wwPDB X-ray Structure Validation Summary Report (i)

Aug 5, 2026 – 07:17 AM EDT

PDB ID	:	3RMZ / pdb_00003rmz
Title	:	Crystal Structure of the W199F-MauG/pre-Methylamine Dehydrogenase Complex
Authors	:	Jensen, L.M.R.; Wilmot, C.M.
Deposited on	:	2011-04-21
Resolution	:	1.72 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 (i) 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 (i)) were used in the production of this report:

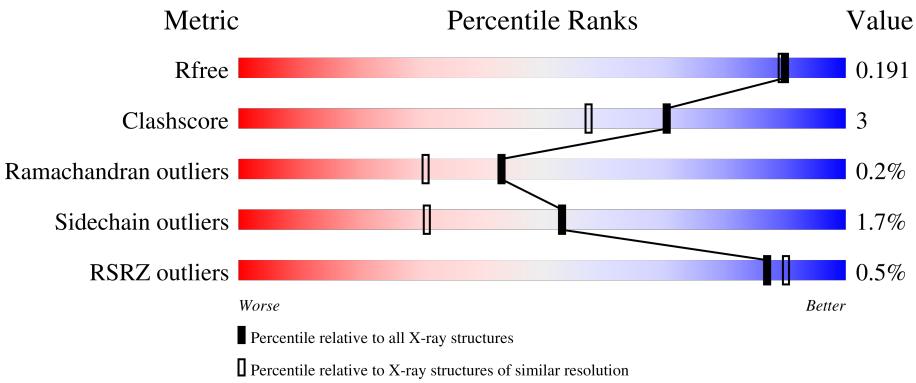
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.72 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	1039 (1.72-1.72)
Clashscore	190562	1049 (1.72-1.72)
Ramachandran outliers	187476	1041 (1.72-1.72)
Sidechain outliers	187428	1041 (1.72-1.72)
RSRZ outliers	180081	1039 (1.72-1.72)

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 <=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	373	86% 9% 5%
1	B	373	89% 5% • 5%
2	C	137	% 82% 10% • •
2	E	137	% 78% 12% • 9%
3	D	386	% 87% 10% •

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Mol	Chain	Length	Quality of chain
3	F	386	% 85% 11%

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
6	HEC	A	500	X	-	-	-
6	HEC	A	600	X	-	-	-
6	HEC	B	500	X	-	-	-
6	HEC	B	600	X	-	-	-

2 Entry composition (i)

There are 13 unique types of molecules in this entry. The entry contains 15575 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 Methylamine utilization protein MauG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	354	2773	1734	496	532	11	0	7	0
1	B	355	2757	1721	494	531	11	0	3	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	199	PHE	TRP	engineered mutation	UNP Q51658
A	368	HIS	-	expression tag	UNP Q51658
A	369	HIS	-	expression tag	UNP Q51658
A	370	HIS	-	expression tag	UNP Q51658
A	371	HIS	-	expression tag	UNP Q51658
A	372	HIS	-	expression tag	UNP Q51658
A	373	HIS	-	expression tag	UNP Q51658
B	199	PHE	TRP	engineered mutation	UNP Q51658
B	368	HIS	-	expression tag	UNP Q51658
B	369	HIS	-	expression tag	UNP Q51658
B	370	HIS	-	expression tag	UNP Q51658
B	371	HIS	-	expression tag	UNP Q51658
B	372	HIS	-	expression tag	UNP Q51658
B	373	HIS	-	expression tag	UNP Q51658

- Molecule 2 is a protein called Methylamine dehydrogenase light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	131	1032	638	180	199	15	0	5	0
2	E	124	968	603	161	189	15	0	4	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	132	HIS	-	expression tag	UNP A1BBA0
C	133	HIS	-	expression tag	UNP A1BBA0
C	134	HIS	-	expression tag	UNP A1BBA0
C	135	HIS	-	expression tag	UNP A1BBA0
C	136	HIS	-	expression tag	UNP A1BBA0
C	137	HIS	-	expression tag	UNP A1BBA0
E	132	HIS	-	expression tag	UNP A1BBA0
E	133	HIS	-	expression tag	UNP A1BBA0
E	134	HIS	-	expression tag	UNP A1BBA0
E	135	HIS	-	expression tag	UNP A1BBA0
E	136	HIS	-	expression tag	UNP A1BBA0
E	137	HIS	-	expression tag	UNP A1BBA0

- Molecule 3 is a protein called Methylamine dehydrogenase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	376	2957	1882	504	562	9	0	7	0
			Total	C	N	O	S			
3	F	376	2971	1888	507	567	9	0	9	0

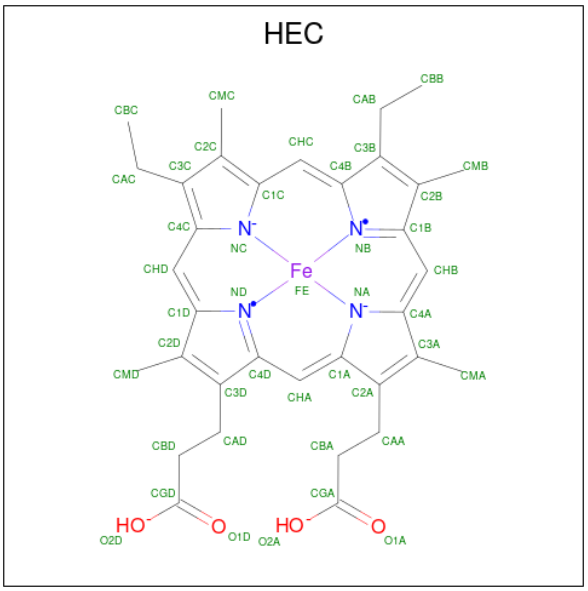
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
4	A	1	1	1	0	0
			Total	Ca		
4	B	1	1	1	0	0

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

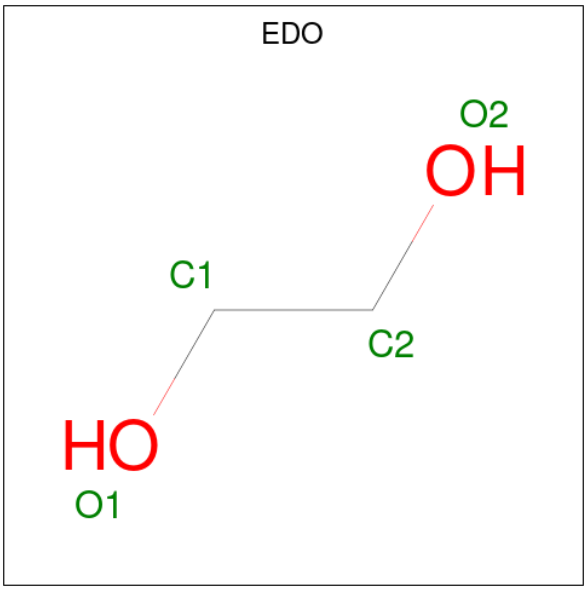
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
5	A	2	2	2	0	0
			Total	Na		
5	B	2	2	2	0	0

