



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 25, 2022 – 12:02 PM EDT

PDB ID : 7UAY
Title : Crystal structure of human CYP3A4 with the caged inhibitor
Authors : Sevrioukova, I.F.
Deposited on : 2022-03-14
Resolution : 2.78 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

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>.

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 : 2.29
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) : 2.29

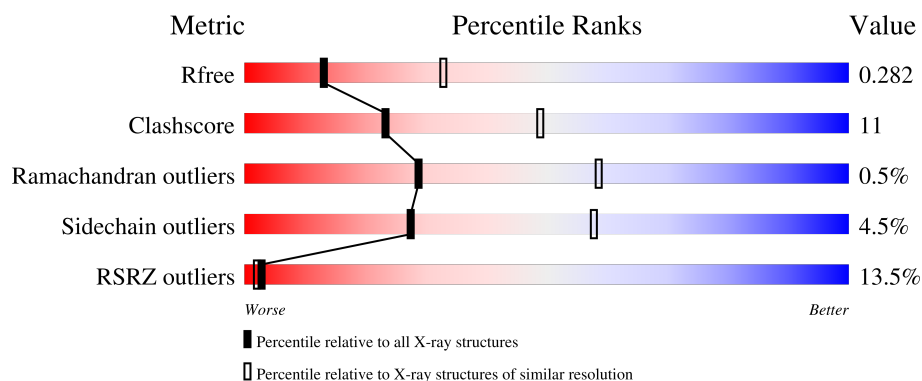
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.78 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	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)
RSRZ outliers	127900	4027 (2.80-2.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	<div> <div>12%</div> <div>70%</div> <div>19%</div> <div>10%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3595 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	436	Total	C	N	O	S	0	0	0
			3493	2278	568	623	24			

There are 24 discrepancies between the modelled and reference sequences:

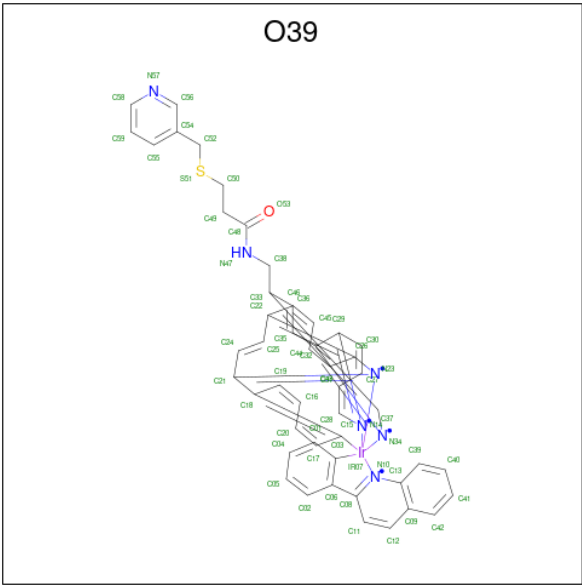
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LEU	deletion	UNP P08684
A	?	-	ILE	deletion	UNP P08684
A	?	-	PRO	deletion	UNP P08684
A	?	-	ASP	deletion	UNP P08684
A	?	-	LEU	deletion	UNP P08684
A	?	-	ALA	deletion	UNP P08684
A	?	-	MET	deletion	UNP P08684
A	?	-	GLU	deletion	UNP P08684
A	?	-	THR	deletion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

- Molecule 3 is (N-[(2,2'-bipyridin]-5-yl-kappa 2 N 1 ,N 1 ')methyl]-3-[(pyridin-3-yl)methyl]sulfanyl}propanamide)bis[2-(quinolin-2-yl-kappaN)phenyl-kappaC 1]iridium (three-letter code: O39) (formula: C₅₀H₄₀IrN₆OS) (labeled as "Ligand of Interest" by depositor).

