



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:08 PM UTC

PDB ID : 4FB1 / pdb_00004fb1
Title : Crystal Structure of WT MauG in Complex with Pre-Methylamine Dehydrogenase Aged 60 Days
Authors : Yukl, E.T.; Wilmot, C.M.
Deposited on : 2012-05-22
Resolution : 2.15 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:

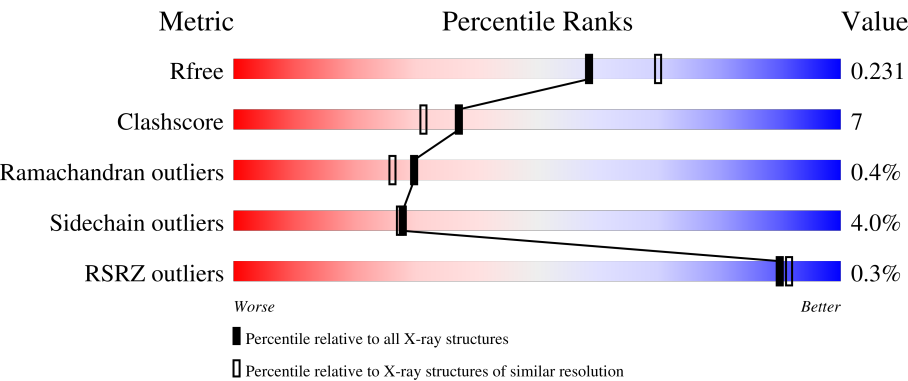
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal 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 i

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

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	373	71%21%• 5%
1	B	373	83%12%• •
2	C	137	% 71%19%• 9%
2	E	137	% 66%23%• 9%
3	D	385	78%18%• •

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Mol	Chain	Length	Quality of chain
3	F	385	83% 13% ••

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 14193 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
1	A	354	Total	C	N	O	S	0	2	0
			2751	1717	495	528	11			
1	B	357	Total	C	N	O	S	0	1	0
			2769	1727	498	533	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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	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
2	C	125	Total	C	N	O	S	0	1	0
			957	592	161	190	14			
2	E	125	Total	C	N	O	S	0	4	0
			970	601	162	191	16			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	132	HIS	-	expression tag	UNP P22619
C	133	HIS	-	expression tag	UNP P22619
C	134	HIS	-	expression tag	UNP P22619
C	135	HIS	-	expression tag	UNP P22619
C	136	HIS	-	expression tag	UNP P22619
C	137	HIS	-	expression tag	UNP P22619
E	132	HIS	-	expression tag	UNP P22619
E	133	HIS	-	expression tag	UNP P22619
E	134	HIS	-	expression tag	UNP P22619
E	135	HIS	-	expression tag	UNP P22619
E	136	HIS	-	expression tag	UNP P22619
E	137	HIS	-	expression tag	UNP P22619

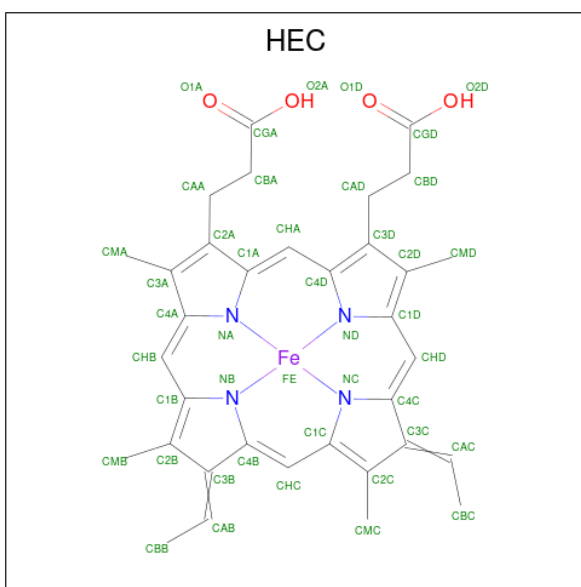
- Molecule 3 is a protein called Methylamine dehydrogenase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	376	Total	C	N	O	S	0	2	0
			2934	1859	503	563	9			
3	F	376	Total	C	N	O	S	0	4	0
			2955	1871	508	567	9			

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

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

- Molecule 5 is HEME C (CCD ID: HEC) (formula: C₃₄H₃₄FeN₄O₄).



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

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Na 1 1	0	0
6	B	2	Total Na 2 2	0	0

- Molecule 7 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



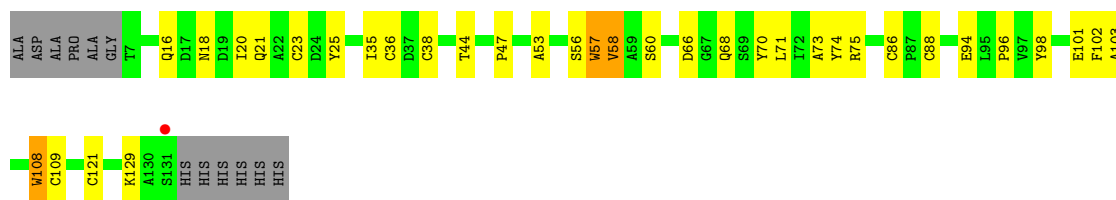
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
7	F	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	81	Total	O	0	0
			81	81		
8	B	155	Total	O	0	2
			157	157		
8	C	36	Total	O	0	0
			36	36		
8	D	101	Total	O	0	0
			101	101		
8	E	63	Total	O	0	0
			63	63		
8	F	218	Total	O	0	0
			218	218		

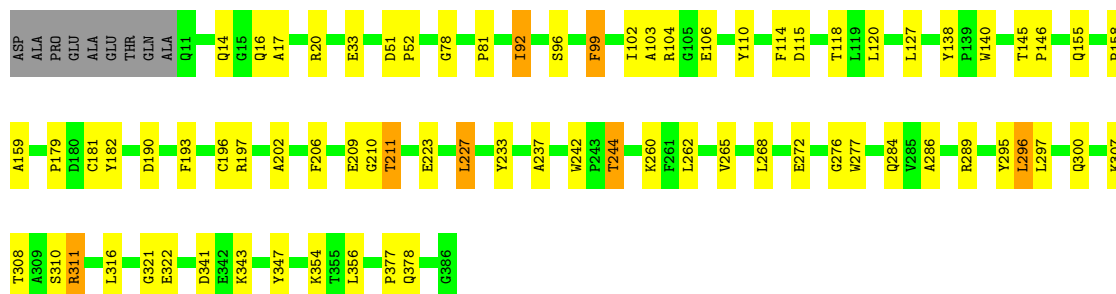
- Molecule 1: Methylamine utilization protein MauG





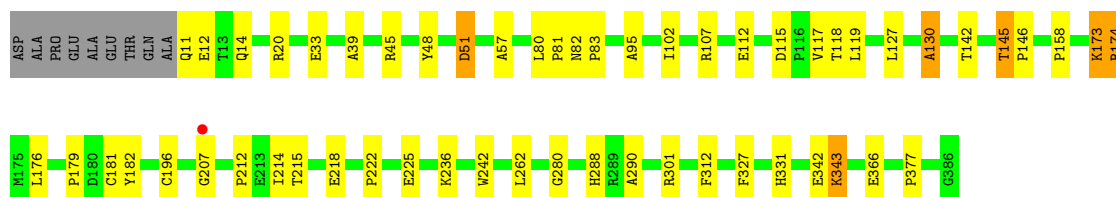
• Molecule 3: Methylamine dehydrogenase heavy chain

Chain D: 78% 18% ..



• Molecule 3: Methylamine dehydrogenase heavy chain

Chain F: 83% 13% ..



4 Data and refinement statistics

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)	44.49 – 2.15 44.49 – 2.15	Depositor EDS
% Data completeness (in resolution range)	97.0 (44.49-2.15) 97.0 (44.49-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.162 , 0.222 0.175 , 0.231	Depositor DCC
R_{free} test set	4746 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	38.8	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14193	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NA, MES, CA, 0AF, HEC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.04	2/2818 (0.1%)	1.13	8/3823 (0.2%)
1	B	1.25	2/2833 (0.1%)	1.17	5/3842 (0.1%)
2	C	1.18	3/969 (0.3%)	1.18	4/1323 (0.3%)
2	E	1.35	2/988 (0.2%)	1.25	1/1350 (0.1%)
3	D	1.04	1/3015 (0.0%)	1.13	13/4108 (0.3%)
3	F	1.32	6/3035 (0.2%)	1.23	12/4134 (0.3%)
All	All	1.18	16/13658 (0.1%)	1.17	43/18580 (0.2%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	112	VAL	CA-CB	8.23	1.64	1.54
3	F	51	ASP	N-CA	-7.25	1.39	1.46
2	C	108	TRP	C-N	7.13	1.42	1.33
3	F	95	ALA	CA-CB	-7.04	1.43	1.53
3	F	130	ALA	N-CA	6.64	1.51	1.46
2	C	86	CYS	CA-C	-6.45	1.48	1.53
2	E	108	TRP	CA-CB	6.37	1.60	1.52
2	C	53	ALA	CA-CB	-6.37	1.43	1.53
1	A	66	ASN	C-O	6.00	1.31	1.23
1	B	304	ALA	CA-CB	-5.80	1.43	1.53
2	E	60	SER	N-CA	-5.60	1.39	1.46
3	D	103	ALA	CA-CB	5.35	1.61	1.53
3	F	33	GLU	CA-C	5.25	1.58	1.52
1	B	227	GLY	N-CA	5.25	1.52	1.45
3	F	207	GLY	N-CA	5.19	1.49	1.44
3	F	83	PRO	CA-C	-5.12	1.46	1.52

