



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2025 – 10:22 PM JST

PDB ID : 9ILT
Title : Crystal structure of alternative complex III from *Chloroflexus aurantiacus*
Authors : Xu, X.; Wu, W.
Deposited on : 2024-07-01
Resolution : 3.25 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:

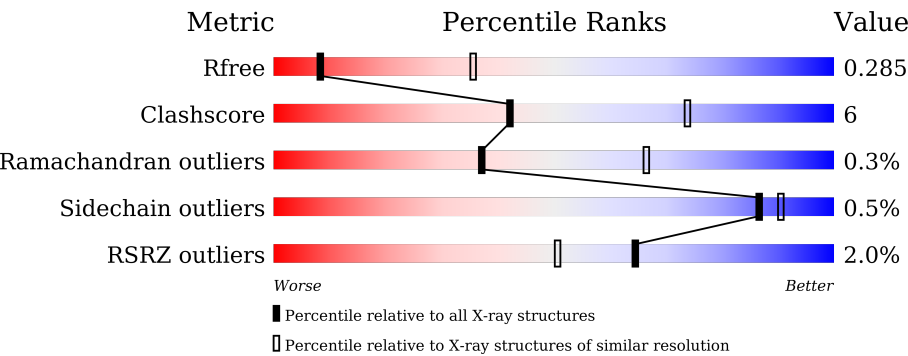
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.21
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.2

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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	1482 (3.30-3.22)
Clashscore	180529	1546 (3.30-3.22)
Ramachandran outliers	177936	1536 (3.30-3.22)
Sidechain outliers	177891	1535 (3.30-3.22)
RSRZ outliers	164620	1483 (3.30-3.22)

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	219	<div><div>3%</div><div><div></div><div>86%</div><div>14%</div></div></div>
2	B	1029	<div><div>%</div><div><div></div><div>78%</div><div>14%</div><div>7%</div></div></div>
3	C	486	<div><div>2%</div><div><div></div><div>78%</div><div>14%</div><div>8%</div></div></div>
4	D	179	<div><div>2%</div><div><div></div><div>77%</div><div>20%</div><div>..</div></div></div>
5	E	205	<div><div>2%</div><div><div></div><div>67%</div><div>13%</div><div>20%</div></div></div>
6	F	411	<div><div>2%</div><div><div></div><div>86%</div><div>11%</div><div>.</div></div></div>

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Mol	Chain	Length	Quality of chain
7	G	112	
8	I	37	

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
11	F3S	B	1104	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 19668 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 Cytochrome c7-like domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	0	0
			1763	1129	306	313	15			

- Molecule 2 is a protein called Fe-S-cluster-containing hydrogenase components 1-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	952	Total	C	N	O	S	0	0	0
			7356	4625	1304	1397	30			

- Molecule 3 is a protein called Polysulphide reductase NrfD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	449	Total	C	N	O	S	0	0	0
			3655	2476	576	586	17			

- Molecule 4 is a protein called Quinol:cytochrome c oxidoreductase membrane protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	175	Total	C	N	O	S	0	0	0
			1350	884	215	245	6			

- Molecule 5 is a protein called Cytochrome c domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	164	Total	C	N	O	S	0	0	0
			1292	819	220	246	7			

- Molecule 6 is a protein called Quinol:cytochrome c oxidoreductase quinone-binding subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	396	Total	C	N	O	S	0	0	0
			3120	2087	504	512	17			

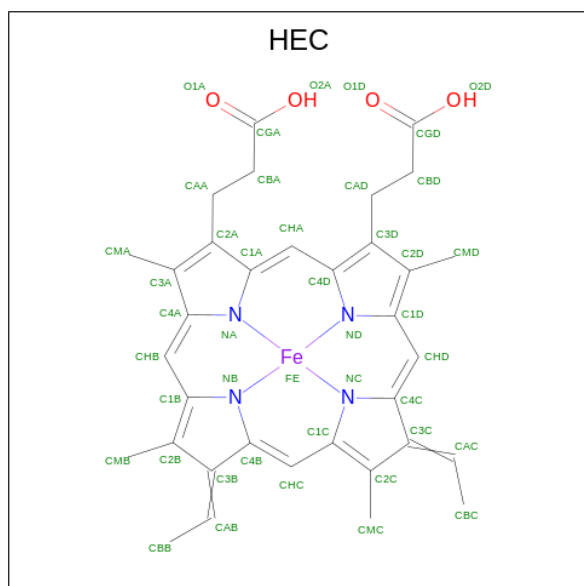
- Molecule 7 is a protein called ActG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	80	Total 619	C 401	N 107	O 107	S 4	0	0	0

- Molecule 8 is a protein called subunit I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	27	Total 224	C 162	N 30	O 30	S 2	0	0	0

- Molecule 9 is HEME C (three-letter code: HEC) (formula: $\text{C}_{34}\text{H}_{34}\text{FeN}_4\text{O}_4$).



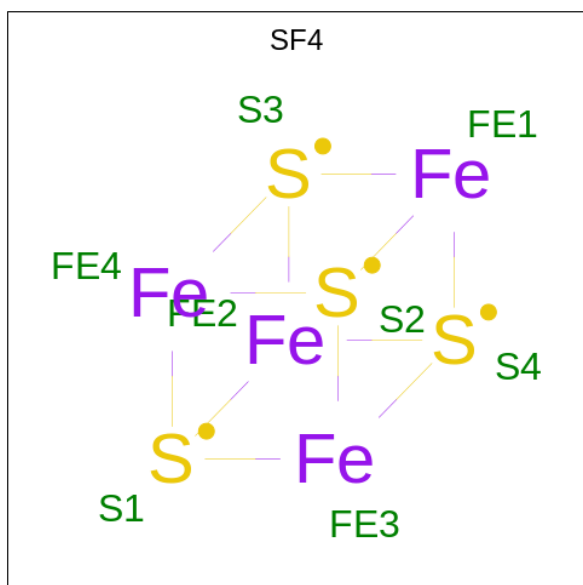
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
9	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
9	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
9	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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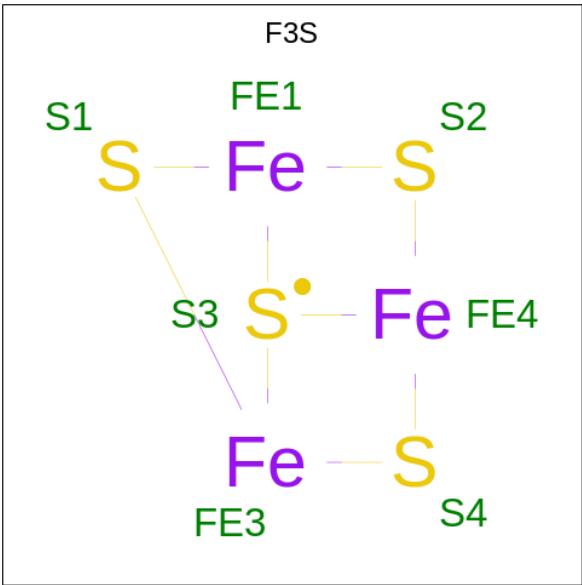
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
9	E	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 10 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).

