



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 08:12 AM UTC

PDB ID : 9ESD / pdb\_00009esd  
Title : Holo TDO with a bound inhibitor  
Authors : Wicki, M.; Mac Sweeney, A.  
Deposited on : 2024-03-26  
Resolution : 2.10 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](mailto: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>.

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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)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

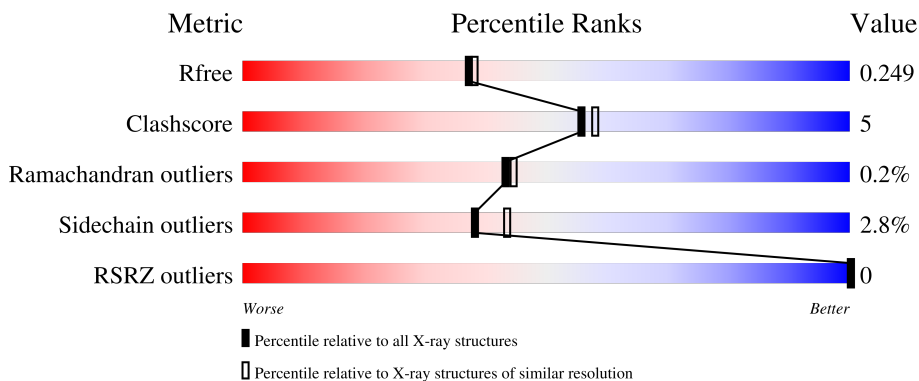
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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  $\geq 3$ , 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	365	80% 9% • 10%
1	B	365	80% 8% • 11%
1	C	365	81% 12% • 6%
1	D	365	78% 11% • 9%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 11368 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 Tryptophan 2,3-dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	328	2735	1753	468	502	12	0	1	0
1	B	326	2715	1740	469	494	12	0	1	0
1	C	344	2849	1820	493	524	12	0	1	0
1	D	331	2755	1763	475	505	12	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

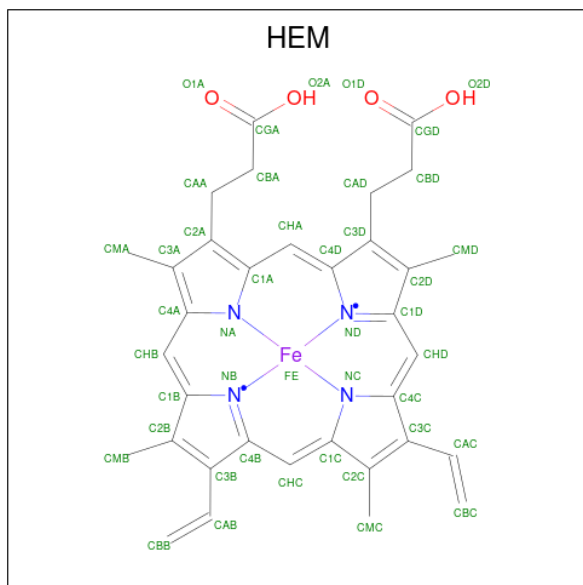
Chain	Residue	Modelled	Actual	Comment	Reference
A	23	MET	-	initiating methionine	UNP P20351
A	380	LEU	-	expression tag	UNP P20351
A	381	GLU	-	expression tag	UNP P20351
A	382	HIS	-	expression tag	UNP P20351
A	383	HIS	-	expression tag	UNP P20351
A	384	HIS	-	expression tag	UNP P20351
A	385	HIS	-	expression tag	UNP P20351
A	386	HIS	-	expression tag	UNP P20351
A	387	HIS	-	expression tag	UNP P20351
B	23	MET	-	initiating methionine	UNP P20351
B	380	LEU	-	expression tag	UNP P20351
B	381	GLU	-	expression tag	UNP P20351
B	382	HIS	-	expression tag	UNP P20351
B	383	HIS	-	expression tag	UNP P20351
B	384	HIS	-	expression tag	UNP P20351
B	385	HIS	-	expression tag	UNP P20351
B	386	HIS	-	expression tag	UNP P20351
B	387	HIS	-	expression tag	UNP P20351
C	23	MET	-	initiating methionine	UNP P20351
C	380	LEU	-	expression tag	UNP P20351
C	381	GLU	-	expression tag	UNP P20351

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Chain	Residue	Modelled	Actual	Comment	Reference
C	382	HIS	-	expression tag	UNP P20351
C	383	HIS	-	expression tag	UNP P20351
C	384	HIS	-	expression tag	UNP P20351
C	385	HIS	-	expression tag	UNP P20351
C	386	HIS	-	expression tag	UNP P20351
C	387	HIS	-	expression tag	UNP P20351
D	23	MET	-	initiating methionine	UNP P20351
D	380	LEU	-	expression tag	UNP P20351
D	381	GLU	-	expression tag	UNP P20351
D	382	HIS	-	expression tag	UNP P20351
D	383	HIS	-	expression tag	UNP P20351
D	384	HIS	-	expression tag	UNP P20351
D	385	HIS	-	expression tag	UNP P20351
D	386	HIS	-	expression tag	UNP P20351
D	387	HIS	-	expression tag	UNP P20351

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



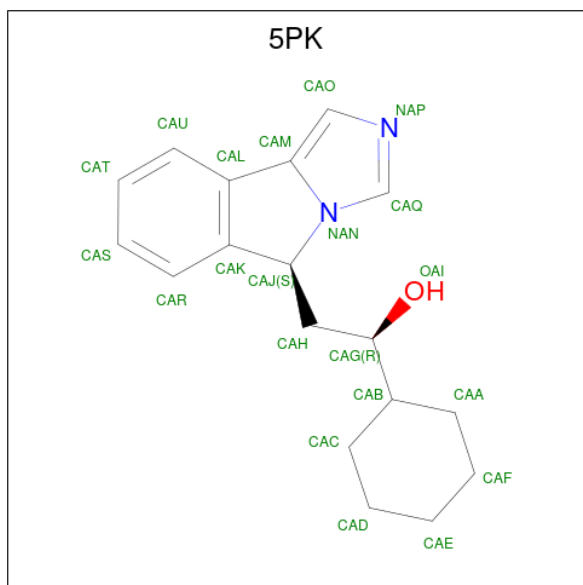
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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

- Molecule 3 is (1 {R})-1-cyclohexyl-2-[(5 {S})-5 {H}-imidazo[1,5-b]isoindol-5-yl]ethanol (CCD ID: 5PK) (formula: C<sub>18</sub>H<sub>22</sub>N<sub>2</sub>O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	21	18	2	1	0	0
3	B	1	21	18	2	1	0	0
3	C	1	21	18	2	1	0	0
3	D	1	21	18	2	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	12	Total	O	0	0
			12	12		
4	B	13	Total	O	0	0
			13	13		
4	C	17	Total	O	0	0
			17	17		
4	D	16	Total	O	0	0
			16	16		



W207	F210	Q211	A233	I251	R267	H270	Q274	M278	F288	P291	M299	D300	V316	Q324	L325	Y333	R337	R343	F351	F368	THR	ILE	ARG	LYS	LYS	LEU	ILE	ASN	LYS	SER	VAL	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	143.74Å 143.74Å 141.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.05 – 2.10 47.05 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.05-2.10) 100.0 (47.05-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.45 (at 2.10Å)	Xtrriage
Refinement program	BUSTER 2.11.8	Depositor
R, $R_{free}$	0.233 , 0.255 0.223 , 0.249	Depositor DCC
$R_{free}$ test set	4796 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.6	Xtrriage
Anisotropy	0.007	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 25.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.124 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	11368	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 5PK, 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	0.71	0/2793	1.03	1/3766 (0.0%)
1	B	0.70	0/2773	1.03	2/3738 (0.1%)
1	C	0.75	3/2910 (0.1%)	1.06	3/3927 (0.1%)
1	D	0.71	0/2811	1.01	1/3790 (0.0%)
All	All	0.72	3/11287 (0.0%)	1.03	7/15221 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	156	ARG	CA-C	7.63	1.60	1.52
1	C	118	THR	CA-C	5.30	1.60	1.52
1	C	154	GLU	CA-C	5.22	1.59	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	C	133	PRO	N-CA-C	6.81	122.99	113.53
1	B	133	PRO	N-CA-C	5.87	121.69	113.53
1	C	134	ALA	CA-C-N	5.59	128.22	120.29
1	C	134	ALA	C-N-CA	5.59	128.22	120.29
1	A	210	PHE	CA-CB-CG	5.53	119.33	113.80

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	2735	0	2734	28	0
1	B	2715	0	2718	25	0
1	C	2849	0	2838	37	0
1	D	2755	0	2761	38	0
2	A	43	0	30	1	0
2	B	43	0	30	2	0
2	C	43	0	30	3	0
2	D	43	0	30	2	0
3	A	21	0	22	2	0
3	B	21	0	22	2	0
3	C	21	0	22	5	0
3	D	21	0	22	2	0
4	A	12	0	0	0	0
4	B	13	0	0	0	0
4	C	17	0	0	0	0
4	D	16	0	0	0	0
All	All	11368	0	11259	107	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 5.