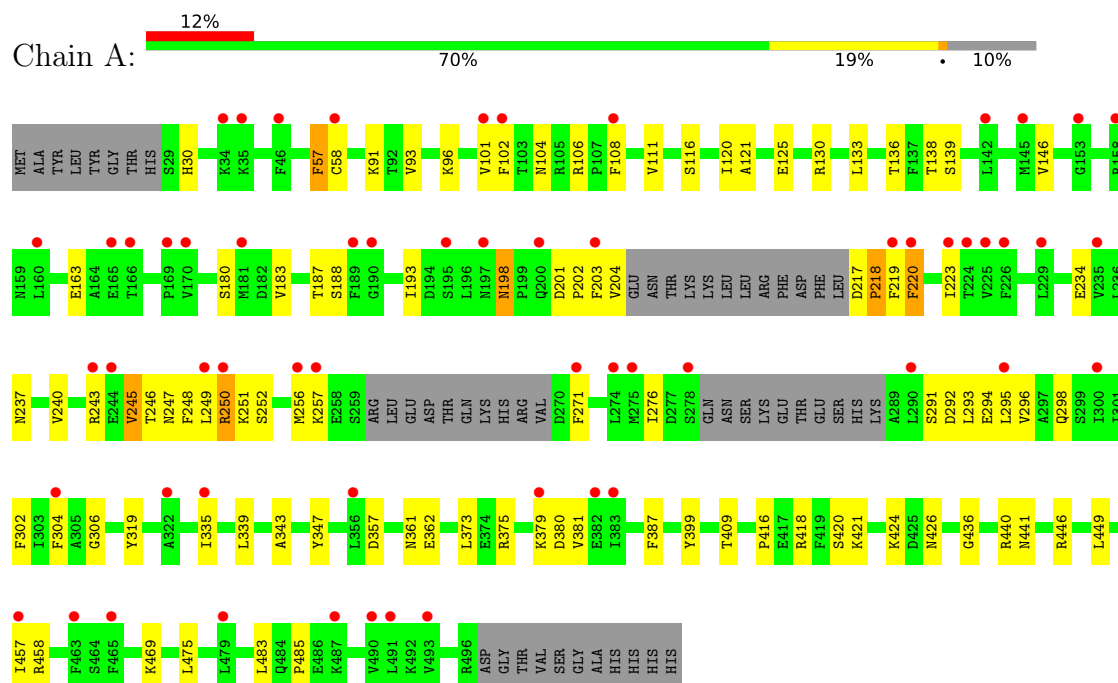


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	A	1	Total	C	Ir	N	O	S	0	0
			59	50	1	6	1	1		

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 3A4



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	76.94Å 99.53Å 135.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.77 – 2.78 49.77 – 2.78	Depositor EDS
% Data completeness (in resolution range)	99.6 (49.77-2.78) 99.6 (49.77-2.78)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.77Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.258 , 0.280 0.260 , 0.282	Depositor DCC
R_{free} test set	660 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	93.1	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 79.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3595	wwPDB-VP
Average B, all atoms (Å ²)	126.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: O39, 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	0.27	0/3578	0.42	0/4841