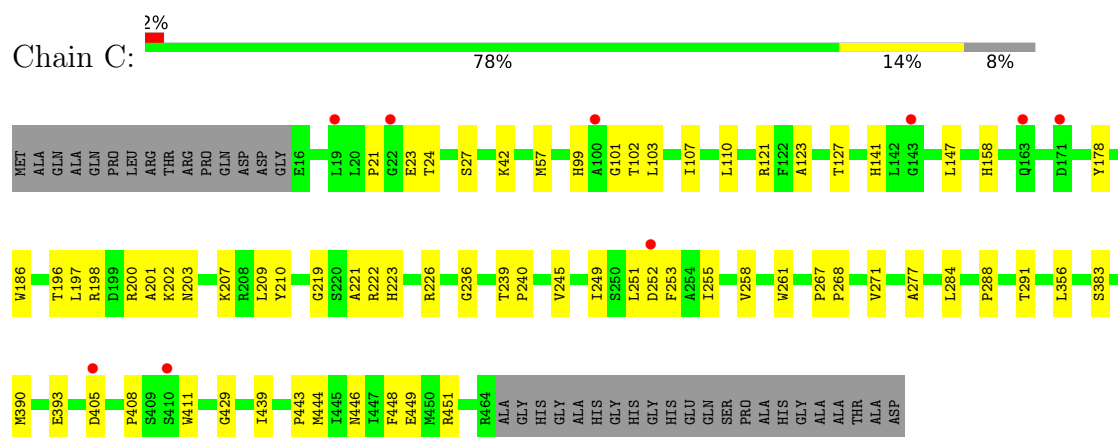


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	Fe	S	0	0
			8	4	4		
10	B	1	Total	Fe	S	0	0
			8	4	4		
10	B	1	Total	Fe	S	0	0
			8	4	4		

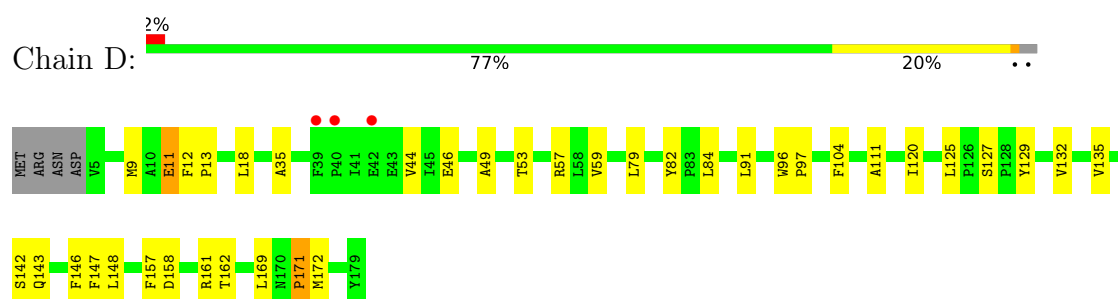
- Molecule 11 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).



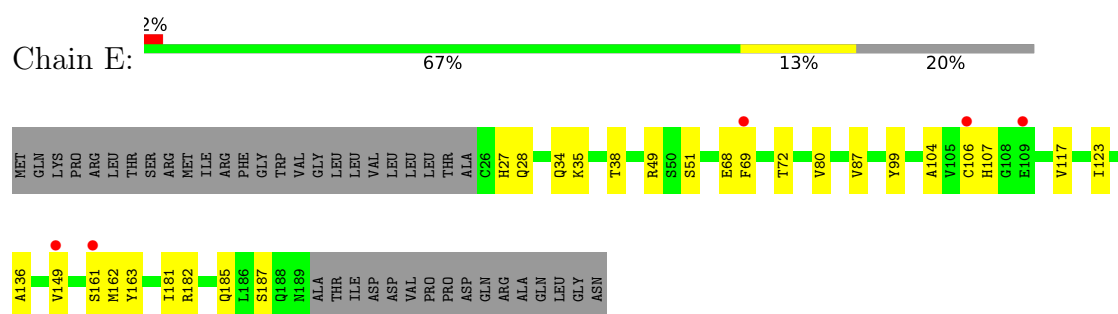
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	Fe	S	0	0
			7	3	4		



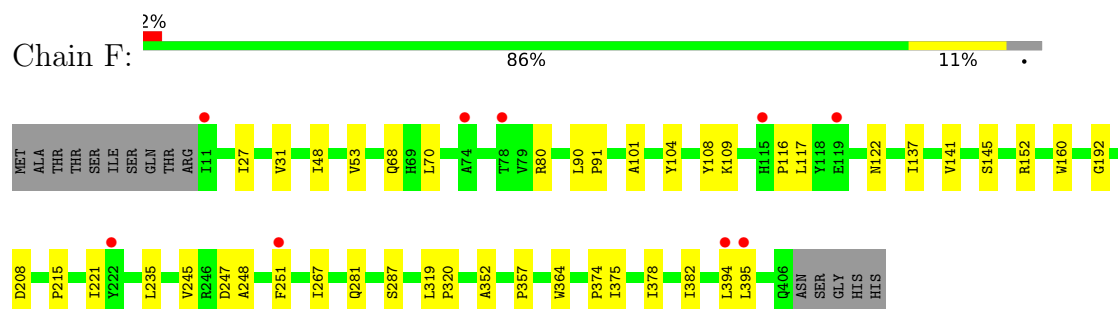
• Molecule 4: Quinol:cytochrome c oxidoreductase membrane protein



• Molecule 5: Cytochrome c domain-containing protein



• Molecule 6: Quinol:cytochrome c oxidoreductase quinone-binding subunit 2



• Molecule 7: ActG



- Molecule 8: subunit I



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	142.02Å 153.06Å 173.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.30 – 3.25 40.30 – 3.25	Depositor EDS
% Data completeness (in resolution range)	89.8 (40.30-3.25) 89.8 (40.30-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 3.25Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158)	Depositor
R, R_{free}	0.249 , 0.286 0.251 , 0.285	Depositor DCC
R_{free} test set	2949 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	88.6	Xtriage
Anisotropy	0.380	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 33.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	19668	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% 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: HEC, SF4, F3S

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	0.24	0/1812	0.44	0/2472
2	B	0.25	0/7524	0.50	0/10257
3	C	0.24	0/3787	0.41	0/5179
4	D	0.27	0/1388	0.47	0/1895
5	E	0.25	0/1327	0.47	0/1803
6	F	0.24	0/3218	0.43	0/4397
7	G	0.23	0/631	0.49	0/861
8	I	0.28	0/233	0.43	0/319
All	All	0.25	0/19920	0.46	0/27183

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	1763	0	1713	30	0
2	B	7356	0	7186	100	0
3	C	3655	0	3688	48	0
4	D	1350	0	1341	28	0
5	E	1292	0	1217	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	3120	0	3169	25	0
7	G	619	0	649	10	0
8	I	224	0	234	8	0
9	A	215	0	149	14	0
9	E	43	0	30	5	0
10	B	24	0	0	1	0
11	B	7	0	0	7	0
All	All	19668	0	19376	240	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 6.

