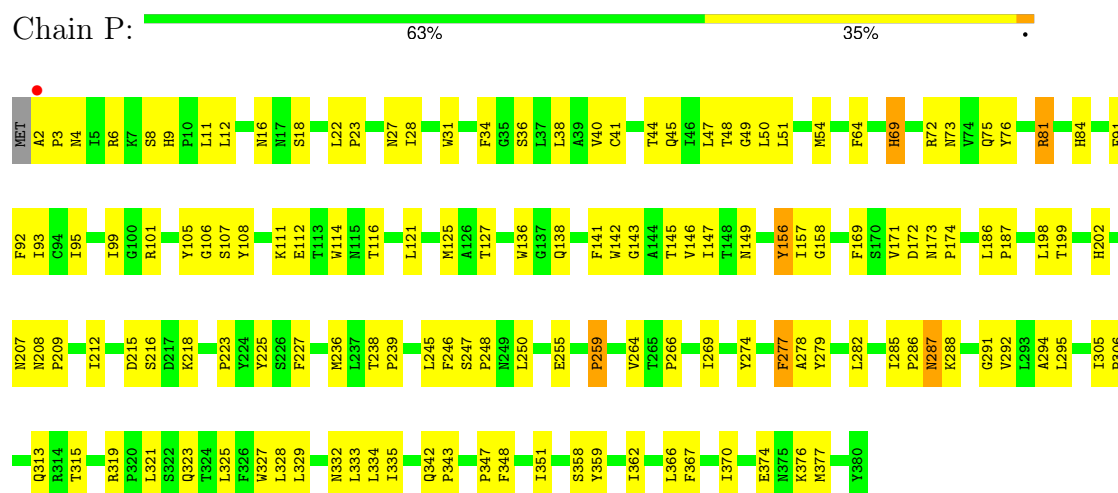




### • Molecule 3: Cytochrome b

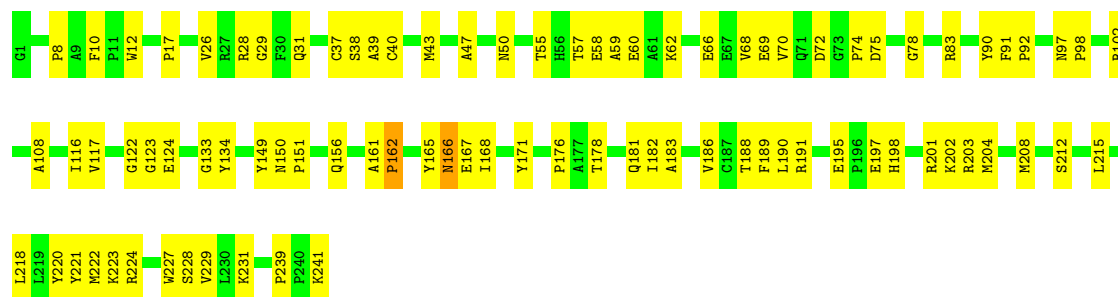


### • Molecule 3: Cytochrome b

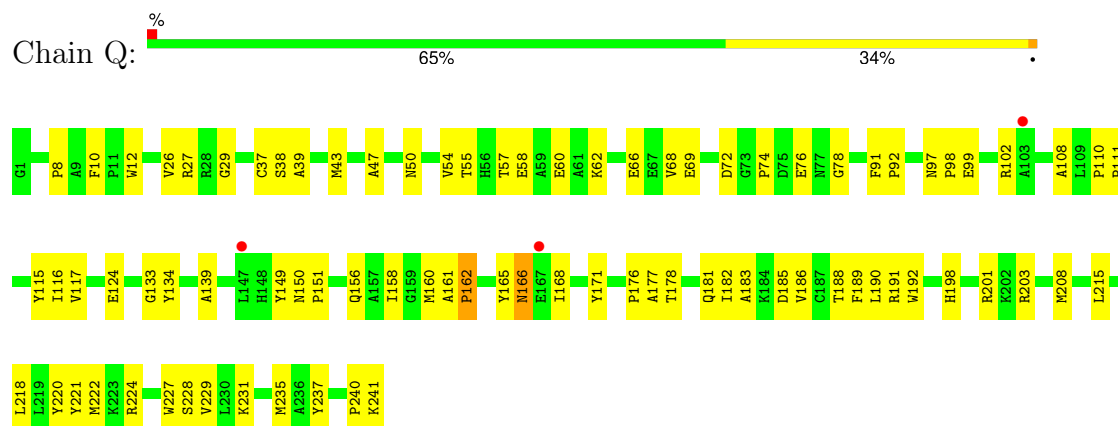


### • Molecule 4: CYTOCHROME C1, HEME PROTEIN, MITOCHONDRIAL

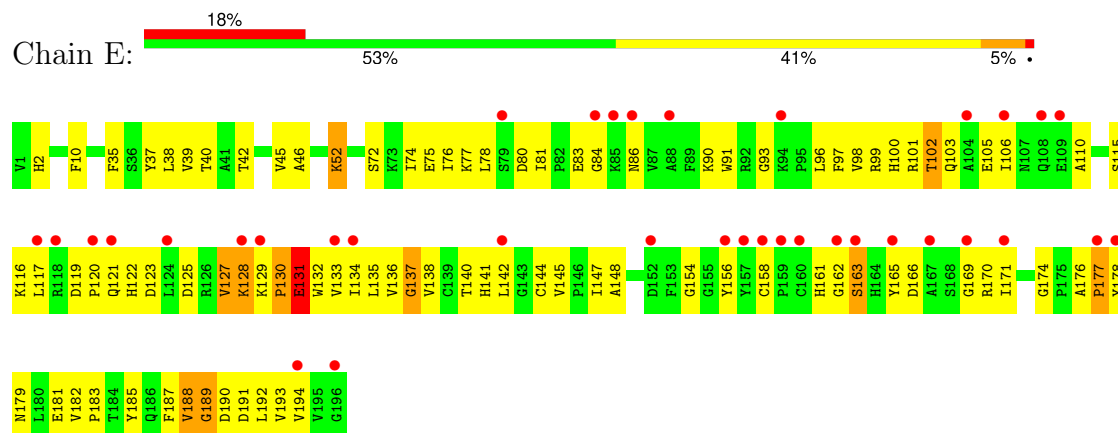




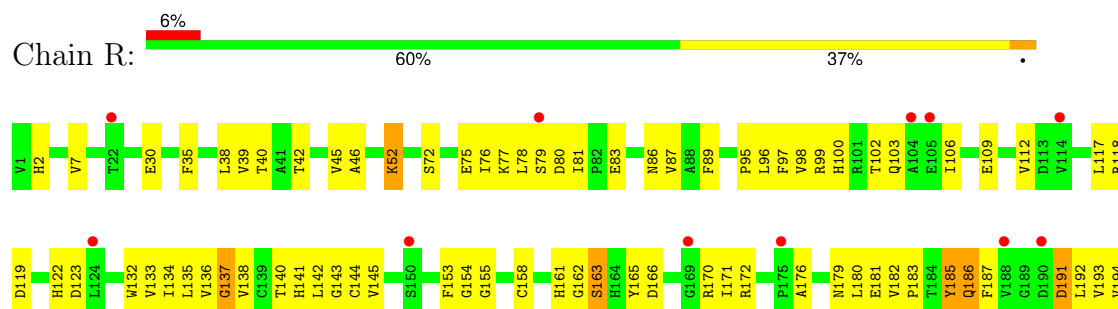
• Molecule 4: CYTOCHROME C1, HEME PROTEIN, MITOCHONDRIAL



• Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



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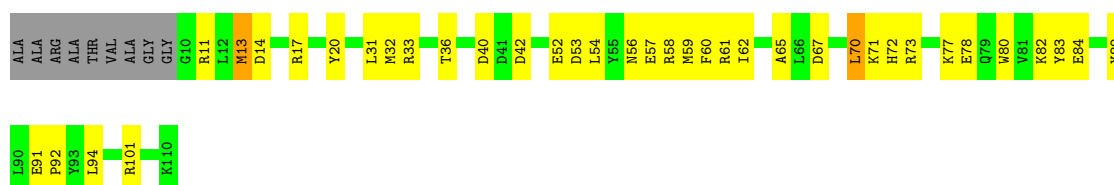




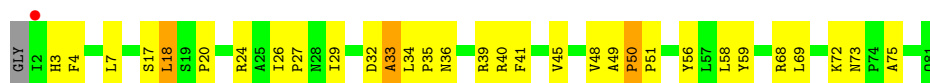
• Molecule 6: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KDA PROTEIN



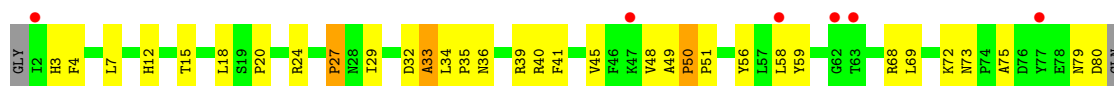
• Molecule 6: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KDA PROTEIN



• Molecule 7: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C



• Molecule 7: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C



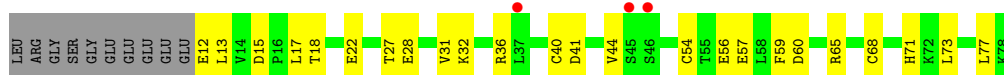
• Molecule 8: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KDA PROTEIN



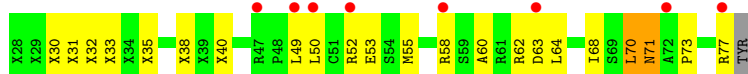
• Molecule 8: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KDA PROTEIN



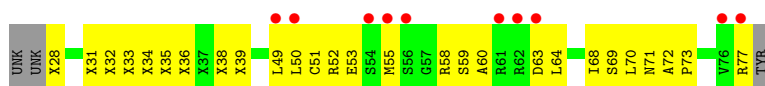




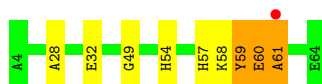
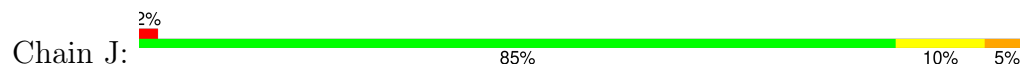
- Molecule 9: Cytochrome b-c1 complex subunit Rieske, mitochondrial



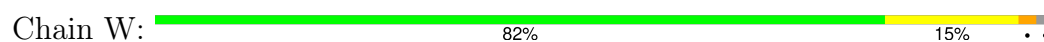
- Molecule 9: Cytochrome b-c1 complex subunit Rieske, mitochondrial



- Molecule 10: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2 KDA PROTEIN



- Molecule 10: UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2 KDA PROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.59Å 182.52Å 240.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.16 20.00 – 3.16	Depositor EDS
% Data completeness (in resolution range)	97.1 (20.00-3.16) 96.7 (20.00-3.16)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.00 (at 3.19Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.253 , 0.291 0.236 , 0.276	Depositor DCC
$R_{free}$ test set	2451 reflections (1.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	75.4	Xtriage
Anisotropy	0.738	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 64.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	32608	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.98% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: UNL, CDL, PEE, HEM, GOL, UQ, BOG, FES, 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	A	0.48	0/3513	0.67	0/4760
1	N	0.46	0/3508	0.66	0/4753
2	B	0.41	0/3196	0.64	0/4334
2	O	0.44	0/3202	0.67	1/4343 (0.0%)
3	C	0.54	0/3119	0.69	0/4270
3	P	0.48	0/3114	0.65	0/4263
4	D	0.48	0/1956	0.66	1/2658 (0.0%)
4	Q	0.39	0/1956	0.63	1/2658 (0.0%)
5	E	0.40	0/1547	0.60	0/2103
5	R	0.39	0/1543	0.61	1/2098 (0.0%)
6	F	0.54	0/911	0.66	0/1219
6	S	0.44	0/911	0.62	0/1219
7	G	0.53	0/694	0.69	1/941 (0.1%)
7	T	0.46	0/684	0.66	1/929 (0.1%)
8	H	0.48	0/582	0.65	0/779
8	U	0.36	0/561	0.59	0/751
9	I	0.45	0/218	0.66	0/293
9	V	0.43	0/218	0.65	0/293
10	J	0.46	0/508	0.62	0/682
10	W	0.41	0/490	0.59	0/660
All	All	0.46	0/32431	0.65	6/44006 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	T	18	LEU	CA-CB-CG	5.82	128.69	115.30
4	D	133	GLY	N-CA-C	5.71	127.39	113.10
4	Q	133	GLY	N-CA-C	5.44	126.69	113.10
7	G	18	LEU	CA-CB-CG	5.37	127.65	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	143	GLY	N-CA-C	5.11	125.88	113.10

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	A	3442	0	3354	153	0
1	N	3437	0	3349	155	0
2	B	3141	0	3142	215	0
2	O	3147	0	3146	215	0
3	C	3017	0	3063	108	0
3	P	3012	0	3058	126	0
4	D	1898	0	1846	71	0
4	Q	1898	0	1846	75	0
5	E	1513	0	1478	94	0
5	R	1509	0	1474	87	0
6	F	891	0	893	25	0
6	S	891	0	893	35	0
7	G	672	0	653	31	0
7	T	662	0	645	33	0
8	H	574	0	548	18	0
8	U	553	0	535	25	0
9	I	287	0	250	40	0
9	V	278	0	253	38	0
10	J	497	0	490	8	0
10	W	479	0	478	9	0
11	A	3	0	0	0	0
11	C	2	0	0	0	0
11	N	3	0	0	0	0
11	P	1	0	0	0	0
12	C	86	0	60	6	0
12	P	86	0	60	8	0
13	C	19	0	17	5	0
13	P	19	0	17	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	C	40	0	24	2	0
14	D	42	0	28	2	0
14	P	40	0	24	2	0
14	Q	42	0	28	3	0
15	C	70	0	85	2	0
15	E	50	0	77	1	0
15	N	5	0	0	0	0
15	P	49	0	72	2	0
15	R	50	0	77	0	0
16	C	6	0	8	0	0
16	P	6	0	8	0	0
17	D	43	0	30	3	0
17	Q	43	0	30	1	0
18	D	33	0	39	1	0
18	P	12	0	11	1	0
18	Q	33	0	39	0	0
19	E	4	0	0	2	0
19	R	4	0	0	2	0
20	C	8	0	0	1	0
20	E	1	0	0	0	0
20	P	9	0	0	2	0
20	R	1	0	0	0	0
All	All	32608	0	32128	1415	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 1415 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:157:VAL:HG23	9:V:64:LEU:HD21	1.40	1.04
9:I:33:UNK:HG2	9:I:73:PRO:HB3	1.07	1.02
1:N:10:ASN:HD21	2:O:18:CYS:HB3	1.23	1.01
9:I:32:UNK:N	9:I:73:PRO:HG2	1.75	0.99
1:A:178:THR:HG22	1:A:180:ALA:H	1.27	0.99

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	441/446 (99%)	384 (87%)	48 (11%)	9 (2%)	6	28
1	N	440/446 (99%)	385 (88%)	45 (10%)	10 (2%)	5	25
2	B	419/441 (95%)	350 (84%)	51 (12%)	18 (4%)	2	13
2	O	420/441 (95%)	359 (86%)	46 (11%)	15 (4%)	3	16
3	C	378/380 (100%)	346 (92%)	25 (7%)	7 (2%)	6	29
3	P	377/380 (99%)	336 (89%)	33 (9%)	8 (2%)	5	27
4	D	239/241 (99%)	218 (91%)	17 (7%)	4 (2%)	7	32
4	Q	239/241 (99%)	216 (90%)	17 (7%)	6 (2%)	4	23
5	E	194/196 (99%)	148 (76%)	30 (16%)	16 (8%)	1	3
5	R	194/196 (99%)	162 (84%)	27 (14%)	5 (3%)	4	22
6	F	99/110 (90%)	93 (94%)	6 (6%)	0	100	100
6	S	99/110 (90%)	89 (90%)	10 (10%)	0	100	100
7	G	78/81 (96%)	65 (83%)	11 (14%)	2 (3%)	4	22
7	T	77/81 (95%)	65 (84%)	10 (13%)	2 (3%)	4	22
8	H	68/77 (88%)	59 (87%)	9 (13%)	0	100	100
8	U	65/77 (84%)	53 (82%)	12 (18%)	0	100	100
9	I	29/47 (62%)	26 (90%)	3 (10%)	0	100	100
9	V	29/47 (62%)	23 (79%)	6 (21%)	0	100	100
10	J	59/61 (97%)	53 (90%)	5 (8%)	1 (2%)	7	32
10	W	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
All	All	4002/4160 (96%)	3481 (87%)	418 (10%)	103 (3%)	4	22

5 of 103 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	282	ARG

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Mol	Chain	Res	Type
2	B	26	ILE
2	B	29	LEU
2	B	171	ALA
2	B	224	LEU

