



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 05:21 am BST

PDB ID : 6BD8  
Title : Crystal structure of human CYP3A4 bound to an inhibitor  
Authors : Sevrioukova, I.  
Deposited on : 2017-10-21  
Resolution : 2.38 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

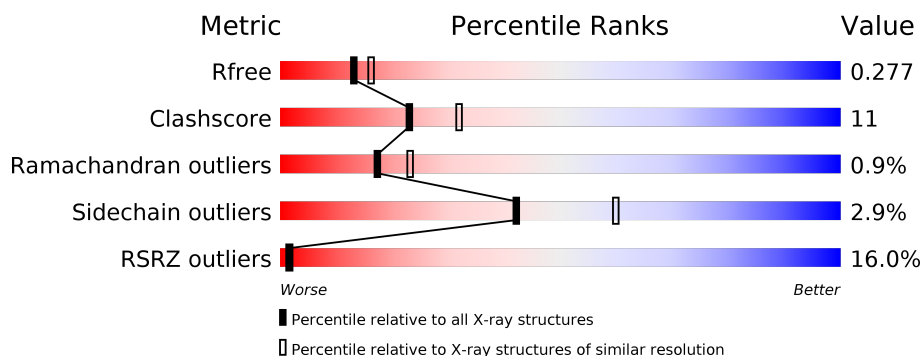
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.38 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	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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 on 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	487	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3834 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 3A4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	457	Total	C	N	O	S	0	14	0
			3753	2449	612	665	27			

There are 24 discrepancies between the modelled and reference sequences:

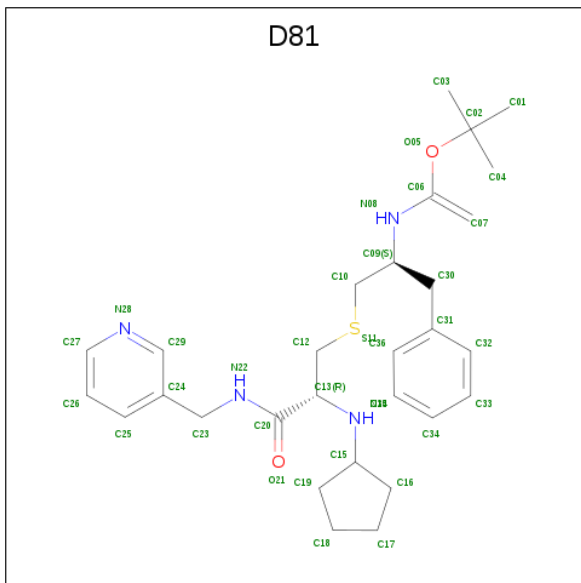
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LEU	deletion	UNP P08684
A	?	-	ILE	deletion	UNP P08684
A	?	-	PRO	deletion	UNP P08684
A	?	-	ASP	deletion	UNP P08684
A	?	-	LEU	deletion	UNP P08684
A	?	-	ALA	deletion	UNP P08684
A	?	-	MET	deletion	UNP P08684
A	?	-	GLU	deletion	UNP P08684
A	?	-	THR	deletion	UNP P08684
A	?	-	TRP	deletion	UNP P08684
A	?	-	LEU	deletion	UNP P08684
A	?	-	LEU	deletion	UNP P08684
A	?	-	LEU	deletion	UNP P08684
A	?	-	ALA	deletion	UNP P08684
A	?	-	VAL	deletion	UNP P08684
A	?	-	SER	deletion	UNP P08684
A	?	-	LEU	deletion	UNP P08684
A	?	-	VAL	deletion	UNP P08684
A	?	-	LEU	deletion	UNP P08684
A	?	-	LEU	deletion	UNP P08684
A	504	HIS	-	expression tag	UNP P08684
A	505	HIS	-	expression tag	UNP P08684
A	506	HIS	-	expression tag	UNP P08684
A	507	HIS	-	expression tag	UNP P08684

- 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
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is S-{(2S)-2-[(1-tert-butoxyethenyl)amino]-3-phenylpropyl}-N 2 -cyclopentyl-N-[pyridin-3-yl)methyl]-L-cysteinamide (three-letter code: D81) (formula: C<sub>29</sub>H<sub>42</sub>N<sub>4</sub>O<sub>2</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			36	29	4	2	1		

