



# Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2021 – 06:02 PM EDT

PDB ID : 7KS8  
Title : Crystal structure of human CYP3A4 with the caged inhibitor  
Authors : Sevrioukova, I.S.  
Deposited on : 2020-11-21  
Resolution : 2.50 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 : 2.18  
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) : 2.18

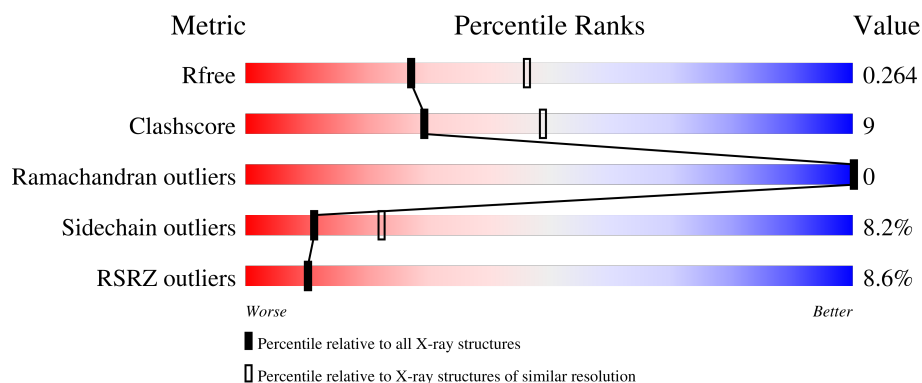
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	

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	GOL	A	602	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3753 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.

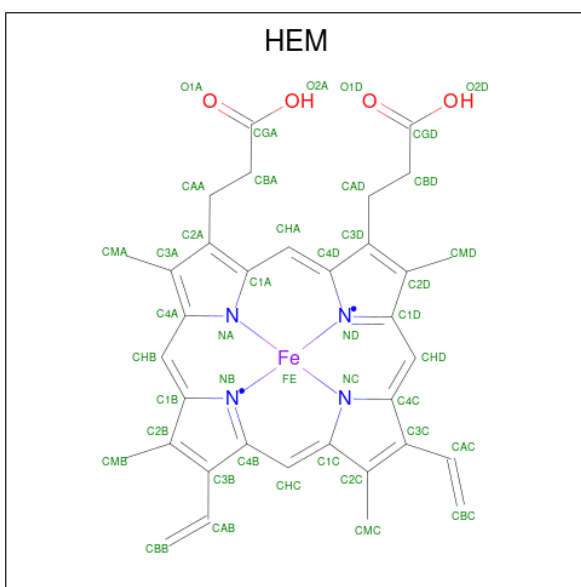
- Molecule 1 is a protein called Cytochrome P450 3A4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	0	0	0
			3641	2369	596	652	24			

There are 24 discrepancies between the modelled and reference sequences:

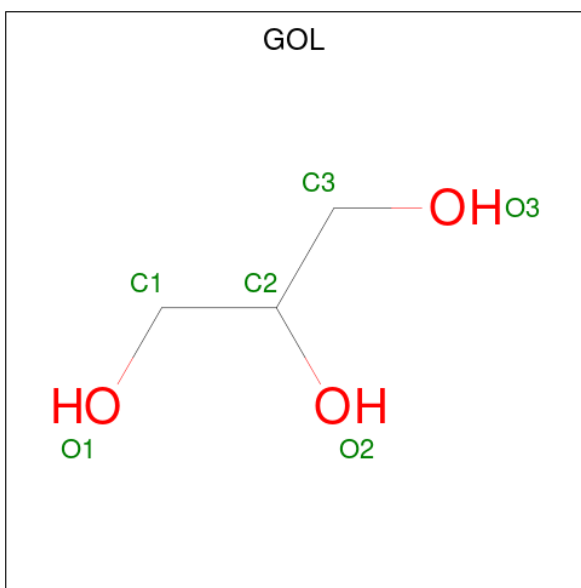
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LEU	deletion	UNP P08684
A	?	-	ILE	deletion	UNP P08684
A	?	-	PRO	deletion	UNP P08684
A	?	-	ASP	deletion	UNP P08684
A	?	-	LEU	deletion	UNP P08684
A	?	-	ALA	deletion	UNP P08684
A	?	-	MET	deletion	UNP P08684
A	?	-	GLU	deletion	UNP P08684
A	?	-	THR	deletion	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 43	C 34	Fe 1	N 4	O 4	0	0