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	57	ALA	N-CA-C	-7.86	103.14	112.89
2	C	107	ILE	O-C-N	7.40	130.74	122.68
3	D	120	LEU	CA-C-N	-6.99	112.77	119.76
3	D	120	LEU	C-N-CA	-6.99	112.77	119.76
1	A	200	ASN	N-CA-C	6.74	119.46	111.71
1	B	76	VAL	CA-C-N	-6.71	113.39	120.03
1	B	76	VAL	C-N-CA	-6.71	113.39	120.03
3	F	118	THR	N-CA-C	-6.35	105.54	113.28
1	A	7	ASP	N-CA-C	-6.21	104.59	111.36
2	C	26	TRP	N-CA-C	6.11	118.72	111.33
3	D	115	ASP	CA-C-N	-6.01	113.78	120.45
3	D	115	ASP	C-N-CA	-6.01	113.78	120.45
3	D	343	LYS	CA-C-N	6.00	125.96	119.78
3	D	343	LYS	C-N-CA	6.00	125.96	119.78
3	D	244	THR	N-CA-C	-5.96	101.39	110.14
3	D	99	PHE	N-CA-C	-5.69	100.41	109.23
3	D	33	GLU	N-CA-C	5.65	117.10	109.24
3	D	296	LEU	N-CA-C	5.62	117.59	108.26
2	E	16	GLN	N-CA-C	-5.53	100.94	109.52
1	A	301	ARG	CA-C-N	5.50	126.72	119.84
1	A	301	ARG	C-N-CA	5.50	126.72	119.84
3	F	51	ASP	CA-C-N	5.43	125.14	119.82
3	F	51	ASP	C-N-CA	5.43	125.14	119.82
3	F	127	LEU	CA-C-N	-5.42	114.37	119.85
3	F	127	LEU	C-N-CA	-5.42	114.37	119.85
1	B	283	VAL	N-CA-C	5.41	116.14	110.62
3	D	118	THR	N-CA-C	-5.36	106.74	113.28
2	C	108	TRP	CA-C-N	-5.35	114.26	122.60
2	C	108	TRP	C-N-CA	-5.35	114.26	122.60
1	A	174	LYS	N-CA-C	-5.33	105.55	111.36
3	D	211	THR	N-CA-C	-5.32	103.49	109.60
1	A	266	VAL	CA-C-N	-5.29	114.33	119.78
1	A	266	VAL	C-N-CA	-5.29	114.33	119.78
3	F	242	TRP	CA-C-N	-5.28	114.80	120.03
3	F	242	TRP	C-N-CA	-5.28	114.80	120.03
1	B	106	GLN	O-C-N	5.26	124.54	120.38
1	B	303	GLU	N-CA-C	-5.16	106.08	112.38
1	A	331	GLY	N-CA-C	-5.11	109.00	115.08
3	F	145	THR	CA-C-N	5.05	124.83	119.28
3	F	145	THR	C-N-CA	5.05	124.83	119.28
3	D	17	ALA	N-CA-C	-5.03	105.80	111.28
3	F	48	TYR	CA-C-N	-5.03	116.42	123.10
3	F	48	TYR	C-N-CA	-5.03	116.42	123.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2751	0	2628	58	0
1	B	2769	0	2643	31	0
2	C	957	0	863	17	0
2	E	970	0	881	31	0
3	D	2934	0	2814	38	0
3	F	2955	0	2835	32	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	86	0	60	2	0
5	B	86	0	60	2	0
6	A	1	0	0	0	0
6	B	2	0	0	0	0
7	D	12	0	12	0	0
7	F	12	0	12	0	0
8	A	81	0	0	4	0
8	B	157	0	0	4	0
8	C	36	0	0	0	0
8	D	101	0	0	3	0
8	E	63	0	0	1	0
8	F	218	0	0	6	0
All	All	14193	0	12808	186	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 7.

