



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 5, 2026 – 11:29 AM JST

PDB ID : 6IQ5 / pdb_00006iq5
Title : Crystal Structure of CYP1B1 and Inhibitor Having Azide Group
Authors : Kubo, M.; Yamamoto, K.; Itoh, T.
Deposited on : 2018-11-06
Resolution : 3.70 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

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 : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

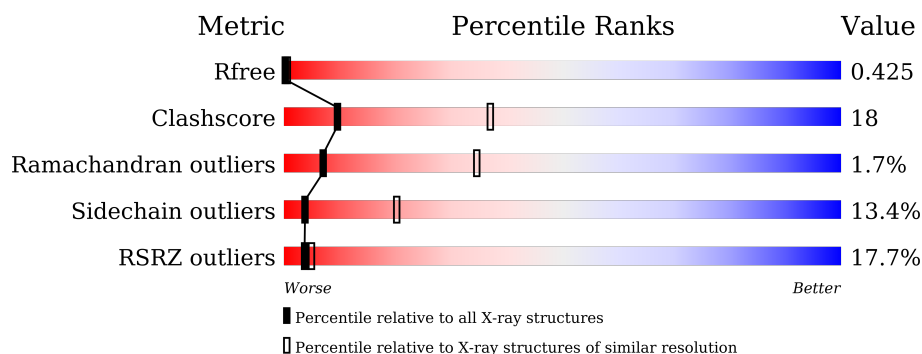
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1131 (3.80-3.60)
Clashscore	190562	1171 (3.80-3.60)
Ramachandran outliers	187476	1129 (3.80-3.60)
Sidechain outliers	187428	1126 (3.80-3.60)
RSRZ outliers	180081	1130 (3.80-3.60)

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.

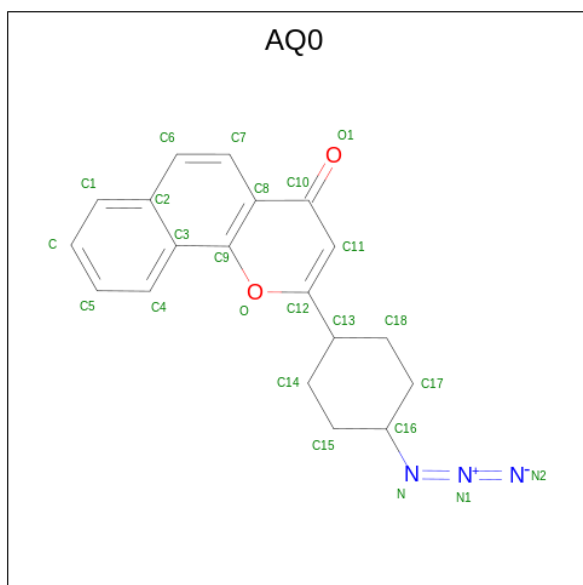
Mol	Chain	Length	Quality of chain
1	A	463	16% 62% 30% 7%
1	B	463	19% 59% 30% 5% 6%

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	AQ0	A	902	-	-	-	X

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

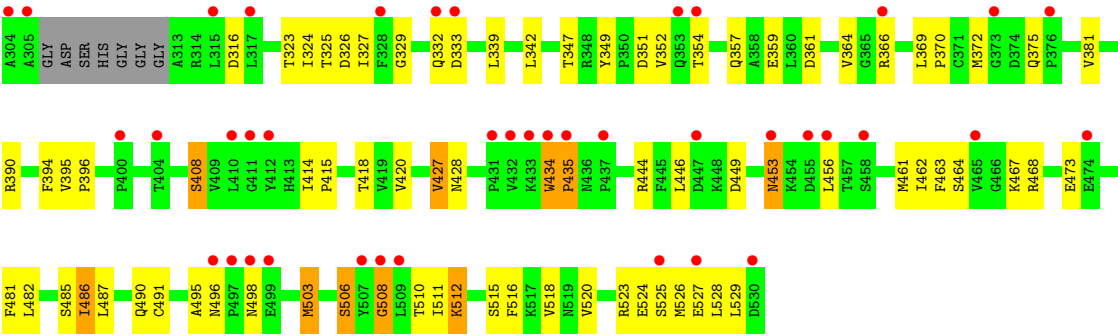
- Molecule 3 is 2-(cis-4-azidocyclohexyl)-4H-naphtho[1,2-b]pyran-4-one (CCD ID: AQ0) (formula: C₁₉H₁₇N₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O		
			24	19	3	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O		
			2	2	0	0
4	B	1	Total	O		
			1	1	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	135.19Å 135.19Å 302.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.80 – 3.70 47.80 – 3.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (47.80-3.70) 99.3 (47.80-3.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.06 (at 3.67Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.356 , 0.396 0.419 , 0.425	Depositor DCC
R_{free} test set	1472 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	111.3	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 354.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
F_o, F_c correlation	0.75	EDS
Total number of atoms	7186	wwPDB-VP
Average B, all atoms (Å ²)	316.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, AQ0

