Full wwPDB X-ray Structure Validation Report (i)

Sep 24, 2023 – 08:26 AM EDT

PDB ID	:	5UCW
Title	:	Cytochrome P411 P-4 A82L A78V F263L amination catalyst
Authors	:	Zhang, R.K.; Buller, A.R.; Arnold, F.H.
Deposited on	:	2016-12-22
Resolution	:	1.70 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 (i) 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 (i)) were used in the production of this report:

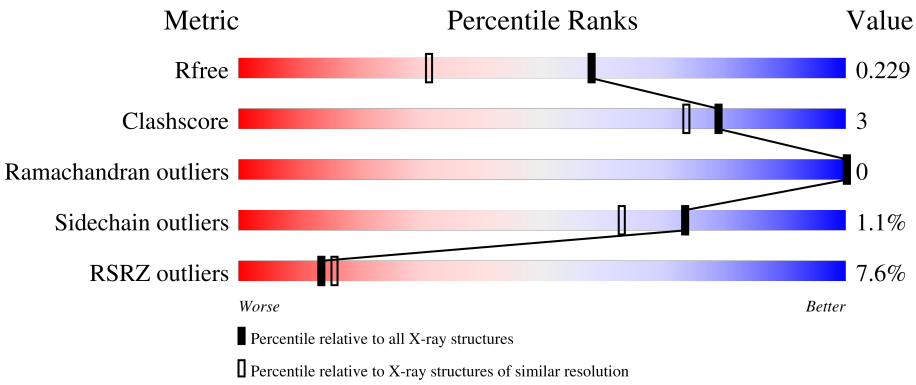
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 <=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	6% 89% 6% ·
1	B	472	9% 90% 6% ·

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7709 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 NADPH-cytochrome P450 reductase 102A1V3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	453	3638	2328	615	677	18	0	7	0
1	B	453	3608	2309	614	668	17	0	4	0

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	LEU	ALA	engineered mutation	UNP F2Q7T0
A	87	ALA	PHE	engineered mutation	UNP F2Q7T0
A	142	SER	PRO	engineered mutation	UNP F2Q7T0
A	175	ILE	THR	engineered mutation	UNP F2Q7T0
A	184	VAL	ALA	engineered mutation	UNP F2Q7T0
A	226	ARG	SER	engineered mutation	UNP F2Q7T0
A	236	GLN	HIS	engineered mutation	UNP F2Q7T0
A	252	GLY	GLU	engineered mutation	UNP F2Q7T0
A	263	LEU	ILE	engineered mutation	UNP F2Q7T0
A	268	GLY	THR	engineered mutation	UNP F2Q7T0
A	290	VAL	ALA	engineered mutation	UNP F2Q7T0
A	328	VAL	ALA	engineered mutation	UNP F2Q7T0
A	353	VAL	LEU	engineered mutation	UNP F2Q7T0
A	366	VAL	ILE	engineered mutation	UNP F2Q7T0
A	400	SER	CYS	engineered mutation	UNP F2Q7T0
A	438	SER	THR	engineered mutation	UNP F2Q7T0
A	442	LYS	GLU	engineered mutation	UNP F2Q7T0
A	464	LEU	-	expression tag	UNP F2Q7T0
A	465	GLU	-	expression tag	UNP F2Q7T0
A	466	HIS	-	expression tag	UNP F2Q7T0
A	467	HIS	-	expression tag	UNP F2Q7T0
A	468	HIS	-	expression tag	UNP F2Q7T0
A	469	HIS	-	expression tag	UNP F2Q7T0
A	470	HIS	-	expression tag	UNP F2Q7T0
A	471	HIS	-	expression tag	UNP F2Q7T0