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

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	3493	0	3573	73	0
2	A	43	0	30	4	0
3	A	59	0	0	14	0
All	All	3595	0	3603	81	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 (81) 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:245:VAL:HG12	1:A:246:THR:H	1.14	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:VAL:HG12	1:A:246:THR:N	1.85	0.92
1:A:108:PHE:HD1	3:A:602:O39:C17	1.86	0.88
3:A:602:O39:C37	3:A:602:O39:N10	2.39	0.85
1:A:245:VAL:CG1	1:A:246:THR:H	1.93	0.82
1:A:201:ASP:N	1:A:202:PRO:HD3	1.98	0.78
3:A:602:O39:C37	3:A:602:O39:C08	2.68	0.72
1:A:373:LEU:HD21	1:A:436:GLY:HA2	1.74	0.69
1:A:188:SER:HA	1:A:271:PHE:HB2	1.76	0.67
1:A:247:ASN:HA	1:A:250:ARG:HB2	1.77	0.66
1:A:409:THR:O	1:A:418:ARG:NH1	2.28	0.65
1:A:139:SER:OG	1:A:446:ARG:NH1	2.31	0.64
1:A:116:SER:O	1:A:298:GLN:NE2	2.31	0.63
1:A:203:PHE:O	1:A:204:VAL:HG12	1.97	0.63
1:A:108:PHE:HB3	3:A:602:O39:C40	2.29	0.62
1:A:203:PHE:C	1:A:204:VAL:HG12	2.20	0.62
1:A:257:LYS:NZ	1:A:292:ASP:OD1	2.28	0.62
1:A:203:PHE:O	1:A:204:VAL:CG1	2.49	0.61
1:A:201:ASP:N	1:A:202:PRO:CD	2.65	0.60
1:A:250:ARG:HH11	1:A:293:LEU:HD13	1.66	0.60
1:A:362:GLU:HG3	1:A:416:PRO:HA	1.85	0.59
3:A:602:O39:C43	3:A:602:O39:C06	2.80	0.59
1:A:203:PHE:CD1	1:A:248:PHE:HE2	2.21	0.58
3:A:602:O39:C17	3:A:602:O39:C28	2.78	0.57
1:A:108:PHE:HE2	1:A:120:ILE:HG13	1.70	0.56
1:A:201:ASP:H	1:A:202:PRO:HD3	1.67	0.56
2:A:601:HEM:HBB2	2:A:601:HEM:HMB2	1.87	0.56
2:A:601:HEM:HMC2	2:A:601:HEM:HBC2	1.88	0.55
1:A:108:PHE:CD1	3:A:602:O39:C17	2.78	0.55
1:A:108:PHE:HD1	3:A:602:O39:C20	2.20	0.54
1:A:130:ARG:NH2	1:A:441:ASN:OD1	2.40	0.54
1:A:219:PHE:HD2	1:A:220:PHE:CD1	2.26	0.53
3:A:602:O39:C43	3:A:602:O39:C03	2.86	0.53
1:A:121:ALA:HB1	1:A:125:GLU:HG3	1.91	0.53
1:A:250:ARG:HA	1:A:296:VAL:HG21	1.90	0.52
1:A:180:SER:OG	1:A:306:GLY:O	2.27	0.51
1:A:436:GLY:HA3	2:A:601:HEM:HBA1	1.92	0.51
1:A:101:VAL:HG21	1:A:381:VAL:HG11	1.92	0.51
1:A:220:PHE:HB2	3:A:602:O39:C24	2.42	0.50
1:A:257:LYS:HG2	1:A:276:ILE:HD13	1.93	0.50
1:A:106:ARG:HG2	3:A:602:O39:C41	2.42	0.49
3:A:602:O39:C03	3:A:602:O39:C26	2.87	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:PHE:CD1	3:A:602:O39:C20	2.97	0.48
1:A:375:ARG:NH2	1:A:440:ARG:HB3	2.29	0.48
1:A:183:VAL:O	1:A:187:THR:OG1	2.30	0.47
1:A:249:LEU:HA	1:A:252:SER:HB3	1.96	0.47
1:A:146:VAL:HG21	1:A:347:TYR:HB2	1.97	0.47
1:A:217:ASP:OD2	3:A:602:O39:C45	2.63	0.47
1:A:248:PHE:O	1:A:252:SER:N	2.43	0.47
1:A:91:LYS:HG2	1:A:96:LYS:HE3	1.96	0.46
1:A:319:TYR:CZ	1:A:475:LEU:HB2	2.50	0.46
1:A:133:LEU:HD13	1:A:302:PHE:HZ	1.79	0.46
1:A:339:LEU:HB3	1:A:343:ALA:HB3	1.96	0.46
1:A:375:ARG:NH2	2:A:601:HEM:O1A	2.30	0.45
1:A:420:SER:O	1:A:424:LYS:N	2.47	0.45
1:A:421:LYS:HA	1:A:424:LYS:HE3	1.97	0.45
1:A:203:PHE:C	1:A:204:VAL:CG1	2.85	0.45
1:A:93:VAL:HG13	1:A:102:PHE:CG	2.51	0.45
1:A:421:LYS:HA	1:A:424:LYS:HG2	1.99	0.45
1:A:58:CYS:HB3	1:A:399:TYR:CD2	2.52	0.45
1:A:246:THR:O	1:A:250:ARG:N	2.43	0.44
1:A:102:PHE:HB3	1:A:375:ARG:HB3	1.99	0.44
1:A:198:ASN:O	1:A:202:PRO:HG3	2.17	0.44
1:A:219:PHE:HE2	1:A:240:VAL:HG12	1.81	0.44
1:A:203:PHE:CE1	1:A:248:PHE:CE2	3.05	0.44
1:A:380:ASP:HB3	1:A:387:PHE:HE2	1.82	0.43
1:A:291:SER:OG	1:A:292:ASP:N	2.50	0.43
1:A:257:LYS:HE3	1:A:295:LEU:HD22	2.00	0.42
1:A:111:VAL:N	1:A:234:GLU:OE2	2.52	0.42
1:A:357:ASP:OD2	1:A:361:ASN:ND2	2.53	0.42
1:A:475:LEU:HD11	1:A:485:PRO:HB3	2.00	0.42
1:A:203:PHE:CD1	1:A:248:PHE:CE2	3.06	0.41
1:A:217:ASP:OD1	1:A:217:ASP:N	2.53	0.41
1:A:294:GLU:O	1:A:298:GLN:HG2	2.20	0.41
1:A:217:ASP:HA	1:A:218:PRO:HD3	1.82	0.41
1:A:223:ILE:HD13	1:A:223:ILE:HA	1.98	0.41
1:A:469:LYS:HE3	1:A:469:LYS:HB2	1.91	0.41
1:A:483:LEU:HD12	1:A:483:LEU:HA	1.95	0.41
1:A:104:ASN:HA	1:A:440:ARG:NH1	2.36	0.41
1:A:57:PHE:HD2	1:A:57:PHE:HA	1.75	0.40
1:A:335:ILE:HD13	1:A:457:ILE:HA	2.03	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	428/487 (88%)	399 (93%)	27 (6%)	2 (0%)	29	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	218	PRO
1	A	245	VAL