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	365/368 (99%)	353 (97%)	12 (3%)	33	60
1	N	365/368 (99%)	352 (96%)	13 (4%)	30	58
2	B	332/347 (96%)	319 (96%)	13 (4%)	27	55
2	O	333/347 (96%)	319 (96%)	14 (4%)	25	53
3	C	328/329 (100%)	323 (98%)	5 (2%)	60	78
3	P	328/329 (100%)	322 (98%)	6 (2%)	54	74
4	D	200/200 (100%)	197 (98%)	3 (2%)	60	78
4	Q	200/200 (100%)	197 (98%)	3 (2%)	60	78
5	E	166/166 (100%)	163 (98%)	3 (2%)	54	74
5	R	165/166 (99%)	162 (98%)	3 (2%)	54	74
6	F	93/96 (97%)	90 (97%)	3 (3%)	34	61
6	S	93/96 (97%)	88 (95%)	5 (5%)	18	46
7	G	71/71 (100%)	69 (97%)	2 (3%)	38	64
7	T	70/71 (99%)	68 (97%)	2 (3%)	37	63
8	H	65/71 (92%)	64 (98%)	1 (2%)	60	78
8	U	63/71 (89%)	62 (98%)	1 (2%)	58	77
9	I	23/26 (88%)	21 (91%)	2 (9%)	8	29
9	V	23/26 (88%)	22 (96%)	1 (4%)	25	53
10	J	49/49 (100%)	47 (96%)	2 (4%)	26	54
10	W	47/49 (96%)	46 (98%)	1 (2%)	48	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3379/3446 (98%)	3284 (97%)	95 (3%)	38 64

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	432	LEU
2	O	402	ILE
2	O	19	PRO
2	O	104	LYS
3	P	259	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
3	P	313	GLN
4	Q	35	GLN
7	T	23	GLN
3	C	342	GLN
3	C	332	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 [i](#)

Of 36 ligands modelled in this entry, 9 are unknown - leaving 27 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
12	HEM	P	501	3	42,50,50	1.54	6 (14%)	46,82,82	1.53	10 (21%)
17	HEC	Q	501	4	32,50,50	2.11	4 (12%)	30,82,82	2.25	3 (10%)
15	PEE	C	2007	-	48,48,50	1.47	6 (12%)	51,53,55	0.82	3 (5%)
14	CDL	C	2004	-	39,39,99	1.24	2 (5%)	45,51,111	1.16	3 (6%)
14	CDL	D	2003	-	41,41,99	1.18	2 (4%)	47,53,111	1.09	4 (8%)
16	GOL	C	2011	-	5,5,5	1.22	0	5,5,5	0.48	0
12	HEM	C	501	3	42,50,50	1.65	6 (14%)	46,82,82	1.89	13 (28%)
15	PEE	P	3007	-	48,48,50	1.40	5 (10%)	51,53,55	0.77	2 (3%)
14	CDL	Q	3003	-	41,41,99	1.16	1 (2%)	47,53,111	1.08	4 (8%)
18	BOG	D	2009	-	20,20,20	1.00	1 (5%)	25,25,25	0.94	1 (4%)
15	PEE	R	3005	-	49,49,50	1.56	10 (20%)	52,54,55	0.88	3 (5%)
12	HEM	C	502	3	42,50,50	2.17	12 (28%)	46,82,82	2.22	13 (28%)
13	UQ	C	2002	-	19,19,63	2.73	11 (57%)	24,26,79	1.29	3 (12%)
18	BOG	Q	3091	-	13,13,20	1.42	3 (23%)	18,18,25	1.12	2 (11%)
19	FES	R	501	5	0,4,4	-	-	-	-	-
15	PEE	N	3008	-	4,4,50	3.83	4 (100%)	6,6,55	0.66	0
15	PEE	E	2005	-	49,49,50	1.61	11 (22%)	52,54,55	0.89	3 (5%)
18	BOG	D	2091	-	13,13,20	1.40	3 (23%)	18,18,25	1.20	2 (11%)
18	BOG	Q	3009	-	20,20,20	0.95	1 (5%)	25,25,25	0.96	1 (4%)
14	CDL	P	3004	-	39,39,99	1.21	3 (7%)	45,51,111	1.19	4 (8%)
13	UQ	P	3002	-	19,19,63	2.63	10 (52%)	24,26,79	1.33	3 (12%)
15	PEE	C	2008	-	20,20,50	1.87	6 (30%)	23,25,55	0.68	0
12	HEM	P	502	3	42,50,50	1.63	6 (14%)	46,82,82	1.83	10 (21%)
17	HEC	D	501	4	32,50,50	2.94	6 (18%)	30,82,82	2.29	4 (13%)
19	FES	E	501	5	0,4,4	-	-	-	-	-
18	BOG	P	2010	-	12,12,20	1.40	3 (25%)	17,17,25	0.62	0
16	GOL	P	3011	-	5,5,5	1.32	1 (20%)	5,5,5	0.55	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
12	HEM	P	501	3	-	5/12/54/54	-
17	HEC	Q	501	4	-	4/10/54/54	-
15	PEE	C	2007	-	-	29/52/52/54	-
14	CDL	C	2004	-	-	23/49/49/110	-
14	CDL	D	2003	-	-	27/51/51/110	-
16	GOL	C	2011	-	-	4/4/4/4	-
12	HEM	C	501	3	-	5/12/54/54	-
15	PEE	P	3007	-	-	28/52/52/54	-
14	CDL	Q	3003	-	-	28/51/51/110	-
18	BOG	D	2009	-	-	8/11/31/31	0/1/1/1
15	PEE	R	3005	-	-	28/53/53/54	-
12	HEM	C	502	3	-	6/12/54/54	-
13	UQ	C	2002	-	-	4/11/35/87	0/1/1/1
18	BOG	Q	3091	-	-	4/4/24/31	0/1/1/1
19	FES	R	501	5	-	-	0/1/1/1
15	PEE	E	2005	-	-	28/53/53/54	-
18	BOG	D	2091	-	-	0/4/24/31	0/1/1/1
18	BOG	Q	3009	-	-	8/11/31/31	0/1/1/1
14	CDL	P	3004	-	-	21/49/49/110	-
13	UQ	P	3002	-	-	4/11/35/87	0/1/1/1
15	PEE	C	2008	-	-	8/24/24/54	-
12	HEM	P	502	3	-	7/12/54/54	-
17	HEC	D	501	4	-	4/10/54/54	-
19	FES	E	501	5	-	-	0/1/1/1
18	BOG	P	2010	-	-	0/2/22/31	0/1/1/1
16	GOL	P	3011	-	-	3/4/4/4	-

The worst 5 of 123 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	D	501	HEC	C3C-C2C	-10.98	1.28	1.40
17	D	501	HEC	C2B-C3B	-10.13	1.29	1.40
17	Q	501	HEC	C2B-C3B	-7.38	1.32	1.40
17	Q	501	HEC	C3C-C2C	-6.85	1.33	1.40
12	C	502	HEM	C3C-C2C	-6.39	1.31	1.40

The worst 5 of 91 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	D	501	HEC	CBB-CAB-C3B	-8.33	107.99	127.49
17	Q	501	HEC	CBC-CAC-C3C	-7.11	110.84	127.49
17	Q	501	HEC	CBB-CAB-C3B	-7.03	111.03	127.49
12	C	502	HEM	C3B-C2B-C1B	-6.48	101.54	106.41
17	D	501	HEC	CBC-CAC-C3C	-5.87	113.75	127.49

There are no chirality outliers.

5 of 286 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	C	501	HEM	C2B-C3B-CAB-CBB
12	C	501	HEM	C4B-C3B-CAB-CBB
12	P	501	HEM	C2B-C3B-CAB-CBB
12	P	501	HEM	C4B-C3B-CAB-CBB
13	C	2002	UQ	C1-C6-C7-C8

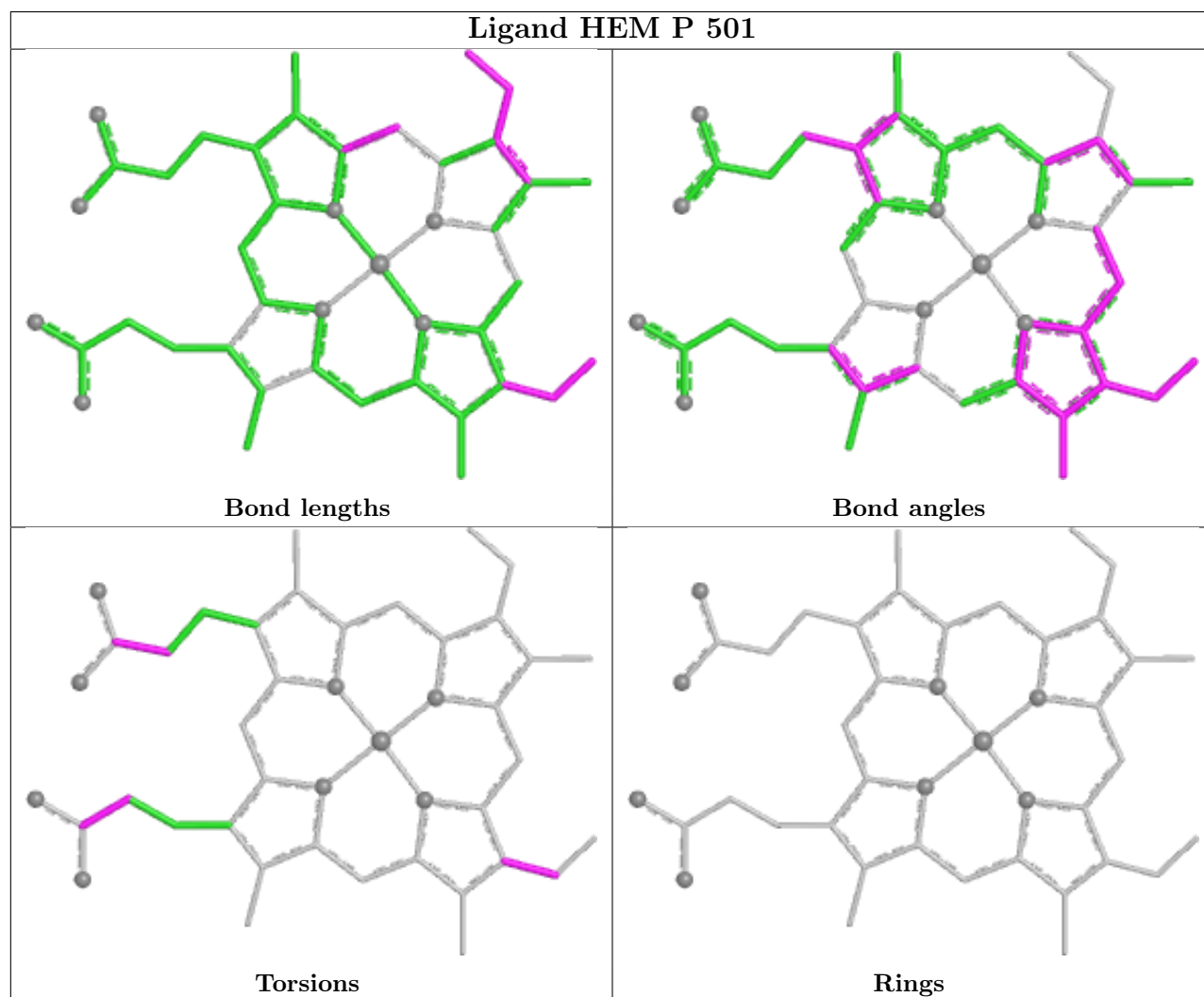
There are no ring outliers.

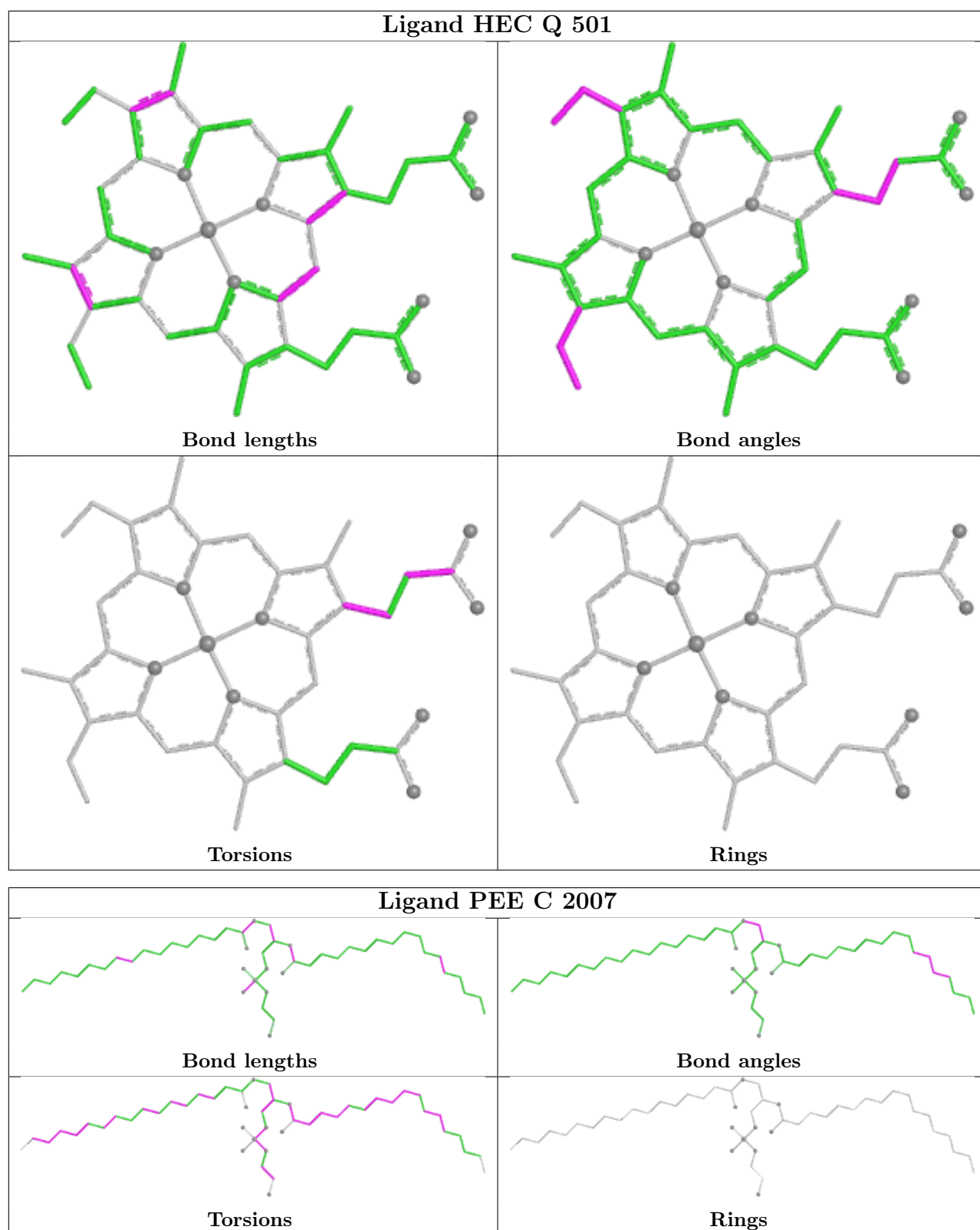
19 monomers are involved in 47 short contacts:

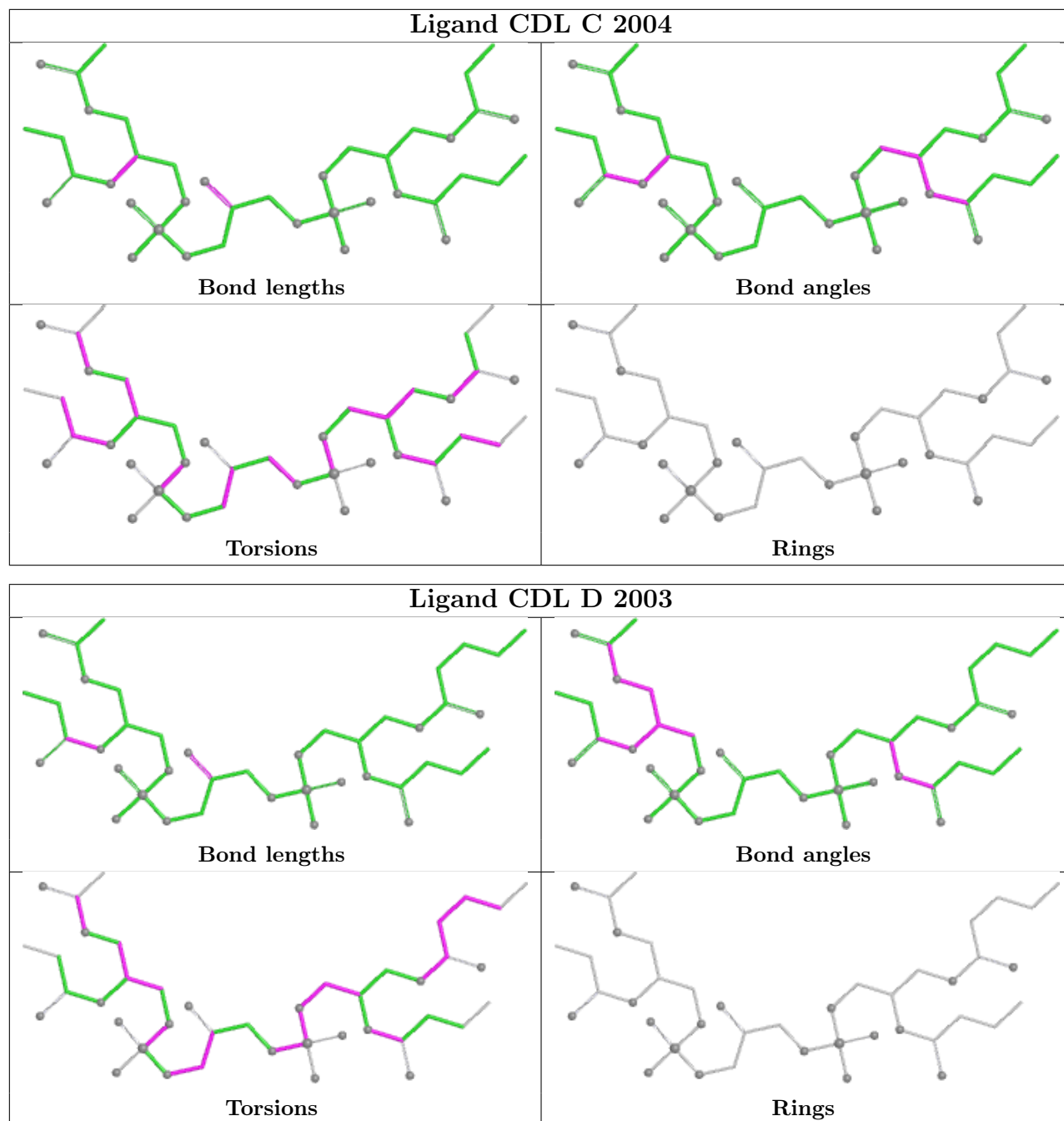
Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	P	501	HEM	5	0
17	Q	501	HEC	1	0
15	C	2007	PEE	2	0
14	C	2004	CDL	2	0
14	D	2003	CDL	2	0
12	C	501	HEM	5	0
15	P	3007	PEE	2	0
14	Q	3003	CDL	3	0
18	D	2009	BOG	1	0
12	C	502	HEM	1	0
13	C	2002	UQ	5	0
19	R	501	FES	2	0
15	E	2005	PEE	1	0
14	P	3004	CDL	2	0
13	P	3002	UQ	4	0
12	P	502	HEM	3	0
17	D	501	HEC	3	0
19	E	501	FES	2	0
18	P	2010	BOG	1	0

