



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2026 – 03:33 am BST

PDB ID : 2BVJ / pdb_00002bvj
Title : Ligand-free structure of cytochrome P450 PikC (CYP107L1)
Authors : Sherman, D.H.; Li, S.; Yermalitskaya, L.V.; Kim, Y.; Smith, J.A.; Waterman, M.R.; Podust, L.M.
Deposited on : 2005-06-28
Resolution : 2.10 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 : 1.8.4, 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

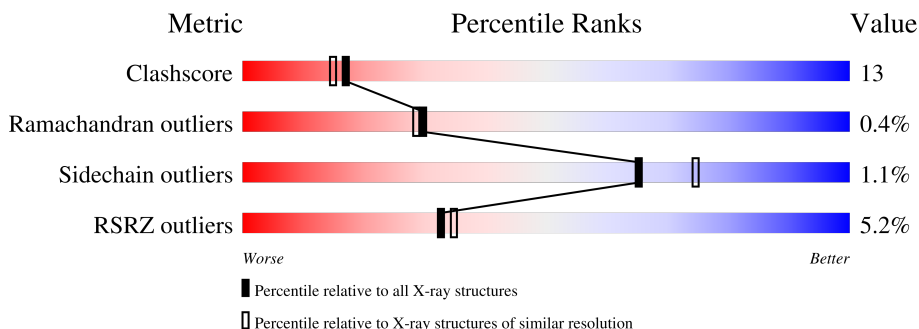
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	436	3% 66% 23% • 9%
1	B	436	6% 68% 22% • 10%

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:

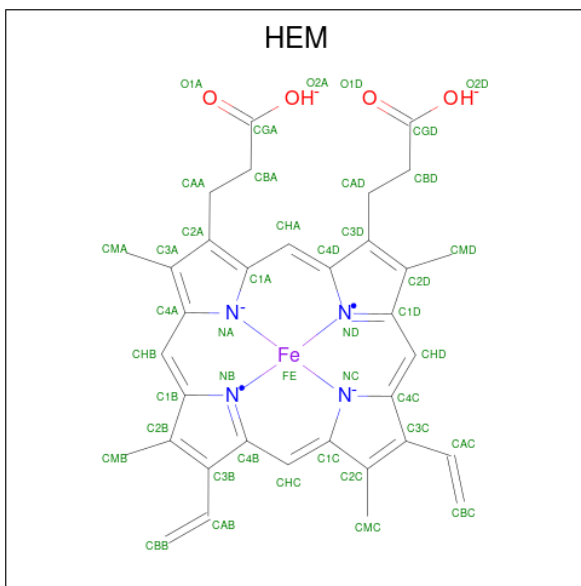
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BME	A	1409	-	-	X	-
3	BME	B	1409	-	-	X	-

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CYTOCHROME P450 MONOOXYGENASE.

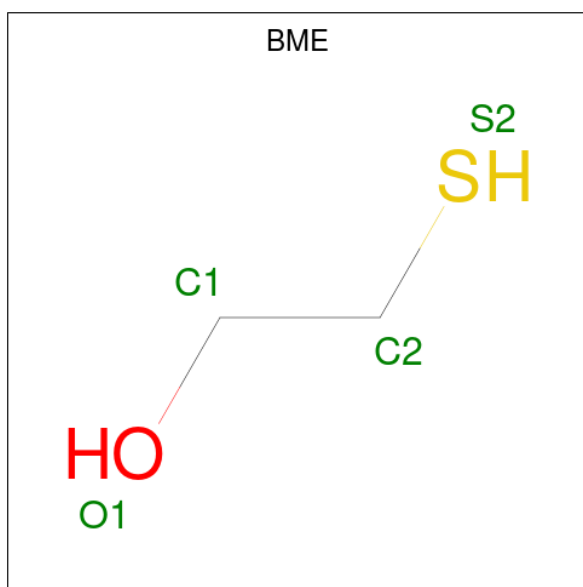
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total 3039	C 1916	N 549	O 561	S 13	0	0	1
1	B	392	Total 3007	C 1897	N 545	O 553	S 12	0	0	1

