



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 03:39 PM EDT

PDB ID : 3SLE / pdb_00003sle
Title : Crystal Structure of the P107C-MauG/pre-Methylamine Dehydrogenase Complex
Authors : Yukl, E.T.; Wilmot, C.M.
Deposited on : 2011-06-24
Resolution : 2.52 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (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

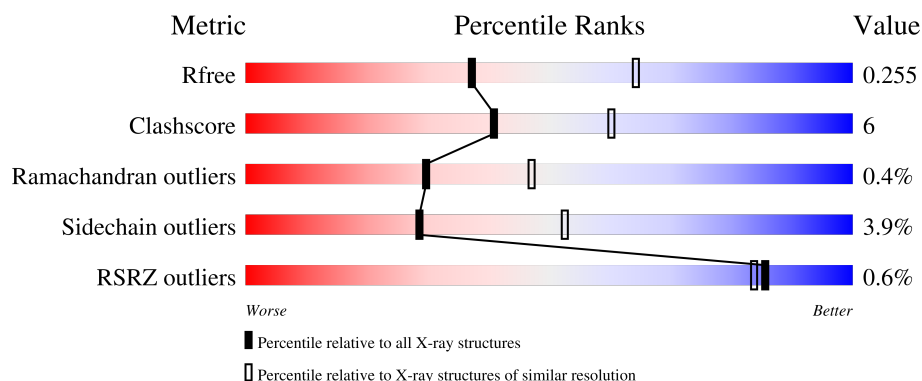
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.52 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	7383 (2.54-2.50)
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (2.54-2.50)

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	82% 12% • 5%
1	B	373	81% 13% • 5%
2	C	137	3% 80% 13% •• 6%
2	E	137	72% 17% •• 9%
3	D	385	75% 22% ••

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Mol	Chain	Length	Quality of chain
3	F	385	 83% 14%

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
2	0AF	C	57	-	-	X	-
2	0AF	E	57	-	-	X	-
5	HEC	A	402	X	-	-	-
5	HEC	A	403	X	-	-	-
5	HEC	B	402	X	-	-	-
5	HEC	B	404	X	-	-	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 13939 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	1	0
			2744	1710	492	530	12			
1	B	355	Total	C	N	O	S	0	5	0
			2788	1736	500	540	12			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	CSD	PRO	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	107	CSD	PRO	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
2	C	129	Total	C	N	O	S	0	0	0
			994	614	173	194	13			
2	E	125	Total	C	N	O	S	0	4	0
			972	601	162	193	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

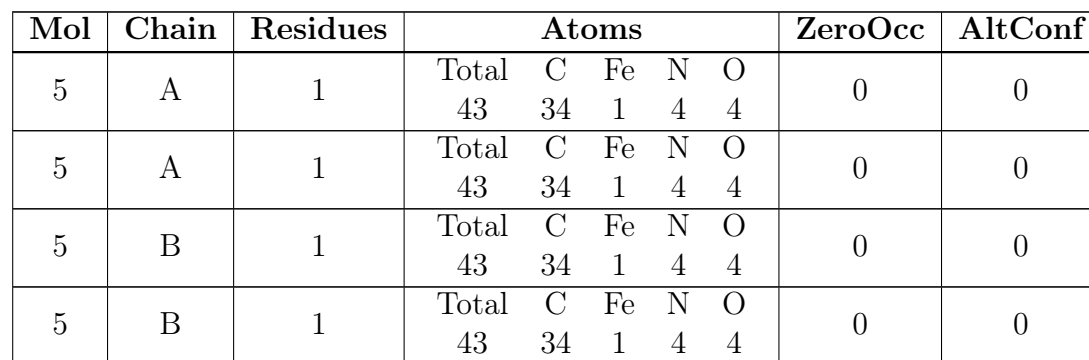
- Molecule 3 is a protein called Methylamine dehydrogenase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	376	Total	C	N	O	S	0	1	0
			2929	1857	502	562	8			
3	F	376	Total	C	N	O	S	0	1	0
			2926	1855	502	560	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		

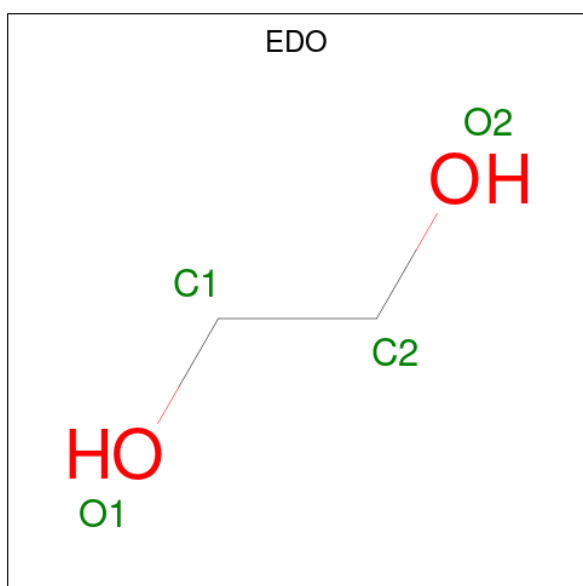
- Molecule 5 is HEME C (CCD ID: HEC) (formula: C₃₄H₃₆FeN₄O₄).



