



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 03:38 PM UTC

PDB ID : 6NHH / pdb_00006nhh
Title : Rhodobacter sphaeroides bc1 with azoxystrobin
Authors : Xia, D.; Zhou, F.; Yu, C.A.
Deposited on : 2018-12-21
Resolution : 3.00 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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

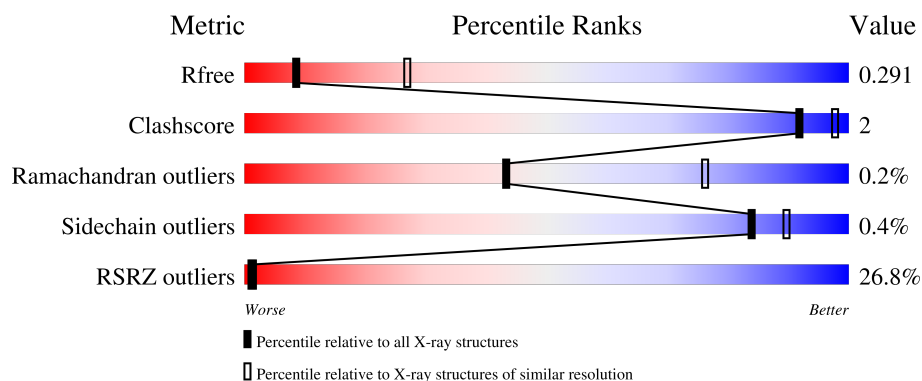
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	A	445	8% 91% 6%
1	E	445	12% 91% 5%
2	B	272	12% 90% 6%
2	F	272	16% 90% 6%
3	C	187	81% 93% 6%

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Mol	Chain	Length	Quality of chain
3	G	187	78% 93% 6%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 27403 atoms, of which 13476 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 Cytochrome b.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	430	Total	C	H	N	O	S	0	0	0
			6878	2334	3421	549	559	15			
1	E	430	Total	C	H	N	O	S	0	0	0
			6878	2334	3421	549	559	15			

- Molecule 2 is a protein called Cytochrome c1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	256	Total	C	H	N	O	S	0	0	0
			3792	1240	1839	326	374	13			
2	F	256	Total	C	H	N	O	S	0	0	0
			3792	1240	1839	326	374	13			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	264	GLY	-	expression tag	UNP A0A344Q9J2
B	265	THR	-	expression tag	UNP A0A344Q9J2
B	266	GLY	-	expression tag	UNP A0A344Q9J2
B	267	HIS	-	expression tag	UNP A0A344Q9J2
B	268	HIS	-	expression tag	UNP A0A344Q9J2
B	269	HIS	-	expression tag	UNP A0A344Q9J2
B	270	HIS	-	expression tag	UNP A0A344Q9J2
B	271	HIS	-	expression tag	UNP A0A344Q9J2
B	272	HIS	-	expression tag	UNP A0A344Q9J2
F	264	GLY	-	expression tag	UNP A0A344Q9J2
F	265	THR	-	expression tag	UNP A0A344Q9J2
F	266	GLY	-	expression tag	UNP A0A344Q9J2
F	267	HIS	-	expression tag	UNP A0A344Q9J2
F	268	HIS	-	expression tag	UNP A0A344Q9J2
F	269	HIS	-	expression tag	UNP A0A344Q9J2
F	270	HIS	-	expression tag	UNP A0A344Q9J2

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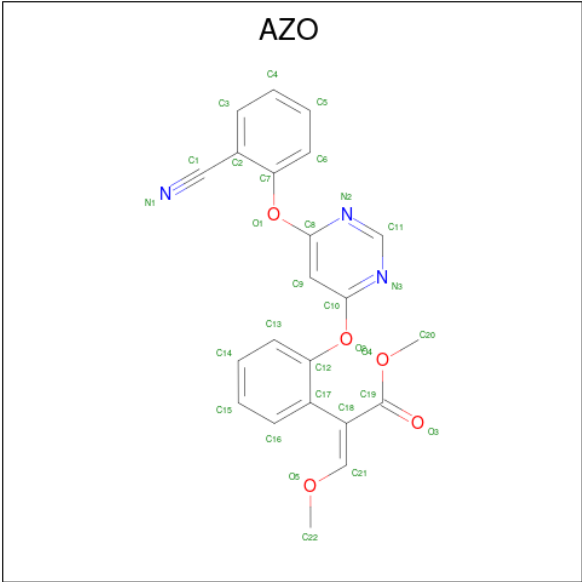
Chain	Residue	Modelled	Actual	Comment	Reference
F	271	HIS	-	expression tag	UNP A0A344Q9J2
F	272	HIS	-	expression tag	UNP A0A344Q9J2

- | Mol | Chain | Residues | Atoms | | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|---------------|----------|-----------|----------|----------|--------|---------|---------|-------|
| 3 | C | 175 | Total
2576 | C
827 | H
1268 | N
227 | O
248 | S
6 | 0 | 0 | 0 |
| 3 | G | 175 | Total
2576 | C
827 | H
1268 | N
227 | O
248 | S
6 | 0 | 0 | 0 |

- # HEM

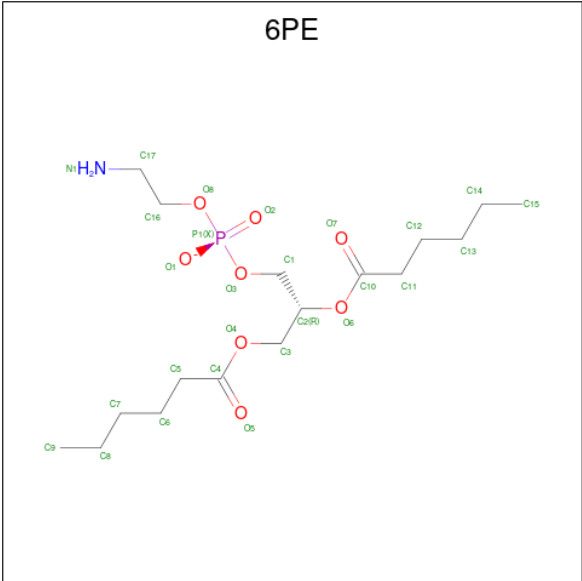
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0
4	A	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0
4	E	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0
4	E	1	Total 73	C 34	Fe 1	H 30	N 4	O 4	0	0

- 



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0	0
			47	22	17	3	5		
5	E	1	Total	C	H	N	O	0	0
			47	22	17	3	5		

- Molecule 6 is 1,2-DIHEXANOYL-SN-GLYCERO-3-PHOSPHOETHANOLAMINE (CCD ID: 6PE) (formula: C₁₇H₃₃NO₈P).



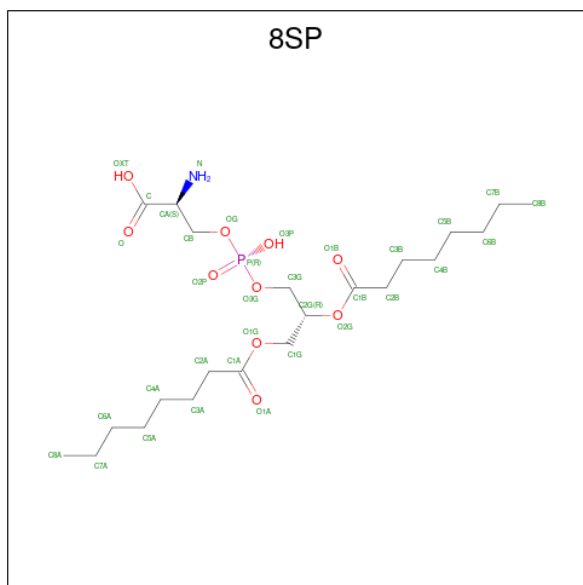
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total	C	H	N	O	P	0	0
			60	17	33	1	8	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
6	E	1	Total	C	H	N	O	P	0	0
			60	17	33	1	8	1		

- Molecule 7 is O-[(R)-{[(2R)-2,3-bis(octanoyloxy)propyl]oxy}(hydroxy)phosphoryl]-L-serine (CCD ID: 8SP) (formula: C₂₂H₄₂NO₁₀P).

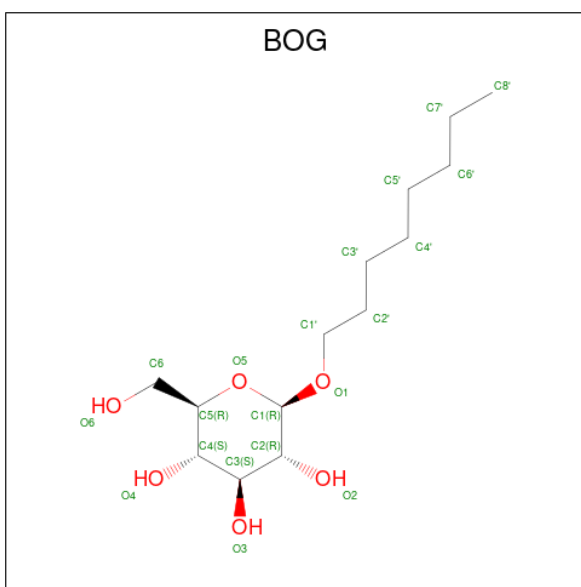


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
7	A	1	Total	C	H	N	O	P	0	0
			74	22	40	1	10	1		
7	F	1	Total	C	H	N	O	P	0	0
			74	22	40	1	10	1		

- Molecule 8 is STRONTIUM ION (CCD ID: SR) (formula: Sr).

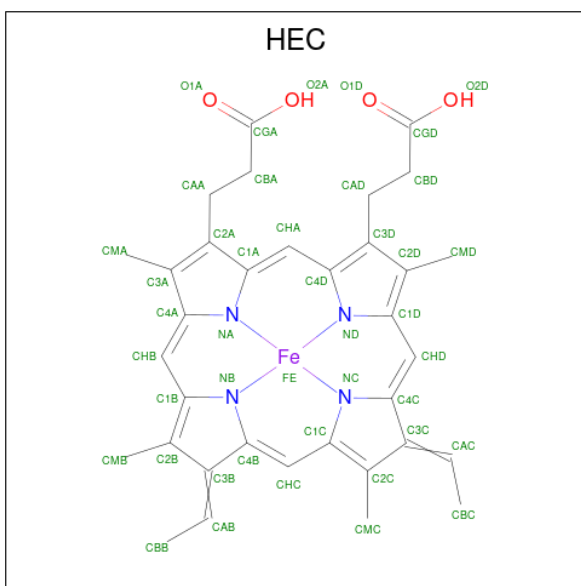
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Sr	0	0
			1	1		
8	B	1	Total	Sr	0	0
			1	1		
8	F	1	Total	Sr	0	0
			1	1		

- Molecule 9 is octyl beta-D-glucopyranoside (CCD ID: BOG) (formula: C₁₄H₂₈O₆).



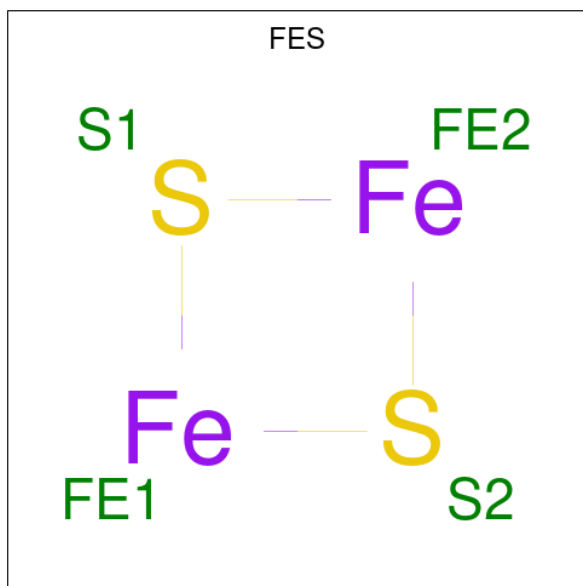
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total 48	C 14	H 28	O 6	0	0
9	F	1	Total 48	C 14	H 28	O 6	0	0

- Molecule 10 is HEME C (CCD ID: HEC) (formula: $\text{C}_{34}\text{H}_{34}\text{FeN}_4\text{O}_4$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
10	B	1	Total 75	C 34	Fe 1	H 32	N 4	O 4	0	0
10	F	1	Total 75	C 34	Fe 1	H 32	N 4	O 4	0	0

- Molecule 11 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).