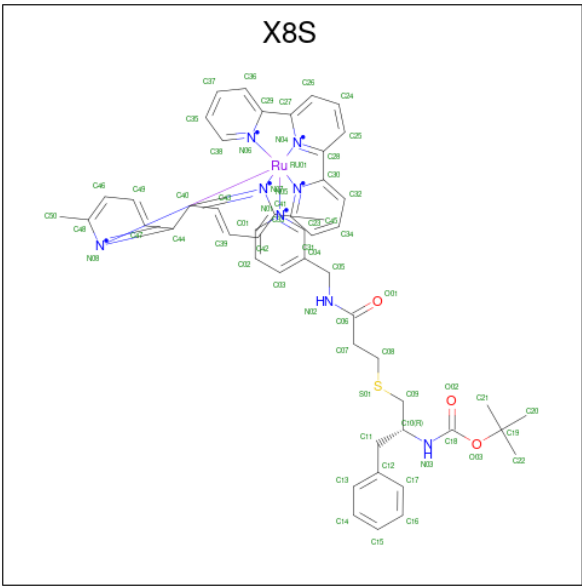
- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $\text{C}_3\text{H}_8\text{O}_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is (tert-butyl {1-[(3-oxo-3-[(pyridin-3-yl-kappaN)methyl]amino}propyl)sulfanyl]-3-phenylpropan-2-yl}carbamate)(6,6'-dimethyl-2,2'-bipyridine-kappa 2 N 1 ,N 1' )(1 2 ,2 2 :2 6 ,3 2 -terpyridine-kappa 3 N 1 ^{1 },N 2 ^{1 },N 3 ^{1 })ruthenium (three-letter code:

X8S) (formula: C<sub>50</sub>H<sub>54</sub>N<sub>8</sub>O<sub>3</sub>RuS) (labeled as "Ligand of Interest" by depositor).

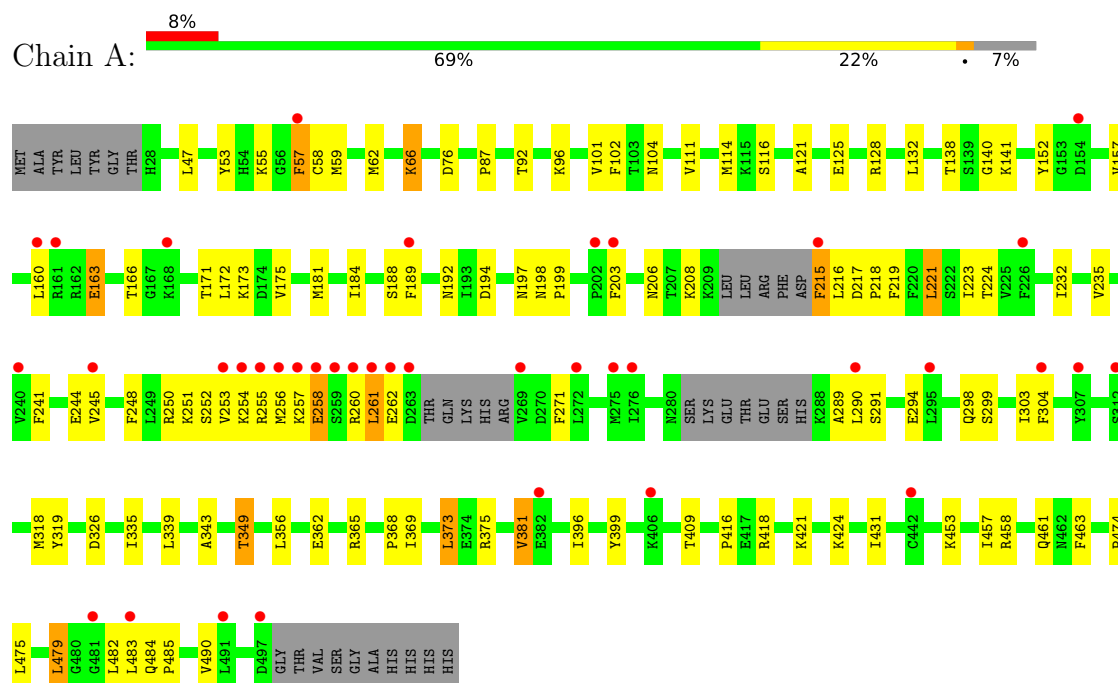


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	Ru	S		
4	A	1	63	50	8	3	1	1	0	0

### 3 Residue-property plots

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 3A4



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.76Å 101.16Å 127.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.09 – 2.50 40.09 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.1 (40.09-2.50) 96.1 (40.09-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.04 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575)	Depositor
R, $R_{free}$	0.211 , 0.262 0.212 , 0.264	Depositor DCC
$R_{free}$ test set	823 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	85.6	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 72.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3753	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% 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, GOL, X8S

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	0.25	0/3728	0.42	0/5041

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	3641	0	3719	69	0
2	A	43	0	30	3	0
3	A	6	0	8	6	0
4	A	63	0	0	0	0
All	All	3753	0	3757	71	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 9.