The worst 5 of 107 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:D:61:HIS:NE2	3:D:402:5PK:H22	1.87	0.89
1:B:101:ARG:HE	1:C:118:THR:CG2	1.87	0.88
1:A:101:ARG:HE	1:D:118:THR:CG2	1.88	0.87
1:A:118:THR:CG2	1:D:101:ARG:HE	1.89	0.86
1:B:118:THR:CG2	1:C:101:ARG:HE	1.90	0.84

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	323/365 (88%)	318 (98%)	5 (2%)	0	100	100
1	B	321/365 (88%)	316 (98%)	5 (2%)	0	100	100
1	C	343/365 (94%)	333 (97%)	7 (2%)	3 (1%)	14	10
1	D	327/365 (90%)	322 (98%)	5 (2%)	0	100	100
All	All	1314/1460 (90%)	1289 (98%)	22 (2%)	3 (0%)	43	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	134	ALA
1	C	154	GLU
1	C	157	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	302/337 (90%)	293 (97%)	9 (3%)	36	41
1	B	298/337 (88%)	292 (98%)	6 (2%)	48	56
1	C	313/337 (93%)	302 (96%)	11 (4%)	32	35
1	D	304/337 (90%)	296 (97%)	8 (3%)	40	46
All	All	1217/1348 (90%)	1183 (97%)	34 (3%)	38	43

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	131	LEU
1	D	152	LEU
1	D	200	GLU
1	B	131	LEU
1	B	118	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	190	GLN
1	D	221	GLN
1	D	292	HIS
1	B	190	GLN
1	B	141	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

8 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	HEM	A	401	1,3	50,50,50	1.26	7 (14%)	67,82,82	0.71	2 (2%)
2	HEM	C	401	1,3	50,50,50	1.22	7 (14%)	67,82,82	0.59	0
2	HEM	B	401	1,3	50,50,50	1.26	6 (12%)	67,82,82	0.67	2 (2%)
2	HEM	D	401	1,3	50,50,50	1.23	5 (10%)	67,82,82	0.71	1 (1%)
3	5PK	D	402	2	24,24,24	3.18	8 (33%)	27,34,34	3.12	7 (25%)
3	5PK	B	402	2	24,24,24	3.29	9 (37%)	27,34,34	2.87	6 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	5PK	C	402	2	24,24,24	3.07	8 (33%)	27,34,34	2.54	8 (29%)
3	5PK	A	402	2	24,24,24	3.42	8 (33%)	27,34,34	3.73	6 (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	HEM	A	401	1,3	-	3/14/54/54	-
2	HEM	C	401	1,3	-	2/14/54/54	-
2	HEM	B	401	1,3	-	3/14/54/54	-
2	HEM	D	401	1,3	-	3/14/54/54	-
3	5PK	D	402	2	-	0/8/28/28	0/4/4/4
3	5PK	B	402	2	-	1/8/28/28	0/4/4/4
3	5PK	C	402	2	-	1/8/28/28	0/4/4/4
3	5PK	A	402	2	-	0/8/28/28	0/4/4/4

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	5PK	CAK-CAJ	-10.73	1.39	1.51
3	B	402	5PK	CAK-CAJ	-9.20	1.41	1.51
3	D	402	5PK	CAL-CAM	-9.14	1.33	1.46
3	C	402	5PK	CAL-CAM	-9.11	1.33	1.46
3	B	402	5PK	CAL-CAM	-8.88	1.34	1.46

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	5PK	CAJ-NAN-CAM	-14.77	106.67	113.77
3	D	402	5PK	CAJ-NAN-CAM	-10.41	108.77	113.77
3	B	402	5PK	CAJ-NAN-CAM	-9.26	109.32	113.77
3	A	402	5PK	CAL-CAM-NAN	7.84	110.15	107.44
3	C	402	5PK	CAJ-NAN-CAM	-7.25	110.29	113.77

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

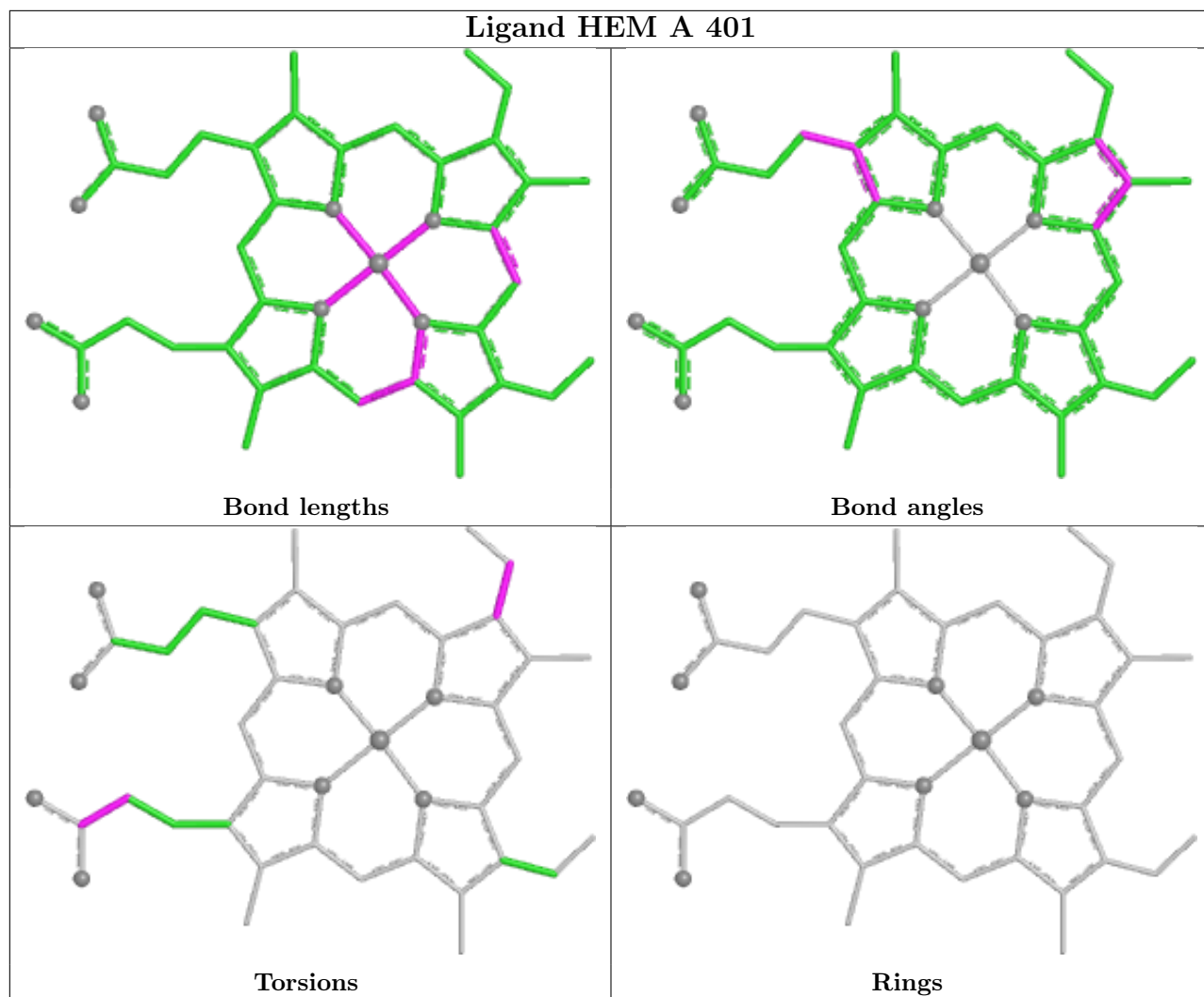
Mol	Chain	Res	Type	Atoms
3	C	402	5PK	CAG-CAH-CAJ-CAK
2	A	401	HEM	C2C-C3C-CAC-CBC
2	A	401	HEM	CAA-CBA-CGA-O1A
2	A	401	HEM	CAA-CBA-CGA-O2A
2	B	401	HEM	CAA-CBA-CGA-O1A