- ACT
- CH₃ C OXT O⁻ O
-
- Chemical structure diagram showing a carboxylate group. The central carbon atom (C) is bonded to a methyl group (CH₃), a carbonyl oxygen (O), and a carboxylate oxygen (OXT) which carries a negative charge (O⁻). A small oxygen atom (O) is also shown below the carbonyl oxygen.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	F	1	Total C O 4 2 2	0	0
6	F	1	Total C O 4 2 2	0	0

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



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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	66	Total O 66 66	0	0
8	B	105	Total O 105 105	0	0
8	C	18	Total O 18 18	0	0
8	D	52	Total O 52 52	0	0

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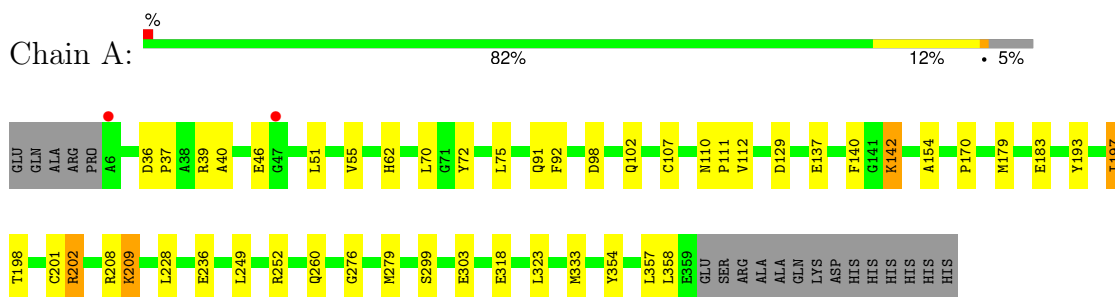
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	E	30	Total 30	O 30	0	0
8	F	117	Total 117	O 117	0	0

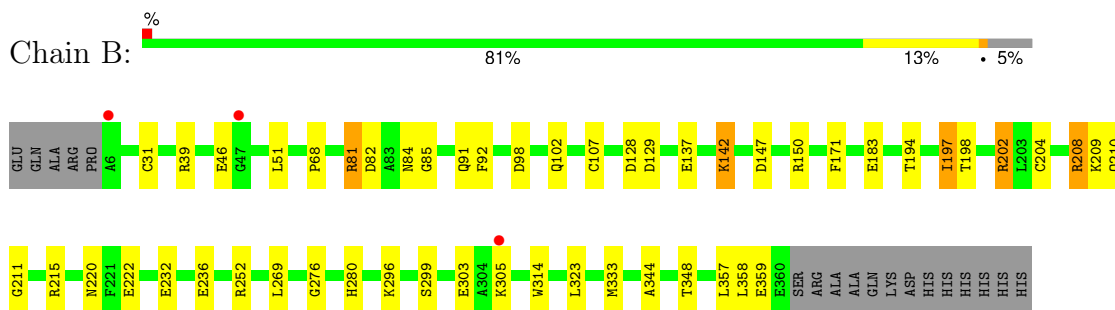
3 Residue-property plots [i](#)

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.

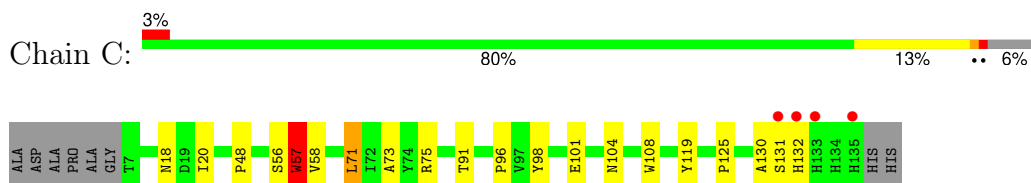
- Molecule 1: Methylamine utilization protein MauG



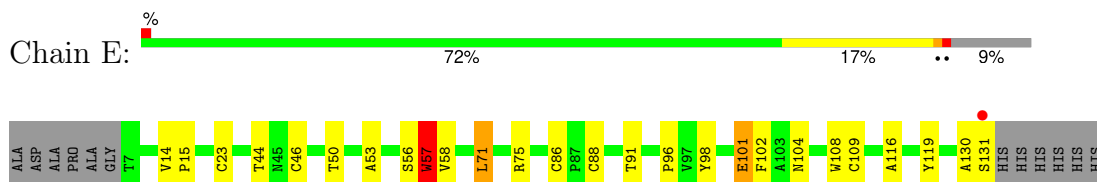
- Molecule 1: Methylamine utilization protein MauG



- Molecule 2: Methylamine dehydrogenase light chain



- Molecule 2: Methylamine dehydrogenase light chain



- Molecule 3: Methylamine dehydrogenase heavy chain

H306	G163	ASP
G310	R174	ALA
G321	V178	GLU
E322	F179	ALA
R323	D180	GLU
G331	C181	THR
G335	Y182	GLN
L336	H183	ALA
K343	D190	Q11
Y347	T191	A41
A348	F192	P42
L349	C193	V47
K354	M194	D51
L355	H195	H54
L356	C196	F55
Y357	A202	Q61
E362	K203	G78
E366	G207	F79
P377	T208	L80
L380	I214	P81
L381	T215	N82
L382	P222	P83
A383	E225	I92
D384	F226	A93
K385	L227	H94
G386	S234	A95
	A237	S96
	V242	T97
	K248	S100
	S255	R101
	Q283	I102
	Q284	Y110
	R289	V111
	Y295	E112
	L296	V113
	L297	A123
		L127
		P128
		P131
		L151
		L152
		F153
		A159
		P160

Chain F: 83% 14% .

ASP	E218	ALA	F226	GLU	L227	ALA	L228	GLU	K229	THR	H230	ALA	A237	Q11	Q16	A19	G29	Q30	E33	N50	D51	Q60	Q61	M74	I76	N82	I102	V117	T118	L119	T122	T142	A159	K173	Y182	A188	P189	C196	R197	G207	T208	T215
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.85Å 88.53Å 107.70Å 116.21° 91.83° 99.35°	Depositor
Resolution (Å)	47.86 – 2.52 47.86 – 2.52	Depositor EDS
% Data completeness (in resolution range)	96.9 (47.86-2.52) 96.9 (47.86-2.52)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.174 , 0.243 0.187 , 0.255	Depositor DCC
R_{free} test set	2992 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	43.3	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.0	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	0.95	EDS
Total number of atoms	13939	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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: CA, OAF, HEC, CSD, ACT, EDO