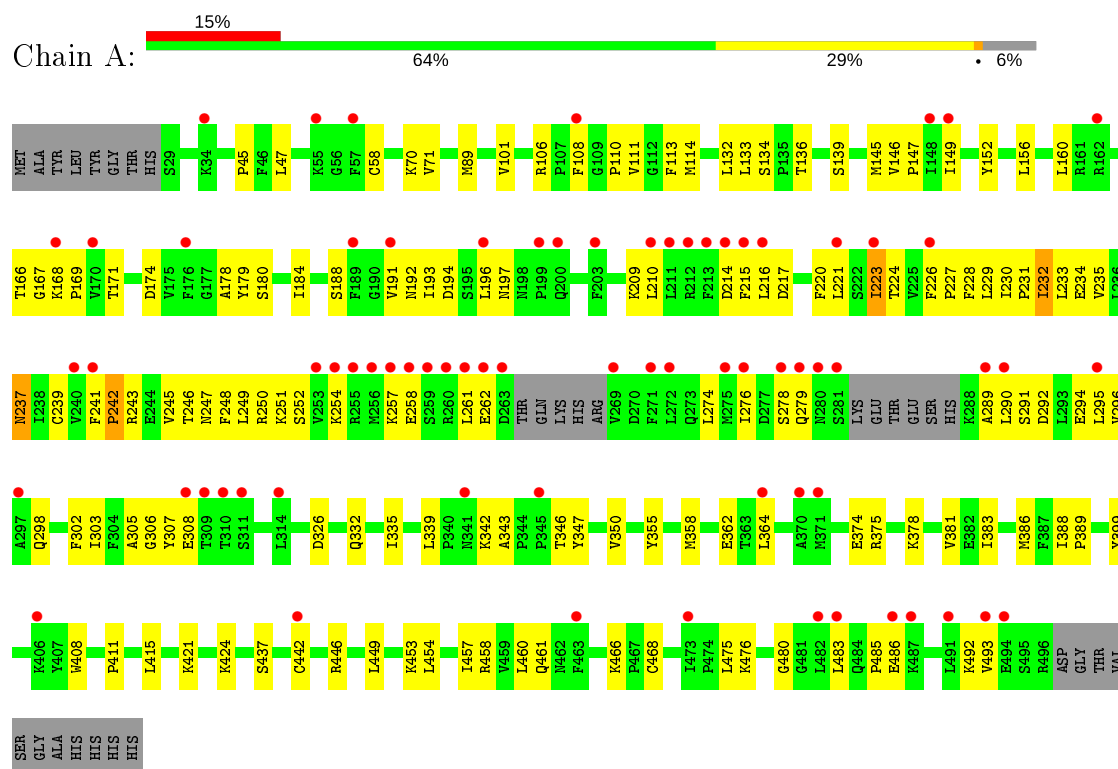
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 3A4



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.74Å 101.29Å 123.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.85 – 2.38 39.85 – 2.38	Depositor EDS
% Data completeness (in resolution range)	95.2 (39.85-2.38) 95.2 (39.85-2.38)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.06 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, $R_{free}$	0.211 , 0.269 0.226 , 0.277	Depositor DCC
$R_{free}$ test set	863 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	87.0	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 94.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3834	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	132.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% 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, D81

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	0.42	0/3871	0.61	0/5234

There are no bond length outliers.

There are no bond angle outliers.

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	3753	0	3869	87	0
2	A	43	0	30	3	0
3	A	36	0	0	1	0
4	A	2	0	0	0	0
All	All	3834	0	3899	88	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 11.