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	0.83	0/3739	1.11	16/5066 (0.3%)
1	B	0.88	0/3506	1.16	17/4759 (0.4%)
All	All	0.85	0/7245	1.13	33/9825 (0.3%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	ALA	N-CA-C	-7.81	103.77	113.38
1	A	284	ARG	CA-C-N	7.50	129.21	119.84
1	A	284	ARG	C-N-CA	7.50	129.21	119.84
1	B	329	GLY	N-CA-C	7.17	121.33	112.73
1	B	183	ARG	N-CA-C	6.99	119.75	111.71

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	3650	0	3606	137	0
1	B	3423	0	3349	115	0
2	A	43	0	30	4	0
2	B	43	0	30	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	24	0	0	1	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
All	All	7186	0	7015	252	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 18.

The worst 5 of 252 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:526:MET:CE	1:A:529:LEU:HD21	1.69	1.22
1:B:327:ILE:HG23	2:B:900:HEM:HBC1	1.17	1.10
1:A:526:MET:HE1	1:A:529:LEU:HD21	1.23	1.06
1:A:526:MET:CE	1:A:529:LEU:CD2	2.38	1.00
1:A:489:HIS:HA	1:A:523:ARG:NH1	1.77	0.99

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	455/463 (98%)	393 (86%)	54 (12%)	8 (2%)	6	34
1	B	429/463 (93%)	367 (86%)	55 (13%)	7 (2%)	7	35
All	All	884/926 (96%)	760 (86%)	109 (12%)	15 (2%)	7	34

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	285	PRO

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Mol	Chain	Res	Type
1	A	436	ASN
1	A	500	PRO
1	B	284	ARG
1	B	435	PRO

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	394/397 (99%)	329 (84%)	65 (16%)	2	14
1	B	362/397 (91%)	326 (90%)	36 (10%)	7	30
All	All	756/794 (95%)	655 (87%)	101 (13%)	4	20

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	484	ILE
1	B	166	LEU
1	B	525	SER
1	A	503	MET
1	B	76	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	319	ASN
1	B	423	ASN
1	A	479	GLN
1	A	490	GLN
1	B	71	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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$
3	AQ0	A	902	-	25,27,27	1.52	4 (16%)	32,38,38	2.47	7 (21%)
2	HEM	A	901	1	50,50,50	1.59	8 (16%)	66,82,82	1.70	16 (24%)
2	HEM	B	900	1	50,50,50	1.58	8 (16%)	66,82,82	1.65	16 (24%)

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	AQ0	A	902	-	-	4/7/17/17	1/4/4/4
2	HEM	A	901	1	-	2/14/54/54	-
2	HEM	B	900	1	-	2/14/54/54	-

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	HEM	FE-NB	5.11	2.10	1.94
2	B	900	HEM	FE-NB	4.98	2.10	1.94
2	B	900	HEM	FE-NC	4.77	2.11	1.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	901	HEM	FE-NC	4.63	2.10	1.95
3	A	902	AQ0	C8-C9	4.12	1.48	1.39

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	902	AQ0	C16-N-N1	8.95	133.12	115.01
3	A	902	AQ0	O-C9-C3	6.94	122.79	114.58
2	B	900	HEM	C1B-NB-C4B	4.48	109.70	105.07
2	A	901	HEM	CHA-C4D-ND	4.13	129.47	124.37
2	A	901	HEM	CHC-C4B-NB	4.04	128.80	124.42

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	HEM	C2C-C3C-CAC-CBC
3	A	902	AQ0	O-C12-C13-C14
3	A	902	AQ0	C11-C12-C13-C14
3	A	902	AQ0	C15-C16-N-N1
2	A	901	HEM	C4C-C3C-CAC-CBC

All (1) ring outliers are listed below:

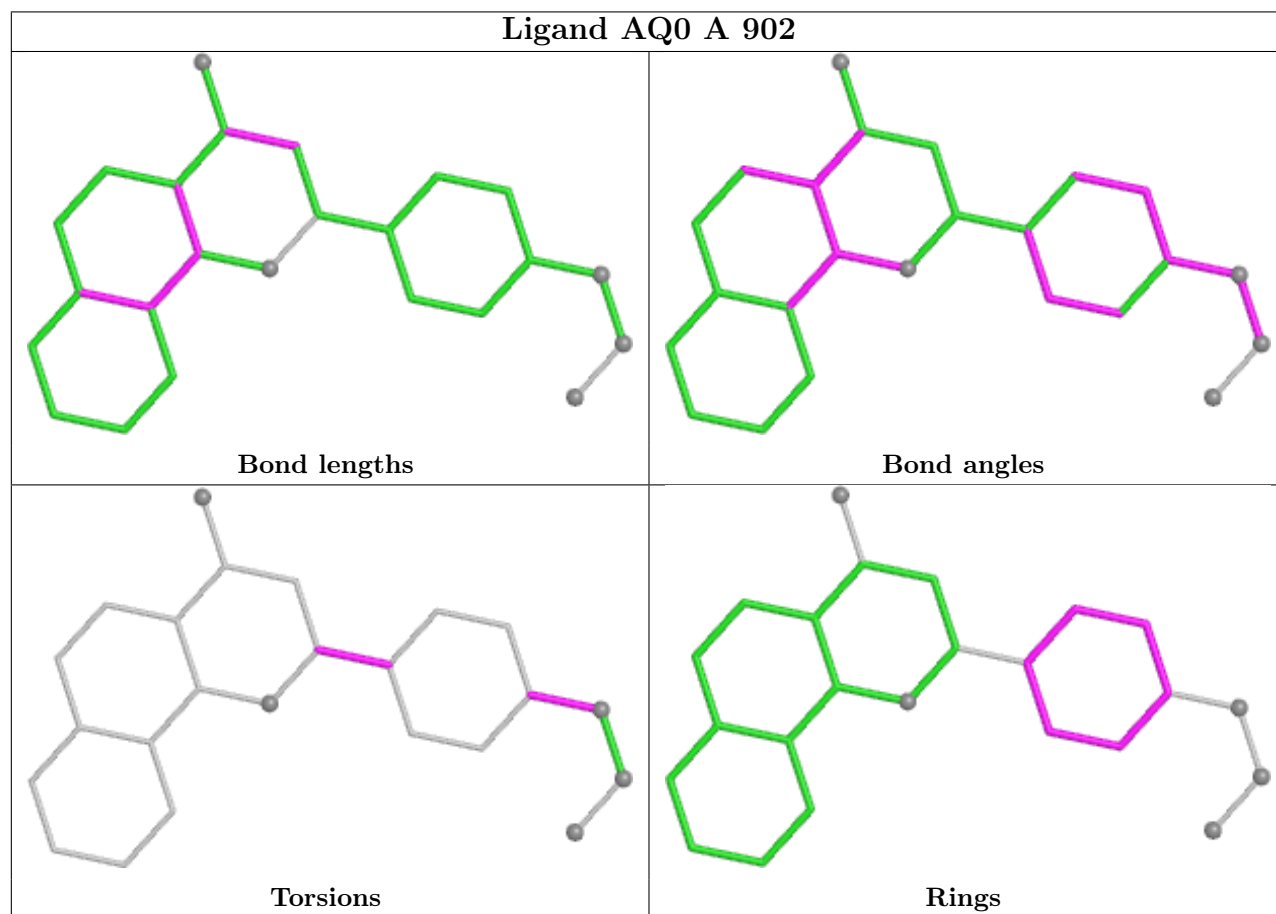
Mol	Chain	Res	Type	Atoms
3	A	902	AQ0	C13-C14-C15-C16-C17-C18