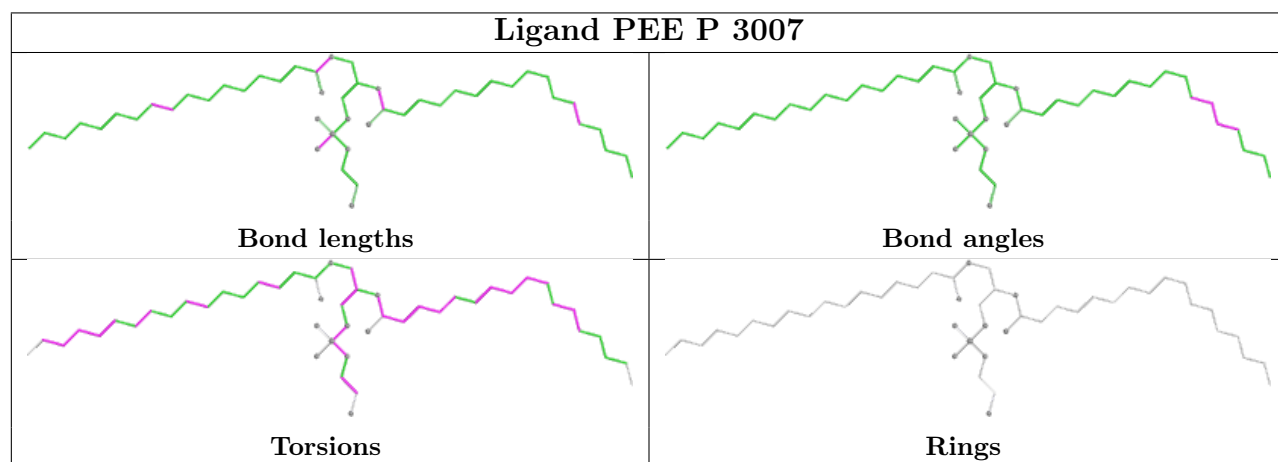
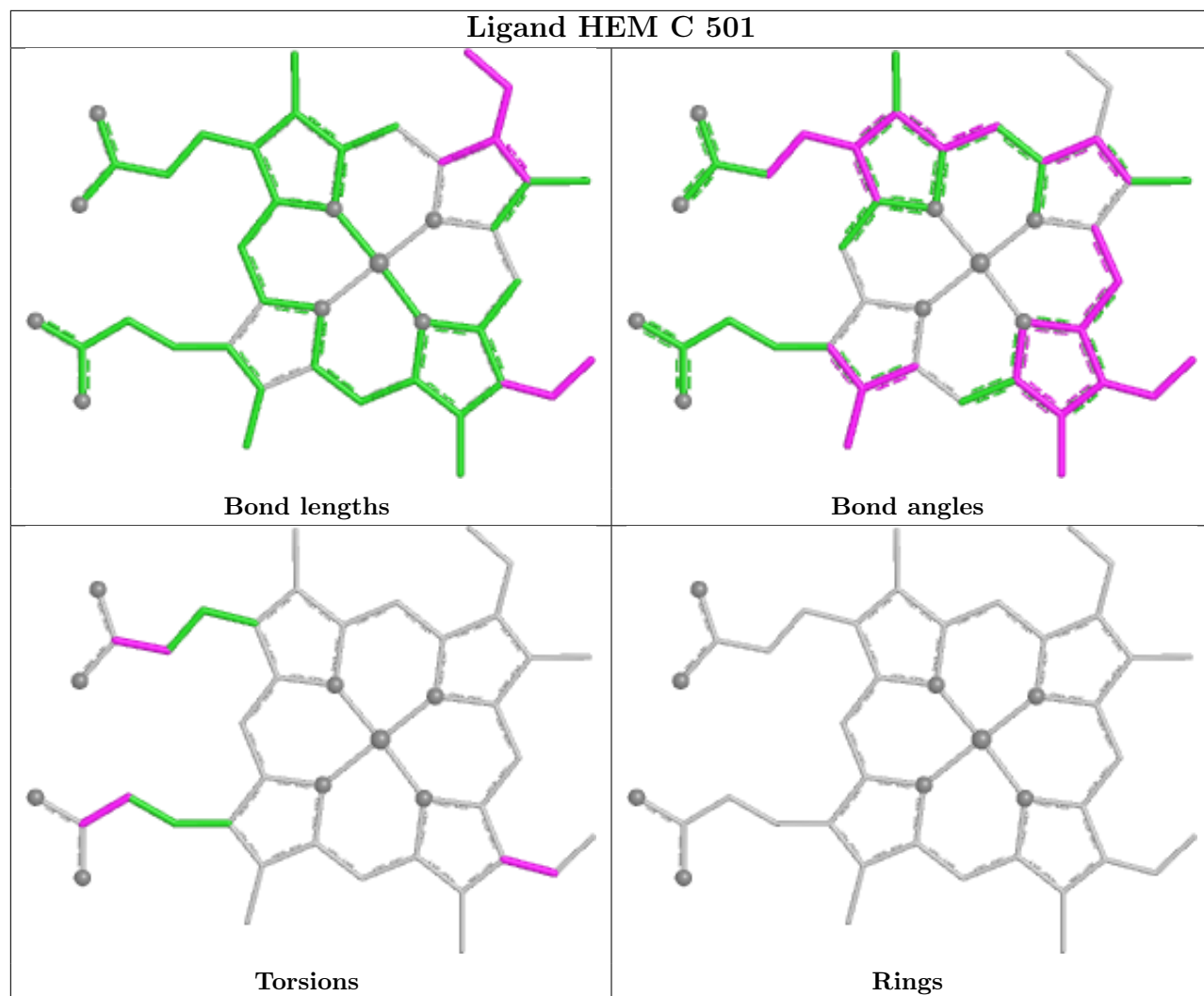
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

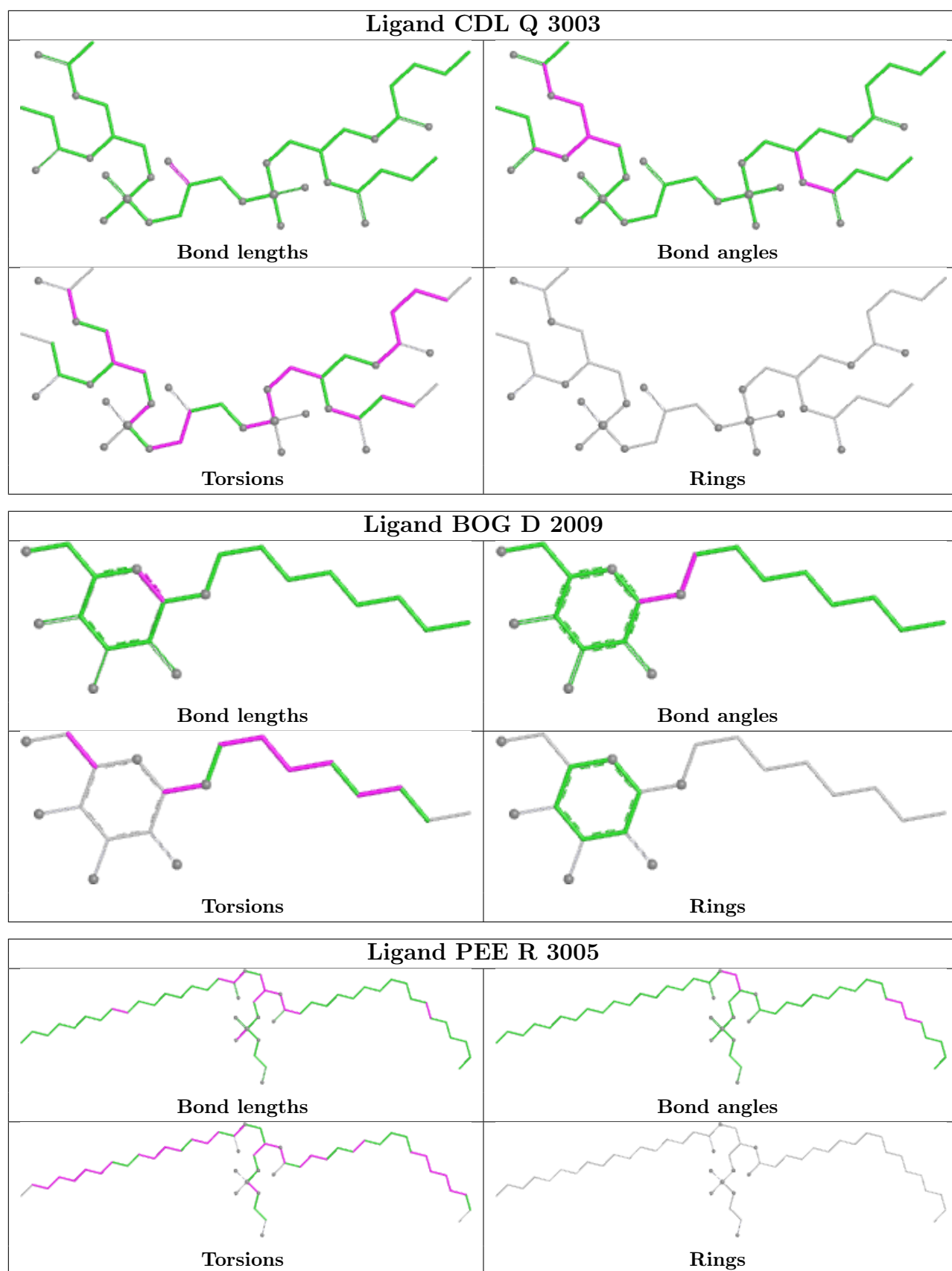
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.