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	0.81	0/2799	1.01	3/3797 (0.1%)
1	B	0.92	0/2846	1.04	7/3858 (0.2%)
2	C	0.81	0/1007	1.00	1/1375 (0.1%)
2	E	0.94	0/990	1.03	5/1352 (0.4%)
3	D	0.87	0/3009	1.03	7/4100 (0.2%)
3	F	0.99	1/3006 (0.0%)	1.07	4/4096 (0.1%)
All	All	0.90	1/13657 (0.0%)	1.03	27/18578 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	2
2	E	0	3
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	228	ILE	CA-CB	5.22	1.59	1.54

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	242	TRP	CA-C-N	-7.72	111.95	120.14
3	F	242	TRP	C-N-CA	-7.72	111.95	120.14
3	D	51	ASP	CA-C-N	6.08	125.76	119.56
3	D	51	ASP	C-N-CA	6.08	125.76	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	129	ASP	CA-C-N	6.03	125.74	119.05

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	56	SER	Peptide
2	C	57	0AF	Mainchain
2	E	56	SER	Peptide,Mainchain
2	E	57	0AF	Mainchain

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	2744	0	2612	27	0
1	B	2788	0	2653	31	0
2	C	994	0	887	20	0
2	E	972	0	878	25	0
3	D	2929	0	2814	49	0
3	F	2926	0	2812	29	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	86	0	60	4	0
5	B	86	0	61	13	0
6	B	4	0	3	0	0
6	D	4	0	3	0	0
6	F	8	0	6	0	0
7	B	4	0	6	0	0
7	D	4	0	6	1	0
8	A	66	0	0	3	0
8	B	105	0	0	2	0
8	C	18	0	0	0	0
8	D	52	0	0	1	0
8	E	30	0	0	1	0
8	F	117	0	0	2	0
All	All	13939	0	12801	169	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 169 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)
2:C:57:0AF:HE3	2:C:108:TRP:CD1	1.30	1.66
2:E:57:0AF:HE3	2:E:108:TRP:CD1	1.20	1.63
2:E:57:0AF:CE3	2:E:108:TRP:CD1	1.98	1.47
1:B:204:CYS:SG	5:B:404:HEC:CAC	2.03	1.47
2:C:57:0AF:CE3	2:C:108:TRP:CD1	2.05	1.39

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	352/373 (94%)	342 (97%)	10 (3%)	0	100	100
1	B	357/373 (96%)	346 (97%)	11 (3%)	0	100	100
2	C	126/137 (92%)	123 (98%)	3 (2%)	0	100	100
2	E	126/137 (92%)	120 (95%)	6 (5%)	0	100	100
3	D	375/385 (97%)	354 (94%)	16 (4%)	5 (1%)	9	17
3	F	375/385 (97%)	357 (95%)	16 (4%)	2 (0%)	24	41
All	All	1711/1790 (96%)	1642 (96%)	62 (4%)	7 (0%)	30	47

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	209	GLU
3	F	218	GLU
3	D	102	ILE

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Mol	Chain	Res	Type
3	D	180	ASP
3	D	283	GLN

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	276/291 (95%)	261 (95%)	15 (5%)	20	39
1	B	281/291 (97%)	264 (94%)	17 (6%)	17	34
2	C	108/112 (96%)	104 (96%)	4 (4%)	30	54
2	E	108/112 (96%)	104 (96%)	4 (4%)	30	54
3	D	305/310 (98%)	298 (98%)	7 (2%)	44	70
3	F	305/310 (98%)	295 (97%)	10 (3%)	33	58
All	All	1383/1426 (97%)	1326 (96%)	57 (4%)	28	50

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	303	GLU
3	F	262	LEU
2	C	132	HIS
3	F	260	LYS
3	F	33	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	235	GLN
3	F	331	HIS
1	B	210	GLN
2	C	132	HIS
3	D	235	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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
1	CSD	B	107	5,1	4,7,8	2.19	1 (25%)	1,8,10	4.05	1 (100%)
2	0AF	E	57	2	15,16,17	1.33	3 (20%)	14,22,24	1.43	3 (21%)
2	0AF	C	57	2	15,16,17	1.38	3 (20%)	14,22,24	1.47	2 (14%)
1	CSD	A	107	5,1	4,7,8	1.68	1 (25%)	1,8,10	2.97	1 (100%)

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
1	CSD	B	107	5,1	-	2/2/6/8	-
2	0AF	E	57	2	-	0/5/6/8	0/2/2/2
2	0AF	C	57	2	-	0/5/6/8	0/2/2/2
1	CSD	A	107	5,1	-	2/2/6/8	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	107	CSD	OD1-SG	-3.79	1.44	1.47
2	C	57	0AF	CD2-CE2	-2.98	1.37	1.41
1	A	107	CSD	OD1-SG	-2.75	1.45	1.47
2	E	57	0AF	CE2-NE1	-2.55	1.33	1.37
2	E	57	0AF	CD2-CE2	-2.31	1.38	1.41

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	107	CSD	OD1-SG-CB	4.05	113.06	105.60
1	A	107	CSD	OD1-SG-CB	2.97	111.07	105.60
2	C	57	0AF	CZ3-CH2-CZ2	-2.94	116.42	120.05
2	E	57	0AF	CZ3-CH2-CZ2	-2.74	116.67	120.05
2	C	57	0AF	CB-CG-CD2	2.39	131.29	126.70

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	107	CSD	N-CA-CB-SG
1	A	107	CSD	CA-CB-SG-OD1
1	B	107	CSD	N-CA-CB-SG
1	B	107	CSD	CA-CB-SG-OD1