- Molecule 6 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



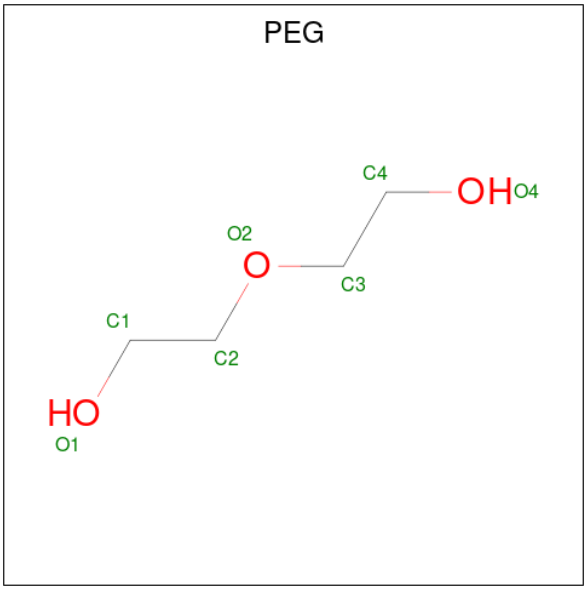
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
6	A	1	43	34	1	4	4	0	0
			Total	C	Fe	N	O		
6	A	1	43	34	1	4	4	0	0
			Total	C	Fe	N	O		
6	B	1	43	34	1	4	4	0	0
			Total	C	Fe	N	O		
6	B	1	43	34	1	4	4	0	0

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



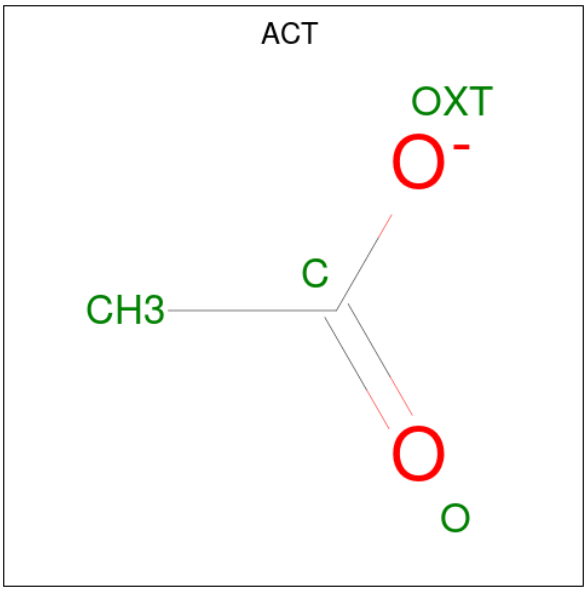
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	4	2	2	0	0
7	B	1	4	2	2	0	0

- Molecule 8 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



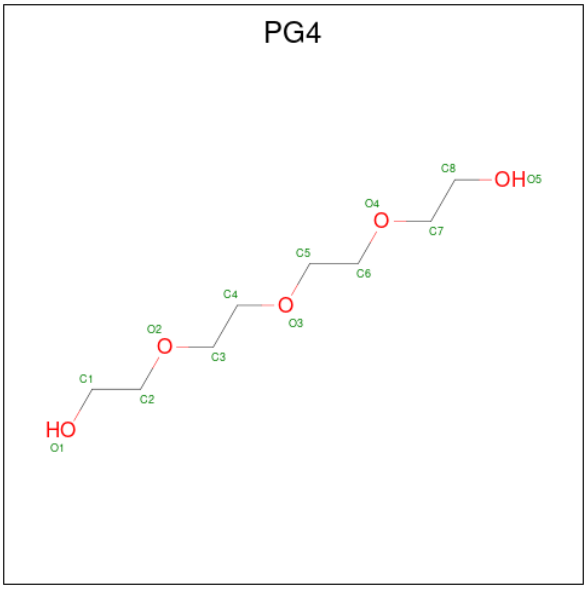
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
8	D	1	7	4	3	0	0

- Molecule 9 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



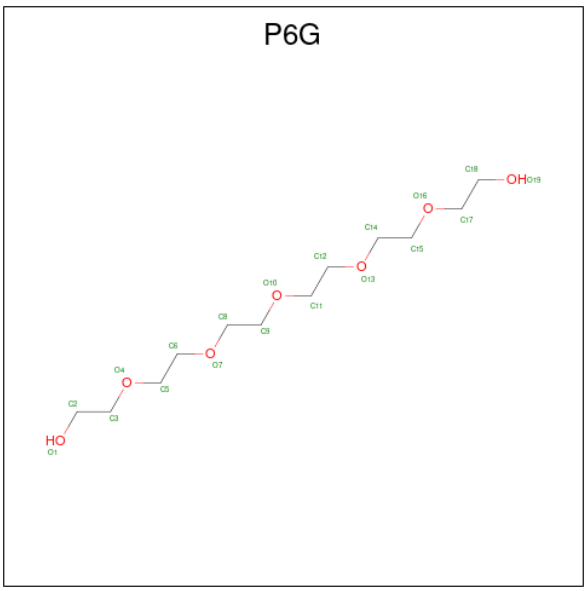
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
9	D	1	4	2	2	0	0

- Molecule 10 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



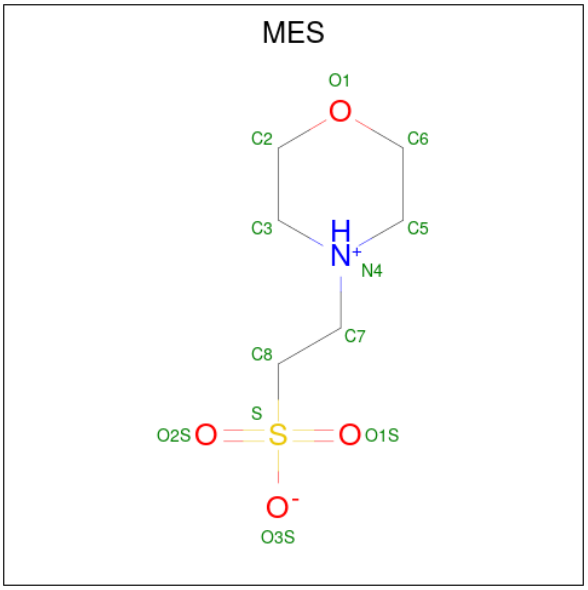
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
10	F	1	13	8	5	0	0

- Molecule 11 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	F	1	Total	C	O		0	0
			19	12	7			

- Molecule 12 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	F	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 13 is water.

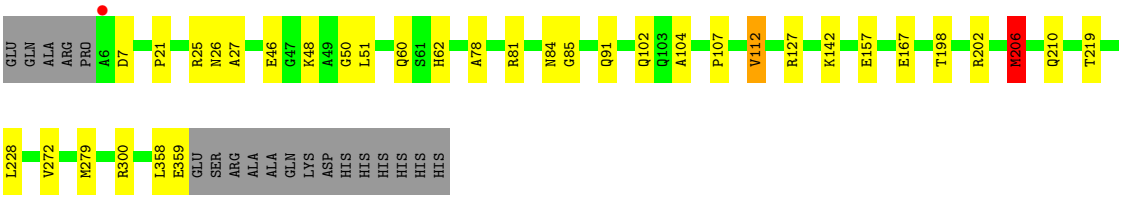
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	381	Total	O	0	0
			381	381		
13	B	387	Total	O	0	0
			387	387		
13	C	134	Total	O	0	0
			134	134		
13	D	371	Total	O	0	0
			371	371		
13	E	132	Total	O	0	0
			132	132		
13	F	471	Total	O	0	0
			471	471		

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.