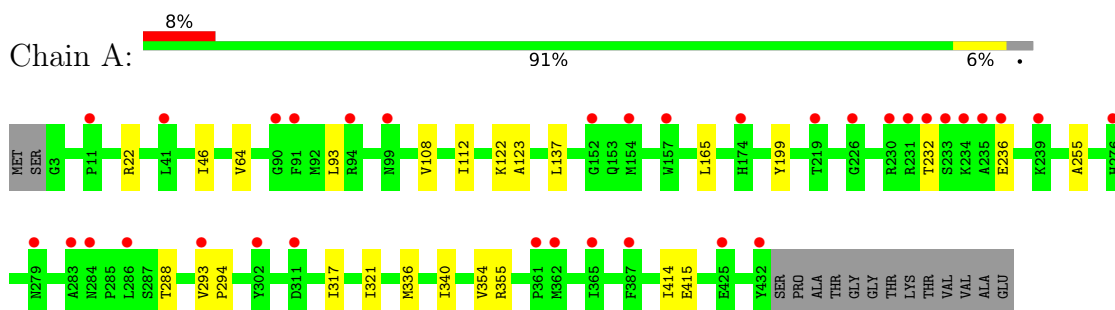


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	C	1	Total	Fe	S	0	0
			4	2	2		
11	G	1	Total	Fe	S	0	0
			4	2	2		

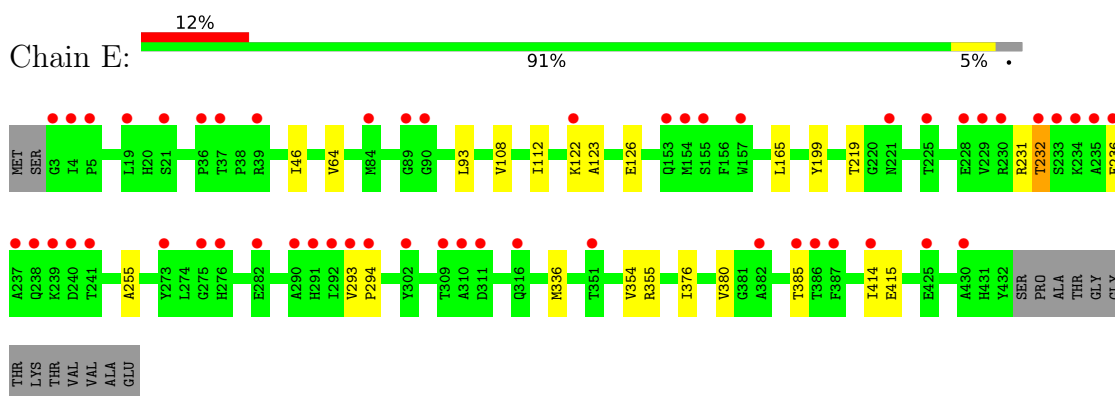
3 Residue-property plots [i](#)

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

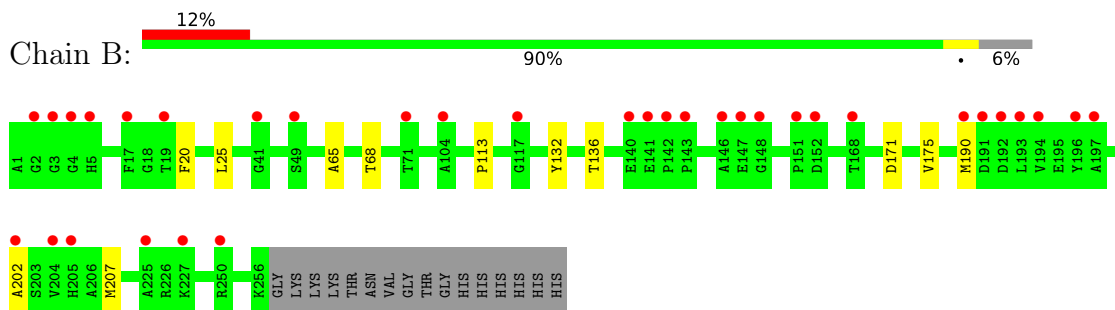
- Molecule 1: Cytochrome b



- Molecule 1: Cytochrome b

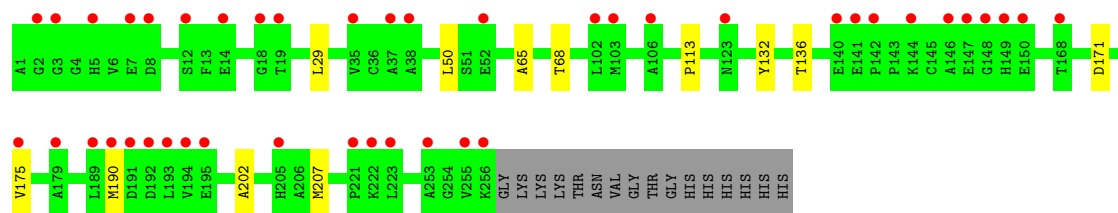


- Molecule 2: Cytochrome c1

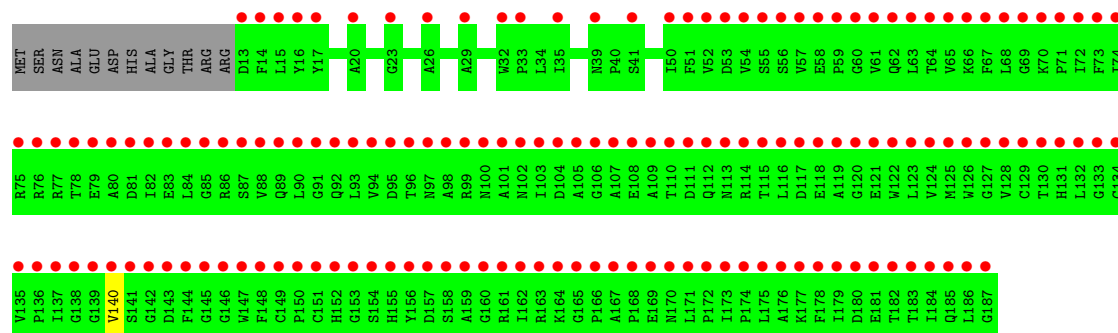
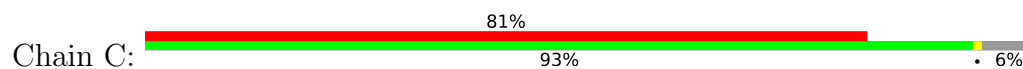


- Molecule 2: Cytochrome c1

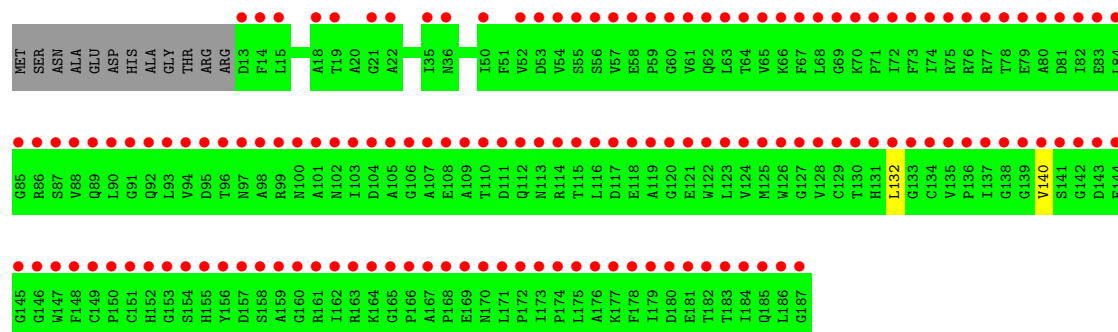
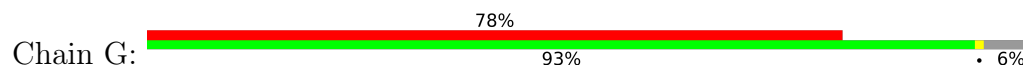




● Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit



● Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.31Å 154.66Å 100.94Å 90.00° 95.36° 90.00°	Depositor
Resolution (Å)	39.28 – 3.00 39.28 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.28-3.00) 93.1 (39.28-3.00)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 3.01Å)	Xtriage
Refinement program	PHENIX dev_3339	Depositor
R, R_{free}	0.264 , 0.282 0.275 , 0.291	Depositor DCC
R_{free} test set	1991 reflections (3.64%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.935	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 46.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	27403	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BOG, SR, HEC, 8SP, FES, HEM, AZO, 6PE

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	0.18	0/3589	0.34	0/4924
1	E	0.17	0/3589	0.33	0/4924
2	B	0.15	0/2010	0.31	0/2733
2	F	0.14	0/2010	0.29	0/2733
3	C	0.15	0/1338	0.27	0/1825
3	G	0.15	0/1338	0.27	0/1825
All	All	0.16	0/13874	0.32	0/18964

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3457	3421	3436	13	0
1	E	3457	3421	3436	12	0
2	B	1953	1839	1848	6	0
2	F	1953	1839	1848	6	0
3	C	1308	1268	1271	0	0
3	G	1308	1268	1271	1	0
4	A	86	60	60	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	86	60	60	2	0
5	A	30	17	17	0	0
5	E	30	17	17	0	0
6	A	27	33	33	0	0
6	E	27	33	33	0	0
7	A	34	40	40	0	0
7	F	34	40	40	0	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
8	F	1	0	0	0	0
9	B	20	28	28	0	0
9	F	20	28	28	0	0
10	B	43	32	30	2	0
10	F	43	32	30	1	0
11	C	4	0	0	0	0
11	G	4	0	0	0	0
All	All	13927	13476	13526	43	0

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

The worst 5 of 43 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:232:THR:OG1	1:E:236:GLU:OE1	2.09	0.68
10:B:302:HEC:HBB3	10:B:302:HEC:HMB3	1.76	0.68
10:B:302:HEC:HMC1	10:B:302:HEC:HBC3	1.76	0.67
10:F:302:HEC:HBB3	10:F:302:HEC:HMB3	1.75	0.67
1:E:123:ALA:O	1:E:355:ARG:NH1	2.28	0.65

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	A	428/445 (96%)	416 (97%)	12 (3%)	0	100	100
1	E	428/445 (96%)	416 (97%)	12 (3%)	0	100	100
2	B	254/272 (93%)	245 (96%)	8 (3%)	1 (0%)	30	65
2	F	254/272 (93%)	245 (96%)	8 (3%)	1 (0%)	30	65
3	C	173/187 (92%)	158 (91%)	14 (8%)	1 (1%)	21	56
3	G	173/187 (92%)	158 (91%)	14 (8%)	1 (1%)	21	56
All	All	1710/1808 (95%)	1638 (96%)	68 (4%)	4 (0%)	43	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	140	VAL
3	G	140	VAL
2	B	113	PRO
2	F	113	PRO

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	355/366 (97%)	353 (99%)	2 (1%)	78	88
1	E	355/366 (97%)	351 (99%)	4 (1%)	65	83
2	B	203/216 (94%)	203 (100%)	0	100	100
2	F	203/216 (94%)	203 (100%)	0	100	100
3	C	135/144 (94%)	135 (100%)	0	100	100
3	G	135/144 (94%)	135 (100%)	0	100	100
All	All	1386/1452 (96%)	1380 (100%)	6 (0%)	84	90

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	385	THR
1	E	414	ILE
1	E	415	GLU
1	A	415	GLU
1	A	414	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	319	ASN
3	G	113	ASN
2	B	200	HIS
3	C	113	ASN
1	E	6	HIS

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 19 ligands modelled in this entry, 3 are monoatomic - leaving 16 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	AZO	E	1003	-	32,32,32	0.62	0	42,42,42	1.62	8 (19%)
9	BOG	B	301	-	20,20,20	0.88	0	25,25,25	1.24	4 (16%)
7	8SP	A	1005	-	32,33,33	0.90	1 (3%)	34,40,40	0.92	2 (5%)
5	AZO	A	1003	-	32,32,32	0.58	0	42,42,42	1.58	7 (16%)
11	FES	C	1001	3	0,4,4	-	-	-	-	-
4	HEM	E	1002	1	50,50,50	1.48	9 (18%)	67,82,82	1.08	4 (5%)
4	HEM	A	1001	1	50,50,50	1.46	9 (18%)	67,82,82	1.29	6 (8%)
4	HEM	A	1002	1	50,50,50	1.56	9 (18%)	67,82,82	1.04	3 (4%)
10	HEC	F	302	2	46,50,50	1.86	6 (13%)	58,82,82	1.73	5 (8%)
9	BOG	F	301	-	20,20,20	0.81	0	25,25,25	1.33	2 (8%)
10	HEC	B	302	2	46,50,50	1.85	6 (13%)	58,82,82	1.69	3 (5%)
6	6PE	A	1004	-	26,26,26	0.88	2 (7%)	29,31,31	0.69	0
6	6PE	E	1004	-	26,26,26	0.89	2 (7%)	29,31,31	0.68	1 (3%)
11	FES	G	1001	3	0,4,4	-	-	-	-	-
7	8SP	F	303	-	32,33,33	0.90	1 (3%)	34,40,40	1.33	3 (8%)
4	HEM	E	1001	1	50,50,50	1.42	9 (18%)	67,82,82	1.10	4 (5%)