The worst 5 of 240 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:C:200:ARG:HG2	4:D:143:GLN:NE2	1.78	0.99
4:D:158:ASP:HB3	4:D:161:ARG:HB2	1.57	0.86
3:C:200:ARG:CG	4:D:143:GLN:NE2	2.45	0.80
2:B:80:PRO:HD3	5:E:28:GLN:HE22	1.49	0.77
2:B:882:CYS:HG	11:B:1104:F3S:FE4	0.96	0.75

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	216/219 (99%)	205 (95%)	11 (5%)	0	100	100
2	B	950/1029 (92%)	882 (93%)	64 (7%)	4 (0%)	30	60
3	C	447/486 (92%)	425 (95%)	20 (4%)	2 (0%)	30	60
4	D	173/179 (97%)	160 (92%)	12 (7%)	1 (1%)	22	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	162/205 (79%)	151 (93%)	11 (7%)	0	100	100
6	F	394/411 (96%)	376 (95%)	17 (4%)	1 (0%)	37	66
7	G	78/112 (70%)	75 (96%)	3 (4%)	0	100	100
8	I	25/37 (68%)	23 (92%)	2 (8%)	0	100	100
All	All	2445/2678 (91%)	2297 (94%)	140 (6%)	8 (0%)	37	66

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	833	PHE
3	C	202	LYS
4	D	171	PRO
2	B	220	TYR
6	F	395	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	198/199 (100%)	197 (100%)	1 (0%)	86	90
2	B	769/830 (93%)	765 (100%)	4 (0%)	86	90
3	C	382/405 (94%)	382 (100%)	0	100	100
4	D	143/147 (97%)	139 (97%)	4 (3%)	38	62
5	E	135/171 (79%)	134 (99%)	1 (1%)	81	87
6	F	317/330 (96%)	316 (100%)	1 (0%)	91	94
7	G	68/95 (72%)	68 (100%)	0	100	100
8	I	23/32 (72%)	23 (100%)	0	100	100
All	All	2035/2209 (92%)	2024 (100%)	11 (0%)	86	90

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	57	ARG
4	D	157	PHE
6	F	364	TRP
5	E	163	TYR
2	B	930	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	588	ASN
5	E	28	GLN
7	G	82	ASN
2	B	90	GLN
1	A	168	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](#)

10 ligands are 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
10	SF4	B	1102	2	0,12,12	-	-	-		
9	HEC	A	303	1	32,50,50	2.22	4 (12%)	24,82,82	1.37	2 (8%)
9	HEC	A	301	1	32,50,50	2.22	3 (9%)	24,82,82	1.54	4 (16%)
11	F3S	B	1104	2	0,9,9	-	-	-		
10	SF4	B	1103	2	0,12,12	-	-	-		
9	HEC	A	304	1	32,50,50	2.21	3 (9%)	24,82,82	1.46	4 (16%)
9	HEC	A	302	1	32,50,50	2.18	3 (9%)	24,82,82	1.48	4 (16%)
9	HEC	E	301	5	32,50,50	2.18	3 (9%)	24,82,82	1.49	2 (8%)
10	SF4	B	1101	2	0,12,12	-	-	-		
9	HEC	A	305	1	32,50,50	2.20	3 (9%)	24,82,82	1.41	2 (8%)

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
10	SF4	B	1102	2	-	-	0/6/5/5
9	HEC	A	303	1	-	1/10/54/54	-
9	HEC	A	301	1	-	0/10/54/54	-
11	F3S	B	1104	2	-	-	0/3/3/3
10	SF4	B	1103	2	-	-	0/6/5/5
9	HEC	A	304	1	-	2/10/54/54	-
9	HEC	A	302	1	-	3/10/54/54	-
9	HEC	E	301	5	-	2/10/54/54	-
10	SF4	B	1101	2	-	-	0/6/5/5
9	HEC	A	305	1	-	0/10/54/54	-

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	301	HEC	C3C-C2C	-6.59	1.33	1.40
9	A	305	HEC	C3C-C2C	-6.41	1.34	1.40
9	A	304	HEC	C3C-C2C	-6.38	1.34	1.40
9	A	303	HEC	C3C-C2C	-6.35	1.34	1.40
9	A	303	HEC	C2B-C3B	-6.35	1.34	1.40

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	E	301	HEC	CMC-C2C-C1C	-3.96	122.38	128.46
9	A	301	HEC	CBA-CAA-C2A	-3.30	107.05	112.60
9	A	302	HEC	CMC-C2C-C1C	-3.11	123.69	128.46
9	A	303	HEC	CMC-C2C-C1C	-2.98	123.88	128.46
9	A	301	HEC	CMC-C2C-C1C	-2.81	124.14	128.46

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

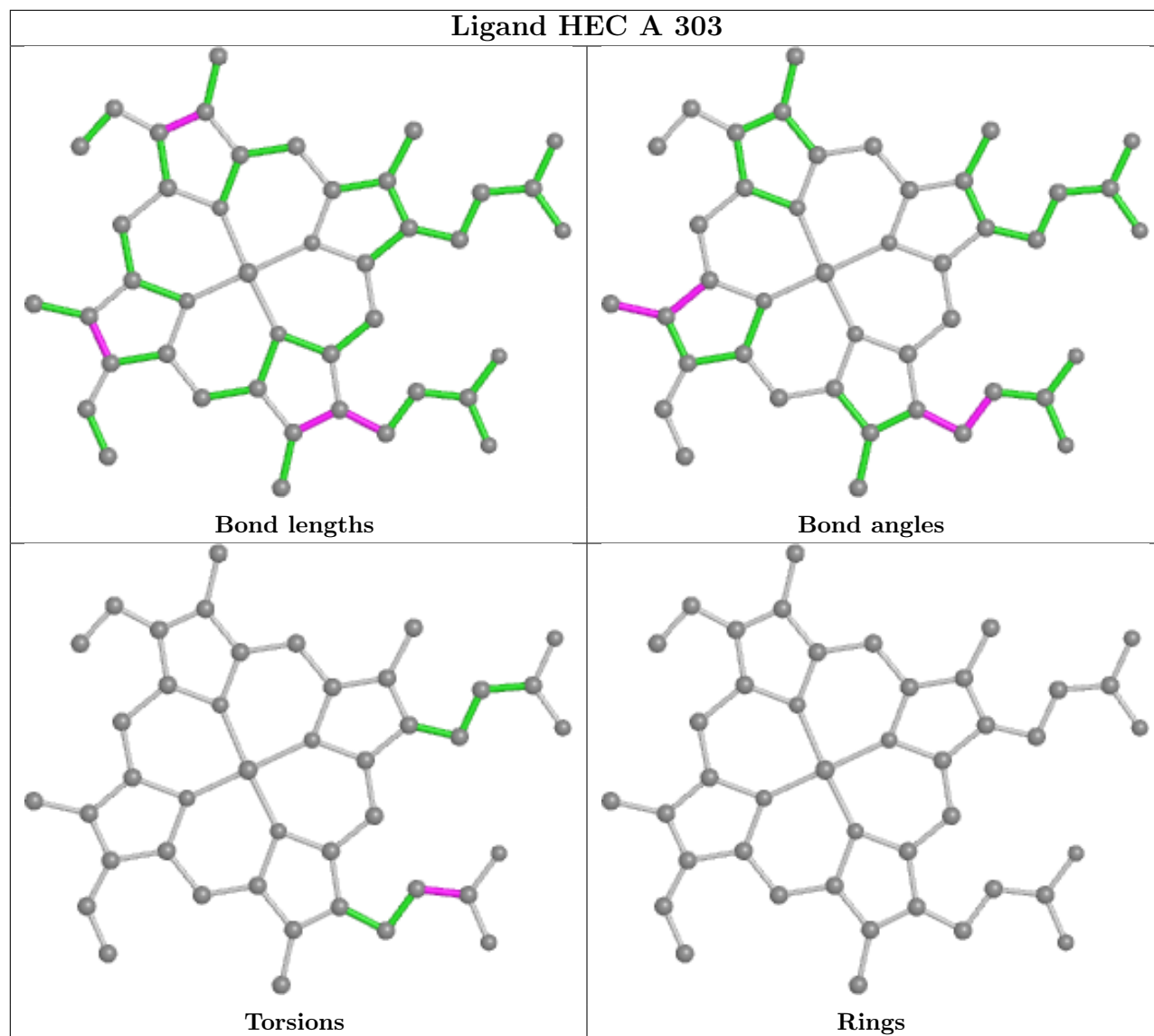
Mol	Chain	Res	Type	Atoms
9	A	302	HEC	C2A-CAA-CBA-CGA
9	A	304	HEC	C1A-C2A-CAA-CBA
9	A	304	HEC	C3A-C2A-CAA-CBA
9	E	301	HEC	CAD-CBD-CGD-O2D
9	E	301	HEC	CAD-CBD-CGD-O1D