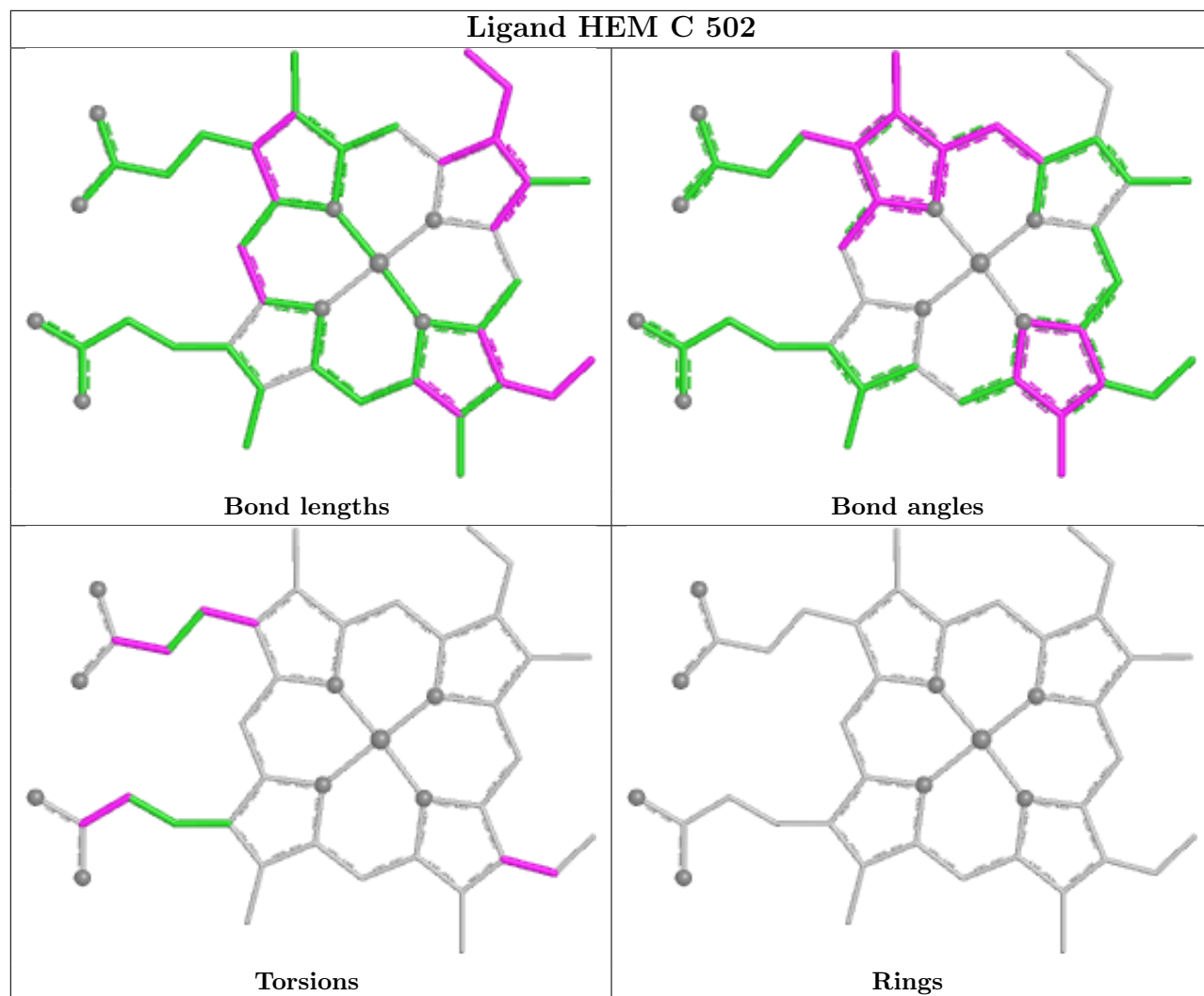


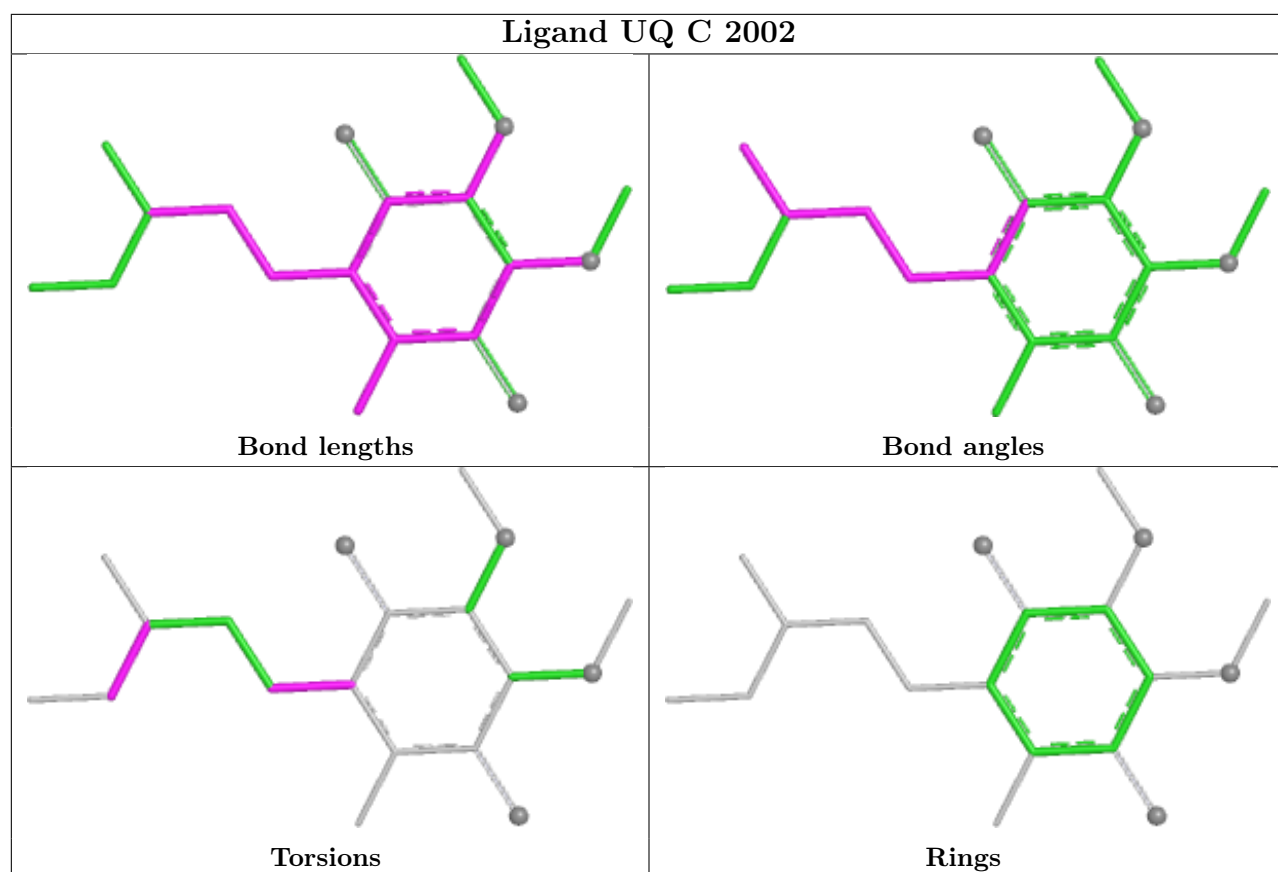




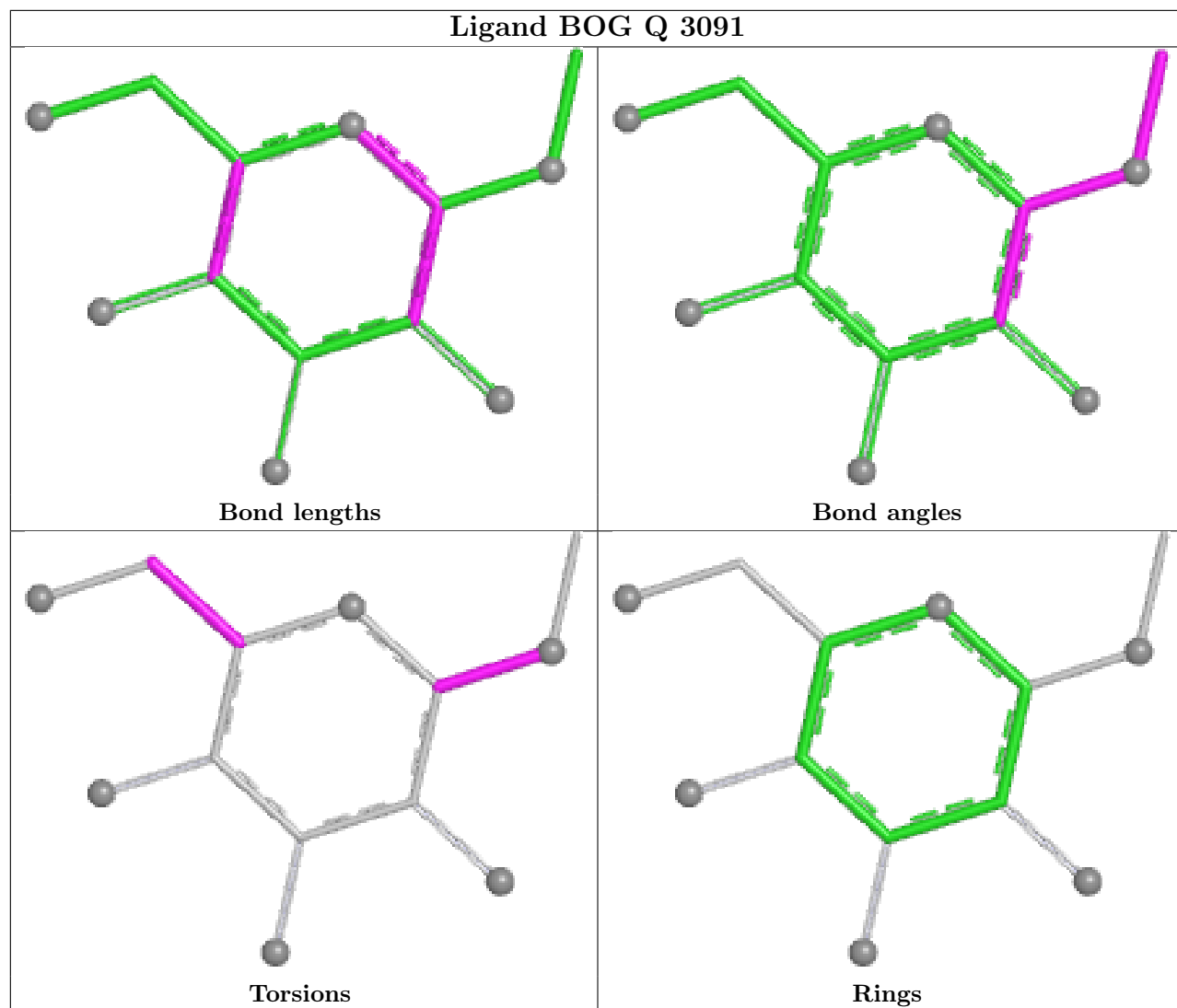


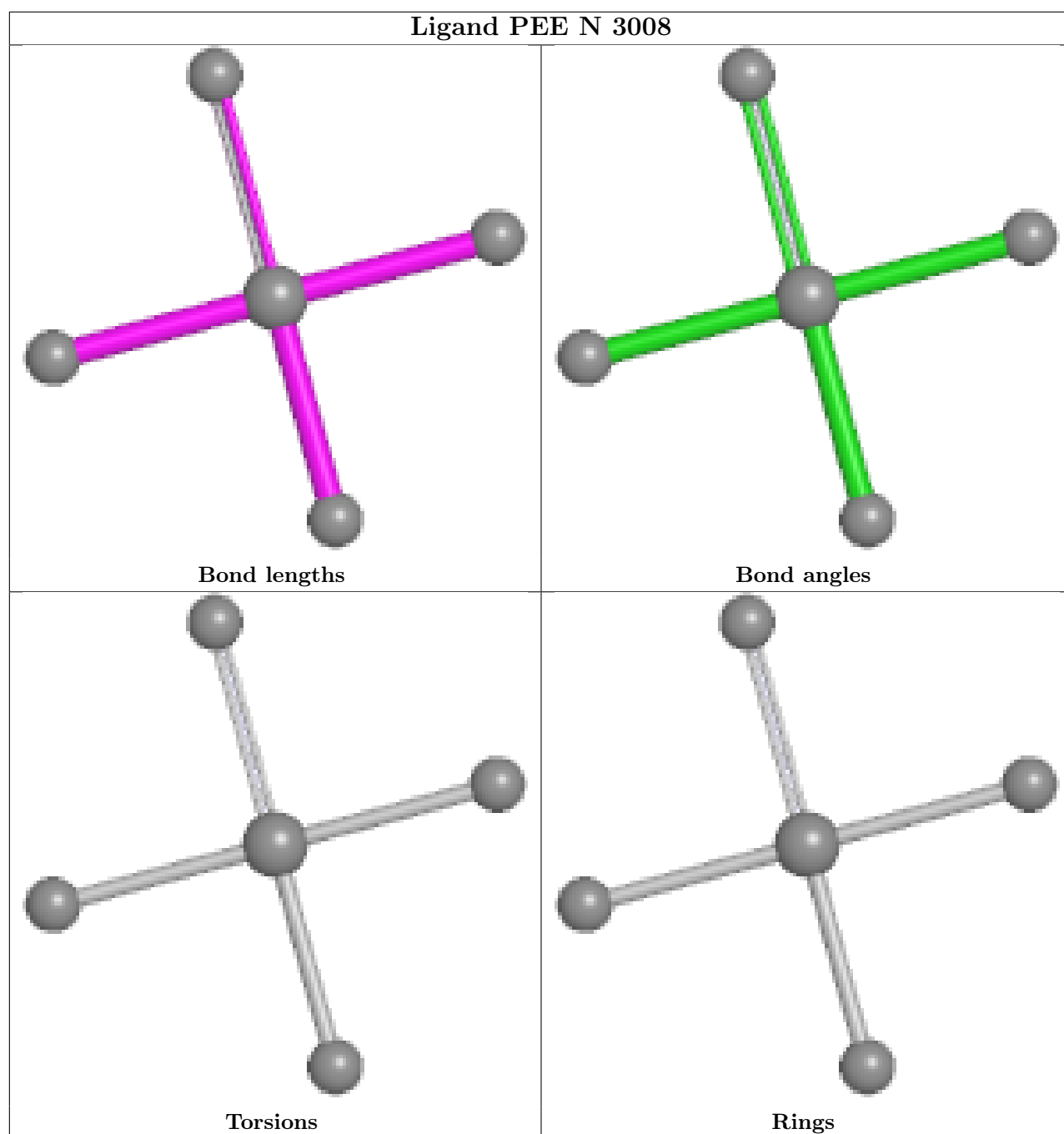


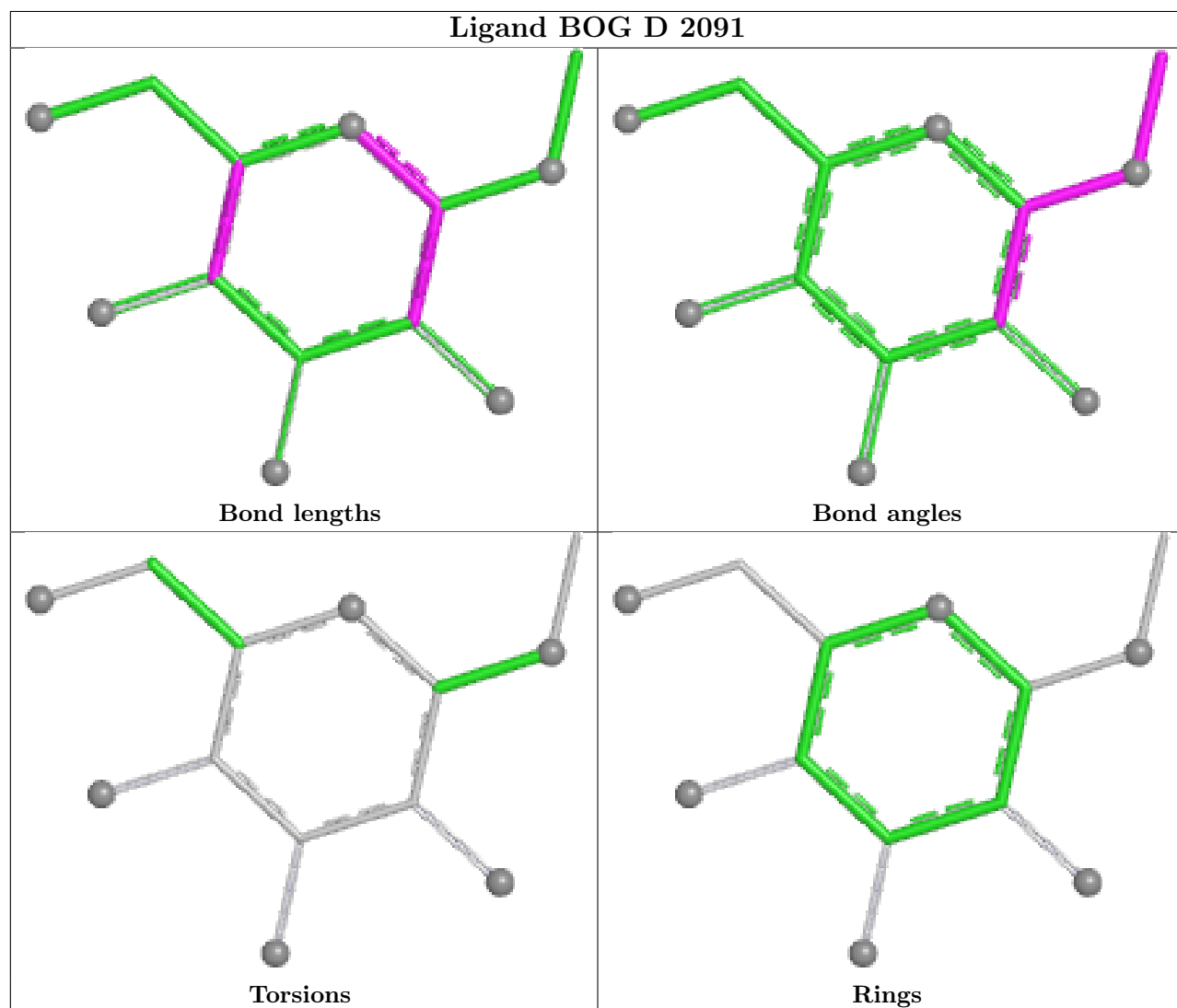
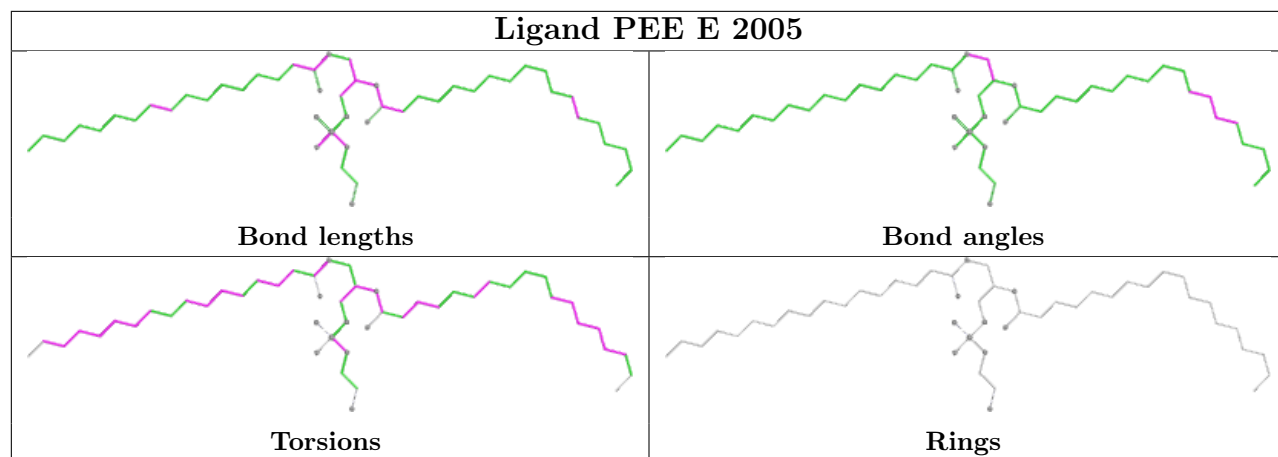


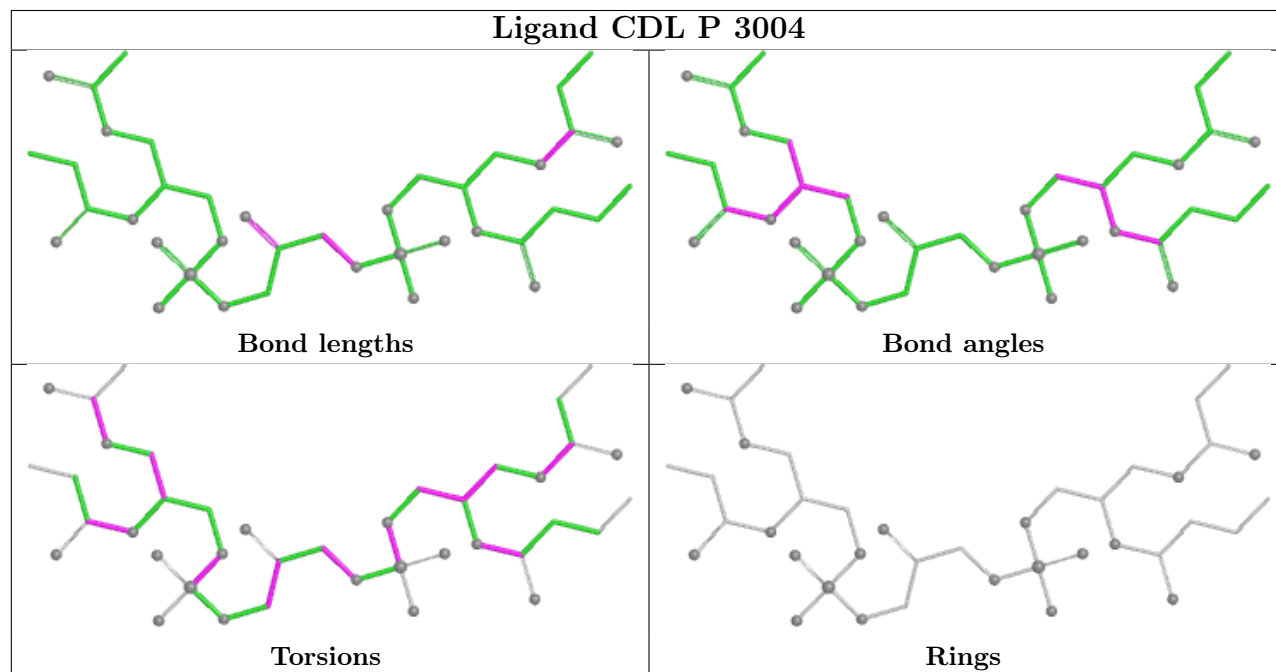
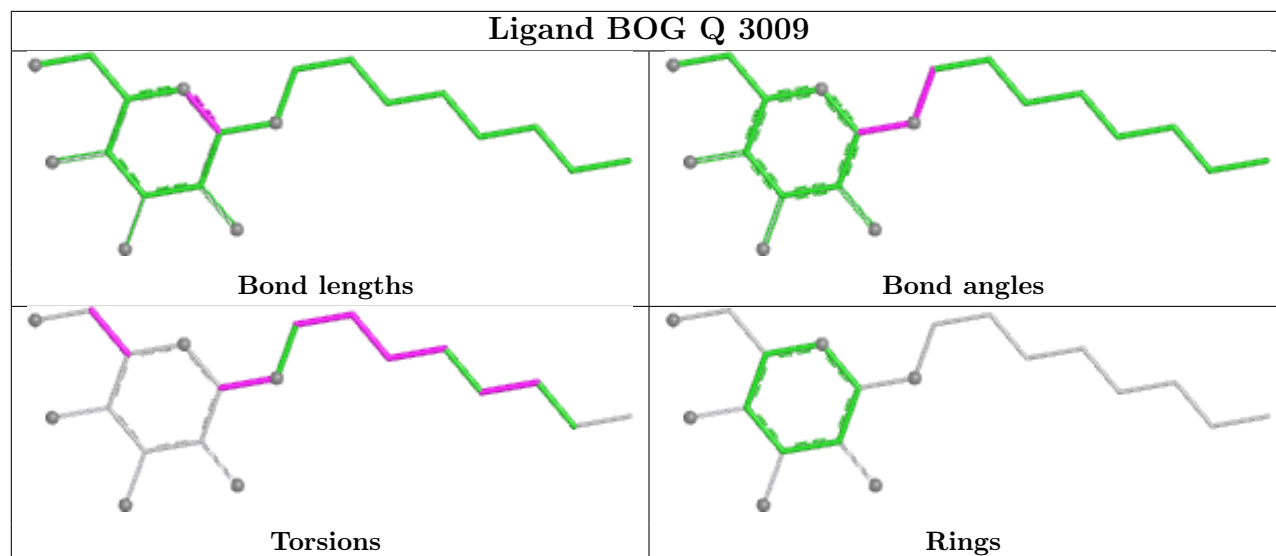


