wwPDB X-ray Structure Validation Summary Report (i)

Aug 5, 2026 – 10:47 PM JST

PDB ID	:	7E0O / pdb_00007e0o
Title	:	Crystal Structure of Human Indoleamine 2,3-dioxygenagse 1 (hIDO1) Complexed with 6-Bromo-1H-indazol-4-amine (1)
Authors	:	Li, G.-B.; Ning, X.-L.
Deposited on	:	2021-01-28
Resolution	:	3.34 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:

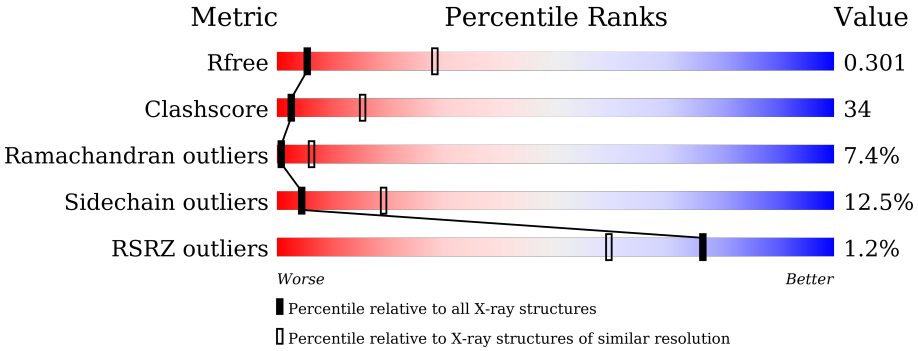
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
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 3.34 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	1434 (3.38-3.30)
Clashscore	190562	1479 (3.38-3.30)
Ramachandran outliers	187476	1456 (3.38-3.30)
Sidechain outliers	187428	1455 (3.38-3.30)
RSRZ outliers	180081	1434 (3.38-3.30)

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	392	2% 37% 44% 12% • 6%
1	B	392	% 39% 45% 10% • 6%

2 Entry composition (i)

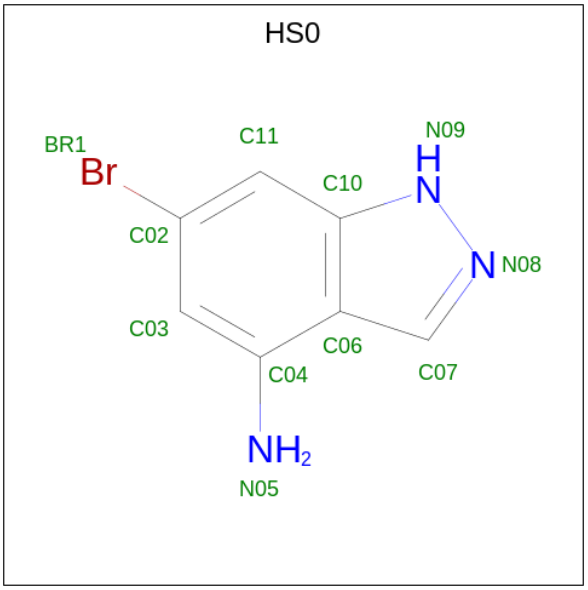
There are 3 unique types of molecules in this entry. The entry contains 5966 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Indoleamine 2,3-dioxygenase 1.

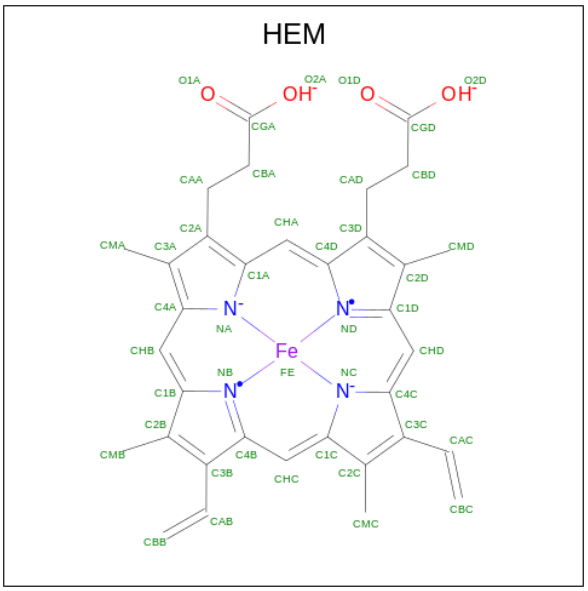
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	370	2929	1883	499	530	17	0	0	0
1	B	370	2929	1883	499	530	17	0	0	0

- Molecule 2 is 6-bromanyl-1 {H}-indazol-4-amine (CCD ID: HS0) (formula: $C_7H_6BrN_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	Br	C	N		
2	A	1	11	1	7	3	0	0
2	B	1	11	1	7	3	0	0