All (71) 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:475:LEU:HD11	1:A:485:PRO:HB3	1.75	0.69
1:A:101:VAL:HG21	1:A:381:VAL:HG11	1.75	0.68
1:A:57:PHE:N	3:A:602:GOL:H12	2.09	0.66
1:A:116:SER:O	1:A:298:GLN:NE2	2.29	0.65
1:A:479:LEU:HD13	1:A:479:LEU:H	1.63	0.64
1:A:87:PRO:HG3	1:A:431:ILE:HD11	1.82	0.61
1:A:479:LEU:H	1:A:479:LEU:HD22	1.65	0.61
1:A:458:ARG:NH2	1:A:461:GLN:OE1	2.34	0.60
1:A:369:ILE:HA	1:A:483:LEU:HD23	1.82	0.60
1:A:132:LEU:HD13	1:A:290:LEU:HG	1.83	0.59
1:A:58:CYS:HB3	1:A:399:TYR:CD2	2.37	0.59
1:A:215:PHE:CD2	1:A:482:LEU:HD21	2.38	0.59
1:A:421:LYS:HA	1:A:424:LYS:HG2	1.85	0.59
1:A:479:LEU:HD22	1:A:479:LEU:N	2.17	0.58
2:A:601:HEM:HMC2	2:A:601:HEM:HBC2	1.85	0.58
1:A:206:ASN:HB3	1:A:245:VAL:HG13	1.85	0.58
1:A:184:ILE:HG21	1:A:303:ILE:HG23	1.88	0.56
1:A:194:ASP:O	1:A:198:ASN:N	2.37	0.56
1:A:189:PHE:HE2	1:A:303:ILE:HD11	1.71	0.55
1:A:121:ALA:HB1	1:A:125:GLU:HG3	1.89	0.54
1:A:335:ILE:HG23	1:A:457:ILE:HG23	1.90	0.54
2:A:601:HEM:HBB2	2:A:601:HEM:HMB2	1.89	0.54
1:A:59:MET:HG2	3:A:602:GOL:O3	2.08	0.53
1:A:362:GLU:HG3	1:A:416:PRO:HA	1.90	0.53
1:A:59:MET:HG2	3:A:602:GOL:HO3	1.74	0.53
1:A:368:PRO:C	1:A:483:LEU:HD23	2.30	0.52
1:A:217:ASP:HB3	1:A:221:LEU:HG	1.91	0.52
1:A:92:THR:HA	1:A:96:LYS:HB2	1.91	0.52
1:A:152:TYR:OH	1:A:192:ASN:OD1	2.28	0.51
1:A:362:GLU:OE2	1:A:365:ARG:NE	2.36	0.50
1:A:339:LEU:HB3	1:A:343:ALA:HB3	1.94	0.49
1:A:128:ARG:NH2	1:A:289:ALA:O	2.46	0.49
1:A:217:ASP:N	1:A:218:PRO:HD2	2.28	0.49
1:A:368:PRO:O	1:A:483:LEU:CD2	2.61	0.49
1:A:101:VAL:HG11	1:A:381:VAL:HG21	1.97	0.47
1:A:479:LEU:HD13	1:A:479:LEU:N	2.27	0.47
1:A:248:PHE:O	1:A:252:SER:HB2	2.14	0.47
1:A:197:ASN:C	1:A:199:PRO:HD3	2.36	0.46
1:A:294:GLU:O	1:A:298:GLN:HG2	2.15	0.46
1:A:157:VAL:HG13	1:A:463:PHE:HE2	1.81	0.46
1:A:114:MET:HG3	1:A:241:PHE:CD1	2.51	0.46
1:A:163:GLU:HA	1:A:166:THR:HB	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:SER:HA	1:A:271:PHE:HB2	1.99	0.45
1:A:59:MET:HG2	3:A:602:GOL:C3	2.46	0.45
1:A:409:THR:O	1:A:418:ARG:NH1	2.40	0.45
1:A:339:LEU:HD21	1:A:349:THR:HG21	2.00	0.44
1:A:57:PHE:H	3:A:602:GOL:H12	1.81	0.44
1:A:172:LEU:HD13	1:A:318:MET:HB2	1.99	0.44
1:A:76:ASP:HB3	1:A:224:THR:HG21	2.00	0.43
1:A:184:ILE:O	1:A:188:SER:OG	2.29	0.43
1:A:53:TYR:CZ	1:A:57:PHE:HE2	2.37	0.43
1:A:256:MET:HA	1:A:260:ARG:HB2	2.01	0.43
1:A:102:PHE:HB3	1:A:375:ARG:HB3	2.00	0.42
1:A:138:THR:HB	1:A:141:LYS:HG2	2.00	0.42
1:A:335:ILE:HD13	1:A:457:ILE:HA	2.01	0.42
1:A:58:CYS:H	3:A:602:GOL:C1	2.33	0.42
1:A:217:ASP:O	1:A:219:PHE:N	2.53	0.42
1:A:253:VAL:O	1:A:257:LYS:HB2	2.20	0.42
1:A:319:TYR:CZ	1:A:475:LEU:HB2	2.55	0.42
1:A:171:THR:HG22	1:A:173:LYS:HG2	2.01	0.41
1:A:66:LYS:NZ	1:A:66:LYS:HB3	2.36	0.41
1:A:223:ILE:HD13	1:A:223:ILE:HA	1.79	0.41
1:A:261:LEU:HD23	1:A:261:LEU:HA	1.88	0.41
1:A:232:ILE:O	1:A:235:VAL:HG12	2.21	0.41
1:A:138:THR:HG22	1:A:140:GLY:H	1.86	0.40
1:A:373:LEU:HB2	1:A:396:ILE:HB	2.02	0.40
1:A:375:ARG:HH22	2:A:601:HEM:CGA	2.34	0.40
1:A:258:GLU:O	1:A:260:ARG:N	2.55	0.40
1:A:356:LEU:HD21	1:A:453:LYS:HB3	2.03	0.40
1:A:482:LEU:O	1:A:484:GLN:N	2.55	0.40
1:A:189:PHE:HB3	1:A:256:MET:SD	2.61	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	445/487 (91%)	427 (96%)	18 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	414/443 (94%)	380 (92%)	34 (8%)	11	22