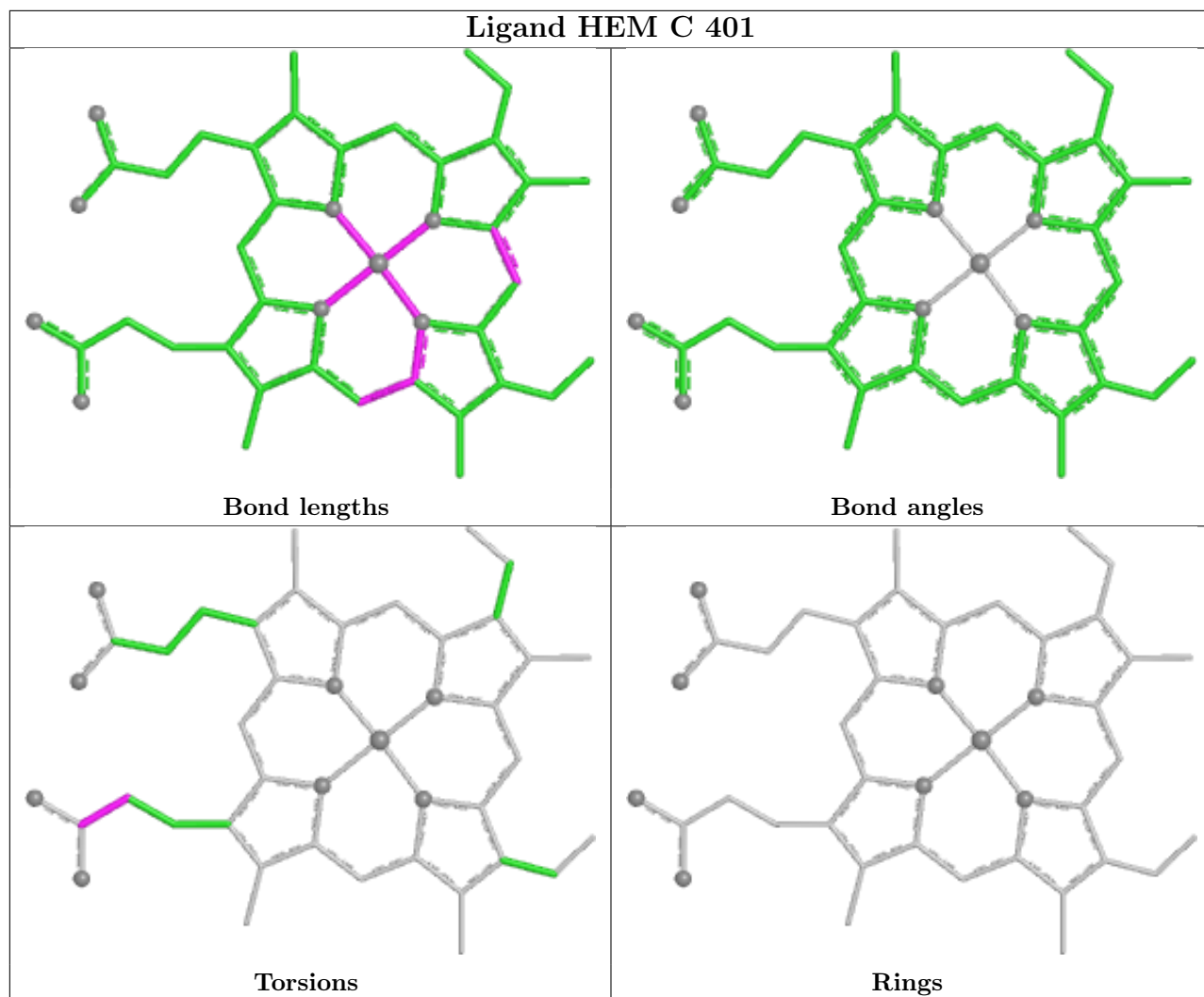
There are no ring outliers.

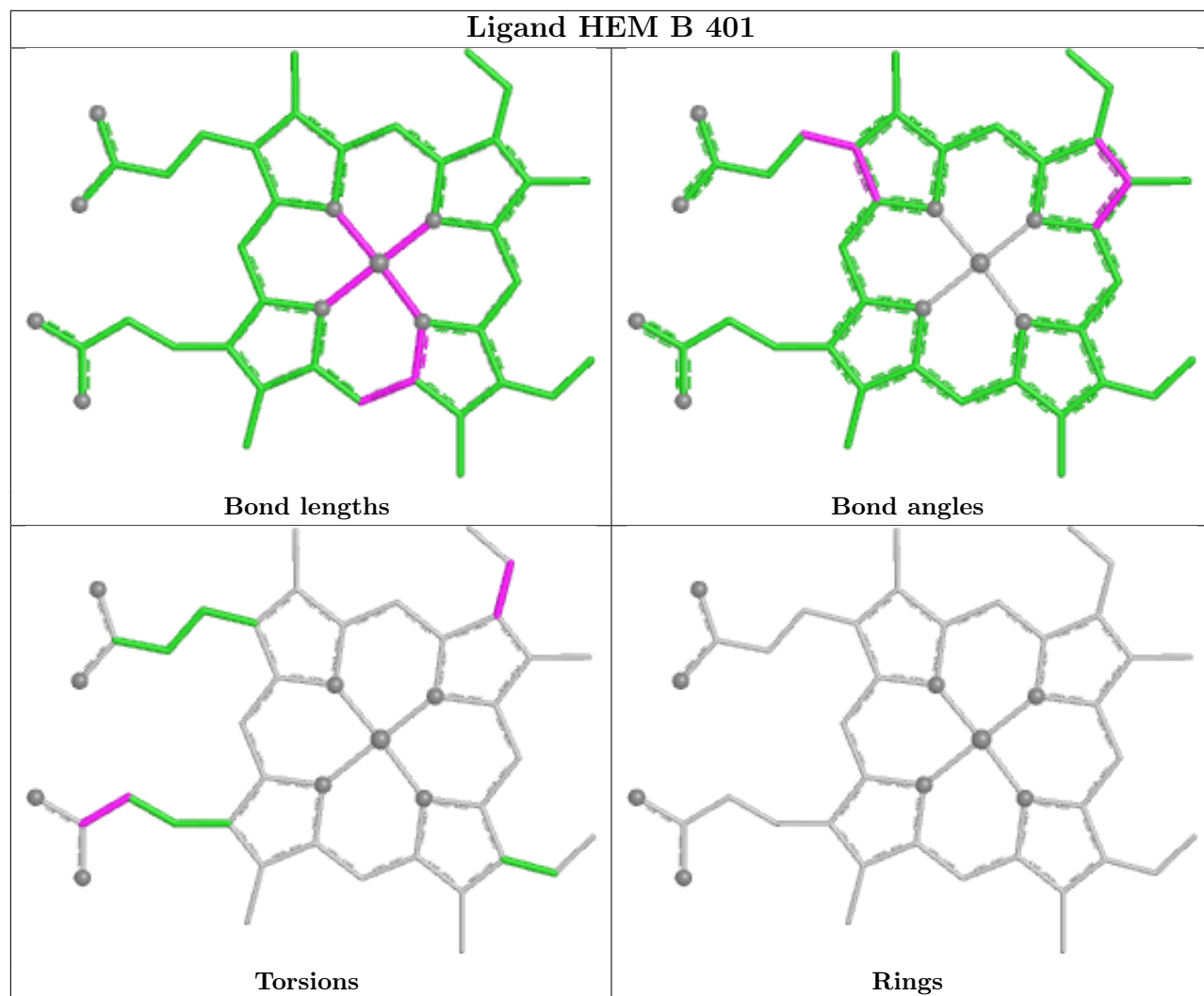
8 monomers are involved in 15 short contacts:

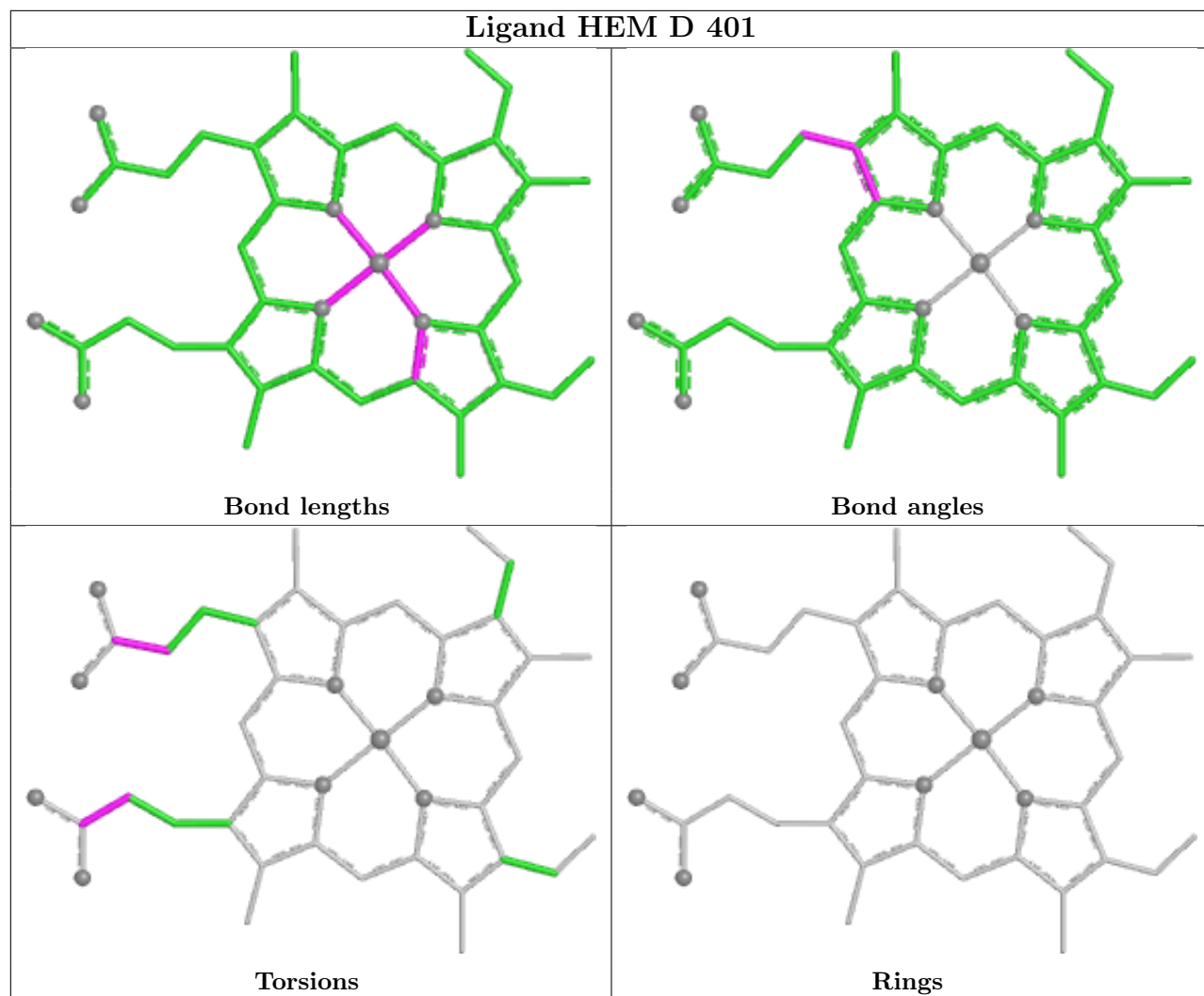
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	HEM	1	0
2	C	401	HEM	3	0
2	B	401	HEM	2	0
2	D	401	HEM	2	0
3	D	402	5PK	2	0
3	B	402	5PK	2	0
3	C	402	5PK	5	0
3	A	402	5PK	2	0

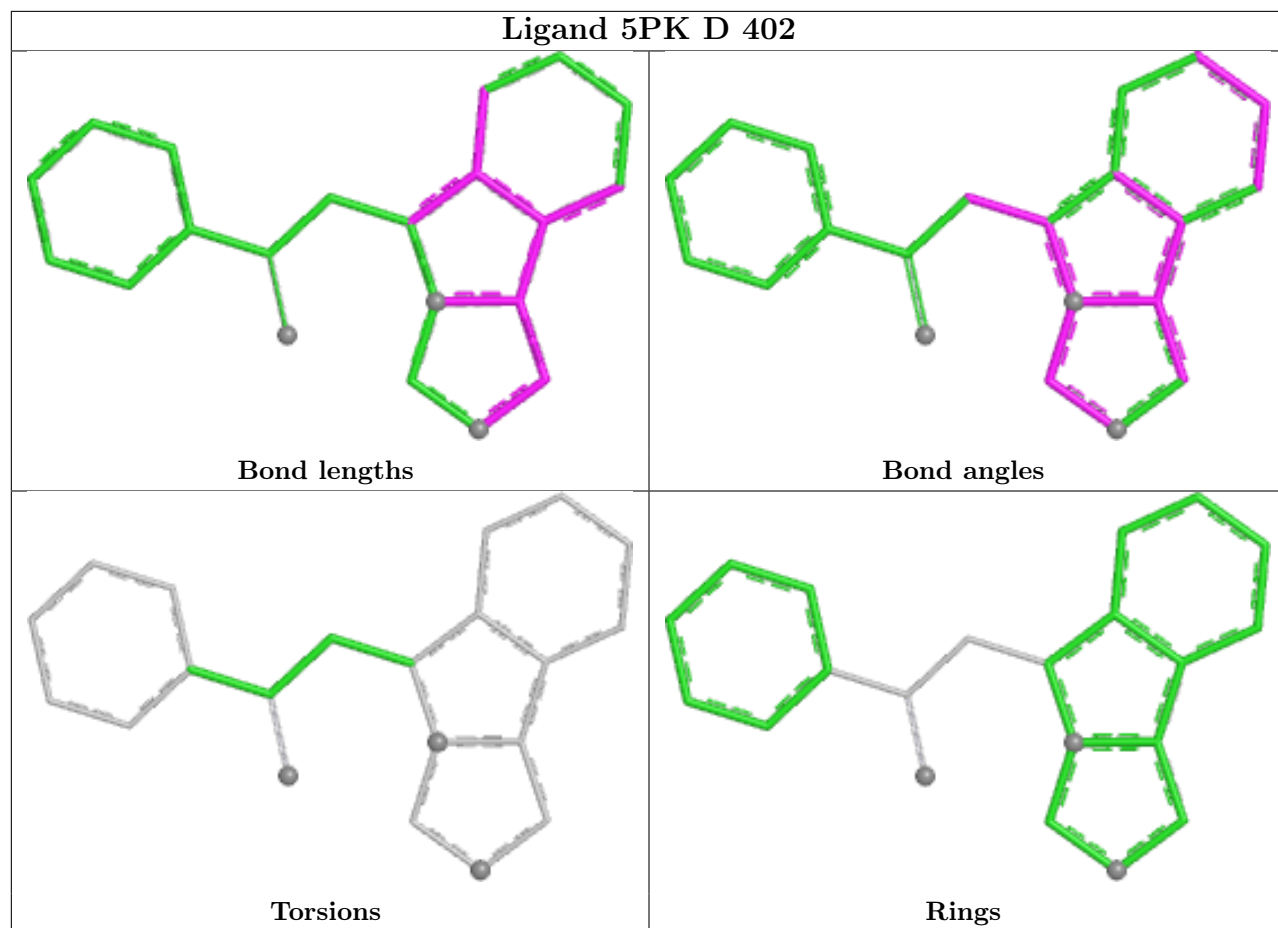
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