All (88) 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:A:239[B]:CYS:SG	1:A:243:ARG:NH2	2.50	0.84
1:A:70:LYS:HG3	1:A:71[A]:VAL:HG23	1.64	0.79
2:A:601:HEM:HBC2	2:A:601:HEM:HHD	1.66	0.77
1:A:166:THR:O	1:A:168:LYS:N	2.26	0.68
1:A:291:SER:OG	1:A:292:ASP:N	2.29	0.66
1:A:421:LYS:HA	1:A:424:LYS:HE3	1.79	0.64
1:A:237:ASN:OD1	1:A:243:ARG:NH2	2.32	0.62
1:A:257:LYS:NZ	1:A:292:ASP:OD1	2.35	0.60
1:A:194:ASP:OD2	1:A:197:ASN:ND2	2.22	0.60
1:A:160:LEU:HD22	1:A:493:VAL:HG11	1.83	0.60
1:A:220:PHE:HA	1:A:223:ILE:HB	1.83	0.59
1:A:216:LEU:HD23	1:A:221:LEU:HD21	1.83	0.59
1:A:408:TRP:HB2	1:A:411:PRO:HB3	1.86	0.58
1:A:294:GLU:O	1:A:298:GLN:HG2	2.05	0.56
1:A:362:GLU:OE1	1:A:415:LEU:N	2.37	0.56
1:A:101:VAL:O	1:A:378:LYS:HG2	2.06	0.56
1:A:332:GLN:HG2	1:A:460:LEU:HB3	1.88	0.55
1:A:249:LEU:HA	1:A:252:SER:HB2	1.87	0.55
1:A:442:CYS:HB2	2:A:601:HEM:NA	2.22	0.55
1:A:106[B]:ARG:HH21	1:A:374:GLU:CD	2.11	0.54
1:A:169:PRO:HG3	1:A:468:CYS:SG	2.48	0.53
1:A:226:PHE:HA	1:A:228:PHE:CE2	2.43	0.53
1:A:229:LEU:O	1:A:232:ILE:HB	2.08	0.53
1:A:58:CYS:HB3	1:A:399:TYR:CD2	2.43	0.53
1:A:355:TYR:HA	1:A:358:MET:SD	2.48	0.53
1:A:132:LEU:HD13	1:A:290:LEU:HG	1.91	0.53
1:A:111:VAL:O	1:A:114:MET:HB2	2.10	0.52
1:A:184:ILE:O	1:A:188:SER:OG	2.23	0.52
1:A:210:LEU:HD21	1:A:245:VAL:HG11	1.91	0.52
1:A:113:PHE:CZ	1:A:246:THR:HB	2.45	0.52
1:A:101:VAL:HG21	1:A:381[A]:VAL:HG11	1.92	0.51
1:A:209:LYS:HB2	1:A:245:VAL:HG21	1.93	0.51
1:A:136:THR:HG23	1:A:274:LEU:HD12	1.93	0.51
1:A:106[B]:ARG:NH2	1:A:374:GLU:OE2	2.28	0.51
1:A:229:LEU:HA	1:A:232:ILE:HG13	1.93	0.50
1:A:229:LEU:O	1:A:233:LEU:HG	2.11	0.50
1:A:184:ILE:HD11	1:A:306:GLY:C	2.32	0.50
1:A:279:GLN:HA	1:A:289:ALA:HB1	1.95	0.49
1:A:257:LYS:HG2	1:A:276:ILE:HD11	1.95	0.48
1:A:139:SER:HB3	1:A:446[B]:ARG:CZ	2.44	0.48
1:A:466:LYS:O	1:A:492:LYS:N	2.35	0.48
1:A:231:PRO:O	1:A:235:VAL:HG12	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:ASP:HB3	1:A:217:ASP:HB3	1.95	0.47
1:A:223:ILE:HA	1:A:223:ILE:HD13	1.65	0.47
1:A:230:ILE:O	1:A:234:GLU:HG2	2.15	0.47
1:A:342:LYS:HE2	1:A:461:GLN:O	2.15	0.46
1:A:58:CYS:HB3	1:A:399:TYR:CE2	2.50	0.46
1:A:346:THR:O	1:A:350:VAL:HG23	2.15	0.46
1:A:339:LEU:HB3	1:A:343:ALA:HB3	1.98	0.46
1:A:146:VAL:HG21	1:A:347:TYR:HB2	1.98	0.46
1:A:375:ARG:HH22	2:A:601:HEM:CGA	2.29	0.46
1:A:250:ARG:HA	1:A:296:VAL:HG11	1.97	0.45
1:A:230:ILE:HB	1:A:231:PRO:HD3	1.99	0.45
1:A:113:PHE:HZ	1:A:246:THR:HB	1.81	0.45
1:A:145:MET:O	1:A:149:ILE:HG13	2.17	0.45
1:A:261:LEU:HA	1:A:262:GLU:HA	1.66	0.45
1:A:454:LEU:HA	1:A:454:LEU:HD23	1.79	0.44
1:A:383:ILE:O	1:A:383:ILE:HG13	2.18	0.44
1:A:171:THR:OG1	1:A:174:ASP:OD2	2.31	0.44
1:A:152:TYR:OH	1:A:192:ASN:HA	2.18	0.44
1:A:278:SER:OG	1:A:290:LEU:HD12	2.17	0.44
1:A:227:PRO:C	1:A:229:LEU:H	2.20	0.44
1:A:184:ILE:HD13	1:A:303:ILE:O	2.17	0.43
1:A:476:LYS:O	1:A:486:GLU:HB2	2.18	0.43
1:A:108[B]:PHE:O	1:A:223:ILE:HG21	2.18	0.43
1:A:180:SER:OG	1:A:306:GLY:O	2.35	0.43
1:A:386:MET:HB2	1:A:386:MET:HE3	1.78	0.43
1:A:388:ILE:HA	1:A:389:PRO:HD3	1.91	0.43
1:A:146:VAL:HB	1:A:147:PRO:HD3	2.01	0.42
1:A:483:LEU:HA	1:A:483:LEU:HD12	1.68	0.42
1:A:178:ALA:HB1	1:A:196:LEU:HB2	2.00	0.42
1:A:305:ALA:HB2	3:A:602:D81:C23	2.49	0.42
1:A:364:LEU:HA	1:A:364:LEU:HD23	1.76	0.42
1:A:184:ILE:HD11	1:A:307:TYR:N	2.35	0.42
1:A:232:ILE:HG22	1:A:233:LEU:HD23	2.02	0.42
1:A:133:LEU:HD13	1:A:302:PHE:HZ	1.85	0.41
1:A:335:ILE:HD13	1:A:457:ILE:HA	2.03	0.41
1:A:421:LYS:HA	1:A:424:LYS:HG2	2.03	0.41
1:A:245:VAL:O	1:A:248:PHE:HB3	2.20	0.41
1:A:449:LEU:O	1:A:453:LYS:HG3	2.20	0.41
1:A:110[B]:PRO:HA	1:A:234:GLU:OE2	2.20	0.40
1:A:247:ASN:O	1:A:251:LYS:HG2	2.21	0.40
1:A:45:PRO:O	1:A:47:LEU:N	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:VAL:HG12	1:A:193:ILE:HG13	2.02	0.40
1:A:89:MET:HG3	1:A:383:ILE:HD12	2.03	0.40
1:A:475:LEU:HD11	1:A:485:PRO:HB3	2.03	0.40
1:A:241:PHE:HA	1:A:242:PRO:HD2	1.70	0.40
1:A:156:LEU:HD13	1:A:179:TYR:HB2	2.02	0.40