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



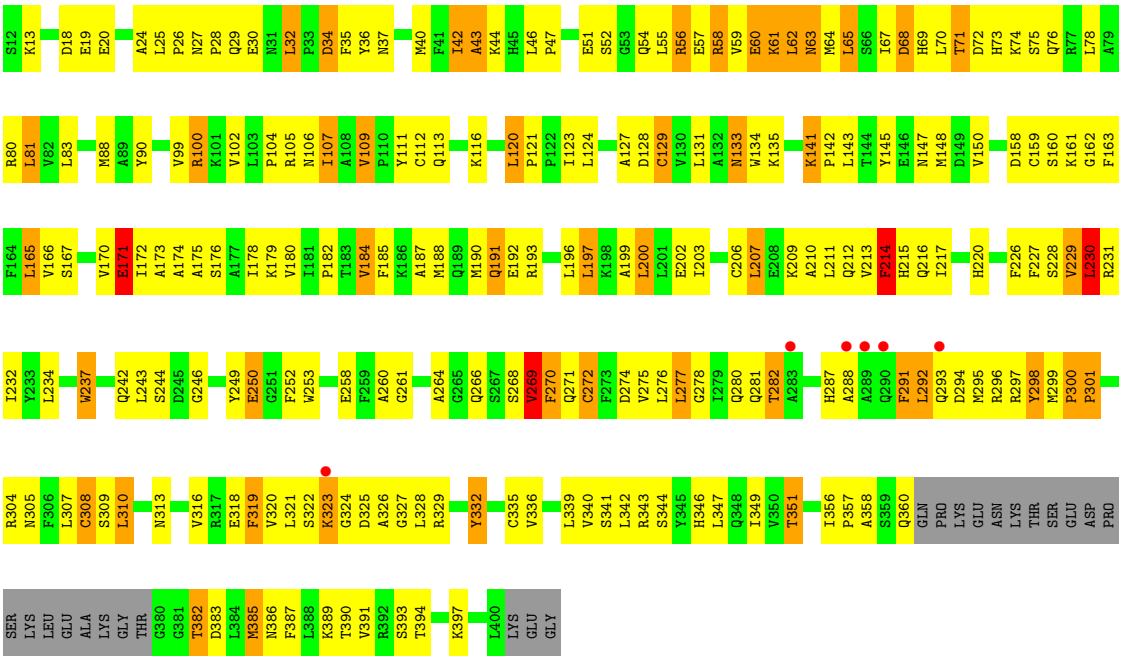
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
3	A	1	43	34	1	4	4	0	0
			Total	C	Fe	N	O		
3	B	1	43	34	1	4	4	0	0

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.

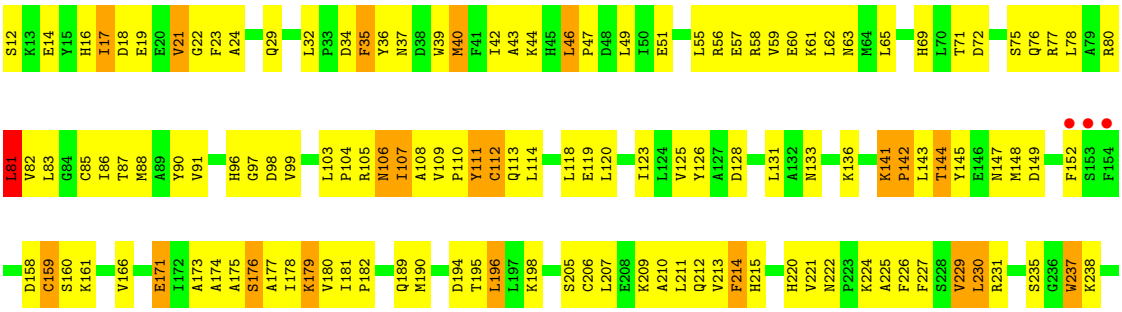
• Molecule 1: Indoleamine 2,3-dioxygenase 1