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



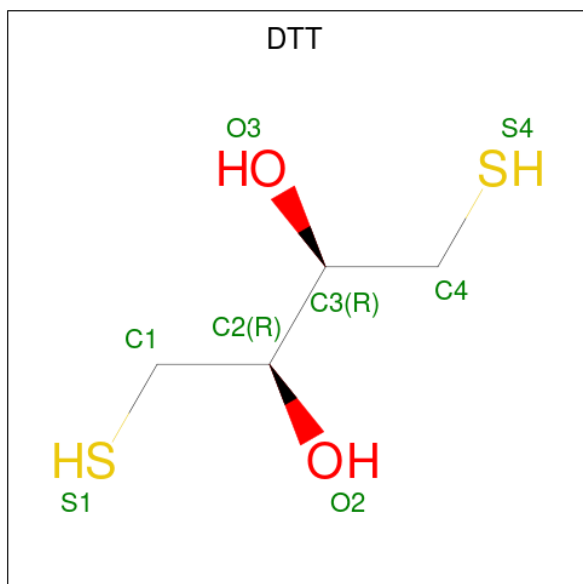
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is BETA-MERCAPTOETHANOL (CCD ID: BME) (formula: $\text{C}_2\text{H}_6\text{OS}$).



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

- Molecule 4 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (CCD ID: DTT) (formula: $C_4H_{10}O_2S_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			8	4	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	144	Total 144	O 144	0	0
5	B	171	Total 171	O 171	0	0

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.

Chain A:

3% 66% 23% 9%

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Arg Pro Arg Gly Ser His His Ser Ser Gly Thr Thr Thr Ala Ser Pro Pro V14 L15 D16 Q22 A25 R34 L35 E38 H42 R45 E48 Q49 Y58 P59 R60 A66 R60

W74 T78 M89 D96 R99 A108 F111 T112 M113 R114 R115 E116 Y117 R120 P121 L135 M145 L148 A149 W150 P151 L152 P153 I154 T155 E159 L180 L161 E165 P166 D167 R168 W174 A177 F178 V179 F180 P181 D182 D183 P184 A185 Q186 W190

L198 R219 R224 D225 S226 E231 L239 L240 L241 V242 A243 G244 V249 H262 Q265 T274 A279 V280 E281 E282 M283 L284 M285 Y286 E287 E291 Y295 P298 L304 D305 G306 P310 A311 G312 D313 R324 R328 P329 P330 D331 P332 H333 W335

F335 D336 I337 R338 R339 D340 H344 L345 A346 H352 F353 C354 I355 G356 A357 P358 L371 C375 V382 E386 W389 Y390 P391 N392 P393 M394 M395 Y405 R406 R407 R408 ARG GLU ALA GLY ARG ARG ARG THR GLY

Chain B:

68% 22% 6% 10%

MET GLY SER SER HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG ARG GLY SER HIS MET ARG ARG THR GLN GLY THR THR ALA S11 P12 A19 Q22 R36 P40 P47 E48 G49 R60 K72 T79 P80 L81 THR GLU ALA GLU ALA T58

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	218.19Å 64.17Å 73.59Å 90.00° 107.15° 90.00°	Depositor
Resolution (Å)	36.98 – 2.10 36.98 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.2 (36.98-2.10) 94.3 (36.98-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.61 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.202 , 0.243 0.197 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.628	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6463	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.25% 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: DTT, BME, 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	0.40	1/3109 (0.0%)	0.89	11/4245 (0.3%)
1	B	0.41	1/3078 (0.0%)	0.89	14/4203 (0.3%)
All	All	0.41	2/6187 (0.0%)	0.89	25/8448 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	407	ARG	C-N	-5.76	1.25	1.33
1	A	407	ARG	C-N	-5.45	1.25	1.33

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	331	ASP	CA-C-N	6.59	127.11	119.47
1	A	331	ASP	C-N-CA	6.59	127.11	119.47
1	A	274	THR	N-CA-C	-6.24	105.62	113.18
1	B	325	THR	CA-C-N	6.18	125.66	119.24
1	B	325	THR	C-N-CA	6.18	125.66	119.24

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	3039	0	2998	94	0
1	B	3007	0	2949	66	0
2	A	43	0	30	4	0
2	B	43	0	30	0	0
3	A	4	0	6	3	1
3	B	4	0	6	4	1
4	A	8	0	10	0	0
5	A	144	0	0	6	0
5	B	171	0	0	9	0
All	All	6463	0	6029	155	2

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 13.