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	AZO	E	1003	-	-	0/23/23/23	0/3/3/3
9	BOG	B	301	-	-	6/11/31/31	0/1/1/1
7	8SP	A	1005	-	-	20/39/39/39	-
5	AZO	A	1003	-	-	1/23/23/23	0/3/3/3
11	FES	C	1001	3	-	-	0/1/1/1
4	HEM	E	1002	1	-	0/14/54/54	-
4	HEM	A	1001	1	-	4/14/54/54	-
4	HEM	A	1002	1	-	5/14/54/54	-
10	HEC	F	302	2	-	6/14/54/54	-
9	BOG	F	301	-	-	3/11/31/31	0/1/1/1
10	HEC	B	302	2	-	6/14/54/54	-
6	6PE	A	1004	-	-	11/30/30/30	-
6	6PE	E	1004	-	-	20/30/30/30	-
11	FES	G	1001	3	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	8SP	F	303	-	-	16/39/39/39	-
4	HEM	E	1001	1	-	4/14/54/54	-

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	302	HEC	CAC-C3C	6.36	1.55	1.35
10	F	302	HEC	CAC-C3C	6.31	1.55	1.35
10	F	302	HEC	CAB-C3B	6.29	1.55	1.35
10	B	302	HEC	CAB-C3B	6.22	1.55	1.35
4	A	1002	HEM	FE-NB	5.93	2.13	1.94

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	302	HEC	CBB-CAB-C3B	-7.71	112.02	127.43
10	F	302	HEC	CBB-CAB-C3B	-7.56	112.33	127.43
10	F	302	HEC	CBC-CAC-C3C	-6.81	113.82	127.43
10	B	302	HEC	CBC-CAC-C3C	-6.35	114.75	127.43
5	E	1003	AZO	C11-N3-C10	6.09	119.14	114.50

There are no chirality outliers.

5 of 102 torsion outliers are listed below:

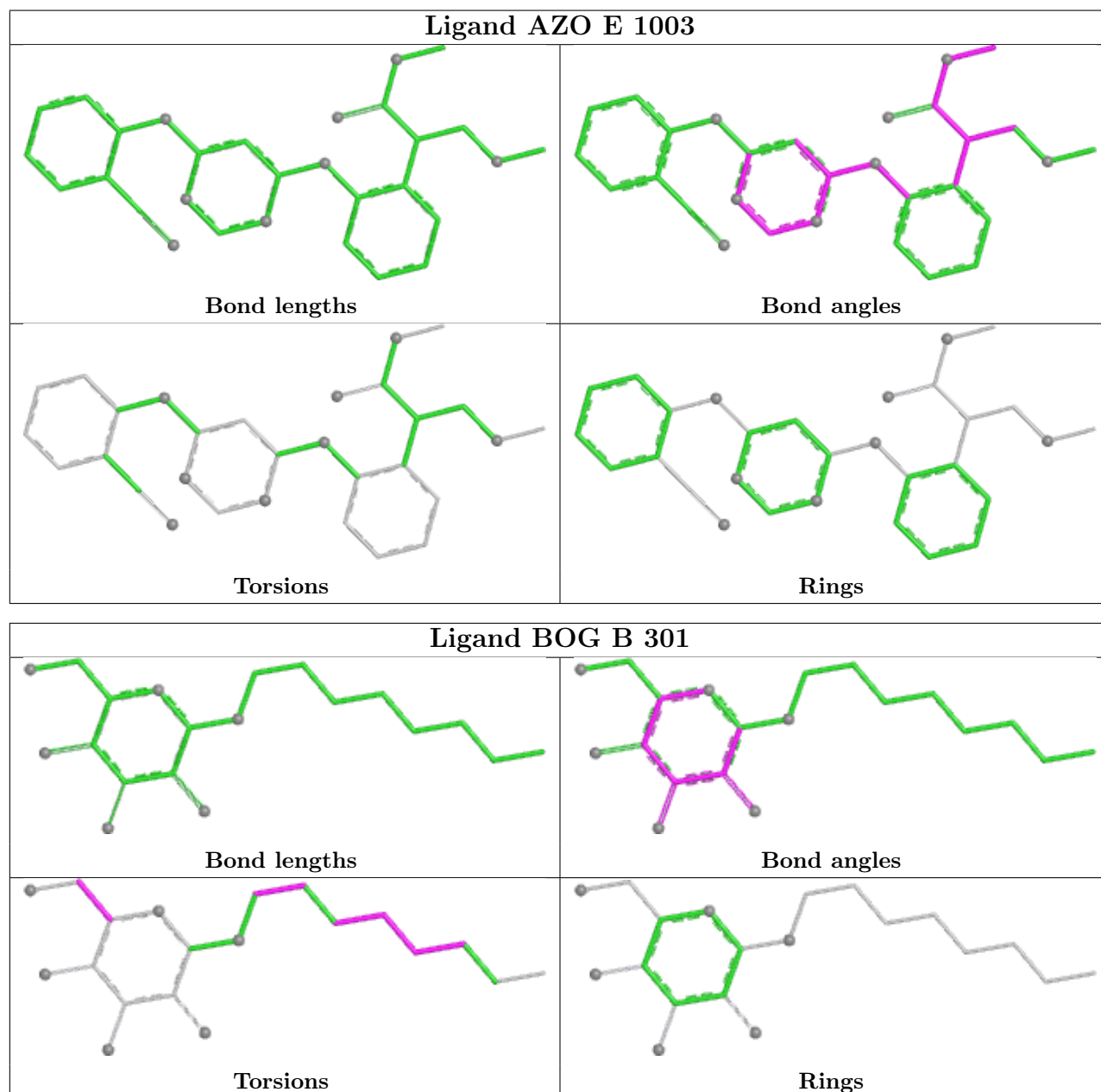
Mol	Chain	Res	Type	Atoms
6	E	1004	6PE	C1-O3-P1-O1
6	E	1004	6PE	C1-O3-P1-O8
6	E	1004	6PE	C16-O8-P1-O2
6	E	1004	6PE	O8-C16-C17-N1
7	A	1005	8SP	CB-OG-P-O3G

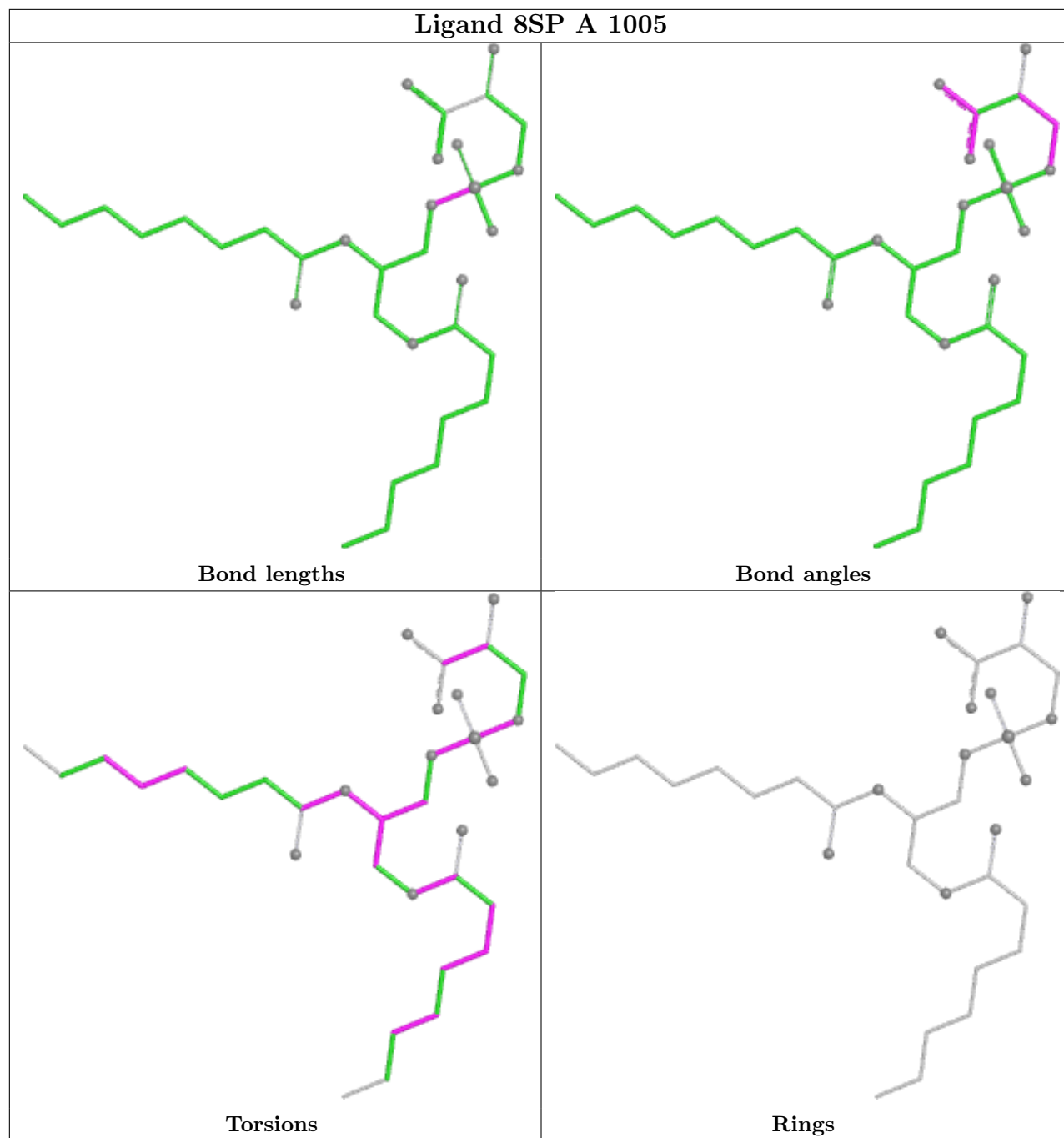
There are no ring outliers.