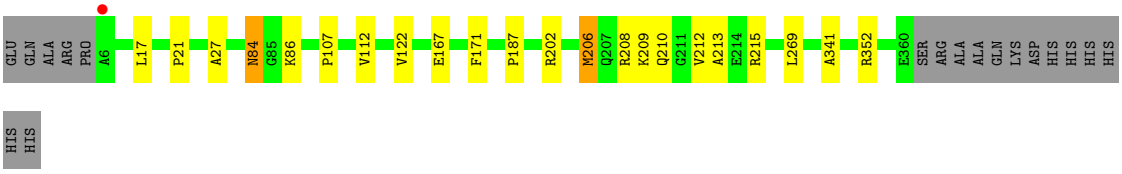
• Molecule 1: Methylamine utilization protein MauG

Chain A:



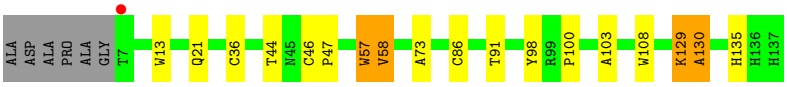
• Molecule 1: Methylamine utilization protein MauG

Chain B:



• Molecule 2: Methylamine dehydrogenase light chain

Chain C:

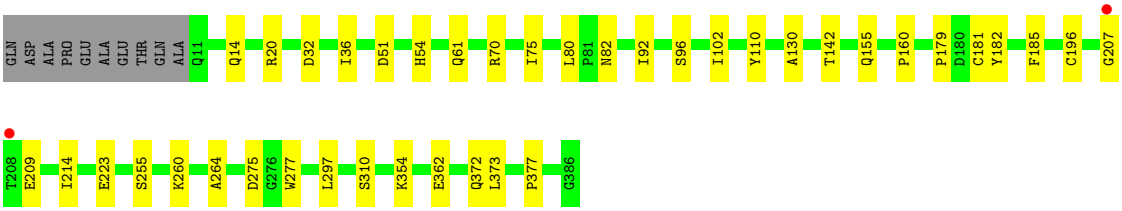


• Molecule 2: Methylamine dehydrogenase light chain

Chain E:

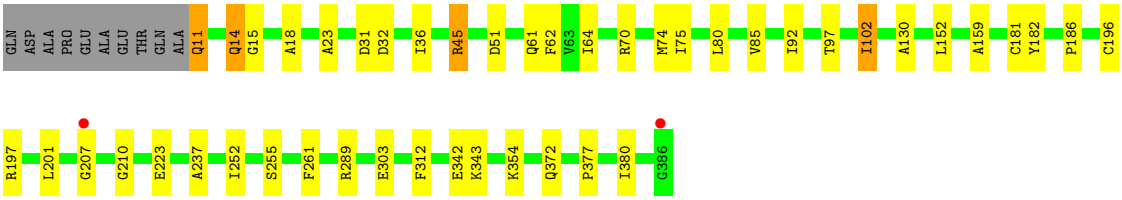
• Molecule 3: Methylamine dehydrogenase heavy chain

Chain D:



• Molecule 3: Methylamine dehydrogenase heavy chain

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	55.53Å 83.52Å 107.78Å 109.94° 91.54° 105.78°	Depositor
Resolution (Å)	39.58 – 1.72 39.58 – 1.72	Depositor EDS
% Data completeness (in resolution range)	94.8 (39.58-1.72) 94.7 (39.58-1.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	1.27 (at 1.72Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.138 , 0.181 0.149 , 0.191	Depositor DCC
R_{free} test set	8789 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å^2)	17.3	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 35.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	15575	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.44% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: P6G, PG4, CA, HEC, EDO, MES, NA, 0AF, PEG, ACT

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	1.37	4/2854 (0.1%)	1.26	3/3870 (0.1%)
1	B	1.45	4/2826 (0.1%)	1.24	5/3833 (0.1%)
2	C	1.39	2/1063 (0.2%)	1.33	3/1447 (0.2%)
2	E	1.49	6/990 (0.6%)	1.35	2/1351 (0.1%)
3	D	1.38	7/3055 (0.2%)	1.24	5/4163 (0.1%)
3	F	1.57	15/3075 (0.5%)	1.33	9/4189 (0.2%)
All	All	1.45	38/13863 (0.3%)	1.28	27/18853 (0.1%)

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	130	ALA	C-O	9.24	1.28	1.23
3	D	277	TRP	C-O	8.15	1.33	1.23
3	F	80	LEU	N-CA	7.69	1.51	1.46
3	F	80	LEU	C-O	7.45	1.27	1.23
3	D	80	LEU	N-CA	7.12	1.51	1.46

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	206	MET	CG-SD-CE	-11.51	75.58	100.90
1	A	206	MET	CG-SD-CE	-7.19	85.08	100.90
3	F	14	GLN	CA-CB-CG	6.63	127.36	114.10
1	B	122	VAL	N-CA-C	-6.46	104.46	110.53
3	F	210	GLY	N-CA-C	-6.36	105.91	111.95

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	2773	0	2664	23	0
1	B	2757	0	2636	10	0
2	C	1032	0	918	16	0
2	E	968	0	880	8	0
3	D	2957	0	2871	26	0
3	F	2971	0	2881	19	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	86	0	60	1	0
6	B	86	0	60	0	0
7	A	4	0	6	0	0
7	B	4	0	6	0	0
8	D	7	0	10	3	0
9	D	4	0	3	0	0
10	F	13	0	18	3	0
11	F	19	0	26	6	0
12	F	12	0	12	0	0
13	A	381	0	0	3	0
13	B	387	0	0	3	0
13	C	134	0	0	2	0
13	D	371	0	0	3	0
13	E	132	0	0	1	0
13	F	471	0	0	6	0
All	All	15575	0	13051	91	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 3.

The worst 5 of 91 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)
11:F:388:P6G:H21	13:F:903:HOH:O	1.70	0.90
3:F:255:SER:HA	10:F:387:PG4:H32	1.56	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:255:SER:HB2	8:D:387:PEG:H22	1.58	0.85
1:B:107:PRO:HG3	13:B:1931:HOH:O	1.81	0.81
3:D:255:SER:HA	8:D:387:PEG:H32	1.66	0.78

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	359/373 (96%)	349 (97%)	10 (3%)	0	100	100
1	B	356/373 (95%)	346 (97%)	10 (3%)	0	100	100
2	C	133/137 (97%)	128 (96%)	4 (3%)	1 (1%)	16	5
2	E	125/137 (91%)	122 (98%)	3 (2%)	0	100	100
3	D	381/386 (99%)	366 (96%)	13 (3%)	2 (0%)	24	11
3	F	383/386 (99%)	370 (97%)	12 (3%)	1 (0%)	36	24
All	All	1737/1792 (97%)	1681 (97%)	52 (3%)	4 (0%)	43	31

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	130	ALA
3	D	102[A]	ILE
3	D	102[B]	ILE
3	F	102	ILE

5.3.2 Protein sidechains (i)

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

resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	282/292 (97%)	276 (98%)	6 (2%)	47	23
1	B	279/292 (96%)	275 (99%)	4 (1%)	59	40
2	C	115/112 (103%)	113 (98%)	2 (2%)	53	31
2	E	107/112 (96%)	104 (97%)	3 (3%)	38	15
3	D	311/311 (100%)	307 (99%)	4 (1%)	61	43
3	F	313/311 (101%)	307 (98%)	6 (2%)	50	27
All	All	1407/1430 (98%)	1382 (98%)	25 (2%)	53	29

