



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 10, 2023 – 12:45 am GMT

PDB ID : 2VZ7  
Title : Crystal structure of the YC-17-bound PikC D50N mutant  
Authors : Li, S.; Sherman, D.H.; Podust, L.M.  
Deposited on : 2008-07-30  
Resolution : 3.20 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 : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

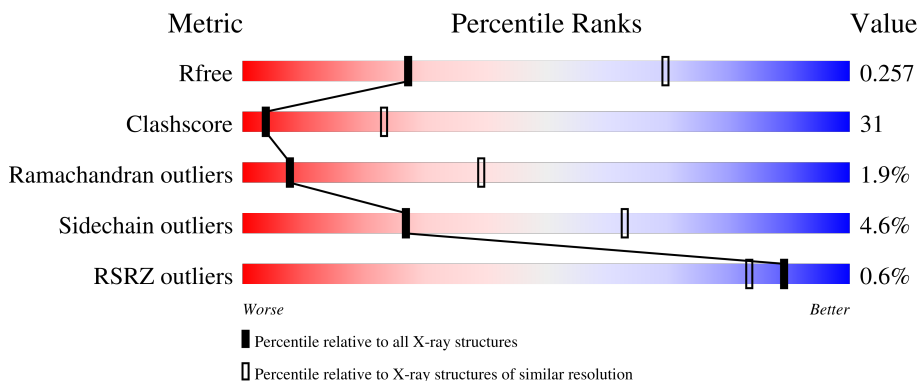
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	436	
1	B	436	

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
3	PXI	A	1408	X	-	-	-
3	PXI	B	1408	X	-	-	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6441 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.

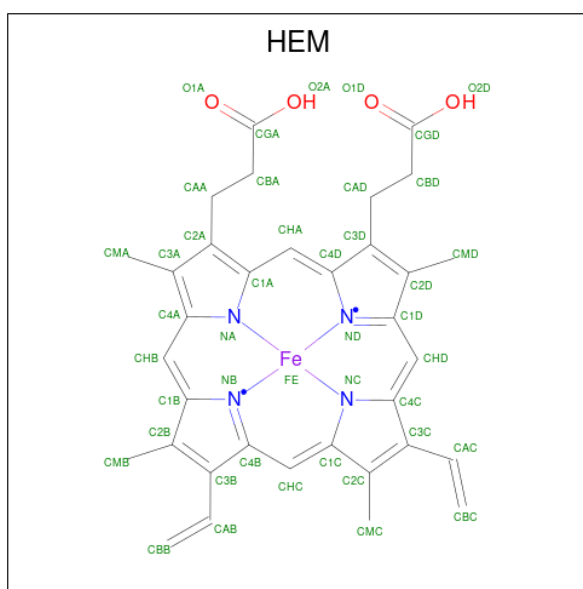
- Molecule 1 is a protein called CYTOCHROME P450 MONOOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	396	Total 3068	C 1937	N 552	O 566	S 13	0	0	0
1	B	393	Total 3048	C 1924	N 546	O 565	S 13	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	ASN	ASP	engineered mutation	UNP O87605
B	50	ASN	ASP	engineered mutation	UNP O87605

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



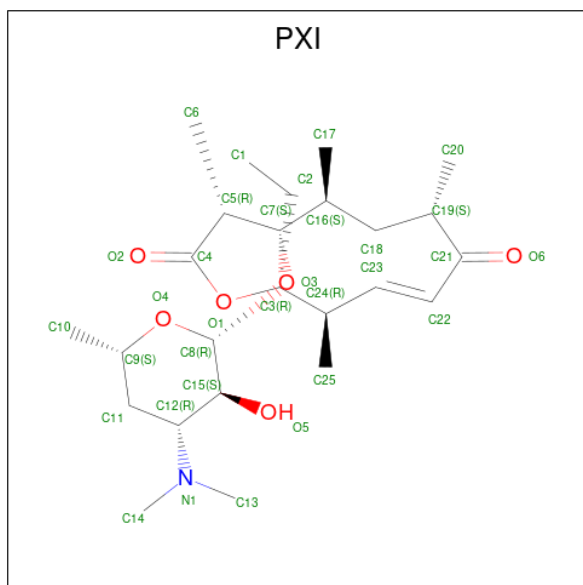
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	N	O		
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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

- Molecule 3 is 4-{{4-(DIMETHYLAMINO)-3-HYDROXY-6-METHYLTETRAHYDRO-2H-PYRAN-2-YL}OXY}-12-ETHYL-3,5,7,11-TETRAMETHYLOXACYCLODODEC-9-ENE-2,8-DIONE (three-letter code: PXI) (formula: C<sub>25</sub>H<sub>43</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	32	25	1	6	0	0
3	B	1	32	25	1	6	0	0