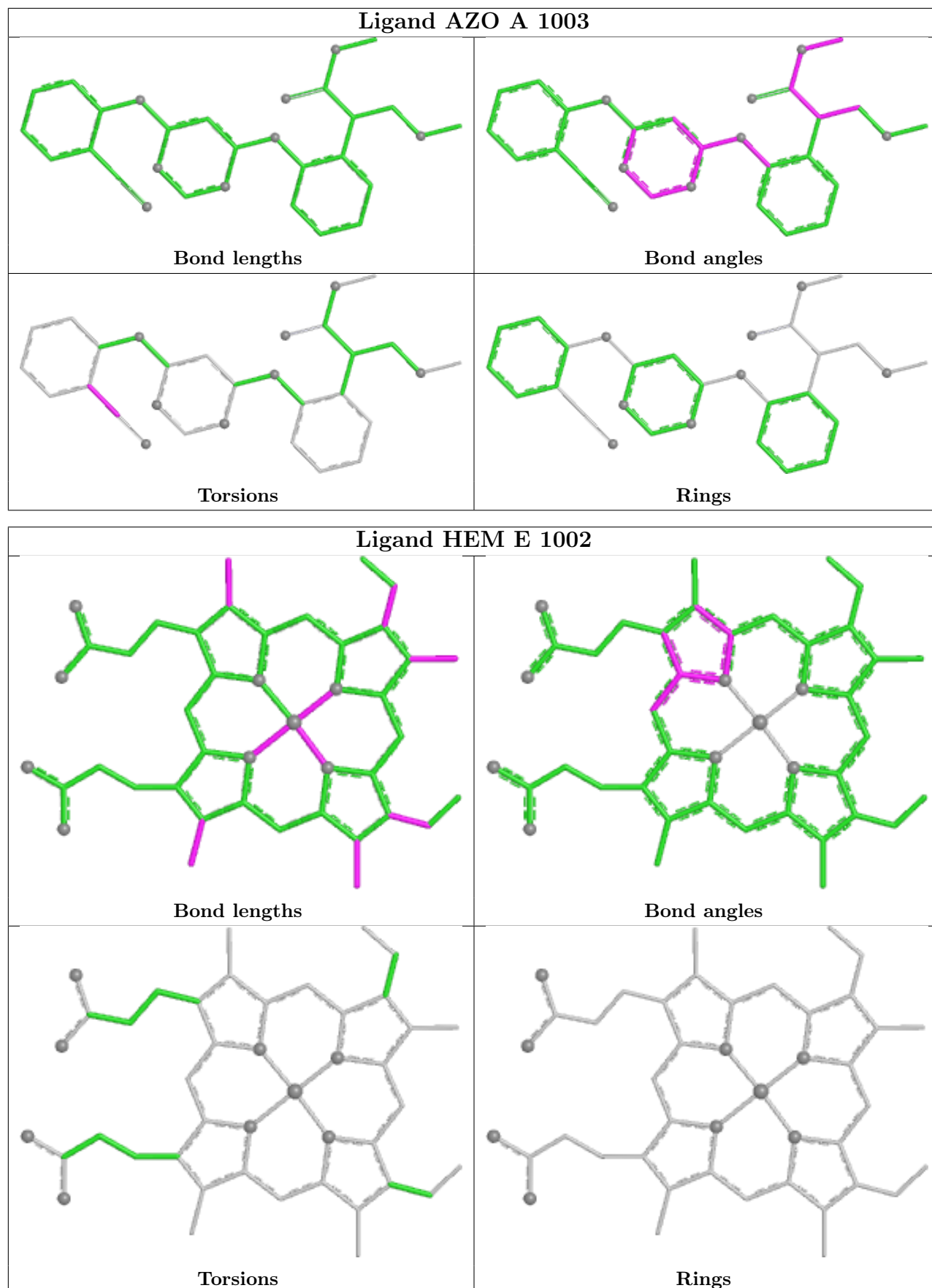
5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1001	HEM	3	0
4	A	1002	HEM	1	0
10	F	302	HEC	1	0
10	B	302	HEC	2	0
4	E	1001	HEM	2	0

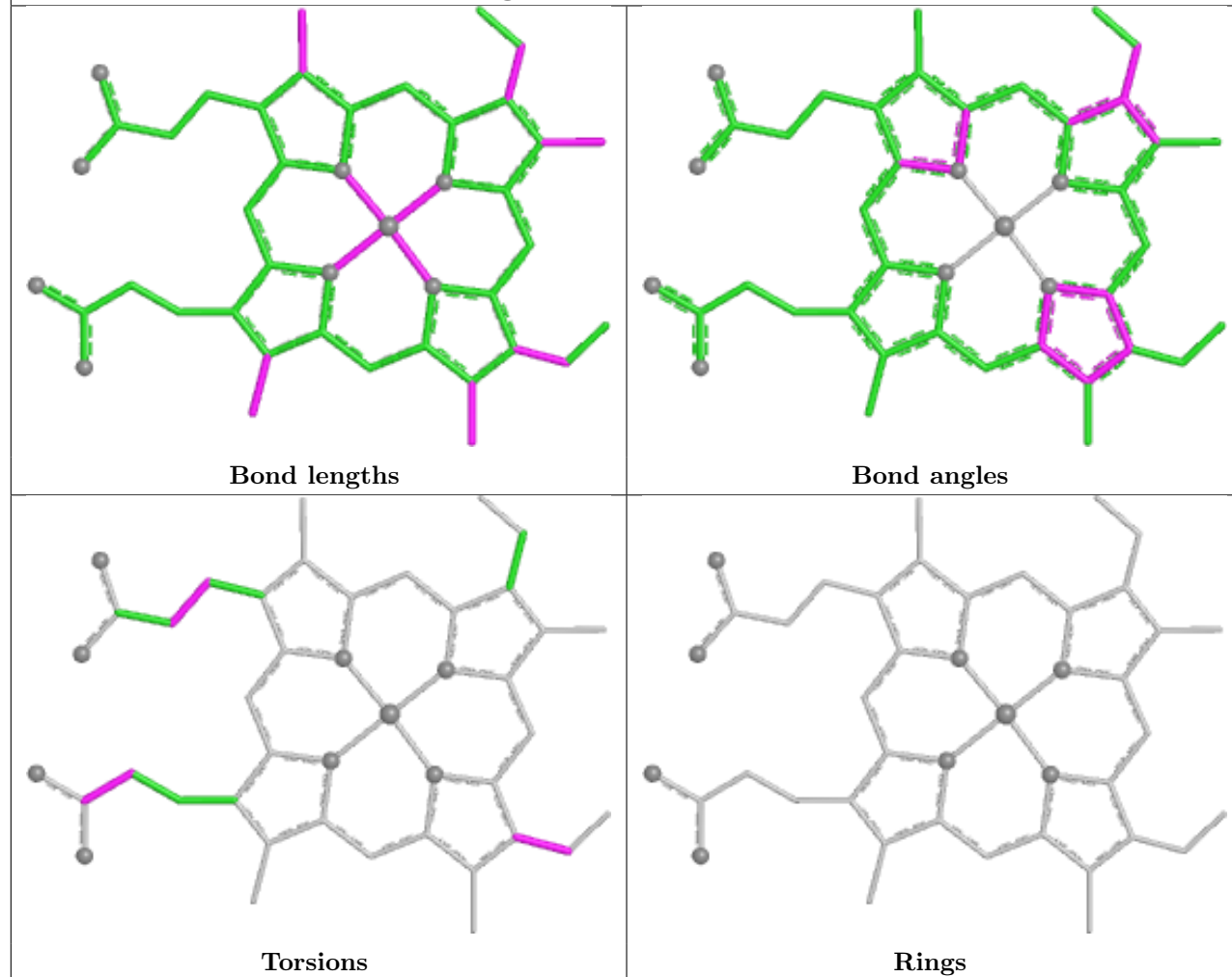
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