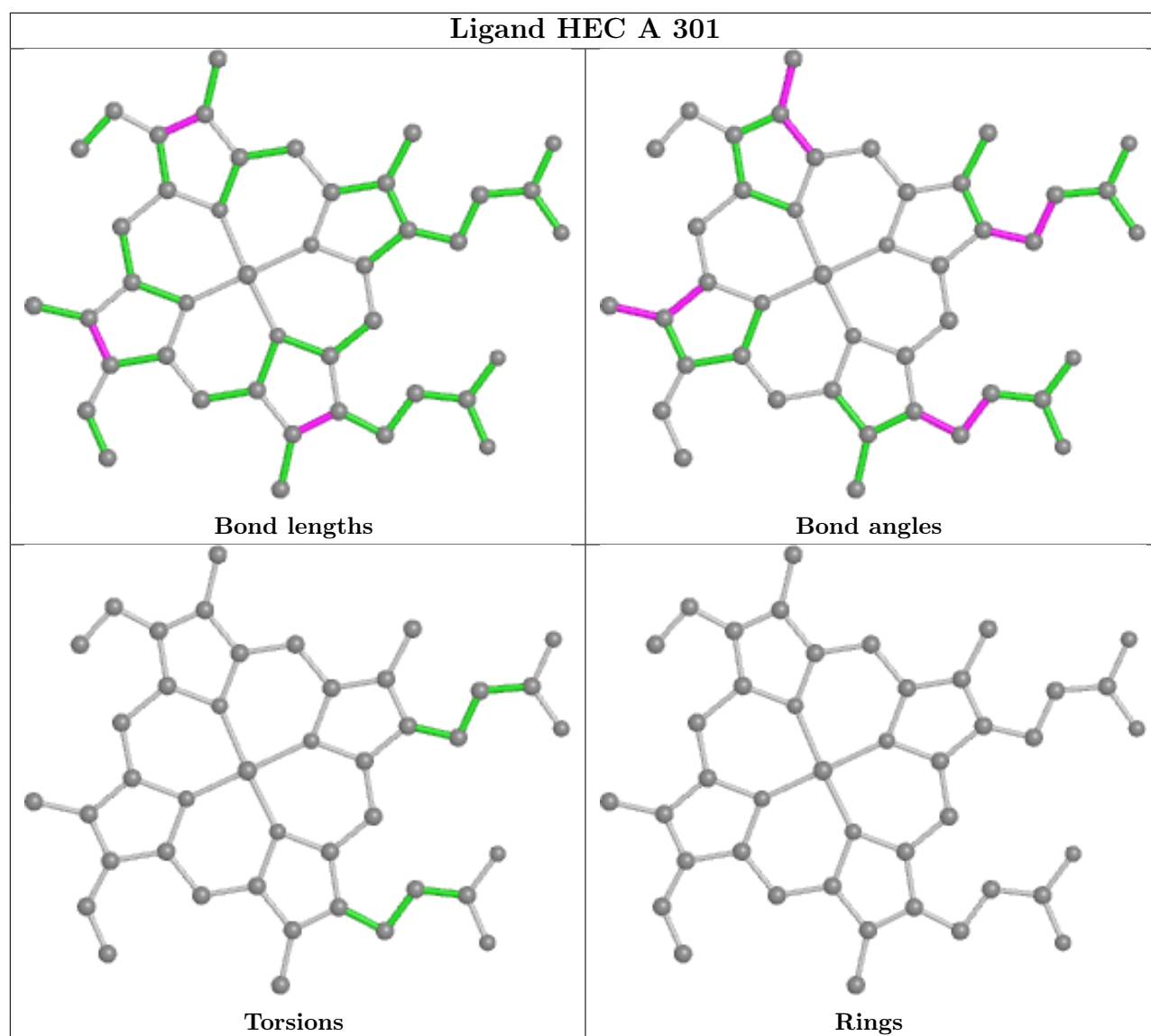
There are no ring outliers.