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	397/443 (90%)	379 (96%)	18 (4%)	27	58

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	HIS
1	A	57	PHE
1	A	136	THR
1	A	138	THR
1	A	163	GLU
1	A	193	ILE
1	A	198	ASN
1	A	220	PHE
1	A	237	ASN

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Mol	Chain	Res	Type
1	A	243	ARG
1	A	250	ARG
1	A	251	LYS
1	A	256	MET
1	A	304	PHE
1	A	379	LYS
1	A	426	ASN
1	A	449	LEU
1	A	458	ARG

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

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](#)

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	$\# Z > 2$
3	O39	A	602	2	70,70,70	2.06	17 (24%)	81,110,110	4.39	49 (60%)
2	HEM	A	601	1,3	41,50,50	1.46	4 (9%)	45,82,82	1.42	8 (17%)

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	O39	A	602	2	-	3/12/156/156	0/12/12/12
2	HEM	A	601	1,3	-	1/12/54/54	-

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	O39	C48-N47	6.45	1.48	1.33
3	A	602	O39	C52-S51	-5.69	1.72	1.82
3	A	602	O39	C38-C33	-5.59	1.39	1.51
3	A	602	O39	C03-IR07	-5.36	1.87	2.01
3	A	602	O39	C06-C08	-4.55	1.37	1.46
3	A	602	O39	C38-N47	4.09	1.53	1.46
3	A	602	O39	C15-C18	-4.08	1.33	1.41
2	A	601	HEM	C3C-CAC	3.86	1.55	1.47
2	A	601	HEM	C3C-C2C	-3.71	1.35	1.40
3	A	602	O39	C18-C21	-3.55	1.39	1.46
3	A	602	O39	IR07-N10	-3.17	1.95	2.13
2	A	601	HEM	CAB-C3B	3.04	1.55	1.47
3	A	602	O39	C29-N14	-2.60	1.31	1.37
3	A	602	O39	IR07-N14	-2.50	1.95	2.08
3	A	602	O39	C50-S51	-2.45	1.72	1.81
3	A	602	O39	C26-N23	2.31	1.43	1.39
3	A	602	O39	C08-N10	2.17	1.38	1.35
3	A	602	O39	C49-C48	2.14	1.55	1.51
3	A	602	O39	C13-N10	-2.07	1.35	1.39
2	A	601	HEM	CMB-C2B	2.06	1.55	1.50
3	A	602	O39	C15-IR07	-2.04	1.96	2.01