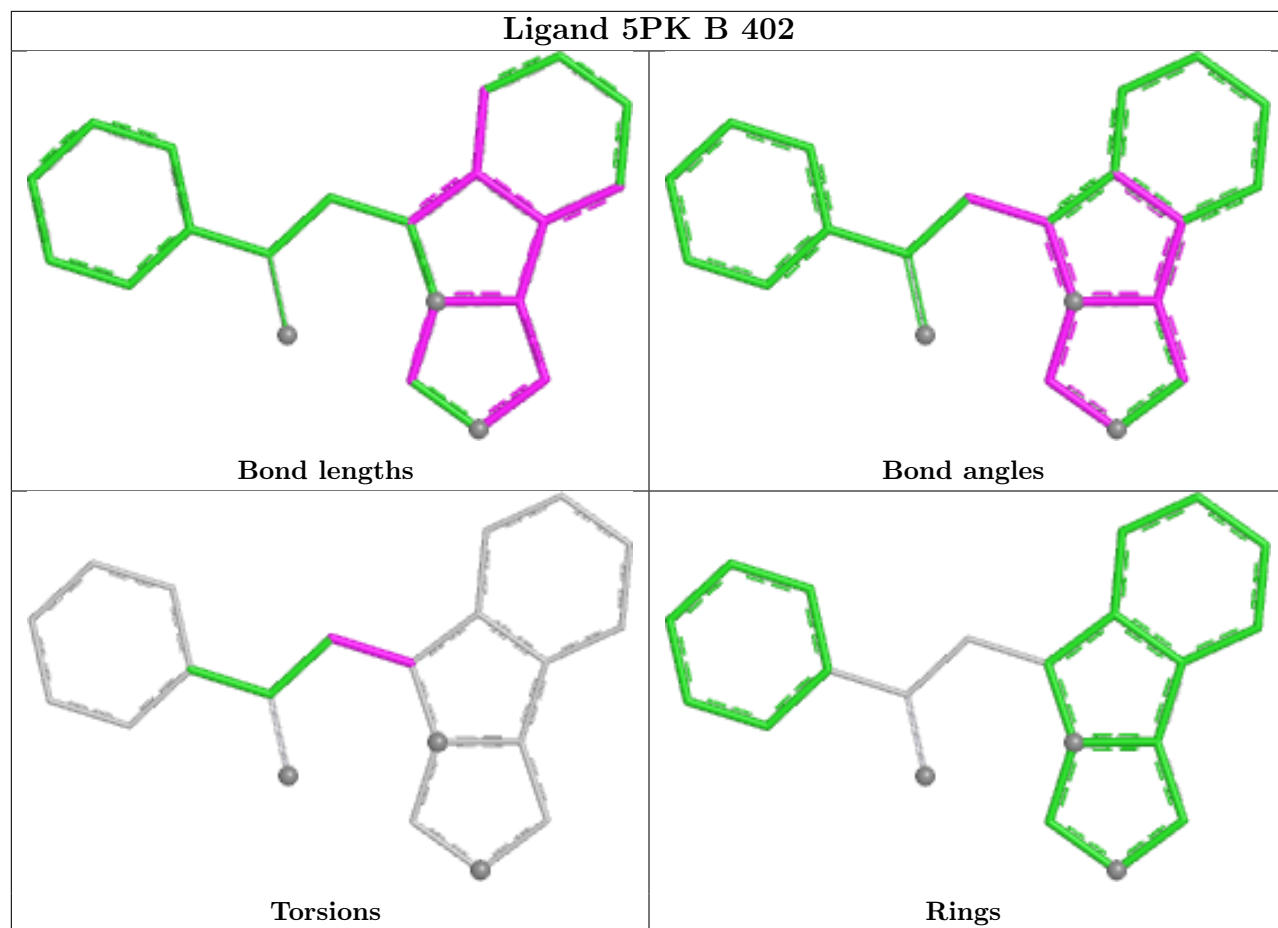


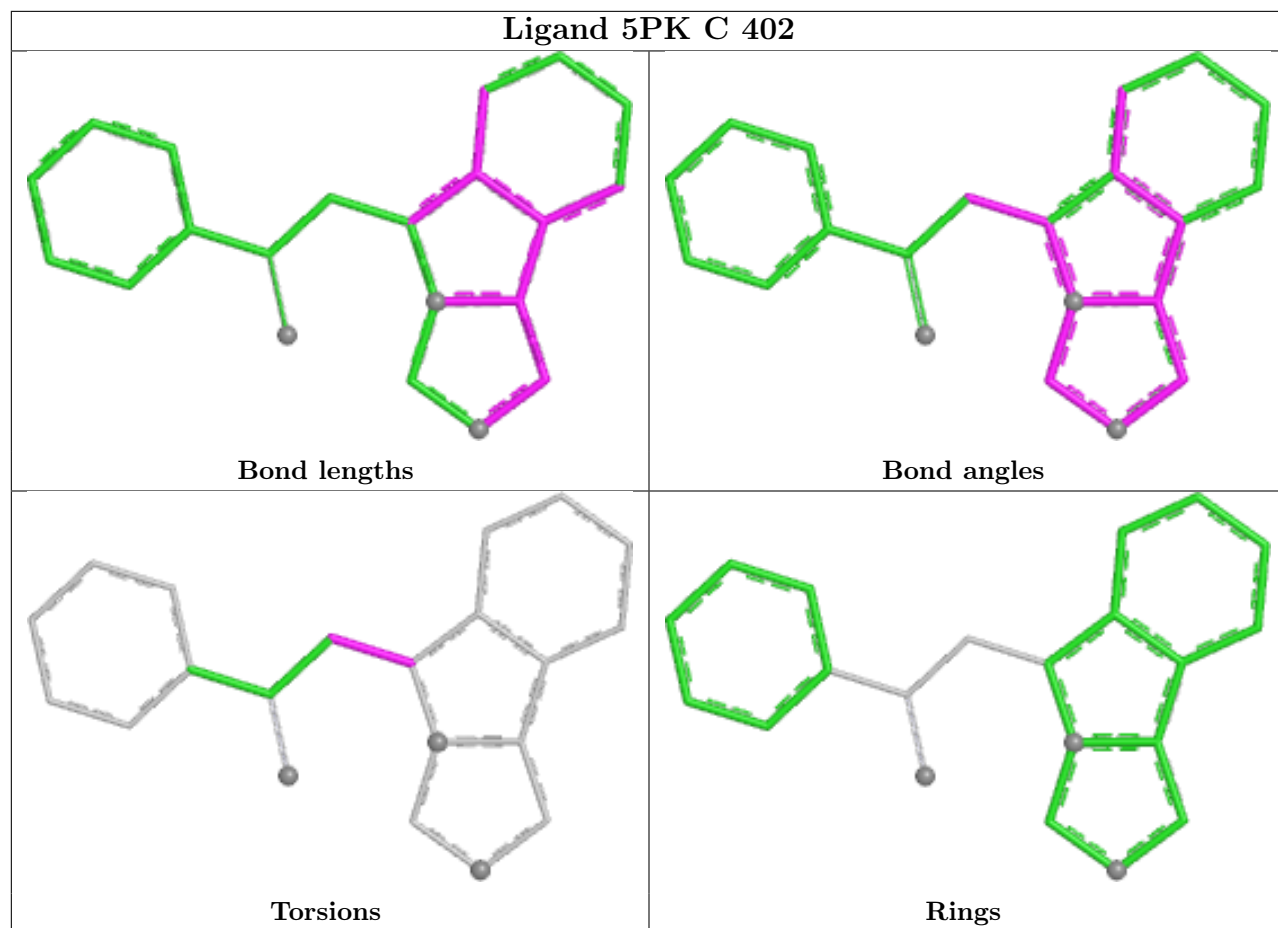


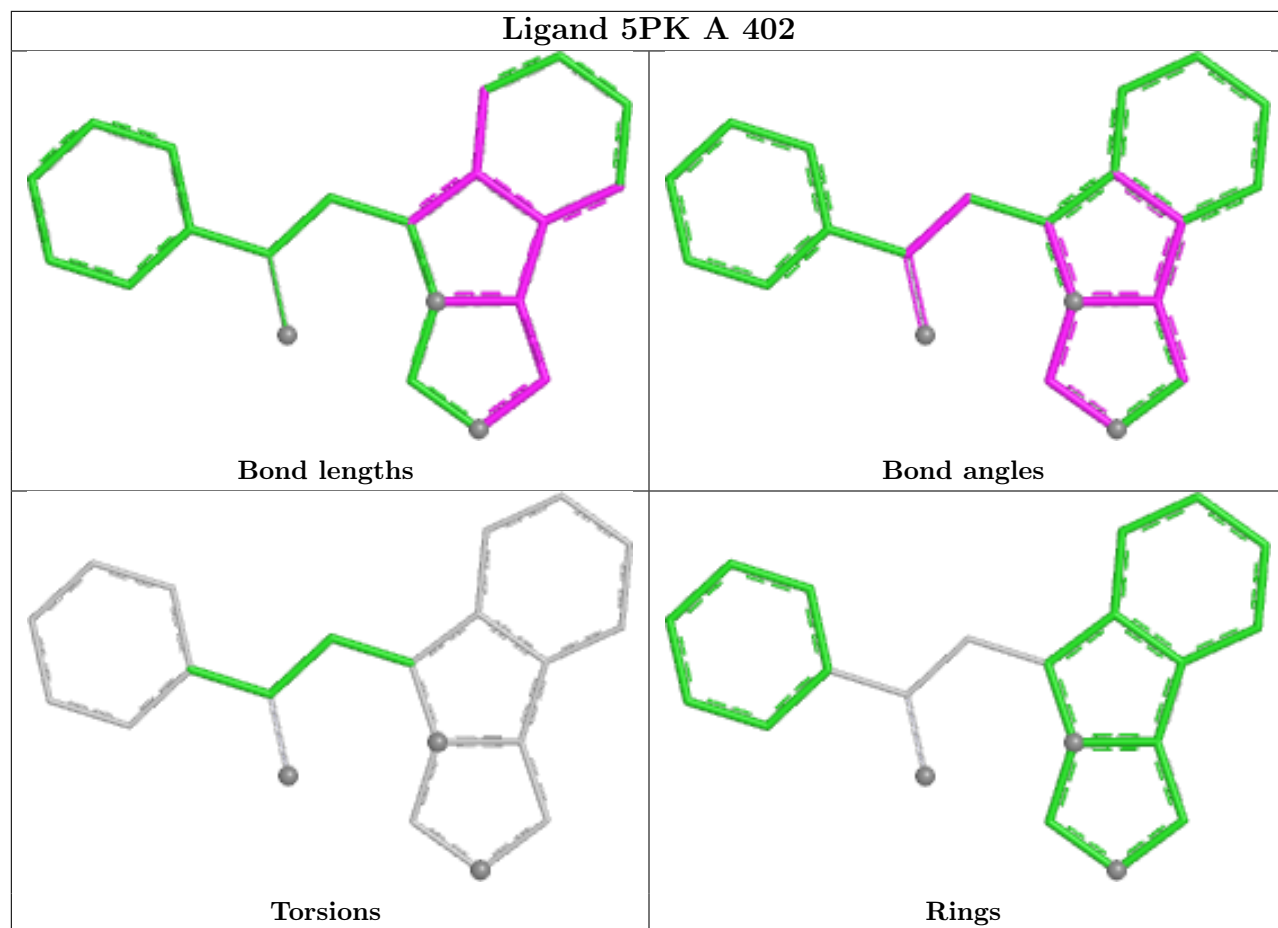












## 5.7 Other polymers [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	328/365 (89%)	-1.02	0 100 100	29, 48, 73, 89	1 (0%)
1	B	326/365 (89%)	-0.99	0 100 100	30, 49, 75, 94	1 (0%)
1	C	344/365 (94%)	-0.99	0 100 100	30, 47, 74, 92	1 (0%)
1	D	331/365 (90%)	-1.01	0 100 100	33, 48, 76, 91	0
All	All	1329/1460 (91%)	-1.00	0 100 100	29, 48, 75, 94	3 (0%)

There are no RSRZ outliers to report.