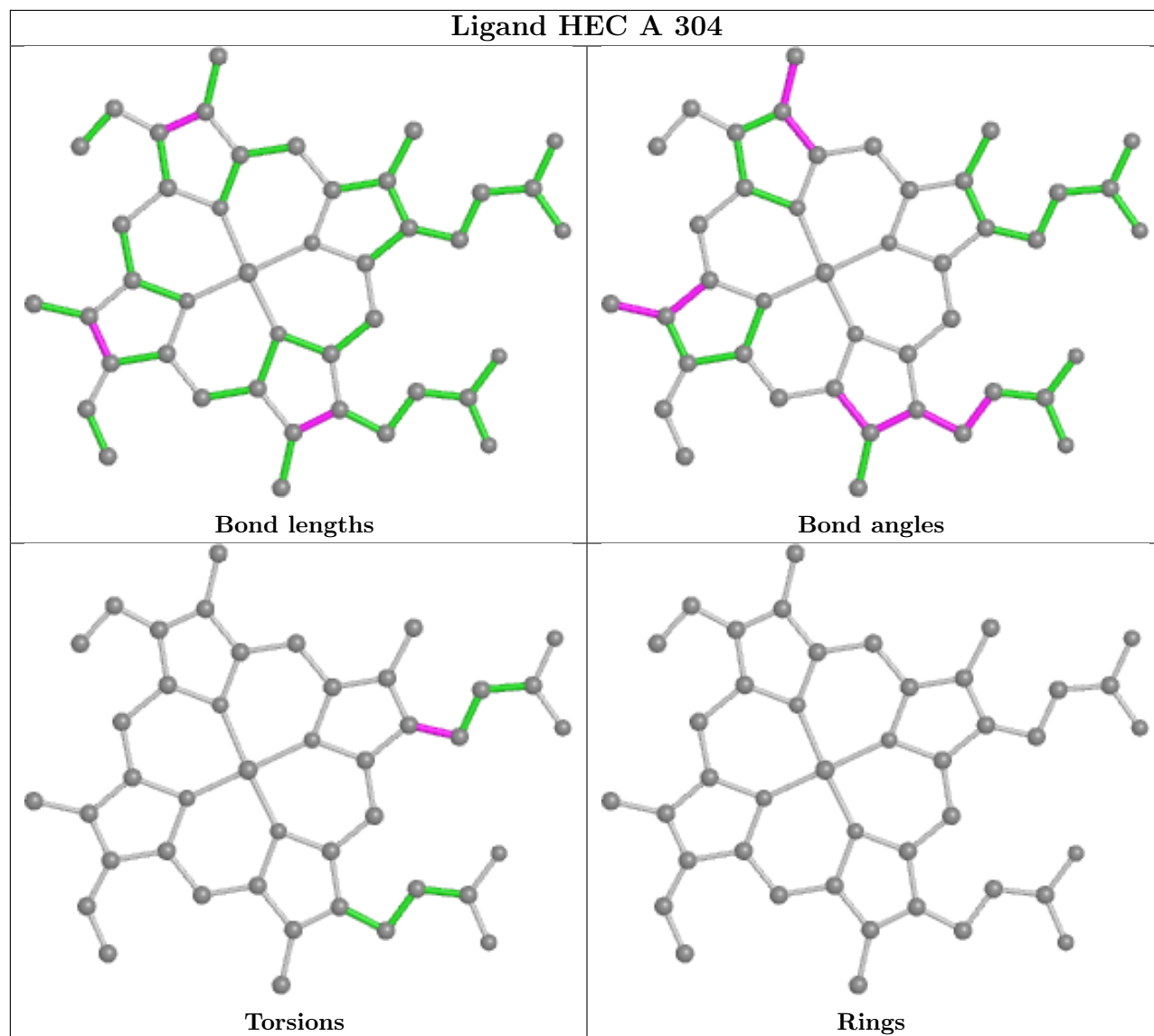
8 monomers are involved in 27 short contacts:

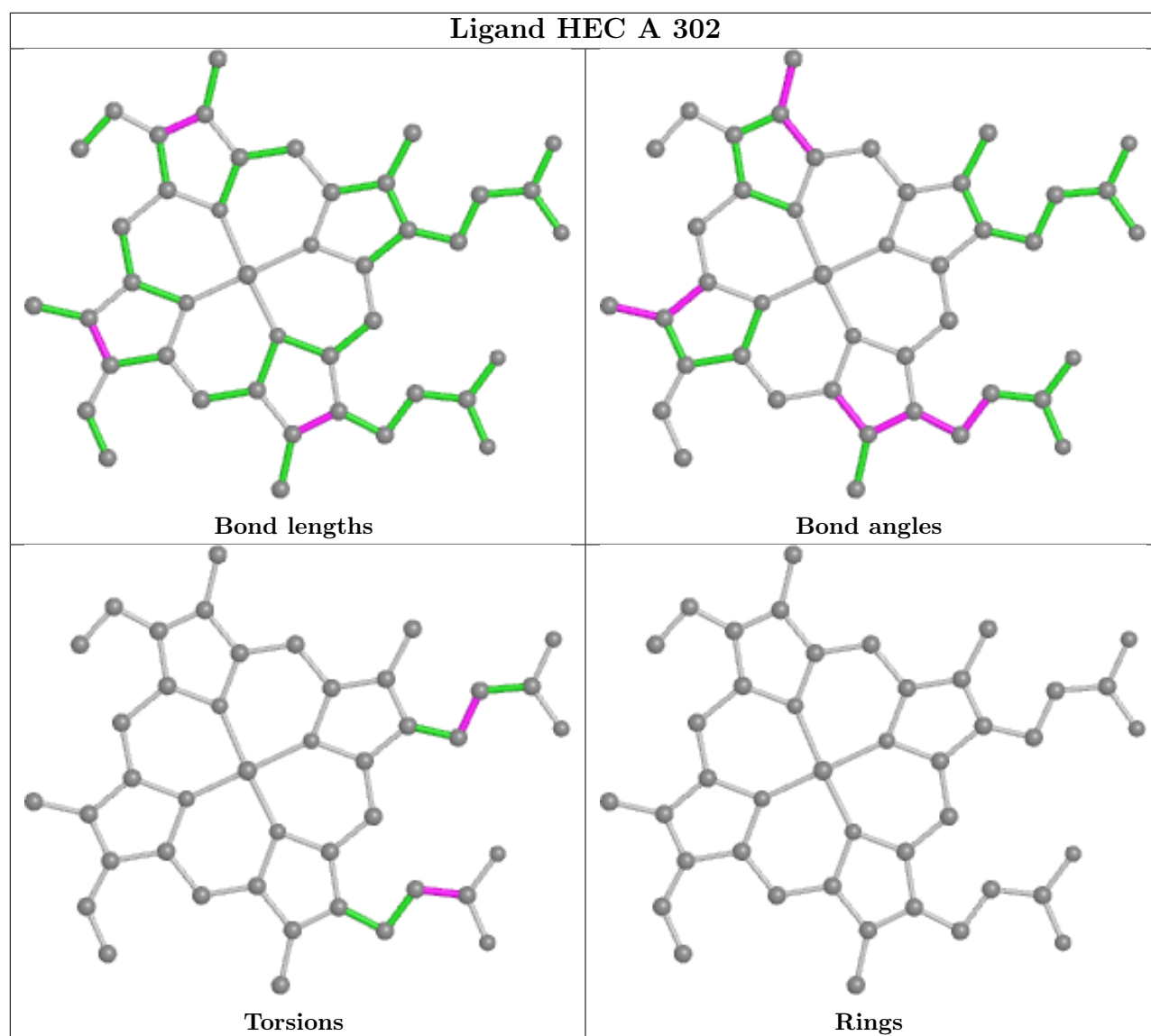
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	303	HEC	2	0
9	A	301	HEC	2	0
11	B	1104	F3S	7	0
10	B	1103	SF4	1	0
9	A	304	HEC	2	0
9	A	302	HEC	6	0
9	E	301	HEC	5	0
9	A	305	HEC	2	0