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	465/487 (96%)	421 (90%)	40 (9%)	4 (1%)	17 23

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	GLY
1	A	237	ASN
1	A	480	GLY
1	A	242	PRO

### 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	431/443 (97%)	419 (97%)	12 (3%)	43 61

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	134	SER
1	A	215	PHE
1	A	223	ILE
1	A	224	THR
1	A	232	ILE
1	A	254	LYS
1	A	258	GLU
1	A	295	LEU
1	A	308	GLU
1	A	326	ASP
1	A	437	SER
1	A	458	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

2 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	601	1,3	27,50,50	2.21	6 (22%)	17,82,82	2.50	8 (47%)
3	D81	A	602	2	36,38,38	1.52	7 (19%)	44,50,50	1.83	8 (18%)

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	601	1,3	-	0/6/54/54	-
3	D81	A	602	2	-	13/28/39/39	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	HEM	C3C-C2C	-5.53	1.32	1.40
2	A	601	HEM	C3D-C2D	5.23	1.53	1.37
3	A	602	D81	C20-N22	4.55	1.43	1.33
2	A	601	HEM	C3B-C2B	-4.26	1.34	1.40
2	A	601	HEM	C3C-CAC	3.40	1.54	1.47
2	A	601	HEM	C3B-CAB	3.35	1.54	1.47
3	A	602	D81	O05-C06	3.14	1.41	1.33
3	A	602	D81	C10-S11	2.84	1.92	1.80
3	A	602	D81	C09-N08	2.59	1.52	1.46
3	A	602	D81	O21-C20	-2.51	1.18	1.23
2	A	601	HEM	CAA-C2A	2.47	1.55	1.52
3	A	602	D81	C23-N22	-2.16	1.41	1.46
3	A	602	D81	C13-C20	2.13	1.58	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	D81	C12-S11-C10	6.47	113.14	102.13
2	A	601	HEM	CBD-CAD-C3D	-5.93	101.55	112.48
2	A	601	HEM	CMA-C3A-C4A	-4.29	121.87	128.46
3	A	602	D81	O05-C06-C07	-3.98	121.37	126.81
2	A	601	HEM	CBA-CAA-C2A	-3.81	105.46	112.49
3	A	602	D81	C12-C13-C20	3.74	117.84	109.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	D81	C31-C30-C09	-3.61	105.59	113.78
2	A	601	HEM	CMD-C2D-C3D	2.79	130.20	124.94
2	A	601	HEM	CMA-C3A-C2A	2.73	130.09	124.94
2	A	601	HEM	C1D-C2D-C3D	-2.61	105.18	107.00
2	A	601	HEM	CMD-C2D-C1D	-2.52	124.59	128.46
3	A	602	D81	C10-C09-C30	2.48	116.70	111.76
3	A	602	D81	C12-C13-N14	2.47	117.59	110.96
3	A	602	D81	C03-C02-C04	-2.16	105.50	111.16
2	A	601	HEM	CMB-C2B-C3B	2.13	128.66	124.68
3	A	602	D81	C24-C23-N22	-2.05	108.66	113.05