The worst 5 of 155 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:334:ARG:HE	1:A:335:PHE:H	1.15	0.94
1:B:323:HIS:HE1	1:B:345:LEU:H	1.06	0.91
1:A:45:ARG:HE	1:A:49:GLY:HA2	1.34	0.90
1:B:22:GLN:HE22	1:B:389:TRP:H	1.26	0.83
1:A:334:ARG:HE	1:A:335:PHE:N	1.75	0.83

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1409:BME:C1	3:A:1409:BME:C1[2_556]	1.58	0.62
3:B:1409:BME:C1	3:B:1409:BME:C1[2_557]	1.77	0.43

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	393/436 (90%)	377 (96%)	15 (4%)	1 (0%)	36	36
1	B	388/436 (89%)	372 (96%)	14 (4%)	2 (0%)	24	22
All	All	781/872 (90%)	749 (96%)	29 (4%)	3 (0%)	30	28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	187	ALA
1	A	179	VAL
1	B	207	GLY

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	314/355 (88%)	311 (99%)	3 (1%)	68	76
1	B	309/355 (87%)	305 (99%)	4 (1%)	61	69
All	All	623/710 (88%)	616 (99%)	7 (1%)	65	74

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	72	LYS
1	B	109	ARG
1	B	273	MET
1	B	150	TRP
1	A	285	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	245	HIS
1	B	262	HIS
1	B	349	HIS

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Mol	Chain	Res	Type
1	B	323	HIS
1	A	344	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 ⓘ

5 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	1408	1	50,50,50	1.17	4 (8%)	66,82,82	0.85	3 (4%)
3	BME	B	1409	-	3,3,3	0.51	0	1,2,2	0.95	0
3	BME	A	1409	-	3,3,3	0.97	0	1,2,2	1.35	0
4	DTT	A	1410	-	7,7,7	0.56	0	4,8,8	1.14	0
2	HEM	B	1408	1	50,50,50	1.28	6 (12%)	66,82,82	0.79	1 (1%)

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	1408	1	-	5/14/54/54	-
3	BME	B	1409	-	-	1/1/1/1	-
3	BME	A	1409	-	-	1/1/1/1	-
4	DTT	A	1410	-	-	0/8/8/8	-
2	HEM	B	1408	1	-	2/14/54/54	-

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1408	HEM	CBC-CAC	3.16	1.45	1.30
2	A	1408	HEM	CAC-C3C	-2.94	1.39	1.47
2	B	1408	HEM	CBB-CAB	2.93	1.44	1.30
2	B	1408	HEM	CBC-CAC	2.76	1.44	1.30
2	B	1408	HEM	CAC-C3C	-2.74	1.40	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1408	HEM	CAD-C3D-C4D	2.19	128.48	124.66
2	A	1408	HEM	CMC-C2C-C1C	2.16	128.52	124.71
2	A	1408	HEM	C4B-C3B-C2B	-2.14	105.41	107.11
2	A	1408	HEM	CAC-C3C-C4C	2.08	129.91	124.90