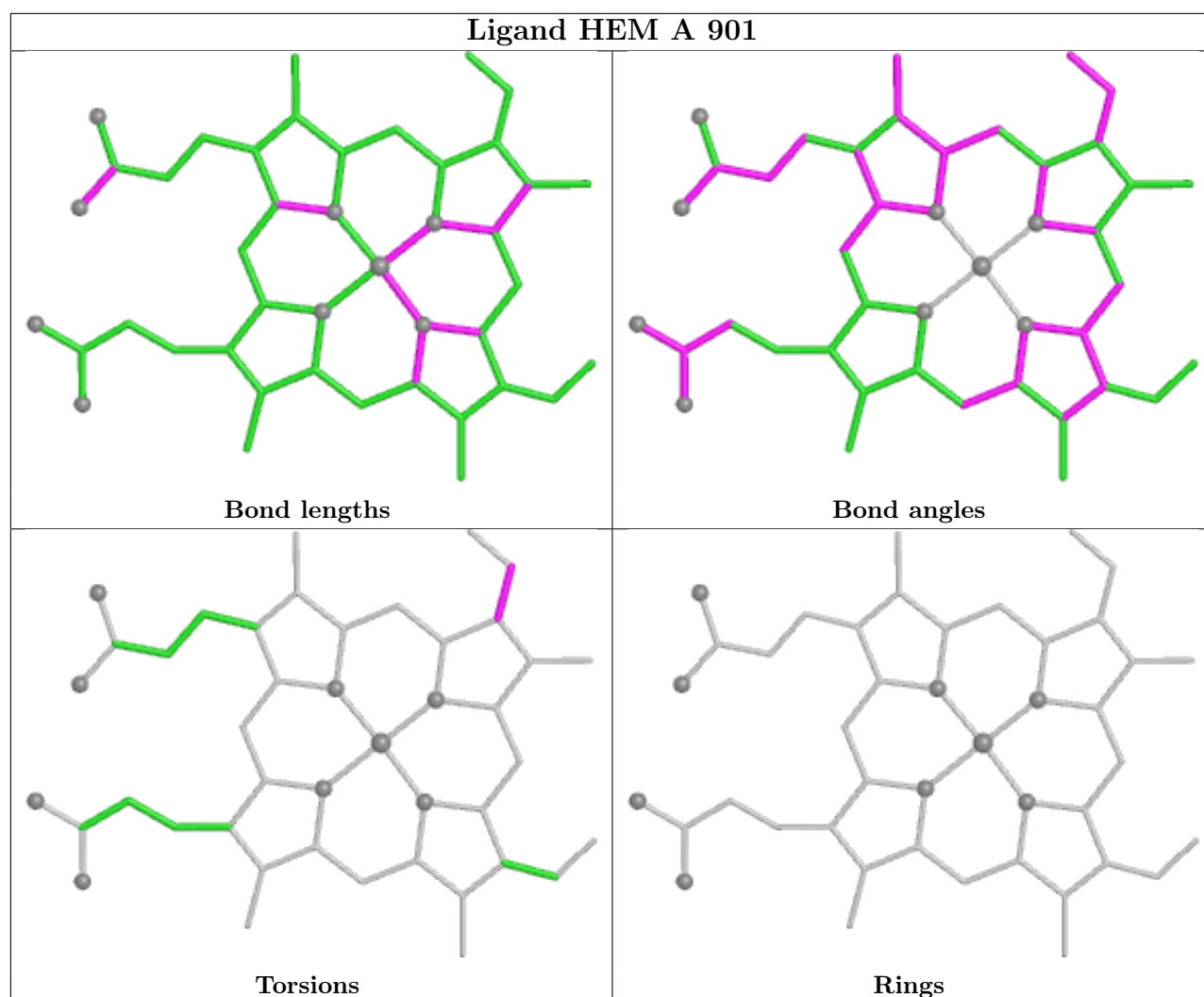
3 monomers are involved in 10 short contacts:

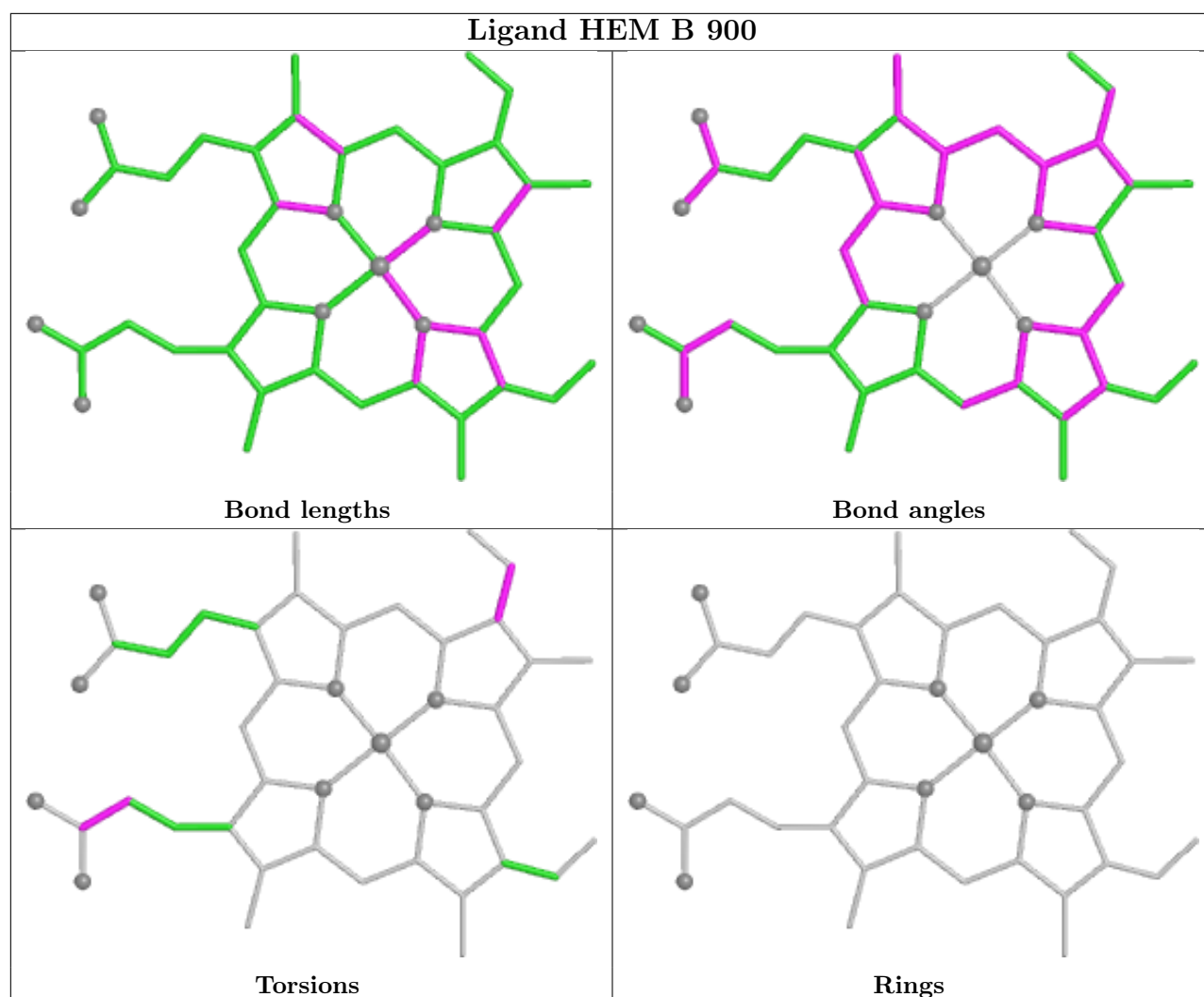
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	902	AQ0	1	0
2	A	901	HEM	4	0
2	B	900	HEM	5	0

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, 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	459/463 (99%)	1.17	73 (15%) 5 6	241, 305, 413, 474	0
1	B	437/463 (94%)	1.31	86 (19%) 3 3	213, 303, 392, 507	0
All	All	896/926 (96%)	1.24	159 (17%) 4 5	213, 304, 402, 507	0

The worst 5 of 159 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	508	GLY	7.3
1	B	254	VAL	6.4
1	B	509	LEU	6.4
1	B	241	VAL	5.4
1	B	251	PRO	5.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