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	D81	S11-C12-C13-C20
3	A	602	D81	S11-C12-C13-N14
3	A	602	D81	C12-C13-N14-C15
3	A	602	D81	C16-C15-N14-C13
3	A	602	D81	C19-C15-N14-C13
3	A	602	D81	C10-C09-N08-C06
3	A	602	D81	N08-C09-C30-C31
3	A	602	D81	C20-C13-N14-C15
3	A	602	D81	C01-C02-O05-C06
3	A	602	D81	C04-C02-O05-C06
3	A	602	D81	N08-C09-C10-S11
3	A	602	D81	C09-C10-S11-C12
3	A	602	D81	C03-C02-O05-C06

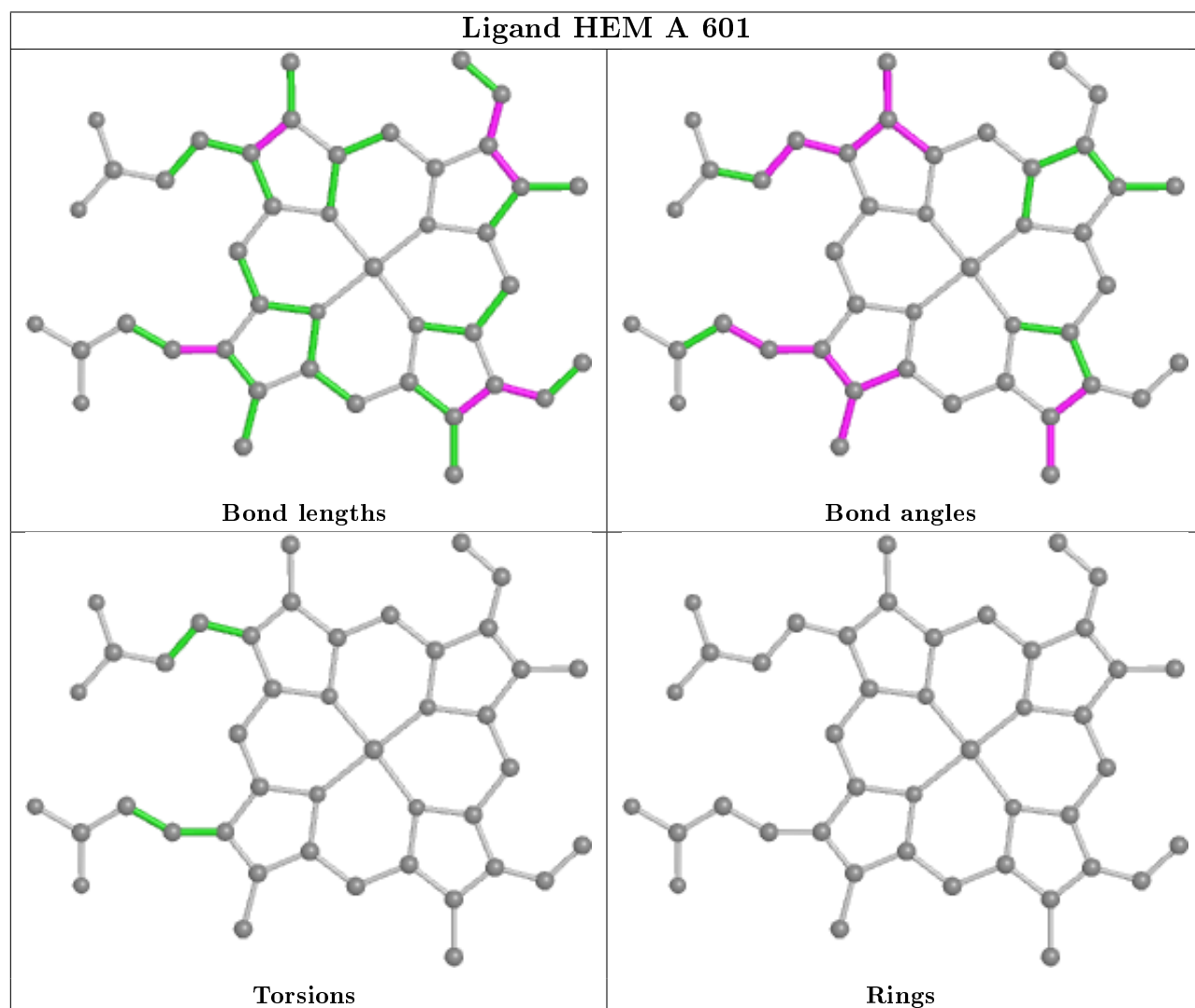
There are no ring outliers.