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

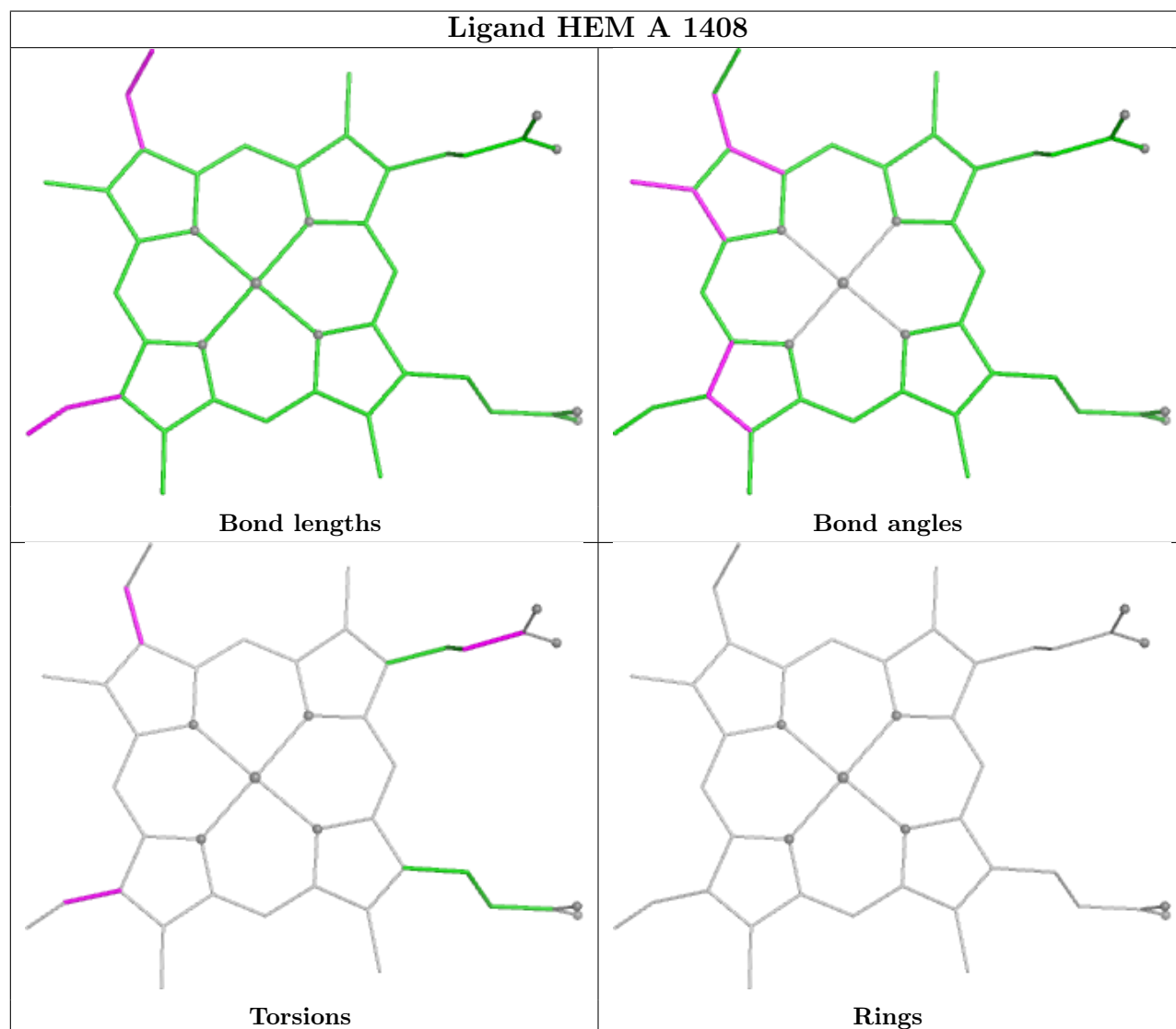
Mol	Chain	Res	Type	Atoms
2	A	1408	HEM	C2B-C3B-CAB-CBB
3	A	1409	BME	O1-C1-C2-S2
3	B	1409	BME	O1-C1-C2-S2
2	A	1408	HEM	C2C-C3C-CAC-CBC
2	A	1408	HEM	C4C-C3C-CAC-CBC