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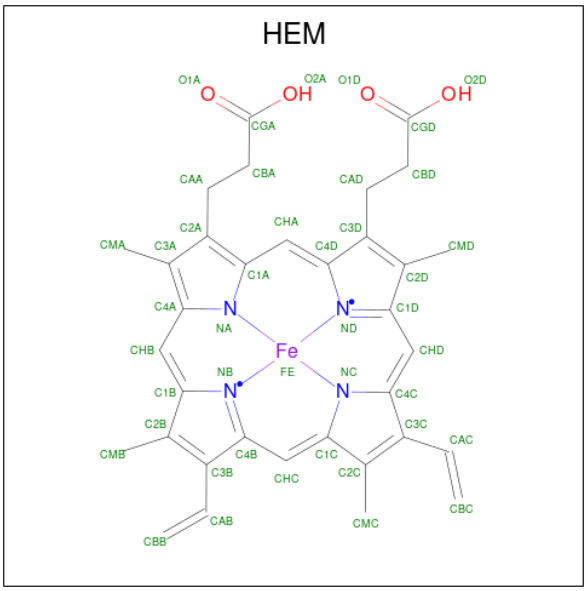
Chain	Residue	Modelled	Actual	Comment	Reference
B	82	LEU	ALA	engineered mutation	UNP F2Q7T0
B	87	ALA	PHE	engineered mutation	UNP F2Q7T0
B	142	SER	PRO	engineered mutation	UNP F2Q7T0
B	175	ILE	THR	engineered mutation	UNP F2Q7T0
B	184	VAL	ALA	engineered mutation	UNP F2Q7T0
B	226	ARG	SER	engineered mutation	UNP F2Q7T0
B	236	GLN	HIS	engineered mutation	UNP F2Q7T0
B	252	GLY	GLU	engineered mutation	UNP F2Q7T0
B	263	LEU	ILE	engineered mutation	UNP F2Q7T0
B	268	GLY	THR	engineered mutation	UNP F2Q7T0
B	290	VAL	ALA	engineered mutation	UNP F2Q7T0
B	328	VAL	ALA	engineered mutation	UNP F2Q7T0
B	353	VAL	LEU	engineered mutation	UNP F2Q7T0
B	366	VAL	ILE	engineered mutation	UNP F2Q7T0
B	400	SER	CYS	engineered mutation	UNP F2Q7T0
B	438	SER	THR	engineered mutation	UNP F2Q7T0
B	442	LYS	GLU	engineered mutation	UNP F2Q7T0
B	464	LEU	-	expression tag	UNP F2Q7T0
B	465	GLU	-	expression tag	UNP F2Q7T0
B	466	HIS	-	expression tag	UNP F2Q7T0
B	467	HIS	-	expression tag	UNP F2Q7T0
B	468	HIS	-	expression tag	UNP F2Q7T0
B	469	HIS	-	expression tag	UNP F2Q7T0
B	470	HIS	-	expression tag	UNP F2Q7T0
B	471	HIS	-	expression tag	UNP F2Q7T0

- 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		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is water.

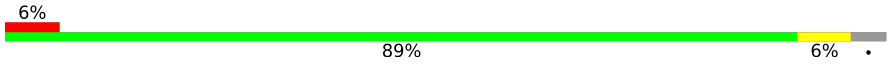
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	221	Total	O	0	0
			221	221		
3	B	156	Total	O	0	0
			156	156		

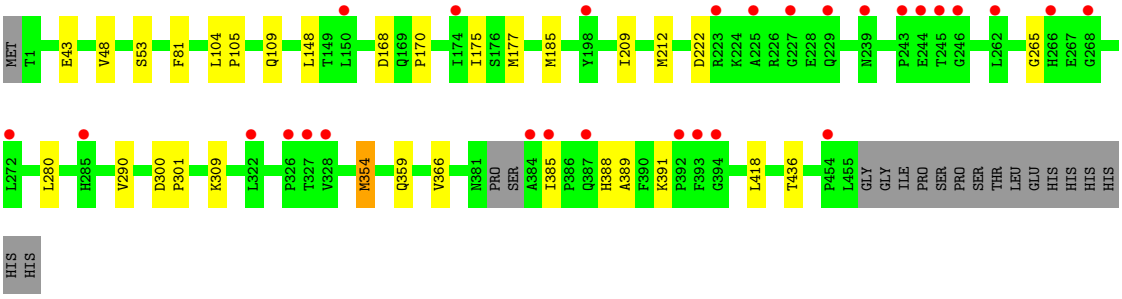
3 Residue-property plots (i)