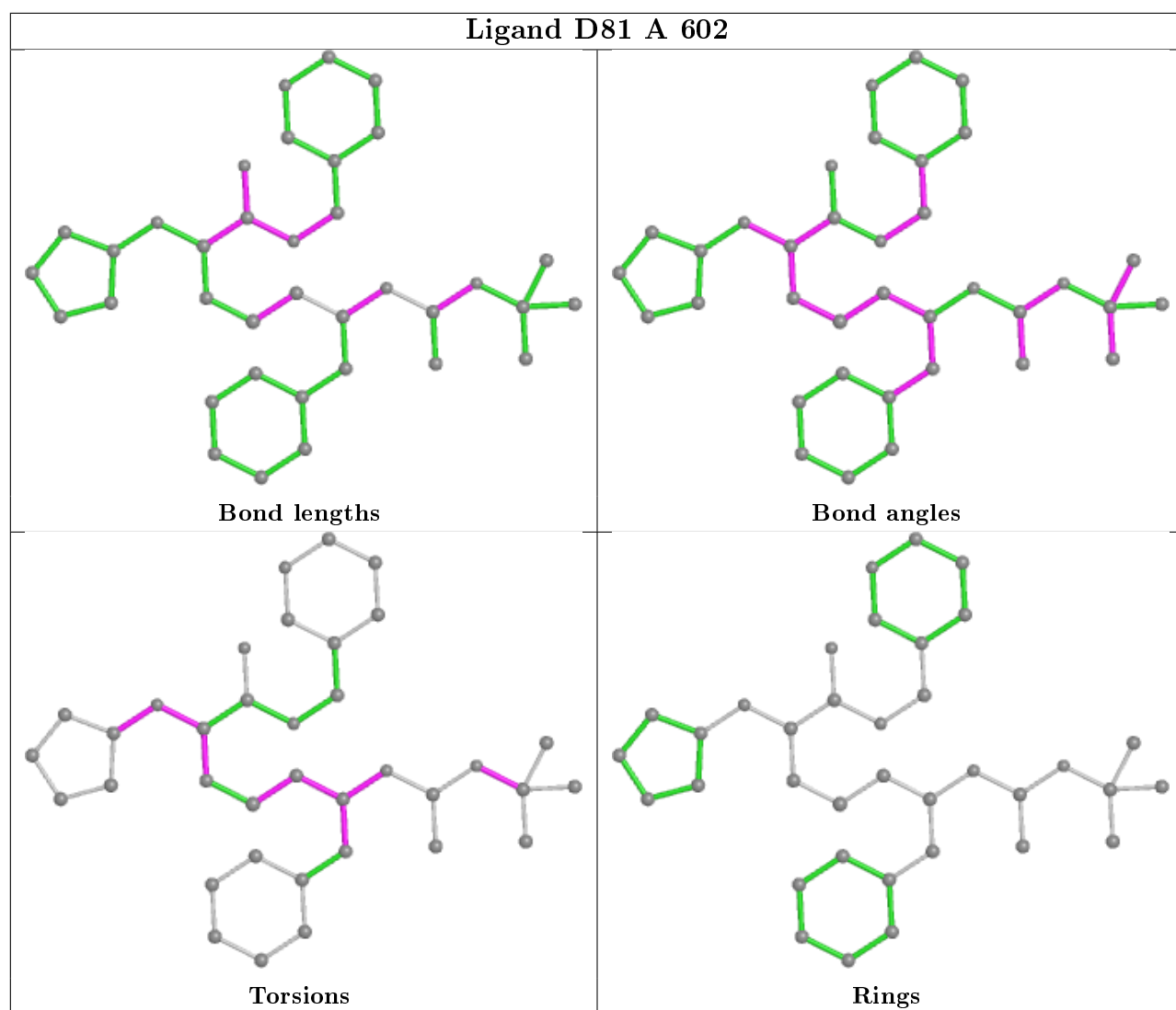
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	HEM	3	0
3	A	602	D81	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	457/487 (93%)	0.86	73 (15%) <b>1</b> <b>2</b>	69, 128, 196, 252	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	261	LEU	9.2
1	A	258	GLU	7.9
1	A	189	PHE	7.6
1	A	263	ASP	6.6
1	A	256	MET	6.4
1	A	272	LEU	6.4
1	A	255	ARG	5.4
1	A	191	VAL	5.3
1	A	269	VAL	5.3
1	A	211	LEU	5.3
1	A	149	ILE	5.0
1	A	281	SER	4.9
1	A	148	ILE	4.8
1	A	260	ARG	4.7
1	A	262	GLU	4.7
1	A	463	PHE	4.6
1	A	290	LEU	4.4
1	A	212	ARG	4.3
1	A	240	VAL	4.2
1	A	215	PHE	4.2
1	A	487	LYS	4.2
1	A	491	LEU	4.1
1	A	253	VAL	4.0
1	A	297	ALA	4.0
1	A	210	LEU	3.9
1	A	203	PHE	3.8
1	A	310	THR	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	276	ILE	3.7
1	A	213	PHE	3.7
1	A	257	LYS	3.7
1	A	221	LEU	3.6
1	A	259	SER	3.6
1	A	309	THR	3.5
1	A	254	LYS	3.5
1	A	442	CYS	3.5
1	A	271	PHE	3.4
1	A	482	LEU	3.4
1	A	200	GLN	3.4
1	A	295	LEU	3.3
1	A	311	SER	3.3
1	A	34	LYS	3.3
1	A	494	GLU	3.2
1	A	275	MET	3.2
1	A	406	LYS	3.2
1	A	345	PRO	3.1
1	A	280	ASN	3.0
1	A	473	ILE	3.0
1	A	199	PRO	3.0
1	A	483	LEU	2.9
1	A	308	GLU	2.8
1	A	216	LEU	2.8
1	A	214	ASP	2.7
1	A	278	SER	2.6
1	A	196	LEU	2.3
1	A	341	ASN	2.3
1	A	223	ILE	2.3
1	A	493	VAL	2.2
1	A	55	LYS	2.2
1	A	370	ALA	2.2
1	A	314	LEU	2.2
1	A	371	MET	2.2
1	A	279	GLN	2.2
1	A	486	GLU	2.2
1	A	162	ARG	2.1
1	A	108[A]	PHE	2.1
1	A	364	LEU	2.1
1	A	170	VAL	2.1
1	A	226	PHE	2.1
1	A	176	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	289	ALA	2.1
1	A	57	PHE	2.0
1	A	241	PHE	2.0
1	A	168	LYS	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