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	O39	C21-N23-C26	-13.83	103.35	118.69
3	A	602	O39	C43-C26-C22	-11.91	103.29	119.25
3	A	602	O39	C49-C48-N47	11.59	135.93	116.42
3	A	602	O39	C24-C21-C18	-9.42	107.86	126.37
3	A	602	O39	C24-C21-N23	9.26	134.34	121.27
3	A	602	O39	C43-C26-N23	8.42	131.67	120.36
3	A	602	O39	O53-C48-N47	-8.31	107.33	123.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	O39	C44-C43-C26	7.53	133.88	119.44
3	A	602	O39	C21-C18-C15	-7.40	104.95	115.33
3	A	602	O39	C46-C22-C25	-6.48	108.04	123.19
3	A	602	O39	C50-S51-C52	6.47	117.00	102.05
3	A	602	O39	C46-C22-C26	6.38	127.31	118.54
3	A	602	O39	C24-C25-C22	-6.07	111.42	120.82
3	A	602	O39	C35-C36-C33	-5.81	113.04	121.03
3	A	602	O39	C11-C08-C06	-5.52	115.52	126.37
3	A	602	O39	C37-N34-C32	-5.26	109.48	119.19
3	A	602	O39	C38-N47-C48	4.90	129.97	122.34
3	A	602	O39	C52-C54-C55	4.66	130.00	120.86
3	A	602	O39	C12-C09-C42	-4.61	112.40	123.19
3	A	602	O39	C35-C32-N34	4.58	126.24	119.86
3	A	602	O39	C08-N10-C13	-4.49	113.70	118.69
3	A	602	O39	C25-C22-C26	4.45	124.66	118.54
3	A	602	O39	C01-C03-C06	4.33	123.74	117.12
3	A	602	O39	C44-C45-C46	-4.00	114.83	120.44
3	A	602	O39	C42-C09-C13	3.99	124.02	118.54
3	A	602	O39	C22-C26-N23	3.73	124.87	120.46
3	A	602	O39	C12-C09-C13	3.66	123.57	118.54
3	A	602	O39	C11-C12-C09	-3.49	115.42	120.82
3	A	602	O39	C11-C08-N10	3.27	125.89	121.27
3	A	602	O39	C19-C18-C21	3.22	129.66	123.45
3	A	602	O39	C39-C13-C09	-3.08	115.13	119.25
3	A	602	O39	C54-C52-S51	3.07	120.96	114.06
3	A	602	O39	C17-C15-C18	-3.06	112.42	117.12
3	A	602	O39	C02-C06-C08	2.95	129.15	123.45
3	A	602	O39	C20-C17-C15	2.91	125.62	121.30
3	A	602	O39	C35-C32-C29	-2.90	118.01	123.75
3	A	602	O39	O53-C48-C49	-2.88	116.74	122.02
2	A	601	HEM	C4D-ND-C1D	2.84	108.01	105.07
2	A	601	HEM	C1B-NB-C4B	2.84	108.00	105.07
2	A	601	HEM	C4B-CHC-C1C	2.83	126.30	122.56
3	A	602	O39	C19-C18-C15	2.79	125.39	121.10
3	A	602	O39	C58-N57-C56	2.65	121.44	116.85
2	A	601	HEM	C4C-CHD-C1D	2.64	126.04	122.56
3	A	602	O39	C08-C06-C03	-2.54	111.76	115.33
3	A	602	O39	C30-C29-N14	2.50	123.34	119.86
3	A	602	O39	C18-C21-N23	2.50	117.67	115.14
3	A	602	O39	C39-C13-N10	2.40	123.58	120.36
3	A	602	O39	C52-C54-C56	-2.32	111.26	120.71
3	A	602	O39	C04-C01-C03	-2.32	117.85	121.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	O39	C20-C16-C19	-2.26	116.74	120.19
3	A	602	O39	C06-C08-N10	2.24	117.41	115.14
2	A	601	HEM	CMC-C2C-C3C	2.21	128.80	124.68
2	A	601	HEM	C3B-C2B-C1B	2.08	108.03	106.49
2	A	601	HEM	CBA-CAA-C2A	-2.05	109.13	112.62
3	A	602	O39	C28-N14-C29	-2.04	116.07	119.06
3	A	602	O39	C31-C27-C30	-2.02	117.11	120.19
2	A	601	HEM	C3D-C4D-ND	-2.01	107.93	110.17

There are no chirality outliers.