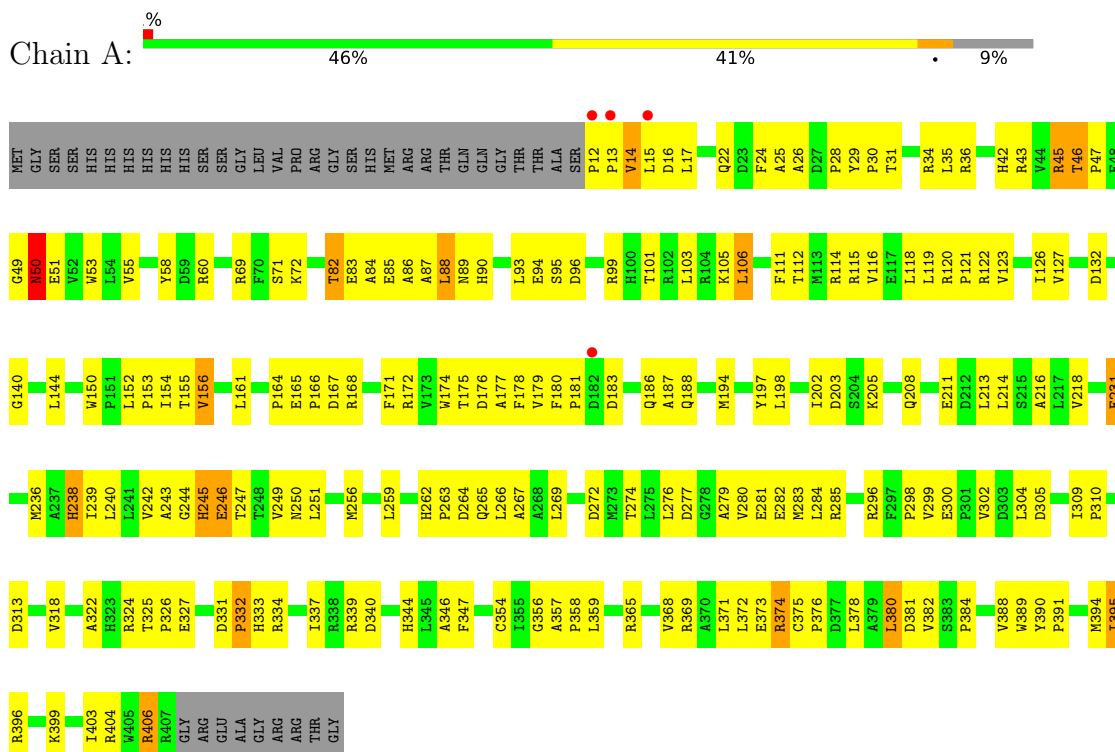
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	81	Total O 81 81	0	0
4	B	94	Total O 94 94	0	0

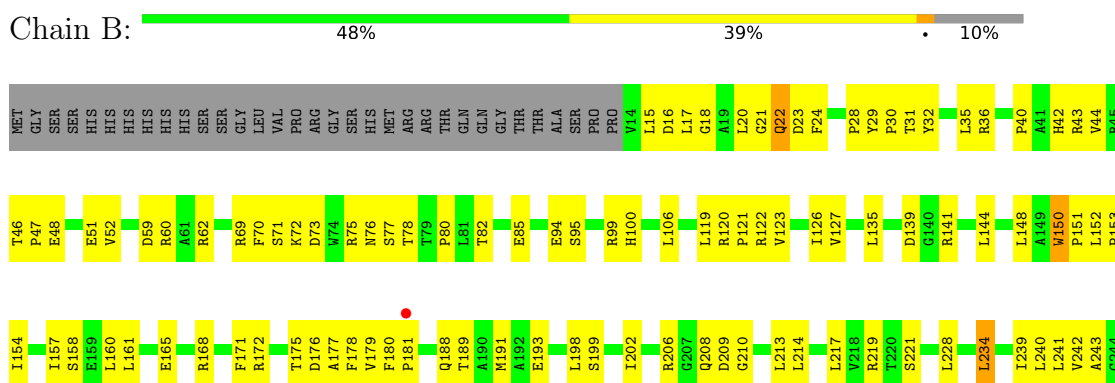
### 3 Residue-property plots i

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: CYTOCHROME P450 MONOOXYGENASE



#### • Molecule 1: CYTOCHROME P450 MONOOXYGENASE



H245	H246	T247	T248	L251	L252	A253	N254	M255	M256	L259	H262	P263	D264	Q265	L266	A267	A268	L269	R270	L276	D277	V280	E281	E282	M283	L284	R285	Y286	E287	V290	T294	Y295	R296	F297	P298	V302	D303	L304	D305	I309	P310	A311	G312	D313	L316	V317	V318	L319	A320			
D321	R324	T325	P326	F329	P330	D331	P332	H333	R334	F335	D336	I337	R338	R339	H344	L345	A346	H352	R361	R365	I366	R369	A370	L371	L372	E373	R374	C375	P376	A379	L380	D381	V382	S383	P384	L387	N392	P393	M394	I395	R396	I403	R406	ARG	GLY	ARG	GLU					
ALA	GLY	ARG	ARG	THR	GLY																																															

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.86Å 109.32Å 153.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.67 – 3.20 49.66 – 3.19	Depositor EDS
% Data completeness (in resolution range)	94.5 (49.67-3.20) 94.2 (49.66-3.19)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.77 (at 3.19Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.179 , 0.260 0.175 , 0.257	Depositor DCC
$R_{free}$ test set	1718 reflections (9.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.6	Xtrriage
Anisotropy	0.414	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 56.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6441	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.64% 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: HEM, PXI

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	0.34	0/3140	0.62	1/4285 (0.0%)
1	B	0.35	0/3119	0.59	0/4256
All	All	0.35	0/6259	0.61	1/8541 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	PRO	N-CA-CB	5.63	110.06	103.30

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	3068	0	3036	189	0
1	B	3048	0	3016	184	0
2	A	43	0	30	8	0
2	B	43	0	30	1	0
3	A	32	0	43	15	0
3	B	32	0	43	11	0
4	A	81	0	0	9	0
4	B	94	0	0	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6441	0	6198	384	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 31.