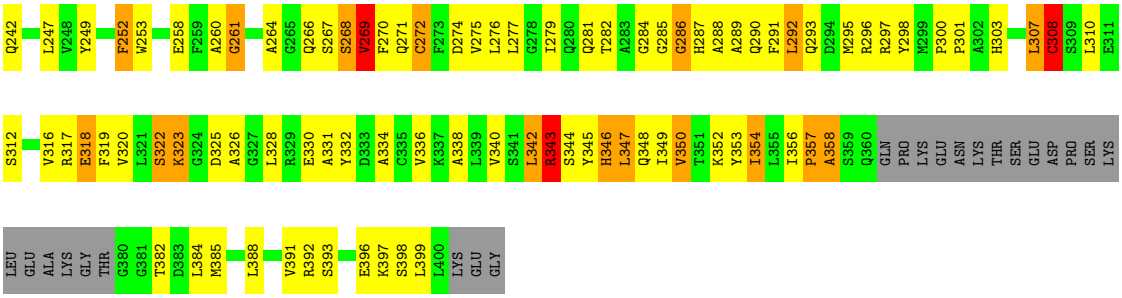
Chain A: 2% 37% 44% 12% • 6%



• Molecule 1: Indoleamine 2,3-dioxygenase 1

Chain B: % 39% 45% 10% • 6%




Q242
L247
V248
Y249
F252
W253
E258
F259
A260
G261
A264
G265
Q266
S267
S268
V269
F270
Q271
C272
F273
D274
V275
L276
L277
G278
I279
Q280
Q281
T282
A283
G284
G285
G286
H287
A288
A289
Q290
F291
L292
Q293
D294
M295
R296
R297
Y298
M299
P300
P301
A302
H303
L307
C308
S309
L310
E311
S312
V316
R317
E318
F319
V320
L321
S322
K323
G324
D325
A326
G327
L328
R329
E330
A331
Y332
D333
A334
C335
V336
K337
A338
L339
V340
S341
L342
R343
S344
Y345
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L347
Q348
I349
V350
T351
K352
Y353
I354
L355
I356
P357
A358
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GLN
PRO
LYS
GLU
ASN
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THR
SER
GLU
ASP
PRO
SER
LYS
LEU
GLU
ALA
LYS
GLY
THR
G380
G381
T382
D383
L384
M385
L388
V391
R392
S393
E396
K397
S398
L399
L400
LYS
GLU
GLY

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	85.59Å 96.79Å 130.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.49 – 3.34 65.49 – 3.34	Depositor EDS
% Data completeness (in resolution range)	96.3 (65.49-3.34) 96.3 (65.49-3.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.14 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.211 , 0.302 0.223 , 0.301	Depositor DCC
R_{free} test set	1587 reflections (9.68%)	wwPDB-VP
Wilson B-factor (Å^2)	101.2	Xtriage
Anisotropy	0.614	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 65.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5966	wwPDB-VP
Average B, all atoms (Å^2)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.58% 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: HS0, HEM

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	0.77	0/2997	0.93	1/4055 (0.0%)
1	B	0.76	2/2997 (0.1%)	0.95	2/4055 (0.0%)
All	All	0.76	2/5994 (0.0%)	0.94	3/8110 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	357	PRO	C-N	5.25	1.41	1.33
1	B	358	ALA	CA-C	5.11	1.59	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	107	ILE	N-CA-C	-6.25	106.70	112.96
1	B	81	LEU	CA-C-N	5.98	128.18	120.70
1	B	81	LEU	C-N-CA	5.98	128.18	120.70

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	2929	0	2934	207	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2929	0	2934	203	0
2	A	11	0	0	0	0
2	B	11	0	0	1	0
3	A	43	0	30	6	0
3	B	43	0	30	5	0
All	All	5966	0	5928	409	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 34.

The worst 5 of 409 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:ARG:NH2	1:B:398:SER:O	2.07	0.87
1:A:109:VAL:O	1:A:113:GLN:HG3	1.76	0.84
1:A:80:ARG:NH2	1:A:128:ASP:OD2	2.09	0.84
1:B:274:ASP:OD2	1:B:343:ARG:NH2	2.14	0.79
1:A:64:MET:N	1:A:106:ASN:OD1	2.17	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	366/392 (93%)	266 (73%)	72 (20%)	28 (8%)	1 5
1	B	366/392 (93%)	261 (71%)	79 (22%)	26 (7%)	1 7
All	All	732/784 (93%)	527 (72%)	151 (21%)	54 (7%)	1 6

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	LYS
1	A	160	SER
1	A	171	GLU
1	A	214	PHE
1	A	269	VAL

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	319/339 (94%)	276 (86%)	43 (14%)	4 16
1	B	319/339 (94%)	282 (88%)	37 (12%)	5 21
All	All	638/678 (94%)	558 (88%)	80 (12%)	4 19

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	144	THR
1	B	308	CYS
1	B	171	GLU
1	B	237	TRP
1	B	343	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	GLN
1	A	242	GLN
1	B	113	GLN
1	B	31	ASN
1	A	73	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	HS0	A	501	3	12,12,12	1.38	2 (16%)	13,17,17	4.15	5 (38%)
2	HS0	B	501	3	12,12,12	1.81	3 (25%)	13,17,17	5.19	8 (61%)
3	HEM	B	502	1,2	50,50,50	1.66	9 (18%)	66,82,82	1.58	16 (24%)
3	HEM	A	502	1,2	50,50,50	1.55	8 (16%)	66,82,82	1.69	15 (22%)

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	HS0	A	501	3	-	-	0/2/2/2
2	HS0	B	501	3	-	-	0/2/2/2
3	HEM	B	502	1,2	-	6/14/54/54	-
3	HEM	A	502	1,2	-	5/14/54/54	-

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	HEM	FE-NB	5.28	2.11	1.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	HEM	FE-NC	4.94	2.11	1.95
3	B	502	HEM	FE-NA	4.62	2.10	1.95
3	A	502	HEM	FE-NB	3.86	2.06	1.94
2	B	501	HS0	C06-C10	-3.69	1.37	1.41

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	501	HS0	C06-C07-N08	-14.25	106.89	111.41
2	A	501	HS0	C06-C07-N08	-10.51	108.07	111.41
2	B	501	HS0	C07-N08-N09	7.97	110.24	106.02
2	A	501	HS0	C07-N08-N09	7.42	109.95	106.02
2	A	501	HS0	C06-C10-N09	5.27	110.74	106.47

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	502	HEM	C1A-C2A-CAA-CBA
3	B	502	HEM	C3A-C2A-CAA-CBA
3	A	502	HEM	C4D-C3D-CAD-CBD
3	A	502	HEM	C3D-CAD-CBD-CGD
3	A	502	HEM	C2D-C3D-CAD-CBD

There are no ring outliers.