All (4) torsion outliers are listed below:

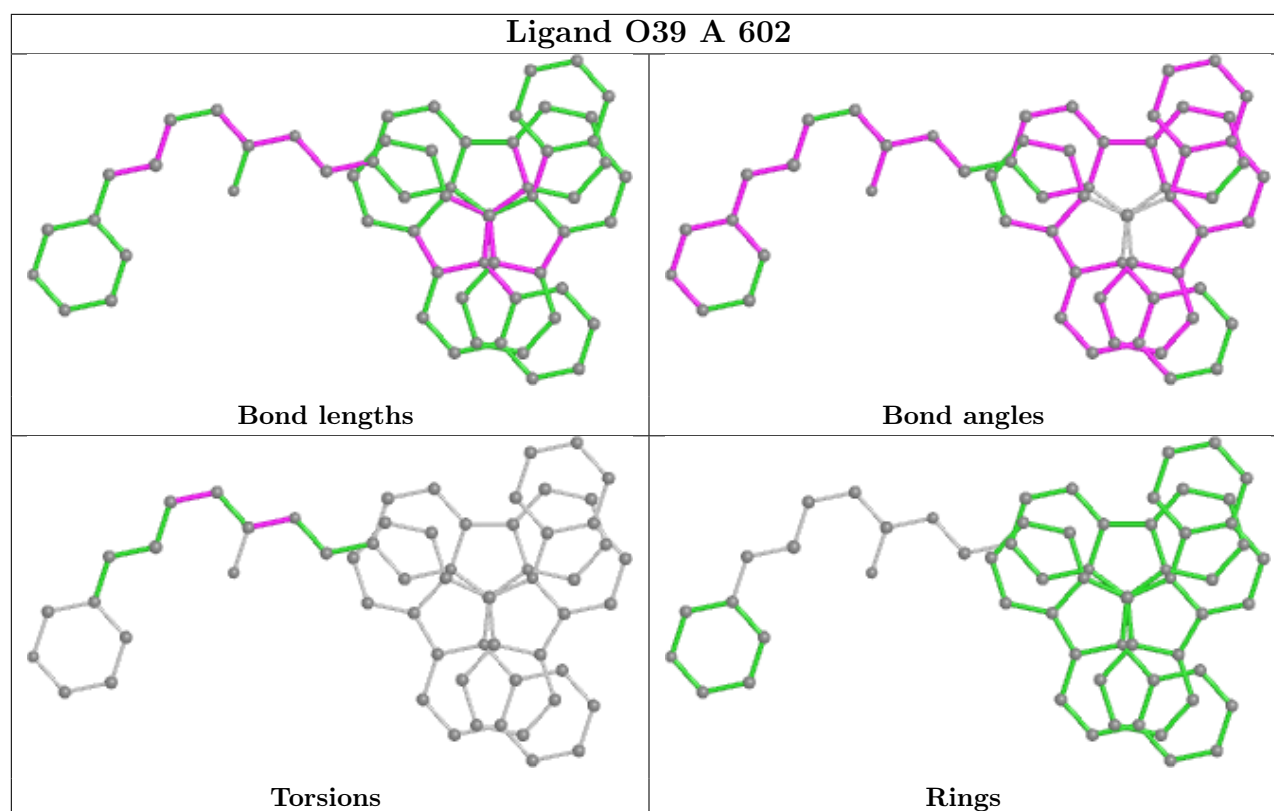
Mol	Chain	Res	Type	Atoms
3	A	602	O39	C48-C49-C50-S51
3	A	602	O39	C49-C48-N47-C38
3	A	602	O39	O53-C48-N47-C38
2	A	601	HEM	CAD-CBD-CGD-O2D