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	260	LYS
2	E	65	THR
3	F	354	LYS
2	E	7	THR
2	E	68	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	135	HIS
3	F	61	GLN
2	C	136	HIS
3	F	331	HIS
3	F	14	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)

2 non-standard protein/DNA/RNA residues 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	0AF	C	57	2	15,16,17	1.97	5 (33%)	14,22,24	1.91	6 (42%)
2	0AF	E	57	2	15,16,17	2.01	8 (53%)	14,22,24	1.50	2 (14%)

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	0AF	C	57	2	-	0/5/6/8	0/2/2/2
2	0AF	E	57	2	-	0/5/6/8	0/2/2/2

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	57	0AF	CB-CA	-3.51	1.46	1.53
2	E	57	0AF	CA-N	-3.41	1.38	1.48
2	C	57	0AF	CA-N	-3.31	1.38	1.48
2	C	57	0AF	CD1-CG	3.20	1.41	1.36
2	E	57	0AF	CB-CG	3.11	1.56	1.50

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	57	0AF	CG-CD1-NE1	-3.39	106.58	110.31
2	C	57	0AF	CH2-CZ2-CE2	3.17	124.17	118.69
2	E	57	0AF	CB-CG-CD2	3.07	132.59	126.70
2	C	57	0AF	CE2-NE1-CD1	2.70	111.26	108.93
2	C	57	0AF	CB-CG-CD2	2.43	131.37	126.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	57	0AF	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 17 ligands modelled in this entry, 6 are monoatomic - leaving 11 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	$\#\|Z\| > 2$
6	HEC	B	600	1	50,50,50	1.98	17 (34%)	68,82,82	2.04	23 (33%)
7	EDO	A	374	-	3,3,3	0.42	0	2,2,2	0.39	0
10	PG4	F	387	-	12,12,12	0.57	0	11,11,11	0.50	0
6	HEC	B	500	1,13	50,50,50	2.18	19 (38%)	68,82,82	1.95	21 (30%)
12	MES	F	389	-	12,12,12	1.39	1 (8%)	15,16,16	3.50	8 (53%)
8	PEG	D	387	-	6,6,6	0.65	0	5,5,5	0.63	0
7	EDO	B	374	-	3,3,3	0.48	0	2,2,2	0.03	0
11	P6G	F	388	-	18,18,18	0.61	0	17,17,17	0.77	0
6	HEC	A	500	1,13	50,50,50	2.26	21 (42%)	68,82,82	2.09	21 (30%)
9	ACT	D	388	-	3,3,3	0.49	0	3,3,3	1.68	1 (33%)
6	HEC	A	600	1	50,50,50	2.10	16 (32%)	68,82,82	2.08	21 (30%)

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
6	HEC	B	600	1	1/1/3/7	6/14/54/54	-
7	EDO	A	374	-	-	1/1/1/1	-
10	PG4	F	387	-	-	7/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HEC	B	500	1,13	1/1/3/7	6/14/54/54	-
12	MES	F	389	-	-	1/6/14/14	0/1/1/1
8	PEG	D	387	-	-	3/4/4/4	-
7	EDO	B	374	-	-	1/1/1/1	-
11	P6G	F	388	-	-	10/16/16/16	-
6	HEC	A	500	1,13	1/1/3/7	9/14/54/54	-
6	HEC	A	600	1	1/1/3/7	5/14/54/54	-

The worst 5 of 74 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	500	HEC	CHD-C1D	5.72	1.49	1.38
6	A	600	HEC	C4C-NC	-5.36	1.29	1.39
6	B	600	HEC	CHB-C4A	5.20	1.48	1.38
6	A	500	HEC	CHD-C1D	5.03	1.48	1.38
6	A	600	HEC	C4A-NA	-4.76	1.30	1.39

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
12	F	389	MES	O1S-S-C8	6.50	116.54	106.73
12	F	389	MES	C5-N4-C3	6.40	122.62	108.84
12	F	389	MES	C2-C3-N4	-5.85	101.23	110.12
6	A	600	HEC	CBD-CAD-C3D	-5.69	96.80	112.53
6	A	500	HEC	C3B-C4B-NB	5.42	116.11	110.17

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	500	HEC	NA
6	A	600	HEC	NA
6	B	500	HEC	NA
6	B	600	HEC	NA

5 of 49 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	600	HEC	C4C-C3C-CAC-CBC
11	F	388	P6G	C11-C12-O13-C14
6	B	600	HEC	C2C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
11	F	388	P6G	C8-C9-O10-C11
10	F	387	PG4	O2-C3-C4-O3

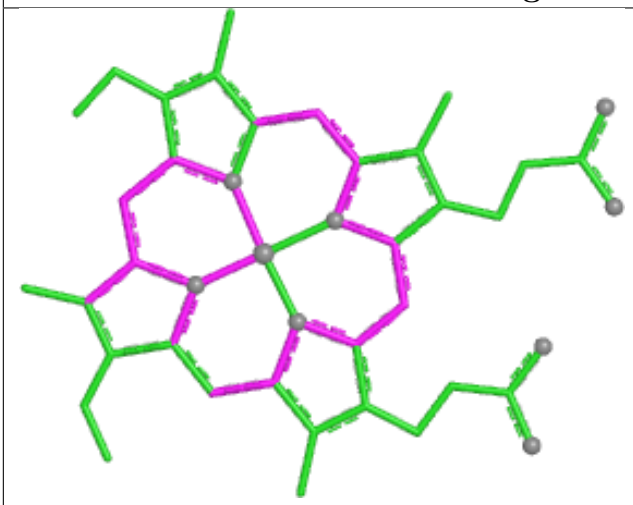
There are no ring outliers.

4 monomers are involved in 13 short contacts:

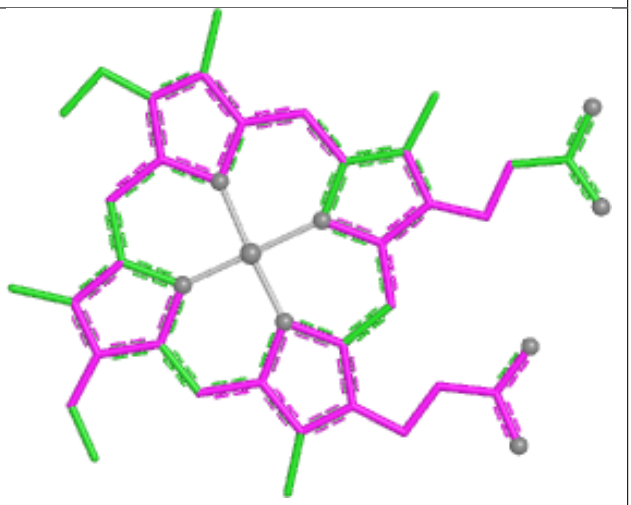
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	F	387	PG4	3	0
8	D	387	PEG	3	0
11	F	388	P6G	6	0
6	A	600	HEC	1	0

