



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:52 PM UTC

PDB ID : 1M6Z / pdb_00001m6z
Title : Crystal structure of reduced recombinant cytochrome c4 from *Pseudomonas stutzeri*
Authors : Noergaard, A.; Harris, P.; Larsen, S.; Christensen, H.E.M.
Deposited on : 2002-07-18
Resolution : 1.35 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

The following versions of software and data (see [references ⓘ](#)) 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

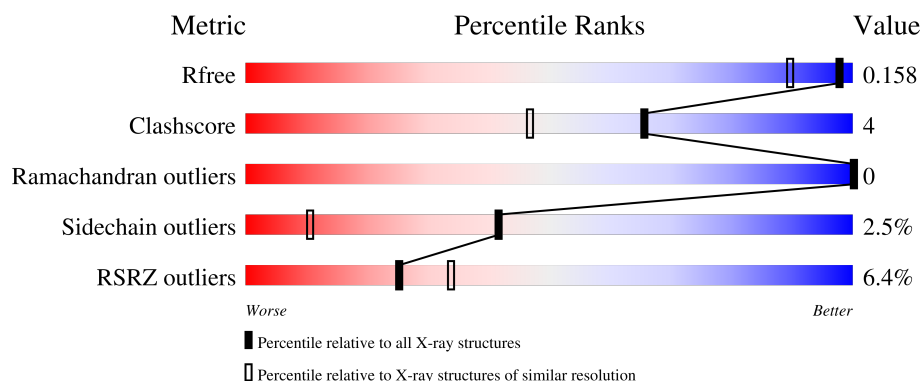
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.35 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	1216 (1.36-1.36)
Clashscore	190562	1232 (1.36-1.36)
Ramachandran outliers	187476	1220 (1.36-1.36)
Sidechain outliers	187428	1220 (1.36-1.36)
RSRZ outliers	180081	1214 (1.36-1.36)

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	190	3% 89% 10% .
1	B	190	12% 86% 11% ..
1	C	190	2% 92% 7% .
1	D	190	9% 92% 8% .

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
4	TRS	D	201	-	X	X	-

2 Entry composition [i](#)

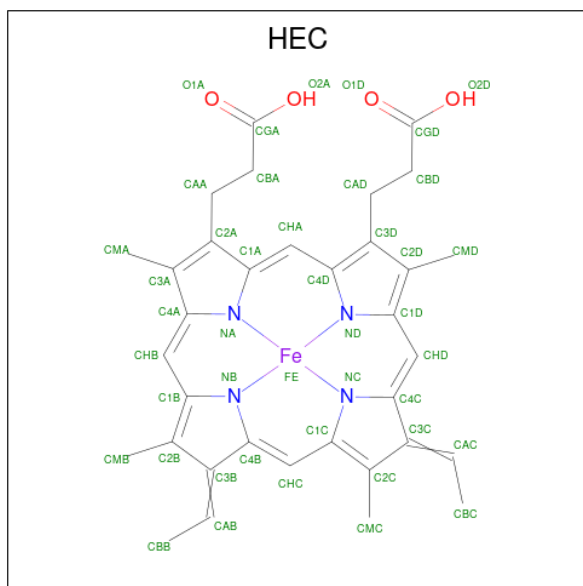
There are 5 unique types of molecules in this entry. The entry contains 6648 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 c4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	0	9	0
			1414	873	254	276	11			
1	B	190	Total	C	N	O	S	0	2	0
			1384	853	248	274	9			
1	C	190	Total	C	N	O	S	0	8	0
			1402	864	251	278	9			
1	D	190	Total	C	N	O	S	0	5	0
			1391	858	248	276	9			

- Molecule 2 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



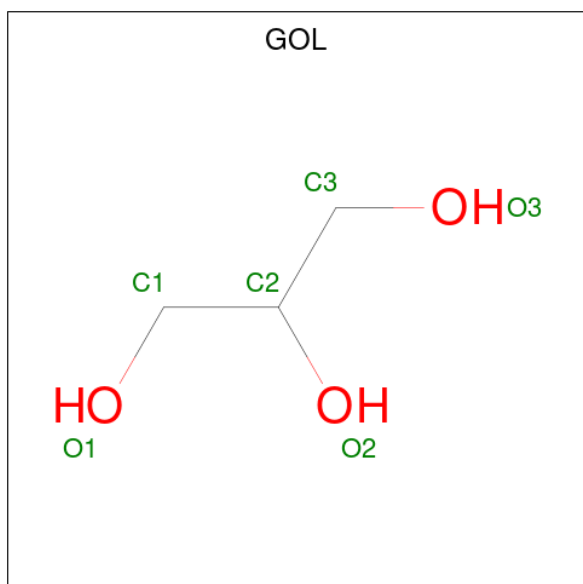
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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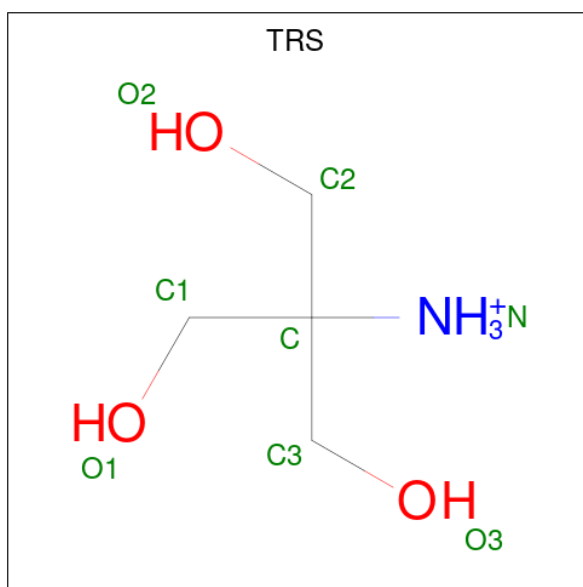
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	Fe	N	O	
			43	34	1	4	4	
2	B	1	Total	C	Fe	N	O	
			43	34	1	4	4	
2	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	
2	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	
2	D	1	Total	C	Fe	N	O	
			43	34	1	4	4	
2	D	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O		
			6	3	3		
3	C	1	Total	C	O		
			6	3	3		

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	188	Total	O	0	0
			188	188		
5	B	135	Total	O	0	0
			135	135		
5	C	201	Total	O	0	0
			201	201		
5	D	169	Total	O	0	0
			169	169		

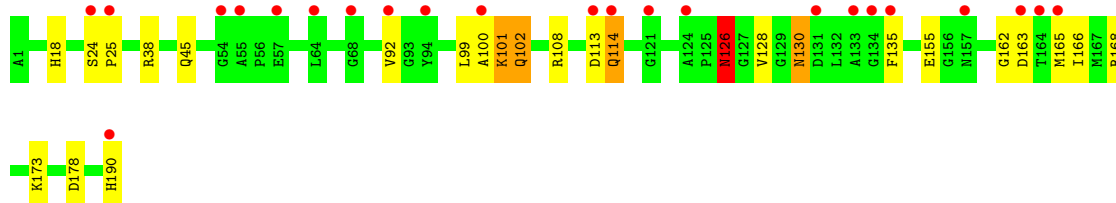
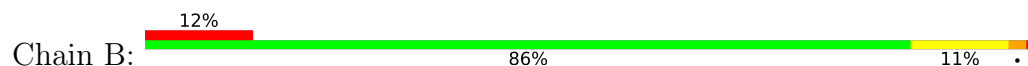
3 Residue-property plots [i](#)

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 c4



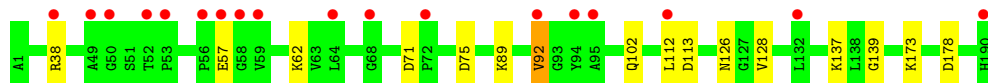
- Molecule 1: Cytochrome c4



- Molecule 1: Cytochrome c4



- Molecule 1: Cytochrome c4



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.11Å 57.56Å 83.75Å 90.00° 104.32° 90.00°	Depositor
Resolution (Å)	30.00 – 1.35 30.00 – 1.35	Depositor EDS
% Data completeness (in resolution range)	92.6 (30.00-1.35) 92.9 (30.00-1.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.38 (at 1.35Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.140 , 0.191 0.145 , 0.158	Depositor DCC
R_{free} test set	7157 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	11.2	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6648	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 84.77 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5182e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, HEC, TRS

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	0.74	0/1477	1.37	11/1986 (0.6%)
1	B	0.62	0/1417	1.47	19/1906 (1.0%)
1	C	0.66	0/1461	1.28	4/1966 (0.2%)
1	D	0.68	0/1437	1.29	7/1934 (0.4%)
All	All	0.68	0/5792	1.36	41/7792 (0.5%)

There are no bond length outliers.

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	38	ARG	NE-CZ-NH2	13.18	131.06	119.20
1	B	126	ASN	CB-CG-ND2	10.24	131.76	116.40
1	B	126	ASN	OD1-CG-ND2	-8.95	113.65	122.60
1	D	38	ARG	CD-NE-CZ	8.31	136.04	124.40
1	A	38[A]	ARG	CD-NE-CZ	7.97	135.56	124.40
1	A	38[B]	ARG	CD-NE-CZ	7.97	135.56	124.40
1	B	135	PHE	CA-C-O	7.43	124.82	119.32
1	A	28	ASN	CA-CB-CG	-7.37	105.23	112.60
1	B	108	ARG	CA-CB-CG	6.94	127.97	114.10
1	A	130	ASN	CA-C-N	-6.79	109.25	121.14
1	A	130	ASN	C-N-CA	-6.79	109.25	121.14
1	A	178	ASP	CA-CB-CG	6.71	119.31	112.60
1	D	71	ASP	CA-CB-CG	-6.62	105.98	112.60
1	B	130	ASN	CB-CG-ND2	6.37	125.95	116.40
1	D	113	ASP	CA-CB-CG	6.29	118.89	112.60
1	B	130	ASN	OD1-CG-ND2	-6.24	116.36	122.60
1	C	96	ASP	CA-CB-CG	-6.13	106.47	112.60
1	B	38	ARG	CD-NE-CZ	6.06	132.89	124.40
1	B	99	LEU	CA-C-N	5.98	128.29	120.28
1	B	99	LEU	C-N-CA	5.98	128.29	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	102	GLN	CG-CD-OE1	5.82	132.44	120.80
1	B	163	ASP	CA-CB-CG	5.77	118.37	112.60
1	D	102	GLN	OE1-CD-NE2	-5.75	116.85	122.60
1	A	163	ASP	CA-CB-CG	5.73	118.33	112.60
1	B	102	GLN	CB-CG-CD	5.66	122.22	112.60
1	C	178	ASP	CA-CB-CG	5.59	118.19	112.60
1	B	166	ILE	CB-CA-C	-5.54	104.61	111.70
1	C	77	ASP	CA-CB-CG	5.48	118.08	112.60
1	B	45	GLN	CG-CD-NE2	5.46	124.59	116.40
1	B	38	ARG	NE-CZ-NH1	-5.44	116.06	121.50
1	B	162	GLY	CA-C-N	5.40	128.06	120.28
1	B	162	GLY	C-N-CA	5.40	128.06	120.28
1	A	162	GLY	CA-C-O	-5.37	114.60	120.40
1	C	26	ALA	CA-C-O	5.34	123.28	119.32
1	A	162	GLY	CA-C-N	5.30	127.92	120.28
1	A	162	GLY	C-N-CA	5.30	127.92	120.28
1	B	178	ASP	CA-CB-CG	5.22	117.82	112.60
1	D	178	ASP	CA-CB-CG	5.21	117.81	112.60
1	B	155	GLU	CG-CD-OE1	5.20	130.35	118.40
1	D	75	ASP	CA-CB-CG	5.08	117.67	112.60
1	A	45	GLN	CG-CD-OE1	5.05	130.91	120.80

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	1414	0	1383	9	0
1	B	1384	0	1352	11	0
1	C	1402	0	1367	10	0
1	D	1391	0	1361	15	0
2	A	86	0	60	1	0
2	B	86	0	60	0	0
2	C	86	0	60	0	0
2	D	86	0	60	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	6	0	7	0	0
3	C	6	0	7	2	0
4	D	8	0	11	9	0
5	A	188	0	0	3	0
5	B	135	0	0	4	0
5	C	201	0	0	5	0
5	D	169	0	0	5	0
All	All	6648	0	5728	44	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 4.