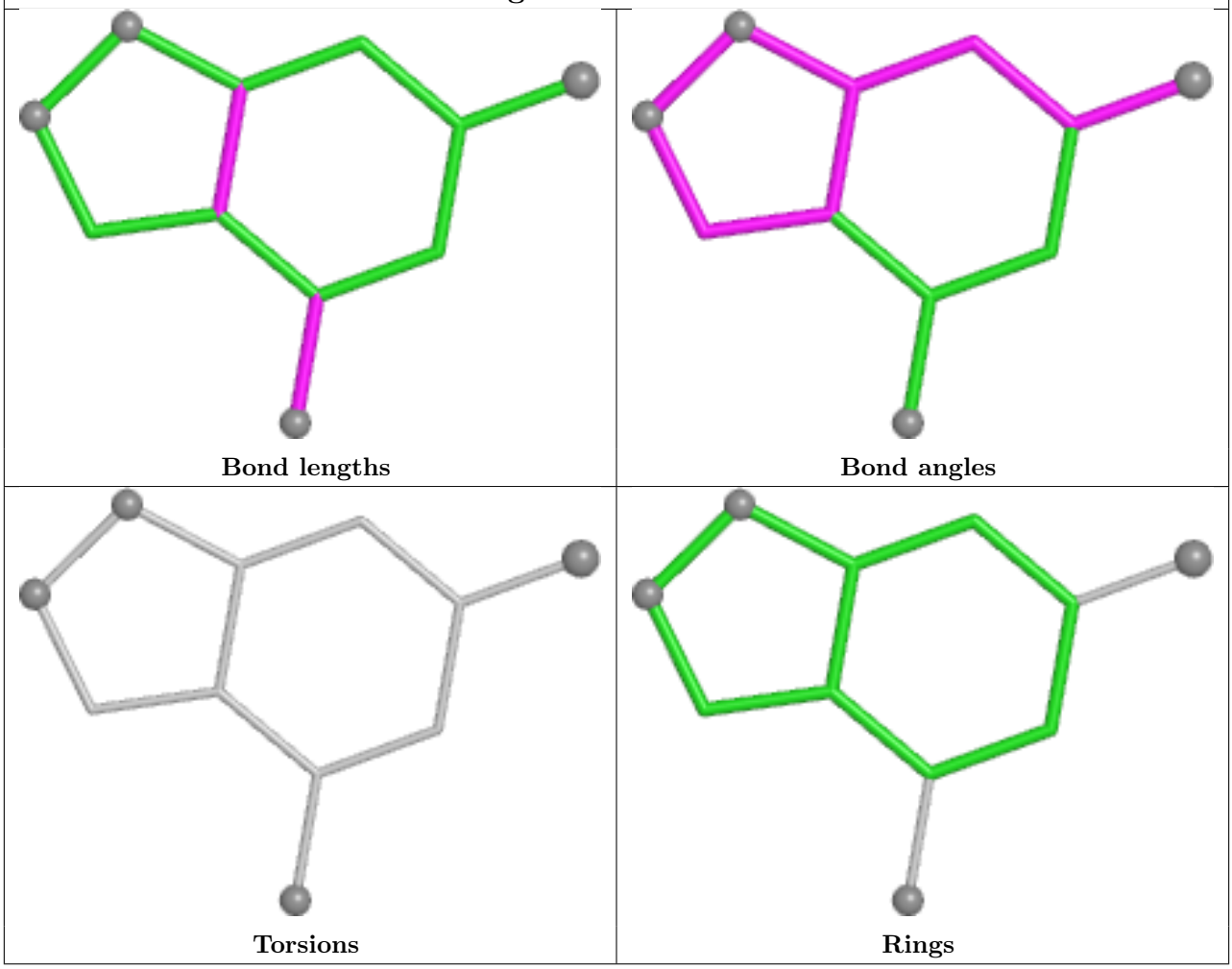
3 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	HS0	1	0
3	B	502	HEM	5	0
3	A	502	HEM	6	0