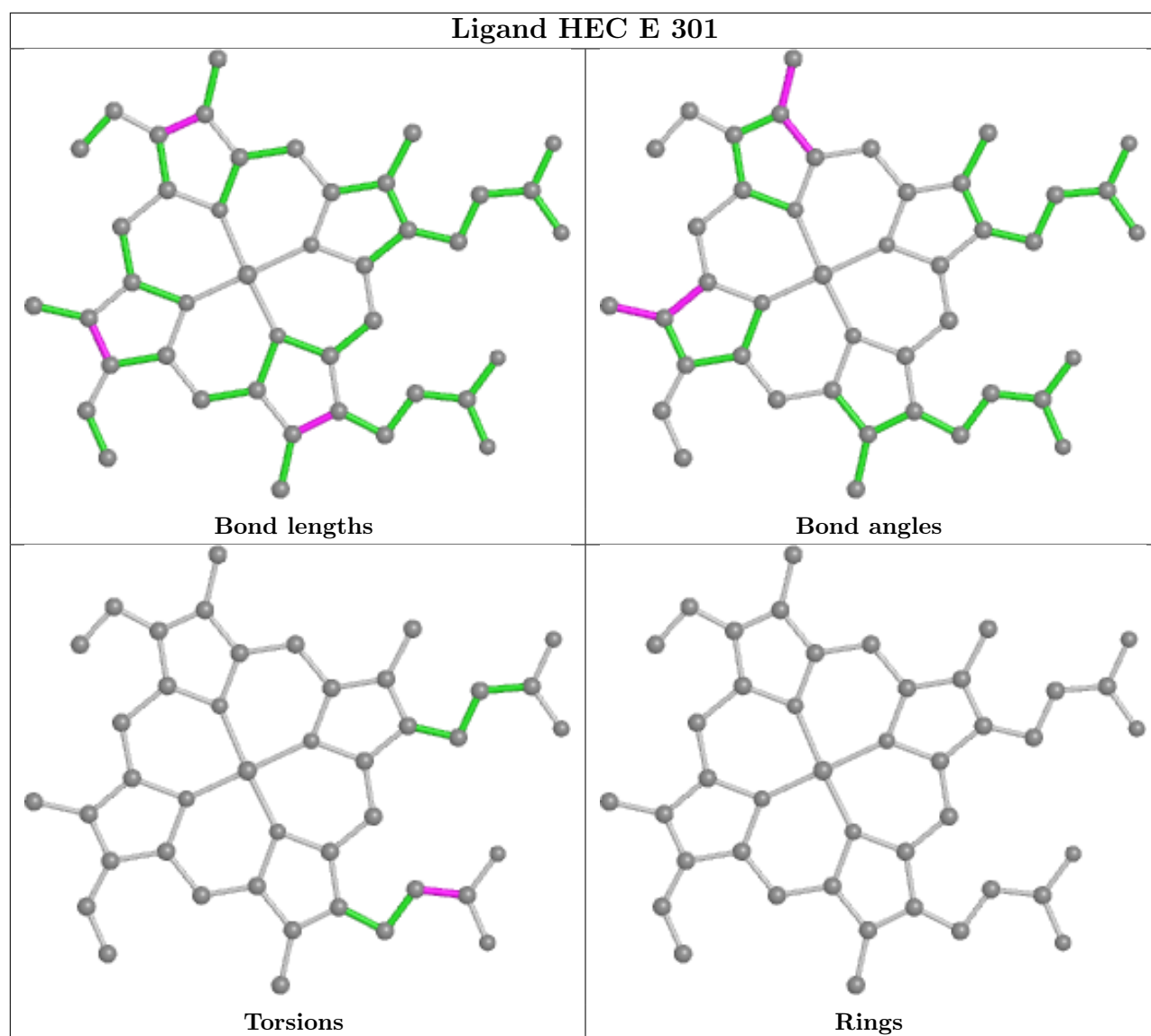
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