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	57	0AF	7	0
2	C	57	0AF	8	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	404	1	50,50,50	1.60	5 (10%)	68,82,82	1.49	11 (16%)
7	EDO	B	405	-	3,3,3	0.70	0	2,2,2	0.10	0
5	HEC	A	403	1	50,50,50	1.62	4 (8%)	68,82,82	1.16	4 (5%)
6	ACT	D	401	-	3,3,3	0.89	0	3,3,3	1.34	0
6	ACT	F	401	-	3,3,3	0.78	0	3,3,3	1.81	2 (66%)
7	EDO	D	402	-	3,3,3	0.54	0	2,2,2	0.08	0
5	HEC	B	402	1	50,50,50	1.76	6 (12%)	68,82,82	1.31	10 (14%)
6	ACT	B	403	-	3,3,3	0.81	0	3,3,3	1.45	0
6	ACT	F	402	-	3,3,3	0.82	0	3,3,3	1.66	2 (66%)
5	HEC	A	402	1	50,50,50	1.77	9 (18%)	68,82,82	1.34	7 (10%)

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	404	1	1/1/3/7	4/14/54/54	-
7	EDO	B	405	-	-	1/1/1/1	-
5	HEC	A	403	1	1/1/3/7	4/14/54/54	-
7	EDO	D	402	-	-	1/1/1/1	-
5	HEC	B	402	1	1/1/3/7	2/14/54/54	-
5	HEC	A	402	1	1/1/3/7	5/14/54/54	-

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	402	HEC	C3D-C2D	7.81	1.53	1.36
5	A	402	HEC	C3D-C2D	7.46	1.52	1.36
5	B	404	HEC	C3D-C2D	7.13	1.52	1.36
5	A	403	HEC	C3D-C2D	7.11	1.52	1.36
5	A	402	HEC	FE-NC	4.30	2.09	1.95

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	403	HEC	C1D-ND-C4D	5.07	111.22	105.21
5	A	402	HEC	C1D-ND-C4D	4.56	110.61	105.21
5	B	404	HEC	CBD-CAD-C3D	-4.43	100.28	112.53
5	B	404	HEC	CMD-C2D-C1D	4.33	131.80	125.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	403	HEC	CBD-CAD-C3D	-3.90	101.76	112.53

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	402	HEC	NA
5	A	403	HEC	NA
5	B	402	HEC	NA
5	B	404	HEC	NA

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	403	HEC	C2C-C3C-CAC-CBC
5	A	403	HEC	C4C-C3C-CAC-CBC
5	B	404	HEC	C2C-C3C-CAC-CBC
5	B	404	HEC	C4C-C3C-CAC-CBC
5	A	402	HEC	C2C-C3C-CAC-CBC

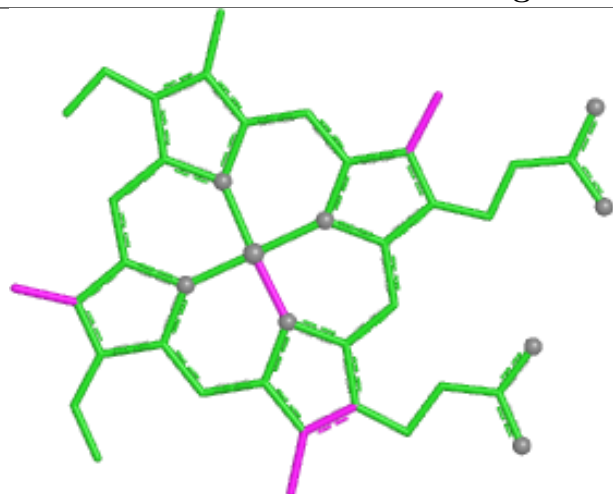
There are no ring outliers.

5 monomers are involved in 18 short contacts:

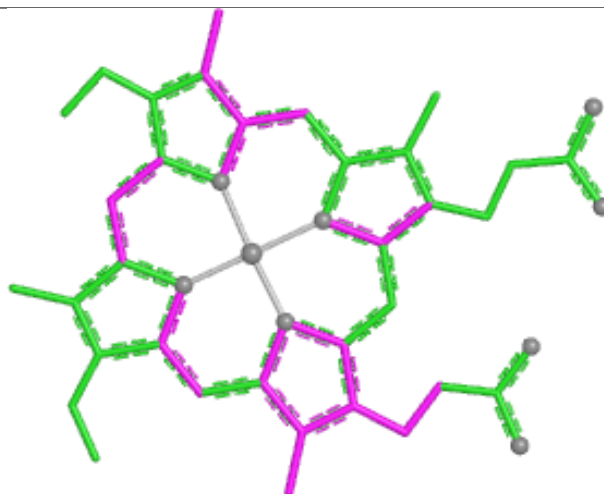
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	404	HEC	10	0
5	A	403	HEC	3	0
7	D	402	EDO	1	0
5	B	402	HEC	3	0
5	A	402	HEC	1	0

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 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.