The worst 5 of 384 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:A:1408:PXI:H16	3:A:1408:PXI:H22	1.38	1.01
1:A:43:ARG:HH11	1:A:43:ARG:HB3	1.23	1.01
1:B:43:ARG:HH12	1:B:51:GLU:HB3	1.21	1.00
1:A:43:ARG:HB3	1:A:43:ARG:NH1	1.80	0.97
1:B:384:PRO:HA	1:B:387:LEU:HD12	1.49	0.92

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	394/436 (90%)	330 (84%)	54 (14%)	10 (2%)	<b>5</b> 32
1	B	391/436 (90%)	337 (86%)	49 (12%)	5 (1%)	<b>12</b> 47
All	All	785/872 (90%)	667 (85%)	103 (13%)	15 (2%)	<b>8</b> 39

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	50	ASN
1	A	14	VAL
1	A	374	ARG
1	B	245	HIS

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Mol	Chain	Res	Type
1	B	305	ASP

### 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	319/355 (90%)	301 (94%)	18 (6%)	21	57
1	B	318/355 (90%)	307 (96%)	11 (4%)	36	69
All	All	637/710 (90%)	608 (95%)	29 (5%)	27	63

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	245	HIS
1	B	394	MET
1	A	395	ILE
1	B	270	ARG
1	A	380	LEU

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

Mol	Chain	Res	Type
1	B	22	GLN
1	B	333	HIS
1	B	76	ASN
1	B	344	HIS
1	B	245	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 monosaccharides 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
3	PXI	B	1408	-	33,33,33	1.59	9 (27%)	40,47,47	2.41	13 (32%)
2	HEM	A	1407	1	41,50,50	1.39	6 (14%)	45,82,82	1.20	3 (6%)
3	PXI	A	1408	-	33,33,33	1.82	8 (24%)	40,47,47	2.36	15 (37%)
2	HEM	B	1407	-	41,50,50	1.51	8 (19%)	45,82,82	1.07	2 (4%)

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
3	PXI	B	1408	-	5/5/13/15	10/43/59/59	0/1/2/2
2	HEM	A	1407	1	-	4/12/54/54	-
3	PXI	A	1408	-	5/5/13/15	7/43/59/59	0/1/2/2
2	HEM	B	1407	-	-	0/12/54/54	-

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1408	PXI	C19-C21	5.05	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1408	PXI	C5-C4	4.58	1.61	1.51
2	A	1407	HEM	C3C-CAC	-4.13	1.39	1.47
3	B	1408	PXI	C5-C4	3.68	1.59	1.51
2	B	1407	HEM	C3C-CAC	-3.58	1.40	1.47

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1408	PXI	C8-O3-C7	-7.91	98.40	117.96
3	A	1408	PXI	C8-O3-C7	-7.43	99.57	117.96
3	B	1408	PXI	O1-C4-C5	5.66	123.99	111.56
3	A	1408	PXI	O1-C4-C5	5.08	122.71	111.56
3	B	1408	PXI	O1-C3-C2	4.92	114.77	106.92

5 of 10 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1408	PXI	C9
3	A	1408	PXI	C15
3	A	1408	PXI	C8
3	A	1408	PXI	C12
3	A	1408	PXI	C19

5 of 21 torsion outliers are listed below:

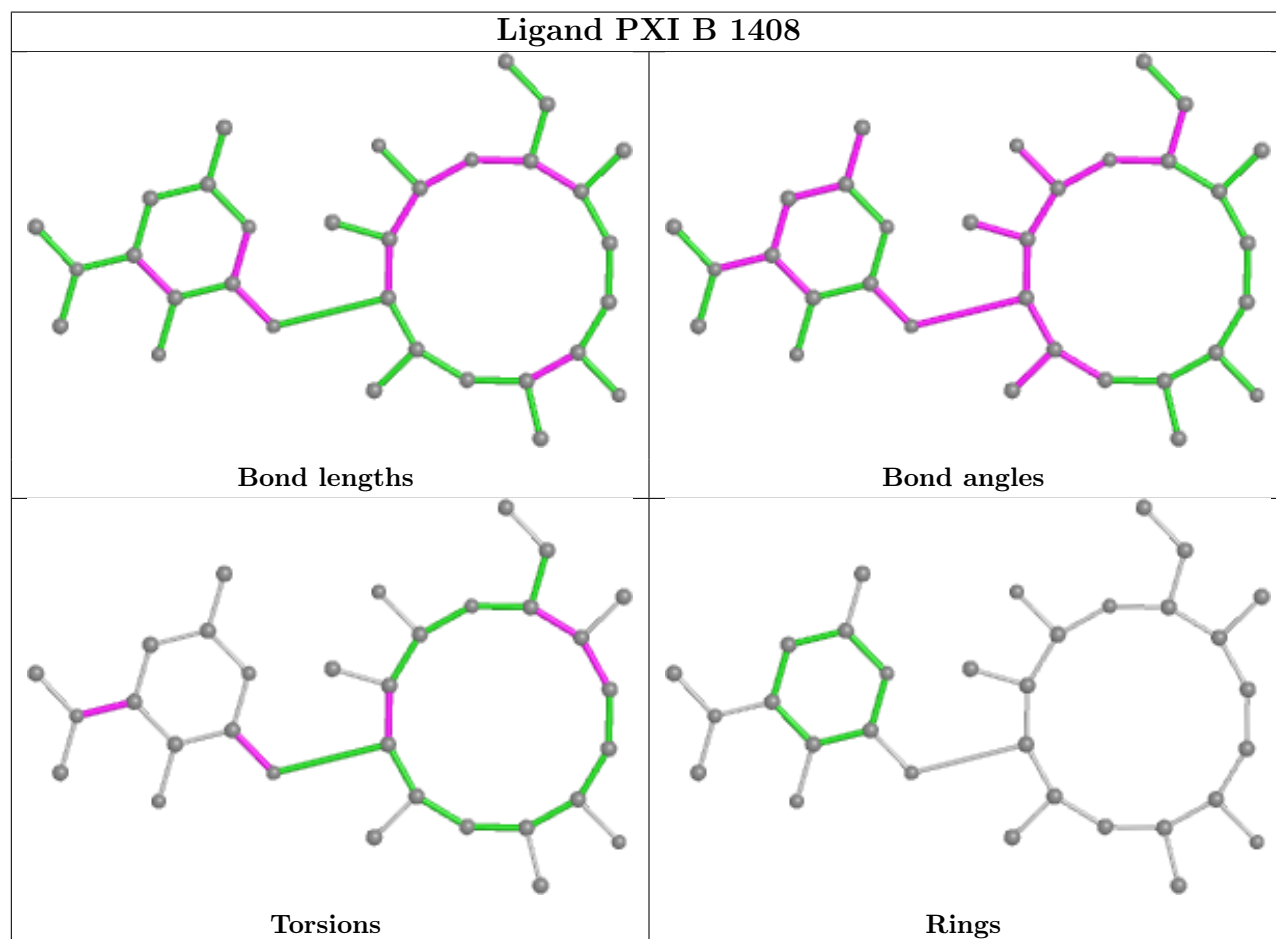
Mol	Chain	Res	Type	Atoms
3	A	1408	PXI	C4-C5-C7-C16
3	A	1408	PXI	C6-C5-C7-O3
3	A	1408	PXI	C18-C19-C21-O6
3	A	1408	PXI	C18-C19-C21-C22
3	B	1408	PXI	C23-C24-C3-C2

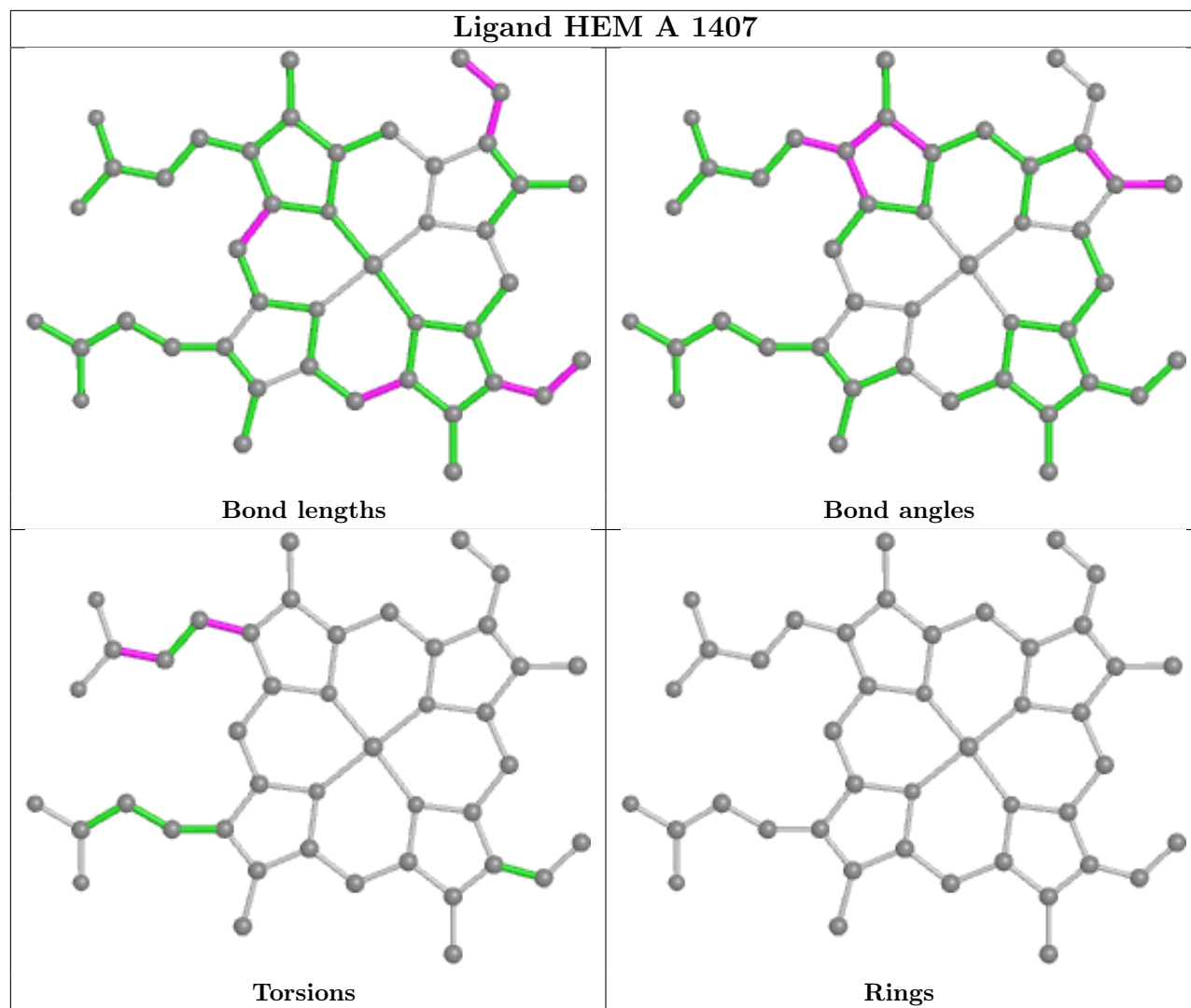
There are no ring outliers.

