



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:20 AM UTC

PDB ID : 8Q2F / pdb_00008q2f
Title : Cytochrome P450 BM3 aMOx-A heme domain
Authors : Klaus, C.; Kowal, J.L.; Hammer, S.C.; Niemann, H.H.
Deposited on : 2023-08-02
Resolution : 3.43 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 : 2022.3.0, CSD as543be (2022)
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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

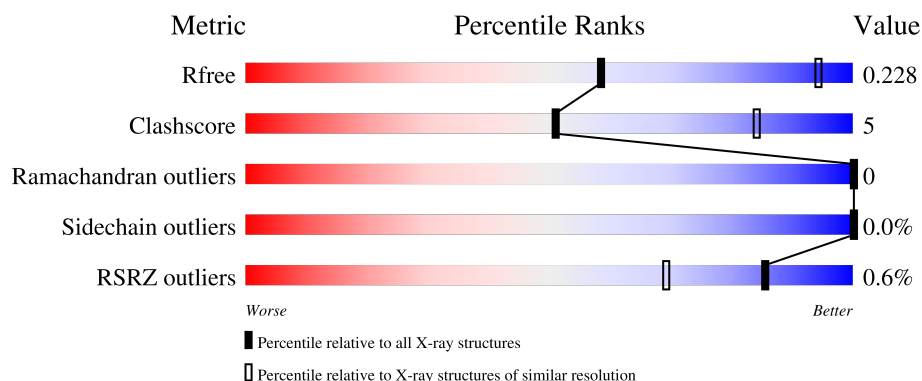
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.43 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	1736 (3.50-3.38)
Clashscore	190562	1808 (3.50-3.38)
Ramachandran outliers	187476	1776 (3.50-3.38)
Sidechain outliers	187428	1777 (3.50-3.38)
RSRZ outliers	180081	1736 (3.50-3.38)

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	472	% 81% 16% .
1	B	472	% 84% 13% .
1	C	472	81% 16% .
1	D	472	86% 11% .
1	E	472	% 86% 12% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	472	% 87% 10% .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 22710 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 Bifunctional cytochrome P450/NADPH-P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	458	Total	C	N	O	S	0	0	0
			3695	2360	632	683	20			
1	B	461	Total	C	N	O	S	0	1	0
			3725	2379	638	688	20			
1	C	457	Total	C	N	O	S	0	0	0
			3687	2354	631	682	20			
1	D	458	Total	C	N	O	S	0	0	0
			3695	2360	632	683	20			
1	E	462	Total	C	N	O	S	0	0	0
			3721	2376	636	689	20			
1	F	461	Total	C	N	O	S	0	1	0
			3725	2379	638	688	20			

There are 204 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	44	MET	ALA	engineered mutation	UNP P14779
A	72	HIS	SER	engineered mutation	UNP P14779
A	77	GLU	PHE	engineered mutation	UNP P14779
A	78	ILE	VAL	engineered mutation	UNP P14779
A	82	CYS	ALA	engineered mutation	UNP P14779
A	87	ALA	PHE	engineered mutation	UNP P14779
A	88	LEU	THR	engineered mutation	UNP P14779
A	89	VAL	SER	engineered mutation	UNP P14779
A	142	ALA	PRO	engineered mutation	UNP P14779
A	174	VAL	ILE	engineered mutation	UNP P14779
A	175	ILE	THR	engineered mutation	UNP P14779
A	184	VAL	ALA	engineered mutation	UNP P14779
A	212	PHE	MET	engineered mutation	UNP P14779
A	226	ARG	SER	engineered mutation	UNP P14779
A	232	CYS	ASP	engineered mutation	UNP P14779
A	236	GLN	HIS	engineered mutation	UNP P14779
A	252	GLY	GLU	engineered mutation	UNP P14779

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	256	ASP	TYR	engineered mutation	UNP P14779
A	269	LEU	THR	engineered mutation	UNP P14779
A	290	VAL	ALA	engineered mutation	UNP P14779
A	315	ASP	GLY	engineered mutation	UNP P14779
A	327	MET	THR	engineered mutation	UNP P14779
A	328	SER	ALA	engineered mutation	UNP P14779
A	353	VAL	LEU	engineered mutation	UNP P14779
A	366	VAL	ILE	engineered mutation	UNP P14779
A	436	HIS	THR	engineered mutation	UNP P14779
A	464	LEU	-	expression tag	UNP P14779
A	465	GLU	-	expression tag	UNP P14779
A	466	HIS	-	expression tag	UNP P14779
A	467	HIS	-	expression tag	UNP P14779
A	468	HIS	-	expression tag	UNP P14779
A	469	HIS	-	expression tag	UNP P14779
A	470	HIS	-	expression tag	UNP P14779
A	471	HIS	-	expression tag	UNP P14779
B	44	MET	ALA	engineered mutation	UNP P14779
B	72	HIS	SER	engineered mutation	UNP P14779
B	77	GLU	PHE	engineered mutation	UNP P14779
B	78	ILE	VAL	engineered mutation	UNP P14779
B	82	CYS	ALA	engineered mutation	UNP P14779
B	87	ALA	PHE	engineered mutation	UNP P14779
B	88	LEU	THR	engineered mutation	UNP P14779
B	89	VAL	SER	engineered mutation	UNP P14779
B	142	ALA	PRO	engineered mutation	UNP P14779
B	174	VAL	ILE	engineered mutation	UNP P14779
B	175	ILE	THR	engineered mutation	UNP P14779
B	184	VAL	ALA	engineered mutation	UNP P14779
B	212	PHE	MET	engineered mutation	UNP P14779
B	226	ARG	SER	engineered mutation	UNP P14779
B	232	CYS	ASP	engineered mutation	UNP P14779
B	236	GLN	HIS	engineered mutation	UNP P14779
B	252	GLY	GLU	engineered mutation	UNP P14779
B	256	ASP	TYR	engineered mutation	UNP P14779
B	269	LEU	THR	engineered mutation	UNP P14779
B	290	VAL	ALA	engineered mutation	UNP P14779
B	315	ASP	GLY	engineered mutation	UNP P14779
B	327	MET	THR	engineered mutation	UNP P14779
B	328	SER	ALA	engineered mutation	UNP P14779
B	353	VAL	LEU	engineered mutation	UNP P14779
B	366	VAL	ILE	engineered mutation	UNP P14779

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	436	HIS	THR	engineered mutation	UNP P14779
B	464	LEU	-	expression tag	UNP P14779
B	465	GLU	-	expression tag	UNP P14779
B	466	HIS	-	expression tag	UNP P14779
B	467	HIS	-	expression tag	UNP P14779
B	468	HIS	-	expression tag	UNP P14779
B	469	HIS	-	expression tag	UNP P14779
B	470	HIS	-	expression tag	UNP P14779
B	471	HIS	-	expression tag	UNP P14779
C	44	MET	ALA	engineered mutation	UNP P14779
C	72	HIS	SER	engineered mutation	UNP P14779
C	77	GLU	PHE	engineered mutation	UNP P14779
C	78	ILE	VAL	engineered mutation	UNP P14779
C	82	CYS	ALA	engineered mutation	UNP P14779
C	87	ALA	PHE	engineered mutation	UNP P14779
C	88	LEU	THR	engineered mutation	UNP P14779
C	89	VAL	SER	engineered mutation	UNP P14779
C	142	ALA	PRO	engineered mutation	UNP P14779
C	174	VAL	ILE	engineered mutation	UNP P14779
C	175	ILE	THR	engineered mutation	UNP P14779
C	184	VAL	ALA	engineered mutation	UNP P14779
C	212	PHE	MET	engineered mutation	UNP P14779
C	226	ARG	SER	engineered mutation	UNP P14779
C	232	CYS	ASP	engineered mutation	UNP P14779
C	236	GLN	HIS	engineered mutation	UNP P14779
C	252	GLY	GLU	engineered mutation	UNP P14779
C	256	ASP	TYR	engineered mutation	UNP P14779
C	269	LEU	THR	engineered mutation	UNP P14779
C	290	VAL	ALA	engineered mutation	UNP P14779
C	315	ASP	GLY	engineered mutation	UNP P14779
C	327	MET	THR	engineered mutation	UNP P14779
C	328	SER	ALA	engineered mutation	UNP P14779
C	353	VAL	LEU	engineered mutation	UNP P14779
C	366	VAL	ILE	engineered mutation	UNP P14779
C	436	HIS	THR	engineered mutation	UNP P14779
C	464	LEU	-	expression tag	UNP P14779
C	465	GLU	-	expression tag	UNP P14779
C	466	HIS	-	expression tag	UNP P14779
C	467	HIS	-	expression tag	UNP P14779
C	468	HIS	-	expression tag	UNP P14779
C	469	HIS	-	expression tag	UNP P14779
C	470	HIS	-	expression tag	UNP P14779