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: NADPH-cytochrome P450 reductase 102A1V3

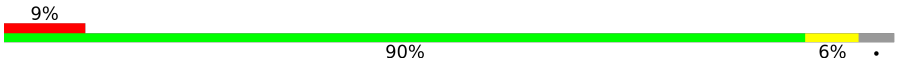
Chain A:

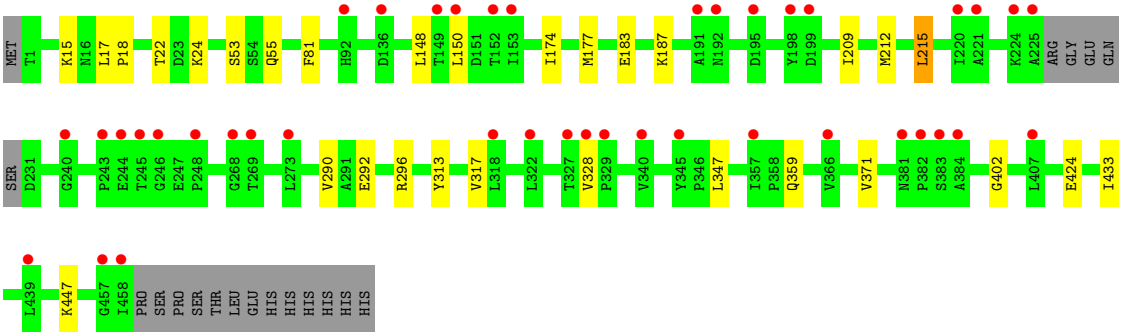




• Molecule 1: NADPH-cytochrome P450 reductase 102A1V3

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	123.86Å 126.96Å 62.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.70 36.17 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.00-1.70) 99.6 (36.17-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.82 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.189 , 0.223 0.199 , 0.229	Depositor DCC
R_{free} test set	5400 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	33.6	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 41.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	7709	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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

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	0.61	0/3719	0.73	3/5034 (0.1%)
1	B	0.61	1/3689 (0.0%)	0.70	1/4996 (0.0%)
All	All	0.61	1/7408 (0.0%)	0.72	4/10030 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	347	LEU	C-O	5.01	1.32	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	354	MET	CA-CB-CG	7.22	125.58	113.30
1	B	215	LEU	CA-CB-CG	-5.85	101.85	115.30
1	A	354	MET	CG-SD-CE	-5.57	91.29	100.20
1	A	168	ASP	CB-CG-OD1	5.53	123.28	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	328	VAL	Peptide

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	3638	0	3559	19	0
1	B	3608	0	3533	16	0
2	A	43	0	30	3	0
2	B	43	0	30	4	0
3	A	221	0	0	1	0
3	B	156	0	0	0	0
All	All	7709	0	7152	40	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 3.