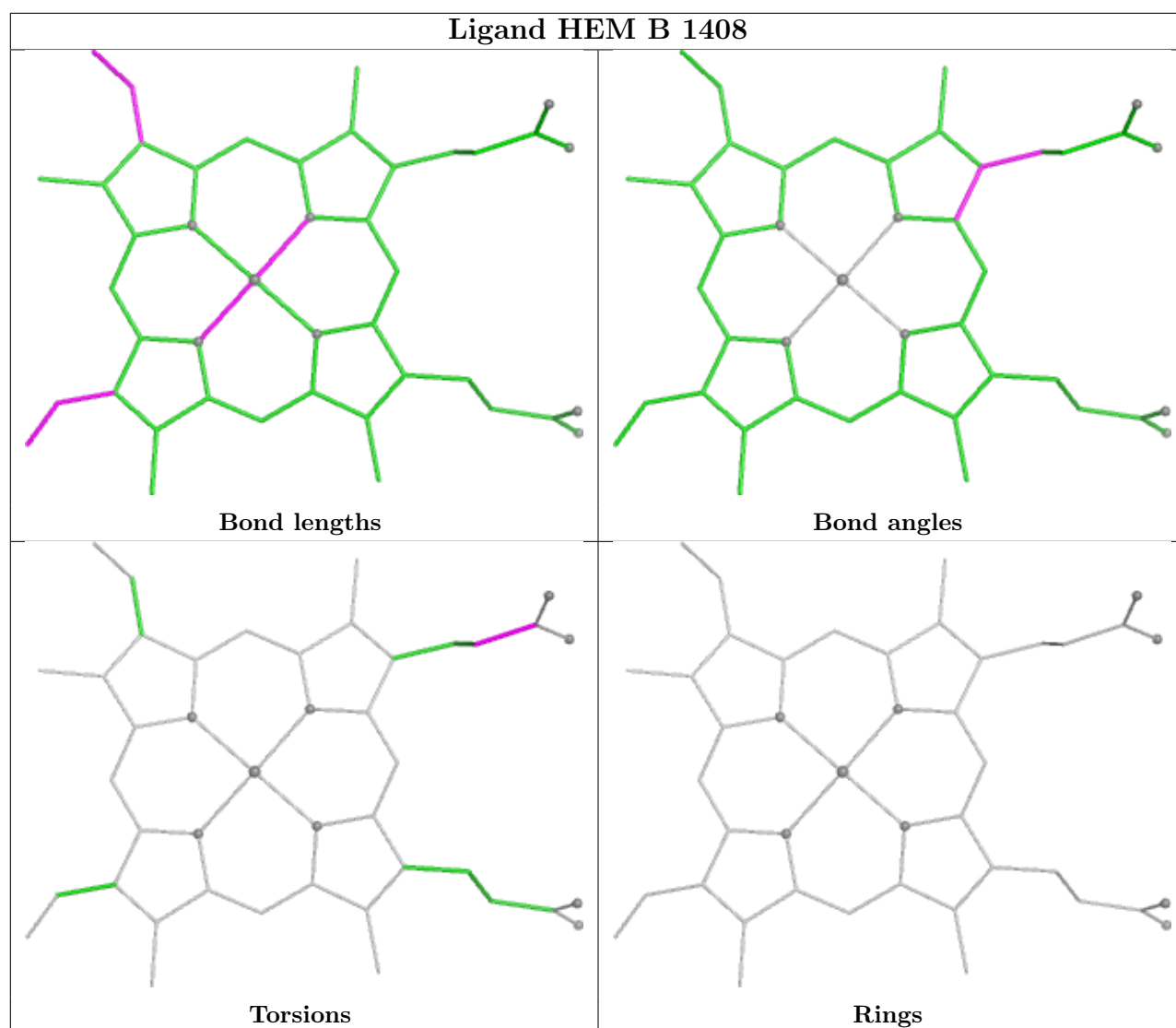
There are no ring outliers.

3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1408	HEM	4	0
3	B	1409	BME	4	1
3	A	1409	BME	3	1

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	395/436 (90%)	0.23	15 (3%) 44 46	14, 27, 47, 65	0
1	B	392/436 (89%)	0.19	26 (6%) 24 26	15, 25, 50, 61	0
All	All	787/872 (90%)	0.21	41 (5%) 33 35	14, 26, 48, 65	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	81	LEU	5.8
1	B	178	PHE	4.8
1	A	182	ASP	4.4
1	B	179	VAL	4.0
1	B	180	PHE	3.8

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](#)