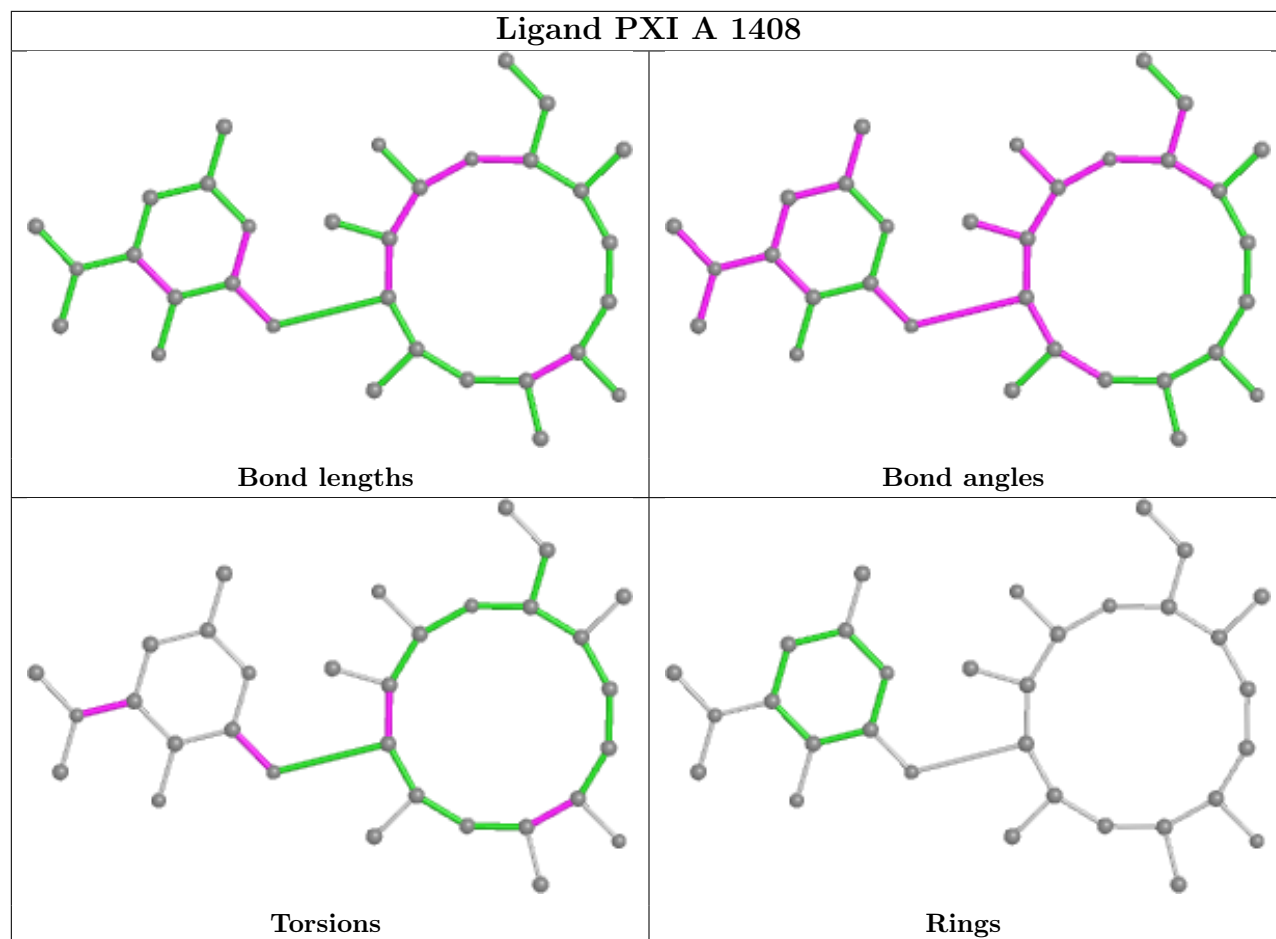
4 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1408	PXI	11	0
2	A	1407	HEM	8	0
3	A	1408	PXI	15	0
2	B	1407	HEM	1	0