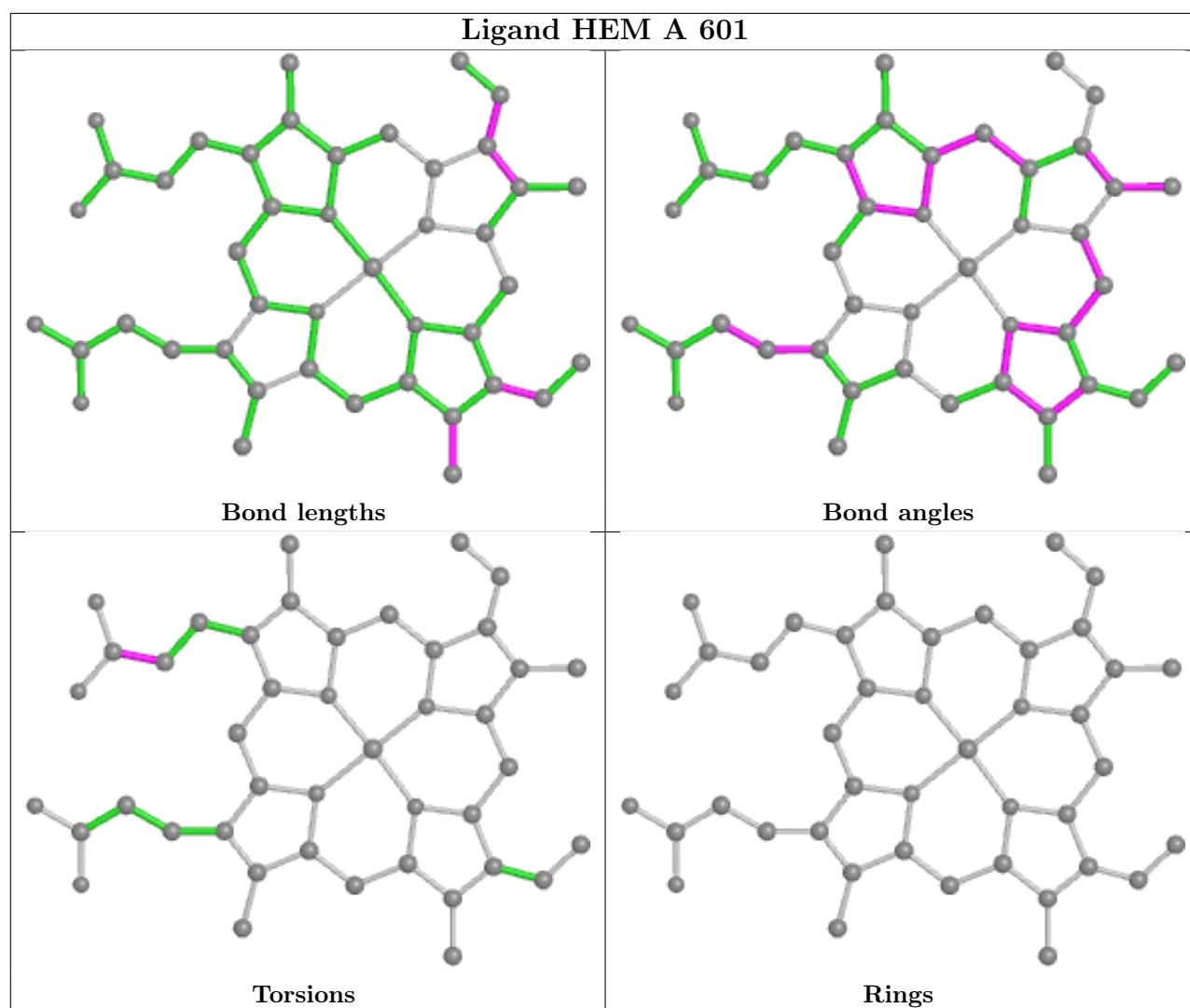
There are no ring outliers.

2 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	O39	14	0
2	A	601	HEM	4	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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	436/487 (89%)	0.73	59 (13%) 3 2	67, 116, 199, 262	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	200	GLN	6.6
1	A	250	ARG	6.4
1	A	220	PHE	5.1
1	A	493	VAL	4.6
1	A	257	LYS	4.3
1	A	219	PHE	4.3
1	A	189	PHE	4.2
1	A	102	PHE	4.0
1	A	142	LEU	3.9
1	A	170	VAL	3.8
1	A	145	MET	3.7
1	A	491	LEU	3.6
1	A	304	PHE	3.5
1	A	166	THR	3.5
1	A	274	LEU	3.5
1	A	195	SER	3.4
1	A	271	PHE	3.4
1	A	224	THR	3.3
1	A	249	LEU	3.3
1	A	383	ILE	3.2
1	A	169	PRO	3.2
1	A	256	MET	3.1
1	A	197	ASN	3.0
1	A	226	PHE	3.0
1	A	290	LEU	3.0
1	A	101	VAL	3.0
1	A	382	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	225	VAL	2.9
1	A	479	LEU	2.8
1	A	153	GLY	2.8
1	A	295	LEU	2.8
1	A	335	ILE	2.7
1	A	244	GLU	2.7
1	A	229	LEU	2.7
1	A	490	VAL	2.7
1	A	356	LEU	2.6
1	A	300	ILE	2.5
1	A	108	PHE	2.4
1	A	160	LEU	2.4
1	A	58	CYS	2.4
1	A	379	LYS	2.4
1	A	190	GLY	2.3
1	A	243	ARG	2.3
1	A	465	PHE	2.3
1	A	165	GLU	2.3
1	A	223	ILE	2.3
1	A	278	SER	2.2
1	A	463	PHE	2.2
1	A	457	ILE	2.2
1	A	322	ALA	2.2
1	A	275	MET	2.1
1	A	34	LYS	2.1
1	A	35	LYS	2.1
1	A	181	MET	2.1
1	A	158	ARG	2.1
1	A	235	VAL	2.0
1	A	46	PHE	2.0
1	A	203	PHE	2.0
1	A	487	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 monosaccharides in this entry.