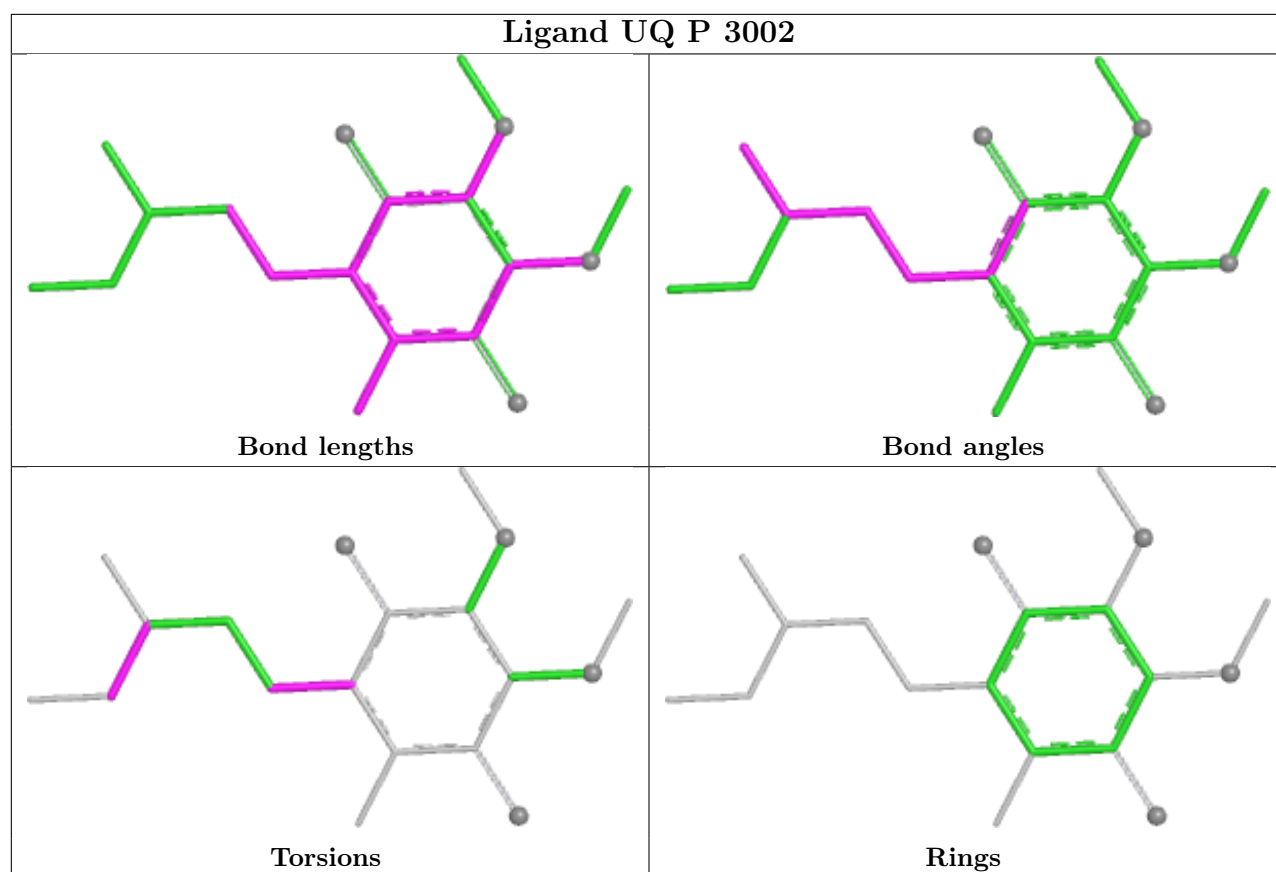
## Ligand BOG Q 3091

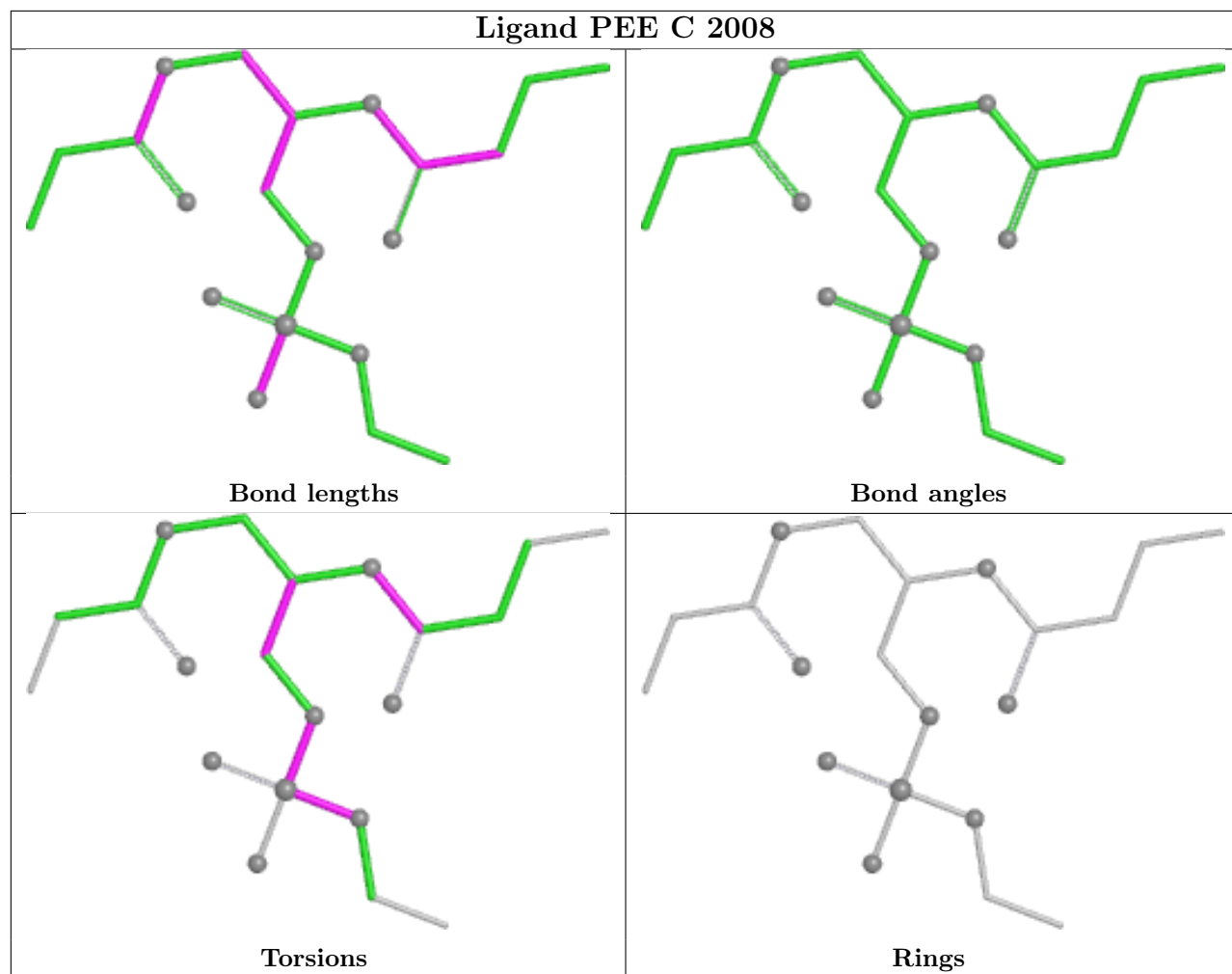




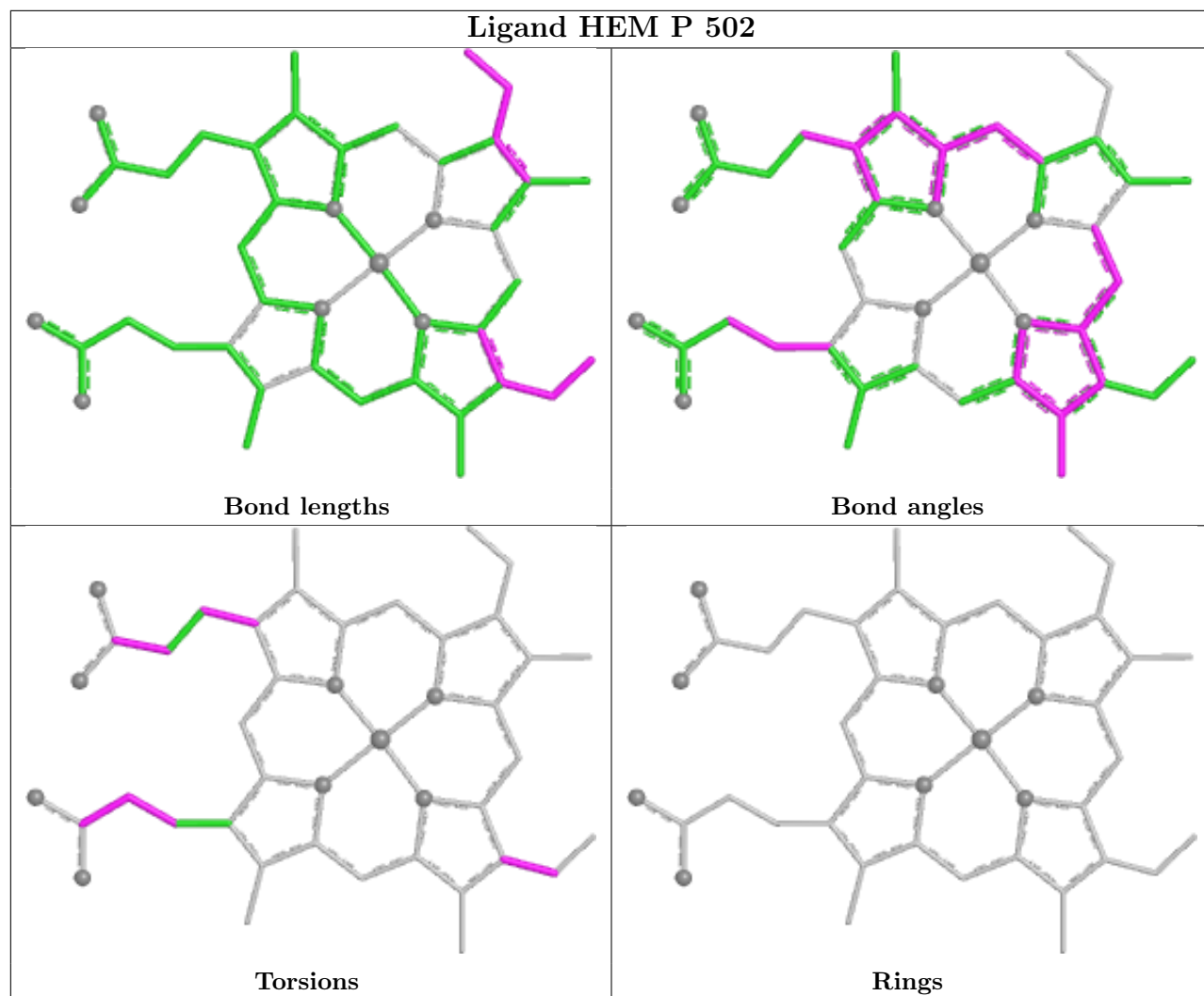


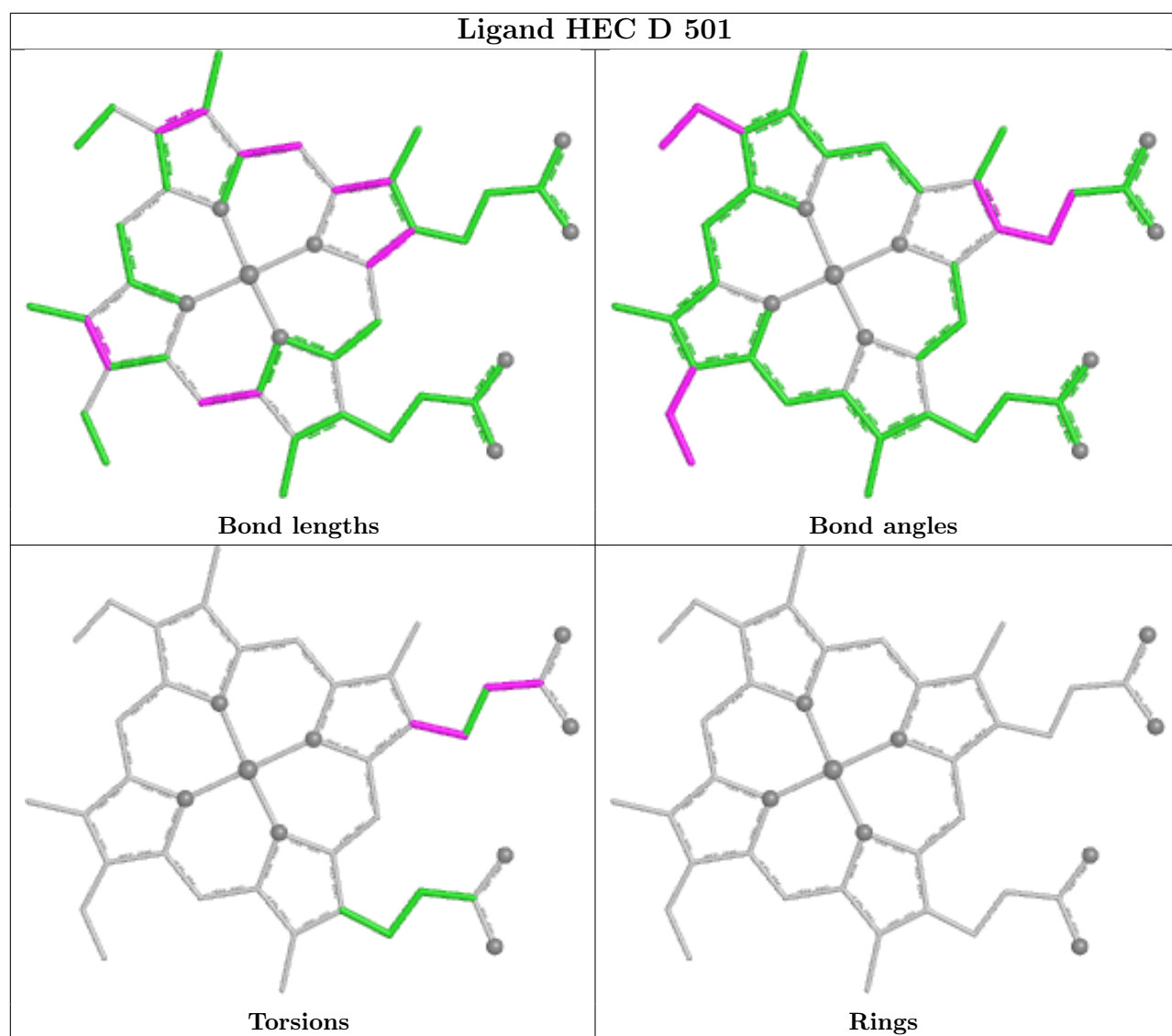


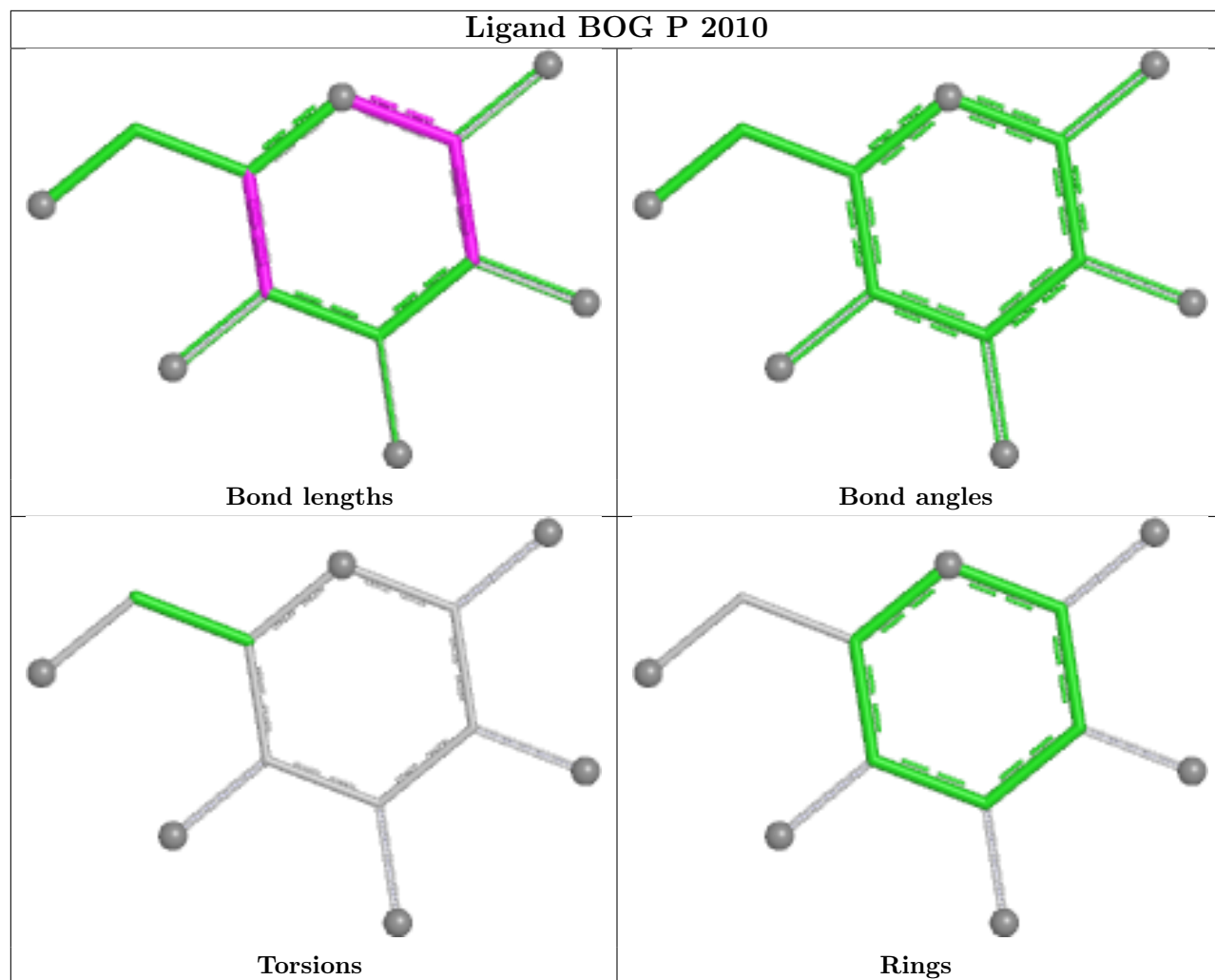












## 5.7 Other polymers [i](#)

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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å <sup>2</sup> )	Q < 0.9
1	A	443/446 (99%)	-0.18	2 (0%) 87 77	38, 72, 106, 123	0
1	N	442/446 (99%)	-0.02	7 (1%) 70 55	41, 79, 111, 121	0
2	B	421/441 (95%)	0.21	11 (2%) 57 41	59, 90, 133, 158	0
2	O	422/441 (95%)	0.11	10 (2%) 59 44	49, 86, 120, 149	0
3	C	380/380 (100%)	-0.58	4 (1%) 77 62	25, 46, 88, 131	0
3	P	379/380 (99%)	-0.28	1 (0%) 90 83	34, 70, 102, 127	0
4	D	241/241 (100%)	-0.53	0 100 100	38, 51, 105, 124	0
4	Q	241/241 (100%)	0.10	3 (1%) 76 60	55, 88, 124, 142	0
5	E	196/196 (100%)	0.79	36 (18%) 4 3	42, 120, 141, 149	125 (63%)
5	R	196/196 (100%)	0.43	11 (5%) 31 20	51, 90, 126, 137	127 (64%)
6	F	101/110 (91%)	-0.59	1 (0%) 79 65	32, 53, 74, 109	0
6	S	101/110 (91%)	-0.02	0 100 100	56, 79, 121, 145	0
7	G	80/81 (98%)	-0.31	1 (1%) 74 59	37, 63, 111, 120	0
7	T	79/81 (97%)	0.41	6 (7%) 21 14	54, 99, 162, 174	0
8	H	70/77 (90%)	-0.08	1 (1%) 73 58	44, 73, 98, 145	0
8	U	67/77 (87%)	0.72	3 (4%) 39 25	110, 132, 150, 155	0
9	I	31/47 (65%)	1.46	8 (25%) 2 1	80, 125, 161, 162	0
9	V	31/47 (65%)	1.82	10 (32%) 1 1	81, 114, 162, 165	0
10	J	61/61 (100%)	-0.20	1 (1%) 70 55	51, 66, 113, 156	0
10	W	60/61 (98%)	0.09	0 100 100	66, 86, 130, 135	0
All	All	4042/4160 (97%)	-0.02	116 (2%) 54 38	25, 77, 131, 174	252 (6%)

The worst 5 of 116 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
9	V	63	ASP	9.4
9	I	63	ASP	6.3
2	B	19	PRO	5.9
5	E	134	ILE	5.7
5	E	158	CYS	5.2

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
15	PEE	C	2008	21/51	0.46	0.29	150,154,158,159	0
15	PEE	N	3008	5/51	0.63	0.19	117,118,119,119	0
18	BOG	Q	3091	13/20	0.65	0.21	195,196,196,196	0
14	CDL	Q	3003	42/100	0.69	0.21	134,150,157,158	0
18	BOG	D	2091	13/20	0.72	0.26	185,187,187,187	0
14	CDL	D	2003	42/100	0.76	0.19	97,106,116,117	0
11	UNL	N	3291	1/-	0.76	0.17	37,37,37,37	0
18	BOG	P	2010	12/20	0.78	0.19	155,156,157,158	0