All (40) 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:290:VAL:HG11	1:A:418:LEU:HD13	1.53	0.90
1:A:290:VAL:CG1	1:A:418:LEU:HD13	2.09	0.82
1:A:109:GLN:OE1	1:A:309:LYS:HE3	1.83	0.78
1:B:290:VAL:HG11	1:B:317:VAL:HG21	1.73	0.71
1:A:290:VAL:HG11	1:A:418:LEU:CD1	2.27	0.63
1:B:292:GLU:OE1	1:B:296:ARG:NH1	2.37	0.57
1:B:177[B]:MET:HE2	1:B:212:MET:SD	2.45	0.56
1:B:290:VAL:CG1	1:B:317:VAL:HG21	2.35	0.56
1:A:280:LEU:CD1	1:A:418:LEU:HD11	2.38	0.53
1:B:177[B]:MET:CE	1:B:212:MET:SD	2.97	0.52
1:B:424:GLU:HG2	1:B:447:LYS:HB2	1.92	0.51
1:A:177[A]:MET:HE2	1:A:212:MET:SD	2.51	0.51
1:A:366:VAL:HG11	1:A:389:ALA:HB1	1.92	0.51
1:B:215:LEU:O	1:B:215:LEU:HG	2.10	0.50
2:B:501:HEM:HMB2	2:B:501:HEM:HBB2	1.92	0.50
2:A:501:HEM:HMC2	2:A:501:HEM:HBC2	1.93	0.50
1:A:177[A]:MET:CE	1:A:212:MET:SD	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:HIS:HA	1:A:391:LYS:HD3	1.94	0.49
1:B:24:LYS:HE2	1:B:433:ILE:O	2.11	0.49
1:B:150:LEU:HD22	1:B:174:ILE:HG12	1.94	0.49
2:B:501:HEM:HBC2	2:B:501:HEM:HMC2	1.95	0.48
1:A:185:MET:SD	1:A:436:THR:HA	2.55	0.47
1:B:402:GLY:HA3	2:B:501:HEM:C3C	2.51	0.46
1:A:385:ILE:HD12	1:A:385:ILE:C	2.36	0.46
1:A:53:SER:HB3	1:A:359:GLN:HB3	1.98	0.46
1:B:81:PHE:HB3	1:B:209:ILE:HG12	1.98	0.46
1:B:53:SER:HB3	1:B:359:GLN:HB3	1.98	0.45
2:B:501:HEM:HBB2	2:B:501:HEM:CMB	2.47	0.44
1:B:183:GLU:O	1:B:187:LYS:HB2	2.18	0.44
1:A:43:GLU:HG2	1:A:48:VAL:HG22	2.00	0.43
2:A:501:HEM:HBC2	2:A:501:HEM:CMC	2.48	0.43
1:A:300:ASP:HB3	1:A:301:PRO:CD	2.49	0.43
1:A:104:LEU:N	1:A:105:PRO:CD	2.82	0.42
1:A:170:PRO:HA	3:A:626:HOH:O	2.19	0.42
1:A:81:PHE:HB3	1:A:209:ILE:HG12	2.01	0.42
1:A:175:ILE:HD13	1:A:175:ILE:HA	1.89	0.41
1:A:265:GLY:HA2	2:A:501:HEM:HMC2	2.02	0.41
1:B:290:VAL:HG12	1:B:313:TYR:CD2	2.54	0.41
1:B:150:LEU:HD22	1:B:174:ILE:CG1	2.49	0.41
1:B:17:LEU:HB3	1:B:18:PRO:HD3	2.01	0.41

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	456/472 (97%)	444 (97%)	12 (3%)	0	100 100
1	B	453/472 (96%)	440 (97%)	13 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	909/944 (96%)	884 (97%)	25 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	387/415 (93%)	384 (99%)	3 (1%)	81	74
1	B	382/415 (92%)	377 (99%)	5 (1%)	69	56
All	All	769/830 (93%)	761 (99%)	8 (1%)	73	67

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	148	LEU
1	A	222	ASP
1	A	354	MET
1	B	15	LYS
1	B	22	THR
1	B	55	GLN
1	B	148	LEU
1	B	371	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	109	GLN
1	B	404	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 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	$\#\|Z\| > 2$
2	HEM	A	501	-	41,50,50	1.27	7 (17%)	45,82,82	1.76	12 (26%)
2	HEM	B	501	-	41,50,50	1.14	2 (4%)	45,82,82	1.65	11 (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
2	HEM	A	501	-	-	2/12/54/54	-
2	HEM	B	501	-	-	2/12/54/54	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	FE-NB	2.76	2.10	1.96
2	B	501	HEM	C1B-NB	-2.36	1.36	1.40
2	A	501	HEM	C4D-ND	-2.35	1.36	1.40
2	A	501	HEM	C4D-C3D	2.30	1.49	1.45
2	A	501	HEM	CHA-C4D	2.29	1.40	1.35
2	A	501	HEM	CHB-C1B	2.29	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEM	CHB-C1B	2.23	1.40	1.35
2	A	501	HEM	C4B-NB	-2.14	1.34	1.38
2	A	501	HEM	C1B-NB	-2.06	1.36	1.40