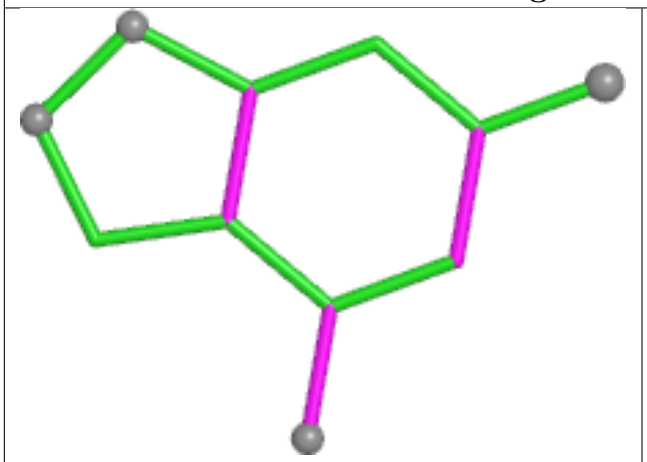
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

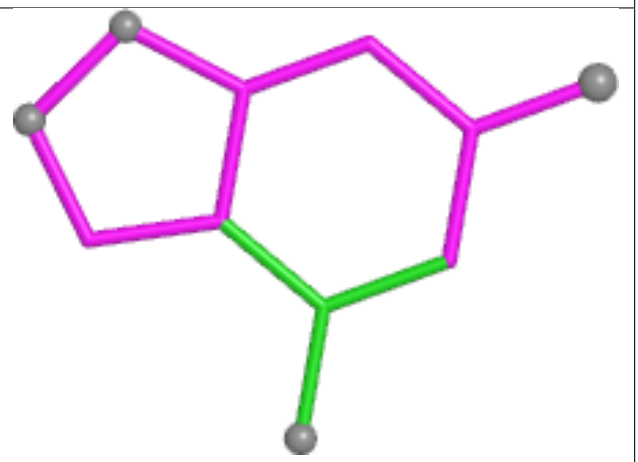
Ligand HS0 A 501



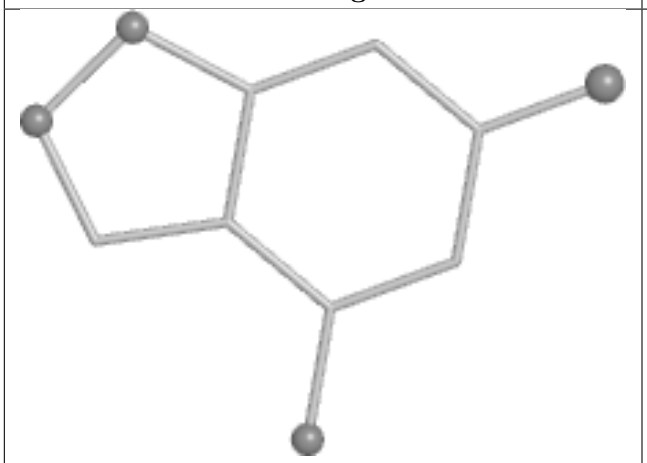
Ligand HS0 B 501



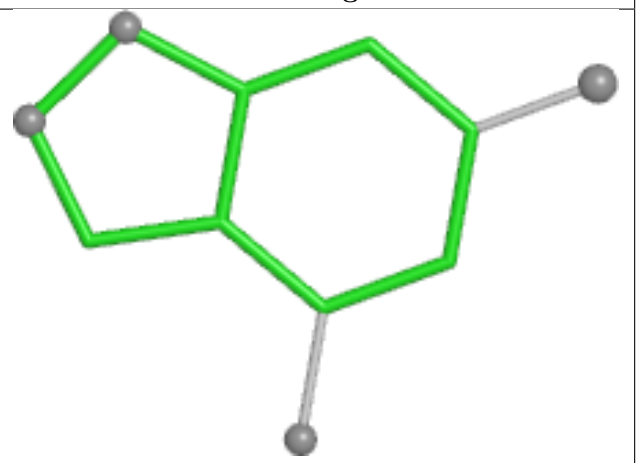
Bond lengths



Bond angles

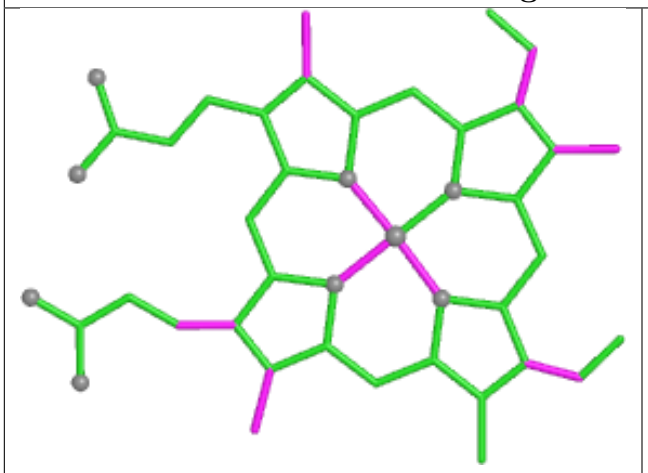


Torsions

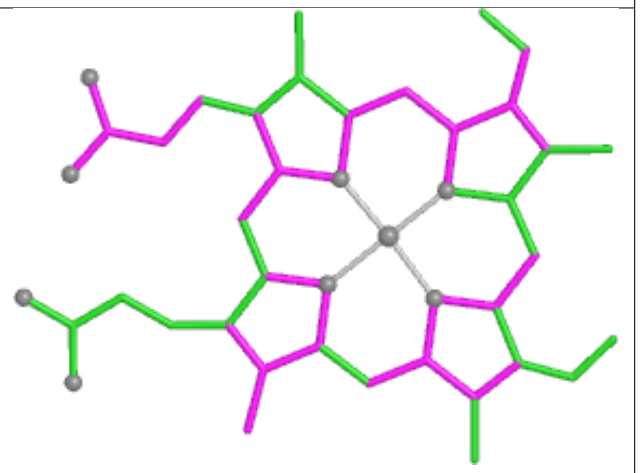


Rings

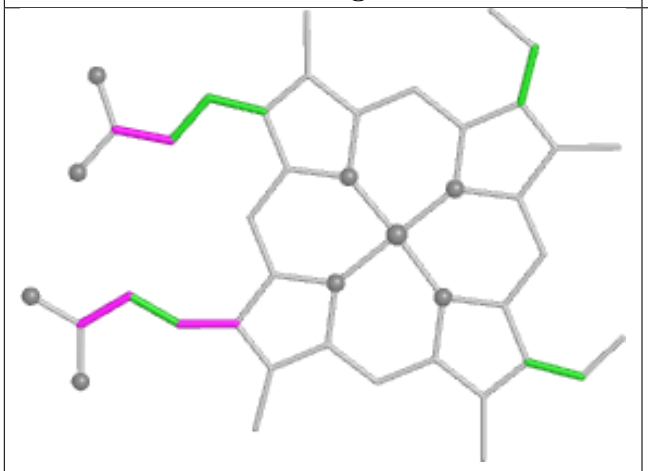
Ligand HEM B 502



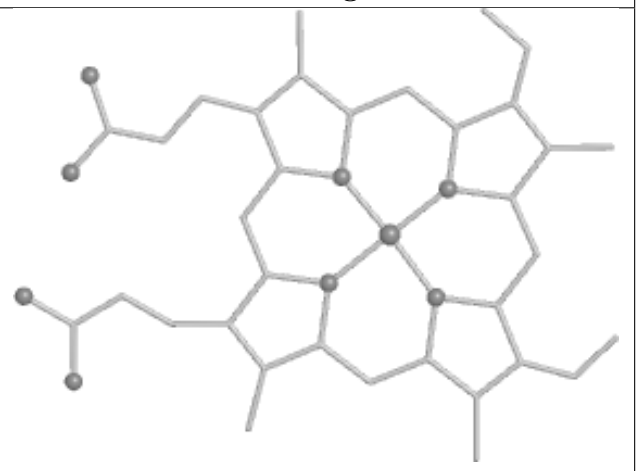
Bond lengths



Bond angles

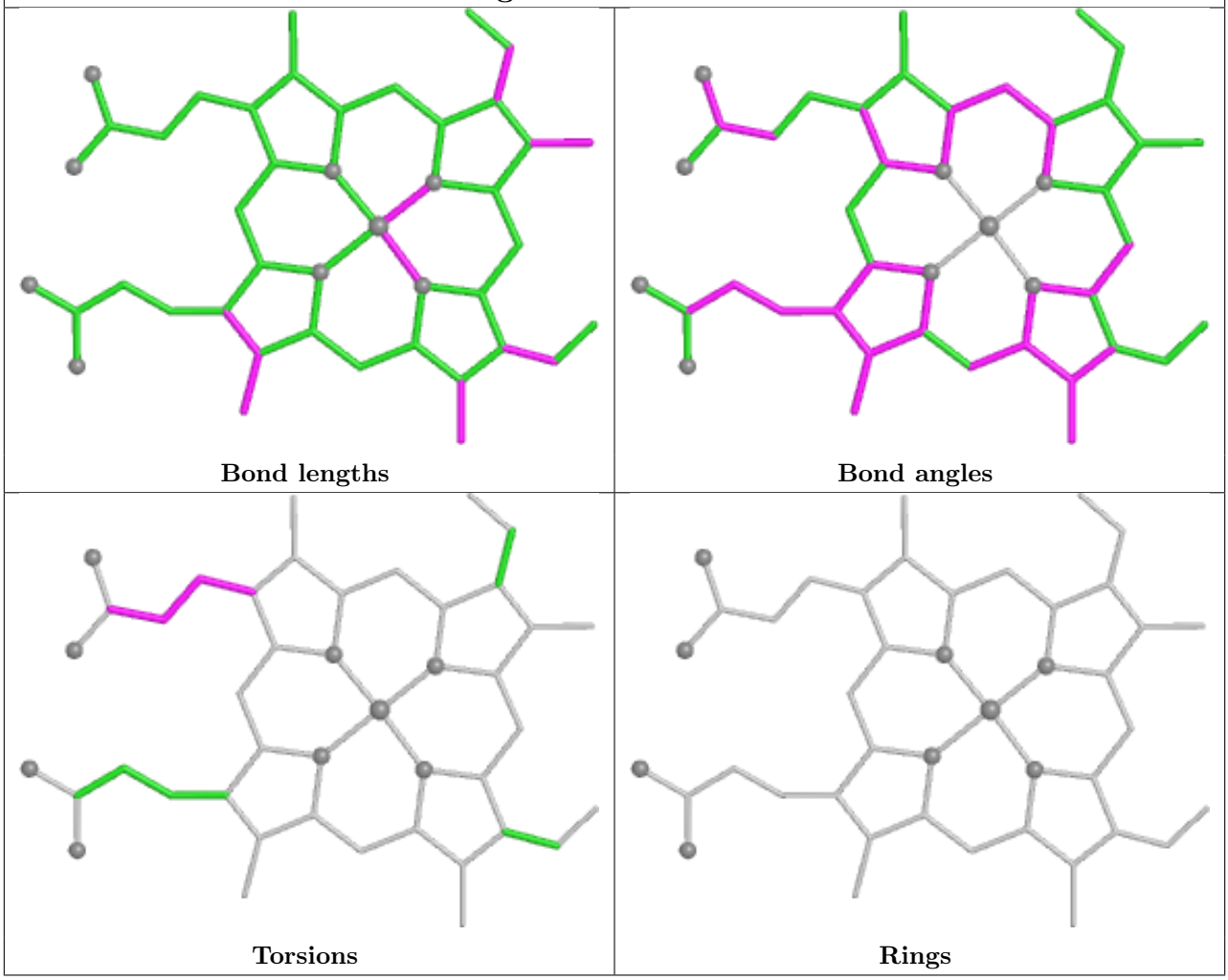