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

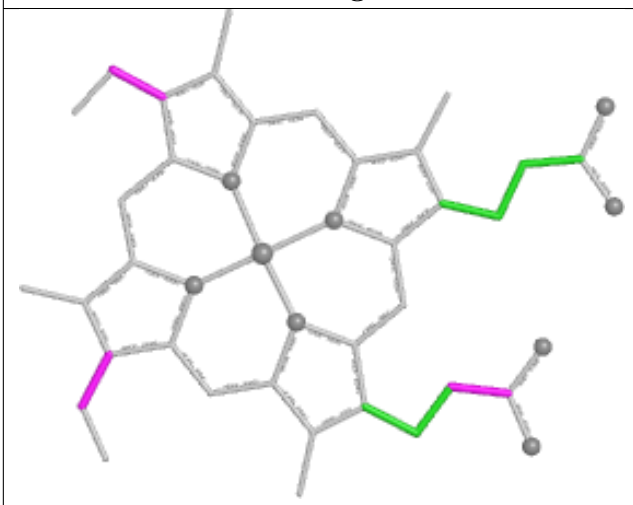
Ligand HEC B 600



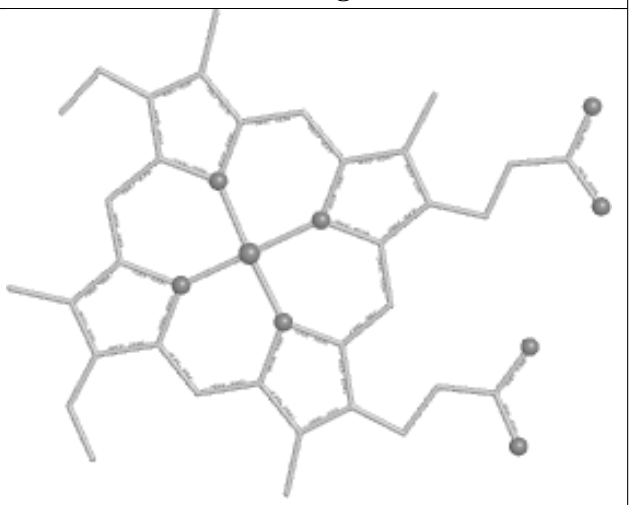
Bond lengths



Bond angles

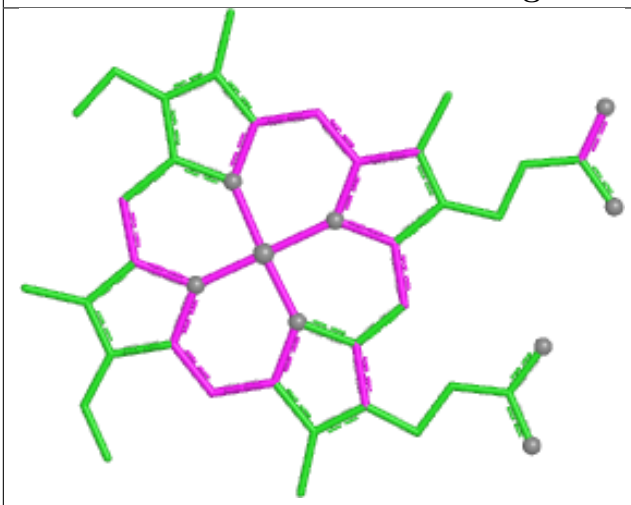


Torsions

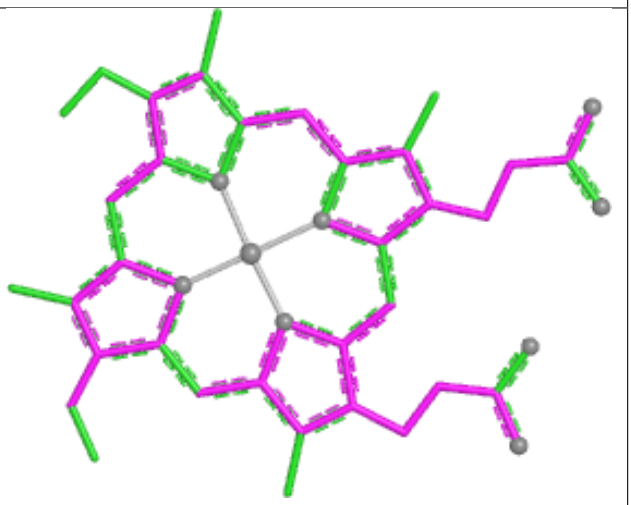


Rings

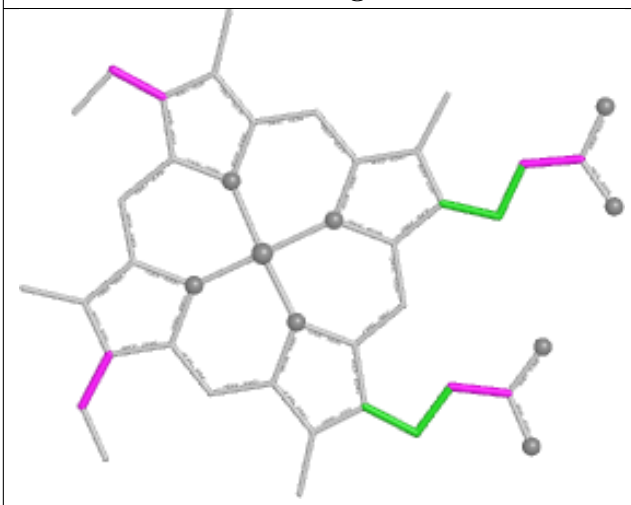
Ligand HEC B 500



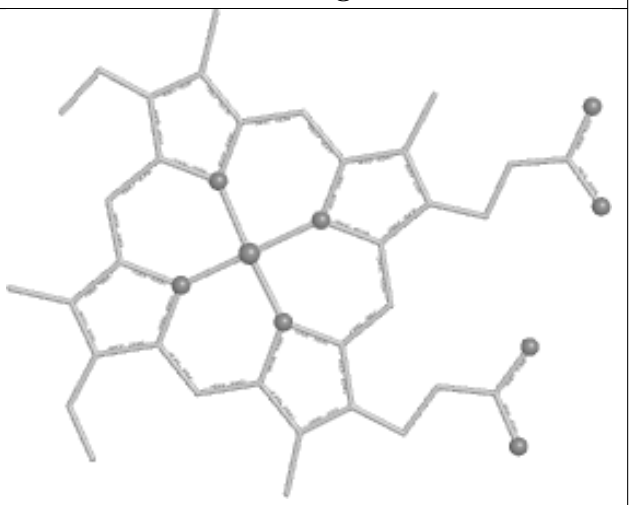
Bond lengths



Bond angles



Torsions

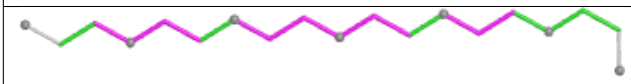


Rings

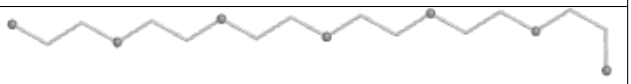
Ligand P6G F 388

Bond lengths

Bond angles

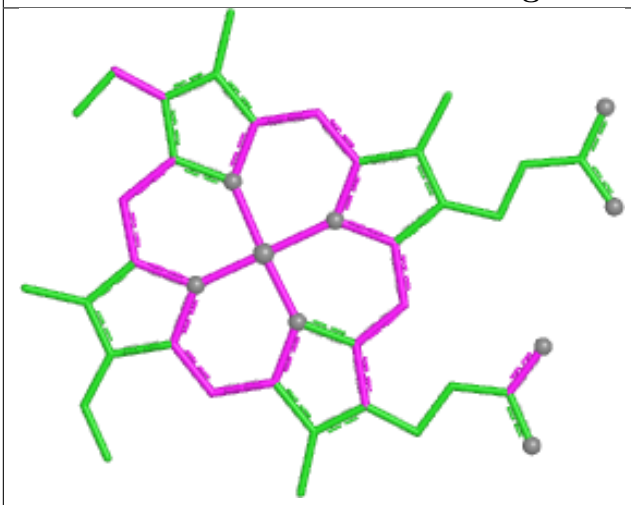


Torsions

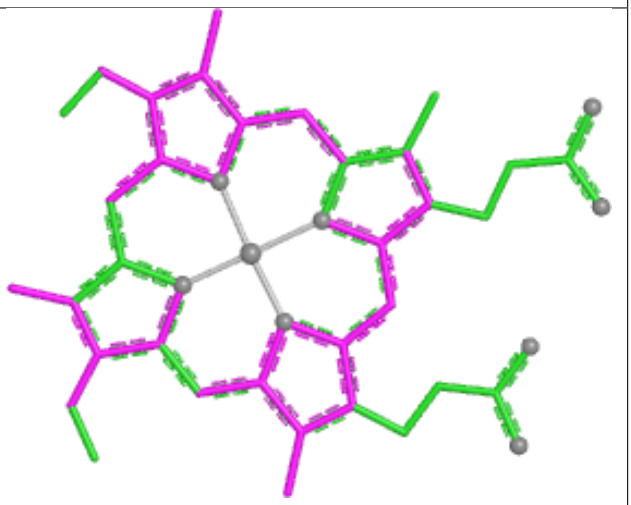


Rings

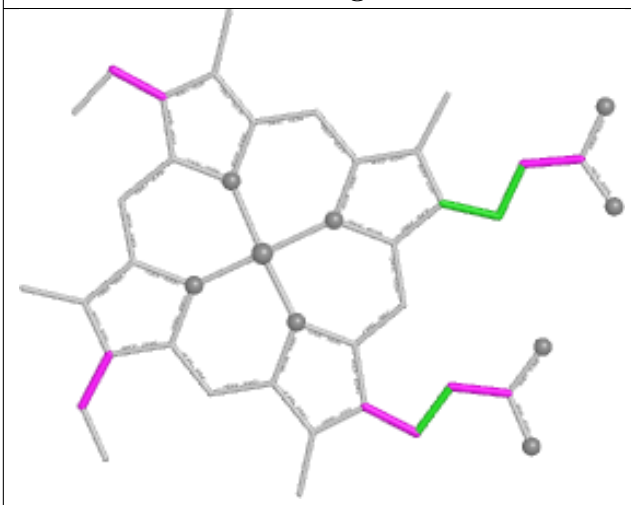
Ligand HEC A 500



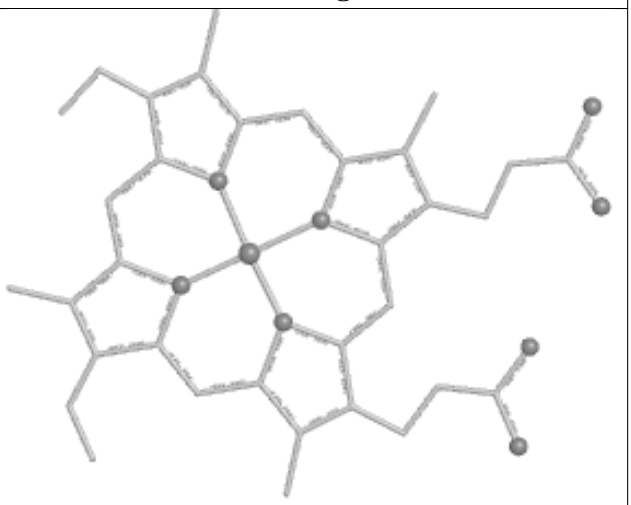
Bond lengths



Bond angles

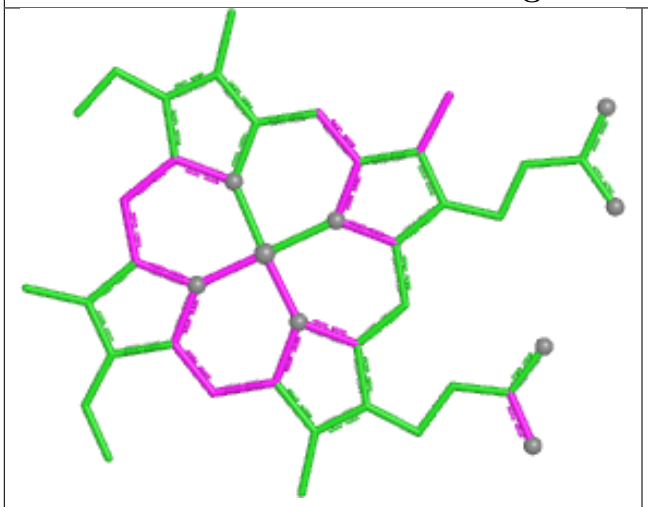


Torsions

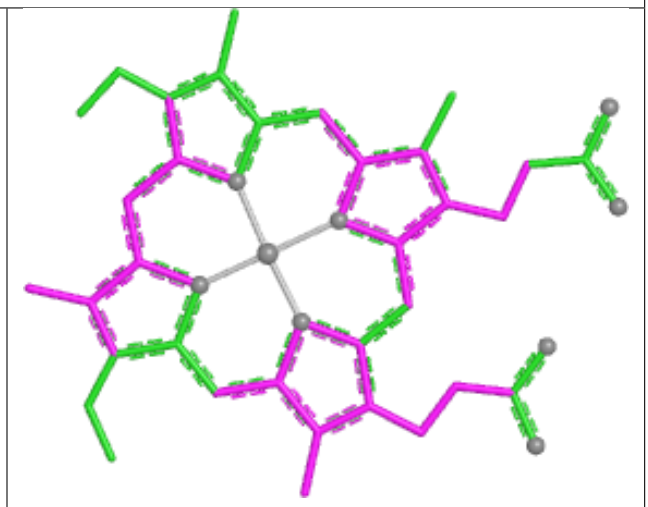


Rings

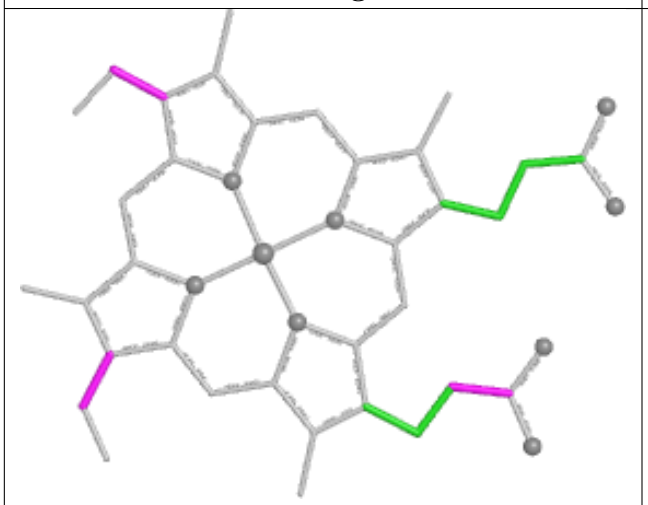
Ligand HEC A 600