All (186) 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:F:174[A]:ARG:HH21	3:F:174[A]:ARG:HG2	1.21	1.03
1:B:107:PRO:HG3	8:B:618[B]:HOH:O	1.63	0.97
1:B:197:ILE:O	1:B:202:ARG:HD3	1.65	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:174[A]:ARG:HH21	3:F:174[A]:ARG:CG	1.81	0.92
1:B:198:THR:HG22	2:E:58[B]:VAL:HG23	1.53	0.90
1:A:48:LYS:H	1:A:62:HIS:HE1	1.18	0.87
2:E:35:ILE:HD12	2:E:86[B]:CYS:SG	2.15	0.86
1:B:198:THR:HG22	2:E:58[B]:VAL:CG2	2.08	0.84
3:D:297:LEU:HD22	3:D:310:SER:HB2	1.62	0.79
3:F:11:GLN:HB3	8:F:585:HOH:O	1.80	0.79
2:E:38:CYS:SG	2:E:86[B]:CYS:HB2	2.25	0.77
2:C:57:0AF:HBC1	2:C:108:TRP:NE1	2.02	0.73
2:E:36[B]:CYS:SG	2:E:47:PRO:HD3	2.29	0.73
1:A:172:ASP:O	1:A:177:ARG:NH1	2.22	0.72
1:A:48:LYS:H	1:A:62:HIS:CE1	2.04	0.72
1:A:210:GLN:HE22	2:C:44:THR:HG21	1.55	0.71
1:B:113:GLU:HG2	5:B:402:HEC:HBC2	1.74	0.70
2:E:56:SER:HB2	2:E:74:TYR:O	1.92	0.70
3:D:52:PRO:HG2	3:D:378:GLN:OE1	1.91	0.70
3:D:14:GLN:HE21	2:E:21:GLN:HE22	1.40	0.69
1:A:301:ARG:CZ	1:A:333:MET:HE1	2.23	0.69
1:B:198:THR:CG2	2:E:58[B]:VAL:HG23	2.23	0.68
3:D:181[B]:CYS:HB3	3:D:196:CYS:SG	2.31	0.68
1:A:60:GLN:O	1:A:62:HIS:HD2	1.76	0.67
3:F:342[B]:GLU:HG3	8:F:596:HOH:O	1.94	0.67
2:E:57:0AF:HBC1	2:E:108:TRP:NE1	2.09	0.67
1:A:353[B]:ARG:HH11	1:A:353[B]:ARG:HG2	1.58	0.67
3:F:45:ARG:NH2	3:F:343:LYS:O	2.28	0.67
3:F:12:GLU:OE1	3:F:20:ARG:NH1	2.28	0.66
1:B:210:GLN:HE22	2:E:44:THR:HG21	1.60	0.66
1:B:198:THR:CG2	2:E:58[B]:VAL:CG2	2.74	0.65
3:D:237:ALA:HB2	3:D:289:ARG:HG3	1.80	0.64
2:E:21:GLN:O	2:E:86[B]:CYS:SG	2.57	0.63
2:E:56:SER:CB	2:E:74:TYR:O	2.47	0.63
1:A:301:ARG:NH1	1:A:333:MET:HE1	2.14	0.62
3:D:51:ASP:HA	3:D:377:PRO:HA	1.82	0.62
3:F:181[B]:CYS:HB3	3:F:196:CYS:SG	2.39	0.61
3:D:227:LEU:HD12	3:D:244:THR:HG22	1.82	0.60
3:F:174[A]:ARG:HD3	8:F:586:HOH:O	2.00	0.60
3:F:222:PRO:HG2	3:F:225:GLU:HB2	1.84	0.60
1:B:186:THR:OG1	1:B:189:GLU:HG3	2.03	0.59
3:D:347:TYR:HB3	3:D:356:LEU:HD11	1.83	0.59
3:F:174[A]:ARG:HG2	3:F:174[A]:ARG:NH2	2.04	0.59
3:F:173:LYS:HD2	8:F:715:HOH:O	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:101:GLU:HA	8:E:253:HOH:O	2.03	0.58
2:E:74:TYR:O	2:E:75:ARG:HG3	2.03	0.58
1:A:113:GLU:HG2	5:A:402:HEC:HBC2	1.86	0.58
1:A:48:LYS:HB2	1:A:62:HIS:CE1	2.39	0.57
1:A:333:MET:HE2	3:D:159:ALA:HB2	1.85	0.57
3:D:268:LEU:HD22	3:D:277:TRP:HB3	1.86	0.57
2:C:21:GLN:HE22	3:F:14:GLN:HE21	1.51	0.56
3:F:331:HIS:HE1	3:F:366:GLU:OE1	1.88	0.56
3:F:174[A]:ARG:CG	3:F:174[A]:ARG:NH2	2.55	0.56
1:A:104:ALA:O	1:A:107:PRO:HD2	2.05	0.56
3:D:190:ASP:HB2	3:D:206:PHE:O	2.06	0.56
1:A:68:PRO:HG2	5:A:402:HEC:HBA1	1.89	0.55
2:C:105:ASP:HB2	3:D:138:TYR:OH	2.07	0.55
1:B:91:GLN:HB3	5:B:402:HEC:HAA1	1.89	0.55
3:D:155:GLN:NE2	8:D:581:HOH:O	2.40	0.54
3:F:312:PHE:HA	3:F:327:PHE:O	2.07	0.54
1:A:21:PRO:O	1:A:27:ALA:HA	2.07	0.54
3:D:284:GLN:O	3:D:296:LEU:HD12	2.08	0.53
3:F:39:ALA:O	3:F:117:VAL:HG13	2.09	0.53
2:C:130:ALA:O	2:C:131:SER:HB3	2.10	0.52
3:F:82:ASN:HB3	3:F:142:THR:HB	1.91	0.52
1:A:195:VAL:HG21	1:A:338:ARG:HG2	1.92	0.51
3:D:104:ARG:NH2	3:F:112:GLU:OE2	2.36	0.51
3:D:193:PHE:HA	3:D:202:ALA:O	2.10	0.51
1:A:136:PHE:CG	1:A:145:LEU:HD21	2.46	0.50
1:A:353[A]:ARG:HD2	8:A:579:HOH:O	2.10	0.50
1:A:333:MET:HE2	3:D:159:ALA:CB	2.42	0.50
1:A:60:GLN:O	1:A:62:HIS:CD2	2.61	0.50
1:A:65:ARG:HH12	1:A:94:ASP:CG	2.19	0.50
1:A:197:ILE:C	1:A:202:ARG:HG2	2.37	0.50
1:A:113:GLU:OE1	8:A:524:HOH:O	2.20	0.49
1:A:19:VAL:HG13	8:A:551:HOH:O	2.12	0.49
1:B:206:MET:O	1:B:207:GLN:C	2.56	0.49
2:E:38:CYS:SG	2:E:86[B]:CYS:CB	2.92	0.49
2:C:57:0AF:HBC1	2:C:108:TRP:HE1	1.77	0.48
1:A:40:ALA:HA	1:A:354:TYR:CZ	2.49	0.48
1:A:119:ARG:HG2	1:A:152:PHE:CG	2.48	0.48
2:E:36[B]:CYS:HG	2:E:47:PRO:HD3	1.78	0.48
1:A:300:ARG:HD3	3:D:158:PRO:HG3	1.96	0.48
1:B:228:LEU:HD13	1:B:279:MET:HB3	1.96	0.47
1:B:198:THR:CG2	2:E:58[B]:VAL:HG21	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:58[B]:VAL:HG22	2:E:73:ALA:HA	1.96	0.47
3:F:236:LYS:NZ	8:F:700:HOH:O	2.45	0.47
3:D:140:TRP:CE2	3:D:233:TYR:HB3	2.50	0.47
3:D:265:VAL:HG21	3:D:321:GLY:HA3	1.94	0.47
3:D:265:VAL:HG21	3:D:321:GLY:CA	2.44	0.47
1:A:95:GLY:HA3	1:A:223:TYR:OH	2.15	0.47
1:B:303:GLU:HB3	8:B:629:HOH:O	2.15	0.47
1:A:206:MET:HA	1:A:206:MET:HE2	1.97	0.47
1:A:28:THR:OG1	1:A:57:ASP:OD1	2.30	0.46
3:F:115:ASP:O	3:F:119:LEU:HA	2.14	0.46
1:A:202:ARG:HB2	1:A:206:MET:HG3	1.96	0.46
1:A:208:ARG:NE	8:A:539:HOH:O	2.41	0.46
1:B:226:ILE:O	1:B:297:TYR:OH	2.28	0.46
3:D:96:SER:HB3	3:D:110:TYR:CZ	2.50	0.46
1:B:81:ARG:HD3	1:B:85:GLY:HA2	1.96	0.46
3:F:107:ARG:HD3	3:F:130:ALA:HB1	1.98	0.46
3:D:197:ARG:HD2	8:D:570:HOH:O	2.16	0.46
1:B:198:THR:HG22	2:E:58[B]:VAL:HG21	1.91	0.46
1:A:40:ALA:HA	1:A:354:TYR:CE1	2.50	0.45
3:D:311:ARG:HE	3:D:311:ARG:HB2	1.45	0.45
1:B:199:TRP:O	1:B:202:ARG:HG2	2.17	0.45
1:A:197:ILE:O	1:A:202:ARG:HG2	2.16	0.45
1:A:171:PHE:CZ	1:A:215:ARG:HB3	2.50	0.45
1:A:206:MET:O	1:A:220:ASN:HB3	2.16	0.45
2:E:20:ILE:HG22	2:E:25:TYR:CZ	2.52	0.45
1:A:257:ASP:HA	1:A:258:PRO:HD2	1.81	0.44
1:B:331:GLY:O	3:F:158:PRO:HA	2.17	0.44
1:A:76:VAL:HG12	1:A:77:PRO:O	2.17	0.44
3:D:227:LEU:HB3	3:D:242:TRP:NE1	2.33	0.44
2:E:53:ALA:HB2	2:E:109:CYS:HA	1.98	0.44
1:A:202:ARG:HD2	1:A:202:ARG:C	2.43	0.44
1:A:359:GLU:CD	1:A:359:GLU:N	2.76	0.44
1:B:208:ARG:HD2	8:B:650:HOH:O	2.17	0.44
2:E:36[B]:CYS:HA	2:E:121:CYS:SG	2.58	0.44
2:C:19:ASP:O	2:C:25:TYR:HB2	2.17	0.44
2:C:46:CYS:HB3	2:C:50:THR:OG1	2.18	0.44
2:C:96:PRO:HB2	2:C:98:TYR:CE1	2.52	0.44
1:A:21:PRO:HA	1:A:29:GLN:O	2.18	0.43
1:B:202:ARG:HG2	1:B:202:ARG:HH11	1.84	0.43
3:D:16:GLN:HA	2:E:18:ASN:O	2.17	0.43
2:C:21:GLN:HE22	3:F:14:GLN:NE2	2.14	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:GLN:CD	1:A:103:GLN:C	2.86	0.43
1:A:140:PHE:O	1:A:150:ARG:NH2	2.51	0.43
1:B:288:ARG:NH1	1:B:340:ASP:OD1	2.46	0.43
3:D:92:ILE:HG12	3:D:114:PHE:HB2	2.01	0.43
1:A:116:MET:HG3	1:A:122:VAL:HG22	2.00	0.43
3:D:145:THR:HB	3:D:146:PRO:HD2	2.01	0.43
1:A:25:ARG:HB2	1:A:115:ALA:O	2.18	0.43
1:A:103:GLN:C	1:A:103:GLN:OE1	2.61	0.43
1:B:353:ARG:HG2	1:B:353:ARG:HH11	1.84	0.43
2:C:56:SER:CB	2:C:74:TYR:O	2.66	0.43
3:F:80:LEU:N	3:F:81:PRO:CD	2.82	0.43
3:F:176:LEU:HD22	3:F:212:PRO:HG3	2.01	0.43
1:A:199:TRP:HH2	1:A:333:MET:O	2.02	0.42
1:B:296:LYS:O	1:B:305[A]:LYS:HE3	2.19	0.42
1:B:305[B]:LYS:HD2	8:B:641:HOH:O	2.19	0.42
3:D:78:GLY:O	3:D:81:PRO:HD3	2.20	0.42
3:D:209:GLU:HG2	3:D:210:GLY:N	2.34	0.42
2:E:36[B]:CYS:SG	2:E:121:CYS:SG	3.06	0.42
2:E:96:PRO:HB2	2:E:98:TYR:CE1	2.55	0.42
1:A:206:MET:HE2	1:A:216:GLU:CD	2.45	0.42
1:B:92:PHE:CZ	1:B:103:GLN:HG2	2.55	0.42
1:A:35:HIS:CE1	1:A:70:LEU:HD21	2.55	0.42
1:B:355:GLU:O	1:B:358:LEU:HB2	2.20	0.42
2:E:23:CYS:HB3	2:E:88[B]:CYS:SG	2.59	0.42
1:A:41:PHE:HB2	1:A:70:LEU:H	1.85	0.42
1:A:191:PHE:CD2	1:A:341:ALA:HB2	2.55	0.42
2:C:14:VAL:HA	2:C:15:PRO:HD2	1.87	0.42
3:D:272:GLU:HB3	3:D:277:TRP:HB2	2.02	0.42
3:F:51:ASP:HA	3:F:377:PRO:HA	2.02	0.42
3:F:182:TYR:CD1	3:F:182:TYR:N	2.87	0.42
2:C:105:ASP:HB2	8:D:575:HOH:O	2.19	0.42
3:D:286:ALA:HB3	3:D:295:TYR:HB2	2.01	0.42
3:D:341:ASP:N	3:D:341:ASP:OD1	2.51	0.42
1:A:91:GLN:O	1:A:92:PHE:HB2	2.20	0.41
1:A:353[B]:ARG:HG2	1:A:353[B]:ARG:NH1	2.30	0.41
1:B:93:TRP:CE2	1:B:280:HIS:HA	2.54	0.41
2:E:94:GLU:HG2	2:E:102:PHE:O	2.21	0.41
3:D:276:GLY:O	3:D:300:GLN:HA	2.20	0.41
1:B:197:ILE:HG22	1:B:206:MET:HE2	2.03	0.41
2:C:9:PRO:O	3:D:308:THR:HG21	2.20	0.41
2:C:105:ASP:OD1	3:D:307:LYS:NZ	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:73:ALA:O	2:C:125:PRO:HD2	2.20	0.41
3:F:280:GLY:HA3	3:F:301:ARG:CZ	2.51	0.41
1:A:70:LEU:HD13	1:A:163:GLN:NE2	2.35	0.41
2:C:95:LEU:HD12	2:C:102:PHE:CD2	2.56	0.41
2:E:66:ASP:OD2	2:E:70:TYR:OH	2.32	0.41
3:F:145:THR:HB	3:F:146:PRO:HD2	2.03	0.41
1:A:192:GLY:N	1:A:341:ALA:HB1	2.36	0.41
1:B:210:GLN:NE2	2:E:44:THR:HG21	2.31	0.41
1:B:263:ARG:HH11	1:B:263:ARG:HD3	1.72	0.41
2:E:103:ALA:HB1	8:F:616:HOH:O	2.21	0.41
3:F:288:HIS:CE1	3:F:290:ALA:HB3	2.55	0.41
1:A:180:ARG:NE	1:A:182:GLU:OE2	2.48	0.40
1:A:223:TYR:CG	1:A:249:LEU:HD22	2.56	0.40
1:A:88:LYS:HD3	1:A:220:ASN:O	2.21	0.40
1:A:93:TRP:CE2	1:A:280:HIS:HA	2.56	0.40
3:D:99:PHE:HA	3:D:106:GLU:O	2.22	0.40
3:F:179:PRO:HD3	3:F:214:ILE:HD13	2.03	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	354/373 (95%)	340 (96%)	14 (4%)	0	100	100
1	B	356/373 (95%)	345 (97%)	10 (3%)	1 (0%)	36	34
2	C	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
2	E	126/137 (92%)	122 (97%)	4 (3%)	0	100	100
3	D	376/385 (98%)	355 (94%)	18 (5%)	3 (1%)	16	10
3	F	378/385 (98%)	364 (96%)	12 (3%)	2 (0%)	24	20
All	All	1713/1790 (96%)	1642 (96%)	65 (4%)	6 (0%)	30	26