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	471	HIS	-	expression tag	UNP P14779
D	44	MET	ALA	engineered mutation	UNP P14779
D	72	HIS	SER	engineered mutation	UNP P14779
D	77	GLU	PHE	engineered mutation	UNP P14779
D	78	ILE	VAL	engineered mutation	UNP P14779
D	82	CYS	ALA	engineered mutation	UNP P14779
D	87	ALA	PHE	engineered mutation	UNP P14779
D	88	LEU	THR	engineered mutation	UNP P14779
D	89	VAL	SER	engineered mutation	UNP P14779
D	142	ALA	PRO	engineered mutation	UNP P14779
D	174	VAL	ILE	engineered mutation	UNP P14779
D	175	ILE	THR	engineered mutation	UNP P14779
D	184	VAL	ALA	engineered mutation	UNP P14779
D	212	PHE	MET	engineered mutation	UNP P14779
D	226	ARG	SER	engineered mutation	UNP P14779
D	232	CYS	ASP	engineered mutation	UNP P14779
D	236	GLN	HIS	engineered mutation	UNP P14779
D	252	GLY	GLU	engineered mutation	UNP P14779
D	256	ASP	TYR	engineered mutation	UNP P14779
D	269	LEU	THR	engineered mutation	UNP P14779
D	290	VAL	ALA	engineered mutation	UNP P14779
D	315	ASP	GLY	engineered mutation	UNP P14779
D	327	MET	THR	engineered mutation	UNP P14779
D	328	SER	ALA	engineered mutation	UNP P14779
D	353	VAL	LEU	engineered mutation	UNP P14779
D	366	VAL	ILE	engineered mutation	UNP P14779
D	436	HIS	THR	engineered mutation	UNP P14779
D	464	LEU	-	expression tag	UNP P14779
D	465	GLU	-	expression tag	UNP P14779
D	466	HIS	-	expression tag	UNP P14779
D	467	HIS	-	expression tag	UNP P14779
D	468	HIS	-	expression tag	UNP P14779
D	469	HIS	-	expression tag	UNP P14779
D	470	HIS	-	expression tag	UNP P14779
D	471	HIS	-	expression tag	UNP P14779
E	44	MET	ALA	engineered mutation	UNP P14779
E	72	HIS	SER	engineered mutation	UNP P14779
E	77	GLU	PHE	engineered mutation	UNP P14779
E	78	ILE	VAL	engineered mutation	UNP P14779
E	82	CYS	ALA	engineered mutation	UNP P14779
E	87	ALA	PHE	engineered mutation	UNP P14779
E	88	LEU	THR	engineered mutation	UNP P14779

Continued on next page...

Continued from previous page...

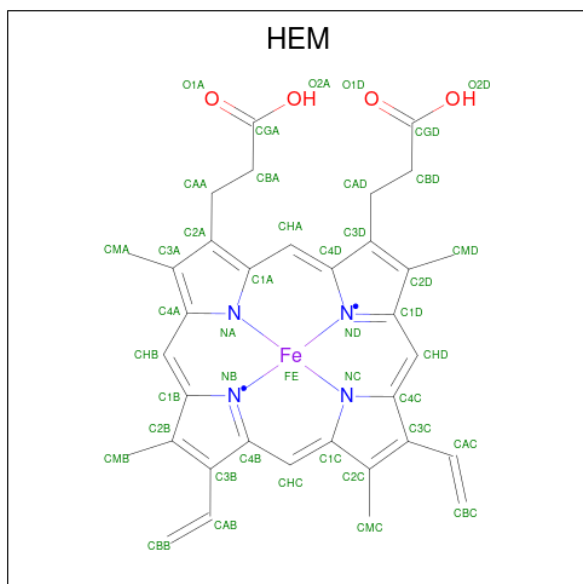
Chain	Residue	Modelled	Actual	Comment	Reference
E	89	VAL	SER	engineered mutation	UNP P14779
E	142	ALA	PRO	engineered mutation	UNP P14779
E	174	VAL	ILE	engineered mutation	UNP P14779
E	175	ILE	THR	engineered mutation	UNP P14779
E	184	VAL	ALA	engineered mutation	UNP P14779
E	212	PHE	MET	engineered mutation	UNP P14779
E	226	ARG	SER	engineered mutation	UNP P14779
E	232	CYS	ASP	engineered mutation	UNP P14779
E	236	GLN	HIS	engineered mutation	UNP P14779
E	252	GLY	GLU	engineered mutation	UNP P14779
E	256	ASP	TYR	engineered mutation	UNP P14779
E	269	LEU	THR	engineered mutation	UNP P14779
E	290	VAL	ALA	engineered mutation	UNP P14779
E	315	ASP	GLY	engineered mutation	UNP P14779
E	327	MET	THR	engineered mutation	UNP P14779
E	328	SER	ALA	engineered mutation	UNP P14779
E	353	VAL	LEU	engineered mutation	UNP P14779
E	366	VAL	ILE	engineered mutation	UNP P14779
E	436	HIS	THR	engineered mutation	UNP P14779
E	464	LEU	-	expression tag	UNP P14779
E	465	GLU	-	expression tag	UNP P14779
E	466	HIS	-	expression tag	UNP P14779
E	467	HIS	-	expression tag	UNP P14779
E	468	HIS	-	expression tag	UNP P14779
E	469	HIS	-	expression tag	UNP P14779
E	470	HIS	-	expression tag	UNP P14779
E	471	HIS	-	expression tag	UNP P14779
F	44	MET	ALA	engineered mutation	UNP P14779
F	72	HIS	SER	engineered mutation	UNP P14779
F	77	GLU	PHE	engineered mutation	UNP P14779
F	78	ILE	VAL	engineered mutation	UNP P14779
F	82	CYS	ALA	engineered mutation	UNP P14779
F	87	ALA	PHE	engineered mutation	UNP P14779
F	88	LEU	THR	engineered mutation	UNP P14779
F	89	VAL	SER	engineered mutation	UNP P14779
F	142	ALA	PRO	engineered mutation	UNP P14779
F	174	VAL	ILE	engineered mutation	UNP P14779
F	175	ILE	THR	engineered mutation	UNP P14779
F	184	VAL	ALA	engineered mutation	UNP P14779
F	212	PHE	MET	engineered mutation	UNP P14779
F	226	ARG	SER	engineered mutation	UNP P14779
F	232	CYS	ASP	engineered mutation	UNP P14779

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	236	GLN	HIS	engineered mutation	UNP P14779
F	252	GLY	GLU	engineered mutation	UNP P14779
F	256	ASP	TYR	engineered mutation	UNP P14779
F	269	LEU	THR	engineered mutation	UNP P14779
F	290	VAL	ALA	engineered mutation	UNP P14779
F	315	ASP	GLY	engineered mutation	UNP P14779
F	327	MET	THR	engineered mutation	UNP P14779
F	328	SER	ALA	engineered mutation	UNP P14779
F	353	VAL	LEU	engineered mutation	UNP P14779
F	366	VAL	ILE	engineered mutation	UNP P14779
F	436	HIS	THR	engineered mutation	UNP P14779
F	464	LEU	-	expression tag	UNP P14779
F	465	GLU	-	expression tag	UNP P14779
F	466	HIS	-	expression tag	UNP P14779
F	467	HIS	-	expression tag	UNP P14779
F	468	HIS	-	expression tag	UNP P14779
F	469	HIS	-	expression tag	UNP P14779
F	470	HIS	-	expression tag	UNP P14779
F	471	HIS	-	expression tag	UNP P14779

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



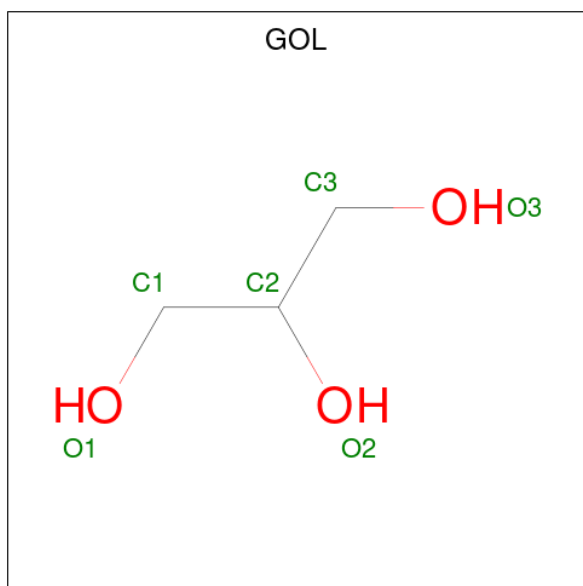
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	

Continued on next page...

Continued from previous page...

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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



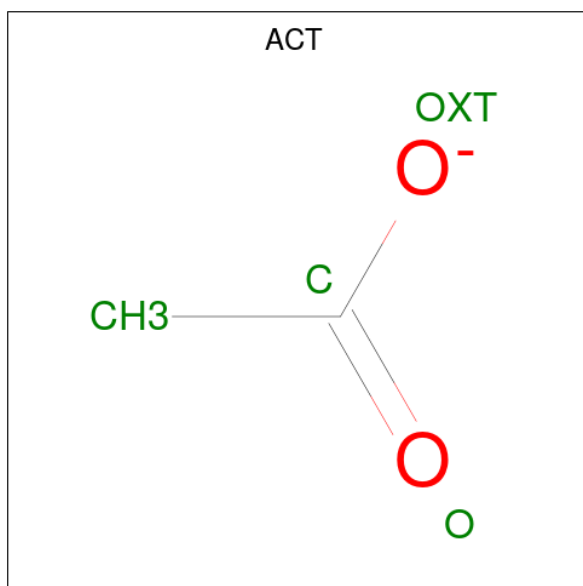
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C O		
			6 3 3		0	0
3	A	1	Total	C O		
			6 3 3		0	0
3	A	1	Total	C O		
			6 3 3		0	0
3	B	1	Total	C O		
			6 3 3		0	0
3	B	1	Total	C O		
			6 3 3		0	0
3	B	1	Total	C O		
			6 3 3		0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