Torsions



Rings

Ligand HEM A 502



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	370/392 (94%)	-0.17	6 (1%)	70	52	67, 104, 131, 162	0
1	B	370/392 (94%)	-0.27	3 (0%)	82	69	72, 103, 131, 152	0
All	All	740/784 (94%)	-0.22	9 (1%)	76	59	67, 104, 131, 162	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	152	PHE	2.8
1	A	289	ALA	2.6
1	A	283	ALA	2.6
1	A	293	GLN	2.4
1	A	290	GLN	2.3

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

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

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

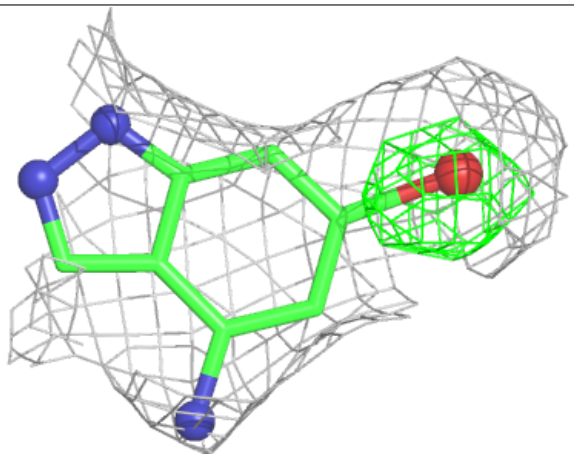
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

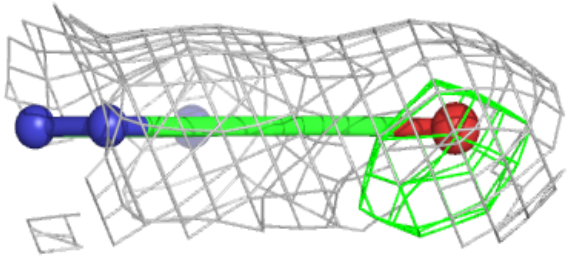
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	HS0	B	501	11/11	0.87	0.12	93,108,129,192	0
2	HS0	A	501	11/11	0.93	0.08	88,100,116,128	0
3	HEM	B	502	43/43	0.95	0.10	67,91,117,131	0
3	HEM	A	502	43/43	0.97	0.09	74,91,110,118	0

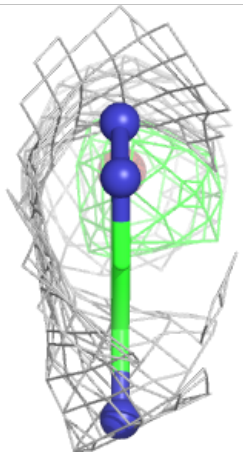
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around HS0 B 501:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