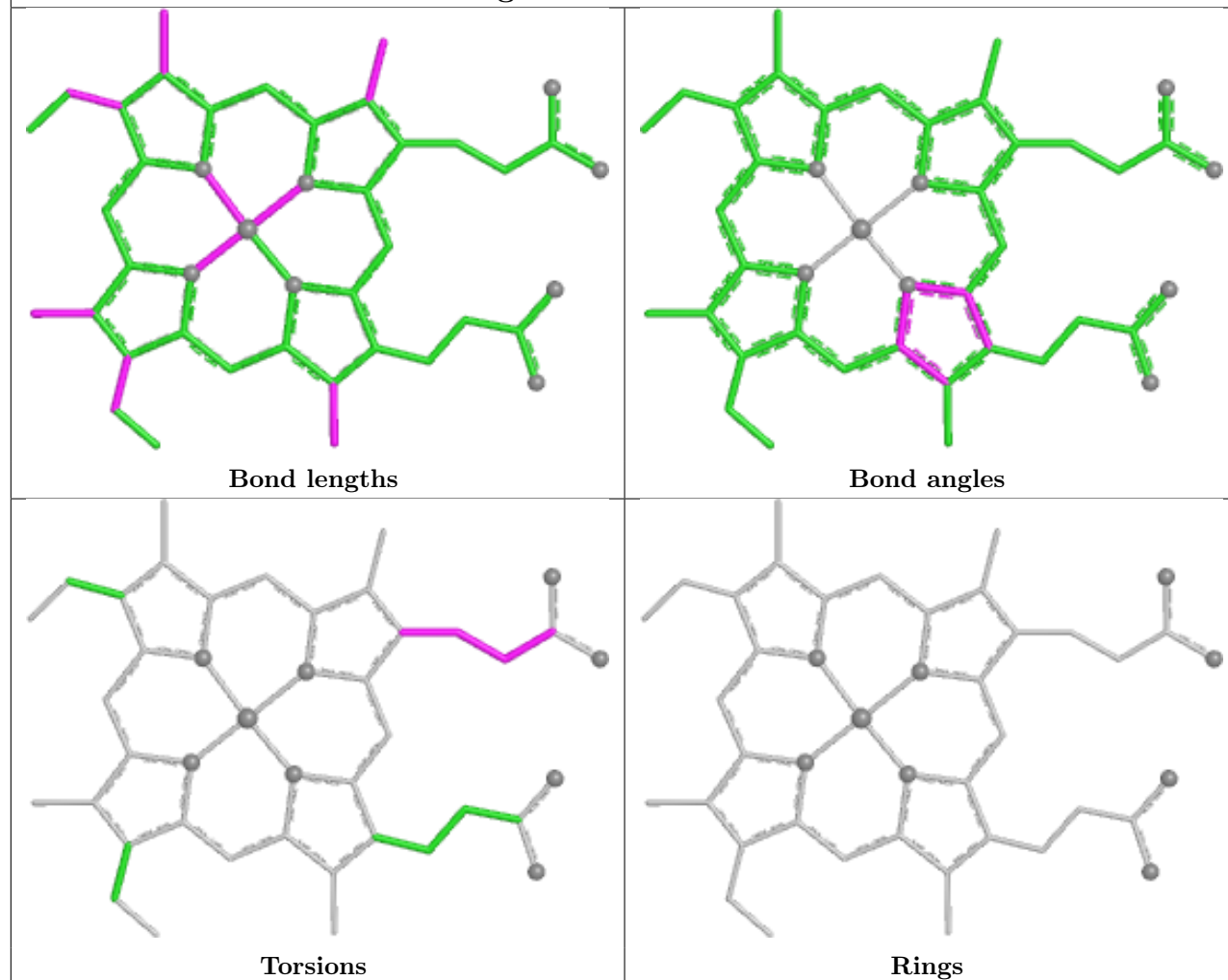




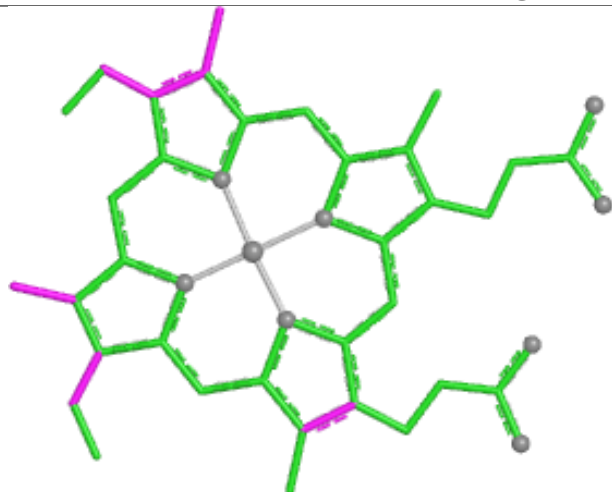
Ligand HEM A 1001



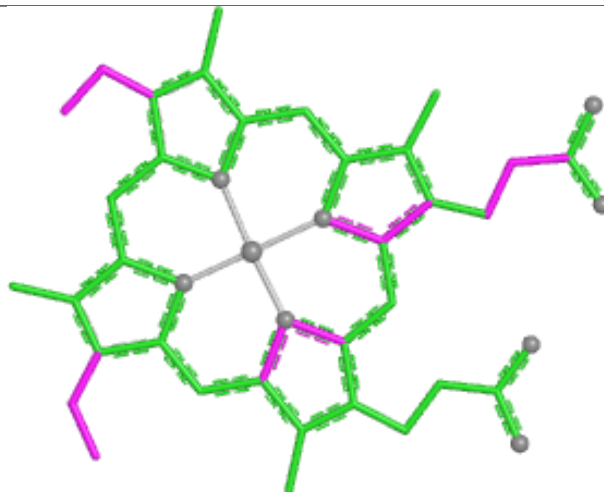
Ligand HEM A 1002



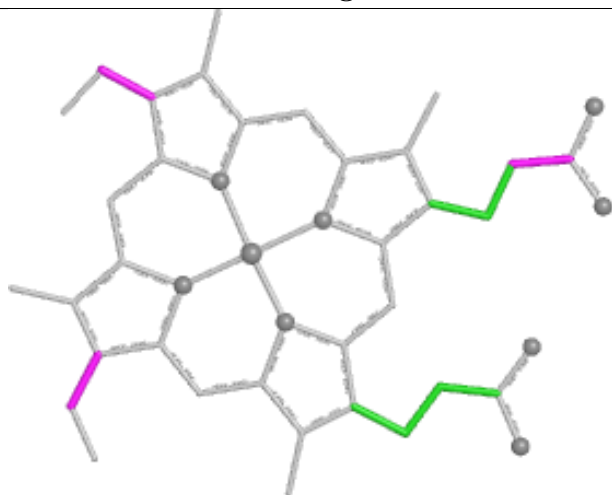
Ligand HEC F 302



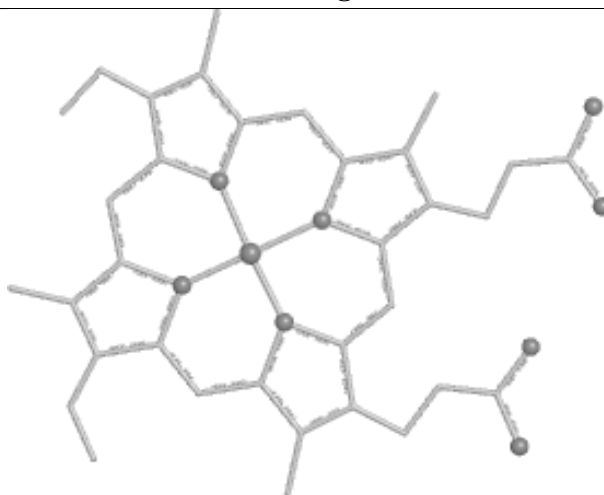
Bond lengths



Bond angles

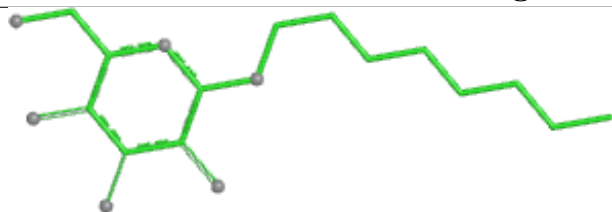


Torsions

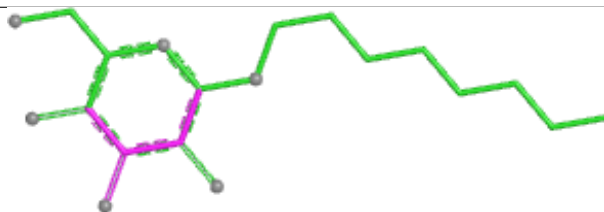


Rings

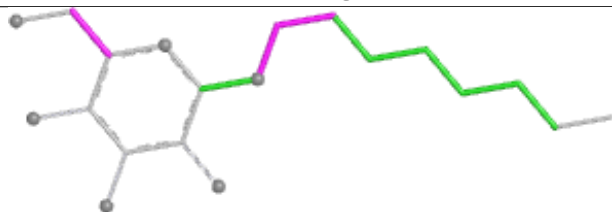
Ligand BOG F 301



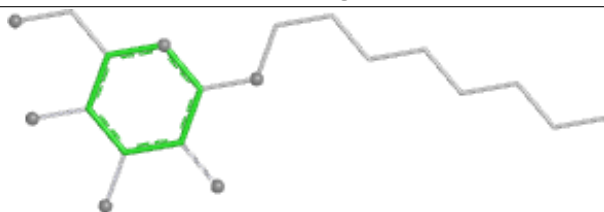
Bond lengths



Bond angles

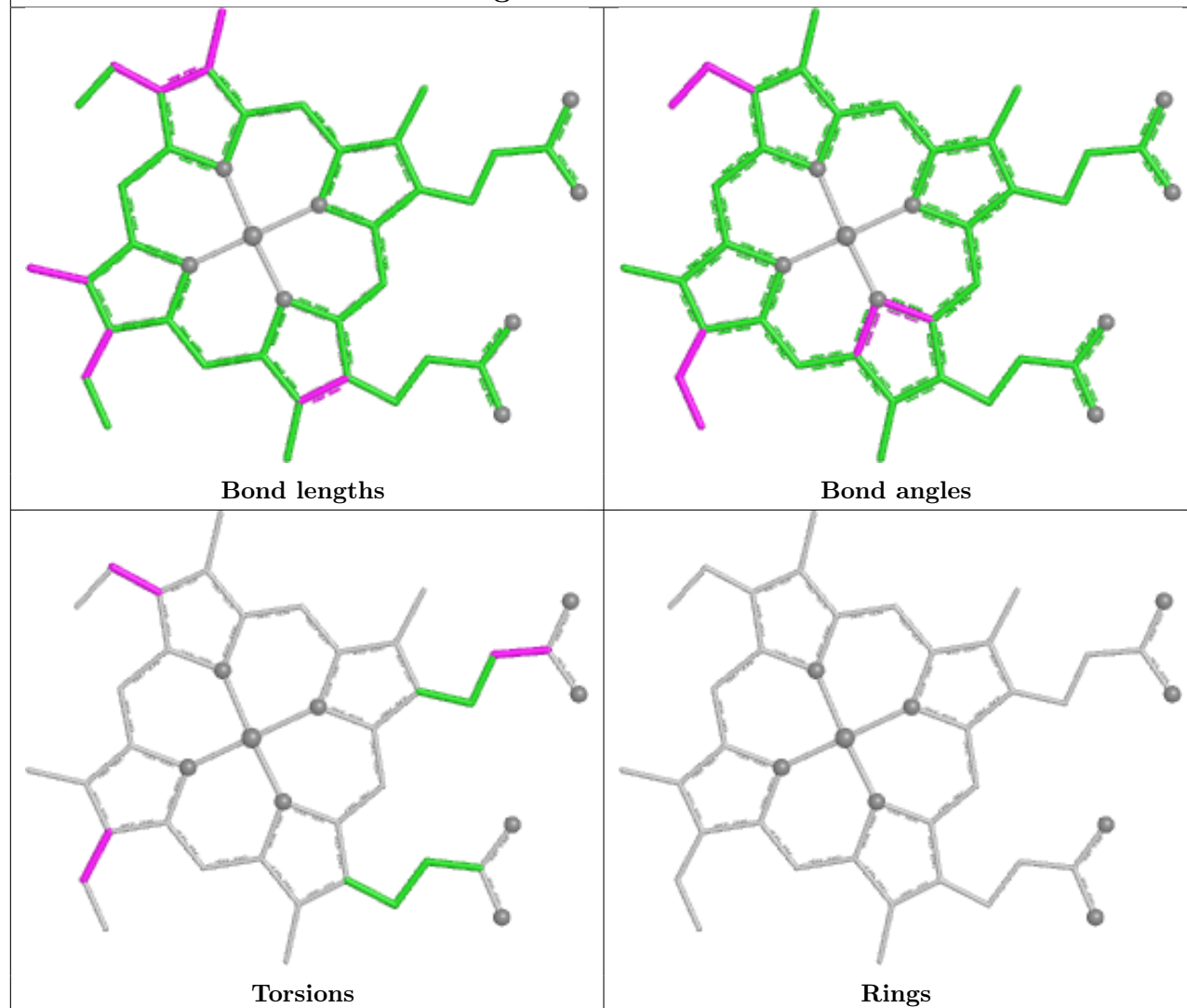


Torsions

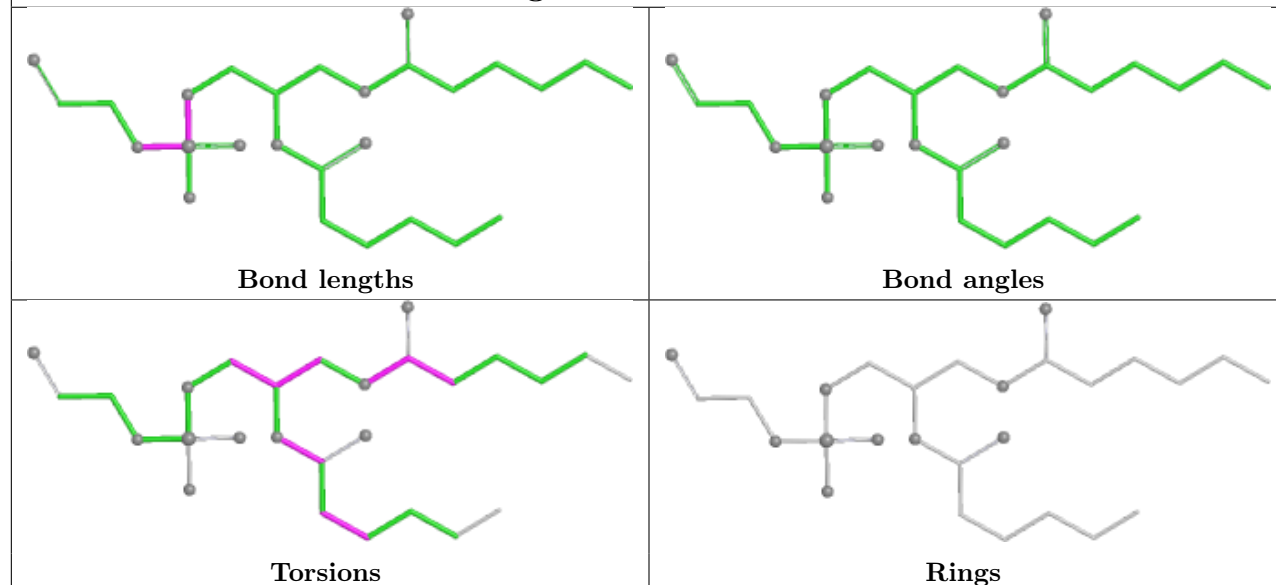


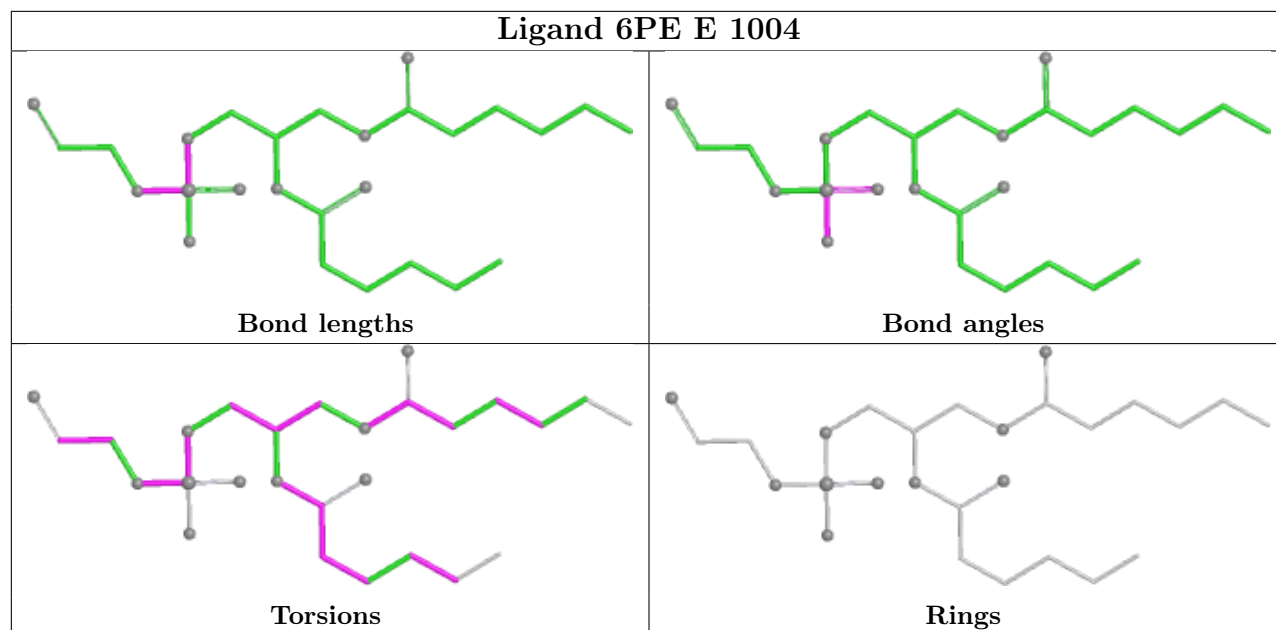
Rings

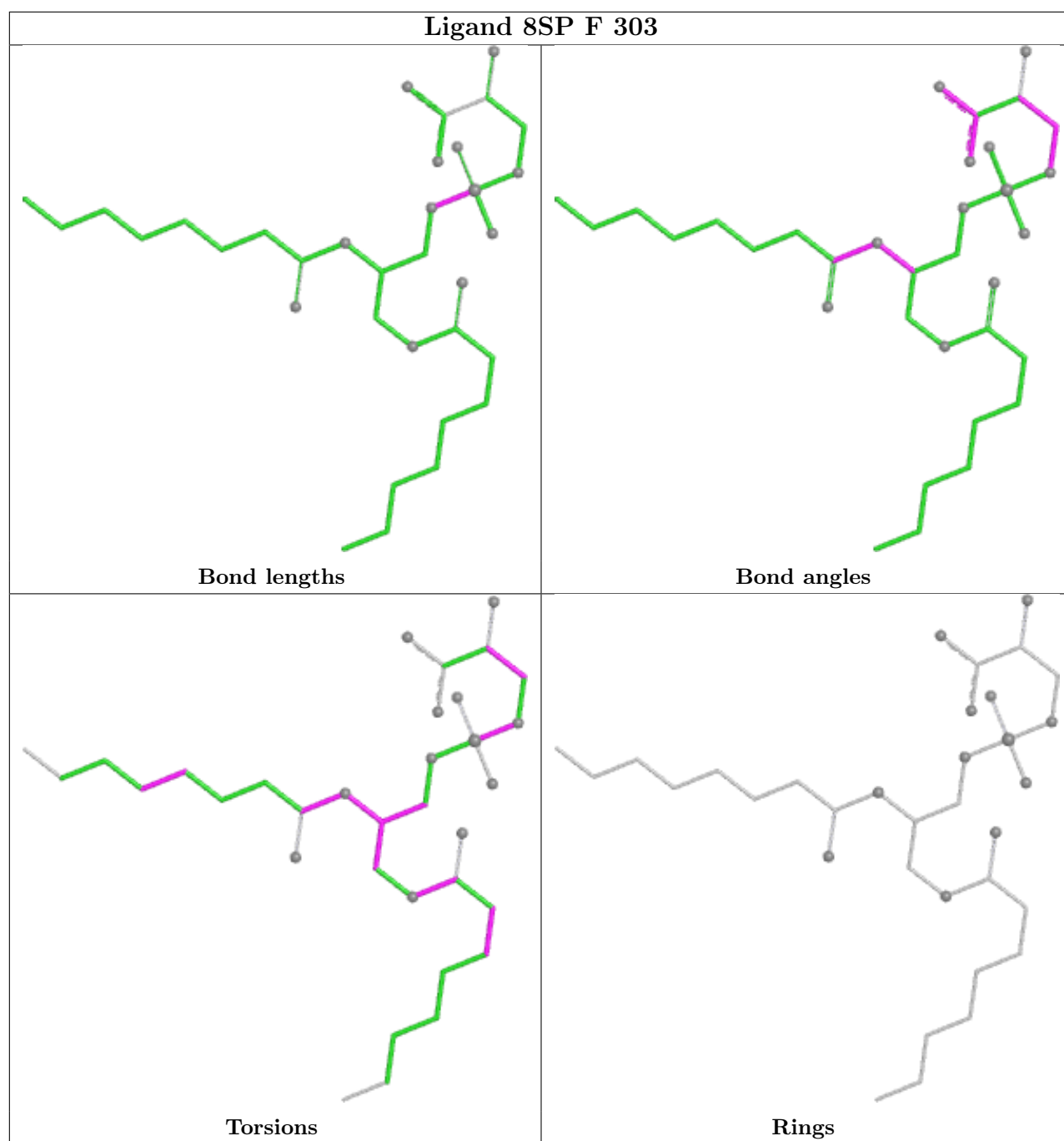
Ligand HEC B 302

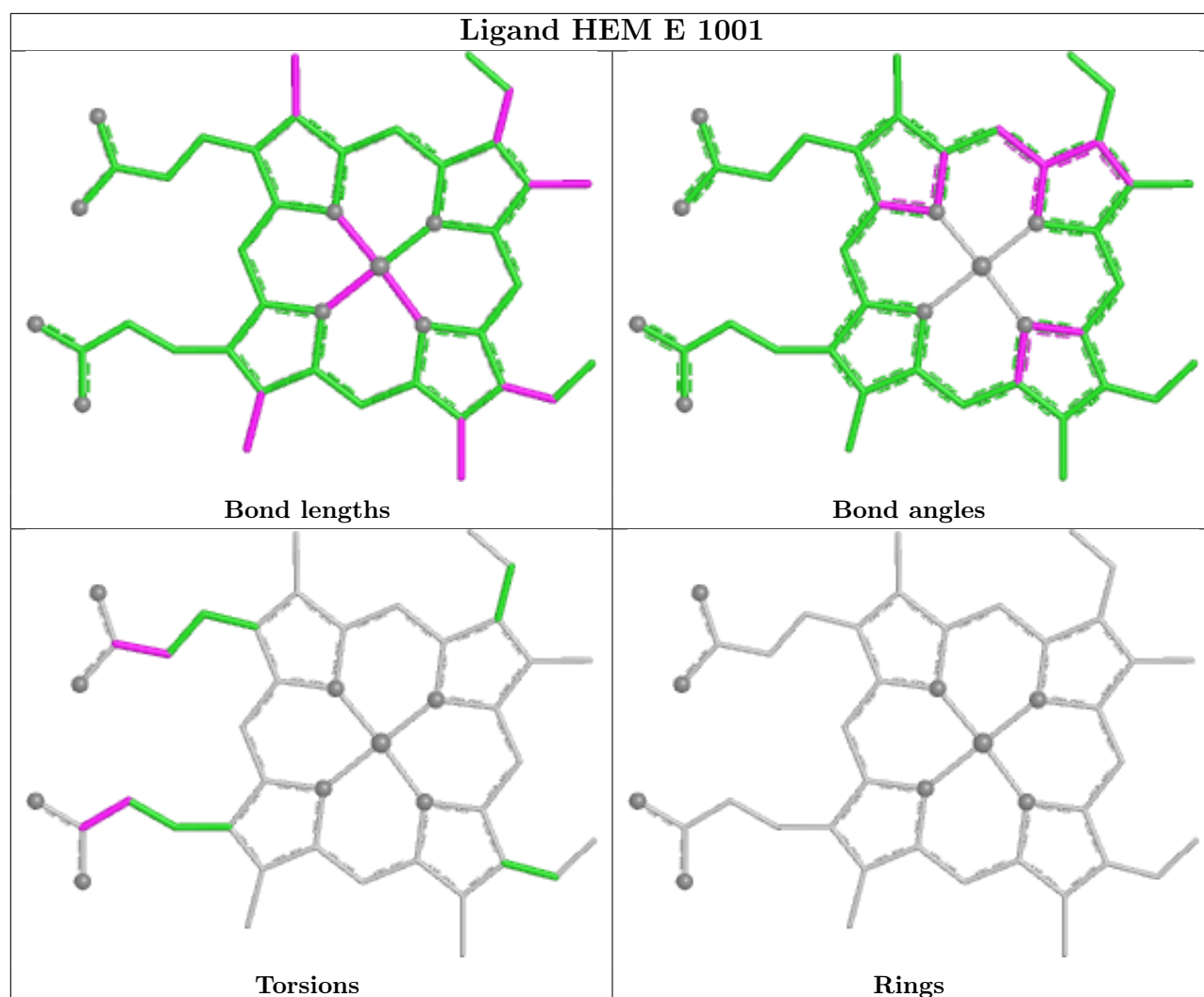


Ligand 6PE A 1004









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	430/445 (96%)	0.65	34 (7%) 18 10	37, 55, 107, 136	0
1	E	430/445 (96%)	0.84	53 (12%) 8 5	18, 64, 114, 178	0
2	B	256/272 (94%)	0.91	34 (13%) 7 4	50, 73, 134, 188	0
2	F	256/272 (94%)	1.13	43 (16%) 4 3	51, 87, 160, 206	0
3	C	175/187 (93%)	7.00	152 (86%) 0 0	23, 34, 92, 107	136 (77%)
3	G	175/187 (93%)	6.69	146 (83%) 0 0	23, 29, 104, 153	136 (77%)
All	All	1722/1808 (95%)	2.07	462 (26%) 1 1	18, 63, 126, 206	272 (15%)