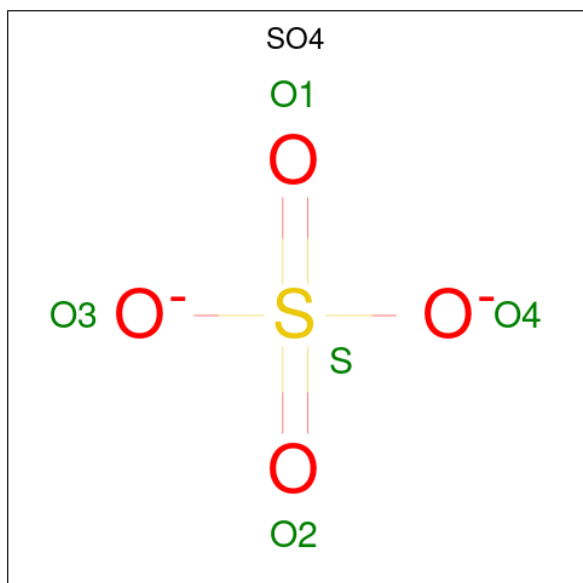
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		
4	E	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

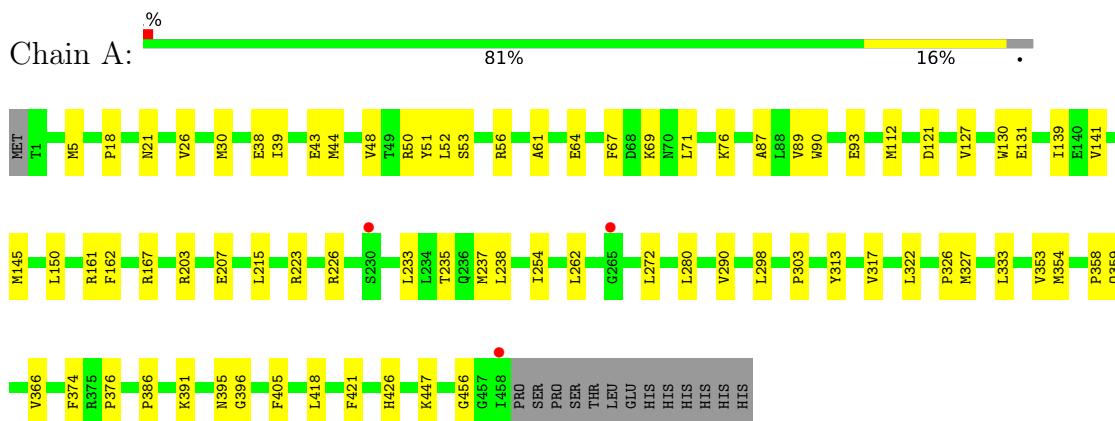
Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		

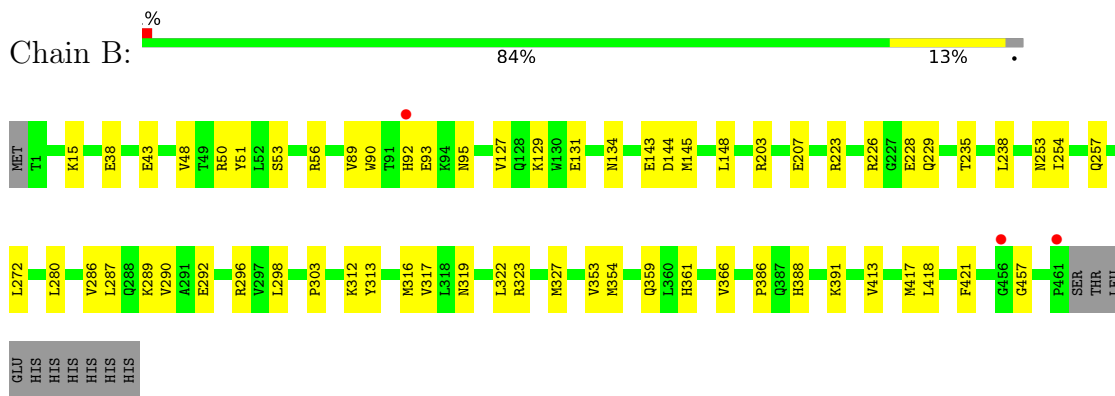
3 Residue-property plots

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.

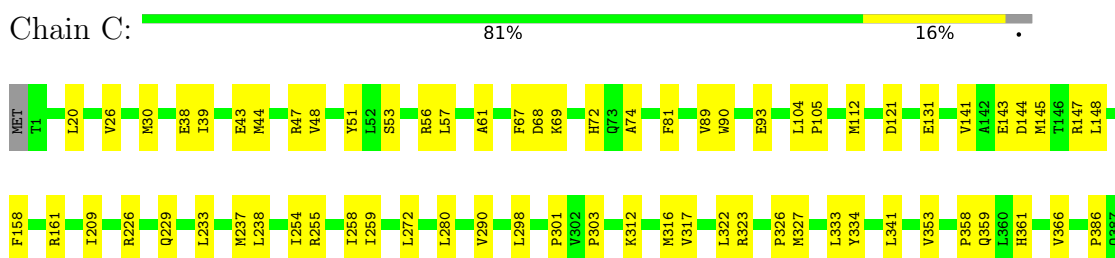
- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase

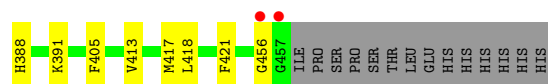


- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase

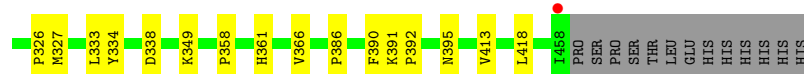
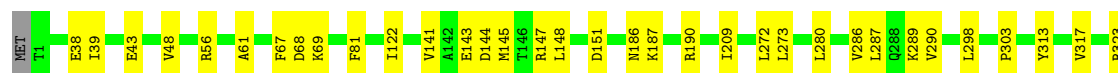


- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase

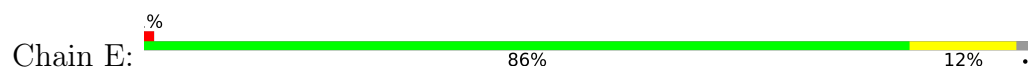




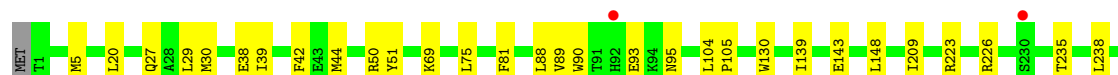
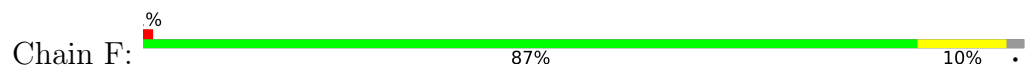
- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase



- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase



- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	167.44Å 167.44Å 364.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	123.34 – 3.43 123.34 – 3.43	Depositor EDS
% Data completeness (in resolution range)	97.9 (123.34-3.43) 99.0 (123.34-3.43)	Depositor EDS
R_{merge}	0.57	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 3.41Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.175 , 0.226 0.177 , 0.228	Depositor DCC
R_{free} test set	3481 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	101.4	Xtriage
Anisotropy	0.195	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 95.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	22710	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.20% 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: GOL, SO4, ACT, 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	0.20	0/3778	0.37	0/5104
1	B	0.18	0/3811	0.35	0/5151
1	C	0.18	0/3770	0.35	0/5093
1	D	0.17	0/3778	0.35	0/5104
1	E	0.19	0/3806	0.37	0/5144
1	F	0.17	0/3811	0.34	0/5151
All	All	0.18	0/22754	0.35	0/30747

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	3695	0	3684	49	0
1	B	3725	0	3709	42	0
1	C	3687	0	3673	41	0
1	D	3695	0	3684	29	0
1	E	3721	0	3708	35	0
1	F	3725	0	3709	30	0
2	A	43	0	30	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	43	0	30	3	0
2	C	43	0	30	3	0
2	D	43	0	30	2	0
2	E	43	0	30	3	0
2	F	43	0	30	4	0
3	A	18	0	24	1	0
3	B	18	0	24	0	0
3	D	6	0	8	0	0
3	E	30	0	40	1	0
3	F	6	0	8	0	0
4	A	8	0	6	0	0
4	B	16	0	12	1	0
4	D	12	0	9	0	0
4	E	8	0	6	0	0
4	F	12	0	9	0	0
5	A	15	0	0	0	0
5	B	5	0	0	0	0
5	C	20	0	0	0	0
5	D	15	0	0	0	0
5	E	10	0	0	0	0
5	F	5	0	0	0	0
All	All	22710	0	22493	234	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 5.