### 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, 95<sup>th</sup> 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.

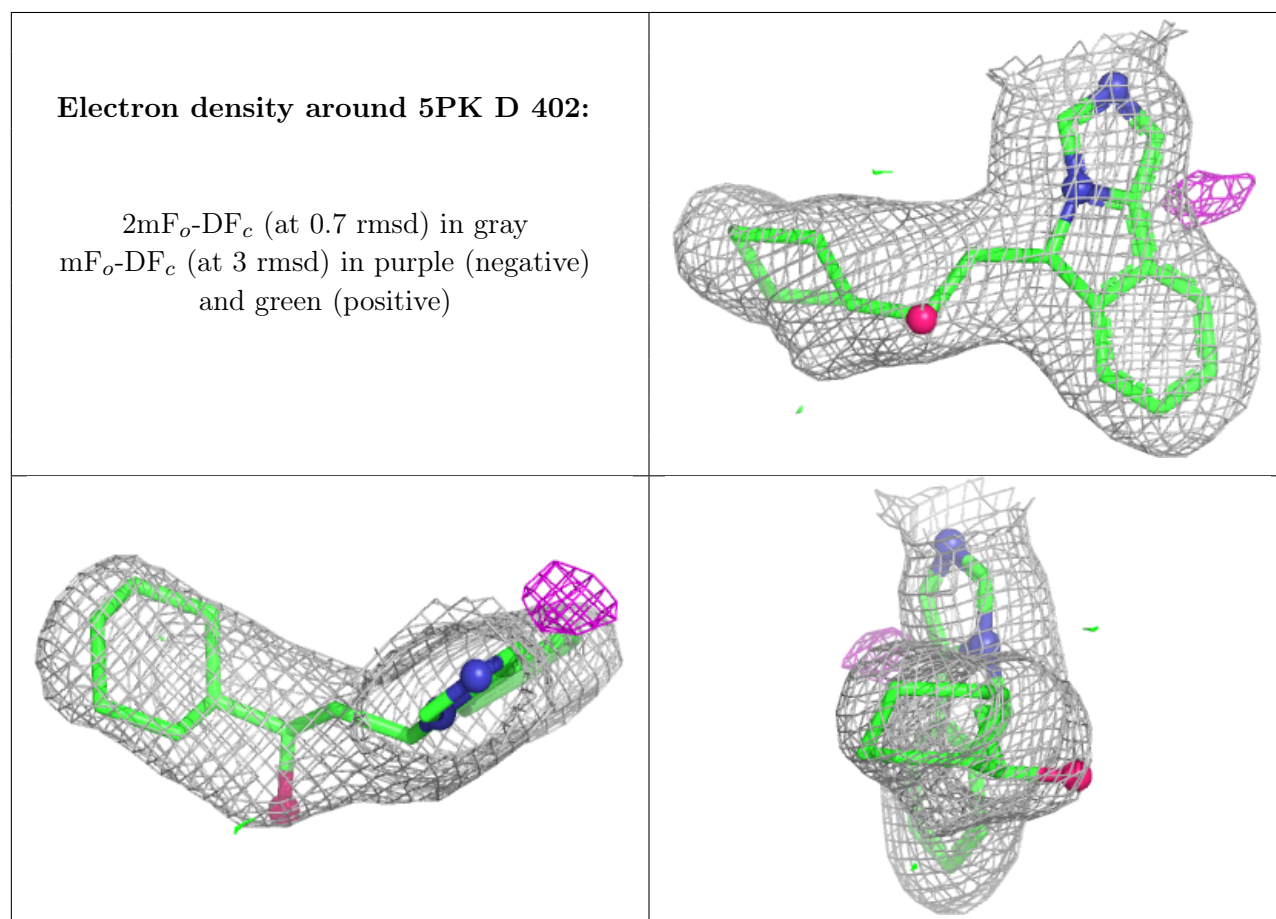
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	5PK	D	402	21/21	0.98	0.06	51,53,56,57	0
2	HEM	B	401	43/43	0.99	0.04	41,43,51,53	0
3	5PK	A	402	21/21	0.99	0.05	54,55,60,60	0
3	5PK	B	402	21/21	0.99	0.05	50,51,57,58	0

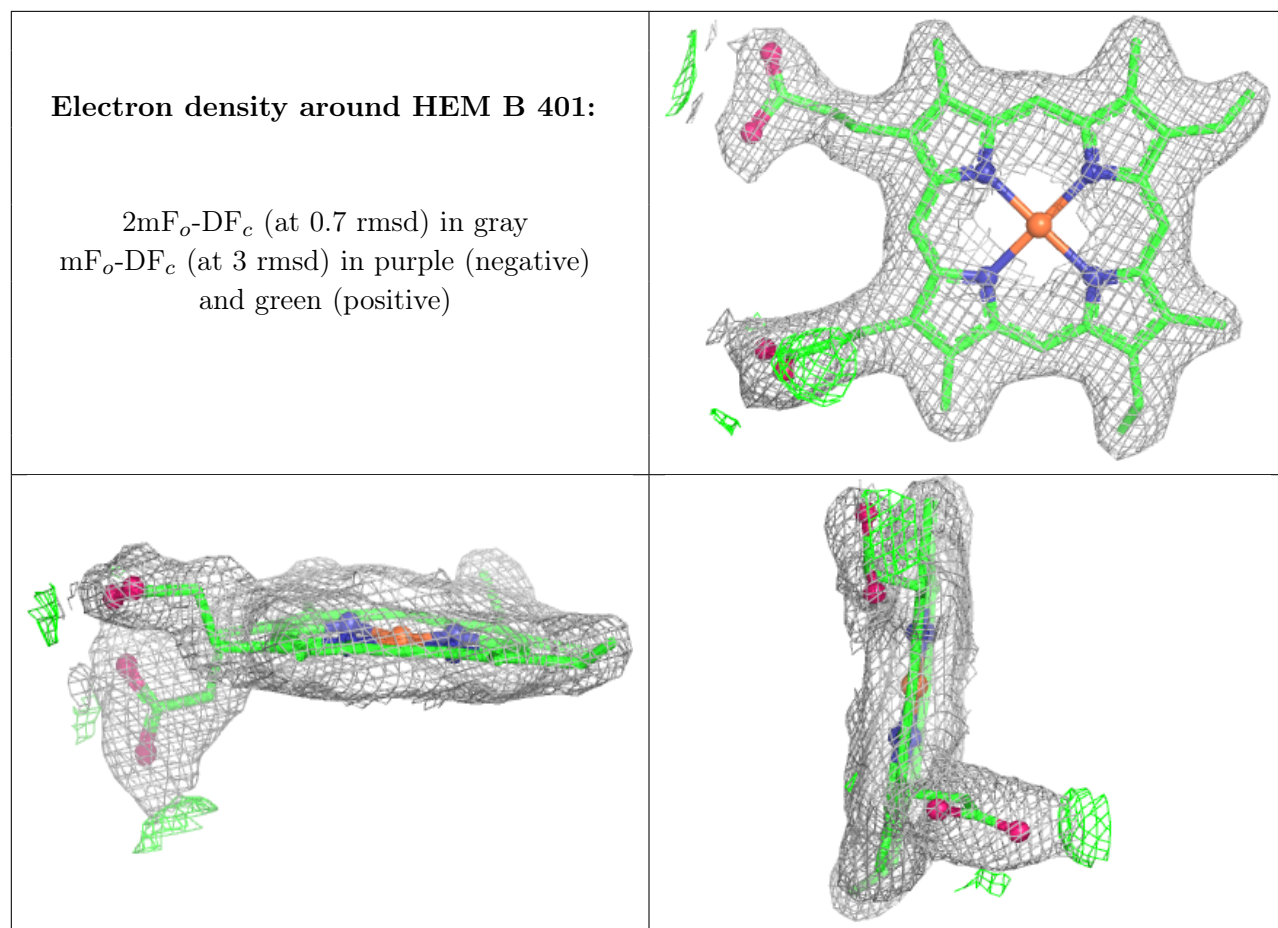
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	5PK	C	402	21/21	0.99	0.05	54,54,60,61	0
2	HEM	A	401	43/43	0.99	0.04	43,45,51,53	0
2	HEM	C	401	43/43	1.00	0.03	40,42,48,50	0
2	HEM	D	401	43/43	1.00	0.03	42,44,50,53	0