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	223	GLU
1	B	361	SER
3	D	102	ILE
3	D	179	PRO
3	F	343	LYS
3	F	102	ILE

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	278/292 (95%)	256 (92%)	22 (8%)	11	7
1	B	280/292 (96%)	269 (96%)	11 (4%)	28	28
2	C	105/112 (94%)	103 (98%)	2 (2%)	50	56
2	E	108/112 (96%)	103 (95%)	5 (5%)	24	22
3	D	306/310 (99%)	295 (96%)	11 (4%)	31	31
3	F	308/310 (99%)	302 (98%)	6 (2%)	50	56
All	All	1385/1428 (97%)	1328 (96%)	57 (4%)	28	26

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASP
1	A	8	ASP
1	A	23	LEU
1	A	48	LYS
1	A	51	LEU
1	A	60	GLN
1	A	75	LEU
1	A	88	LYS
1	A	112	VAL
1	A	157	GLU
1	A	183	GLU

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Mol	Chain	Res	Type
1	A	201	CYS
1	A	202	ARG
1	A	206	MET
1	A	208	ARG
1	A	236	GLU
1	A	306	ILE
1	A	321	ARG
1	A	323	LEU
1	A	357	LEU
1	A	358	LEU
1	A	359	GLU
1	B	81	ARG
1	B	102	GLN
1	B	157	GLU
1	B	167	GLU
1	B	219	THR
1	B	269	LEU
1	B	316	GLU
1	B	321	ARG
1	B	357	LEU
1	B	358	LEU
1	B	359	GLU
2	C	69	SER
2	C	71	LEU
3	D	20	ARG
3	D	92	ILE
3	D	127	LEU
3	D	211	THR
3	D	227	LEU
3	D	260	LYS
3	D	262	LEU
3	D	311	ARG
3	D	316	LEU
3	D	322	GLU
3	D	354	LYS
2	E	58[A]	VAL
2	E	58[B]	VAL
2	E	68	GLN
2	E	71	LEU
2	E	129	LYS
3	F	173	LYS
3	F	174[A]	ARG

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Mol	Chain	Res	Type
3	F	174[B]	ARG
3	F	215	THR
3	F	218	GLU
3	F	262	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	60	GLN
1	A	62	HIS
1	A	84	ASN
1	A	91	GLN
1	A	163	GLN
1	A	210	GLN
1	A	244	HIS
1	B	16	GLN
1	B	91	GLN
1	B	163	GLN
1	B	210	GLN
1	B	329	GLN
2	C	21	GLN
2	C	90	ASN
3	D	14	GLN
3	D	50	ASN
3	D	61	GLN
3	D	155	GLN
3	D	235	GLN
3	D	375	HIS
2	E	68	GLN
3	F	54	HIS
3	F	300	GLN
3	F	375	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	1.51	2 (13%)	14,22,24	2.23	6 (42%)
2	0AF	E	57	2	15,16,17	1.60	3 (20%)	14,22,24	2.45	8 (57%)

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	-	1/5/6/8	0/2/2/2
2	0AF	E	57	2	-	0/5/6/8	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	57	0AF	CE3-CD2	3.67	1.45	1.39
2	C	57	0AF	CE2-NE1	-3.25	1.32	1.37
2	E	57	0AF	CE2-NE1	-2.42	1.33	1.37
2	E	57	0AF	CD1-CG	2.28	1.40	1.36
2	C	57	0AF	CD1-NE1	-2.11	1.33	1.37

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	57	0AF	CB-CG-CD1	-4.11	118.95	126.97
2	E	57	0AF	CE3-CD2-CG	3.92	139.70	133.85
2	E	57	0AF	CB-CG-CD1	-3.77	119.62	126.97
2	C	57	0AF	CB-CG-CD2	3.76	133.92	126.70
2	E	57	0AF	CZ3-CH2-CZ2	-3.45	115.79	120.05
2	C	57	0AF	CE3-CD2-CG	3.16	138.57	133.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	57	0AF	CB-CG-CD2	3.09	132.64	126.70
2	E	57	0AF	CH2-CZ2-CE2	2.95	123.79	118.69
2	C	57	0AF	CE2-NE1-CD1	2.92	111.44	108.93
2	C	57	0AF	CE3-CD2-CE2	-2.81	115.98	119.14
2	E	57	0AF	CD2-CE2-NE1	2.31	110.83	107.54
2	E	57	0AF	CG-CD1-NE1	-2.27	107.82	110.31
2	E	57	0AF	CE3-CD2-CE2	-2.25	116.61	119.14
2	C	57	0AF	CG-CD1-NE1	-2.04	108.07	110.31

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	57	0AF	O-C-CA-CB

There are no ring outliers.

2 monomers are involved in 3 short contacts:

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 5 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	HEC	B	402	1,8	46,50,50	2.68	22 (47%)	58,82,82	2.51	22 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	MES	F	401	-	12,12,12	1.63	1 (8%)	15,16,16	2.97	7 (46%)
5	HEC	A	403	1	46,50,50	2.61	20 (43%)	58,82,82	2.62	16 (27%)
5	HEC	B	403	1	46,50,50	2.52	18 (39%)	58,82,82	2.86	25 (43%)
7	MES	D	401	-	12,12,12	2.20	1 (8%)	15,16,16	2.82	8 (53%)
5	HEC	A	402	1	46,50,50	2.68	22 (47%)	58,82,82	2.54	23 (39%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	HEC	B	402	1,8	-	6/14/54/54	-
7	MES	F	401	-	-	6/6/14/14	0/1/1/1
5	HEC	A	403	1	-	6/14/54/54	-
5	HEC	B	403	1	-	6/14/54/54	-
7	MES	D	401	-	-	4/6/14/14	0/1/1/1
5	HEC	A	402	1	-	4/14/54/54	-

All (84) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	401	MES	C8-S	-7.19	1.67	1.77
5	A	402	HEC	CHC-C4B	5.70	1.49	1.38
5	A	402	HEC	CAC-C3C	5.39	1.52	1.35
5	B	402	HEC	CAC-C3C	5.29	1.52	1.35
5	B	403	HEC	CAC-C3C	5.24	1.52	1.35
5	B	403	HEC	CAB-C3B	5.17	1.51	1.35
5	A	403	HEC	CAC-C3C	5.15	1.51	1.35
7	F	401	MES	C8-S	-5.10	1.70	1.77
5	A	403	HEC	CHB-C4A	5.06	1.48	1.38
5	B	402	HEC	CAB-C3B	5.04	1.51	1.35
5	A	403	HEC	CHD-C4C	4.85	1.47	1.38
5	B	403	HEC	CHC-C4B	4.82	1.47	1.38
5	A	402	HEC	C1D-ND	-4.81	1.30	1.39
5	B	403	HEC	C4D-ND	-4.80	1.30	1.39
5	A	403	HEC	CAB-C3B	4.79	1.50	1.35
5	B	402	HEC	CHD-C4C	4.73	1.47	1.38
5	A	403	HEC	C4A-NA	-4.68	1.30	1.39
5	B	403	HEC	CHB-C4A	4.68	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	402	HEC	CHA-C1A	4.58	1.47	1.38
5	A	403	HEC	CHC-C4B	4.55	1.47	1.38
5	A	402	HEC	CAB-C3B	4.41	1.49	1.35
5	A	402	HEC	C1A-NA	-4.40	1.31	1.39
5	A	402	HEC	CHB-C4A	4.36	1.46	1.38
5	B	402	HEC	CHB-C4A	4.28	1.46	1.38
5	B	402	HEC	C1D-ND	-4.27	1.31	1.39
5	B	402	HEC	C1B-NB	-4.26	1.31	1.39
5	B	403	HEC	C4A-NA	-4.09	1.31	1.39
5	B	402	HEC	CHA-C4D	4.02	1.48	1.39
5	B	402	HEC	C4B-NB	-3.99	1.32	1.39
5	A	402	HEC	CHB-C1B	3.99	1.48	1.39
5	B	403	HEC	C1D-ND	-3.98	1.32	1.39
5	A	402	HEC	CHD-C1D	3.94	1.48	1.39
5	A	402	HEC	C4C-NC	-3.91	1.32	1.39
5	B	402	HEC	CHB-C1B	3.87	1.48	1.39
5	B	403	HEC	C1A-NA	-3.84	1.32	1.39
5	A	403	HEC	CHA-C1A	3.81	1.45	1.38
5	A	403	HEC	C4D-ND	-3.81	1.32	1.39
5	A	403	HEC	C4C-NC	-3.79	1.32	1.39
5	A	403	HEC	C1A-NA	-3.77	1.32	1.39
5	B	402	HEC	C1C-NC	-3.75	1.32	1.39
5	A	402	HEC	CHC-C1C	3.69	1.47	1.39
5	B	402	HEC	CHC-C1C	3.69	1.47	1.39
5	A	402	HEC	CHA-C1A	3.68	1.45	1.38
5	B	402	HEC	CHC-C4B	3.66	1.45	1.38
5	A	402	HEC	CHD-C4C	3.64	1.45	1.38
5	A	402	HEC	C1B-NB	-3.62	1.32	1.39
5	A	403	HEC	C1B-NB	-3.61	1.32	1.39
5	B	402	HEC	CHD-C1D	3.60	1.47	1.39
5	B	403	HEC	CHC-C1C	3.57	1.47	1.39
5	B	403	HEC	CHA-C1A	3.57	1.45	1.38
5	A	403	HEC	CHD-C1D	3.55	1.47	1.39
5	A	403	HEC	CHB-C1B	3.44	1.47	1.39
5	A	403	HEC	CHC-C1C	3.41	1.47	1.39
5	A	402	HEC	CHA-C4D	3.39	1.47	1.39
5	B	402	HEC	C4C-NC	-3.37	1.33	1.39
5	B	403	HEC	CHD-C4C	3.35	1.44	1.38
5	A	403	HEC	C4B-NB	-3.34	1.33	1.39
5	B	402	HEC	C4A-NA	-3.27	1.33	1.39
5	B	403	HEC	C4C-NC	-3.24	1.33	1.39
5	A	403	HEC	CHA-C4D	3.22	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	403	HEC	C1B-NB	-3.08	1.33	1.39
5	A	403	HEC	C1C-NC	-3.07	1.33	1.39
5	B	403	HEC	CHA-C4D	2.96	1.46	1.39
5	A	402	HEC	C4D-ND	-2.75	1.34	1.39
5	B	403	HEC	CHD-C1D	2.74	1.45	1.39
5	B	402	HEC	C1B-C2B	2.73	1.49	1.43
5	B	403	HEC	C4B-NB	-2.73	1.34	1.39
5	A	402	HEC	C4A-NA	-2.72	1.34	1.39
5	A	402	HEC	C1C-C2C	2.62	1.49	1.43
5	A	402	HEC	C3C-C4C	2.58	1.50	1.46
5	B	403	HEC	C1C-NC	-2.57	1.34	1.39
5	A	403	HEC	O2D-CGD	-2.54	1.22	1.30
5	A	402	HEC	C1B-C2B	2.53	1.49	1.43
5	A	402	HEC	CBA-CGA	2.52	1.56	1.50
5	B	402	HEC	C4D-ND	-2.39	1.35	1.39
5	A	402	HEC	C1A-C2A	2.37	1.49	1.45
5	A	403	HEC	C1D-ND	-2.32	1.35	1.39
5	B	403	HEC	CHB-C1B	2.22	1.44	1.39
5	B	402	HEC	C1D-C2D	2.20	1.48	1.43
5	B	402	HEC	C1A-C2A	2.15	1.49	1.45
5	A	402	HEC	C1D-C2D	2.13	1.48	1.43
5	A	403	HEC	C1D-C2D	2.11	1.48	1.43
5	B	402	HEC	C4D-C3D	2.06	1.48	1.44
5	B	402	HEC	C3C-C4C	2.04	1.49	1.46