The worst 5 of 234 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:5:MET:HE1	1:A:50:ARG:HG2	1.57	0.83
1:F:388:HIS:HA	1:F:391:LYS:HE2	1.67	0.77
1:A:167:ARG:HH21	3:A:506:GOL:H31	1.52	0.72
1:B:223:ARG:HH22	1:B:228:GLU:HG3	1.56	0.70
1:E:38:GLU:OE2	1:E:56:ARG:NH2	2.25	0.69

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	456/472 (97%)	442 (97%)	14 (3%)	0	100	100
1	B	460/472 (98%)	446 (97%)	14 (3%)	0	100	100
1	C	455/472 (96%)	441 (97%)	14 (3%)	0	100	100
1	D	456/472 (97%)	443 (97%)	13 (3%)	0	100	100
1	E	460/472 (98%)	443 (96%)	17 (4%)	0	100	100
1	F	460/472 (98%)	445 (97%)	15 (3%)	0	100	100
All	All	2747/2832 (97%)	2660 (97%)	87 (3%)	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	403/417 (97%)	403 (100%)	0	100	100
1	B	407/417 (98%)	407 (100%)	0	100	100
1	C	402/417 (96%)	401 (100%)	1 (0%)	87	85
1	D	403/417 (97%)	403 (100%)	0	100	100
1	E	407/417 (98%)	407 (100%)	0	100	100
1	F	407/417 (98%)	407 (100%)	0	100	100
All	All	2429/2502 (97%)	2428 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	353	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	73	GLN
1	F	72	HIS
1	F	169	GLN
1	E	169	GLN
1	C	359	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

47 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	GOL	A	503	-	5,5,5	1.00	0	5,5,5	1.02	0
5	SO4	D	508	-	4,4,4	0.24	0	6,6,6	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	F	506	-	4,4,4	0.25	0	6,6,6	0.07	0
3	GOL	B	502	-	5,5,5	1.09	0	5,5,5	1.05	0
4	ACT	E	508	-	3,3,3	1.43	1 (33%)	3,3,3	1.35	0
3	GOL	E	506	-	5,5,5	0.99	0	5,5,5	1.00	0
5	SO4	A	507	-	4,4,4	0.23	0	6,6,6	0.21	0
4	ACT	B	507	-	3,3,3	1.47	1 (33%)	3,3,3	1.49	0
4	ACT	D	503	-	3,3,3	1.43	1 (33%)	3,3,3	1.36	0
3	GOL	E	502	-	5,5,5	1.13	0	5,5,5	0.99	0
4	ACT	F	503	-	3,3,3	1.47	1 (33%)	3,3,3	1.35	0
4	ACT	A	504	-	3,3,3	1.42	1 (33%)	3,3,3	1.38	0
5	SO4	A	508	-	4,4,4	0.23	0	6,6,6	0.11	0
3	GOL	B	504	-	5,5,5	1.07	0	5,5,5	0.98	0
2	HEM	B	501	1	50,50,50	1.43	7 (14%)	67,82,82	1.22	5 (7%)
4	ACT	B	508	-	3,3,3	1.43	1 (33%)	3,3,3	1.37	0
4	ACT	D	504	-	3,3,3	1.44	1 (33%)	3,3,3	1.37	0
4	ACT	F	504	-	3,3,3	1.45	1 (33%)	3,3,3	1.36	0
4	ACT	A	505	-	3,3,3	1.49	1 (33%)	3,3,3	1.49	0
2	HEM	F	501	1	50,50,50	1.45	8 (16%)	67,82,82	1.24	5 (7%)
3	GOL	A	502	-	5,5,5	1.05	0	5,5,5	0.99	0
4	ACT	E	504	-	3,3,3	1.42	1 (33%)	3,3,3	1.36	0
5	SO4	D	506	-	4,4,4	0.23	0	6,6,6	0.10	0
4	ACT	B	505	-	3,3,3	1.48	1 (33%)	3,3,3	1.46	0
2	HEM	E	501	1	50,50,50	1.42	8 (16%)	67,82,82	1.26	6 (8%)
5	SO4	D	507	-	4,4,4	0.25	0	6,6,6	0.05	0
4	ACT	B	506	-	3,3,3	1.47	1 (33%)	3,3,3	1.34	0
5	SO4	B	509	-	4,4,4	0.25	0	6,6,6	0.08	0
4	ACT	D	505	-	3,3,3	1.44	1 (33%)	3,3,3	1.36	0
5	SO4	E	509	-	4,4,4	0.27	0	6,6,6	0.07	0
3	GOL	F	502	-	5,5,5	1.09	0	5,5,5	0.96	0
2	HEM	A	501	1	50,50,50	1.40	9 (18%)	67,82,82	1.16	3 (4%)
5	SO4	A	509	-	4,4,4	0.24	0	6,6,6	0.16	0
5	SO4	C	505	-	4,4,4	0.20	0	6,6,6	0.14	0
3	GOL	E	507	-	5,5,5	0.97	0	5,5,5	1.05	0
5	SO4	C	502	-	4,4,4	0.24	0	6,6,6	0.06	0
3	GOL	B	503	-	5,5,5	0.97	0	5,5,5	1.00	0
2	HEM	D	501	1	50,50,50	1.43	7 (14%)	67,82,82	1.21	3 (4%)
4	ACT	F	505	-	3,3,3	1.40	0	3,3,3	1.50	0
5	SO4	C	503	-	4,4,4	0.27	0	6,6,6	0.15	0
3	GOL	D	502	-	5,5,5	1.07	0	5,5,5	0.98	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	C	504	-	4,4,4	0.26	0	6,6,6	0.08	0
3	GOL	E	505	-	5,5,5	1.11	0	5,5,5	0.96	0
2	HEM	C	501	1	50,50,50	1.37	7 (14%)	67,82,82	1.19	5 (7%)
3	GOL	A	506	-	5,5,5	1.05	0	5,5,5	0.92	0
5	SO4	E	510	-	4,4,4	0.26	0	6,6,6	0.10	0
3	GOL	E	503	-	5,5,5	1.08	0	5,5,5	0.98	0

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	GOL	A	503	-	-	2/4/4/4	-
3	GOL	B	502	-	-	1/4/4/4	-
3	GOL	E	506	-	-	0/4/4/4	-
3	GOL	E	502	-	-	1/4/4/4	-
3	GOL	B	504	-	-	2/4/4/4	-
2	HEM	B	501	1	-	2/14/54/54	-
2	HEM	F	501	1	-	2/14/54/54	-
3	GOL	A	502	-	-	0/4/4/4	-
2	HEM	E	501	1	-	1/14/54/54	-
3	GOL	F	502	-	-	0/4/4/4	-
2	HEM	A	501	1	-	1/14/54/54	-
3	GOL	E	507	-	-	0/4/4/4	-
3	GOL	B	503	-	-	2/4/4/4	-
2	HEM	D	501	1	-	1/14/54/54	-
3	GOL	D	502	-	-	0/4/4/4	-
3	GOL	E	505	-	-	0/4/4/4	-
2	HEM	C	501	1	-	1/14/54/54	-
3	GOL	A	506	-	-	2/4/4/4	-
3	GOL	E	503	-	-	2/4/4/4	-

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	501	HEM	FE-NC	4.45	2.09	1.95
2	B	501	HEM	FE-NB	4.18	2.07	1.94
2	F	501	HEM	FE-NB	4.05	2.07	1.94
2	D	501	HEM	FE-NB	3.79	2.06	1.94
2	E	501	HEM	FE-NB	3.64	2.06	1.94

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	501	HEM	C4D-ND-C1D	3.02	108.78	105.21
2	B	501	HEM	C4D-ND-C1D	2.91	108.66	105.21
2	D	501	HEM	C4D-ND-C1D	2.75	108.47	105.21
2	E	501	HEM	C4D-ND-C1D	2.56	108.24	105.21
2	C	501	HEM	CBD-CAD-C3D	-2.55	105.49	112.53

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	503	GOL	O1-C1-C2-O2
3	B	503	GOL	O1-C1-C2-C3
3	E	503	GOL	C1-C2-C3-O3
2	F	501	HEM	C2A-CAA-CBA-CGA
3	A	503	GOL	O1-C1-C2-C3

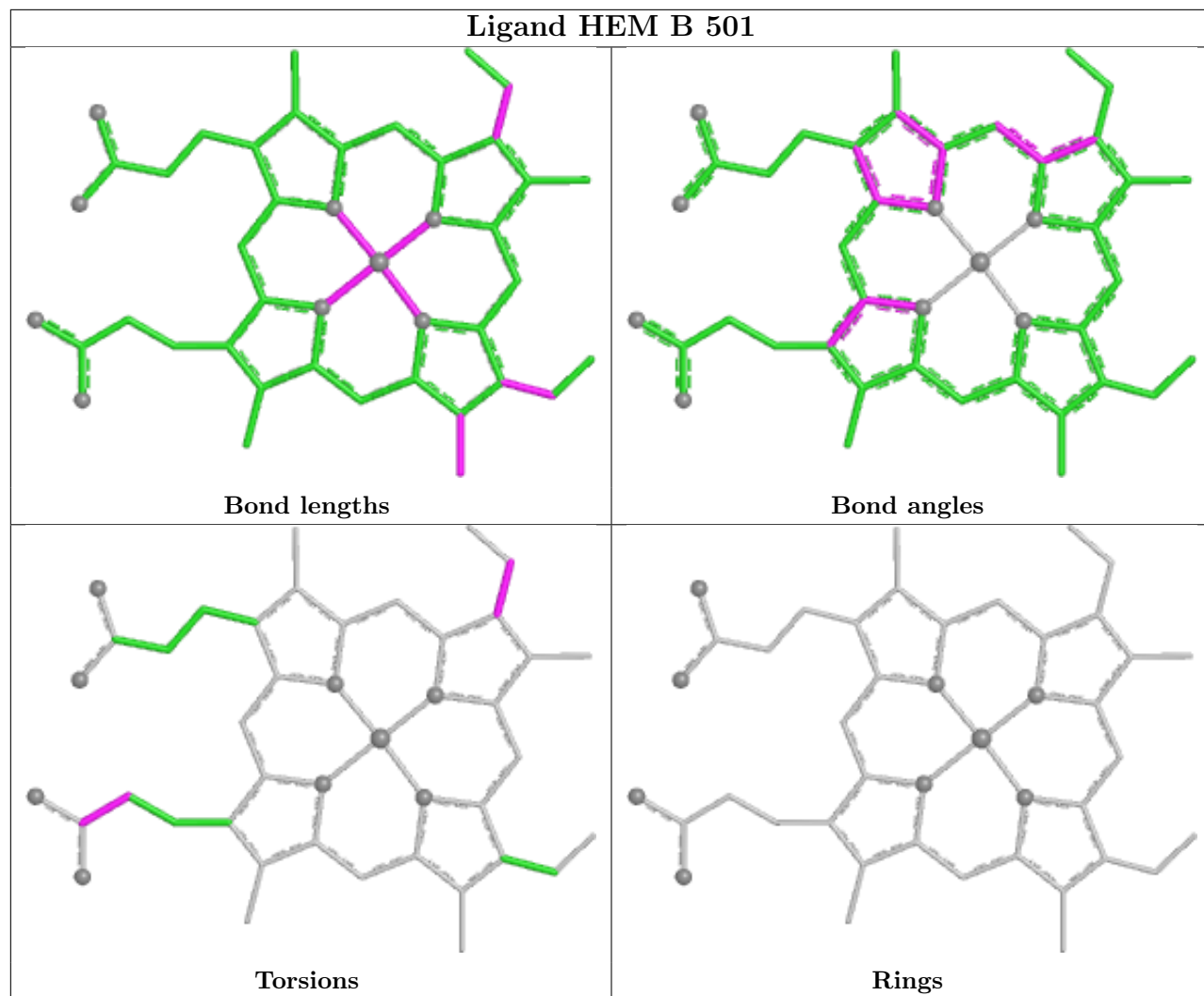
There are no ring outliers.