14	CDL	P	3004	40/100	0.78	0.16	107,115,122,124	0
15	PEE	R	3005	50/51	0.79	0.19	87,109,125,125	0
13	UQ	P	3002	19/63	0.81	0.23	121,130,133,133	0
15	PEE	E	2005	50/51	0.83	0.18	72,96,104,105	0
15	PEE	P	3007	49/51	0.83	0.15	65,94,110,112	0
11	UNL	P	3286	1/-	0.84	0.08	55,55,55,55	0
19	FES	E	501	4/4	0.84	0.15	161,162,162,162	4
11	UNL	C	3288	1/-	0.85	0.26	84,84,84,84	0
13	UQ	C	2002	19/63	0.86	0.16	82,84,86,86	0
11	UNL	A	3289	1/-	0.86	0.11	38,38,38,38	0
14	CDL	C	2004	40/100	0.87	0.13	69,86,100,102	0

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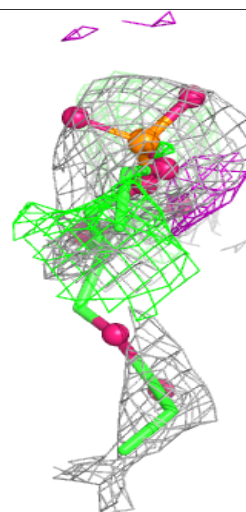
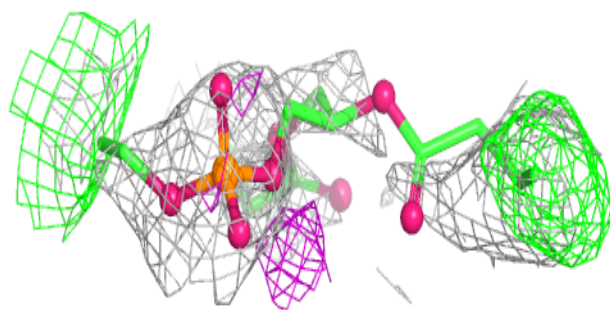
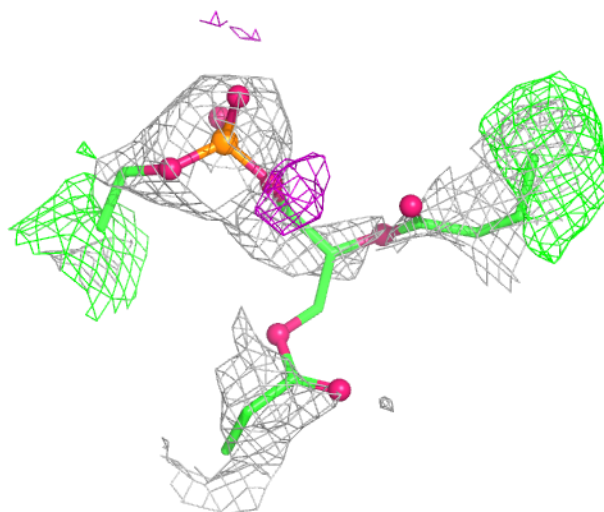
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
15	PEE	C	2007	49/51	0.88	0.13	42,65,85,87	0
11	UNL	C	3287	1/-	0.88	0.18	88,88,88,88	0
11	UNL	A	3284	1/-	0.90	0.09	28,28,28,28	0
18	BOG	D	2009	20/20	0.90	0.10	52,70,74,76	0
11	UNL	N	4231	1/-	0.90	0.11	67,67,67,67	0
16	GOL	P	3011	6/6	0.91	0.16	86,87,88,89	0
18	BOG	Q	3009	20/20	0.91	0.12	82,93,95,95	0
16	GOL	C	2011	6/6	0.92	0.13	70,71,72,75	0
11	UNL	A	3231	1/-	0.92	0.18	91,91,91,91	0
11	UNL	N	3290	1/-	0.93	0.14	53,53,53,53	0
17	HEC	Q	501	43/43	0.95	0.10	70,75,81,84	0
19	FES	R	501	4/4	0.97	0.12	92,94,94,95	4
12	HEM	C	502	43/43	0.98	0.07	23,30,38,44	0
17	HEC	D	501	43/43	0.98	0.06	35,40,48,52	0
12	HEM	P	501	43/43	0.98	0.07	48,52,61,66	0
12	HEM	P	502	43/43	0.98	0.07	43,50,60,65	0
12	HEM	C	501	43/43	0.98	0.07	30,36,47,53	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.

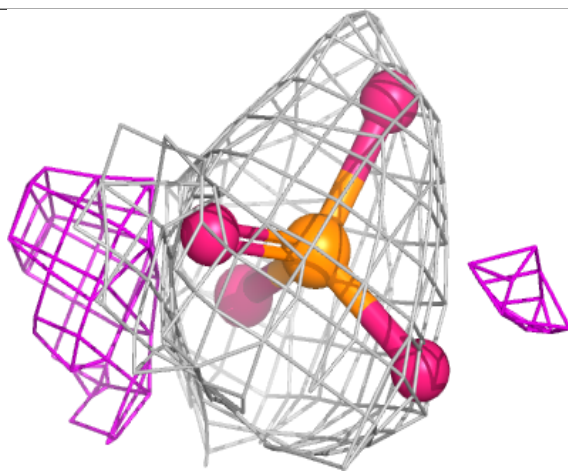
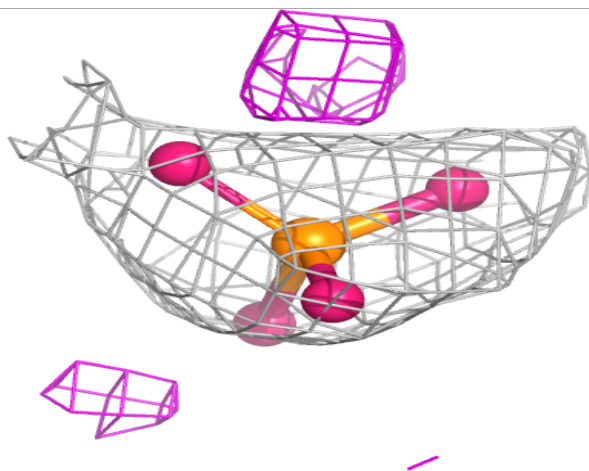
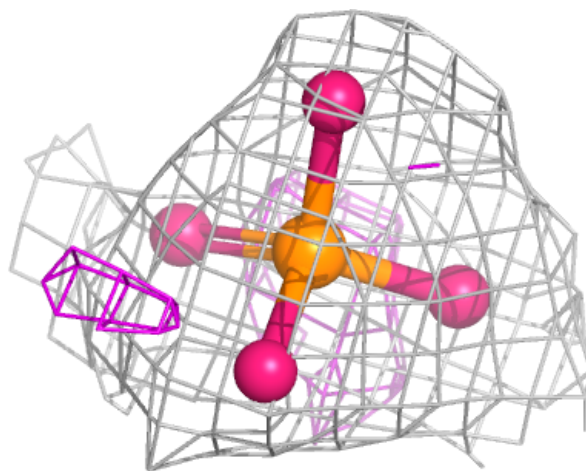
**Electron density around PEE C 2008:**

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



**Electron density around PEE N 3008:**

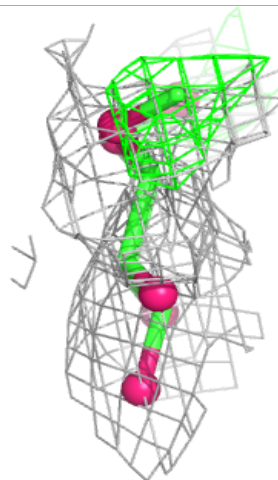
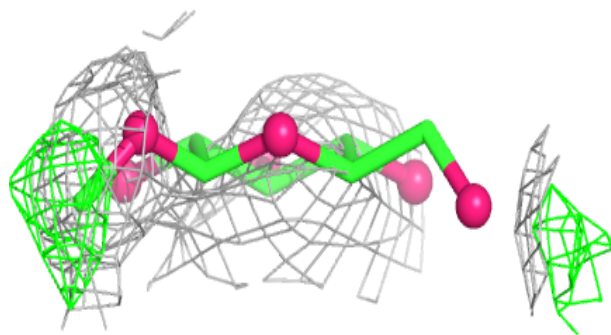
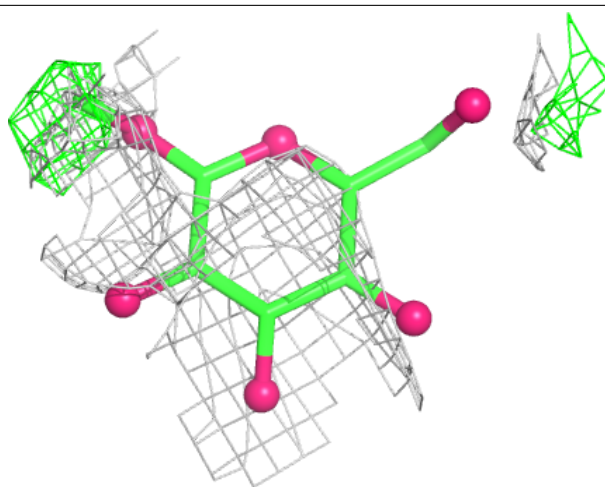
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and green (positive)





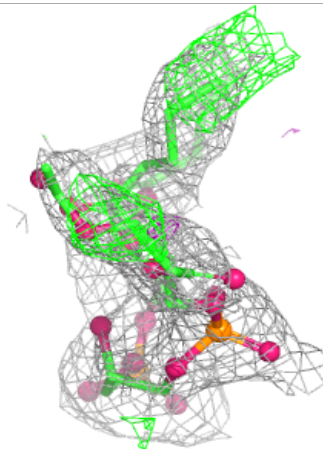
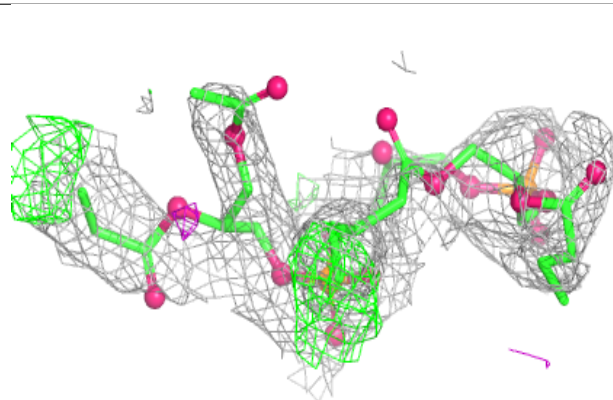
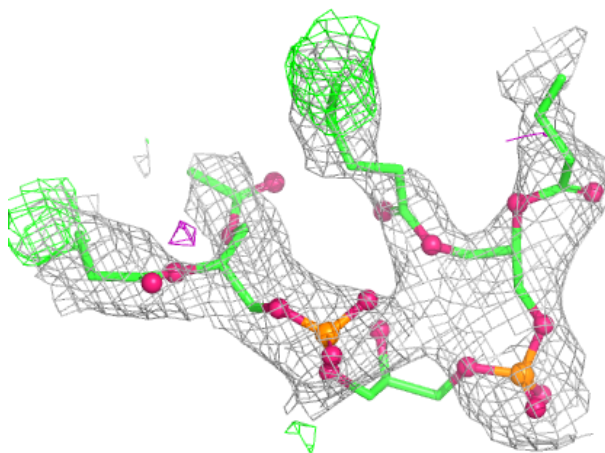
**Electron density around BOG Q 3091:**

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and green (positive)