All (44) 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:C:76:GLN:HB3	3:C:201:GOL:H32	1.58	0.83
1:D:137[A]:LYS:HG2	4:D:201:TRS:H22	1.62	0.79
1:D:139:GLY:O	4:D:201:TRS:H21	1.88	0.74
1:D:137[B]:LYS:HG2	4:D:201:TRS:H22	1.69	0.73
1:C:173:LYS:HE3	5:C:267:HOH:O	1.91	0.70
1:A:62:LYS:HE3	5:A:351:HOH:O	1.94	0.67
1:B:24:SER:HB3	5:B:216:HOH:O	1.95	0.65
1:D:92[A]:VAL:HG12	5:D:365:HOH:O	1.96	0.65
1:D:173:LYS:HE3	5:D:281:HOH:O	1.97	0.63
1:A:102:GLN:HG2	5:A:380:HOH:O	2.00	0.61
1:B:114:GLN:O	1:B:173:LYS:HE2	2.00	0.61
1:D:112:LEU:HG	5:D:254:HOH:O	2.01	0.61
1:D:137[B]:LYS:NZ	4:D:201:TRS:H12	2.16	0.60
1:A:114:GLN:O	1:A:173:LYS:HE2	2.03	0.59
1:D:137[B]:LYS:HZ3	4:D:201:TRS:H12	1.68	0.58
1:C:165:MET:HE2	1:C:168:ARG:NH1	2.19	0.58
1:B:165:MET:HG2	1:B:168:ARG:CZ	2.34	0.57
1:C:20[B]:VAL:HG12	5:C:366:HOH:O	2.09	0.52
1:B:126:ASN:ND2	1:B:128:VAL:HG13	2.25	0.52
1:A:5:GLU:CD	1:B:101:LYS:HD3	2.35	0.51
1:B:190:HIS:HA	5:B:299:HOH:O	2.09	0.51
1:D:137[A]:LYS:HG2	4:D:201:TRS:C2	2.37	0.50
1:B:25:PRO:HD2	5:B:238:HOH:O	2.12	0.49
1:D:62:LYS:HE3	5:D:305:HOH:O	2.12	0.48
1:A:190:HIS:HE1	5:A:294:HOH:O	1.95	0.48
1:B:18:HIS:C	1:B:24:SER:HB2	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38[A]:ARG:NE	5:C:256:HOH:O	2.49	0.46
1:D:137[B]:LYS:HZ3	4:D:201:TRS:H21	1.81	0.46
1:A:126:ASN:OD1	1:A:128[B]:VAL:HG22	2.17	0.45
1:C:45:GLN:NE2	5:C:296:HOH:O	2.49	0.45
1:C:76:GLN:CB	3:C:201:GOL:H32	2.38	0.45
1:D:137[B]:LYS:HG2	4:D:201:TRS:C2	2.41	0.45
1:A:69[B]:MET:HE1	2:A:199:HEC:HMC2	2.00	0.44
1:D:128[A]:VAL:HG12	5:D:363:HOH:O	2.16	0.44
1:C:57:GLU:O	1:C:57:GLU:HG2	2.16	0.44
1:C:137[A]:LYS:HD3	5:C:402:HOH:O	2.18	0.43
1:A:48:LYS:NZ	1:A:73:LEU:O	2.49	0.43
1:B:165:MET:HG2	1:B:168:ARG:NH2	2.35	0.42
1:C:47:ILE:HA	1:C:61:ARG:O	2.20	0.42
1:D:126:ASN:OD1	1:D:128[A]:VAL:HG22	2.19	0.41
1:D:137[B]:LYS:HZ3	4:D:201:TRS:C2	2.33	0.41
1:B:113:ASP:OD1	1:B:113:ASP:N	2.54	0.40
1:A:113:ASP:OD1	1:A:113:ASP:N	2.51	0.40
1:B:100:ALA:HA	5:B:225:HOH:O	2.20	0.40

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	197/190 (104%)	192 (98%)	5 (2%)	0	100	100
1	B	190/190 (100%)	187 (98%)	3 (2%)	0	100	100
1	C	196/190 (103%)	191 (97%)	5 (3%)	0	100	100
1	D	193/190 (102%)	190 (98%)	3 (2%)	0	100	100
All	All	776/760 (102%)	760 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	147/138 (106%)	142 (97%)	5 (3%)	32 6
1	B	140/138 (101%)	134 (96%)	6 (4%)	26 3
1	C	146/138 (106%)	145 (99%)	1 (1%)	76 54
1	D	143/138 (104%)	139 (97%)	4 (3%)	38 9
All	All	576/552 (104%)	560 (97%)	16 (3%)	42 9

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	VAL
1	A	102	GLN
1	A	108[A]	ARG
1	A	108[B]	ARG
1	A	163	ASP
1	B	92	VAL
1	B	101	LYS
1	B	102	GLN
1	B	114	GLN
1	B	126	ASN
1	B	130	ASN
1	C	57	GLU
1	D	57	GLU
1	D	89	LYS
1	D	92[A]	VAL
1	D	92[B]	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	157	ASN
1	A	190	HIS
1	B	88	GLN

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Mol	Chain	Res	Type
1	B	130	ASN
1	B	157	ASN
1	C	28	ASN
1	C	45	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

11 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
2	HEC	A	199	1	46,50,50	2.13	12 (26%)	58,82,82	2.29	17 (29%)
4	TRS	D	201	-	7,7,7	2.02	2 (28%)	9,9,9	2.15	3 (33%)
2	HEC	A	200	1	46,50,50	1.80	8 (17%)	58,82,82	1.94	9 (15%)
3	GOL	A	201	-	5,5,5	0.80	0	5,5,5	2.11	2 (40%)
2	HEC	D	199	1	46,50,50	2.08	11 (23%)	58,82,82	2.29	14 (24%)
2	HEC	D	200	1	46,50,50	1.86	9 (19%)	58,82,82	1.92	9 (15%)
3	GOL	C	201	-	5,5,5	1.16	0	5,5,5	3.87	3 (60%)
2	HEC	C	199	1	46,50,50	2.03	10 (21%)	58,82,82	2.29	15 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEC	C	200	1	46,50,50	1.84	11 (23%)	58,82,82	1.88	9 (15%)
2	HEC	B	199	1	46,50,50	2.20	14 (30%)	58,82,82	2.55	20 (34%)
2	HEC	B	200	1	46,50,50	1.83	8 (17%)	58,82,82	1.84	8 (13%)

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
2	HEC	A	199	1	-	6/14/54/54	-
4	TRS	D	201	-	-	5/9/9/9	-
2	HEC	A	200	1	-	6/14/54/54	-
3	GOL	A	201	-	-	1/4/4/4	-
2	HEC	D	199	1	-	6/14/54/54	-
2	HEC	D	200	1	-	6/14/54/54	-
3	GOL	C	201	-	-	1/4/4/4	-
2	HEC	C	199	1	-	6/14/54/54	-
2	HEC	C	200	1	-	6/14/54/54	-
2	HEC	B	199	1	-	6/14/54/54	-
2	HEC	B	200	1	-	6/14/54/54	-