6.4 Ligands ⓘ

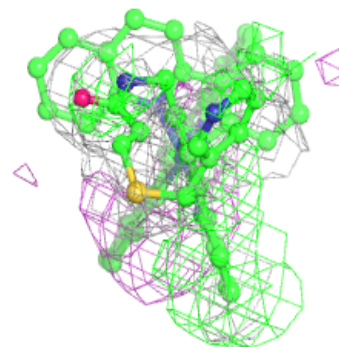
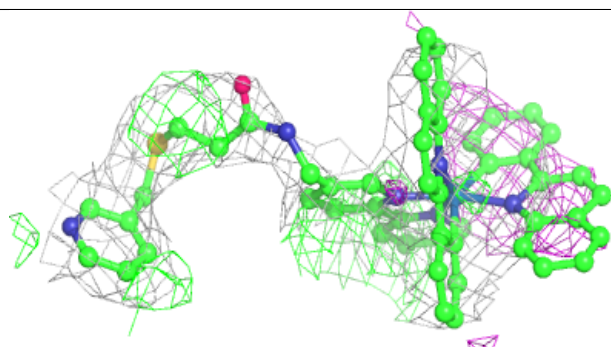
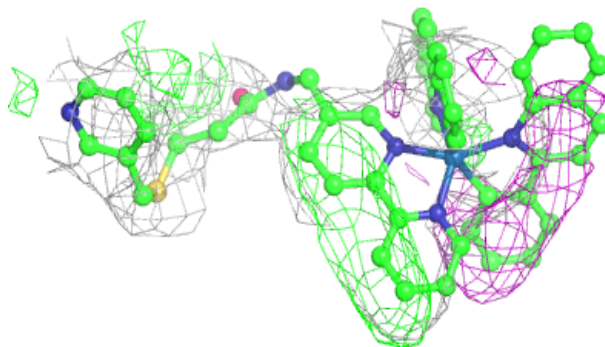
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	O39	A	602	59/59	0.73	0.38	77,223,261,414	0
2	HEM	A	601	43/43	0.97	0.20	56,84,102,118	0

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

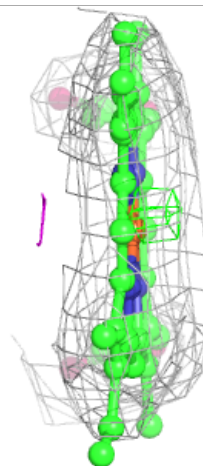
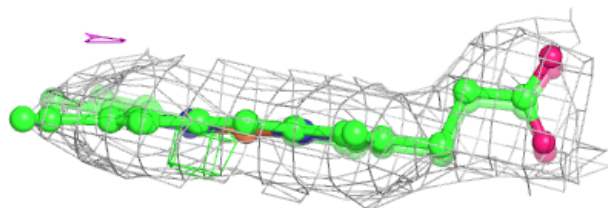
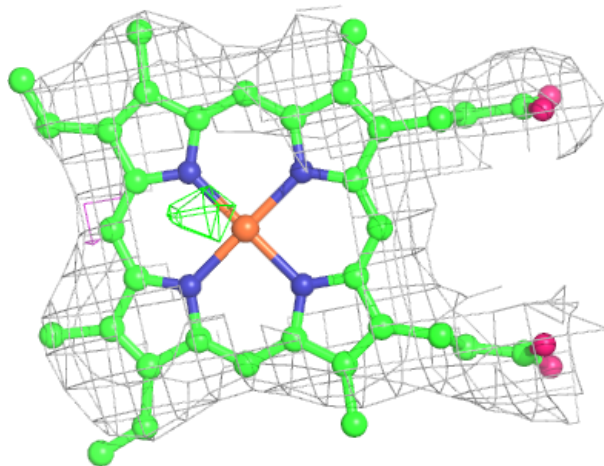
Electron density around O39 A 602:

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



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.