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	LEU
1	A	55	LYS
1	A	57	PHE
1	A	62	MET
1	A	66	LYS
1	A	104	ASN
1	A	111	VAL
1	A	160	LEU
1	A	163	GLU
1	A	175	VAL
1	A	181	MET
1	A	203	PHE
1	A	208	LYS
1	A	215	PHE
1	A	216	LEU
1	A	221	LEU
1	A	244	GLU
1	A	250	ARG
1	A	251	LYS
1	A	254	LYS
1	A	255	ARG
1	A	258	GLU
1	A	261	LEU

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Mol	Chain	Res	Type
1	A	262	GLU
1	A	291	SER
1	A	299	SER
1	A	304	PHE
1	A	326	ASP
1	A	349	THR
1	A	373	LEU
1	A	381	VAL
1	A	474	PRO
1	A	479	LEU
1	A	490	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	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](#)

3 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	27,50,50	1.83	4 (14%)	17,82,82	1.47	3 (17%)
3	GOL	A	602	-	5,5,5	0.26	0	5,5,5	0.28	0
4	X8S	A	603	-	61,72,72	4.57	36 (59%)	58,113,113	4.17	30 (51%)

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	-	0/6/54/54	-
3	GOL	A	602	-	-	0/4/4/4	-
4	X8S	A	603	-	-	11/25/171/171	0/10/10/10