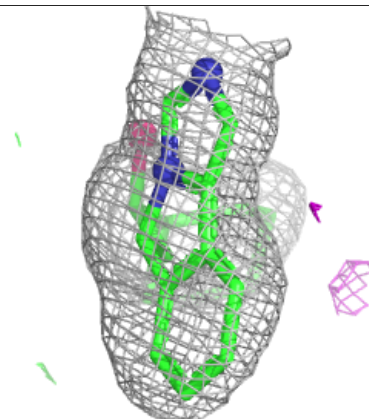
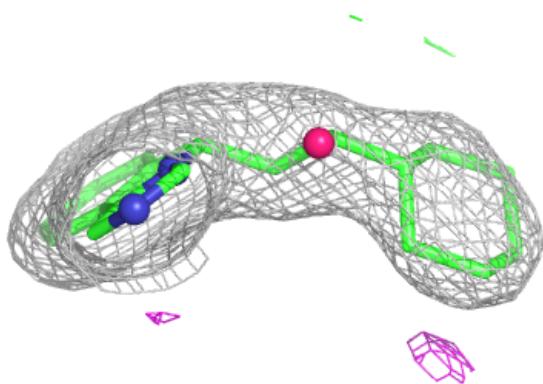
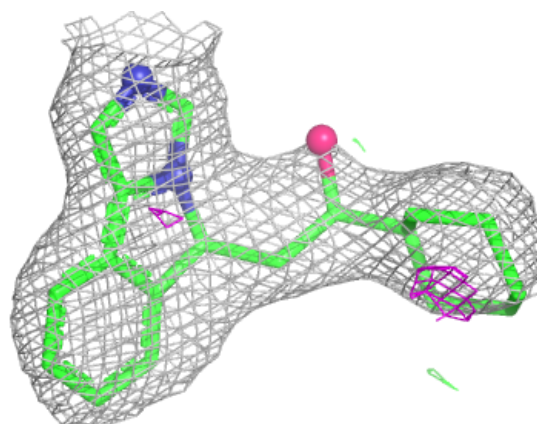
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



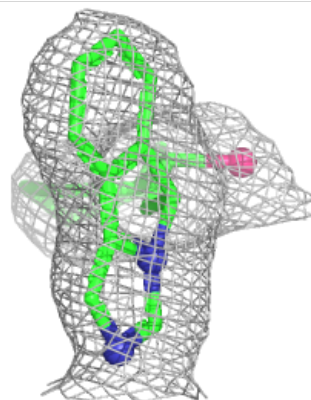
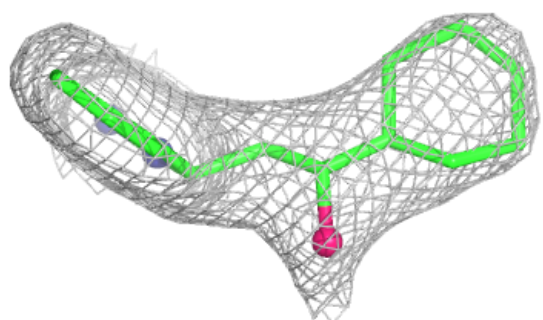
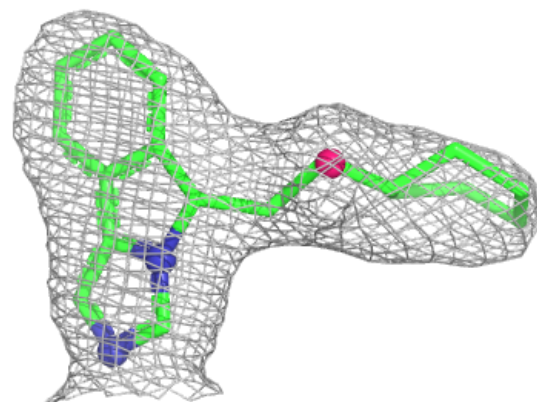


**Electron density around 5PK A 402:**

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

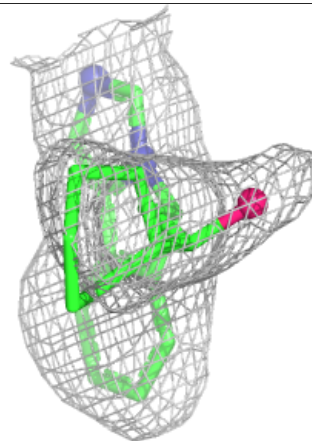
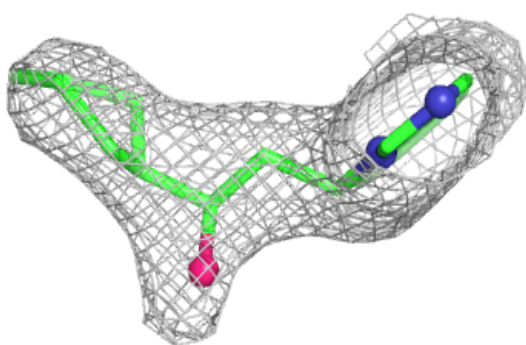
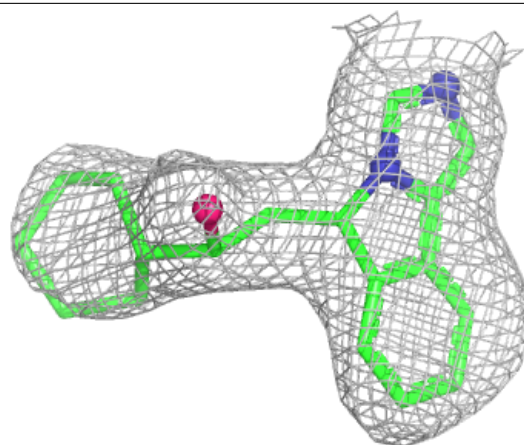
**Electron density around 5PK B 402:**

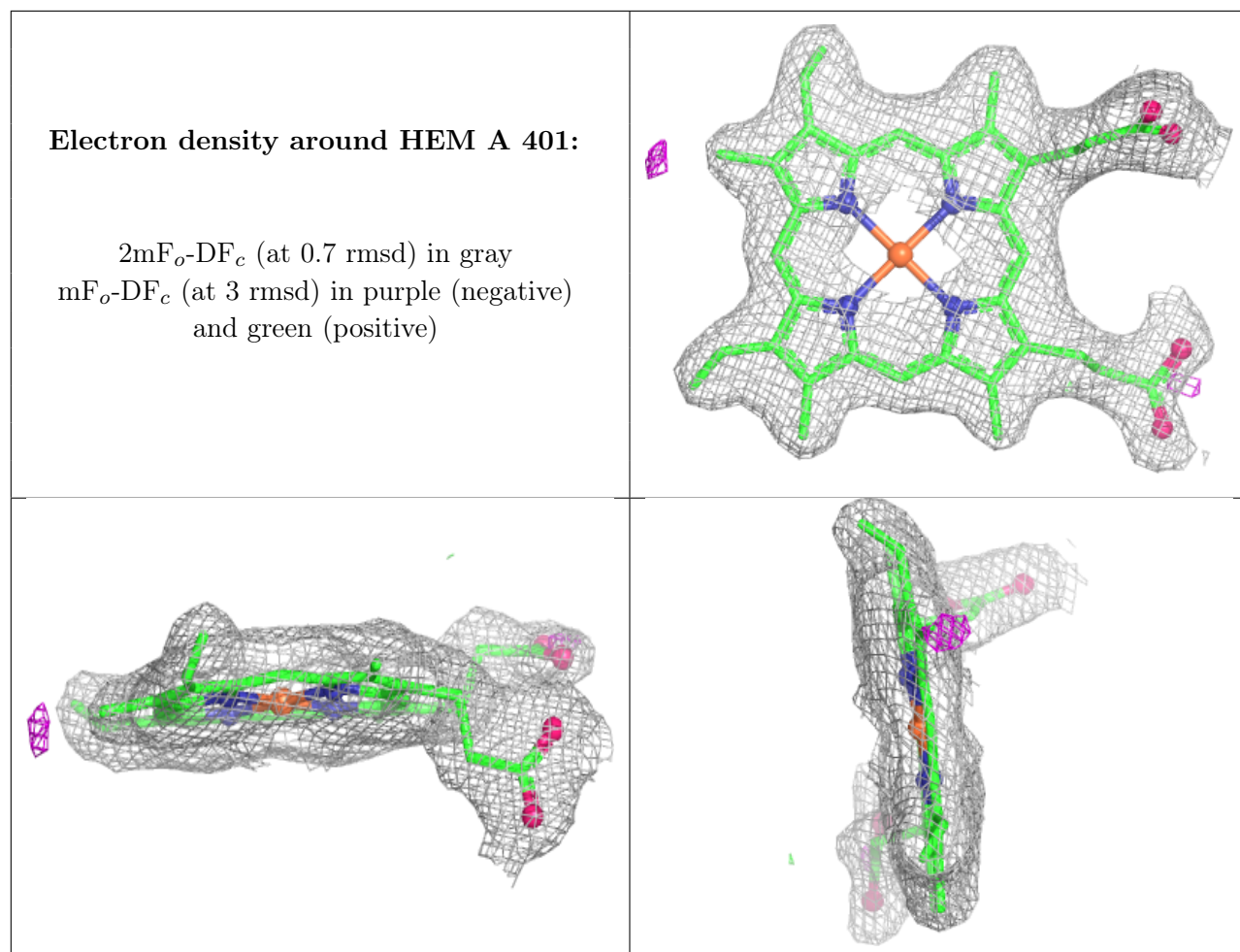
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