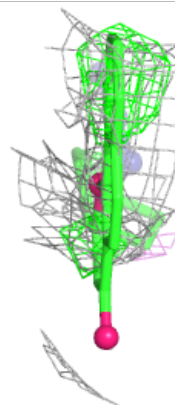
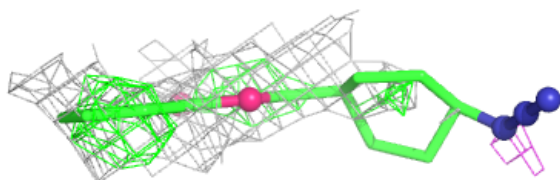
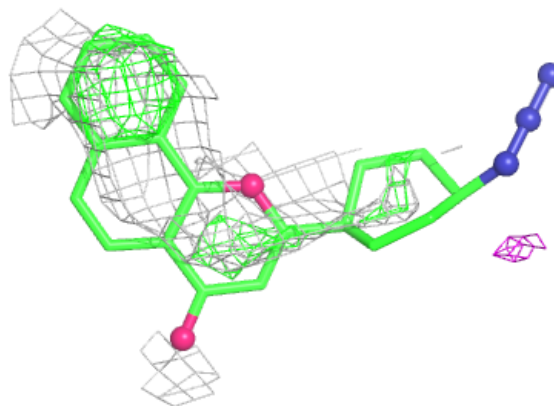
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	AQ0	A	902	24/24	0.76	0.44	493,503,524,557	0
2	HEM	A	901	43/43	0.85	0.35	474,487,497,508	0
2	HEM	B	900	43/43	0.86	0.33	475,489,505,518	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.

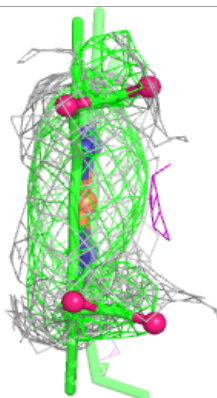
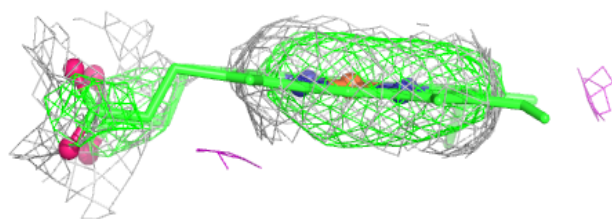
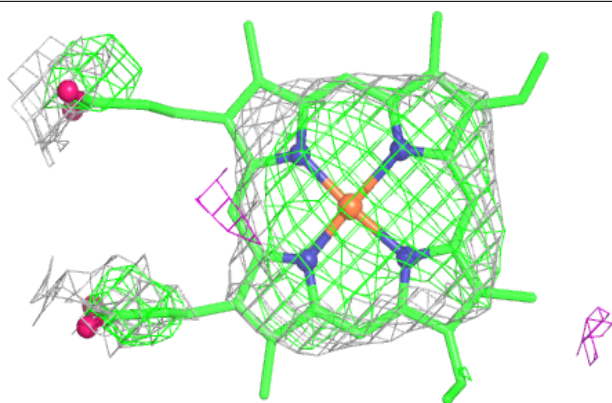
Electron density around AQ0 A 902:

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

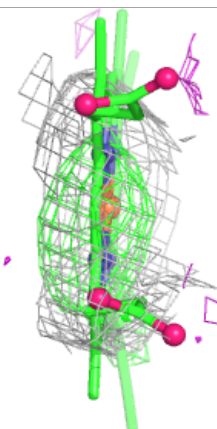
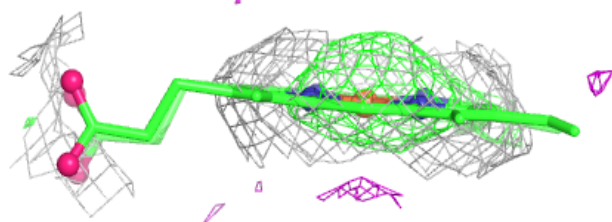
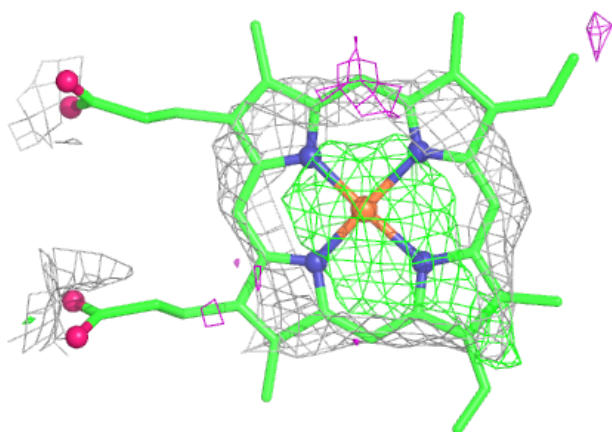


Electron density around HEM A 901:

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

**Electron density around HEM B 900:**

$2mF_o-DF_c$ (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.