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	X8S	C29-C27	-17.63	1.01	1.52
4	A	603	X8S	C30-C28	-12.34	1.16	1.52
4	A	603	X8S	C38-N06	-6.90	1.35	1.49
4	A	603	X8S	C06-N02	6.50	1.48	1.33
4	A	603	X8S	C47-C44	-6.21	1.39	1.53
4	A	603	X8S	C33-N05	-6.15	1.37	1.49
4	A	603	X8S	C26-C27	-6.04	1.40	1.53
4	A	603	X8S	C36-C29	-5.98	1.40	1.53
4	A	603	X8S	C25-C28	-5.84	1.40	1.53
4	A	603	X8S	C32-C30	-5.79	1.40	1.53
4	A	603	X8S	C43-C40	-5.71	1.40	1.53
4	A	603	X8S	C49-C46	-5.36	1.39	1.53
4	A	603	X8S	C23-C04	-5.31	1.40	1.52
4	A	603	X8S	C49-C47	-5.24	1.39	1.53
4	A	603	X8S	C24-C26	-5.15	1.39	1.53
4	A	603	X8S	C18-N03	5.04	1.47	1.34
4	A	603	X8S	C24-C25	-5.04	1.39	1.53
4	A	603	X8S	C39-C43	-5.00	1.40	1.53
4	A	603	X8S	C34-C32	-4.99	1.40	1.53
4	A	603	X8S	C46-C48	-4.98	1.40	1.53
4	A	603	X8S	C37-C36	-4.96	1.40	1.53
4	A	603	X8S	C42-C41	-4.92	1.40	1.53
4	A	603	X8S	C01-N01	-4.68	1.39	1.48
4	A	603	X8S	C02-C03	-4.61	1.41	1.53
4	A	603	X8S	C03-C04	-4.33	1.40	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	X8S	RU01-N06	-4.21	1.97	2.12
4	A	603	X8S	O03-C18	4.19	1.43	1.34
2	A	601	HEM	C3C-CAC	3.88	1.55	1.47
2	A	601	HEM	C3B-CAB	3.84	1.55	1.47
2	A	601	HEM	C3C-C2C	-3.71	1.35	1.40
2	A	601	HEM	C3B-C2B	-3.69	1.35	1.40
4	A	603	X8S	RU01-N08	3.04	2.23	2.12
4	A	603	X8S	C38-C35	-3.04	1.40	1.51
4	A	603	X8S	C33-C31	-3.00	1.40	1.51
4	A	603	X8S	C37-C35	-2.87	1.40	1.51
4	A	603	X8S	C34-C31	-2.87	1.40	1.51
4	A	603	X8S	O03-C19	-2.75	1.43	1.48
4	A	603	X8S	C01-C02	-2.74	1.41	1.51
4	A	603	X8S	RU01-N04	-2.57	2.03	2.12
4	A	603	X8S	RU01-N05	-2.14	2.04	2.12

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	X8S	C50-C48-N08	10.65	130.08	113.06
4	A	603	X8S	C46-C48-N08	9.58	120.97	109.71
4	A	603	X8S	C01-C02-C03	8.96	121.05	111.25
4	A	603	X8S	C42-C41-N07	8.86	120.13	109.71
4	A	603	X8S	C49-C46-C48	7.80	121.46	112.74
4	A	603	X8S	C39-C42-C41	7.64	121.28	112.74
4	A	603	X8S	C23-C04-C03	7.27	118.70	109.71
4	A	603	X8S	O03-C18-N03	6.52	120.98	110.02
4	A	603	X8S	C45-C41-N07	6.15	122.90	113.06
4	A	603	X8S	C35-C38-N06	5.94	122.68	113.00
4	A	603	X8S	C31-C33-N05	5.31	121.65	113.00
4	A	603	X8S	C39-C43-C40	4.97	120.17	111.22
4	A	603	X8S	C34-C32-C30	4.95	120.13	111.22
4	A	603	X8S	C49-C47-C44	4.87	119.99	111.22
4	A	603	X8S	C33-C31-C34	4.70	119.40	111.44
4	A	603	X8S	C24-C25-C28	4.68	119.66	111.22
4	A	603	X8S	C24-C26-C27	4.50	119.33	111.22
4	A	603	X8S	C37-C36-C29	4.34	119.05	111.22
4	A	603	X8S	C02-C03-C04	4.16	120.02	112.15
4	A	603	X8S	C19-O03-C18	-4.14	114.61	120.99
4	A	603	X8S	C35-C37-C36	3.99	119.55	111.42
4	A	603	X8S	C38-C35-C37	3.97	118.17	111.44
4	A	603	X8S	C03-C04-C05	3.84	119.64	111.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	X8S	C02-C01-N01	3.75	118.97	113.21
4	A	603	X8S	O03-C18-O02	-3.58	119.10	125.62
4	A	603	X8S	C31-C34-C32	3.49	118.52	111.42
4	A	603	X8S	O02-C18-N03	-3.01	119.92	124.85
4	A	603	X8S	C23-C04-C05	2.41	121.64	111.50
4	A	603	X8S	C45-C41-C42	2.38	116.96	112.07
2	A	601	HEM	CMB-C2B-C3B	2.25	128.88	124.68
4	A	603	X8S	C07-C08-S01	-2.21	105.38	112.58
2	A	601	HEM	CBD-CAD-C3D	-2.19	108.44	112.48
2	A	601	HEM	CMC-C2C-C3C	2.11	128.63	124.68