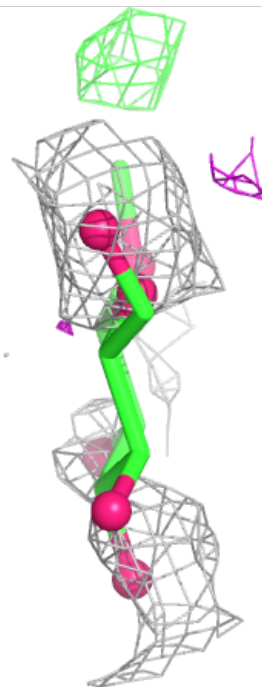
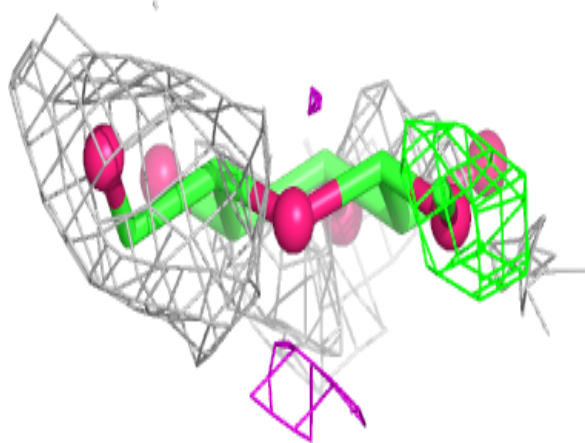
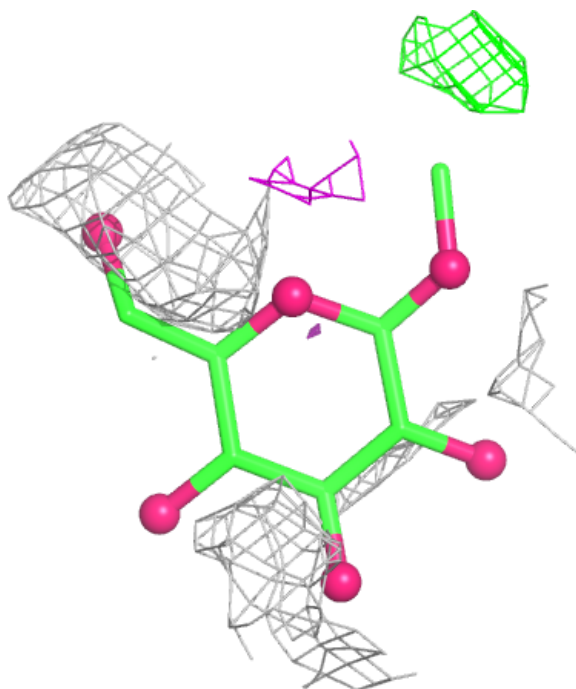
**Electron density around CDL Q 3003:**

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and green (positive)



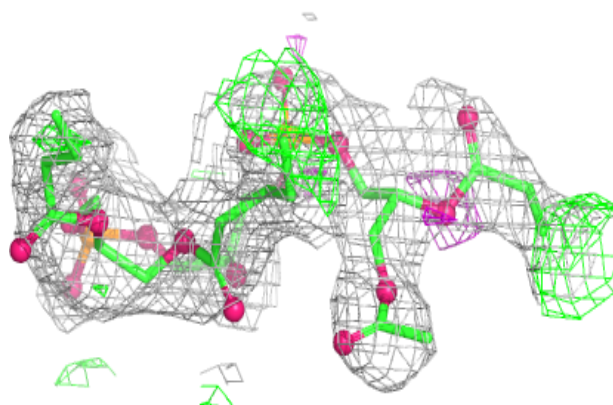
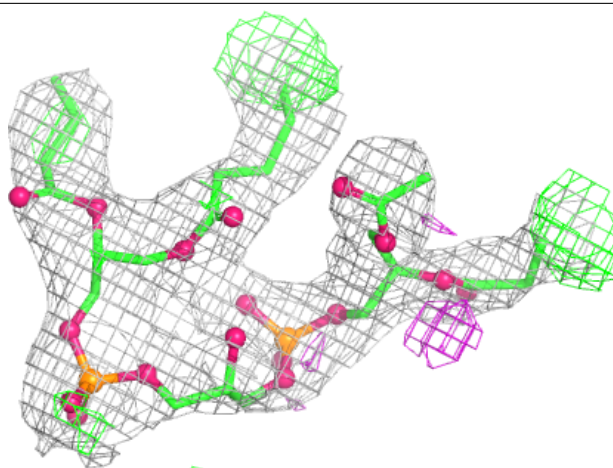
**Electron density around BOG D 2091:**

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



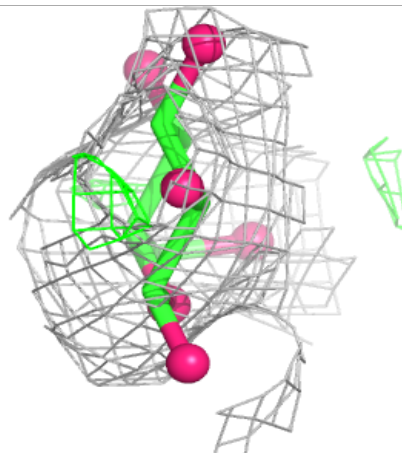
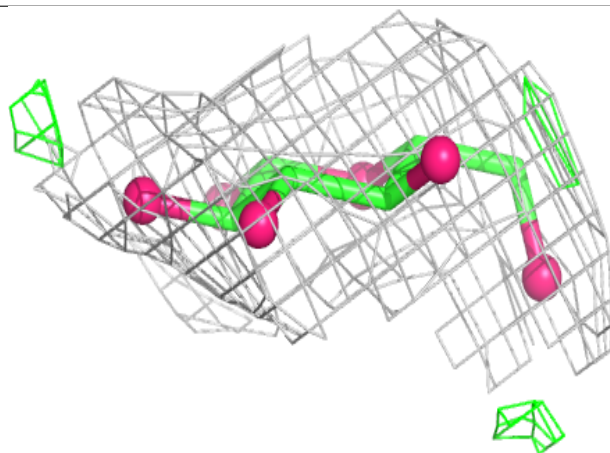
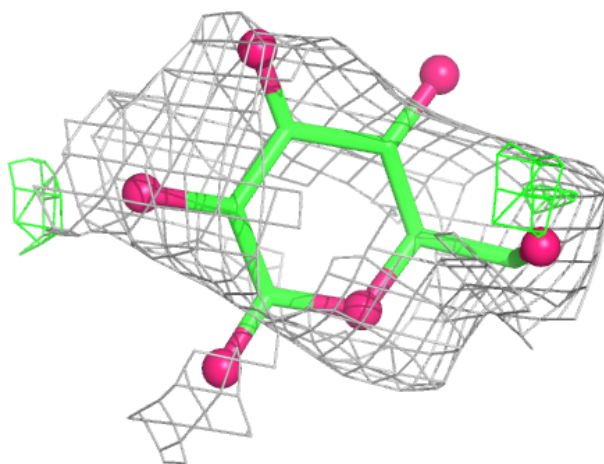
**Electron density around CDL D 2003:**

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



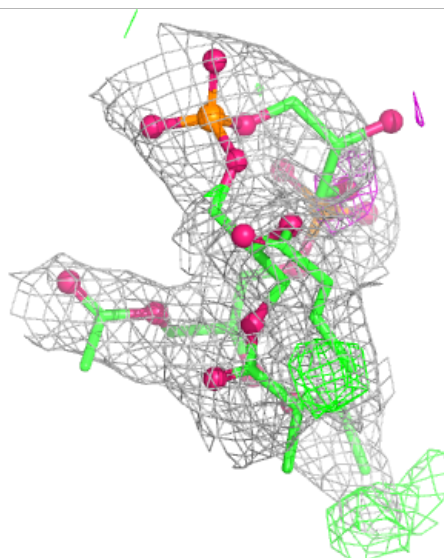
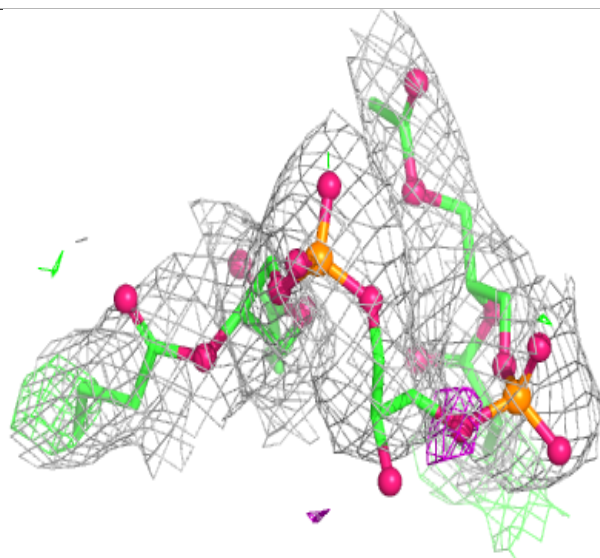
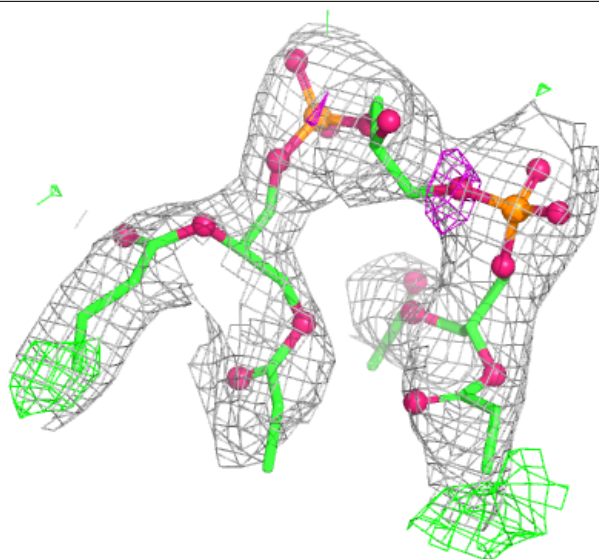
**Electron density around BOG P 2010:**

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and green (positive)



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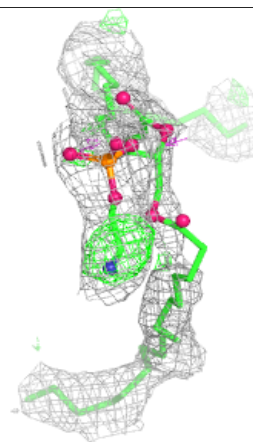
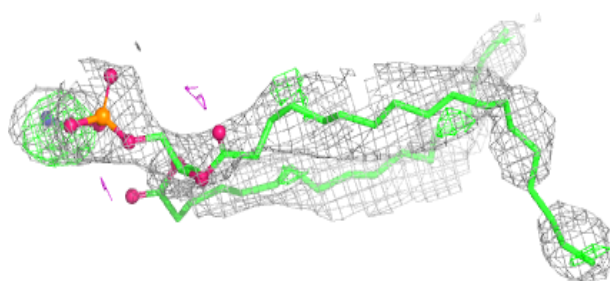
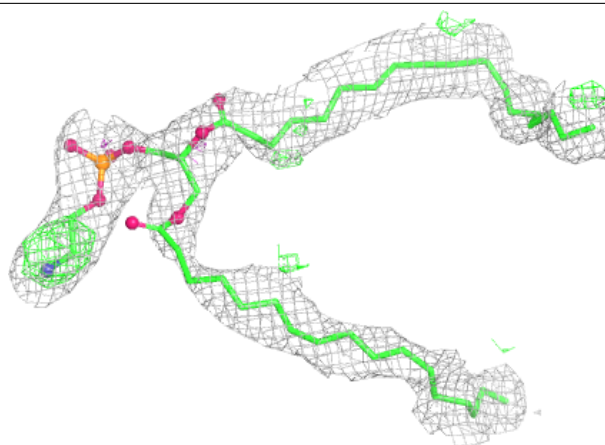
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and green (positive)



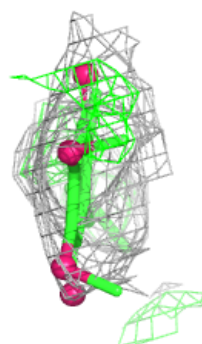
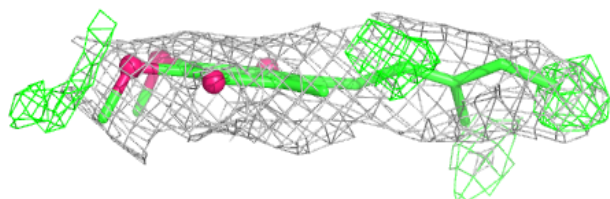
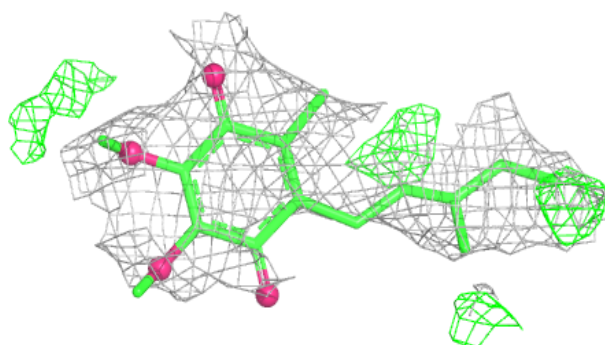


**Electron density around PEE R 3005:**

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and green (positive)

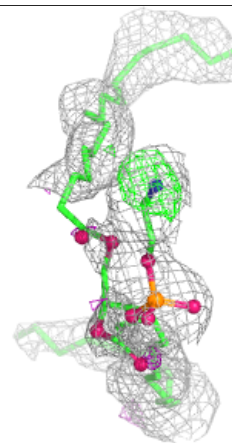
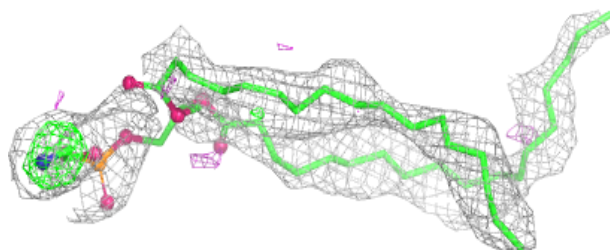
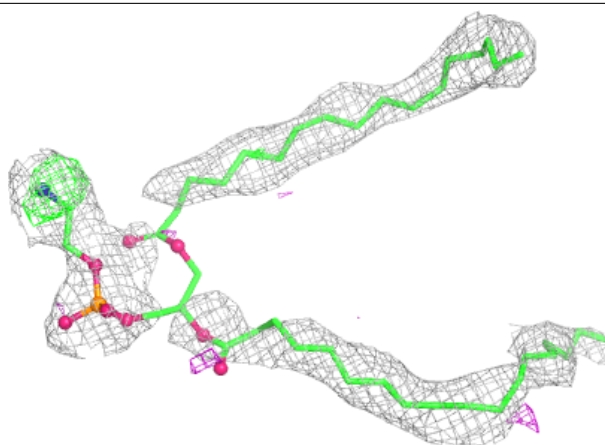
**Electron density around UQ P 3002:**

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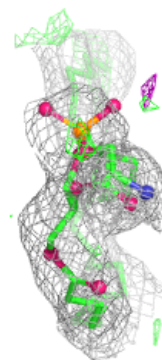
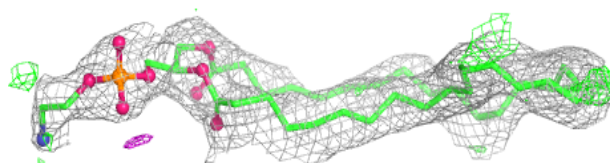
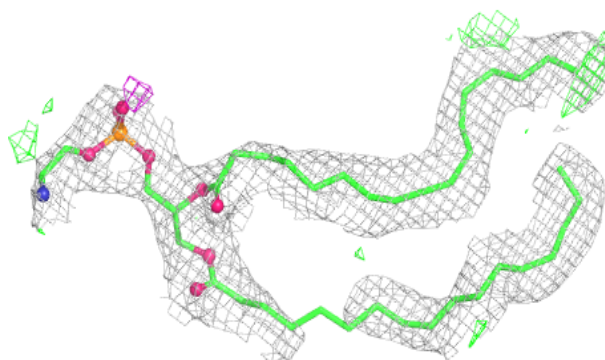


**Electron density around PEE E 2005:**

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and green (positive)

**Electron density around PEE P 3007:**

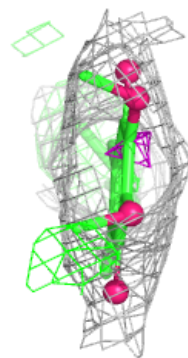
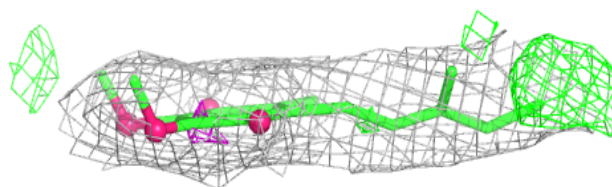
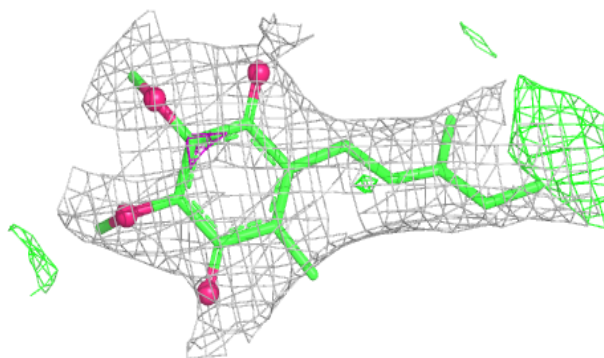
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
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and green (positive)