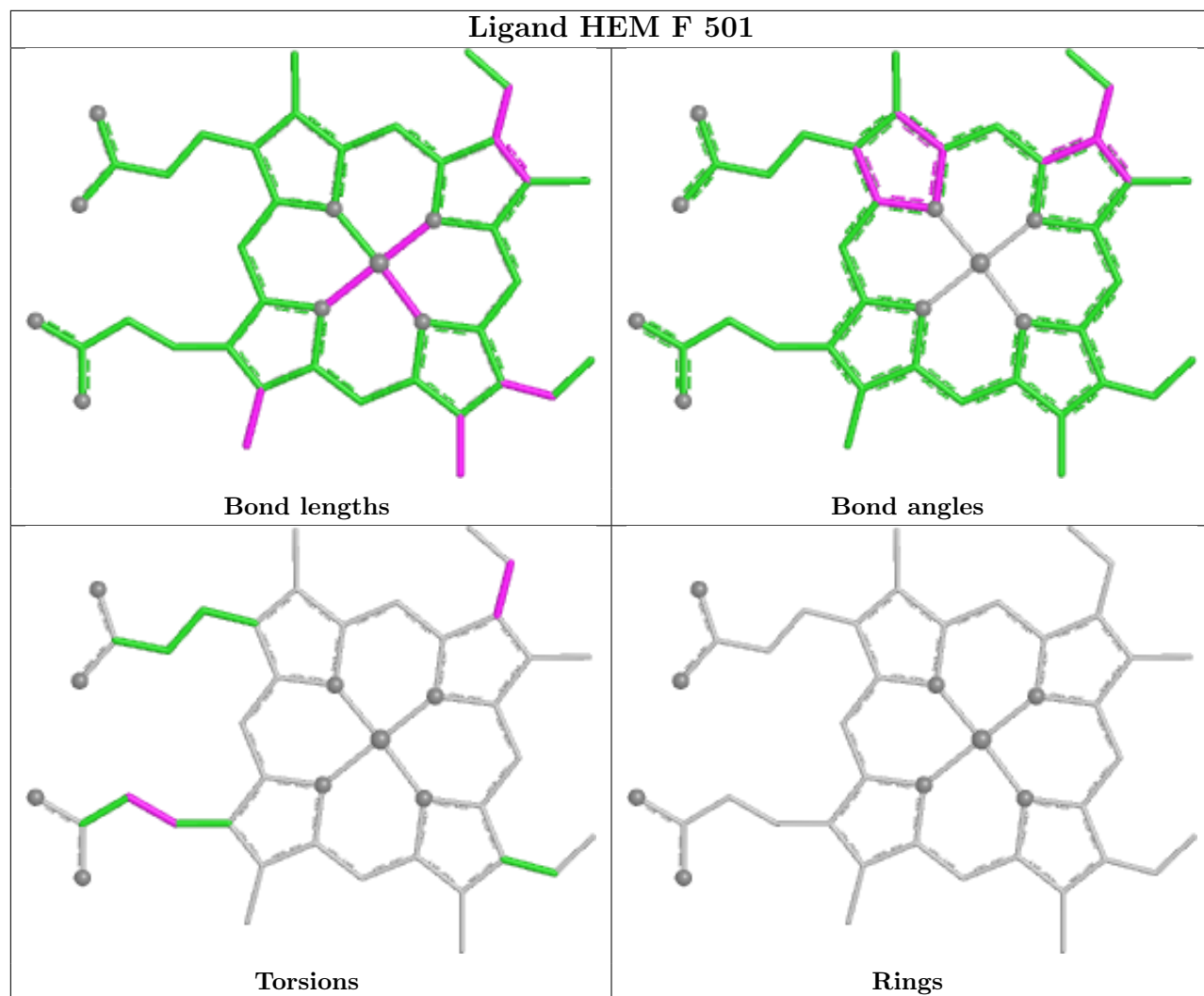
9 monomers are involved in 20 short contacts:

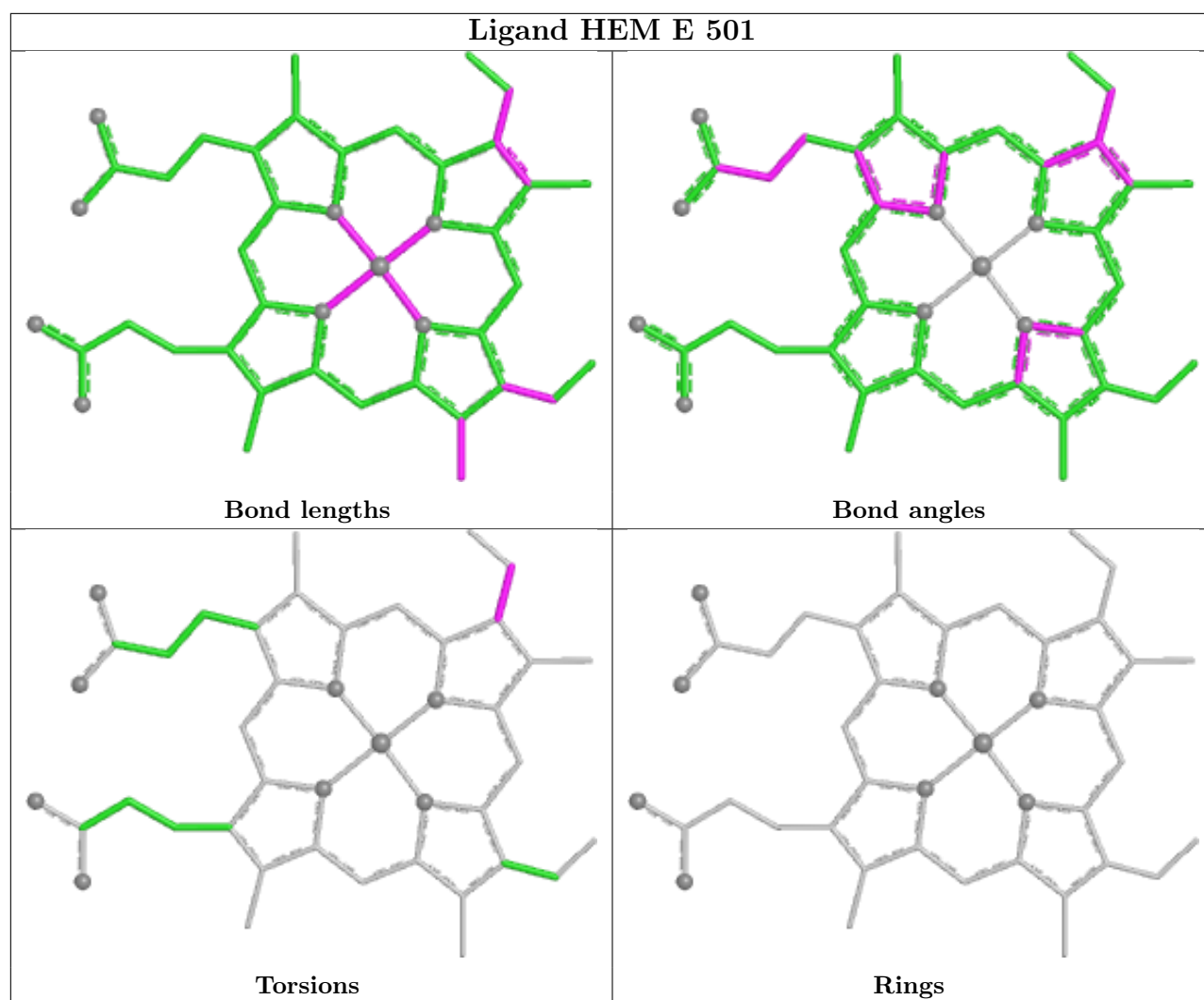
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	HEM	3	0
2	F	501	HEM	4	0
2	E	501	HEM	3	0
4	B	506	ACT	1	0
2	A	501	HEM	2	0
2	D	501	HEM	2	0
2	C	501	HEM	3	0
3	A	506	GOL	1	0
3	E	503	GOL	1	0