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	603	X8S	N03-C18-O03-C19
4	A	603	X8S	O02-C18-O03-C19
4	A	603	X8S	C23-C04-C05-N02
4	A	603	X8S	C03-C04-C05-N02
4	A	603	X8S	O02-C18-N03-C10
4	A	603	X8S	O03-C18-N03-C10
4	A	603	X8S	C21-C19-O03-C18
4	A	603	X8S	C22-C19-O03-C18
4	A	603	X8S	C20-C19-O03-C18
4	A	603	X8S	S01-C09-C10-N03
4	A	603	X8S	C09-C10-N03-C18

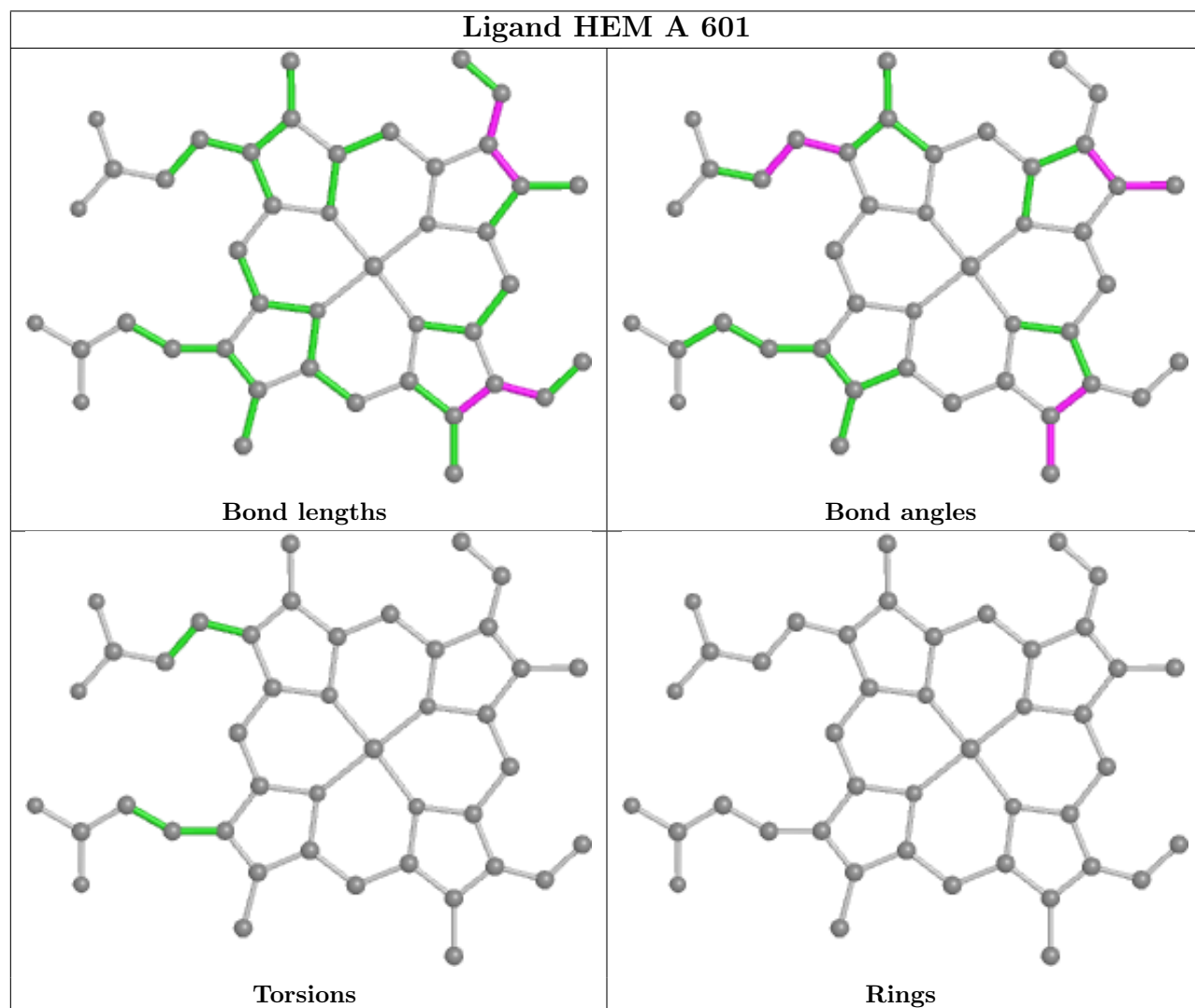
There are no ring outliers.