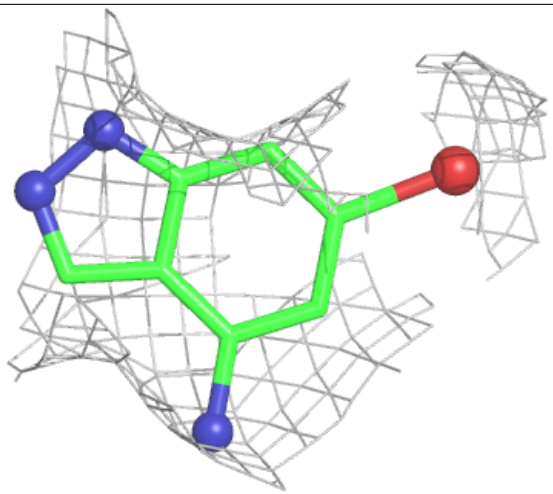


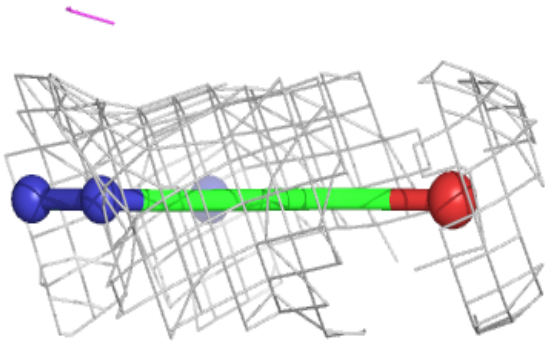


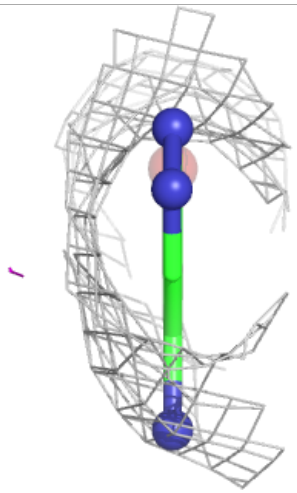


Electron density around HS0 A 501:

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







Electron density around HEM B 502:

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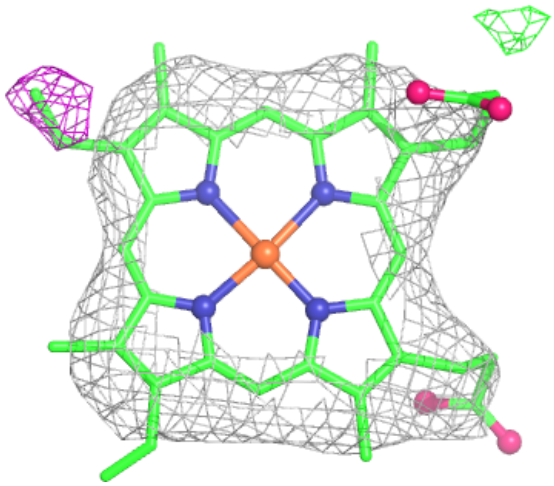
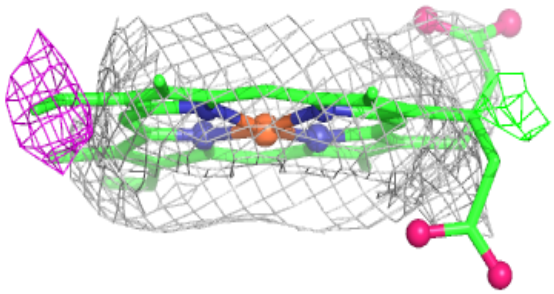
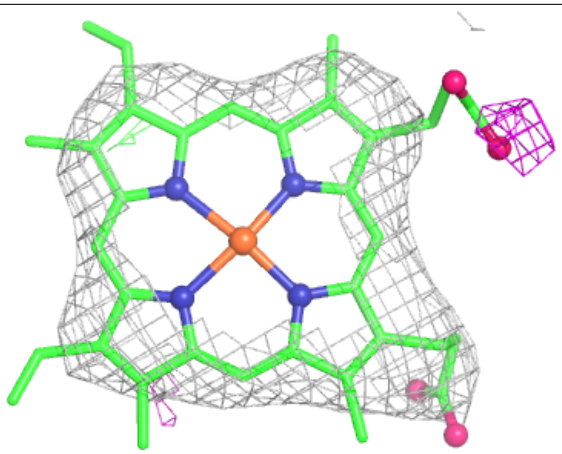
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

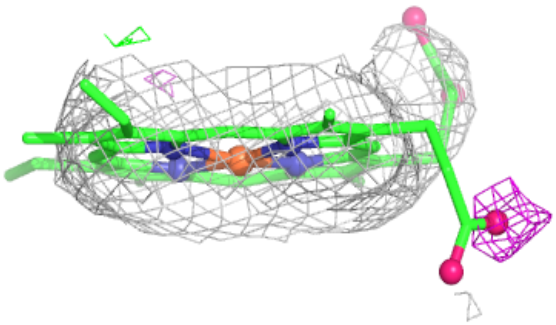


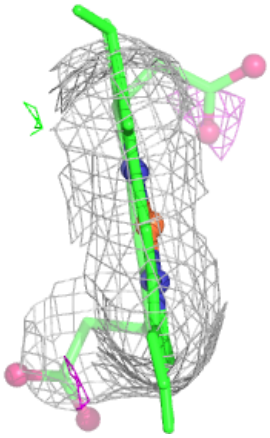


Electron density around HEM A 502:

$2mF_o$-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.