The worst 5 of 462 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	133	GLY	28.6
3	C	87	SER	22.4
3	C	124	VAL	22.3
3	C	119	ALA	21.3
3	C	78	THR	20.7

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

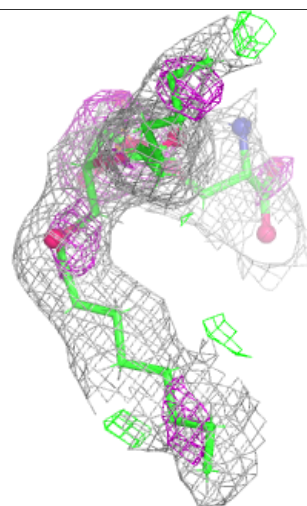
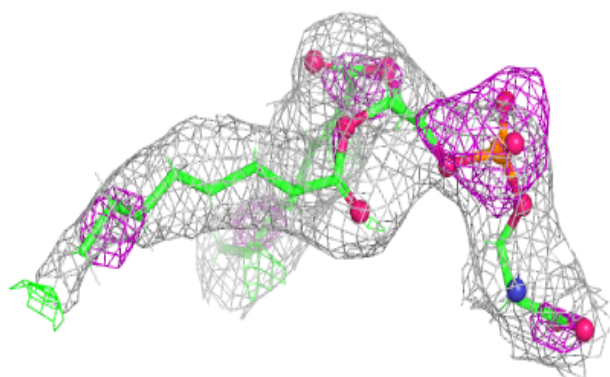
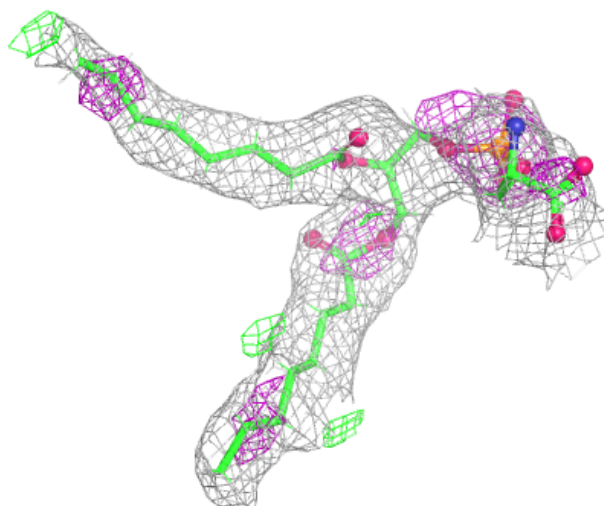
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
11	FES	C	1001	4/4	0.71	0.24	128,129,132,132	4
7	8SP	F	303	34/34	0.81	0.14	11,17,48,49	0
11	FES	G	1001	4/4	0.81	0.28	106,107,109,109	4
7	8SP	A	1005	34/34	0.83	0.14	6,12,35,35	0
6	6PE	E	1004	27/27	0.85	0.13	7,14,19,20	0
6	6PE	A	1004	27/27	0.87	0.13	9,15,19,21	0
5	AZO	A	1003	30/30	0.87	0.15	32,35,43,44	0
9	BOG	B	301	20/20	0.90	0.16	9,12,15,19	0
9	BOG	F	301	20/20	0.90	0.18	12,16,21,25	0
5	AZO	E	1003	30/30	0.91	0.14	39,39,47,49	0
8	SR	A	1006	1/1	0.93	0.07	103,103,103,103	0
10	HEC	F	302	43/43	0.94	0.13	43,48,58,58	0
4	HEM	E	1002	43/43	0.94	0.16	48,54,65,66	0
4	HEM	A	1002	43/43	0.94	0.17	49,54,66,66	0
4	HEM	E	1001	43/43	0.95	0.17	46,52,63,63	0
4	HEM	A	1001	43/43	0.95	0.17	47,53,64,64	0
10	HEC	B	302	43/43	0.96	0.13	43,48,58,58	0
8	SR	F	304	1/1	0.98	0.07	108,108,108,108	0
8	SR	B	303	1/1	0.99	0.08	102,102,102,102	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.