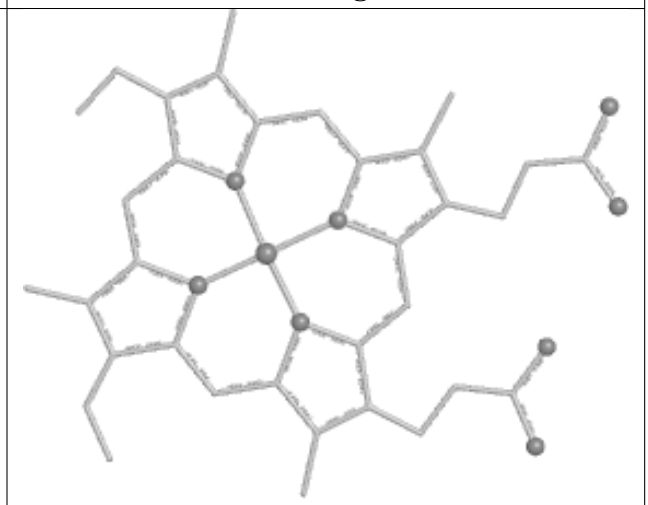
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	354/373 (94%)	-0.47	1 (0%)	90	92	10, 19, 32, 52	7 (1%)
1	B	355/373 (95%)	-0.47	1 (0%)	90	92	9, 20, 34, 56	3 (0%)
2	C	130/137 (94%)	-0.48	1 (0%)	82	87	9, 17, 31, 44	5 (3%)
2	E	123/137 (89%)	-0.67	1 (0%)	82	87	8, 15, 25, 40	4 (3%)
3	D	376/386 (97%)	-0.44	2 (0%)	87	90	8, 20, 36, 60	7 (1%)
3	F	376/386 (97%)	-0.68	2 (0%)	87	90	8, 15, 28, 49	9 (2%)
All	All	1714/1792 (95%)	-0.52	8 (0%)	87	90	8, 18, 33, 60	35 (2%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	6	ALA	4.4
1	B	6	ALA	3.9
3	D	208	THR	3.4
3	F	386	GLY	3.1
3	F	207	GLY	2.7

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	0AF	C	57	15/16	0.97	0.05	17,19,22,23	0
2	0AF	E	57	15/16	0.97	0.05	13,15,18,20	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

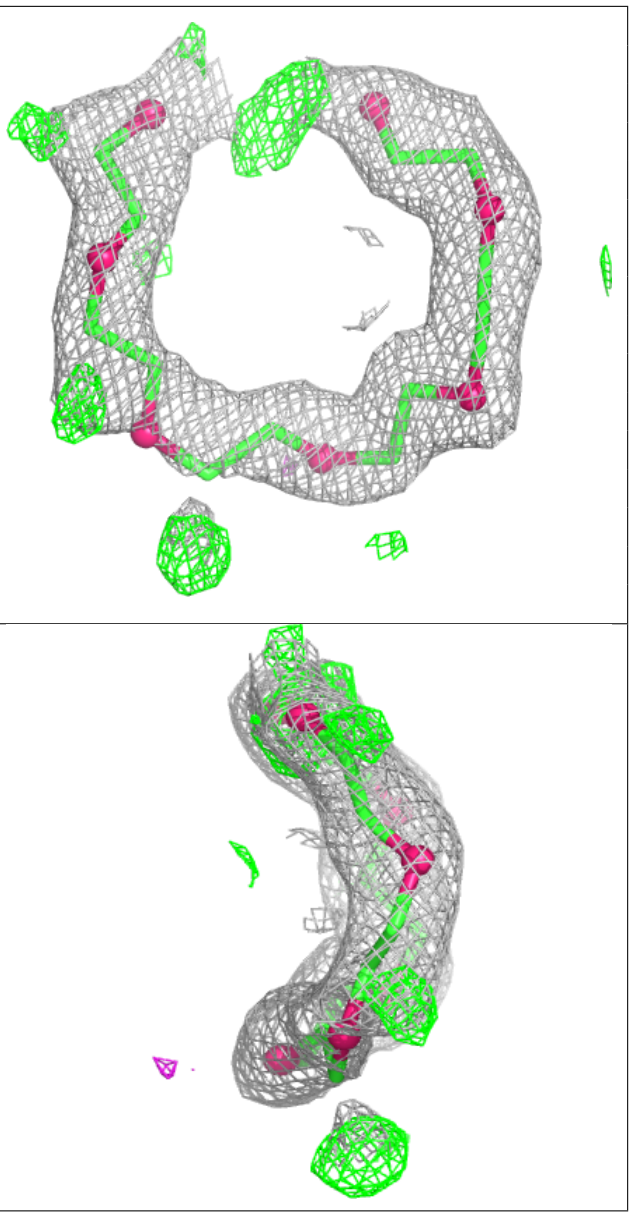
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	PEG	D	387	7/7	0.81	0.15	53,54,55,56	0
10	PG4	F	387	13/13	0.87	0.14	51,55,62,63	0