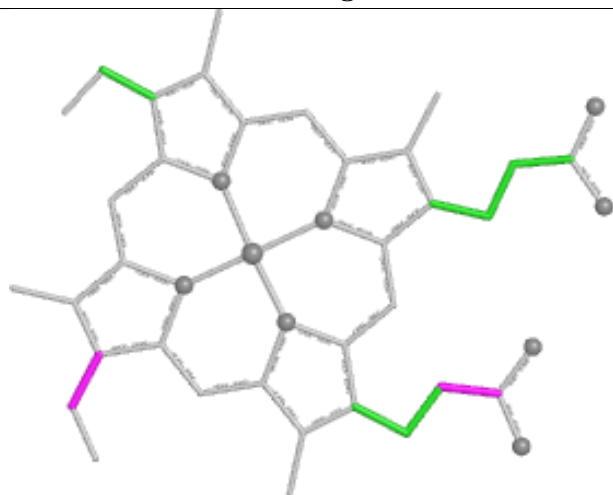
Ligand HEC B 404



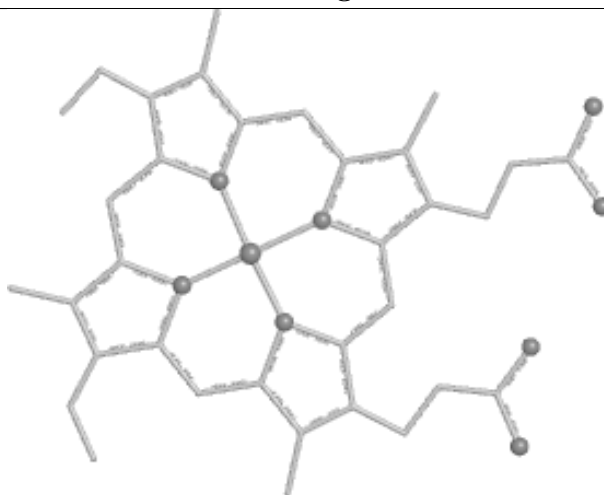
Bond lengths



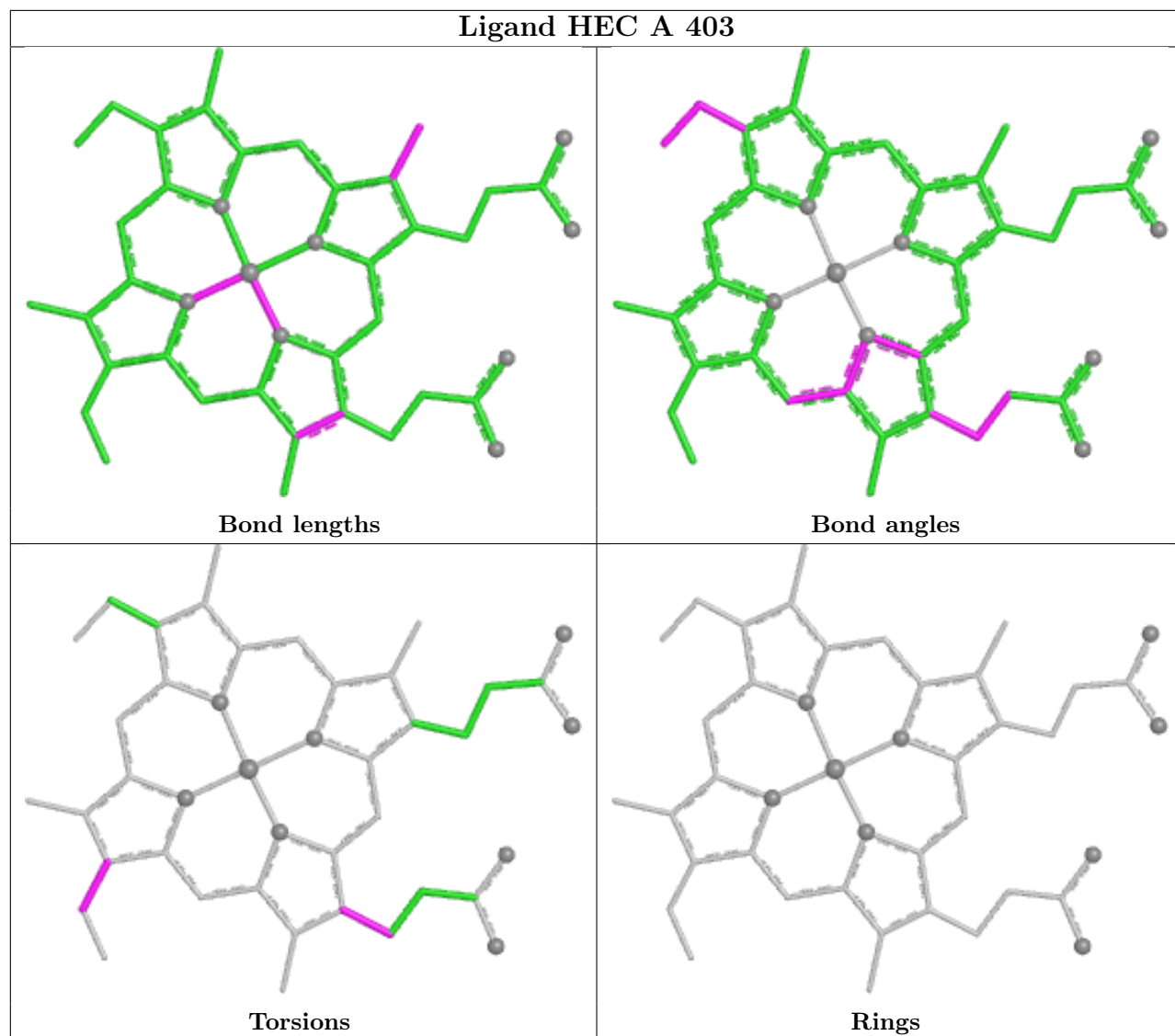
Bond angles



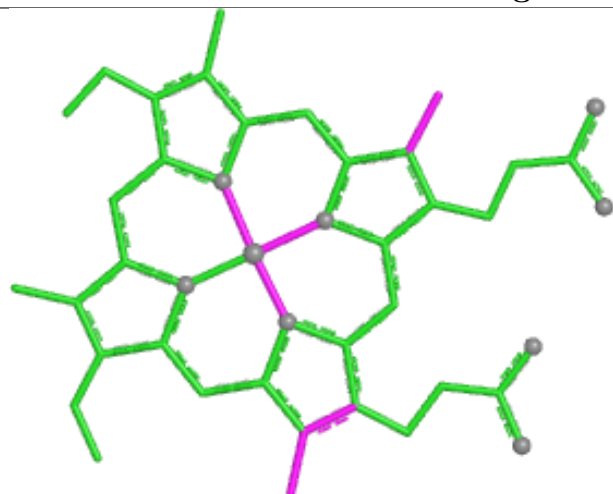
Torsions



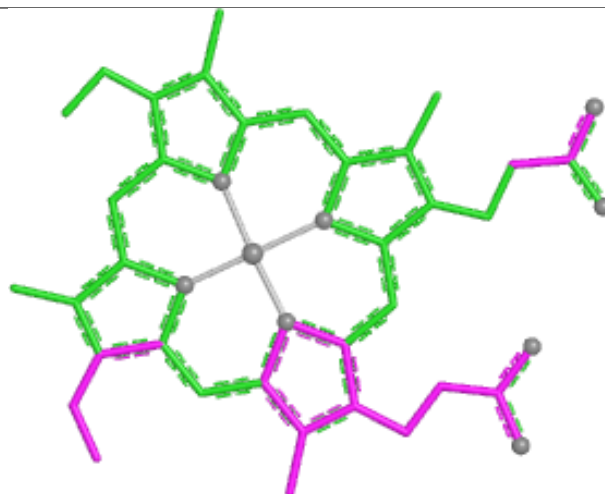
Rings



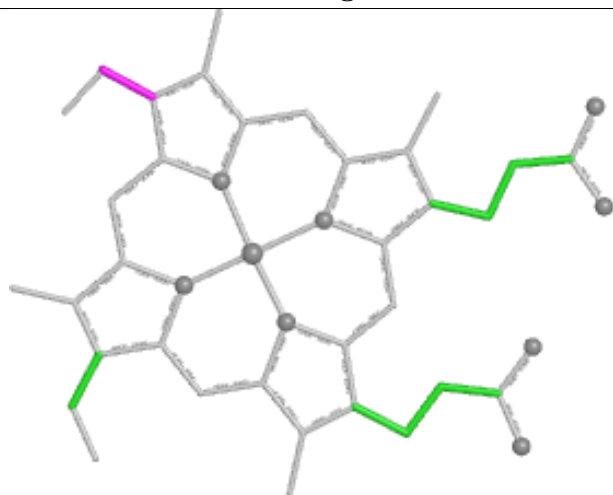
Ligand HEC B 402



Bond lengths



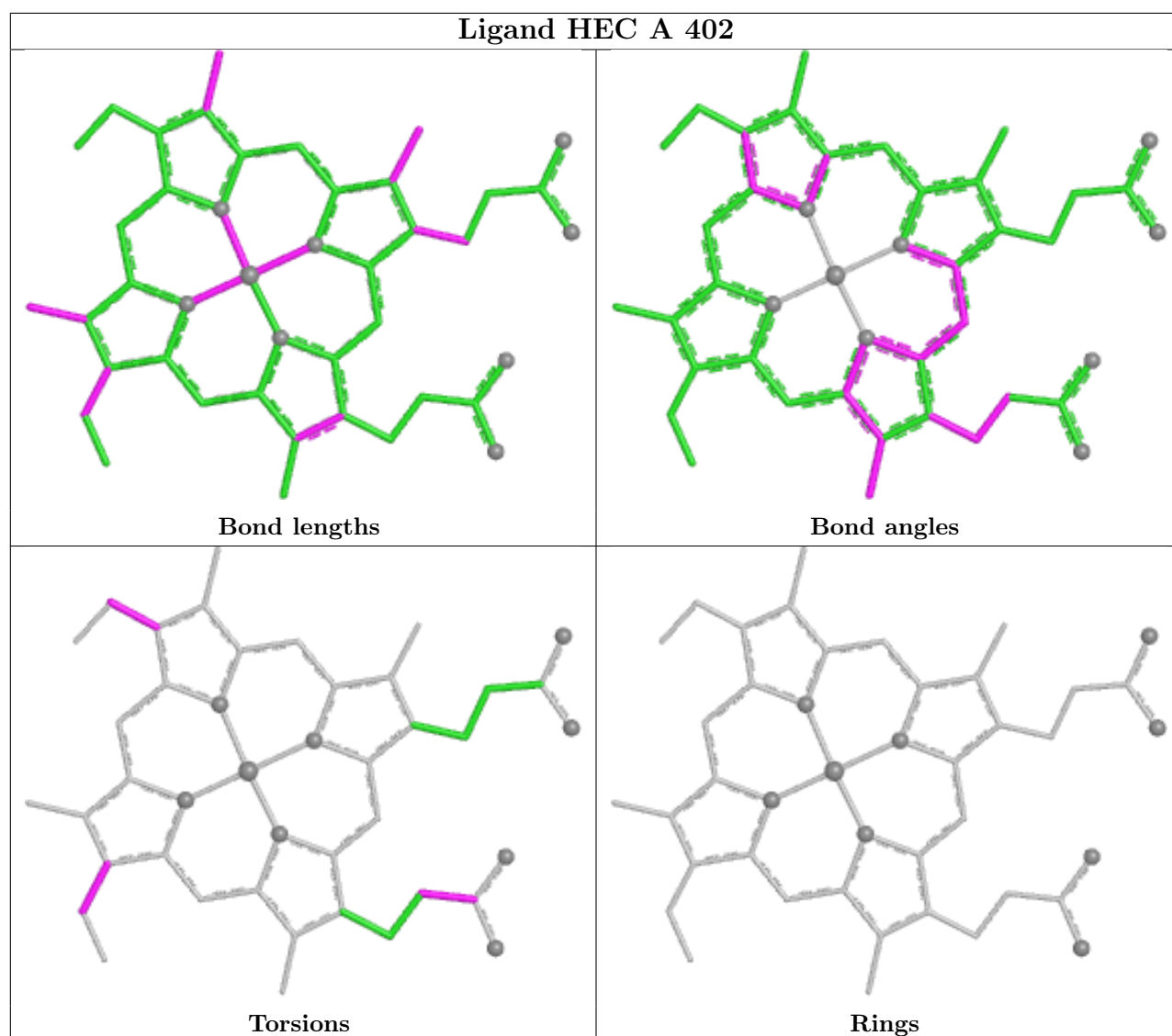
Bond angles



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	353/373 (94%)	-0.12	2 (0%) 85 84	24, 53, 80, 96	1 (0%)
1	B	354/373 (94%)	-0.21	3 (0%) 82 80	20, 48, 79, 96	5 (1%)
2	C	128/137 (93%)	-0.03	4 (3%) 51 48	37, 53, 87, 115	1 (0%)
2	E	124/137 (90%)	-0.26	1 (0%) 82 80	18, 43, 65, 85	4 (3%)
3	D	376/385 (97%)	-0.11	0 100 100	34, 61, 85, 98	1 (0%)
3	F	376/385 (97%)	-0.46	0 100 100	25, 44, 70, 92	3 (0%)
All	All	1711/1790 (95%)	-0.21	10 (0%) 85 84	18, 51, 80, 115	15 (0%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	6	ALA	3.2
2	C	131	SER	2.6
1	B	47	GLY	2.4
1	A	6	ALA	2.3
2	C	132	HIS	2.2