All (85) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	200	HEC	CAC-C3C	6.27	1.55	1.35
2	A	200	HEC	CAC-C3C	6.11	1.54	1.35
2	B	199	HEC	O2D-CGD	-6.06	1.10	1.30
2	C	200	HEC	CAC-C3C	5.89	1.54	1.35
2	A	199	HEC	O2D-CGD	-5.85	1.11	1.30
2	D	199	HEC	O2D-CGD	-5.81	1.11	1.30
2	B	200	HEC	CAC-C3C	5.74	1.53	1.35
2	C	199	HEC	O2D-CGD	-5.67	1.12	1.30
2	C	199	HEC	CAC-C3C	5.63	1.53	1.35
2	B	199	HEC	CAC-C3C	5.60	1.53	1.35
2	A	199	HEC	CAC-C3C	5.44	1.52	1.35
2	D	199	HEC	CAC-C3C	5.37	1.52	1.35
2	A	199	HEC	CAB-C3B	5.11	1.51	1.35
2	B	199	HEC	CAB-C3B	4.96	1.51	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	200	HEC	CAB-C3B	4.96	1.51	1.35
2	D	199	HEC	CAB-C3B	4.90	1.50	1.35
2	C	200	HEC	CAB-C3B	4.90	1.50	1.35
2	D	200	HEC	CAB-C3B	4.81	1.50	1.35
2	C	199	HEC	CAB-C3B	4.77	1.50	1.35
2	A	200	HEC	CAB-C3B	4.63	1.50	1.35
4	D	201	TRS	C2-C	-4.55	1.41	1.53
2	A	199	HEC	CMB-C2B	4.24	1.59	1.50
2	D	199	HEC	CMB-C2B	4.21	1.59	1.50
2	B	199	HEC	CMB-C2B	4.14	1.59	1.50
2	A	199	HEC	C3B-C4B	-4.02	1.39	1.46
2	B	199	HEC	C1D-ND	-3.91	1.32	1.39
2	C	199	HEC	CMB-C2B	3.89	1.58	1.50
2	A	200	HEC	O1D-CGD	3.78	1.34	1.22
2	B	199	HEC	CBB-CAB	3.63	1.62	1.49
2	B	200	HEC	O1D-CGD	3.52	1.33	1.22
2	C	200	HEC	O1D-CGD	3.49	1.33	1.22
2	D	200	HEC	O1D-CGD	3.48	1.33	1.22
2	D	199	HEC	C3B-C4B	-3.38	1.40	1.46
2	C	199	HEC	C3B-C4B	-3.26	1.40	1.46
2	B	199	HEC	C3B-C4B	-3.23	1.40	1.46
2	D	199	HEC	CHA-C4D	3.05	1.46	1.39
2	A	199	HEC	CBB-CAB	3.01	1.60	1.49
2	C	199	HEC	CBB-CAB	2.94	1.60	1.49
2	A	199	HEC	CBA-CGA	2.91	1.57	1.50
2	D	199	HEC	CBB-CAB	2.84	1.60	1.49
2	D	199	HEC	CBD-CGD	2.82	1.57	1.50
2	D	199	HEC	C4D-C3D	-2.77	1.39	1.44
2	C	199	HEC	O2A-CGA	-2.77	1.21	1.30
2	C	200	HEC	O1A-CGA	2.76	1.31	1.22
2	A	199	HEC	O2A-CGA	-2.70	1.21	1.30
2	A	199	HEC	CBD-CGD	2.68	1.56	1.50
2	B	199	HEC	CHD-C1D	2.64	1.45	1.39
2	B	199	HEC	CBD-CGD	2.61	1.56	1.50
2	D	200	HEC	O1A-CGA	2.55	1.30	1.22
2	A	199	HEC	C4D-C3D	-2.54	1.39	1.44
2	C	199	HEC	CBD-CGD	2.54	1.56	1.50
2	B	200	HEC	O1A-CGA	2.54	1.30	1.22
2	D	199	HEC	CBA-CGA	2.52	1.56	1.50
2	C	199	HEC	CBA-CGA	2.51	1.56	1.50
4	D	201	TRS	O1-C1	-2.47	1.34	1.42
2	C	200	HEC	O2D-CGD	-2.47	1.22	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	199	HEC	O2A-CGA	-2.47	1.22	1.30
2	C	199	HEC	C4D-C3D	-2.46	1.39	1.44
2	D	200	HEC	O2D-CGD	-2.45	1.22	1.30
2	D	200	HEC	O2A-CGA	-2.42	1.22	1.30
2	A	200	HEC	O2D-CGD	-2.41	1.22	1.30
2	B	199	HEC	CBA-CGA	2.41	1.56	1.50
2	A	200	HEC	O1A-CGA	2.40	1.30	1.22
2	B	200	HEC	O2D-CGD	-2.40	1.22	1.30
2	D	200	HEC	CMC-C2C	2.36	1.55	1.50
2	B	199	HEC	C4D-C3D	-2.34	1.39	1.44
2	C	200	HEC	CHC-C1C	-2.31	1.34	1.39
2	A	200	HEC	CMC-C2C	2.30	1.55	1.50
2	B	200	HEC	CHC-C1C	-2.29	1.34	1.39
2	A	199	HEC	C3C-C2C	-2.26	1.33	1.41
2	B	200	HEC	C3B-C2B	-2.25	1.33	1.41
2	C	200	HEC	C3B-C2B	-2.21	1.33	1.41
2	B	199	HEC	O2A-CGA	-2.19	1.23	1.30
2	C	200	HEC	O2A-CGA	-2.16	1.23	1.30
2	C	200	HEC	C3D-C2D	-2.15	1.33	1.38
2	A	200	HEC	C3B-C2B	-2.13	1.34	1.41
2	B	199	HEC	CBC-CAC	2.11	1.57	1.49
2	A	200	HEC	O2A-CGA	-2.10	1.23	1.30
2	C	200	HEC	CMC-C2C	2.10	1.55	1.50
2	A	199	HEC	CHA-C4D	2.09	1.44	1.39
2	D	200	HEC	C4A-NA	-2.04	1.35	1.39
2	B	200	HEC	C1B-NB	-2.02	1.35	1.39
2	C	200	HEC	CBB-CAB	2.02	1.57	1.49
2	D	200	HEC	C1A-C2A	2.01	1.48	1.45
2	B	199	HEC	CHA-C4D	2.00	1.43	1.39

All (109) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	199	HEC	CBB-CAB-C3B	-9.37	108.70	127.43
2	A	199	HEC	CBB-CAB-C3B	-9.07	109.31	127.43
2	C	199	HEC	CBB-CAB-C3B	-8.42	110.60	127.43
2	C	199	HEC	CBC-CAC-C3C	-8.37	110.70	127.43
2	C	200	HEC	CBB-CAB-C3B	-8.36	110.73	127.43
2	D	199	HEC	CBB-CAB-C3B	-8.29	110.86	127.43
2	B	199	HEC	CBC-CAC-C3C	-8.21	111.02	127.43
2	A	199	HEC	CBC-CAC-C3C	-8.07	111.31	127.43
2	A	200	HEC	CBB-CAB-C3B	-7.83	111.78	127.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	200	HEC	CBB-CAB-C3B	-7.81	111.83	127.43
2	B	200	HEC	CBB-CAB-C3B	-7.78	111.88	127.43
2	A	200	HEC	CBC-CAC-C3C	-7.49	112.47	127.43
3	C	201	GOL	O2-C2-C1	-7.25	79.15	109.18
2	D	199	HEC	CBC-CAC-C3C	-7.12	113.20	127.43
2	D	200	HEC	CBC-CAC-C3C	-6.67	114.11	127.43
2	B	200	HEC	CBC-CAC-C3C	-6.54	114.36	127.43
2	C	200	HEC	CBC-CAC-C3C	-6.44	114.56	127.43
2	C	199	HEC	CHC-C4B-NB	-5.69	118.26	124.45
2	A	199	HEC	CHC-C4B-NB	-5.66	118.29	124.45
2	D	199	HEC	CHC-C4B-NB	-5.61	118.34	124.45
2	B	199	HEC	CHC-C4B-NB	-5.45	118.52	124.45
2	D	199	HEC	C3D-C4D-ND	5.36	116.10	110.15
2	B	199	HEC	C3D-C4D-ND	5.29	116.02	110.15
2	B	199	HEC	C4D-ND-C1D	-4.33	98.75	105.82
3	A	201	GOL	O2-C2-C1	-3.93	92.90	109.18
2	D	200	HEC	C2A-C1A-NA	-3.66	106.79	110.32
4	D	201	TRS	O3-C3-C	3.61	120.93	110.88
2	B	199	HEC	C2D-C1D-ND	3.59	115.89	110.14
2	A	200	HEC	C2A-C1A-NA	-3.54	106.91	110.32
2	D	199	HEC	C4D-ND-C1D	-3.49	100.13	105.82
2	D	200	HEC	CHB-C4A-NA	3.46	128.22	124.45
2	C	199	HEC	CHD-C4C-NC	3.42	128.17	124.45
2	C	199	HEC	O2D-CGD-CBD	3.42	124.79	114.00
2	C	199	HEC	C3D-C4D-ND	3.41	113.93	110.15
2	D	200	HEC	O1A-CGA-CBA	-3.36	112.44	123.09
2	B	200	HEC	C2A-C1A-NA	-3.31	107.12	110.32
2	B	199	HEC	C2A-C1A-NA	-3.30	107.14	110.32
2	C	199	HEC	O2D-CGD-O1D	-3.28	114.90	123.33
2	A	199	HEC	C3D-C4D-ND	3.26	113.77	110.15
2	D	199	HEC	C2A-C1A-NA	-3.25	107.19	110.32
2	C	200	HEC	CHB-C4A-NA	3.25	127.99	124.45
3	C	201	GOL	C3-C2-C1	3.18	123.47	111.80
2	A	200	HEC	CHB-C4A-NA	3.18	127.92	124.45
2	B	200	HEC	O1A-CGA-CBA	-3.18	113.00	123.09
2	D	199	HEC	CHD-C4C-NC	3.15	127.89	124.45
2	C	200	HEC	C2A-C1A-NA	-3.14	107.29	110.32
2	A	199	HEC	O2D-CGD-O1D	-3.12	115.30	123.33
4	D	201	TRS	C3-C-N	3.11	116.10	108.17
2	C	200	HEC	O1A-CGA-CBA	-3.11	113.24	123.09
2	A	200	HEC	O1A-CGA-CBA	-3.08	113.32	123.09
2	B	200	HEC	CHB-C4A-NA	3.08	127.80	124.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	199	HEC	CHD-C1D-C2D	-3.07	118.50	127.43
2	B	199	HEC	O2D-CGD-CBD	3.06	123.67	114.00
2	C	199	HEC	C4D-ND-C1D	-2.99	100.94	105.82
4	D	201	TRS	C3-C-C1	-2.98	102.72	110.66
2	B	199	HEC	CHD-C4C-NC	2.97	127.69	124.45
2	D	200	HEC	O2A-CGA-CBA	2.93	123.27	114.00
2	D	199	HEC	O2D-CGD-CBD	2.92	123.21	114.00
2	B	199	HEC	CHA-C1A-NA	2.91	127.62	124.45
2	B	199	HEC	O2D-CGD-O1D	-2.90	115.88	123.33
2	C	199	HEC	C2A-C1A-NA	-2.87	107.55	110.32
2	A	199	HEC	C4D-ND-C1D	-2.83	101.22	105.82
3	C	201	GOL	O2-C2-C3	-2.82	97.52	109.18
2	C	199	HEC	C4B-NB-C1B	-2.80	101.26	105.82
2	A	199	HEC	C2A-C1A-NA	-2.79	107.63	110.32
2	D	199	HEC	C4B-NB-C1B	-2.78	101.29	105.82
2	D	199	HEC	O2D-CGD-O1D	-2.75	116.26	123.33
2	C	200	HEC	O2A-CGA-CBA	2.74	122.64	114.00
2	A	199	HEC	O2D-CGD-CBD	2.73	122.64	114.00
2	A	199	HEC	O1A-CGA-CBA	-2.73	114.45	123.09
2	D	199	HEC	CAD-CBD-CGD	-2.69	106.52	113.67
2	A	200	HEC	O2A-CGA-CBA	2.64	122.34	114.00
2	C	200	HEC	CHA-C1A-NA	2.63	127.31	124.45
2	B	199	HEC	C1D-C2D-C3D	-2.57	103.87	106.82
2	B	199	HEC	C4B-NB-C1B	-2.57	101.64	105.82
2	D	199	HEC	CHA-C1A-NA	2.50	127.17	124.45
2	C	199	HEC	O1A-CGA-CBA	-2.45	115.31	123.09
2	C	199	HEC	CAD-CBD-CGD	-2.45	107.17	113.67
2	B	199	HEC	CHA-C4D-ND	-2.43	119.45	123.86
2	A	199	HEC	C4B-NB-C1B	-2.38	101.93	105.82
2	A	199	HEC	CHA-C1A-NA	2.36	127.03	124.45
2	A	200	HEC	CHA-C1A-NA	2.34	127.00	124.45
2	A	200	HEC	CBD-CAD-C3D	2.34	119.01	112.53
2	B	200	HEC	O2A-CGA-CBA	2.27	121.16	114.00
2	A	199	HEC	CHD-C4C-NC	2.26	126.92	124.45
2	D	199	HEC	O1A-CGA-CBA	-2.26	115.91	123.09
2	D	200	HEC	C2D-C1D-ND	2.26	113.76	110.14
2	B	200	HEC	CHA-C1A-NA	2.24	126.89	124.45
2	B	199	HEC	O1A-CGA-CBA	-2.23	116.01	123.09
2	B	200	HEC	C2D-C1D-ND	2.22	113.70	110.14
2	D	200	HEC	C4A-NA-C1A	2.21	109.43	105.82
2	D	200	HEC	CHA-C1A-NA	2.21	126.86	124.45
2	A	199	HEC	CHA-C4D-ND	-2.20	119.88	123.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	199	HEC	CAD-C3D-C4D	2.19	129.22	124.94
2	A	199	HEC	CAD-CBD-CGD	-2.16	107.94	113.67
2	C	199	HEC	CHA-C1A-NA	2.15	126.80	124.45
2	B	199	HEC	CMC-C2C-C1C	-2.15	122.14	125.42
2	A	199	HEC	CHD-C1D-C2D	-2.15	121.18	127.43
2	C	200	HEC	C2D-C1D-ND	2.15	113.59	110.14
2	B	199	HEC	CAD-C3D-C4D	2.09	129.02	124.94
2	B	199	HEC	C4C-NC-C1C	2.08	109.21	105.82
2	C	199	HEC	CMC-C2C-C1C	-2.08	122.25	125.42
2	B	199	HEC	CAD-CBD-CGD	-2.08	108.16	113.67
2	A	199	HEC	CMC-C2C-C1C	-2.05	122.29	125.42
2	C	200	HEC	CMB-C2B-C1B	-2.04	122.32	125.42
2	D	199	HEC	CHD-C1D-C2D	-2.03	121.52	127.43
3	A	201	GOL	C3-C2-C1	2.02	119.20	111.80
2	C	199	HEC	CHA-C4D-ND	-2.01	120.21	123.86
2	A	200	HEC	O2D-CGD-CBD	2.00	120.33	114.00

There are no chirality outliers.