11	P6G	F	388	19/19	0.89	0.12	20,33,52,53	0
7	EDO	B	374	4/4	0.92	0.14	36,40,41,43	0
7	EDO	A	374	4/4	0.92	0.10	40,43,43,46	0
12	MES	F	389	12/12	0.92	0.15	14,31,38,38	12
9	ACT	D	388	4/4	0.94	0.09	26,27,30,31	0
5	NA	A	402	1/1	0.97	0.07	26,26,26,26	0
5	NA	B	402	1/1	0.98	0.04	24,24,24,24	0
5	NA	B	401	1/1	0.98	0.03	22,22,22,22	0
6	HEC	A	600	43/43	0.99	0.04	9,12,15,16	0
6	HEC	B	500	43/43	0.99	0.05	11,14,17,19	0
6	HEC	B	600	43/43	0.99	0.04	7,11,14,16	0
5	NA	A	401	1/1	0.99	0.04	23,23,23,23	0
6	HEC	A	500	43/43	0.99	0.04	11,15,18,21	0
4	CA	B	400	1/1	1.00	0.02	13,13,13,13	0
4	CA	A	400	1/1	1.00	0.02	14,14,14,14	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 P6G F 388:

$2mF_o$-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 600:

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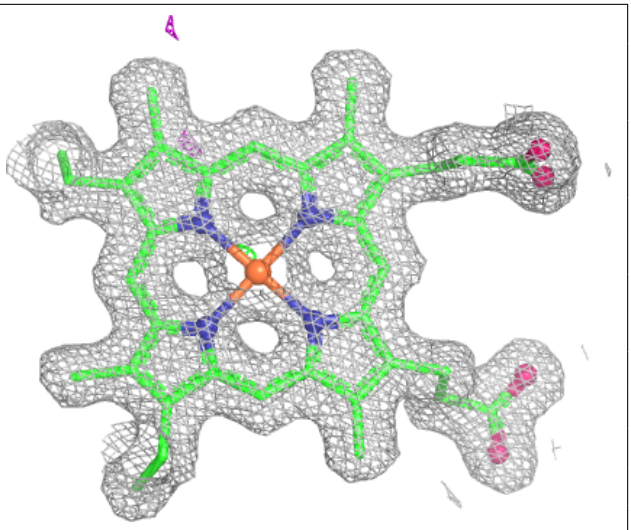
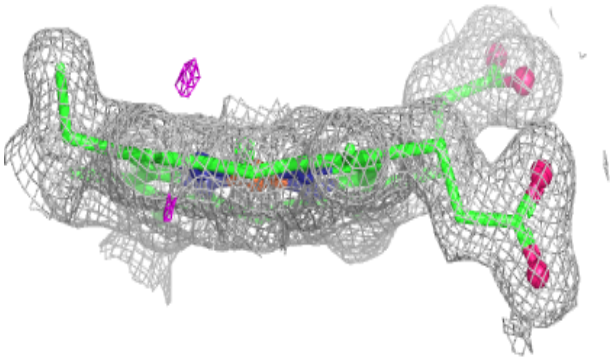
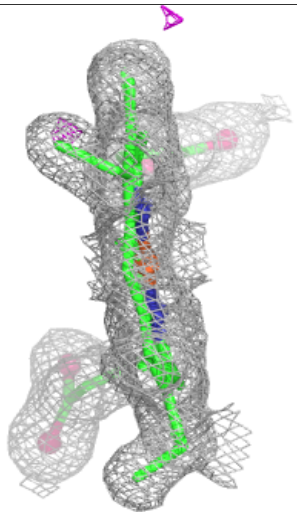
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