All (101) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	403	HEC	CBB-CAB-C3B	-12.30	102.85	127.43
5	B	403	HEC	CBB-CAB-C3B	-12.28	102.88	127.43
5	A	402	HEC	CBB-CAB-C3B	-10.25	106.94	127.43
5	B	403	HEC	CBC-CAC-C3C	-9.78	107.89	127.43
5	B	402	HEC	CBB-CAB-C3B	-8.61	110.23	127.43
5	A	403	HEC	CBC-CAC-C3C	-8.14	111.17	127.43
5	B	402	HEC	CBC-CAC-C3C	-7.88	111.69	127.43
5	A	402	HEC	CBC-CAC-C3C	-7.85	111.75	127.43
7	F	401	MES	C5-N4-C3	5.87	121.48	108.84
7	D	401	MES	C5-N4-C3	5.59	120.88	108.84
7	F	401	MES	C6-C5-N4	-5.43	101.87	110.12
5	A	402	HEC	CHD-C4C-NC	-5.07	118.93	124.45
7	D	401	MES	C6-C5-N4	-5.03	102.48	110.12
5	A	403	HEC	CBD-CAD-C3D	-5.00	98.71	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	403	HEC	C2A-C1A-NA	4.78	114.94	110.32
5	B	403	HEC	CBD-CAD-C3D	-4.75	99.39	112.53
5	A	403	HEC	C2A-C1A-NA	4.71	114.87	110.32
7	F	401	MES	O2S-S-C8	4.70	113.83	106.73
5	B	402	HEC	C3D-C4D-ND	4.52	115.17	110.15
5	A	402	HEC	C2A-C1A-NA	4.36	114.53	110.32
5	B	402	HEC	C2A-C1A-NA	4.00	114.18	110.32
5	B	402	HEC	CMD-C2D-C3D	3.80	133.68	125.62
5	A	403	HEC	C1D-C2D-C3D	-3.68	102.60	106.82
5	B	403	HEC	CHB-C4A-NA	-3.66	120.47	124.45
7	F	401	MES	O1S-S-C8	3.65	112.24	106.73
5	A	402	HEC	C3D-C4D-ND	3.61	114.15	110.15
5	B	402	HEC	C4D-C3D-C2D	-3.51	101.44	106.87
5	A	403	HEC	CBA-CAA-C2A	-3.40	103.12	112.53
7	D	401	MES	C8-C7-N4	-3.36	99.65	112.36
5	B	403	HEC	CMB-C2B-C3B	3.29	134.30	126.55
5	B	403	HEC	CBA-CAA-C2A	-3.27	103.50	112.53
5	B	402	HEC	CHB-C4A-NA	-3.24	120.93	124.45
5	B	402	HEC	CMB-C2B-C3B	3.24	134.16	126.55
5	A	403	HEC	C1A-C2A-C3A	-3.21	102.88	107.11
7	F	401	MES	C7-N4-C3	3.19	119.73	111.24
7	D	401	MES	C7-N4-C3	3.15	119.64	111.24
5	B	403	HEC	C3D-C4D-ND	3.14	113.63	110.15
5	B	402	HEC	CMD-C2D-C1D	-3.10	120.70	125.42
7	D	401	MES	C7-N4-C5	3.09	119.47	111.24
7	D	401	MES	C2-C3-N4	-2.96	105.62	110.12
5	B	402	HEC	C1A-C2A-C3A	-2.95	103.22	107.11
5	B	403	HEC	O2A-CGA-O1A	-2.92	115.82	123.33
5	B	403	HEC	C1A-C2A-C3A	-2.87	103.33	107.11
5	B	403	HEC	C3A-C4A-NA	2.83	114.88	109.64
7	F	401	MES	C7-N4-C5	2.83	118.78	111.24
5	B	402	HEC	C2B-C1B-NB	2.80	114.63	110.14
5	A	402	HEC	C2D-C1D-ND	2.78	114.60	110.14
5	A	402	HEC	CBA-CAA-C2A	-2.78	104.86	112.53
5	A	403	HEC	C3D-C4D-ND	2.72	113.17	110.15
7	D	401	MES	O2S-S-O1S	-2.72	104.99	113.82
5	A	402	HEC	CBD-CAD-C3D	-2.71	105.05	112.53
5	B	402	HEC	CBA-CAA-C2A	-2.70	105.08	112.53
5	B	402	HEC	C2C-C1C-NC	2.68	114.44	110.14
5	A	402	HEC	C1D-C2D-C3D	-2.68	103.75	106.82
5	A	402	HEC	C2B-C1B-NB	2.62	114.34	110.14
5	A	402	HEC	CHD-C1D-ND	-2.60	119.14	123.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	402	HEC	C3A-C4A-NA	2.60	114.45	109.64
7	D	401	MES	O2S-S-C8	2.59	110.64	106.73
5	B	403	HEC	CHD-C1D-C2D	-2.58	119.94	127.43
5	B	402	HEC	O2A-CGA-CBA	2.57	122.12	114.00
5	B	402	HEC	CMC-C2C-C3C	2.55	132.54	126.55
5	B	402	HEC	C3A-C4A-NA	2.55	114.35	109.64
5	A	402	HEC	CMA-C3A-C4A	2.52	129.17	124.73
5	A	403	HEC	C2B-C1B-NB	2.50	114.14	110.14
5	B	402	HEC	CBD-CAD-C3D	-2.46	105.72	112.53
5	A	402	HEC	C2C-C1C-NC	2.45	114.08	110.14
5	B	403	HEC	CAD-C3D-C4D	2.44	129.71	124.94
5	B	403	HEC	CMB-C2B-C1B	-2.43	121.72	125.42
5	B	402	HEC	CAA-C2A-C1A	2.42	129.78	124.85
5	B	403	HEC	CHC-C1C-C2C	-2.42	120.40	127.43
5	B	403	HEC	O2A-CGA-CBA	2.37	121.50	114.00
5	A	402	HEC	C4A-C3A-C2A	-2.36	103.47	106.97
5	A	402	HEC	C4D-C3D-C2D	-2.36	103.22	106.87
5	B	402	HEC	CHC-C4B-NB	-2.35	121.90	124.45
5	A	402	HEC	O1D-CGD-CBD	-2.34	115.69	123.09
5	B	403	HEC	C2C-C1C-NC	2.33	113.88	110.14
5	B	402	HEC	C2D-C1D-ND	2.32	113.86	110.14
5	A	402	HEC	CHA-C1A-NA	-2.32	121.93	124.45
5	B	403	HEC	C2B-C1B-NB	2.31	113.85	110.14
5	B	403	HEC	C2D-C1D-ND	2.30	113.82	110.14
5	A	403	HEC	O2A-CGA-CBA	2.29	121.25	114.00
5	A	402	HEC	CMD-C2D-C1D	2.28	128.90	125.42
5	A	403	HEC	CHB-C4A-NA	-2.26	122.00	124.45
5	A	403	HEC	CMC-C2C-C3C	2.25	131.85	126.55
5	A	402	HEC	C1A-C2A-C3A	-2.25	104.14	107.11
5	A	402	HEC	CHB-C4A-NA	-2.24	122.01	124.45
5	B	403	HEC	C4A-C3A-C2A	-2.22	103.67	106.97
5	A	402	HEC	CAA-C2A-C1A	2.21	129.34	124.85
5	A	403	HEC	O1A-CGA-CBA	-2.19	116.15	123.09
5	B	403	HEC	C4D-C3D-C2D	-2.17	103.51	106.87
7	F	401	MES	O2S-S-O1S	-2.17	106.77	113.82
5	B	403	HEC	CHA-C1A-NA	-2.16	122.10	124.45
5	A	403	HEC	C3A-C4A-NA	2.15	113.62	109.64
5	B	402	HEC	CHA-C1A-NA	-2.13	122.14	124.45
5	B	403	HEC	C1D-C2D-C3D	-2.13	104.38	106.82
5	B	403	HEC	CHD-C4C-C3C	-2.12	121.64	125.21
5	A	402	HEC	O2D-CGD-CBD	2.11	120.68	114.00
5	B	403	HEC	CHB-C1B-C2B	-2.11	121.31	127.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	403	HEC	C2C-C1C-NC	2.07	113.46	110.14
5	A	403	HEC	CAA-C2A-C3A	2.02	131.64	127.87
5	B	402	HEC	C4A-NA-C1A	-2.01	102.55	105.82