All (55) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	199	HEC	C2B-C3B-CAB-CBB
2	A	199	HEC	C4B-C3B-CAB-CBB
2	A	199	HEC	C2C-C3C-CAC-CBC
2	A	199	HEC	C4C-C3C-CAC-CBC
2	A	200	HEC	C2B-C3B-CAB-CBB
2	A	200	HEC	C4B-C3B-CAB-CBB
2	A	200	HEC	C2C-C3C-CAC-CBC
2	A	200	HEC	C4C-C3C-CAC-CBC
2	B	199	HEC	C2B-C3B-CAB-CBB
2	B	199	HEC	C4B-C3B-CAB-CBB
2	B	199	HEC	C2C-C3C-CAC-CBC
2	B	199	HEC	C4C-C3C-CAC-CBC
2	B	200	HEC	C2B-C3B-CAB-CBB
2	B	200	HEC	C4B-C3B-CAB-CBB
2	B	200	HEC	C2C-C3C-CAC-CBC
2	B	200	HEC	C4C-C3C-CAC-CBC
2	C	199	HEC	C2B-C3B-CAB-CBB
2	C	199	HEC	C4B-C3B-CAB-CBB
2	C	199	HEC	C2C-C3C-CAC-CBC
2	C	199	HEC	C4C-C3C-CAC-CBC
2	C	200	HEC	C2B-C3B-CAB-CBB

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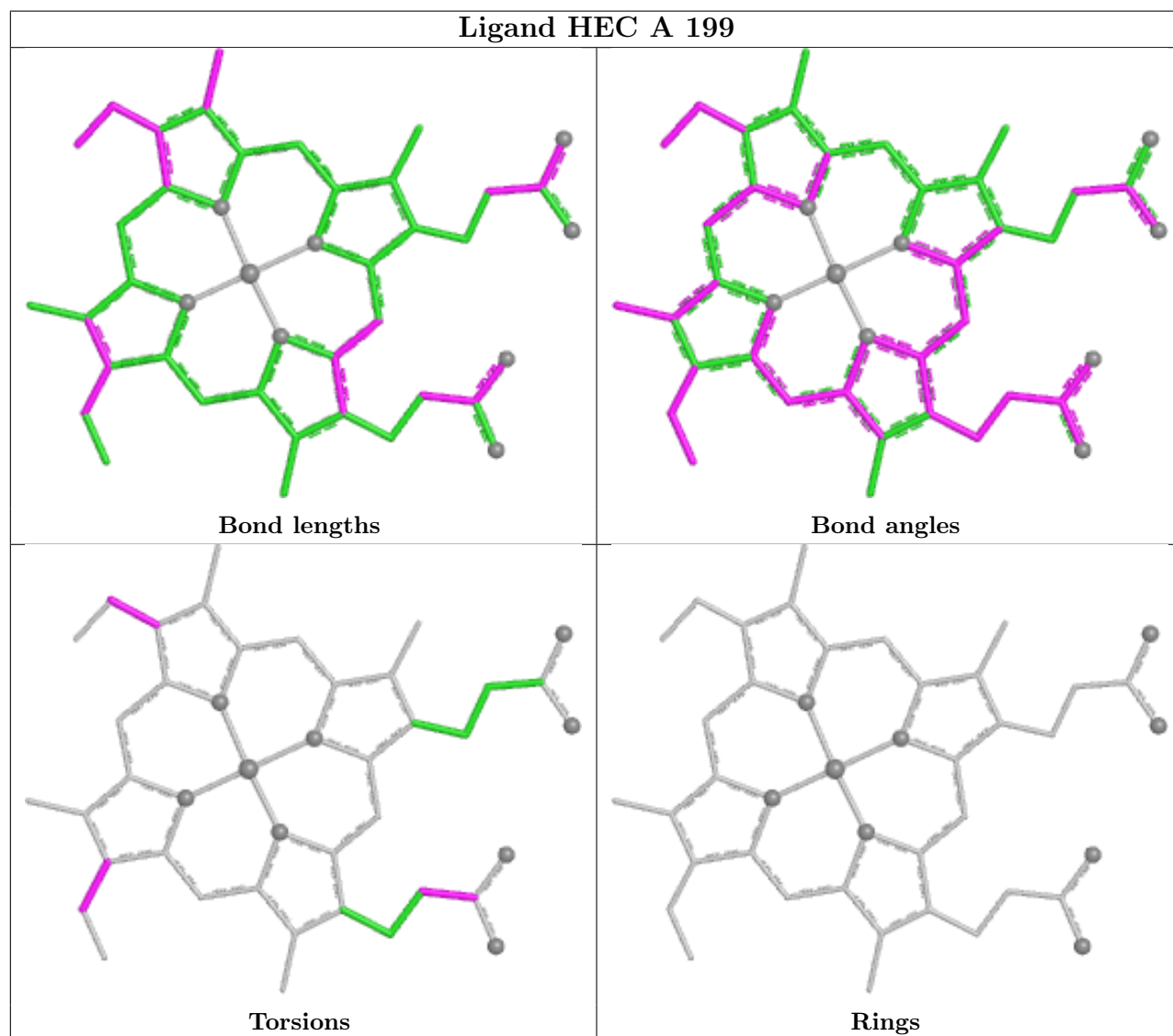
Mol	Chain	Res	Type	Atoms
2	C	200	HEC	C4B-C3B-CAB-CBB
2	C	200	HEC	C2C-C3C-CAC-CBC
2	C	200	HEC	C4C-C3C-CAC-CBC
2	D	199	HEC	C2B-C3B-CAB-CBB
2	D	199	HEC	C4B-C3B-CAB-CBB
2	D	199	HEC	C4C-C3C-CAC-CBC
2	D	200	HEC	C2B-C3B-CAB-CBB
2	D	200	HEC	C4B-C3B-CAB-CBB
2	D	200	HEC	C2C-C3C-CAC-CBC
2	D	200	HEC	C4C-C3C-CAC-CBC
3	C	201	GOL	O1-C1-C2-O2
4	D	201	TRS	C1-C-C3-O3
4	D	201	TRS	C2-C-C3-O3
4	D	201	TRS	N-C-C3-O3
4	D	201	TRS	C3-C-C1-O1
2	D	199	HEC	C2C-C3C-CAC-CBC
2	C	200	HEC	CAD-CBD-CGD-O2D
2	D	200	HEC	CAD-CBD-CGD-O1D
3	A	201	GOL	O1-C1-C2-C3
2	B	200	HEC	CAD-CBD-CGD-O2D
2	B	199	HEC	CAD-CBD-CGD-O1D
2	C	200	HEC	CAD-CBD-CGD-O1D
2	D	200	HEC	CAD-CBD-CGD-O2D
2	A	199	HEC	CAD-CBD-CGD-O2D
2	A	199	HEC	CAD-CBD-CGD-O1D
2	C	199	HEC	CAD-CBD-CGD-O1D
2	C	199	HEC	CAD-CBD-CGD-O2D
2	D	199	HEC	CAD-CBD-CGD-O1D
2	B	199	HEC	CAD-CBD-CGD-O2D
2	D	199	HEC	CAD-CBD-CGD-O2D
2	B	200	HEC	CAD-CBD-CGD-O1D
4	D	201	TRS	C2-C-C1-O1
2	A	200	HEC	CAD-CBD-CGD-O1D
2	A	200	HEC	CAD-CBD-CGD-O2D

There are no ring outliers.

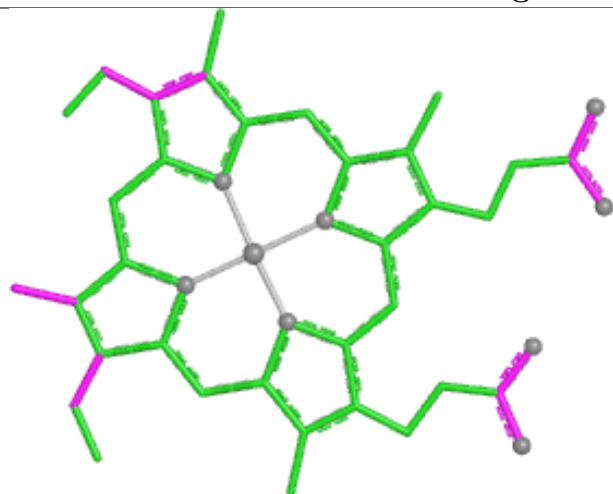
3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	199	HEC	1	0
4	D	201	TRS	9	0
3	C	201	GOL	2	0

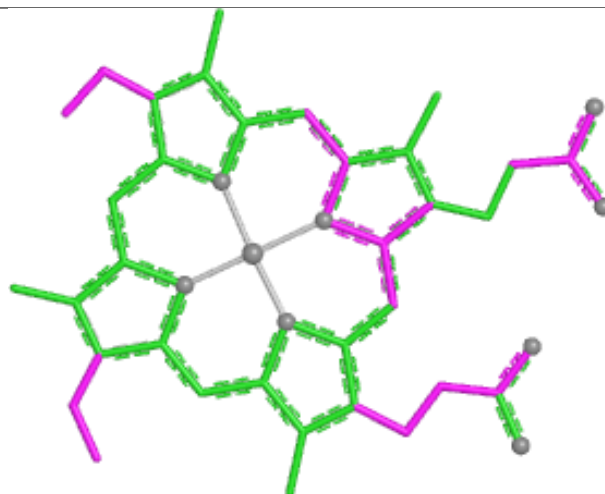
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