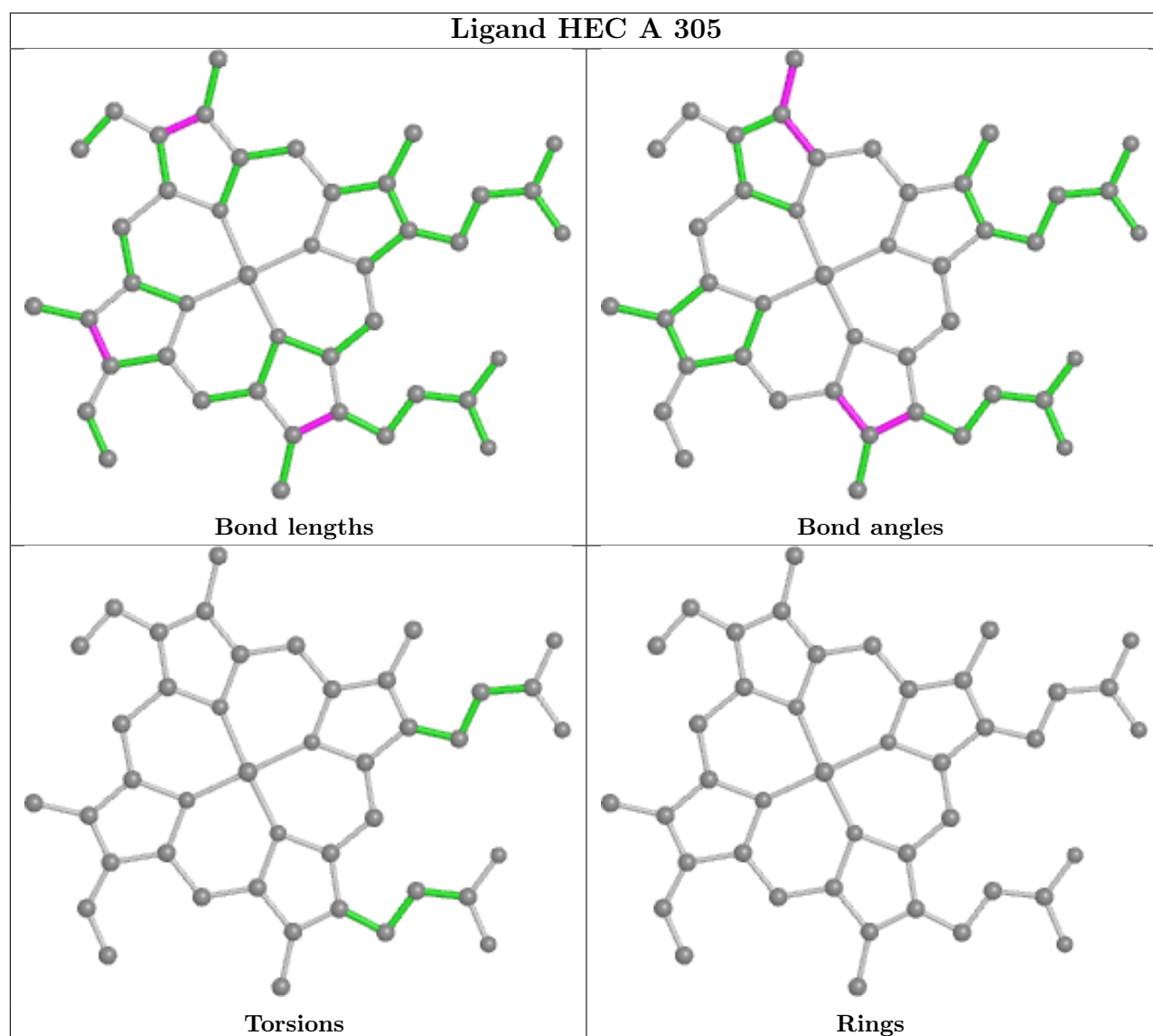












5.7 Other polymers [i](#)

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	218/219 (99%)	0.04	7 (3%)	50 37	37, 77, 127, 160	0
2	B	952/1029 (92%)	-0.06	11 (1%)	76 63	29, 77, 126, 193	0
3	C	449/486 (92%)	0.02	9 (2%)	64 51	49, 92, 142, 214	0
4	D	175/179 (97%)	-0.01	3 (1%)	69 55	39, 109, 166, 218	0
5	E	164/205 (80%)	0.13	5 (3%)	52 39	48, 87, 160, 232	0
6	F	396/411 (96%)	0.01	9 (2%)	61 46	54, 107, 172, 224	0
7	G	80/112 (71%)	0.18	4 (5%)	35 27	66, 103, 172, 241	0
8	I	27/37 (72%)	0.27	1 (3%)	45 34	71, 118, 168, 188	0
All	All	2461/2678 (91%)	0.00	49 (1%)	64 51	29, 88, 150, 241	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	181	VAL	4.7
3	C	143	GLY	4.3
6	F	395	LEU	4.3
5	E	106	CYS	4.1
2	B	481	ASP	3.6

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands

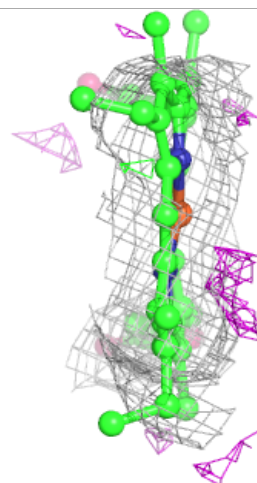
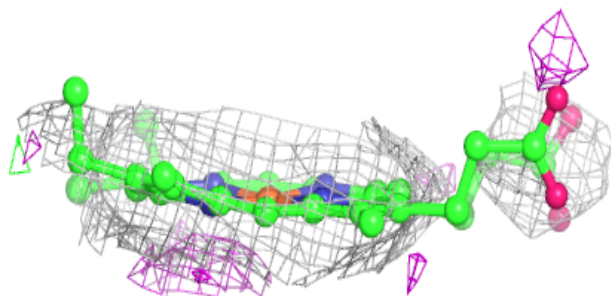
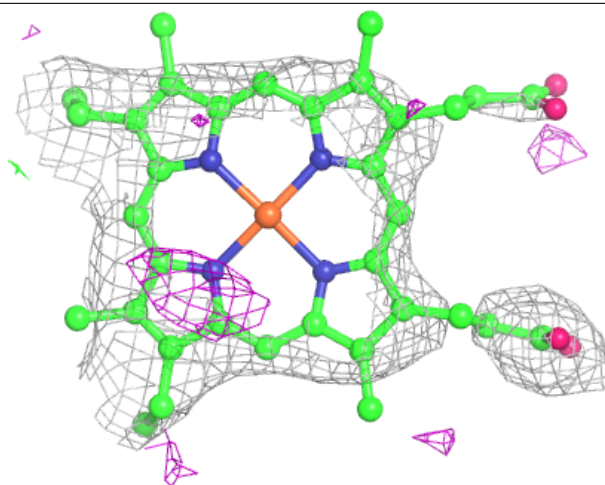
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
9	HEC	E	301	43/43	0.95	0.12	80,96,106,108	0
9	HEC	A	302	43/43	0.96	0.13	63,68,71,72	0
9	HEC	A	301	43/43	0.96	0.11	53,62,65,65	0
9	HEC	A	304	43/43	0.97	0.10	56,66,70,71	0
9	HEC	A	305	43/43	0.97	0.10	69,77,86,90	0
9	HEC	A	303	43/43	0.97	0.09	52,59,63,64	0
10	SF4	B	1101	8/8	0.97	0.05	68,71,74,74	0
11	F3S	B	1104	7/7	0.97	0.07	74,96,109,150	0
10	SF4	B	1103	8/8	0.99	0.04	45,46,48,49	0
10	SF4	B	1102	8/8	0.99	0.04	51,53,55,56	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.

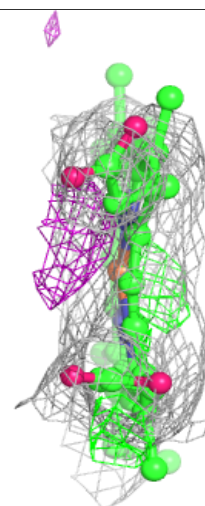
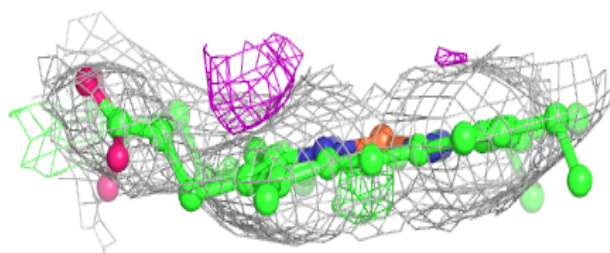
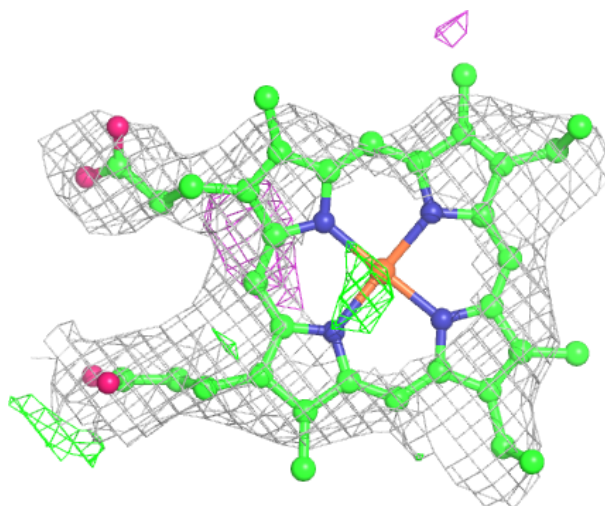
Electron density around HEC E 301:

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



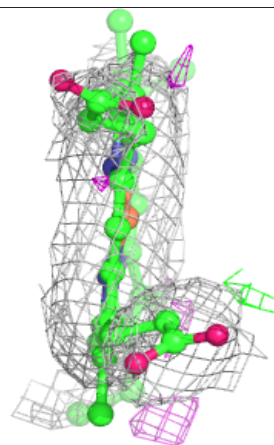
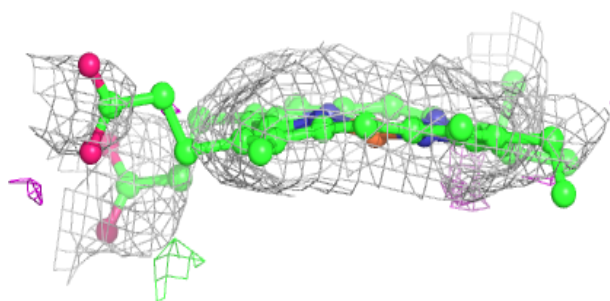
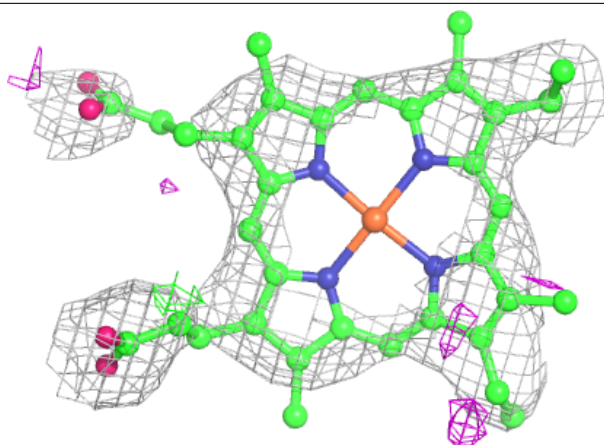
Electron density around HEC A 302:

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



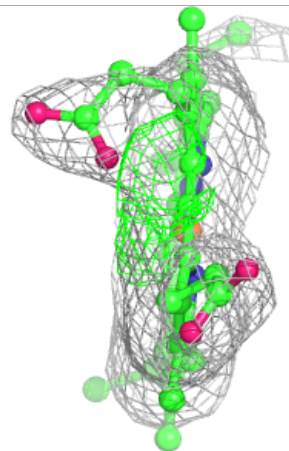
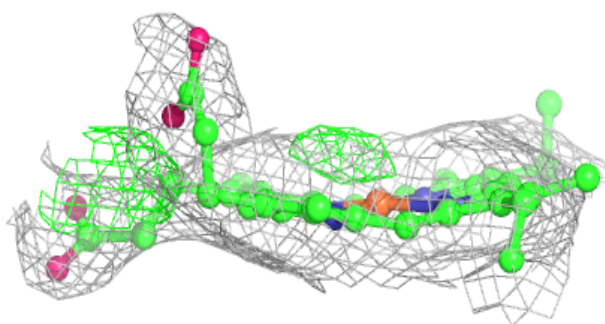
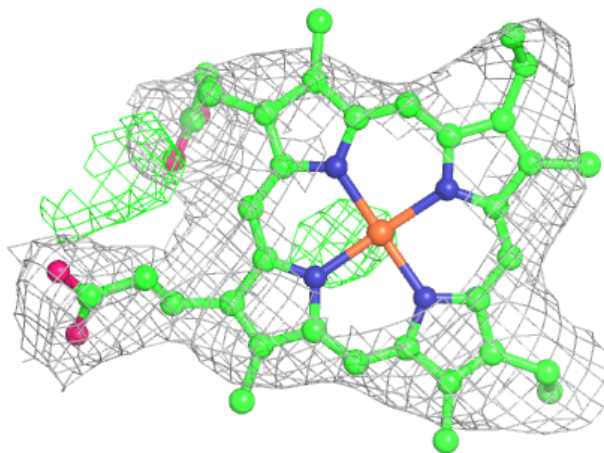
Electron density around HEC A 301:

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



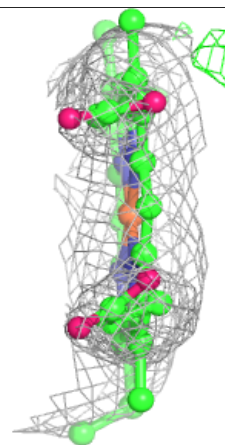
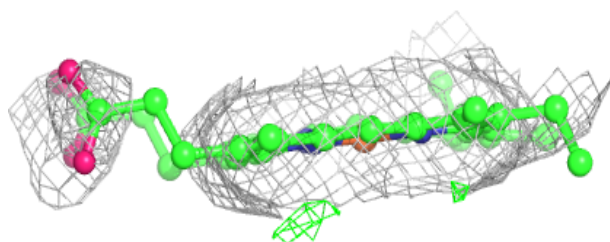
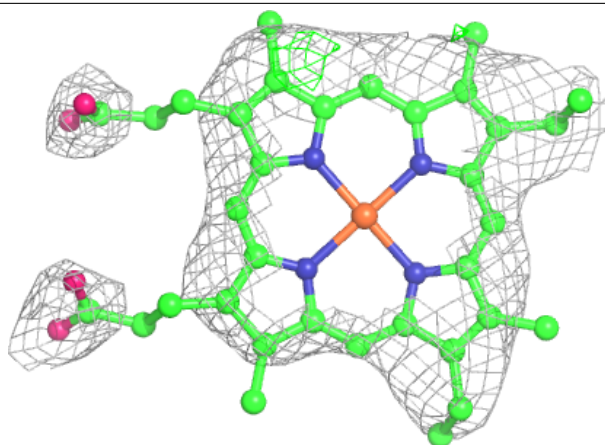
Electron density around HEC A 304:

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



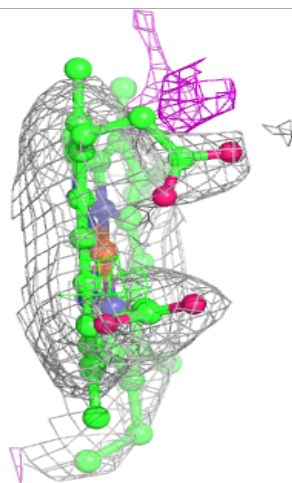
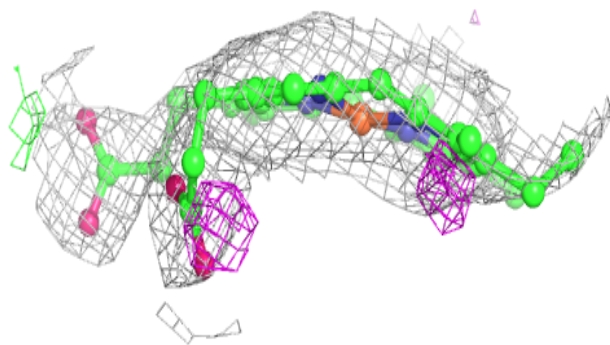
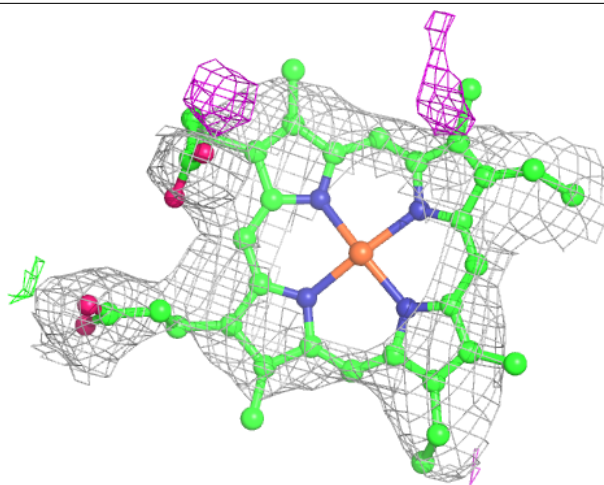
Electron density around HEC A 305:

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



Electron density around HEC A 303:

$2mF_o-DF_c$ (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.