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	402	HEC	C2C-C3C-CAC-CBC
5	A	402	HEC	C4C-C3C-CAC-CBC
5	A	403	HEC	C2B-C3B-CAB-CBB
5	A	403	HEC	C4B-C3B-CAB-CBB
5	A	403	HEC	C2C-C3C-CAC-CBC
5	A	403	HEC	C4C-C3C-CAC-CBC
5	B	402	HEC	C2B-C3B-CAB-CBB
5	B	402	HEC	C4B-C3B-CAB-CBB
5	B	402	HEC	C2C-C3C-CAC-CBC
5	B	403	HEC	C2B-C3B-CAB-CBB
5	B	403	HEC	C4B-C3B-CAB-CBB
5	B	403	HEC	C2C-C3C-CAC-CBC
5	B	403	HEC	C4C-C3C-CAC-CBC
7	D	401	MES	C7-C8-S-O1S
7	D	401	MES	C7-C8-S-O3S
7	F	401	MES	C8-C7-N4-C3
7	F	401	MES	C7-C8-S-O1S
7	F	401	MES	C7-C8-S-O3S
7	D	401	MES	C8-C7-N4-C3
7	D	401	MES	C7-C8-S-O2S
7	F	401	MES	C7-C8-S-O2S
7	F	401	MES	N4-C7-C8-S
5	B	402	HEC	C4C-C3C-CAC-CBC
5	A	402	HEC	C2B-C3B-CAB-CBB
7	F	401	MES	C8-C7-N4-C5
5	B	403	HEC	CAD-CBD-CGD-O2D
5	B	402	HEC	CAA-CBA-CGA-O2A
5	B	403	HEC	CAD-CBD-CGD-O1D
5	A	403	HEC	CAD-CBD-CGD-O2D
5	B	402	HEC	CAA-CBA-CGA-O1A
5	A	402	HEC	C4B-C3B-CAB-CBB
5	A	403	HEC	CAD-CBD-CGD-O1D

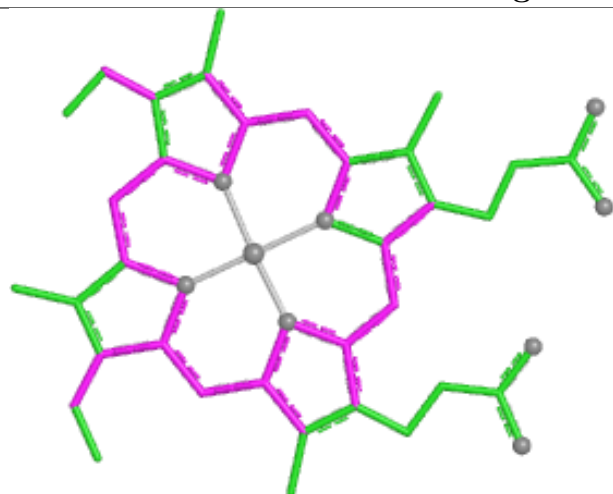
There are no ring outliers.

2 monomers are involved in 4 short contacts:

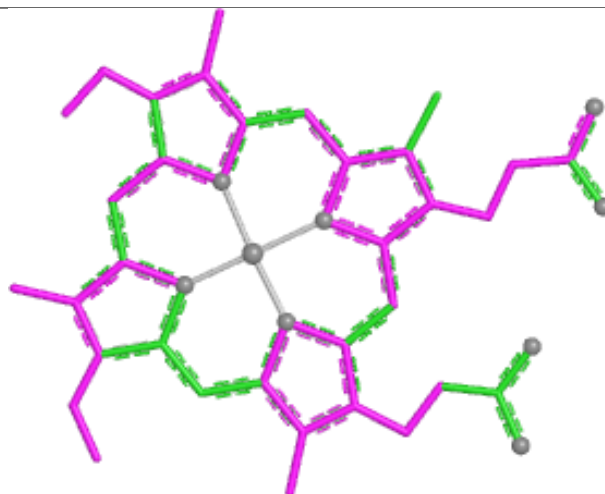
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	402	HEC	2	0
5	A	402	HEC	2	0

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.