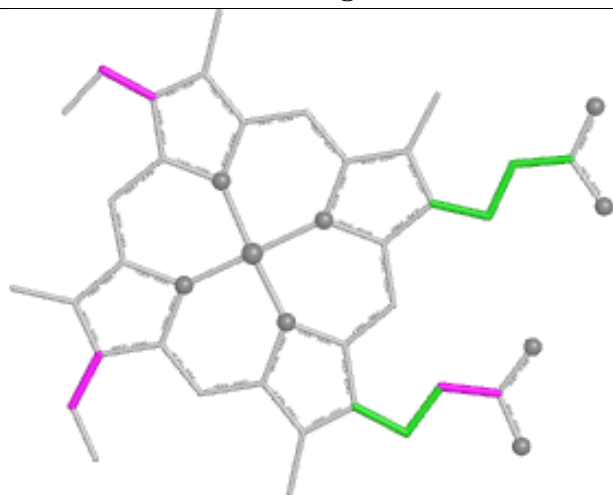
Ligand HEC A 200



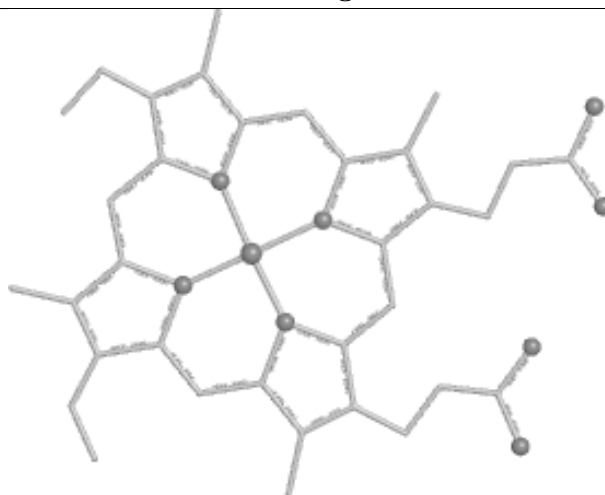
Bond lengths



Bond angles

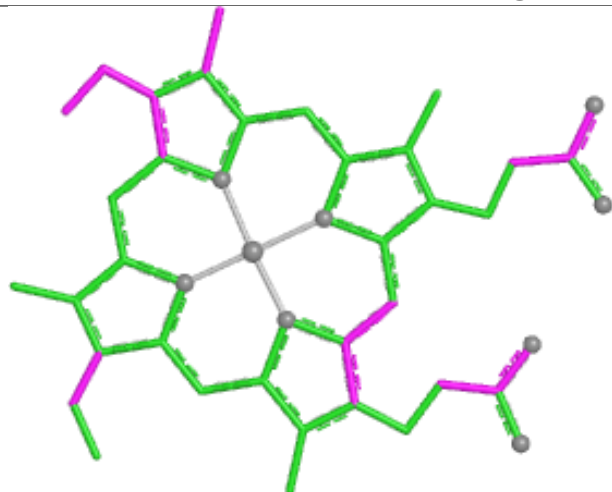


Torsions

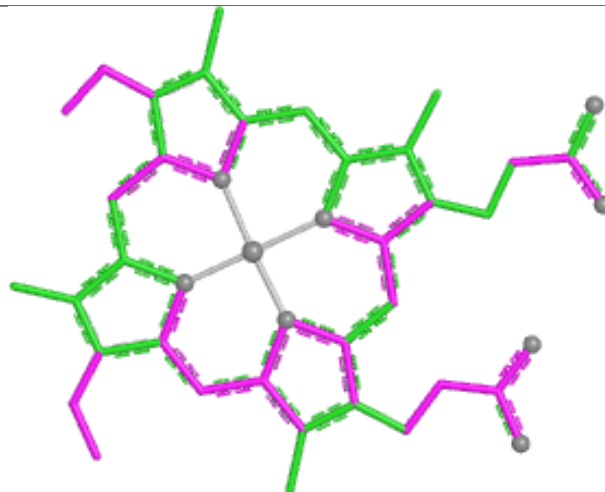


Rings

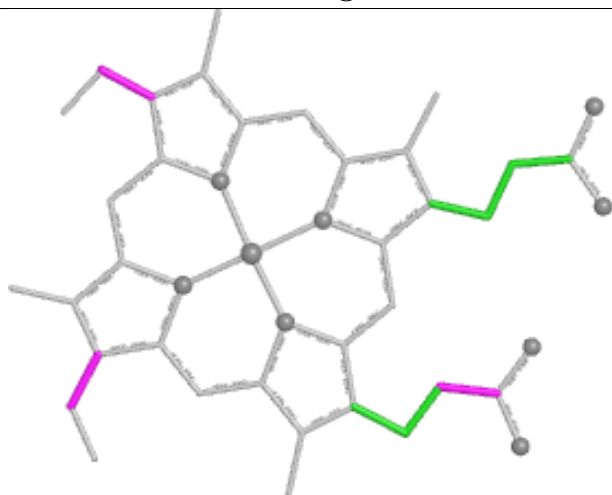
Ligand HEC D 199



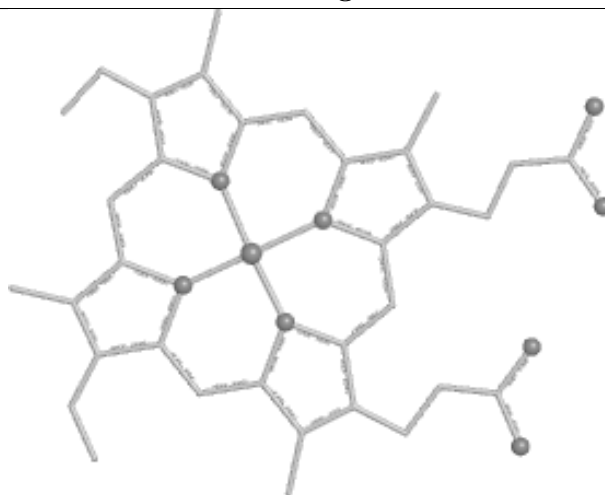
Bond lengths



Bond angles

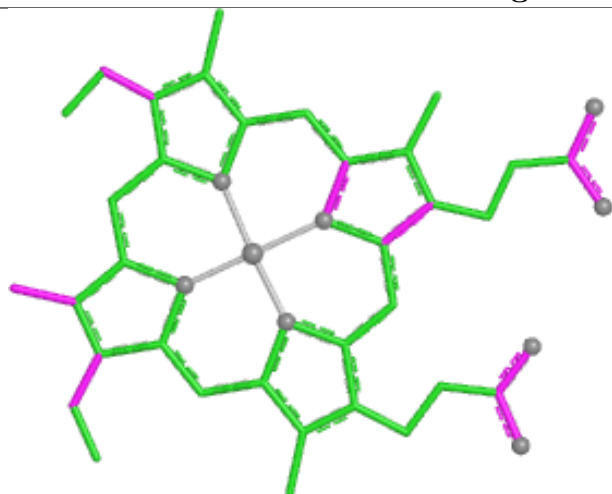


Torsions

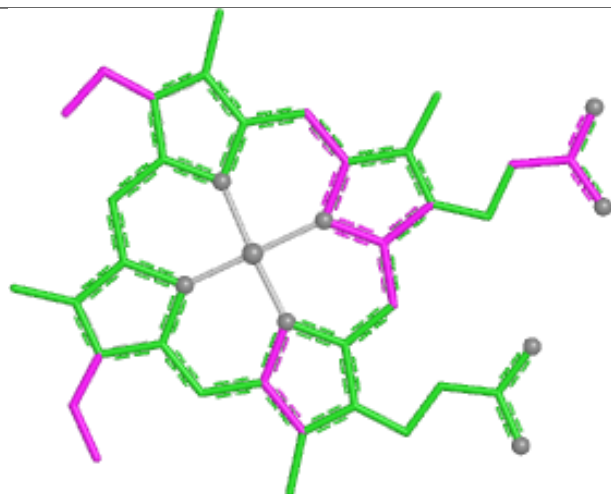


Rings

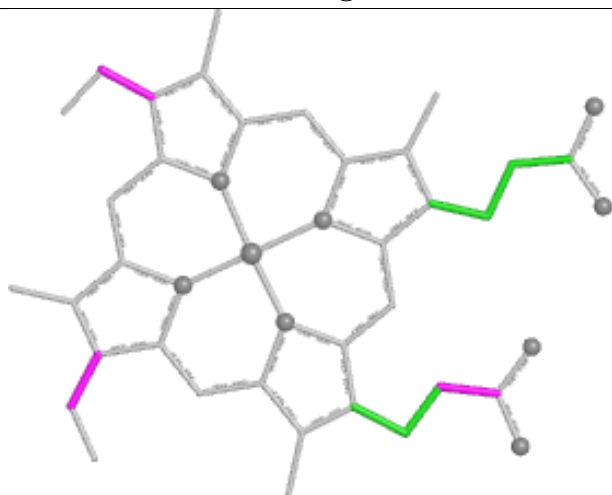
Ligand HEC D 200



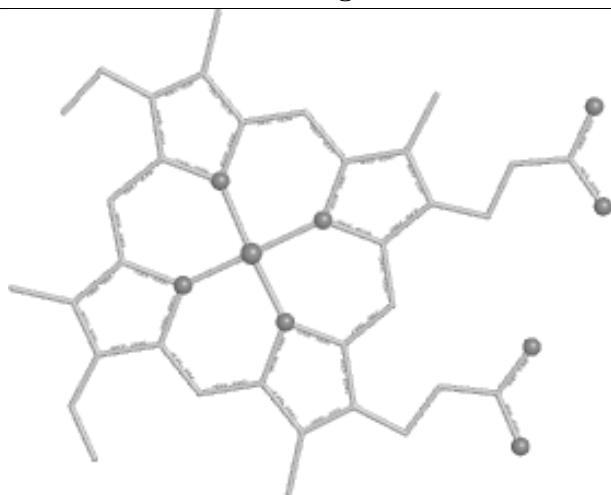
Bond lengths



Bond angles

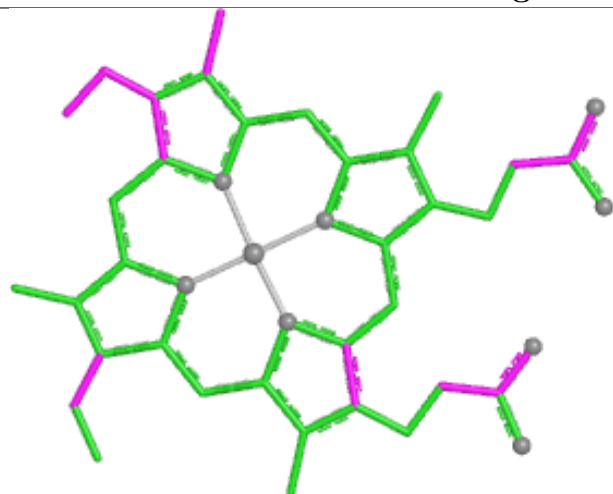


Torsions

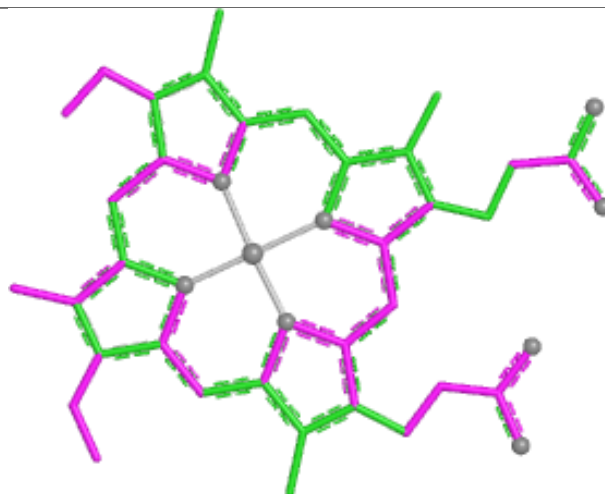


Rings

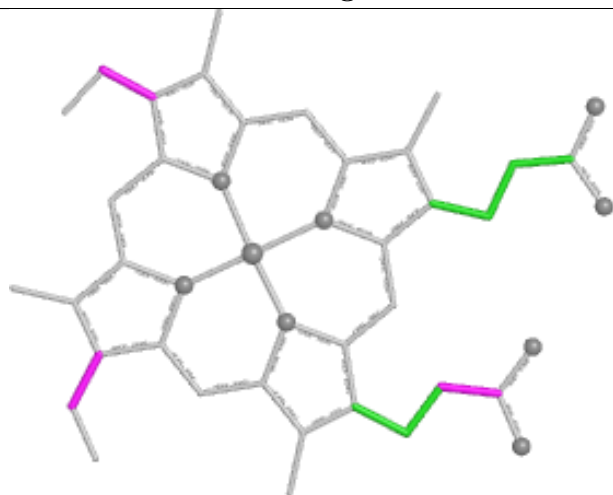
Ligand HEC C 199



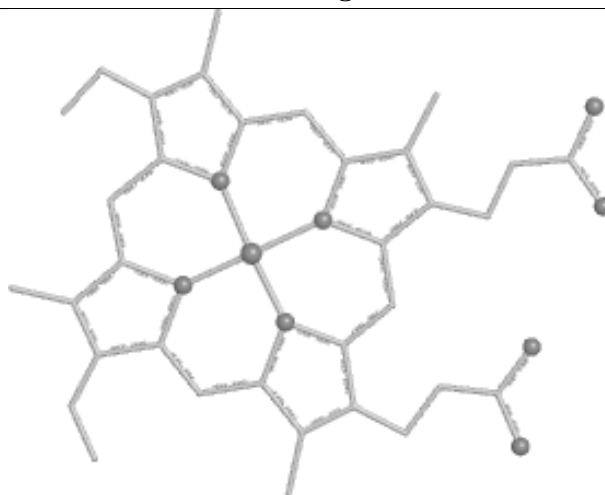
Bond lengths



Bond angles

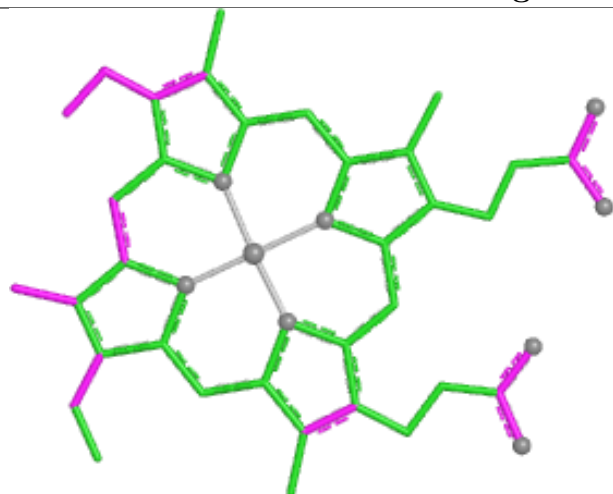


Torsions

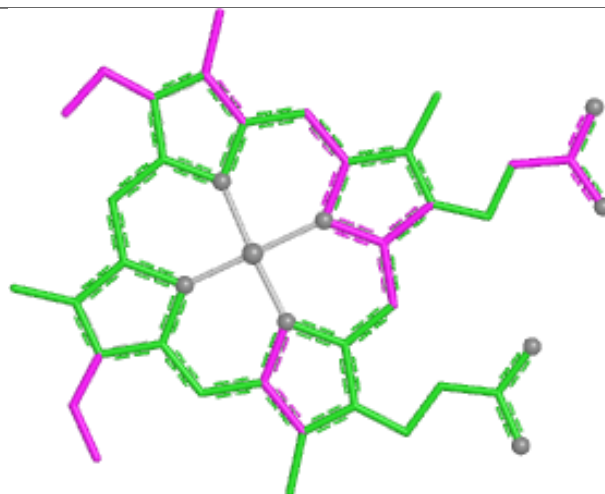


Rings

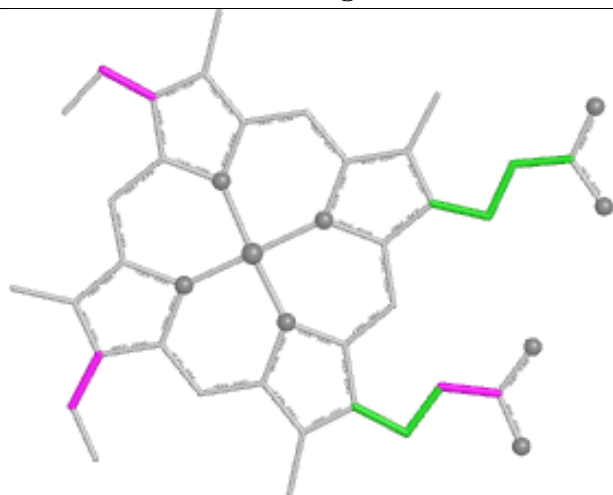
Ligand HEC C 200



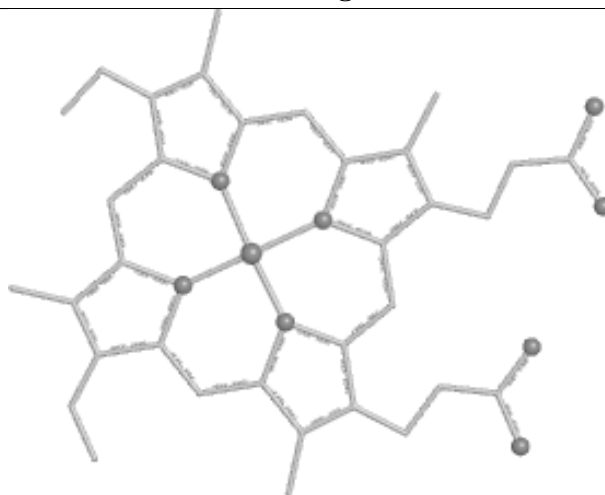
Bond lengths



Bond angles

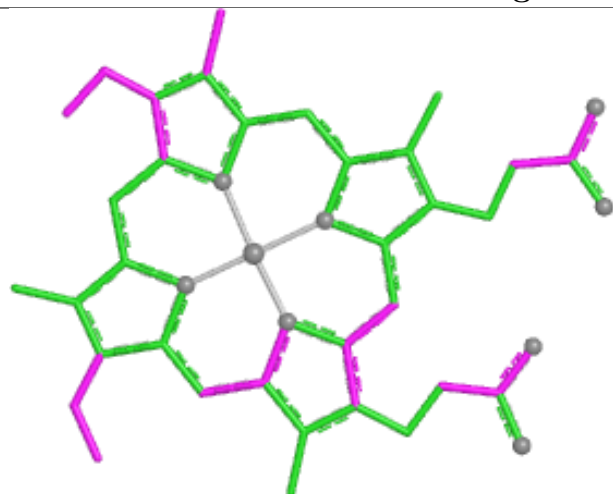


Torsions

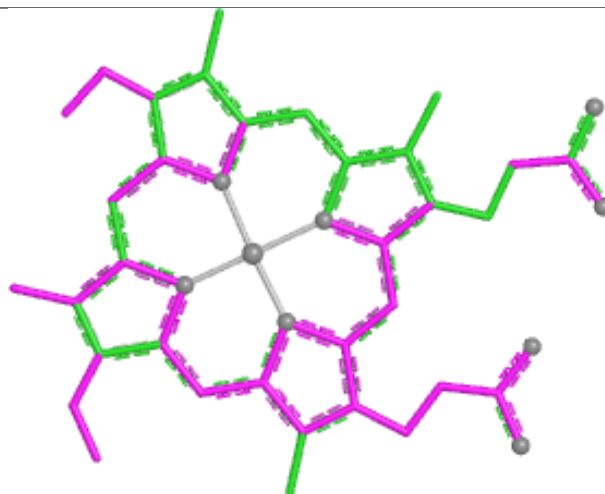


Rings

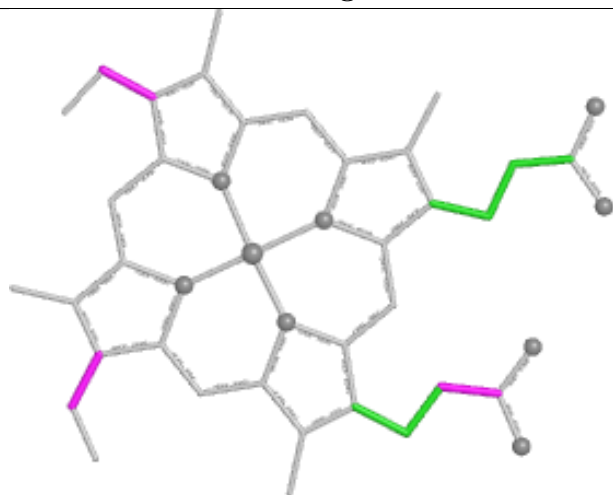