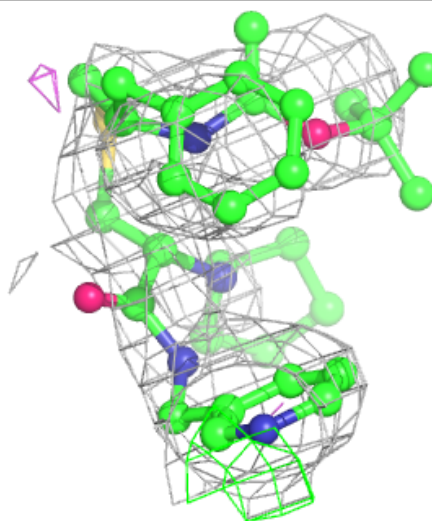
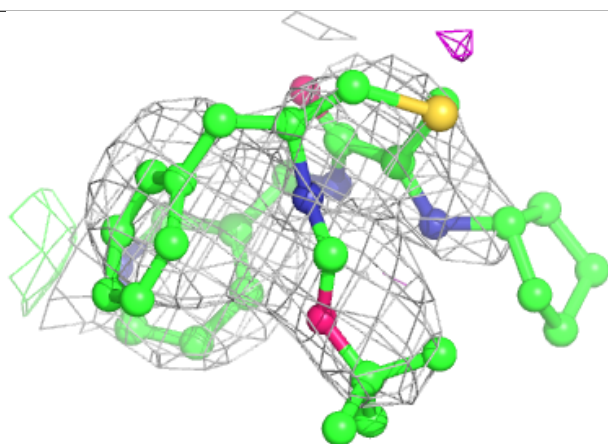
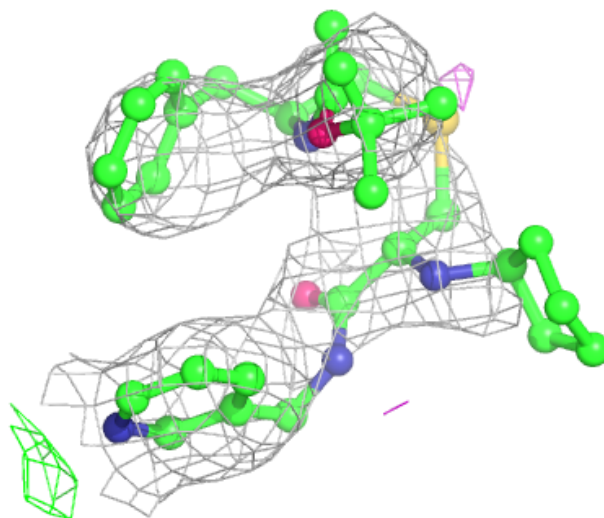
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