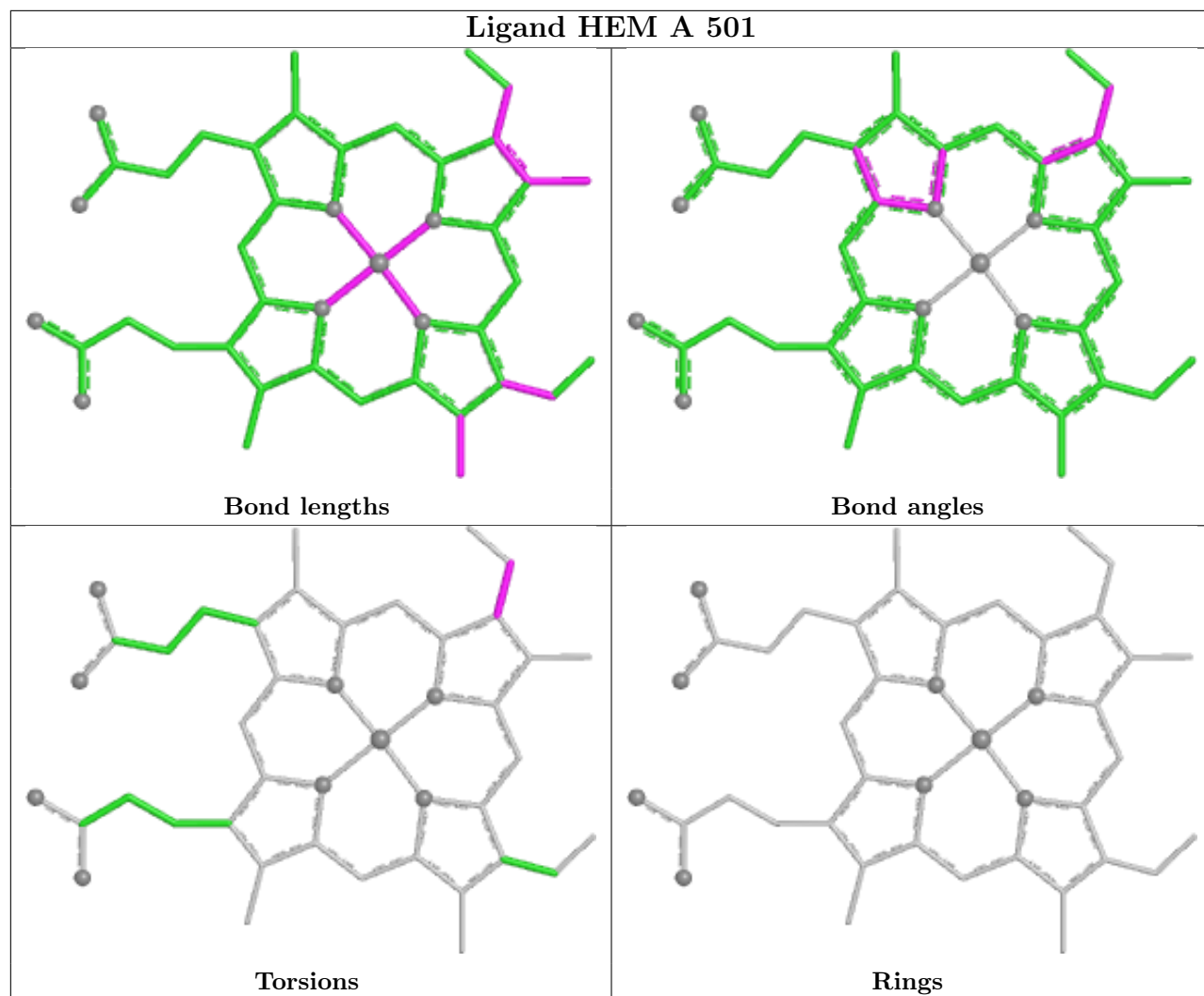
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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

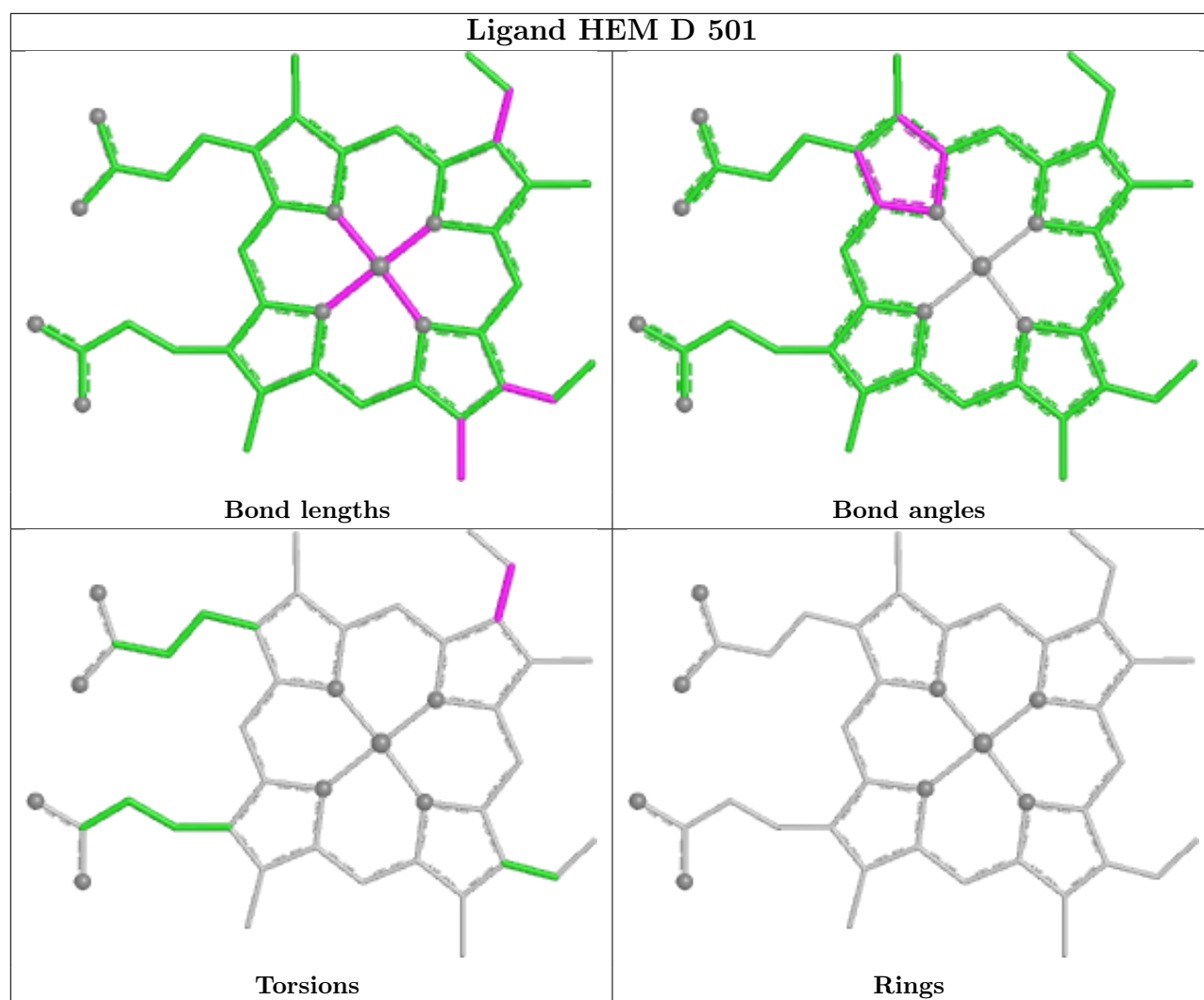
equivalents in the CSD to analyse the geometry.