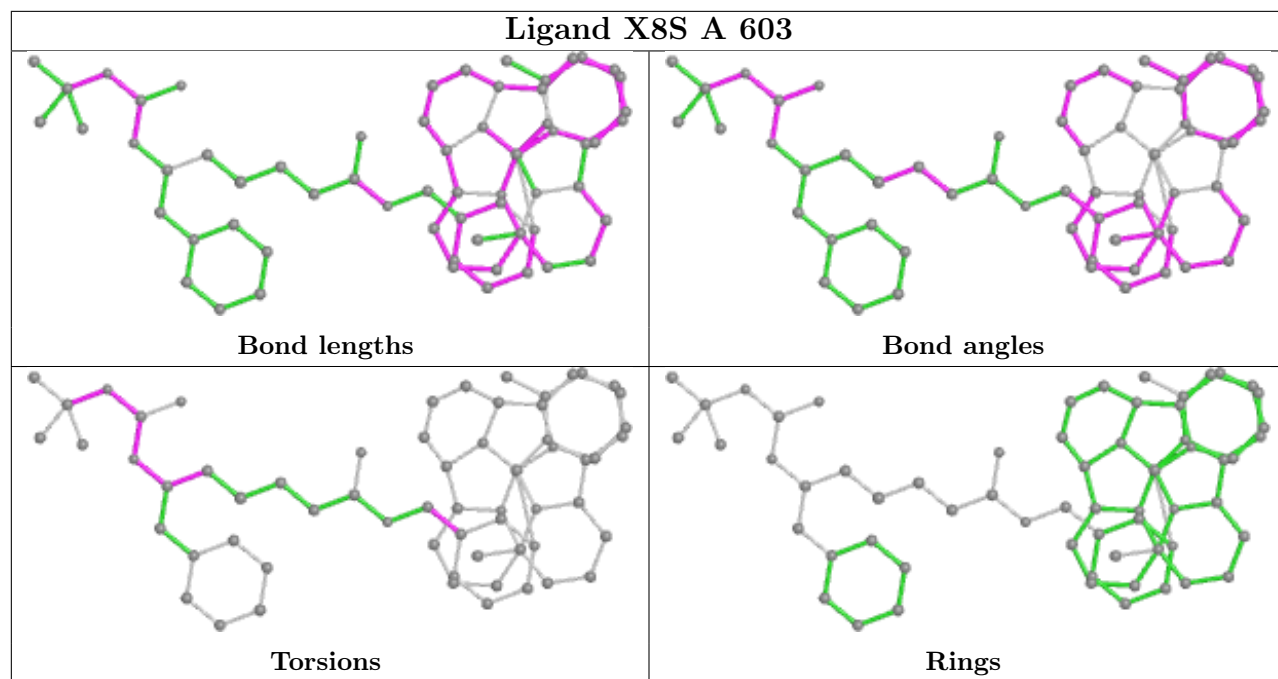
2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	HEM	3	0
3	A	602	GOL	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 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	453/487 (93%)	0.50	39 (8%) 10 10	56, 102, 171, 217	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	259	SER	7.8
1	A	257	LYS	7.0
1	A	260	ARG	6.6
1	A	254	LYS	6.4
1	A	189	PHE	6.2
1	A	258	GLU	5.5
1	A	261	LEU	5.2
1	A	256	MET	5.0
1	A	304	PHE	4.4
1	A	262	GLU	4.4
1	A	276	ILE	4.2
1	A	168	LYS	4.0
1	A	269	VAL	3.9
1	A	255	ARG	3.6
1	A	226	PHE	3.5
1	A	491	LEU	3.4
1	A	275	MET	3.2
1	A	290	LEU	3.1
1	A	263	ASP	3.0
1	A	382	GLU	2.9
1	A	272	LEU	2.8
1	A	497	ASP	2.6
1	A	202	PRO	2.6
1	A	203	PHE	2.5
1	A	154	ASP	2.5
1	A	240	VAL	2.5
1	A	253	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	307	TYR	2.5
1	A	245	VAL	2.3
1	A	160	LEU	2.3
1	A	295	LEU	2.2
1	A	57	PHE	2.2
1	A	161	ARG	2.2
1	A	215	PHE	2.2
1	A	406	LYS	2.1
1	A	312	SER	2.1
1	A	442	CYS	2.1
1	A	483	LEU	2.0
1	A	481	GLY	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](#)