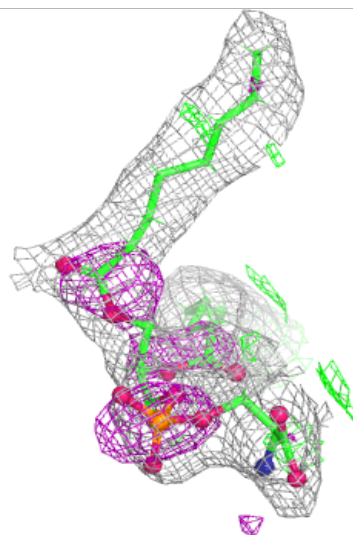
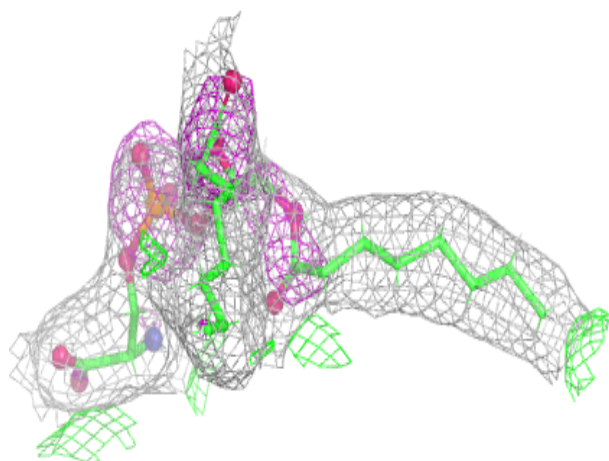
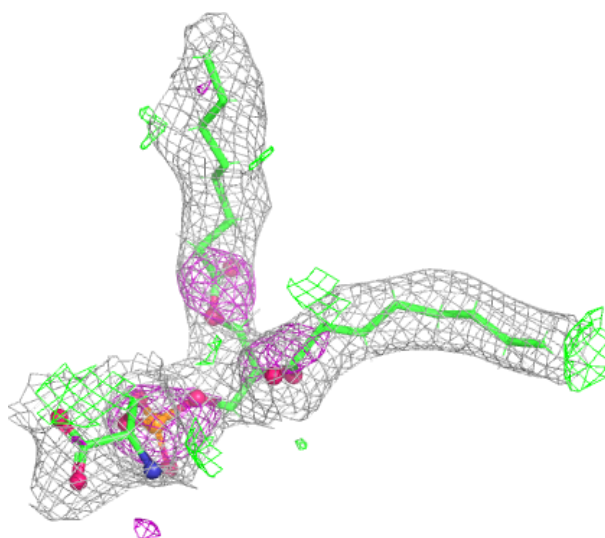
Electron density around 8SP F 303:

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



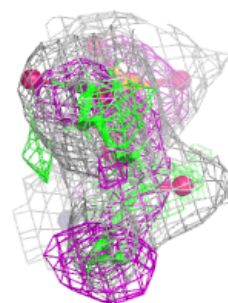
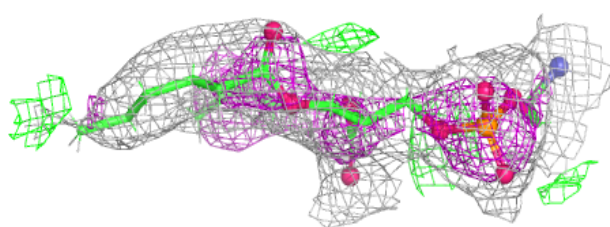
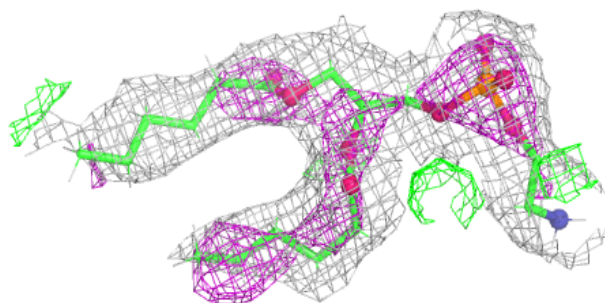
Electron density around 8SP A 1005:

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

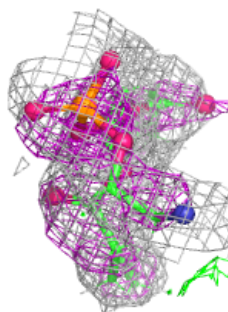
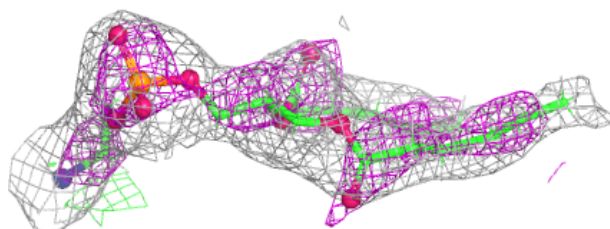
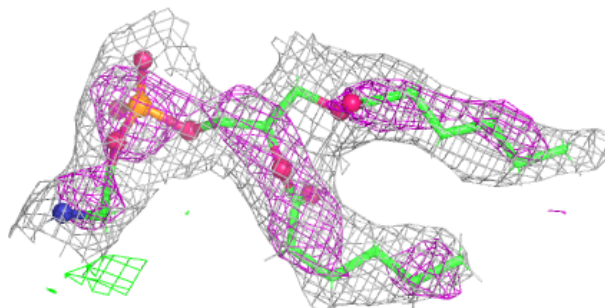


Electron density around 6PE E 1004:

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

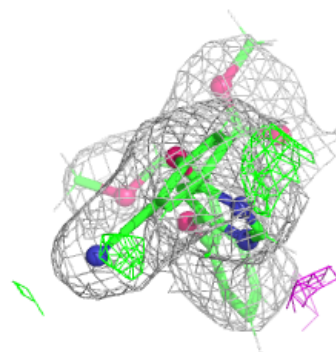
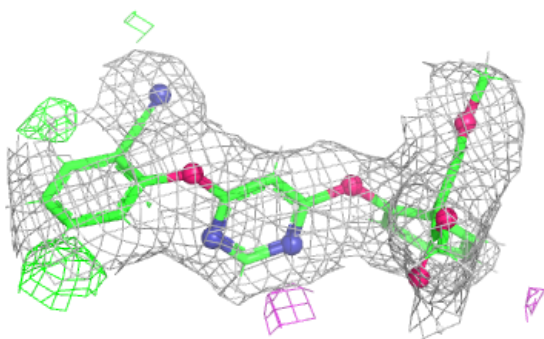
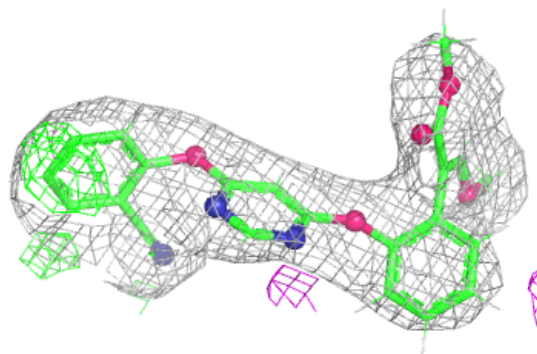
**Electron density around 6PE A 1004:**

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

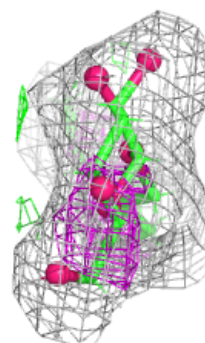
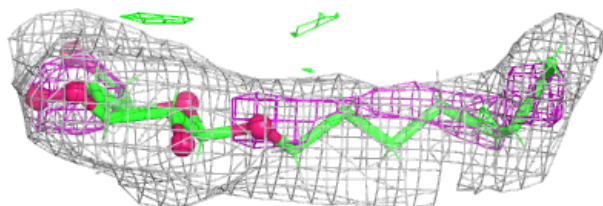
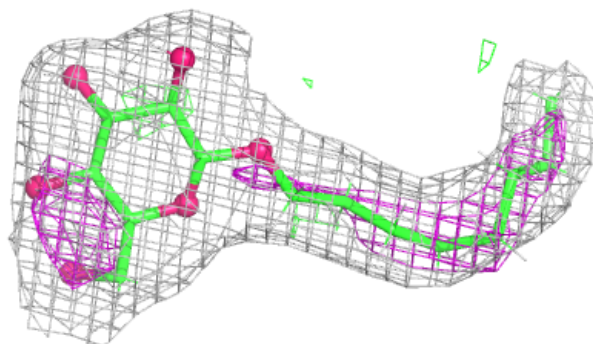


Electron density around AZO A 1003:

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

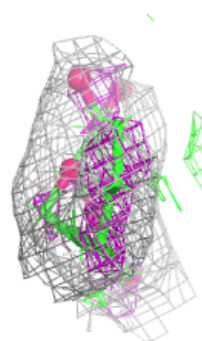
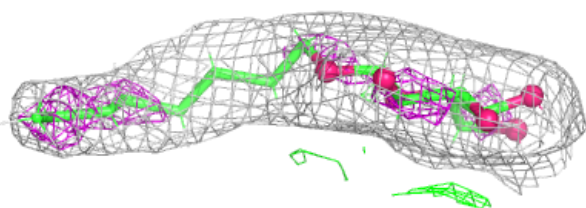
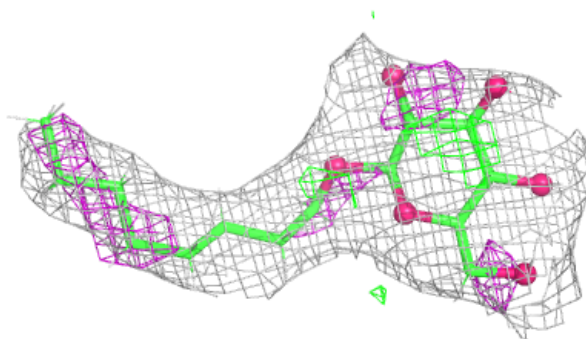
**Electron density around BOG B 301:**

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

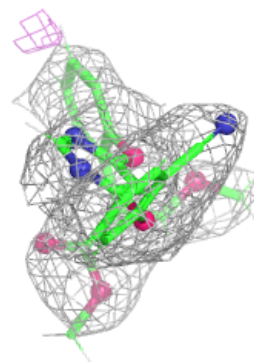
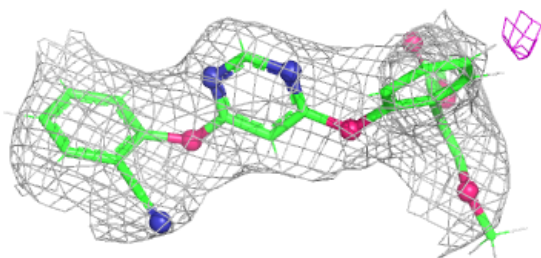
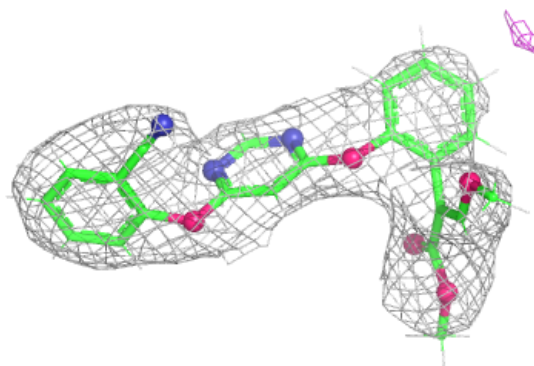


Electron density around BOG F 301:

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and green (positive)

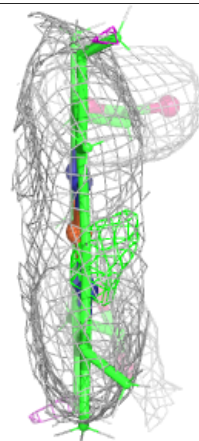
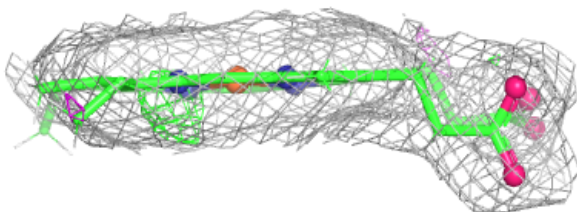
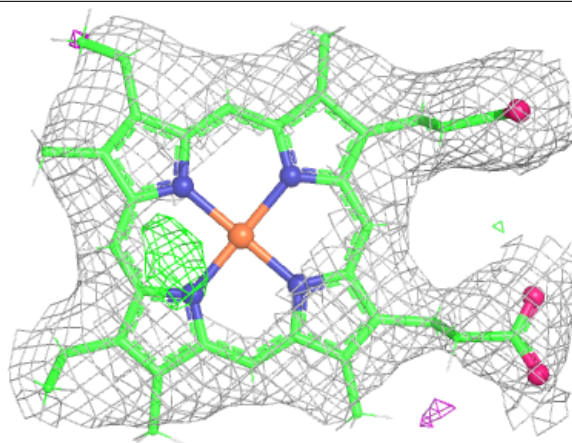
**Electron density around AZO E 1003:**