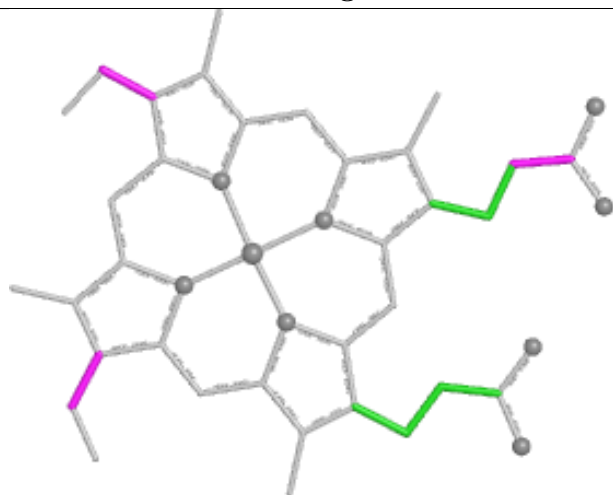
Ligand HEC B 402



Bond lengths



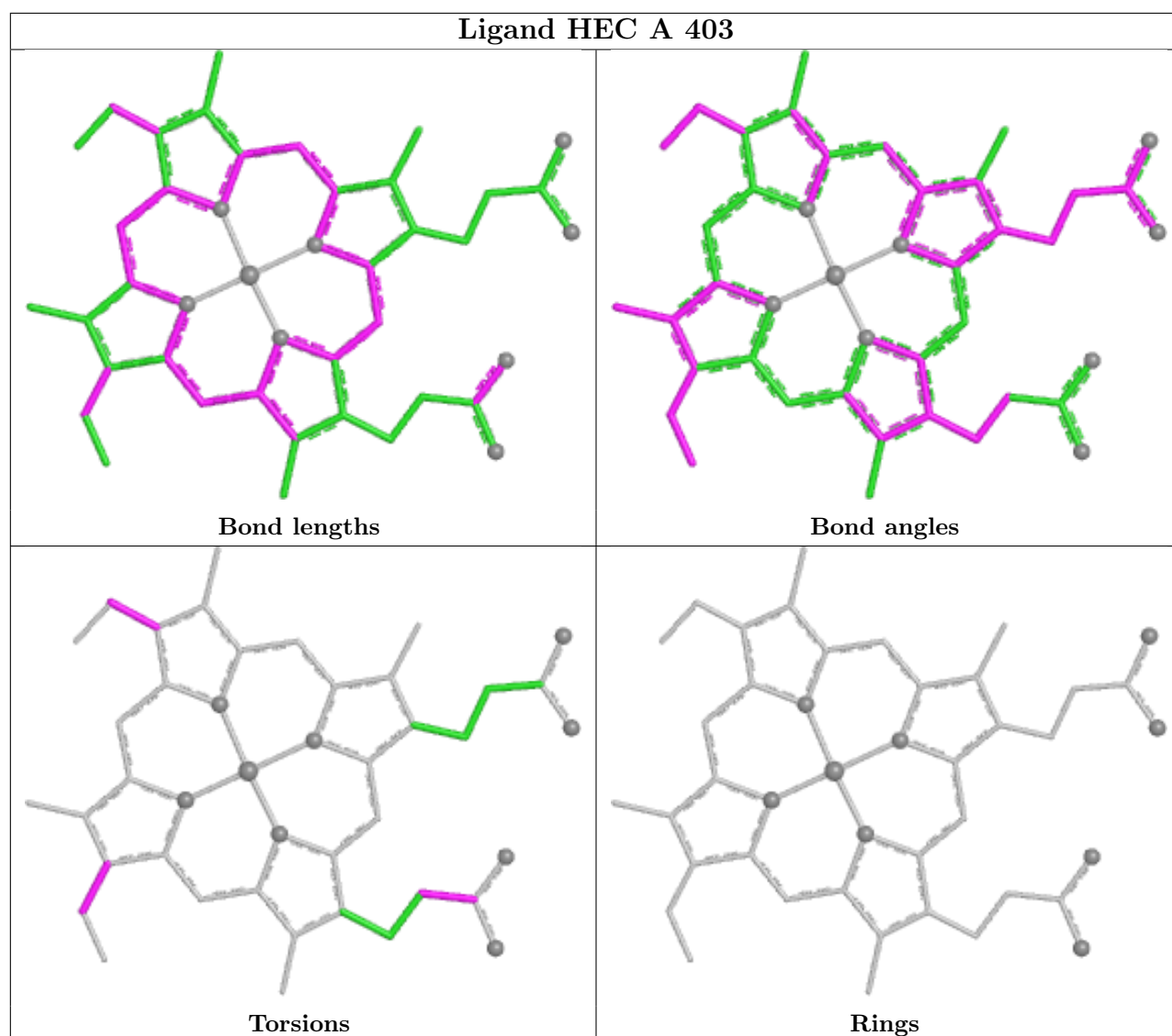
Bond angles



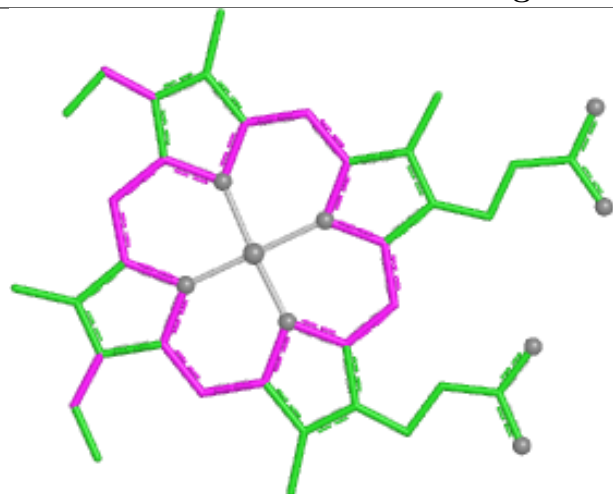
Torsions



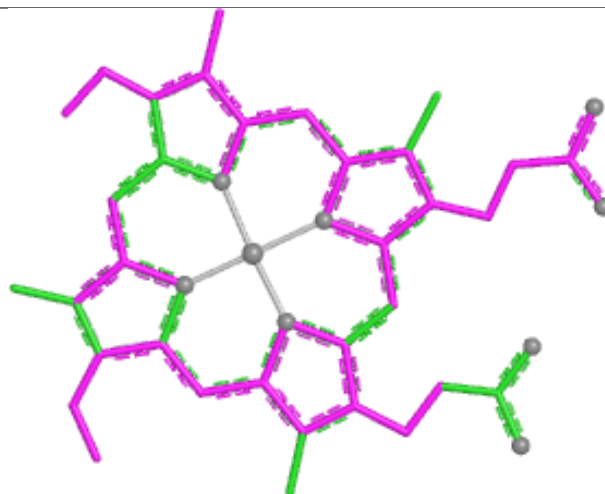
Rings



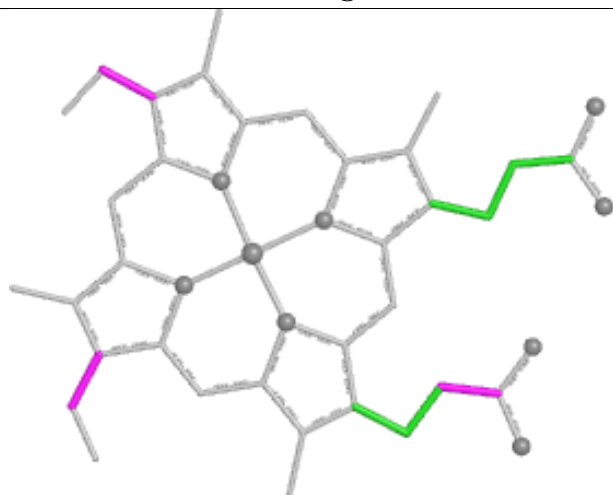
Ligand HEC B 403



Bond lengths



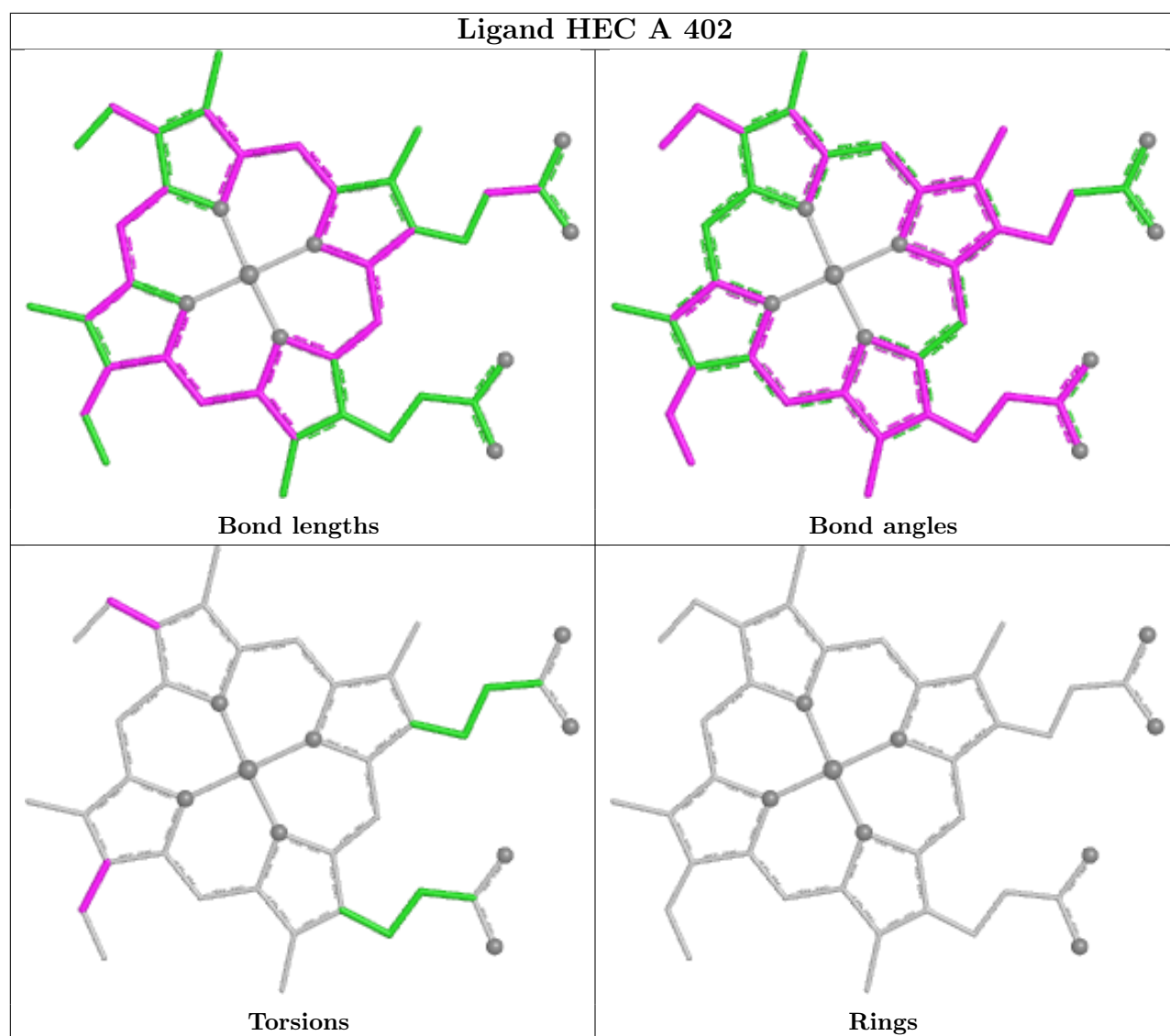
Bond angles



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%)	-0.10	0 100 100	25, 52, 73, 83	2 (0%)
1	B	357/373 (95%)	-0.42	1 (0%) 90 91	17, 40, 60, 83	1 (0%)
2	C	124/137 (90%)	-0.06	2 (1%) 70 74	31, 47, 70, 92	1 (0%)
2	E	124/137 (90%)	-0.46	1 (0%) 82 84	19, 35, 50, 72	4 (3%)
3	D	376/385 (97%)	-0.06	0 100 100	31, 54, 83, 91	2 (0%)
3	F	376/385 (97%)	-0.52	1 (0%) 90 91	18, 36, 56, 74	4 (1%)
All	All	1711/1790 (95%)	-0.27	5 (0%) 90 91	17, 44, 74, 92	14 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	131	SER	4.1
1	B	6	ALA	2.9
2	E	131	SER	2.3
3	F	207	GLY	2.3
2	C	130	ALA	2.1

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	0.91	0.12	53,67,69,70	0
2	0AF	E	57	15/16	0.92	0.11	36,52,56,57	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

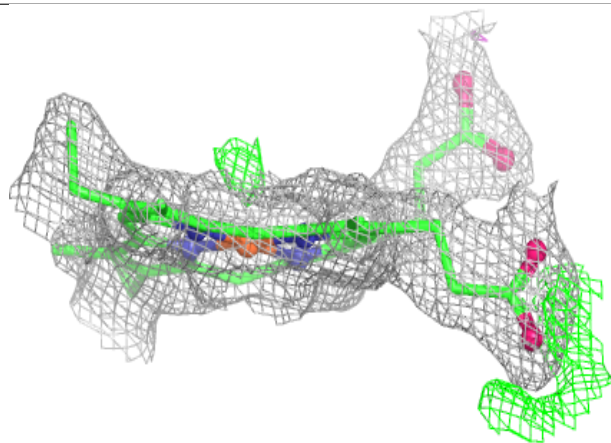
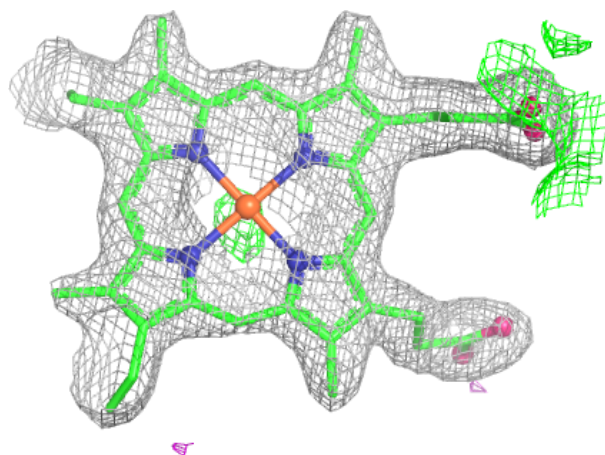
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	NA	A	404	1/1	0.84	0.10	60,60,60,60	0
7	MES	F	401	12/12	0.87	0.16	45,58,61,61	12
7	MES	D	401	12/12	0.89	0.19	34,48,51,52	12
6	NA	B	405	1/1	0.91	0.07	48,48,48,48	0
6	NA	B	404	1/1	0.94	0.05	44,44,44,44	0
5	HEC	A	402	43/43	0.97	0.08	31,41,44,45	0
5	HEC	B	402	43/43	0.98	0.05	27,34,39,40	0
5	HEC	A	403	43/43	0.98	0.06	37,41,44,48	0
5	HEC	B	403	43/43	0.99	0.05	20,25,29,33	0
4	CA	B	401	1/1	0.99	0.03	31,31,31,31	0
4	CA	A	401	1/1	0.99	0.03	43,43,43,43	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.