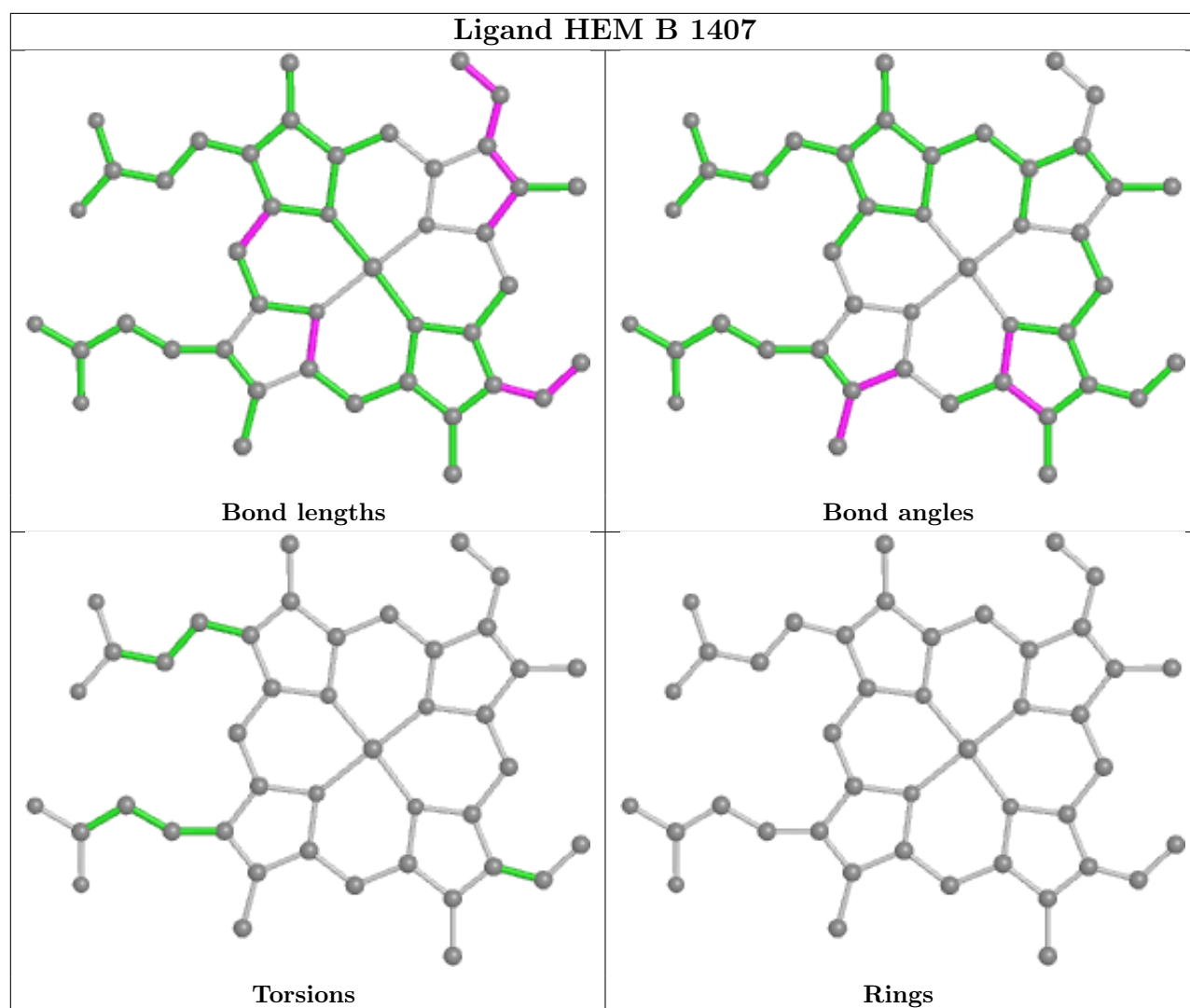
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











## 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	396/436 (90%)	-0.28	4 (1%) 82 72	26, 44, 71, 93	0
1	B	393/436 (90%)	-0.41	1 (0%) 94 92	19, 44, 73, 92	0
All	All	789/872 (90%)	-0.35	5 (0%) 89 83	19, 44, 72, 93	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	12	PRO	2.6
1	A	13	PRO	2.6
1	A	182	ASP	2.4
1	B	181	PRO	2.2
1	A	15	LEU	2.0