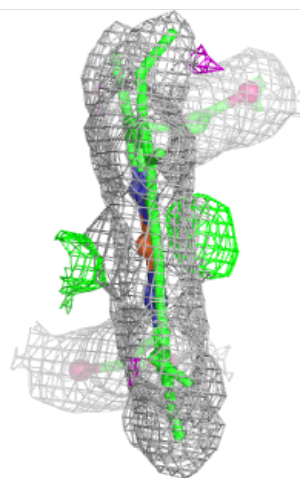
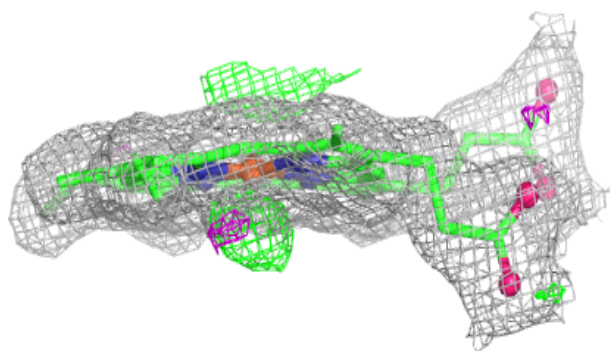
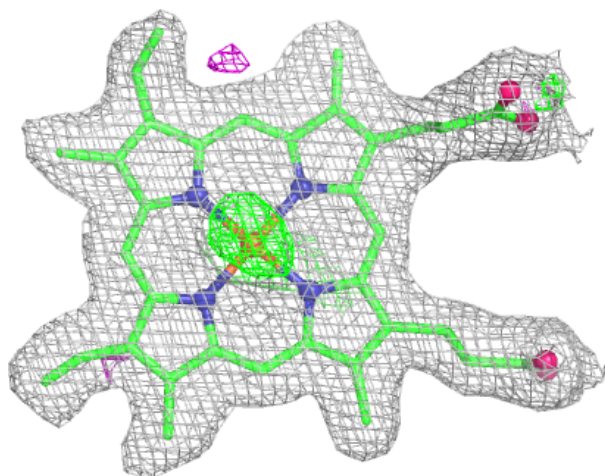
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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
4	DTT	A	1410	8/8	0.62	0.29	48,52,58,69	0
3	BME	B	1409	4/4	0.67	0.24	58,60,62,67	0
3	BME	A	1409	4/4	0.88	0.16	47,47,48,50	0
2	HEM	A	1408	43/43	0.97	0.07	15,17,22,25	0
2	HEM	B	1408	43/43	0.98	0.06	12,16,18,19	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.

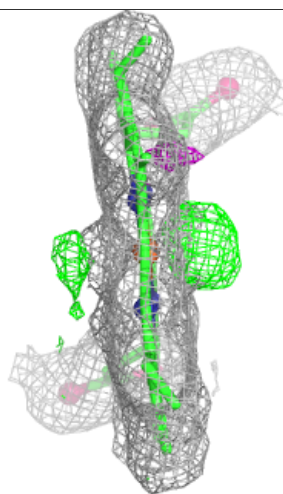
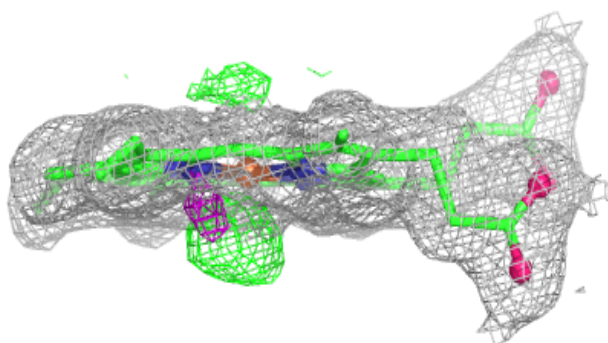
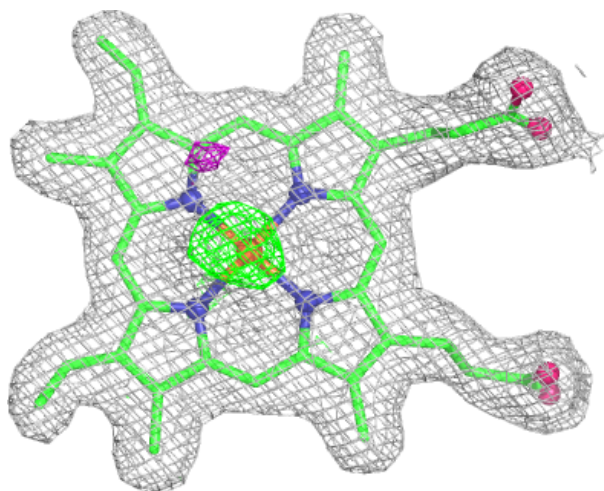
Electron density around HEM A 1408:

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



Electron density around HEM B 1408:

$2mF_o-DF_c$ (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.