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	HEM	CHD-C1D-ND	3.71	128.46	124.43
2	A	501	HEM	CMC-C2C-C3C	3.63	131.48	124.68
2	A	501	HEM	CHD-C1D-C2D	-3.39	119.68	124.98
2	A	501	HEM	C1B-NB-C4B	3.30	108.48	105.07
2	A	501	HEM	CHC-C4B-NB	3.16	127.87	124.43
2	B	501	HEM	CMB-C2B-C1B	3.16	129.85	125.04
2	B	501	HEM	CHD-C1D-C2D	-2.97	120.34	124.98
2	A	501	HEM	CMD-C2D-C1D	2.81	129.32	125.04
2	A	501	HEM	CHA-C4D-C3D	-2.75	120.17	125.33
2	B	501	HEM	CHA-C4D-C3D	-2.68	120.29	125.33
2	A	501	HEM	CBD-CAD-C3D	-2.68	105.17	112.63
2	B	501	HEM	CHC-C4B-NB	2.64	127.30	124.43
2	B	501	HEM	CMA-C3A-C4A	-2.63	124.42	128.46
2	B	501	HEM	CMC-C2C-C3C	2.57	129.48	124.68
2	B	501	HEM	C2D-C1D-ND	2.56	112.95	109.88
2	A	501	HEM	C4B-C3B-C2B	-2.51	105.12	107.11
2	B	501	HEM	C3C-C4C-NC	-2.30	106.59	110.94
2	B	501	HEM	C3D-C4D-ND	2.27	112.69	110.17
2	B	501	HEM	CAD-C3D-C4D	2.20	128.51	124.66
2	B	501	HEM	CMB-C2B-C3B	-2.17	122.98	128.30
2	A	501	HEM	CHA-C4D-ND	2.15	127.04	124.38
2	A	501	HEM	CAD-C3D-C4D	2.08	128.30	124.66
2	A	501	HEM	O2D-CGD-CBD	2.07	120.67	114.03

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	HEM	CAD-CBD-CGD-O1D
2	B	501	HEM	CAD-CBD-CGD-O1D
2	A	501	HEM	CAD-CBD-CGD-O2D
2	B	501	HEM	CAD-CBD-CGD-O2D