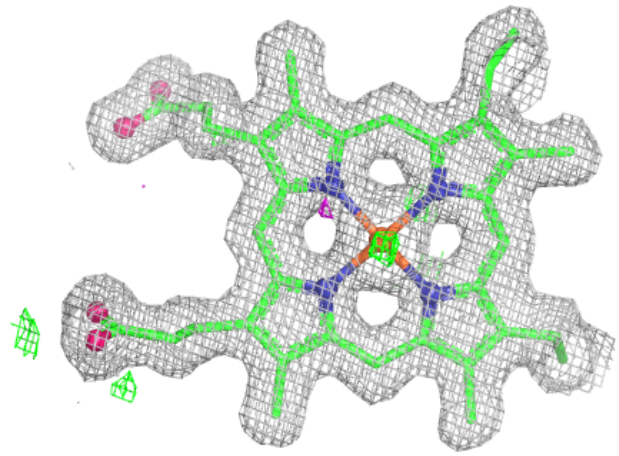


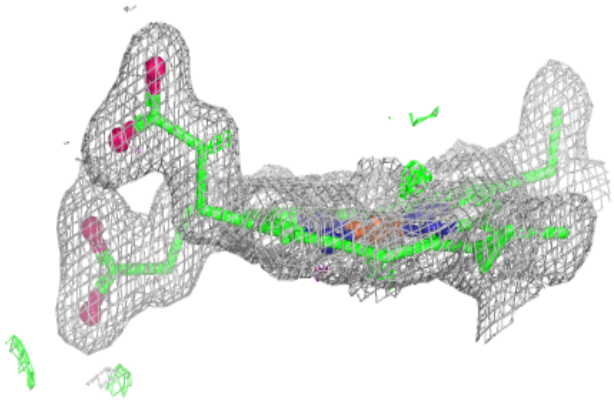


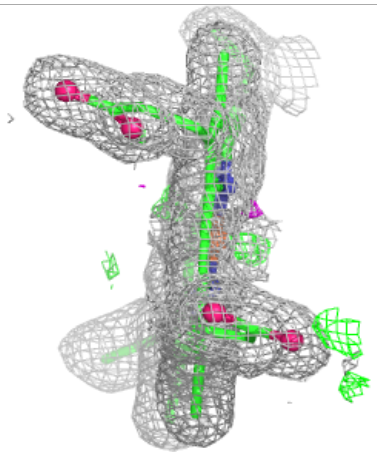


Electron density around HEC B 500:

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

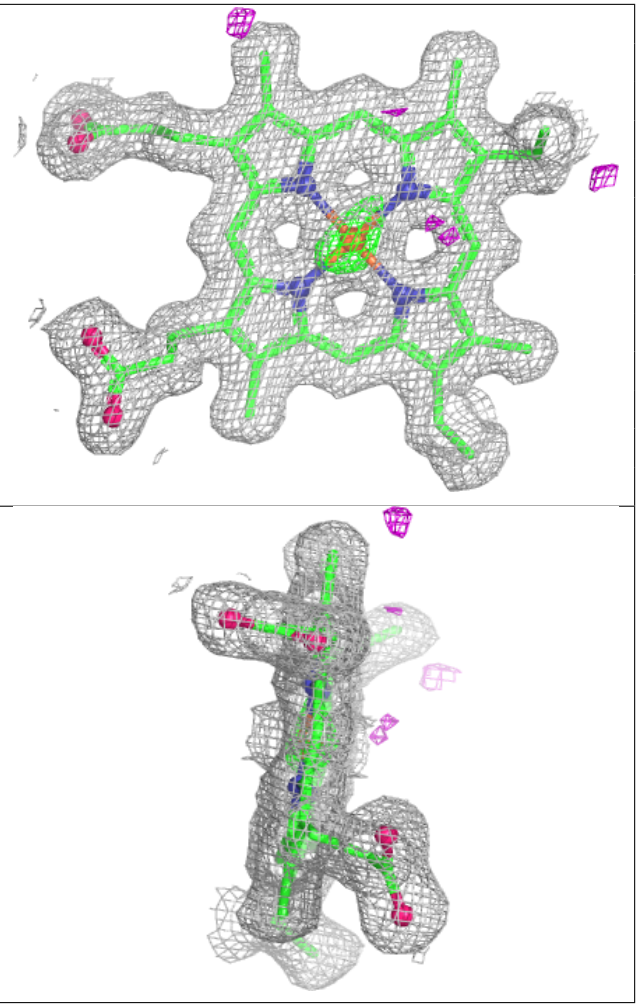






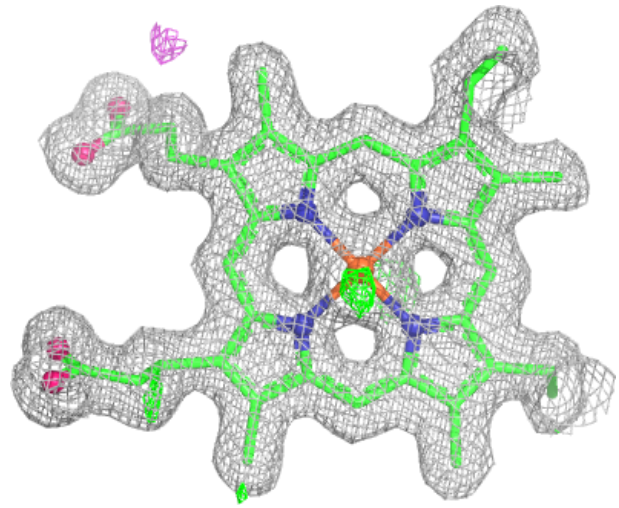
Electron density around HEC B 600:

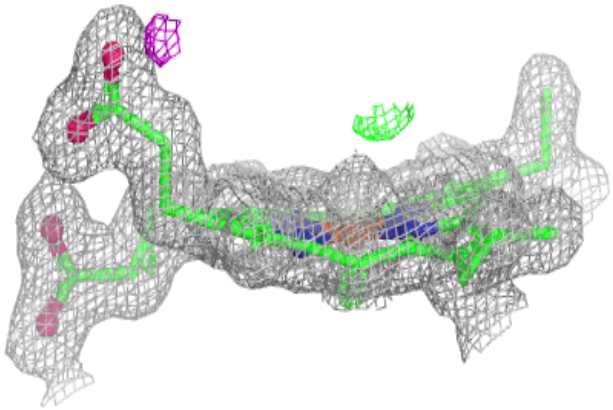
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC A 500:

$2mF_o$-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.