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	E	57	15/16	0.94	0.09	44,47,51,56	0
2	0AF	C	57	15/16	0.95	0.08	56,59,62,65	0
1	CSD	A	107	8/9	0.97	0.05	52,54,55,56	0
1	CSD	B	107	8/9	0.97	0.06	49,52,54,54	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

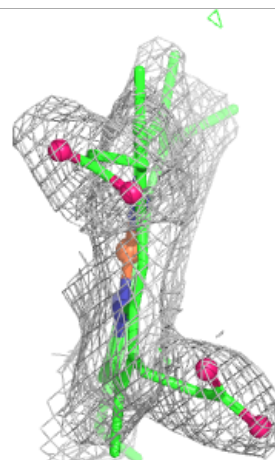
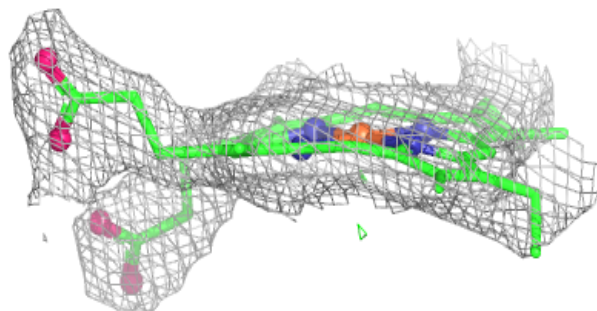
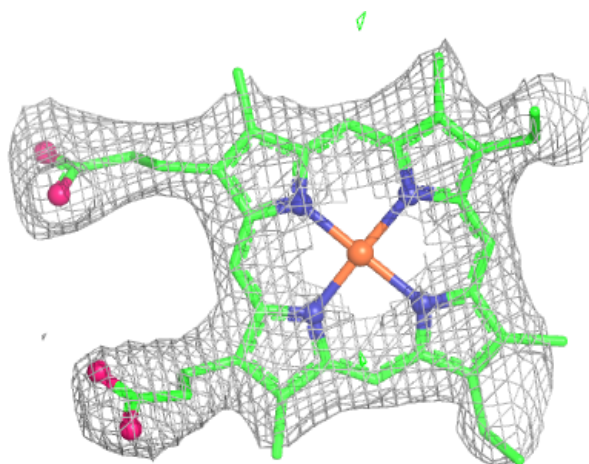
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	ACT	F	402	4/4	0.64	0.16	71,71,72,72	0
6	ACT	B	403	4/4	0.78	0.14	67,67,67,67	0
6	ACT	D	401	4/4	0.90	0.12	62,62,63,63	0
7	EDO	B	405	4/4	0.90	0.12	50,51,51,52	0
6	ACT	F	401	4/4	0.91	0.13	51,51,51,52	0
7	EDO	D	402	4/4	0.91	0.14	63,64,64,65	0
4	CA	A	401	1/1	0.97	0.04	41,41,41,41	0
4	CA	B	401	1/1	0.97	0.04	38,38,38,38	0
5	HEC	A	402	43/43	0.98	0.07	38,44,49,50	0
5	HEC	A	403	43/43	0.98	0.07	34,43,45,45	0
5	HEC	B	402	43/43	0.98	0.07	29,40,45,49	0
5	HEC	B	404	43/43	0.99	0.05	18,27,34,37	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.

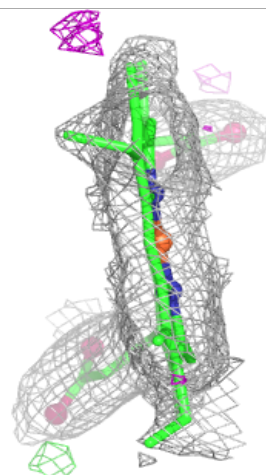
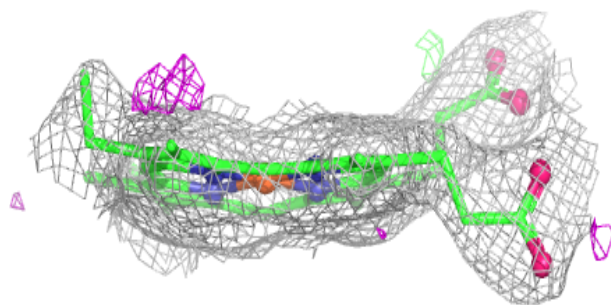
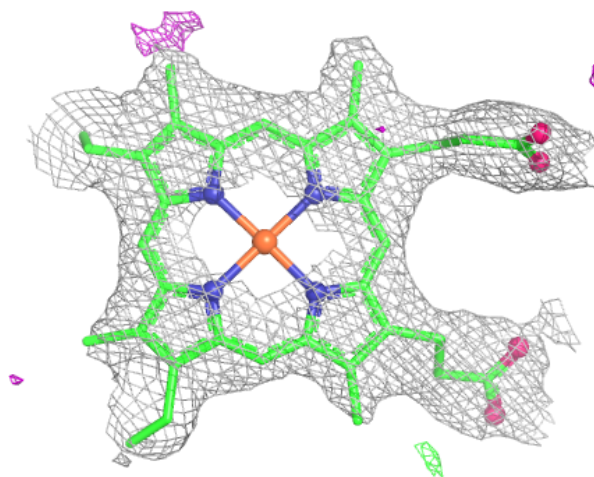
Electron density around HEC A 402:

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



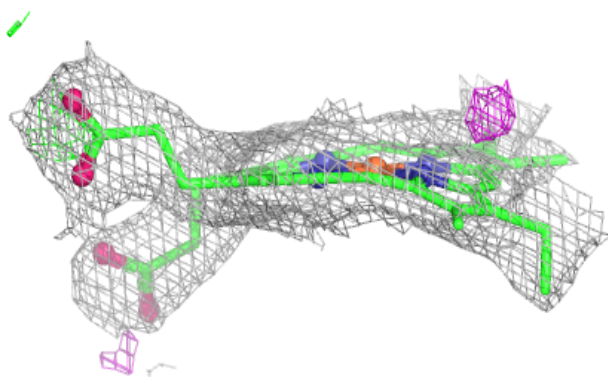
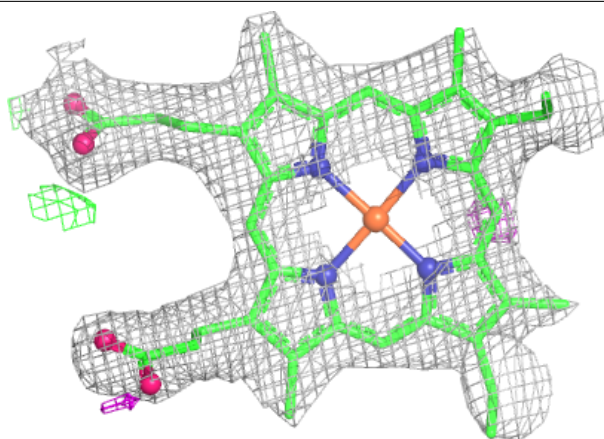
Electron density around HEC A 403:

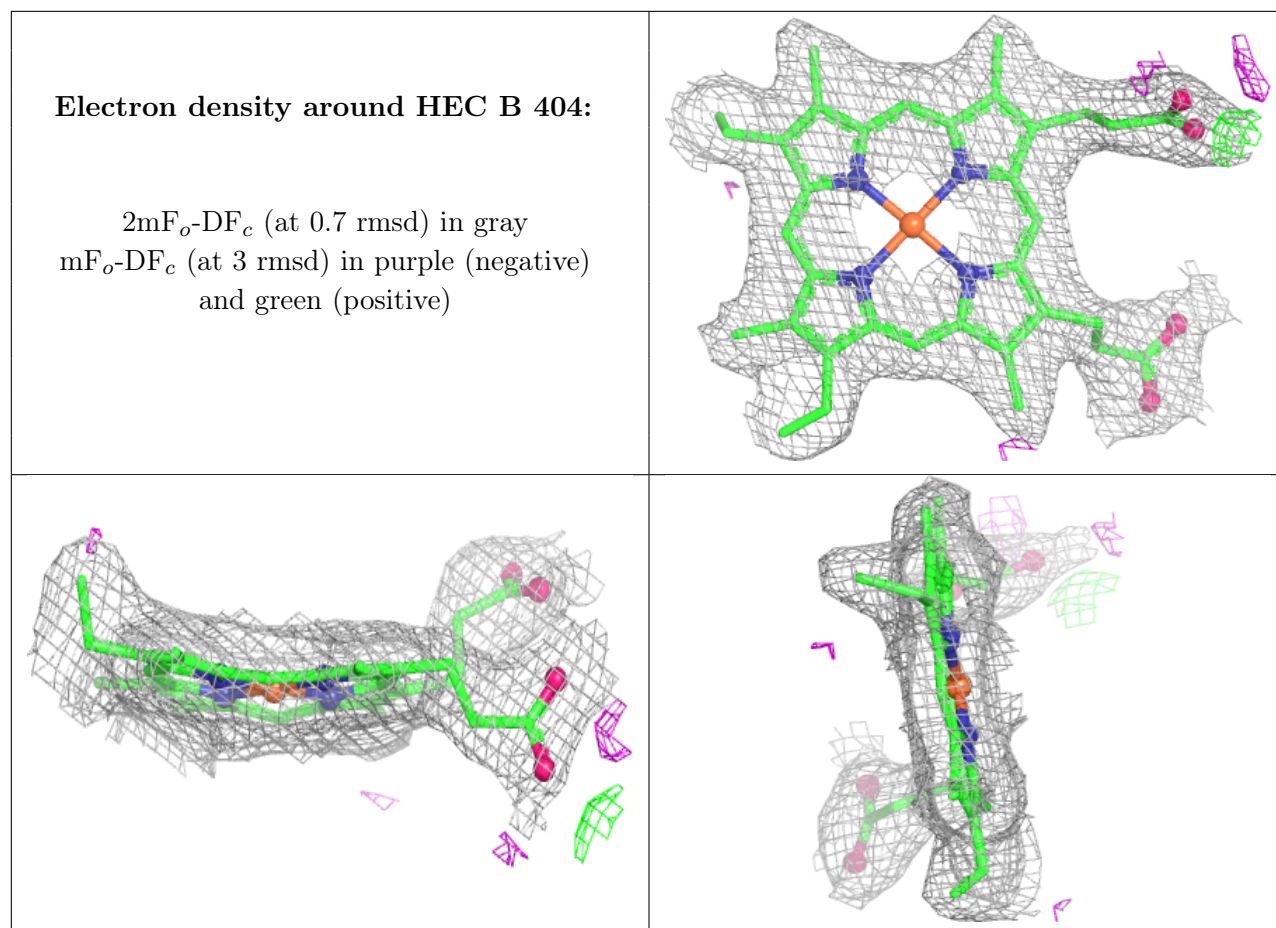
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.5 Other polymers ⓘ

There are no such residues in this entry.