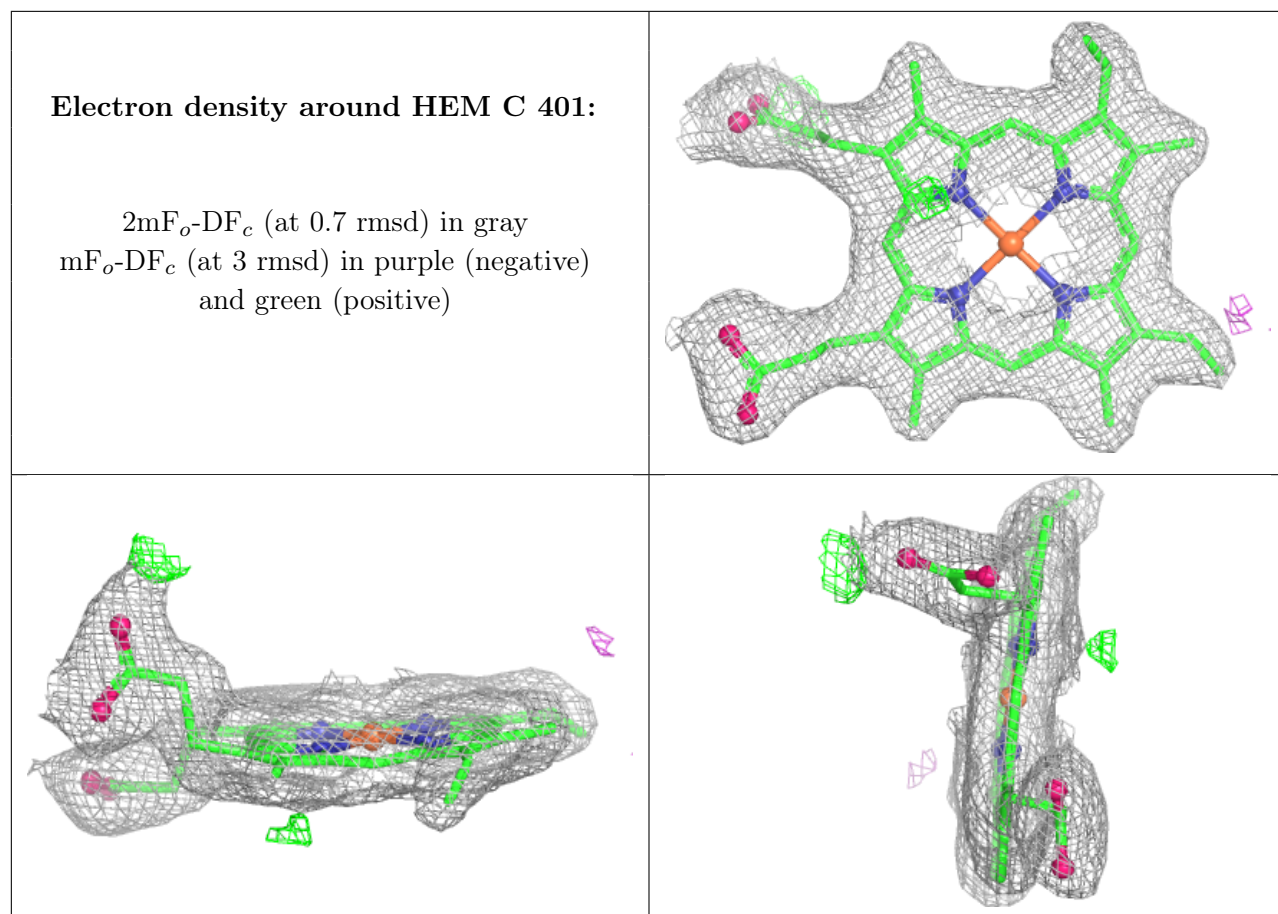


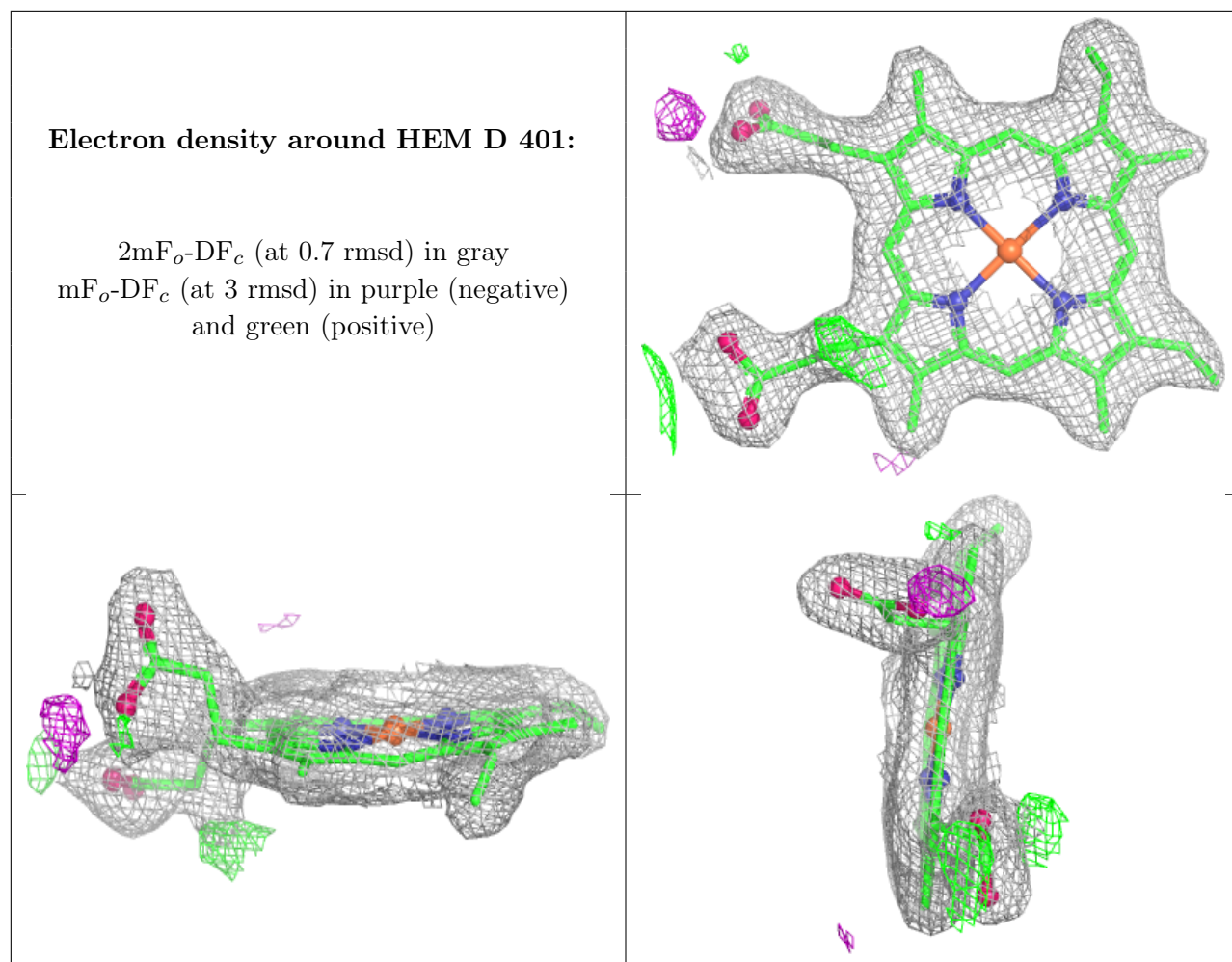
**Electron density around 5PK C 402:**

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









## 6.5 Other polymers [i](#)

There are no such residues in this entry.