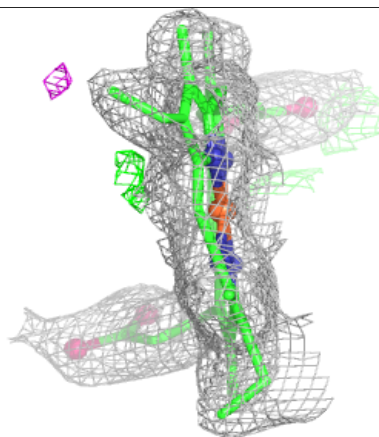
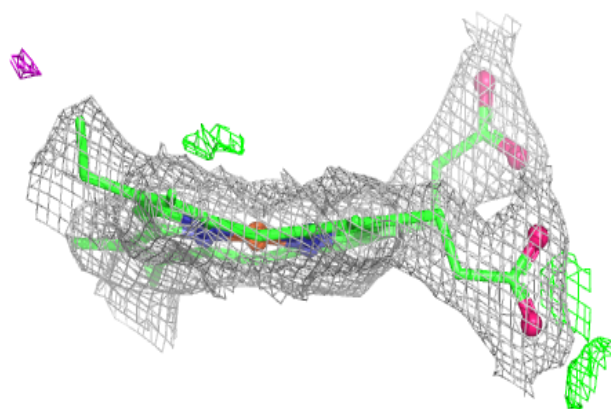
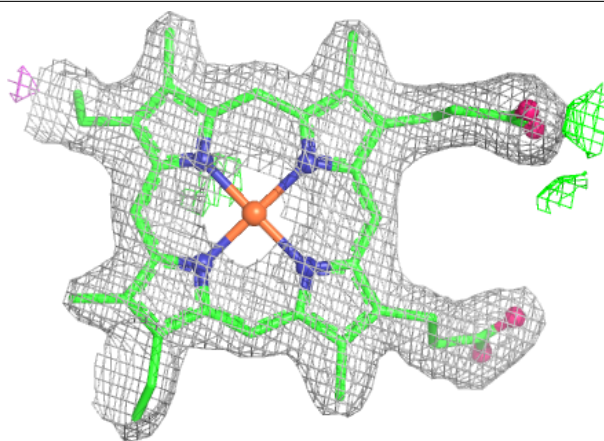
Electron density around HEC A 402:

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



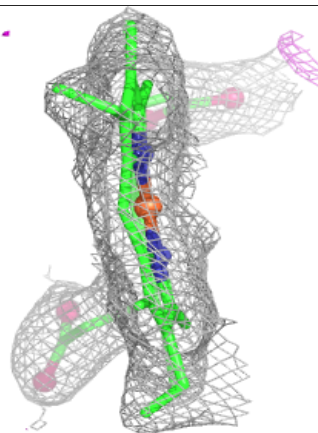
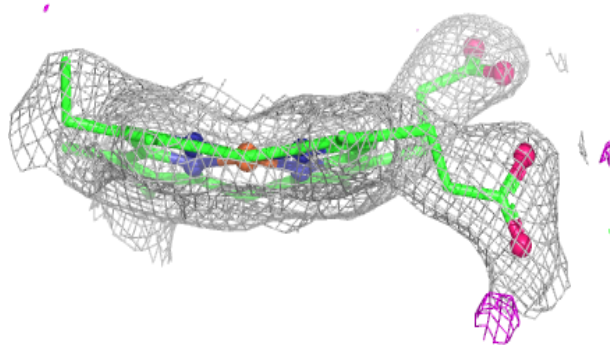
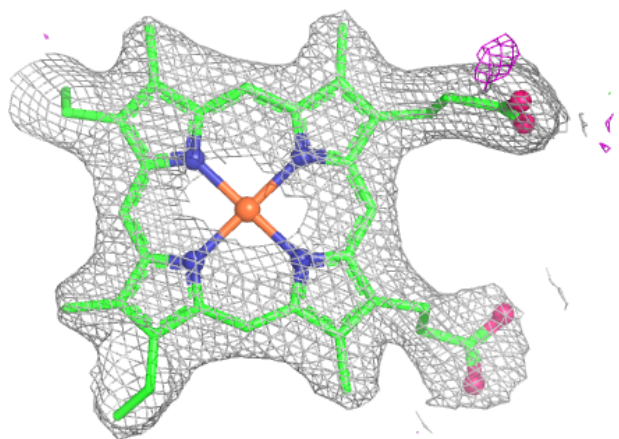
Electron density around HEC B 402:

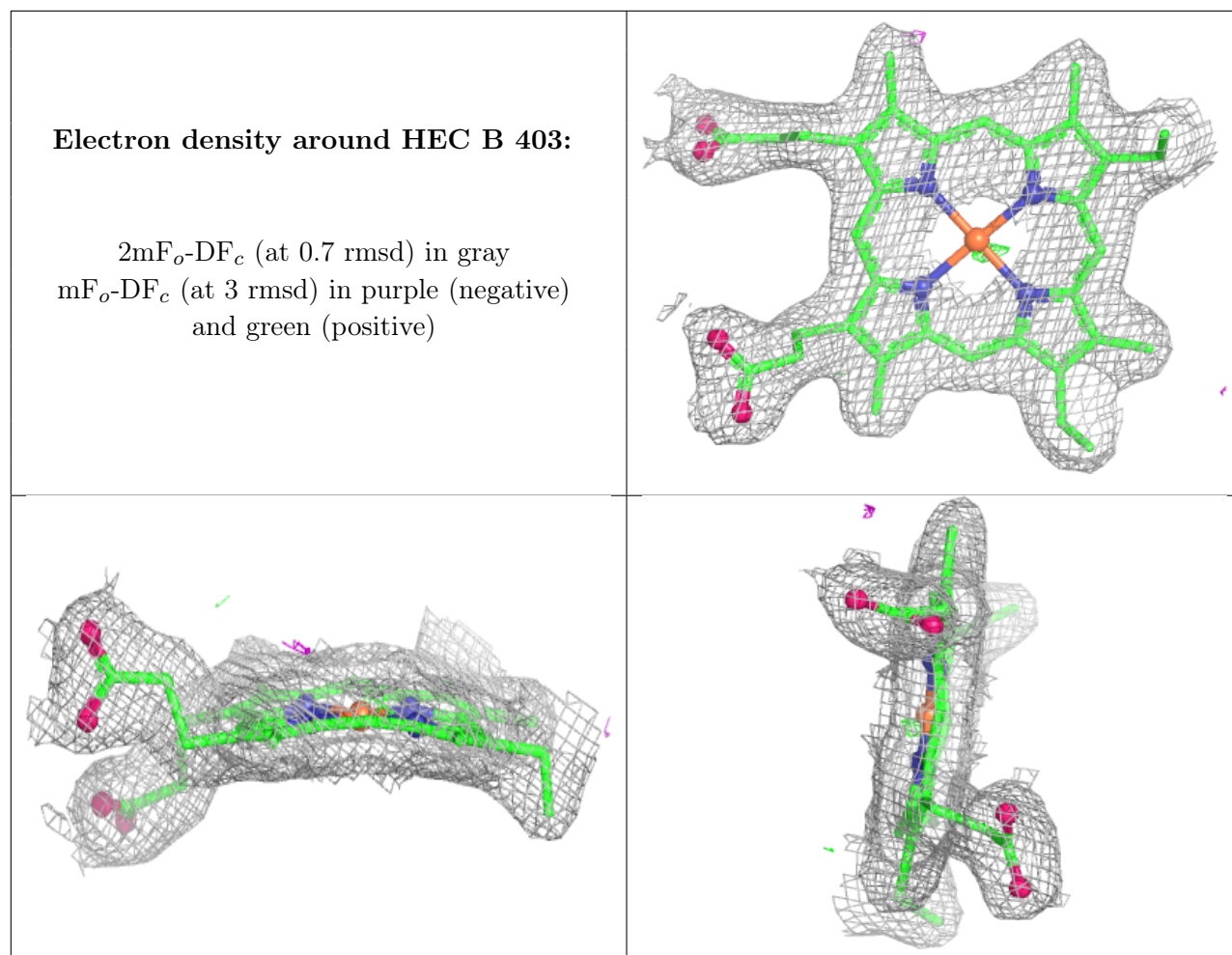
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC A 403:

$2mF_o-DF_c$ (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.