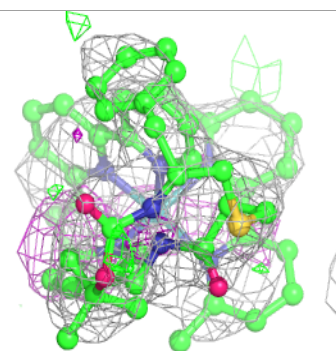
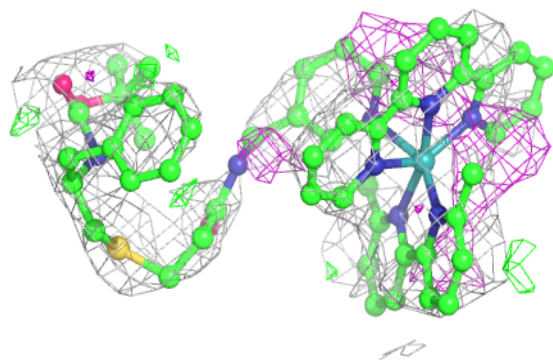
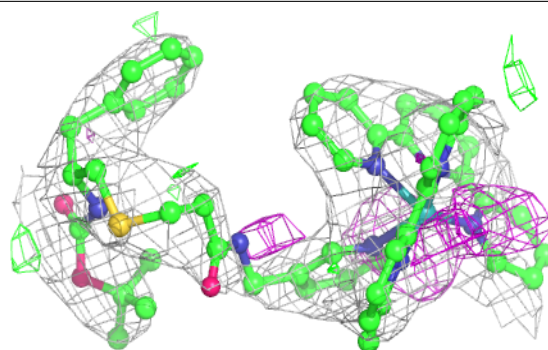
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	GOL	A	602	6/6	0.67	0.28	103,104,112,121	0
4	X8S	A	603	63/63	0.92	0.24	93,138,162,168	0
2	HEM	A	601	43/43	0.98	0.22	52,64,75,80	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.

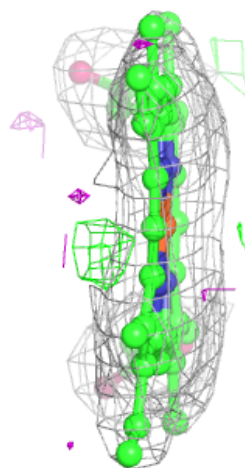
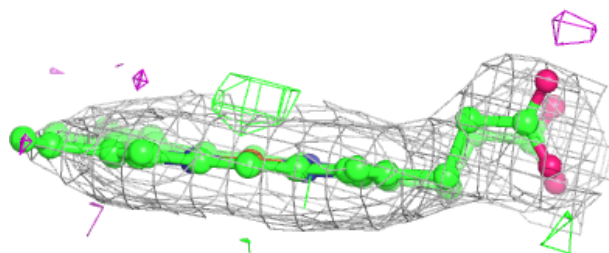
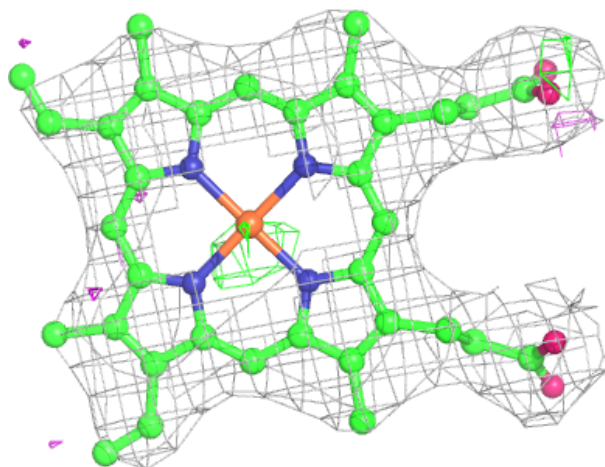
**Electron density around X8S A 603:**

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



**Electron density around HEM A 601:**

$2mF_o-DF_c$  (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.