### 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](#)

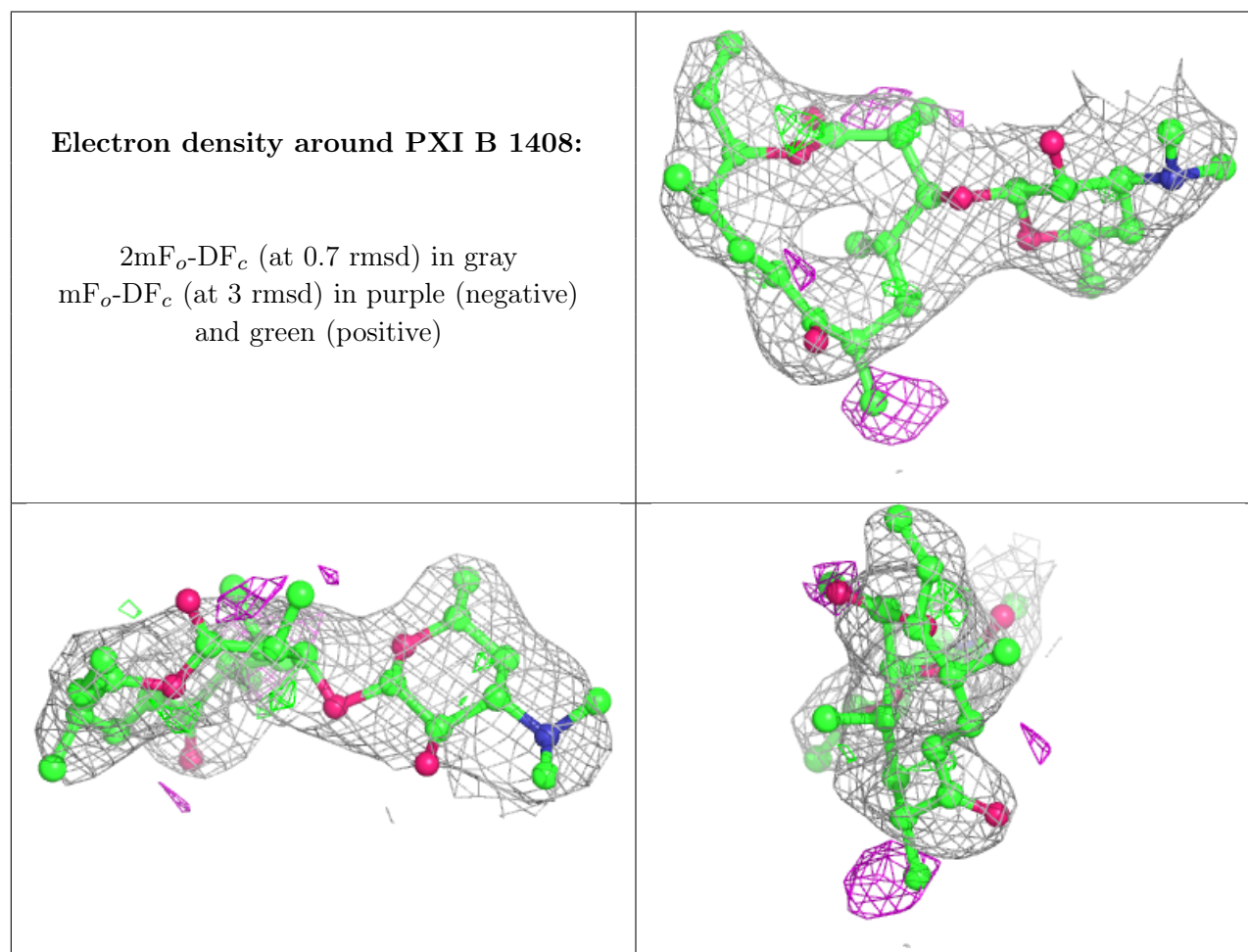
There are no monosaccharides in this entry.

### 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.

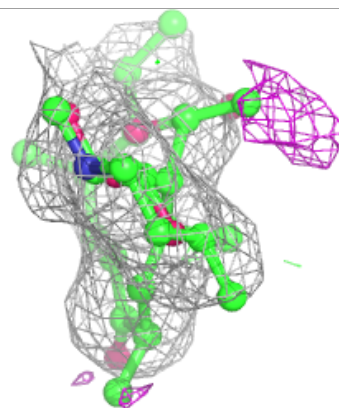
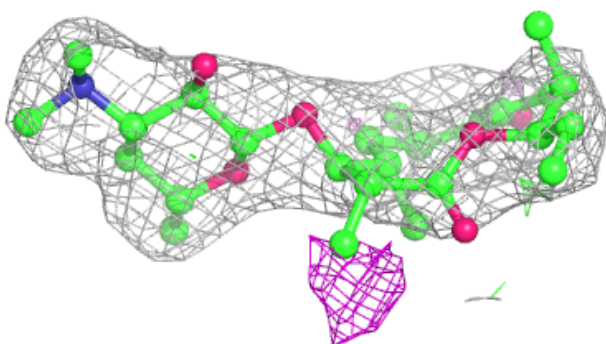
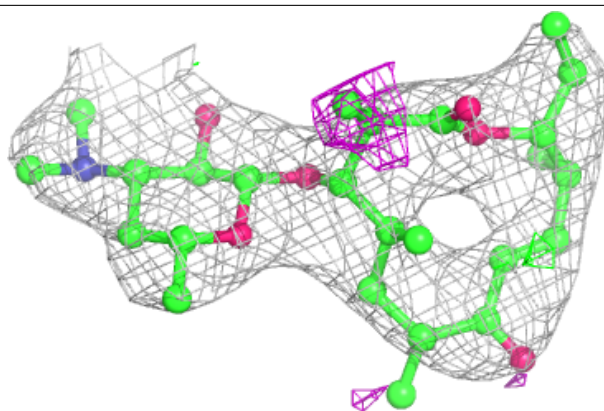
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	PXI	B	1408	32/32	0.91	0.31	36,42,49,52	0
3	PXI	A	1408	32/32	0.93	0.32	38,48,55,56	0
2	HEM	A	1407	43/43	0.98	0.16	25,30,32,33	0
2	HEM	B	1407	43/43	0.98	0.14	24,29,31,33	0

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.