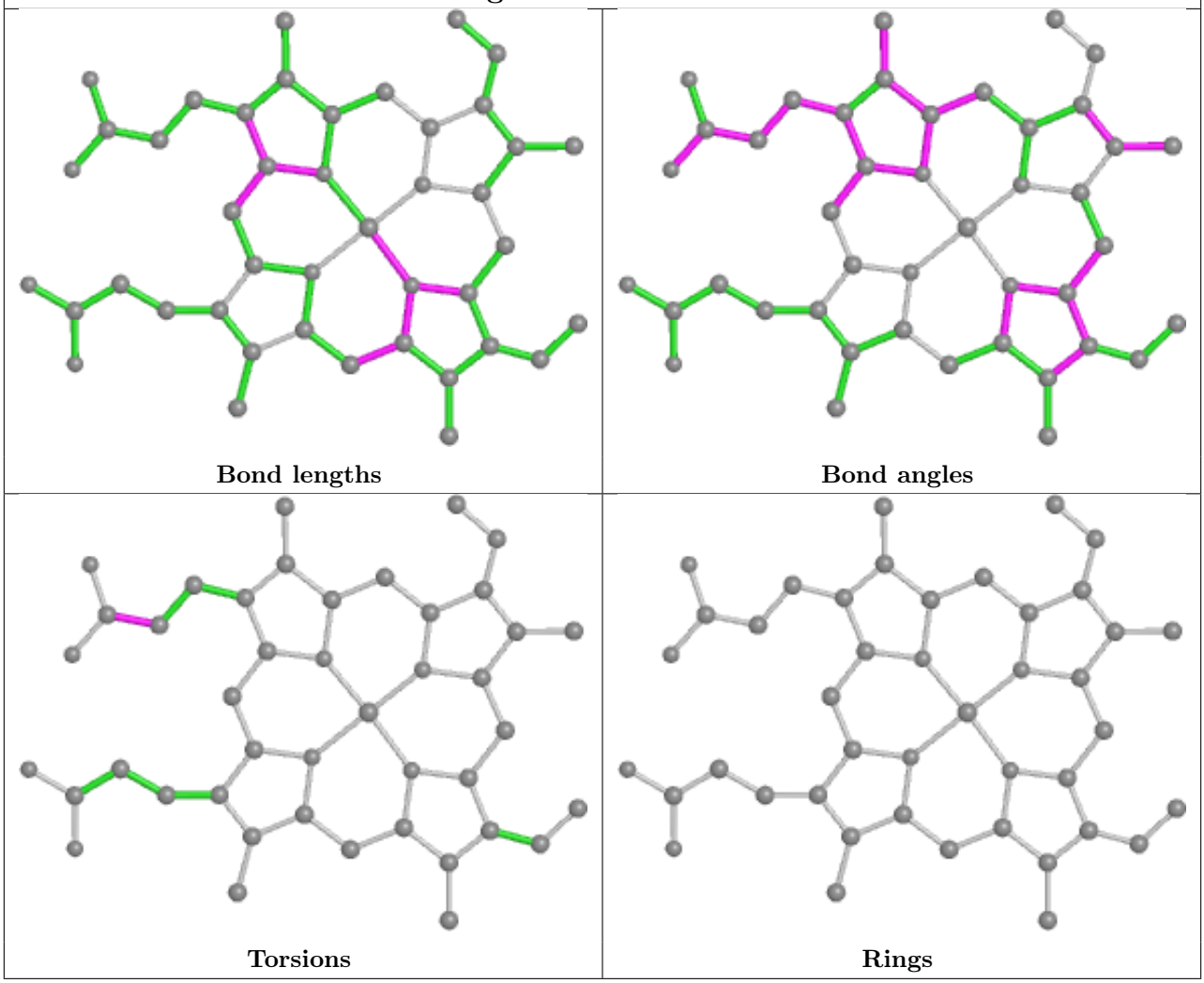
There are no ring outliers.

2 monomers are involved in 7 short contacts:

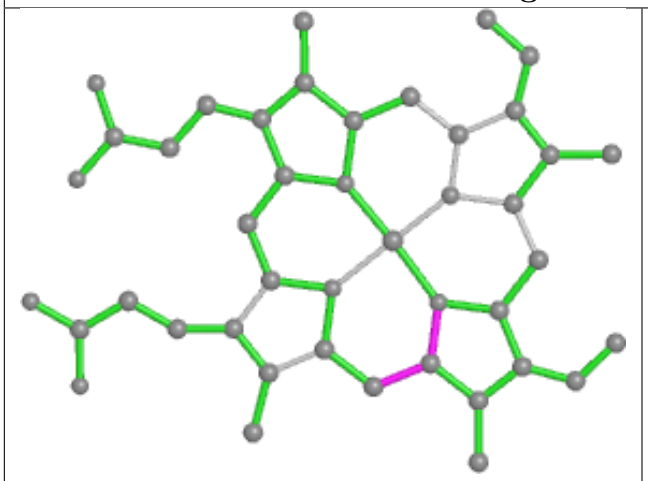
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	3	0
2	B	501	HEM	4	0

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 then 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.