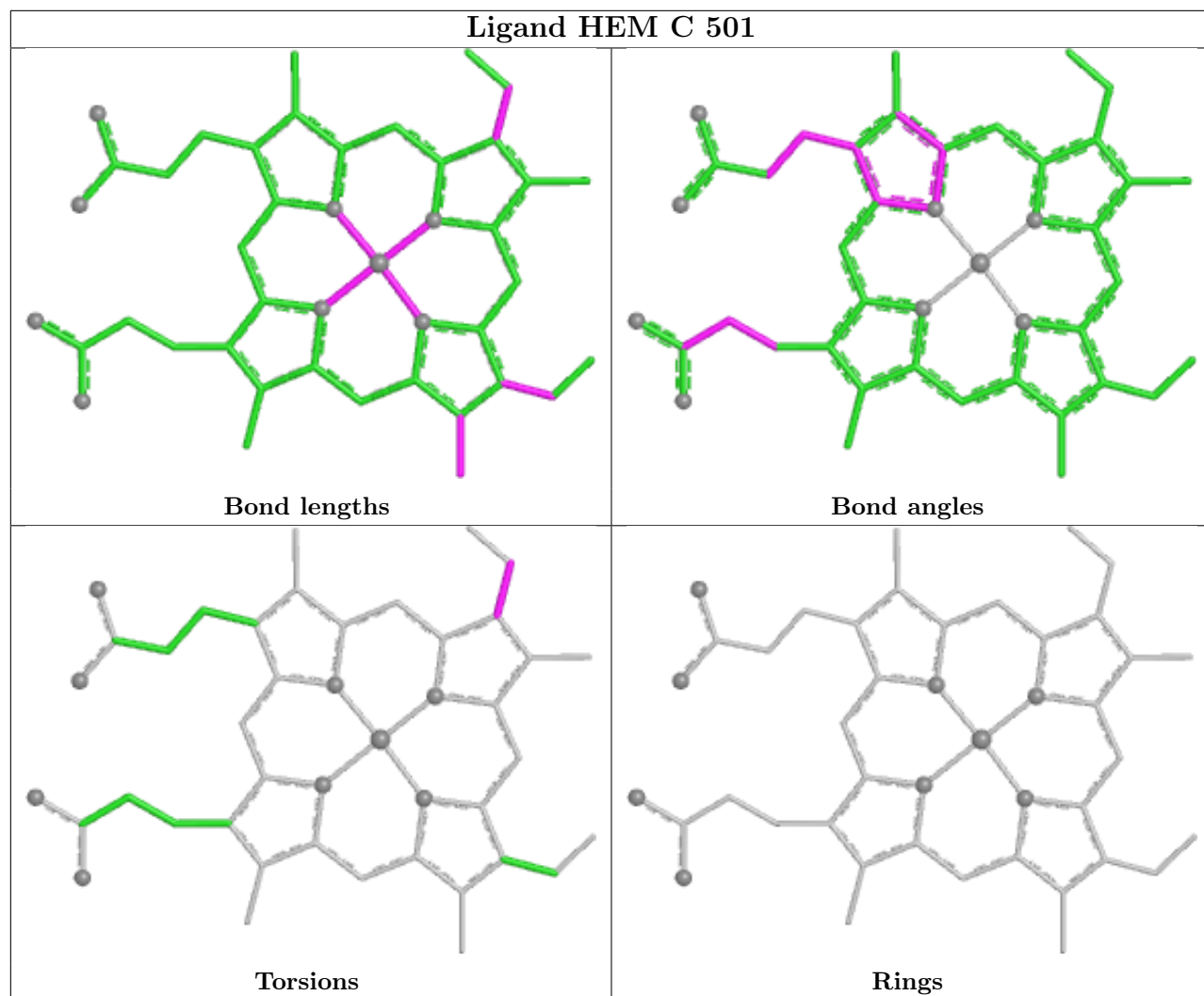












5.7 Other polymers [i](#)

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 [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	458/472 (97%)	-0.50	3 (0%) 84 67	55, 79, 123, 158	0
1	B	461/472 (97%)	-0.53	3 (0%) 84 67	55, 90, 136, 182	1 (0%)
1	C	457/472 (96%)	-0.51	2 (0%) 88 76	65, 95, 138, 177	0
1	D	458/472 (97%)	-0.49	1 (0%) 91 84	70, 99, 132, 192	0
1	E	462/472 (97%)	-0.53	4 (0%) 81 62	57, 83, 128, 170	0
1	F	461/472 (97%)	-0.38	3 (0%) 84 67	63, 106, 150, 188	1 (0%)
All	All	2757/2832 (97%)	-0.49	16 (0%) 85 69	55, 92, 137, 192	2 (0%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	457	GLY	3.5
1	D	458	ILE	3.4
1	F	92[A]	HIS	3.2
1	B	92[A]	HIS	3.1
1	B	461	PRO	3.0

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 oligosaccharides 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
4	ACT	B	505	4/4	0.48	0.16	100,101,129,141	0
4	ACT	E	504	4/4	0.56	0.13	106,114,125,128	0
3	GOL	B	503	6/6	0.59	0.17	96,119,139,149	0
3	GOL	F	502	6/6	0.59	0.14	106,122,146,147	0
4	ACT	F	503	4/4	0.59	0.19	108,109,109,125	0
3	GOL	A	503	6/6	0.60	0.12	92,107,131,133	0
4	ACT	A	504	4/4	0.64	0.18	98,108,127,136	0
3	GOL	E	502	6/6	0.64	0.13	114,124,136,141	0
5	SO4	D	507	5/5	0.64	0.20	158,158,170,178	0
4	ACT	D	503	4/4	0.71	0.23	124,128,137,144	0
4	ACT	F	505	4/4	0.71	0.20	110,127,131,134	0
4	ACT	E	508	4/4	0.71	0.12	87,109,119,121	0
3	GOL	E	507	6/6	0.72	0.11	109,128,142,151	0
4	ACT	B	506	4/4	0.72	0.17	82,101,118,124	0
5	SO4	C	504	5/5	0.73	0.18	130,146,155,166	0
4	ACT	D	505	4/4	0.73	0.16	111,113,124,134	0
3	GOL	E	503	6/6	0.77	0.21	104,124,135,138	0
4	ACT	D	504	4/4	0.79	0.15	117,128,139,139	0
5	SO4	A	508	5/5	0.79	0.17	114,130,141,151	0
4	ACT	B	507	4/4	0.80	0.10	110,113,116,133	0
5	SO4	C	502	5/5	0.80	0.13	141,141,154,159	0
4	ACT	F	504	4/4	0.80	0.12	83,85,93,102	0
3	GOL	A	502	6/6	0.80	0.15	103,127,129,133	0
3	GOL	A	506	6/6	0.81	0.14	94,111,132,134	0
3	GOL	D	502	6/6	0.82	0.15	90,107,118,127	0
3	GOL	E	506	6/6	0.82	0.08	118,127,144,144	0
4	ACT	B	508	4/4	0.83	0.13	94,103,116,117	0
5	SO4	F	506	5/5	0.83	0.20	111,120,149,158	0
3	GOL	B	502	6/6	0.84	0.10	95,96,116,122	0
5	SO4	E	509	5/5	0.84	0.16	111,113,144,147	0
3	GOL	B	504	6/6	0.84	0.11	90,115,123,129	0
5	SO4	E	510	5/5	0.86	0.13	138,157,169,175	0
5	SO4	A	509	5/5	0.86	0.13	78,99,136,137	0
4	ACT	A	505	4/4	0.87	0.14	94,104,105,117	0
5	SO4	B	509	5/5	0.89	0.12	131,136,147,149	0
5	SO4	C	503	5/5	0.90	0.10	88,92,127,136	0
5	SO4	D	506	5/5	0.92	0.10	119,128,138,152	0

Continued on next page...

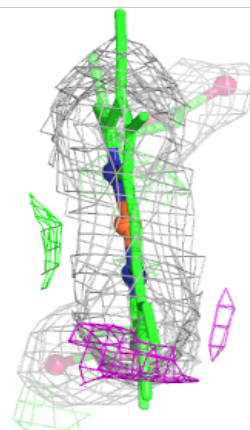
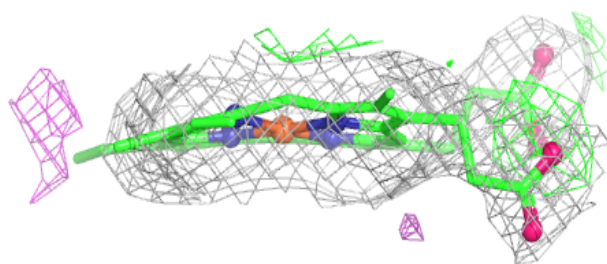
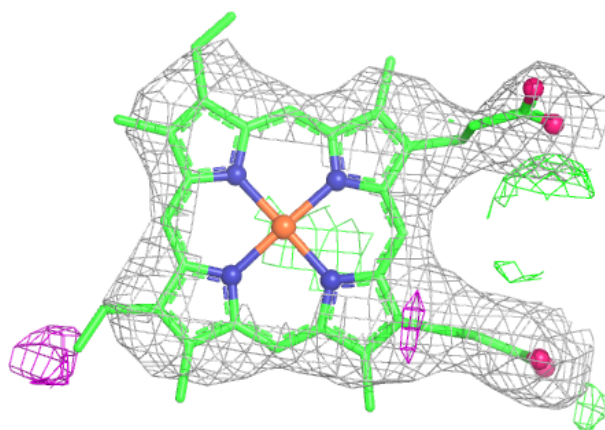
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	E	505	6/6	0.93	0.08	102,113,120,120	0
5	SO4	A	507	5/5	0.95	0.07	61,76,87,101	0
5	SO4	C	505	5/5	0.95	0.07	82,98,105,105	0
2	HEM	C	501	43/43	0.97	0.09	68,84,97,116	0
2	HEM	B	501	43/43	0.97	0.08	60,78,98,110	0
5	SO4	D	508	5/5	0.97	0.05	79,79,91,101	0
2	HEM	D	501	43/43	0.98	0.08	75,93,102,113	0
2	HEM	E	501	43/43	0.98	0.08	57,66,81,86	0
2	HEM	F	501	43/43	0.98	0.08	79,105,119,129	0
2	HEM	A	501	43/43	0.98	0.07	49,68,81,88	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.