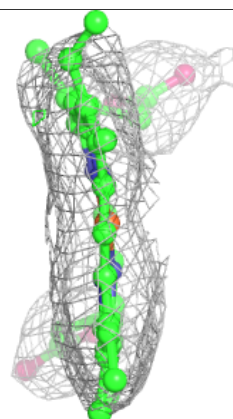
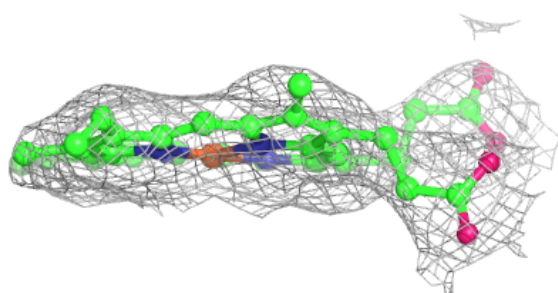
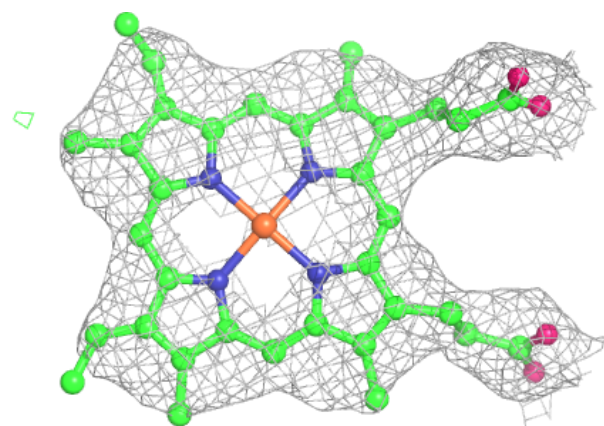


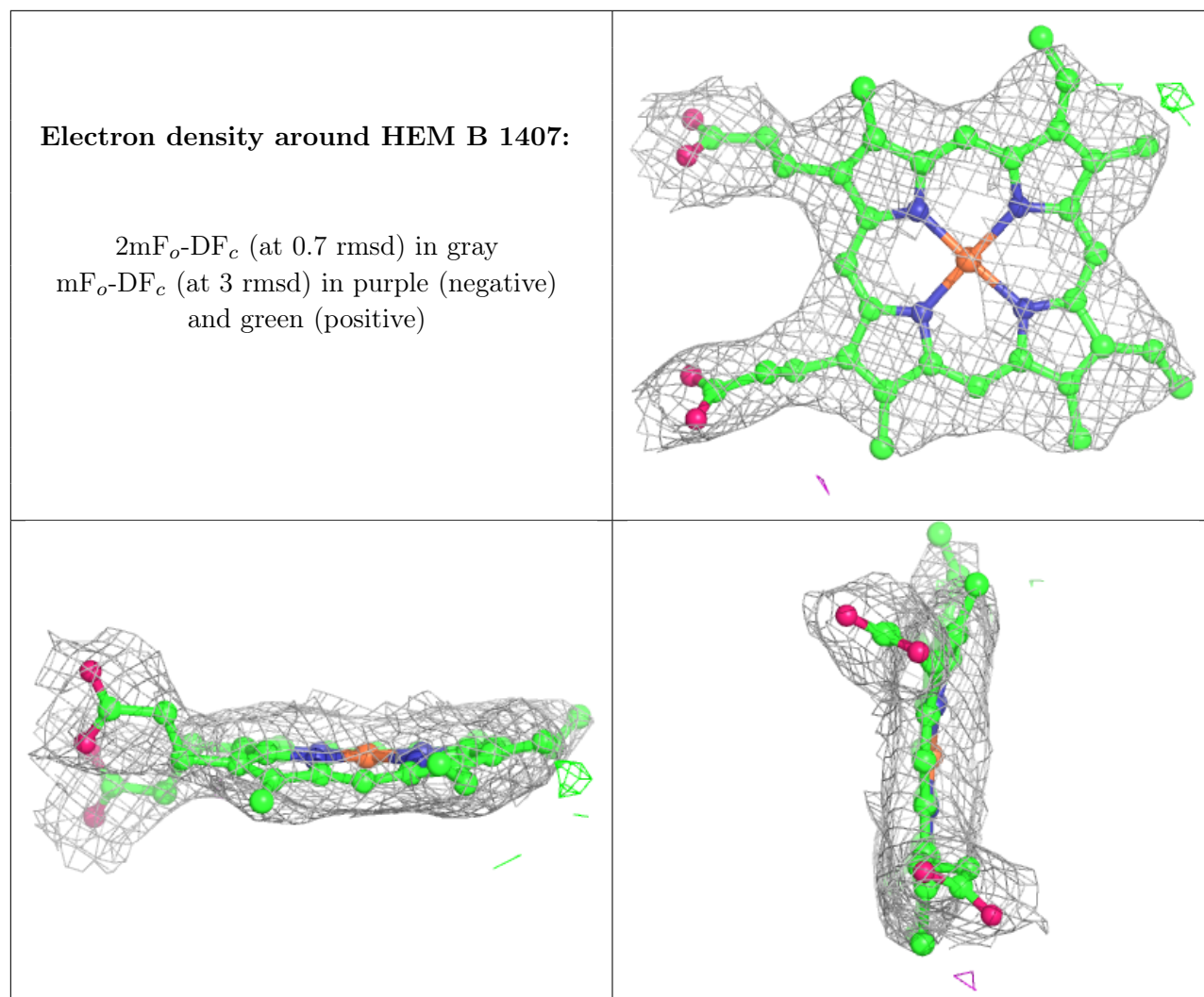
**Electron density around PXI A 1408:**

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

**Electron density around HEM A 1407:**

$2mF_o-DF_c$  (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.