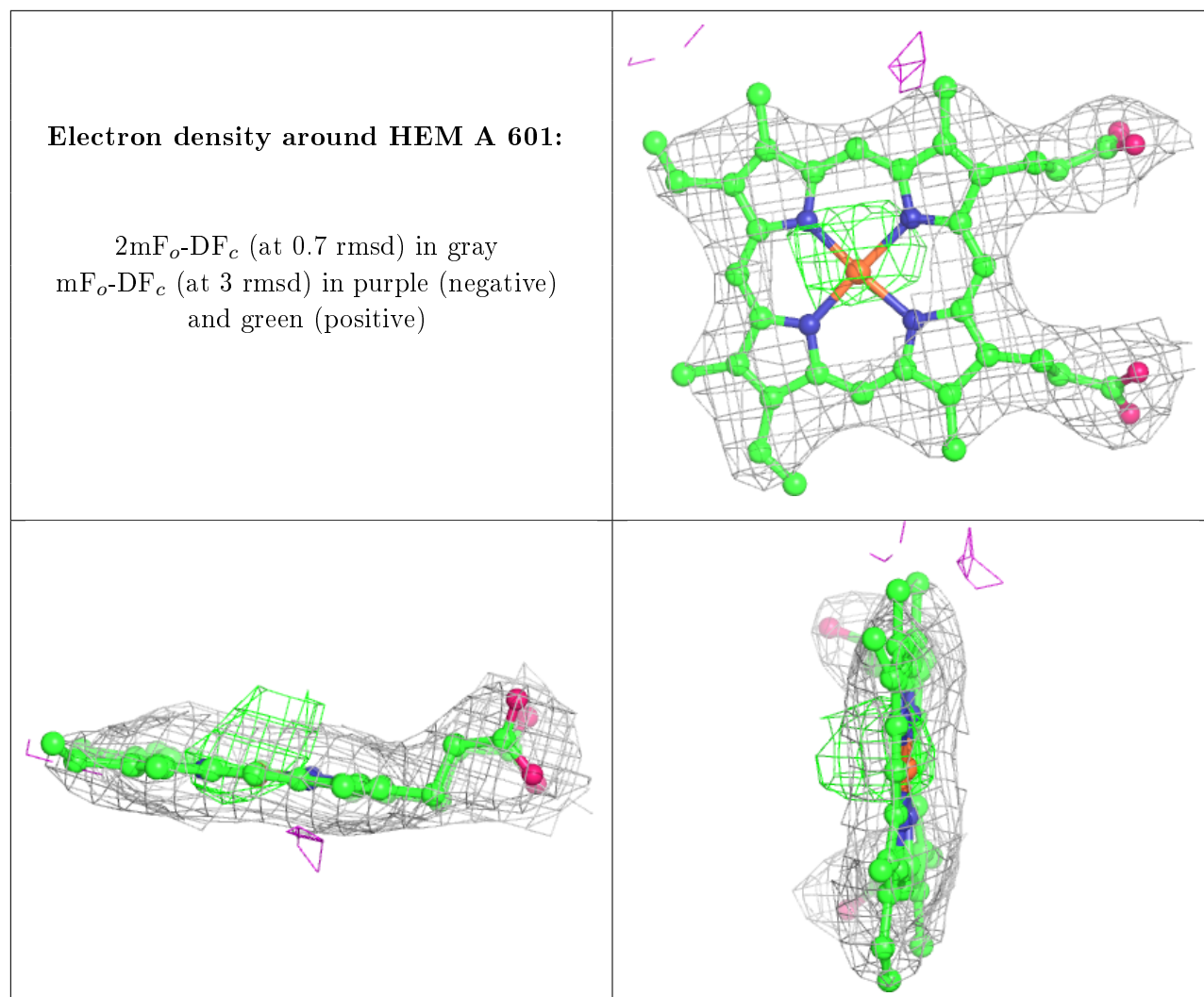
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	D81	A	602	36/36	0.89	0.31	81,144,168,172	0
2	HEM	A	601	43/43	0.98	0.23	68,84,102,115	0

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 D81 A 602:**

$2mF_o-DF_c$  (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.