Ligand HEC B 199



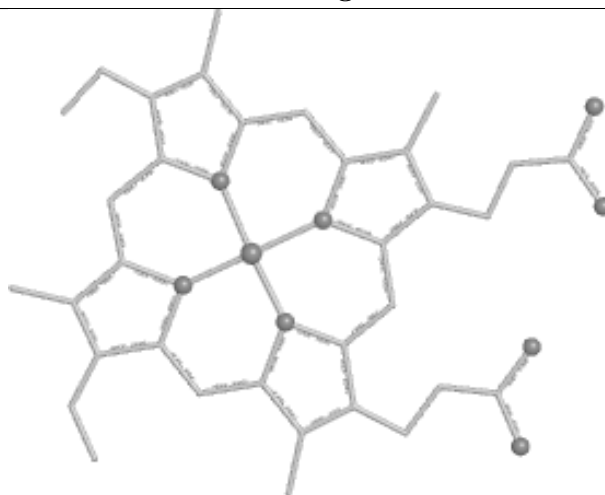
Bond lengths



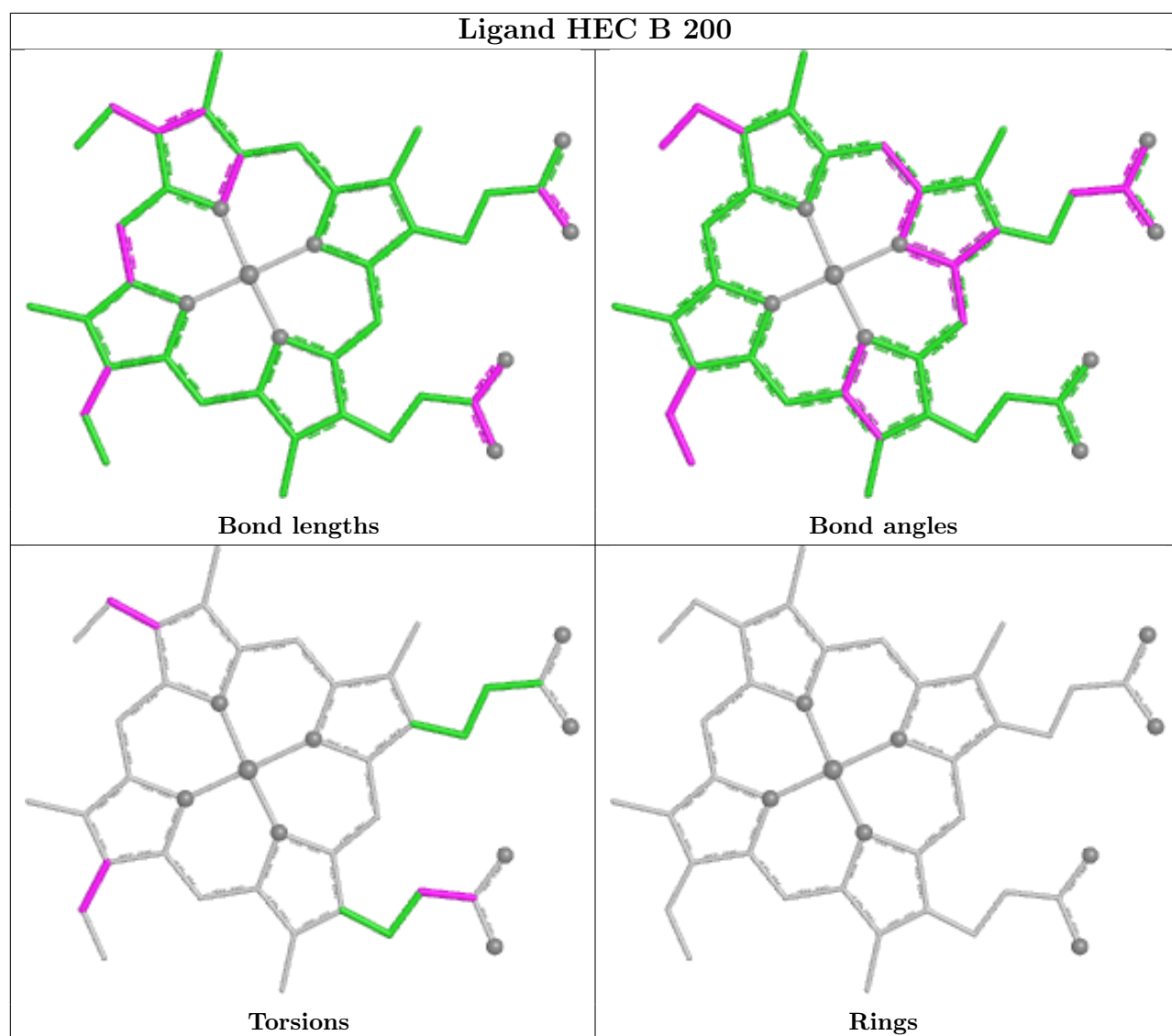
Bond angles



Torsions



Rings



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	190/190 (100%)	-0.02	5 (2%) 57 67	7, 13, 28, 47	9 (4%)
1	B	190/190 (100%)	0.74	23 (12%) 8 13	10, 24, 40, 50	2 (1%)
1	C	190/190 (100%)	0.06	3 (1%) 70 80	8, 14, 27, 54	8 (4%)
1	D	190/190 (100%)	0.51	18 (9%) 14 19	9, 17, 33, 47	5 (2%)
All	All	760/760 (100%)	0.32	49 (6%) 25 34	7, 17, 35, 54	24 (3%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	133	ALA	4.9
1	B	25	PRO	4.0
1	D	64	LEU	3.9
1	D	53	PRO	3.6
1	B	100	ALA	3.6
1	B	92	VAL	3.6
1	B	135	PHE	3.5
1	B	113	ASP	3.4
1	A	163	ASP	3.3
1	C	1	ALA	3.2
1	D	56	PRO	3.2
1	B	64	LEU	3.2
1	B	164	THR	3.1
1	B	165	MET	3.0
1	D	112	LEU	2.9
1	D	92[A]	VAL	2.9
1	D	57	GLU	2.8
1	B	24	SER	2.8
1	B	163	ASP	2.8
1	B	134	GLY	2.8
1	C	57	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	72	PRO	2.7
1	B	114	GLN	2.7
1	B	94	TYR	2.7
1	A	113	ASP	2.7
1	D	132	LEU	2.7
1	A	164	THR	2.6
1	D	52	THR	2.6
1	B	68	GLY	2.5
1	D	68	GLY	2.5
1	D	49	ALA	2.5
1	D	59	VAL	2.5
1	B	190	HIS	2.4
1	D	94	TYR	2.4
1	A	133	ALA	2.4
1	B	157	ASN	2.3
1	B	55	ALA	2.3
1	B	131	ASP	2.3
1	C	112	LEU	2.2
1	D	38	ARG	2.2
1	B	57	GLU	2.2