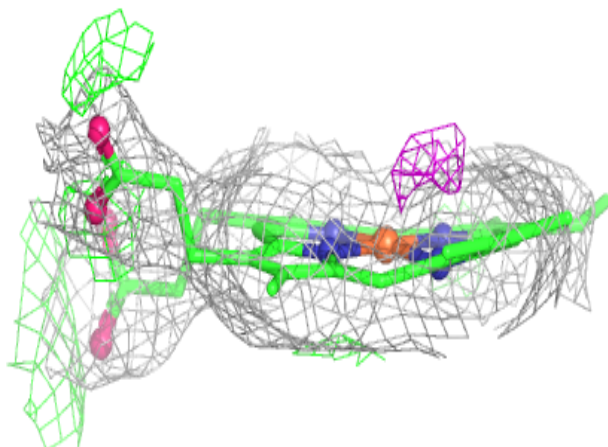
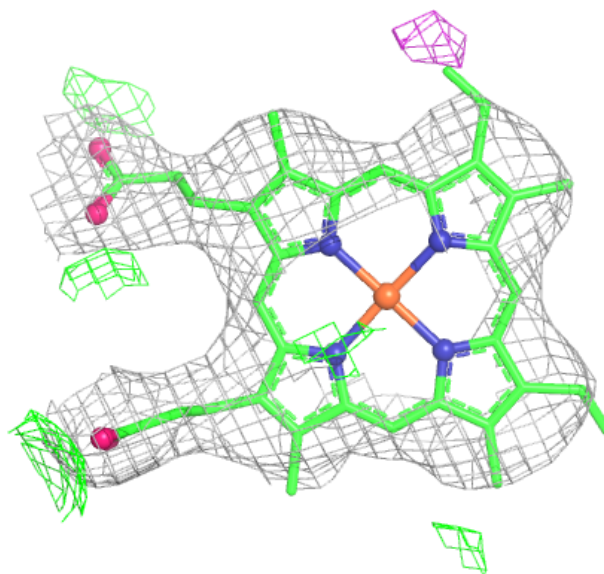
Electron density around HEM C 501:

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



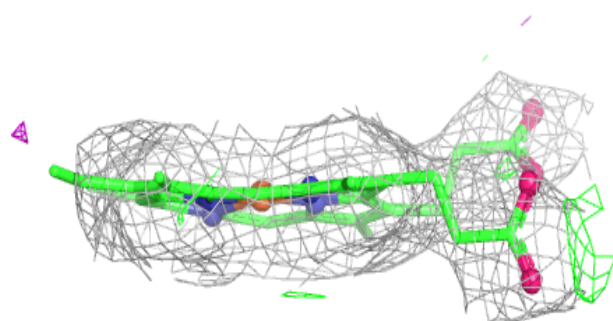
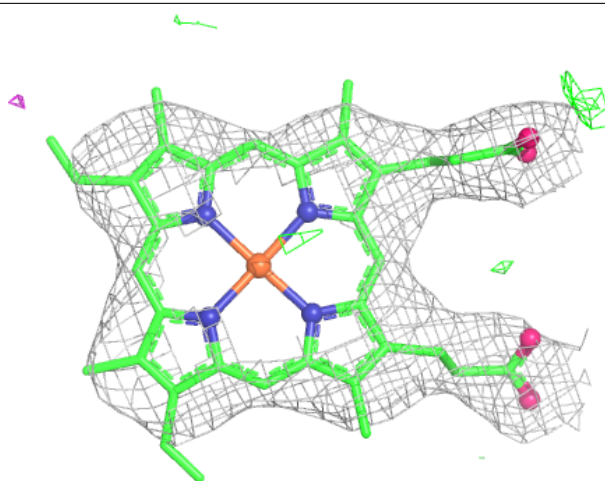
Electron density around HEM B 501:

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



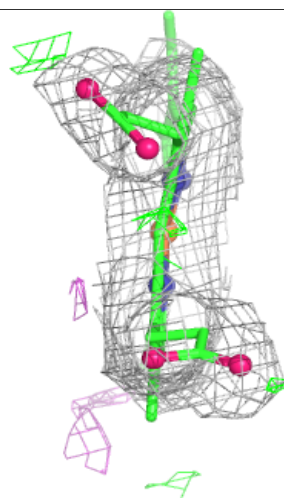
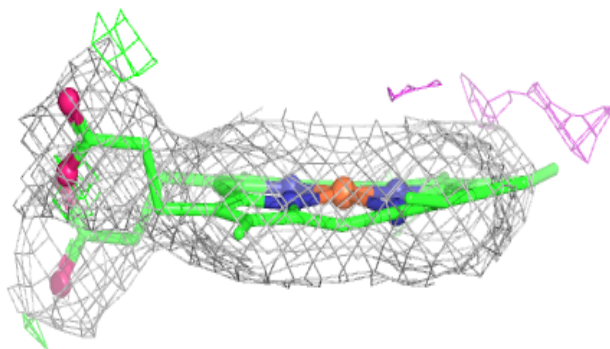
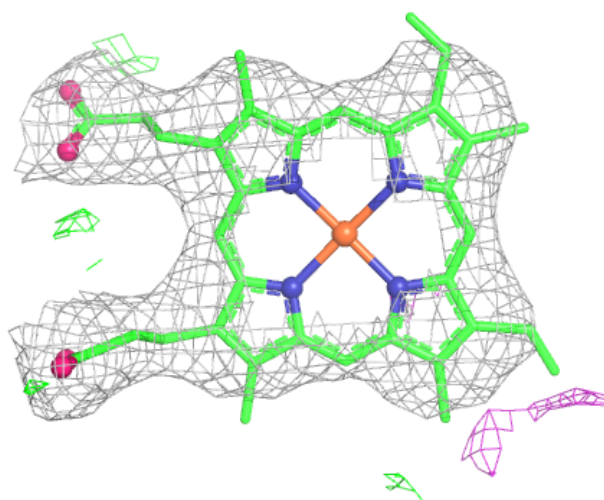
Electron density around HEM D 501:

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



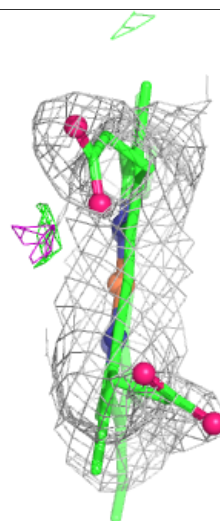
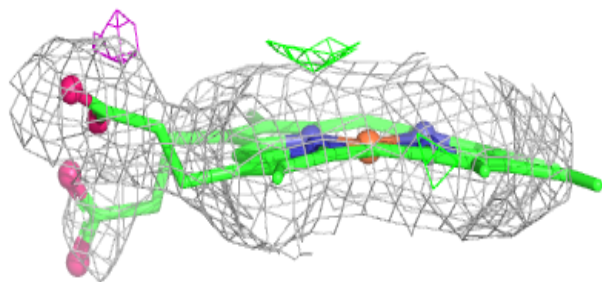
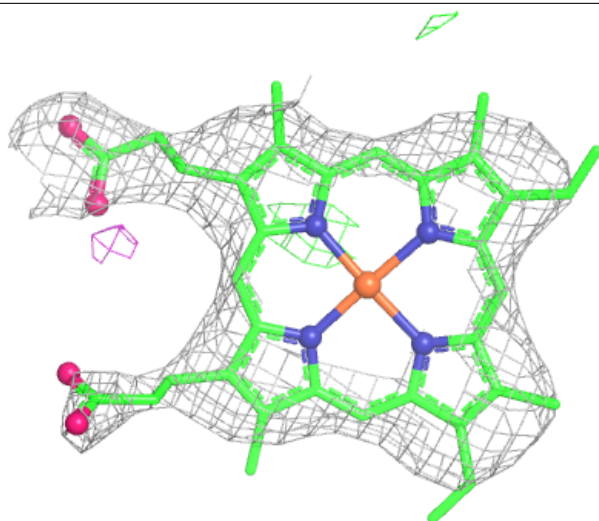
Electron density around HEM E 501:

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



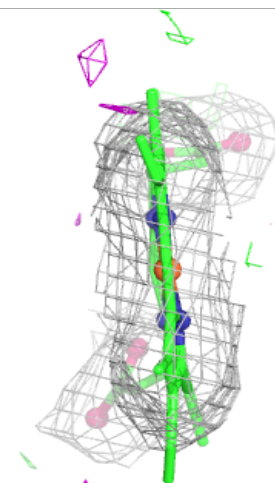
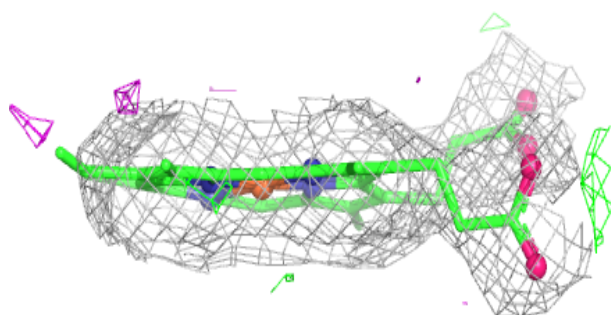
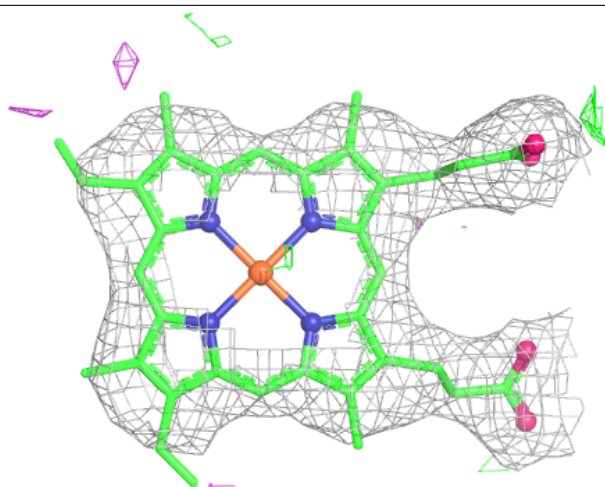
Electron density around HEM F 501:

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



Electron density around HEM A 501:

$2mF_o-DF_c$ (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.