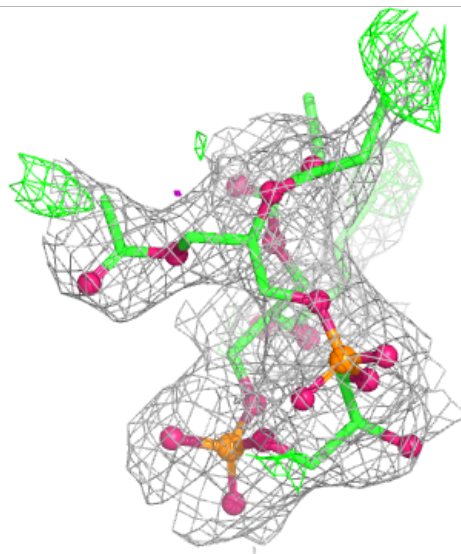
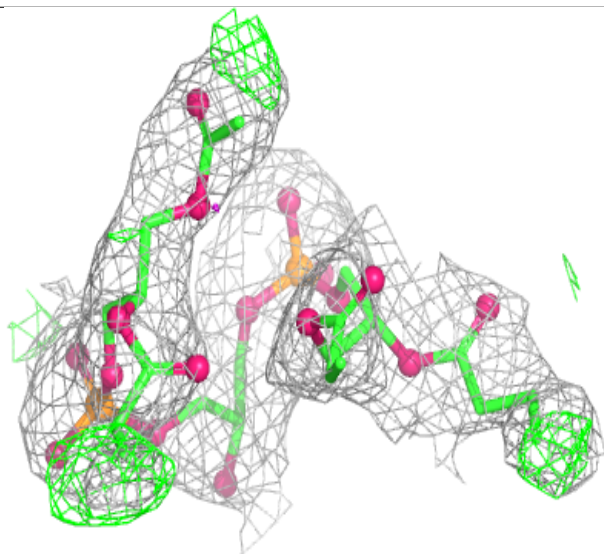
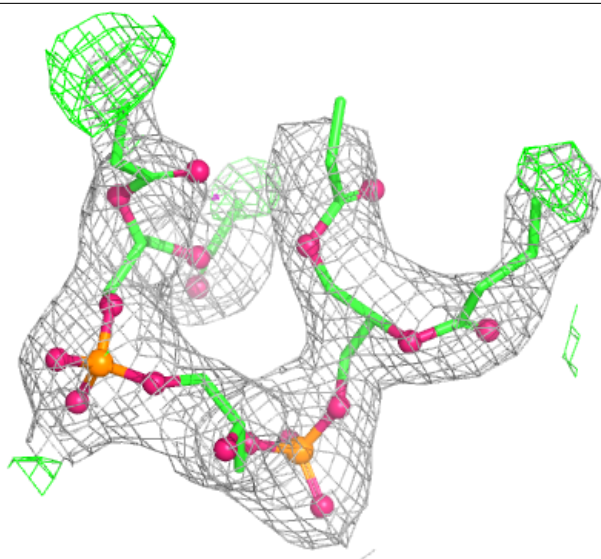
**Electron density around UQ C 2002:**

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and green (positive)



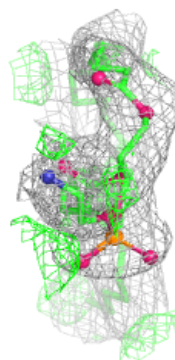
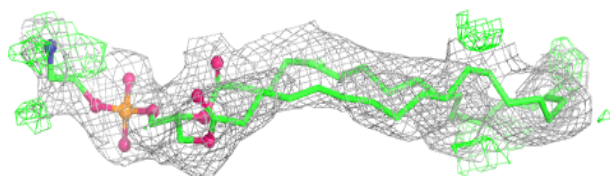
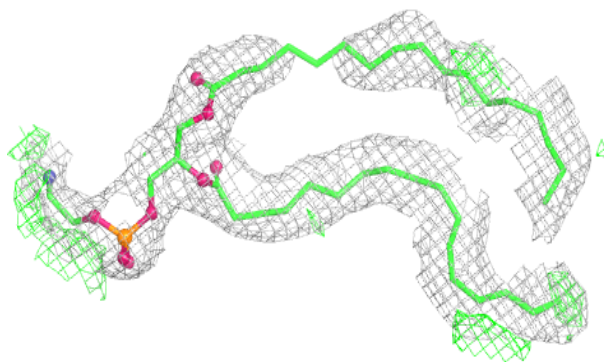
**Electron density around CDL C 2004:**

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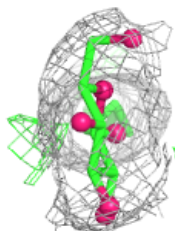
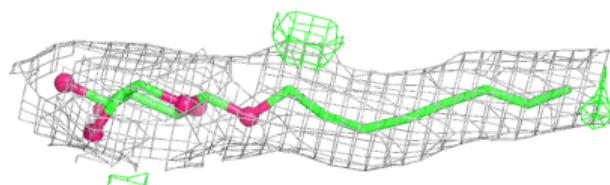
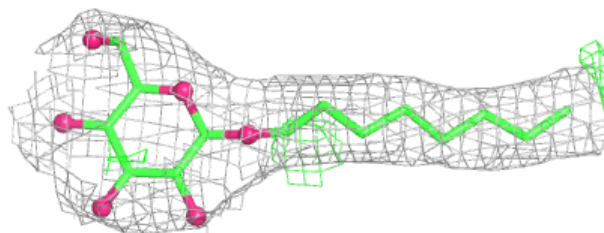


**Electron density around PEE C 2007:**

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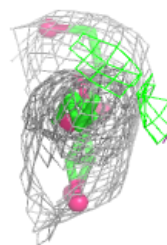
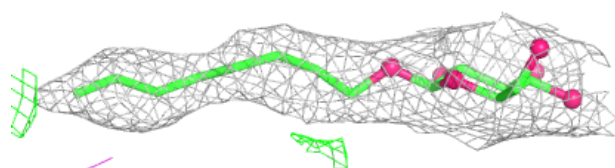
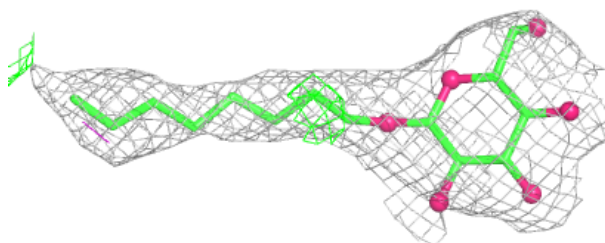
**Electron density around BOG D 2009:**

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and green (positive)

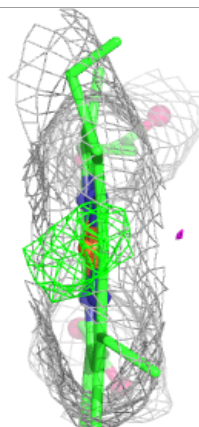
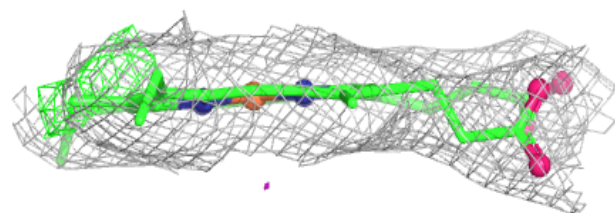
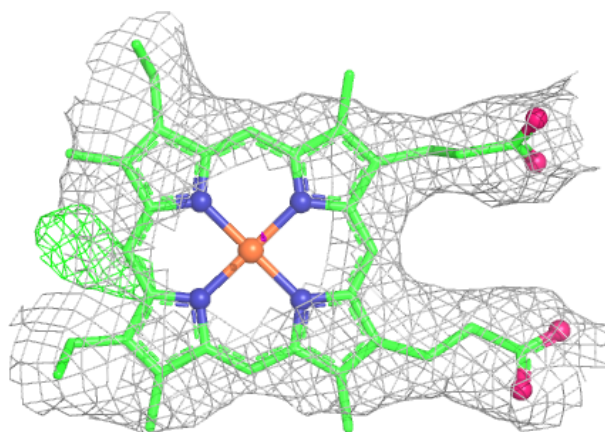


**Electron density around BOG Q 3009:**

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

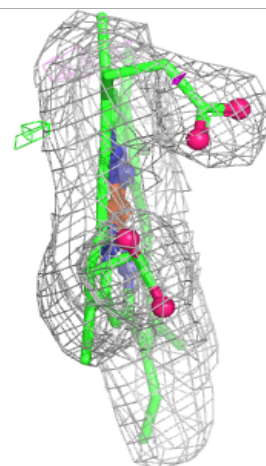
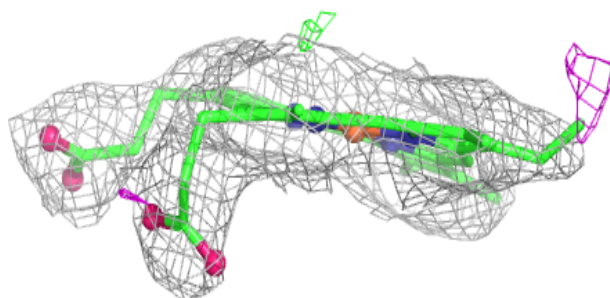
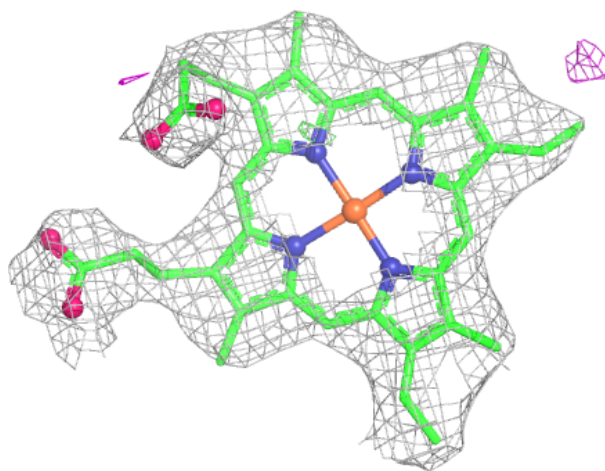
**Electron density around HEC Q 501:**

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



**Electron density around HEM C 502:**

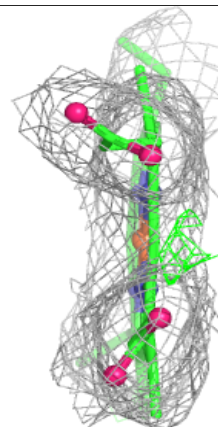
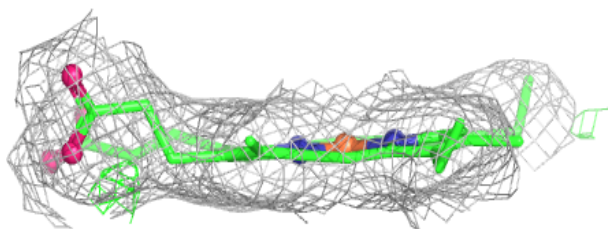
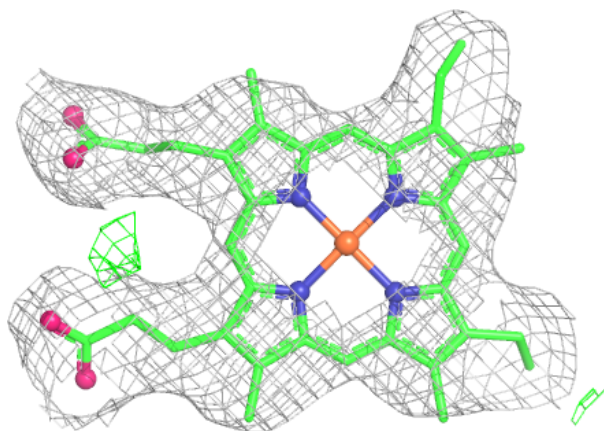
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





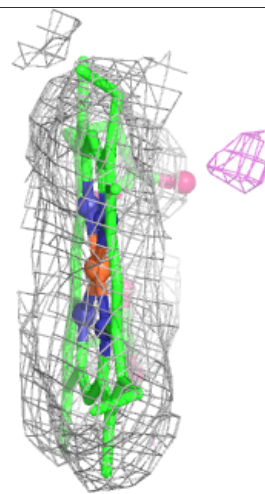
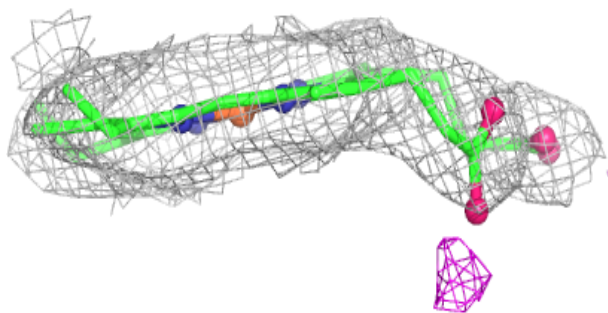
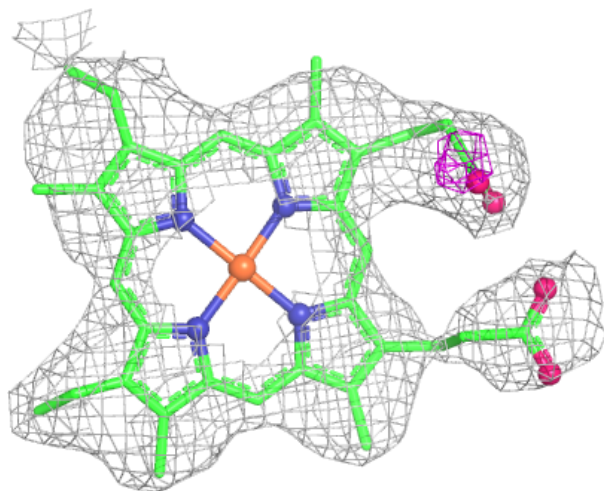
**Electron density around HEC D 501:**

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



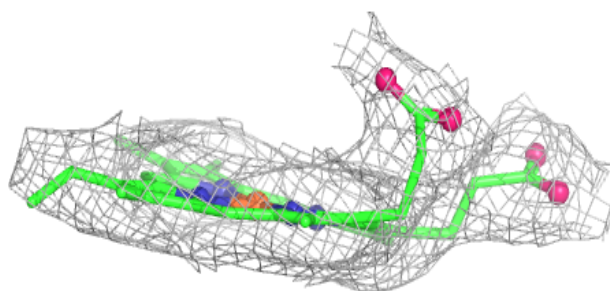
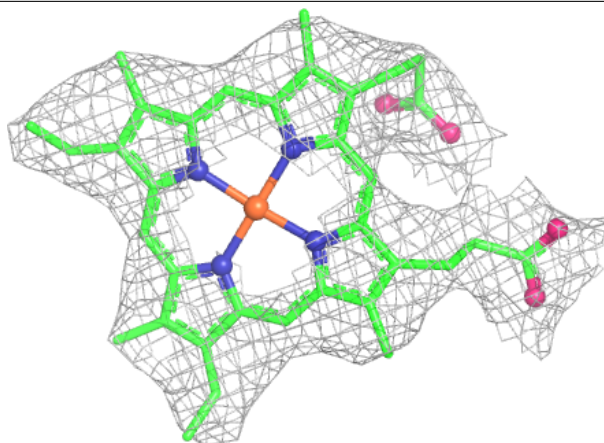
**Electron density around HEM P 501:**

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



**Electron density around HEM P 502:**

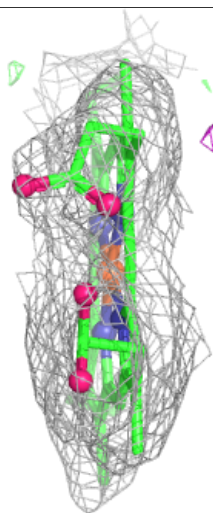
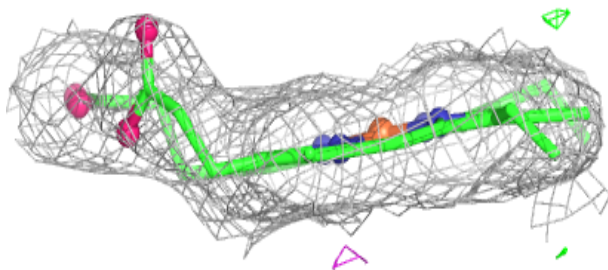
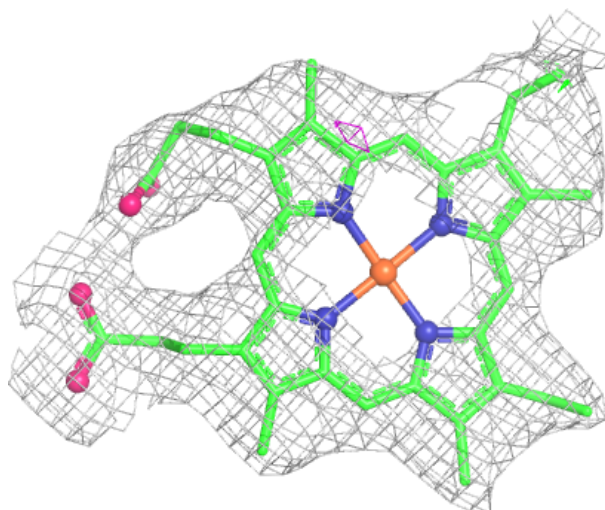
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around HEM C 501:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.