1	B	124	ALA	2.1
1	D	190	HIS	2.1
1	A	131	ASP	2.1
1	B	54	GLY	2.1
1	B	121	GLY	2.1
1	D	58	GLY	2.1
1	D	95	ALA	2.1
1	D	50	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

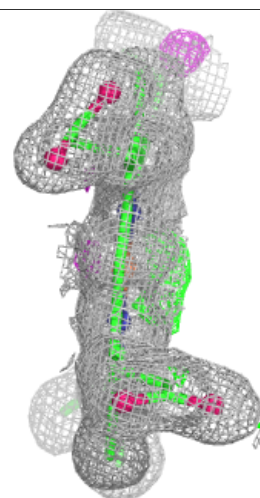
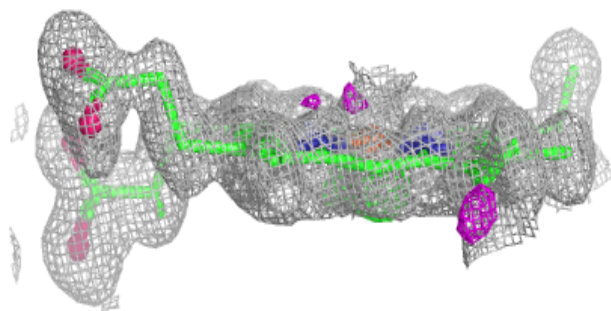
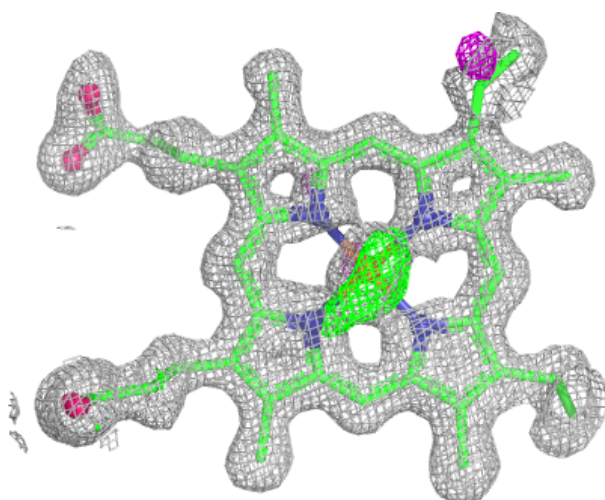
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	TRS	D	201	8/8	0.80	0.17	30,36,50,57	0
3	GOL	C	201	6/6	0.85	0.15	29,55,56,73	0
3	GOL	A	201	6/6	0.96	0.10	14,15,18,18	0
2	HEC	B	200	43/43	0.99	0.05	9,13,20,22	0
2	HEC	C	199	43/43	0.99	0.04	6,8,13,30	0
2	HEC	C	200	43/43	0.99	0.04	6,9,13,15	0
2	HEC	D	199	43/43	0.99	0.05	8,12,15,20	0
2	HEC	D	200	43/43	0.99	0.04	7,9,11,13	0
2	HEC	A	199	43/43	0.99	0.05	7,9,13,30	0
2	HEC	A	200	43/43	0.99	0.04	6,7,13,16	0
2	HEC	B	199	43/43	0.99	0.05	10,13,18,32	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.

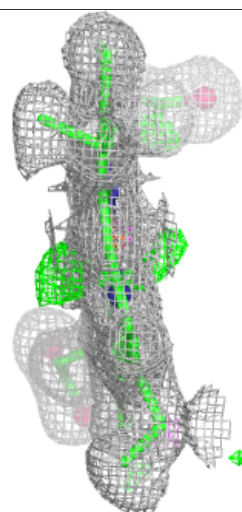
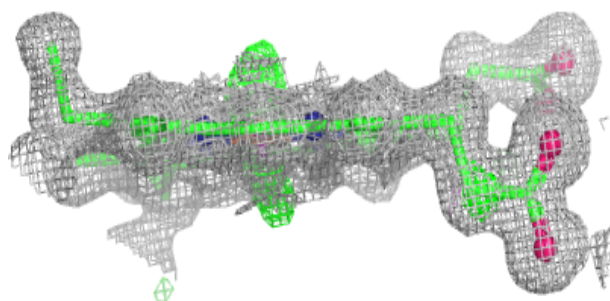
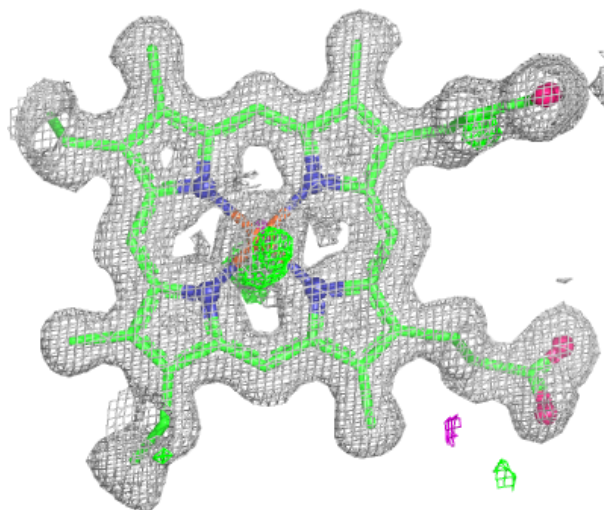
Electron density around HEC B 200:

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



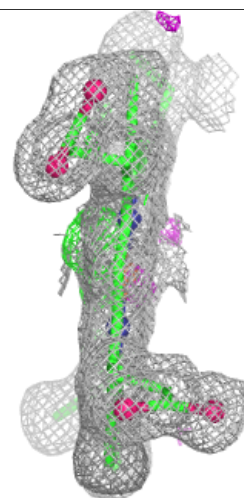
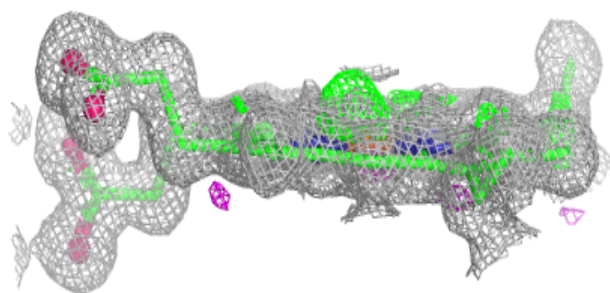
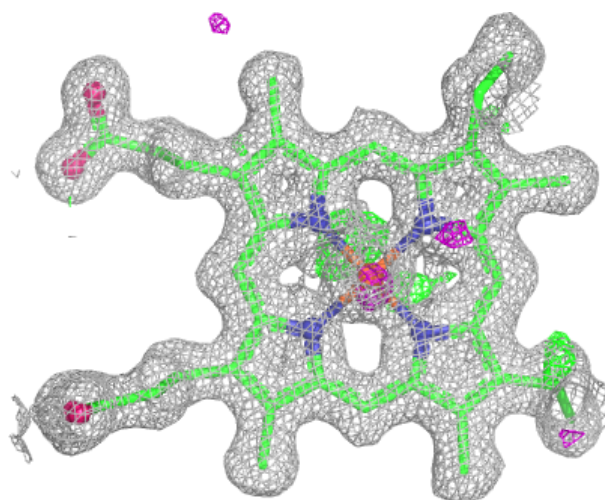
Electron density around HEC C 199:

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



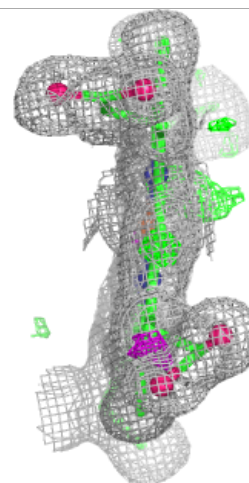
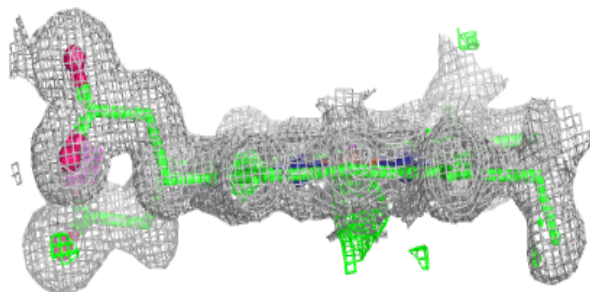
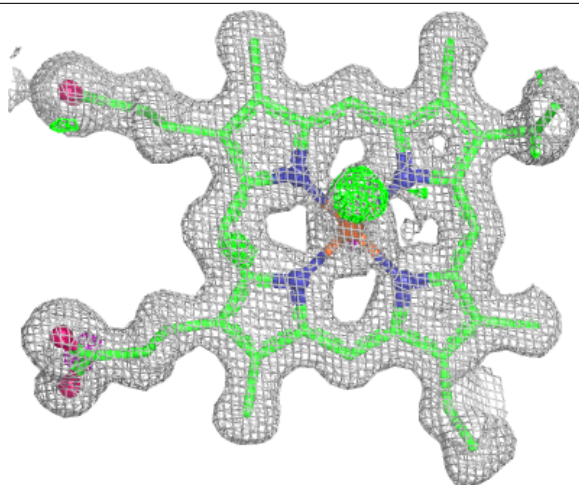
Electron density around HEC C 200:

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



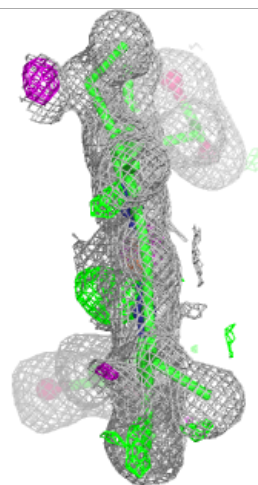
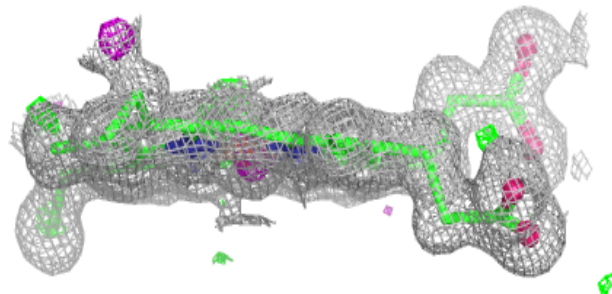
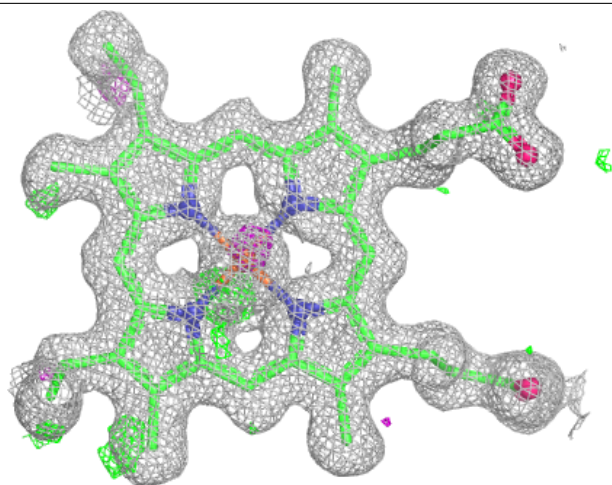
Electron density around HEC D 199:

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



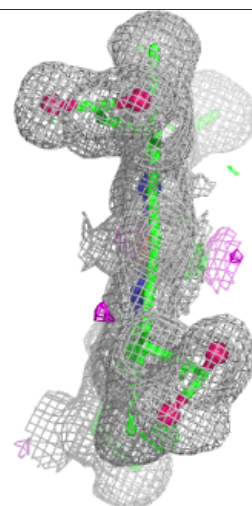
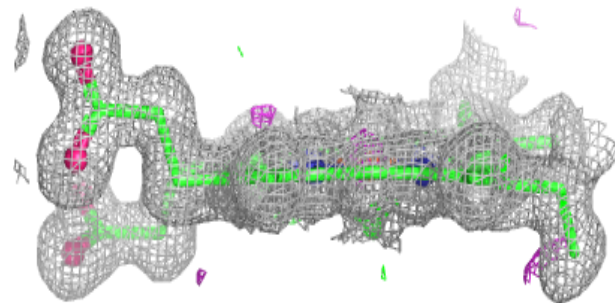
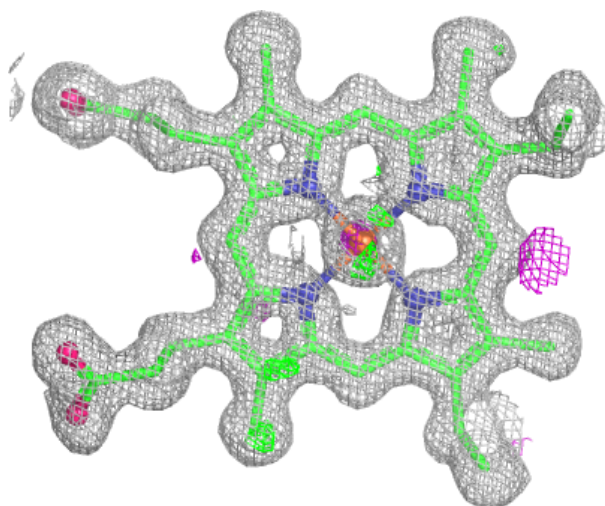
Electron density around HEC D 200:

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



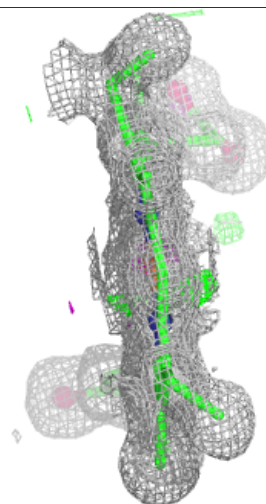
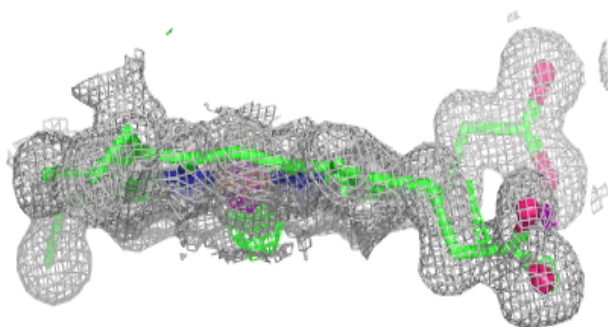
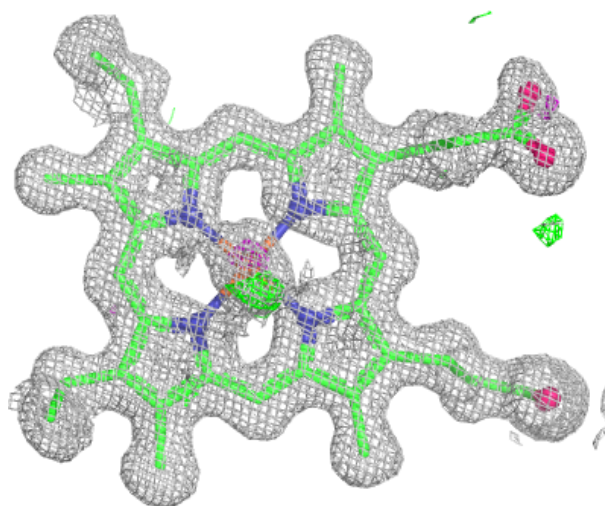
Electron density around HEC A 199:

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



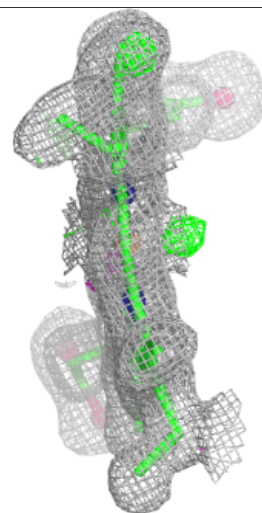
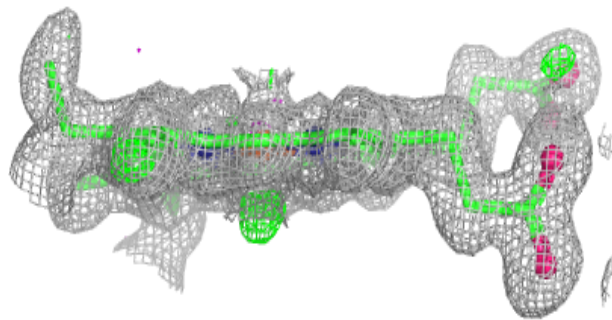
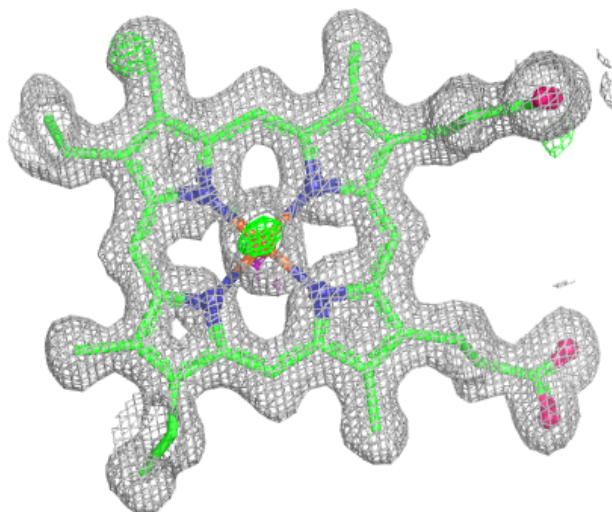
Electron density around HEC A 200:

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



Electron density around HEC B 199:

$2mF_o-DF_c$ (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.