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and green (positive)



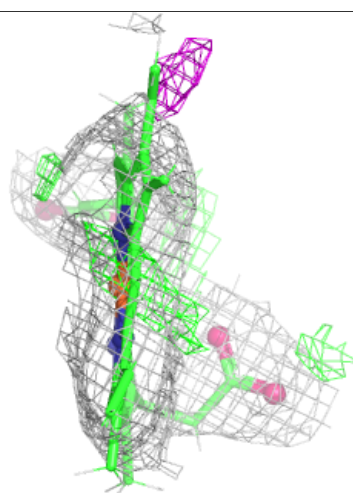
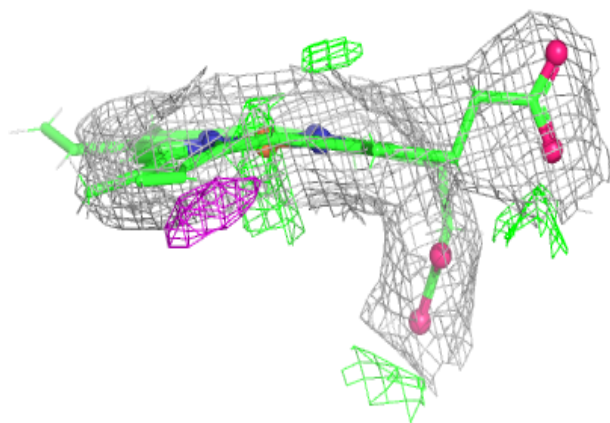
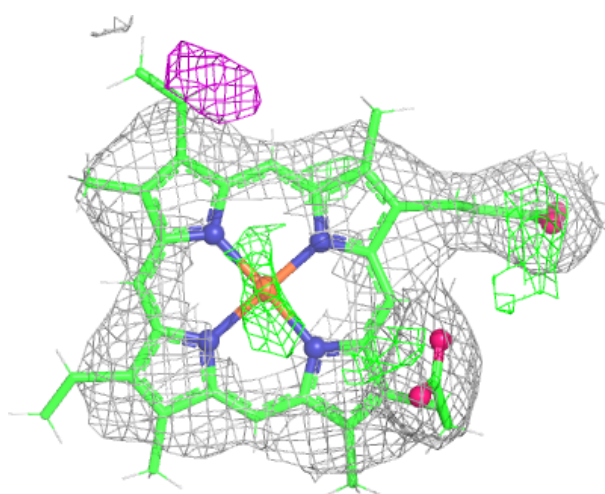
Electron density around HEC F 302:

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



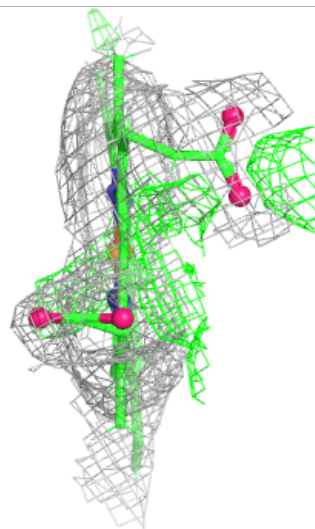
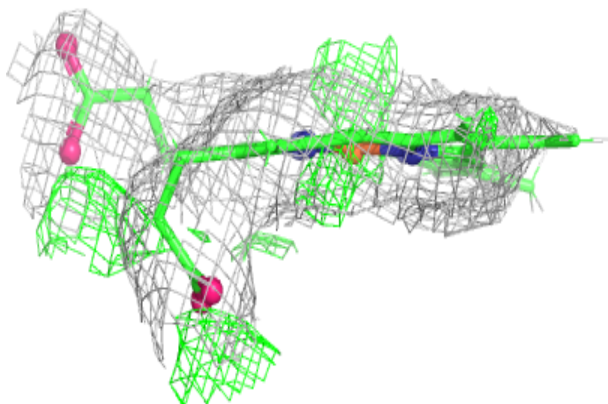
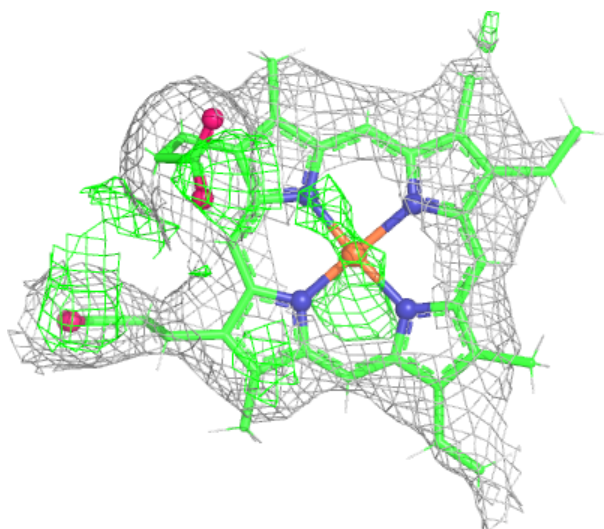
Electron density around HEM E 1002:

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



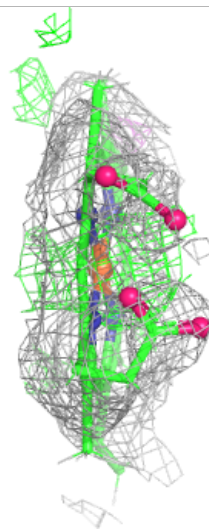
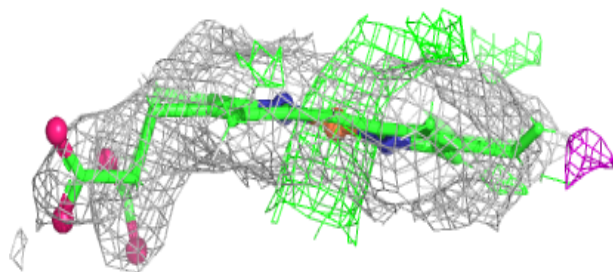
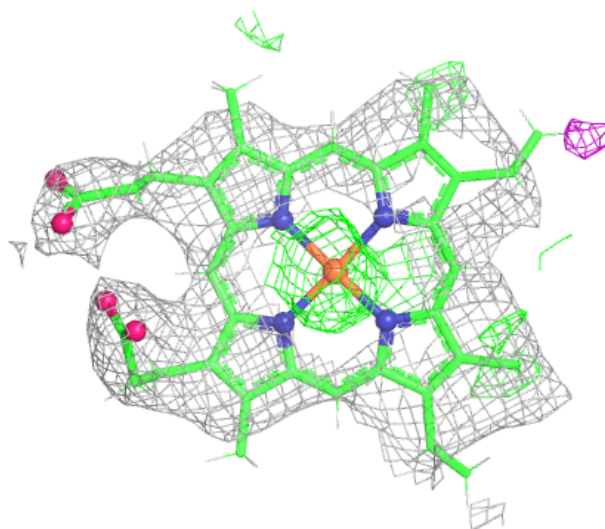
Electron density around HEM A 1002:

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



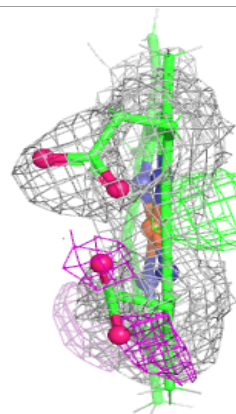
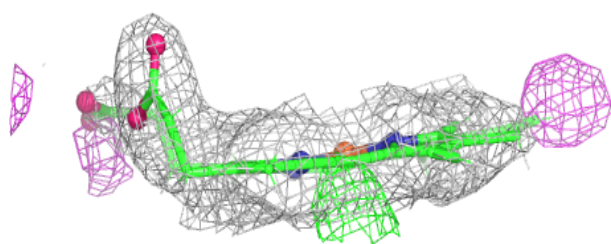
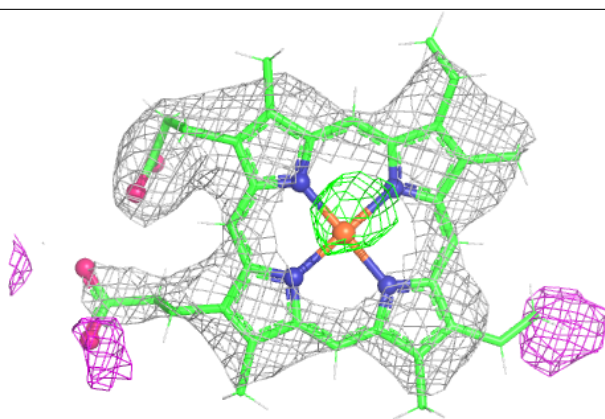
Electron density around HEM E 1001:

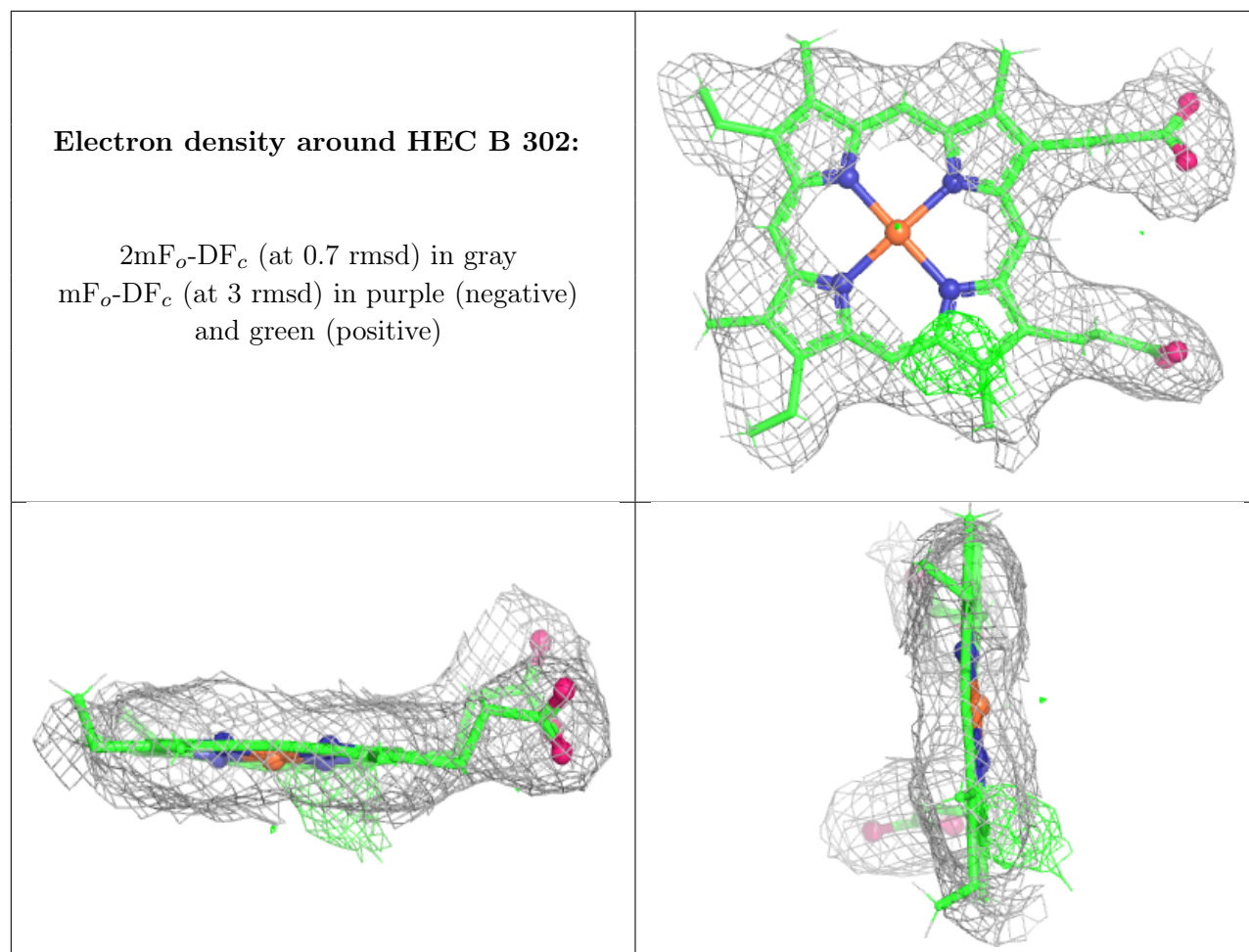
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 1001:

$2mF_o-DF_c$ (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.