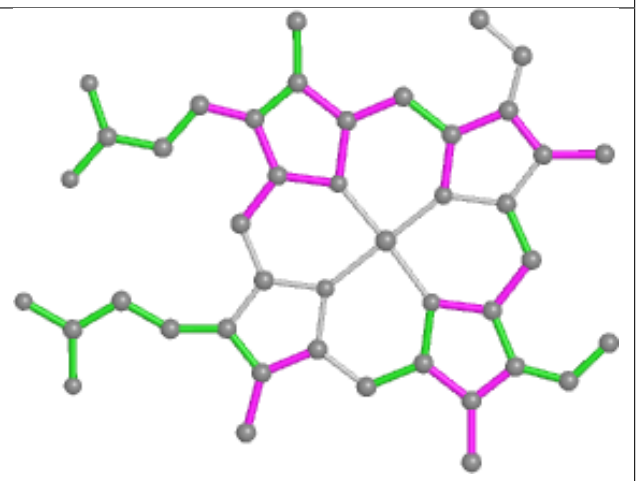
Ligand HEM A 501



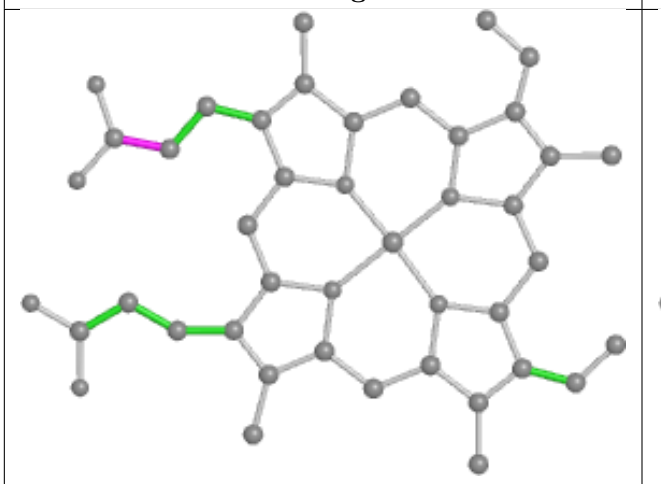
Ligand HEM B 501



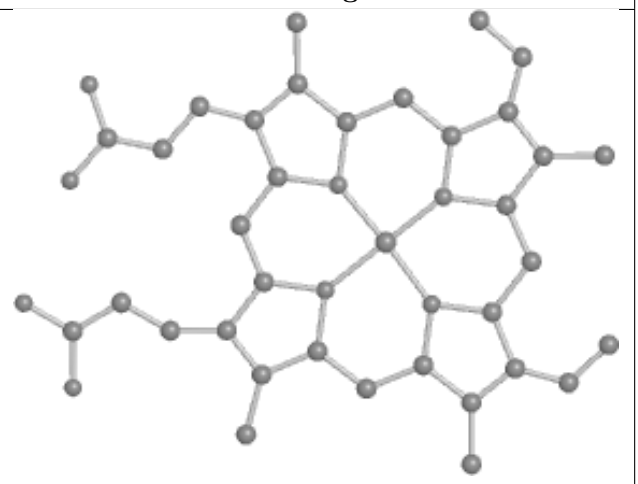
Bond lengths



Bond angles



Torsions



Rings

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	453/472 (95%)	0.36	28 (6%)	20	23	26, 37, 61, 94	0
1	B	453/472 (95%)	0.55	41 (9%)	9	10	24, 45, 70, 88	0
All	All	906/944 (95%)	0.46	69 (7%)	13	16	24, 41, 67, 94	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	191	ALA	7.2
1	A	225	ALA	5.7
1	A	384	ALA	4.9
1	A	243	PRO	4.6
1	B	328	VAL	4.5
1	B	457	GLY	4.3
1	B	384	ALA	4.2
1	B	322	LEU	4.0
1	A	245	THR	3.7
1	B	248	PRO	3.6
1	A	327	THR	3.6
1	B	327	THR	3.6
1	B	243	PRO	3.4
1	A	246	GLY	3.3
1	A	328	VAL	3.3
1	B	153	ILE	3.2
1	B	149	THR	3.2
1	B	318	LEU	3.1
1	B	198	TYR	3.1
1	A	272	LEU	3.1
1	B	245	THR	3.0
1	A	198	TYR	2.9
1	B	382	PRO	2.8
1	B	225	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	381	ASN	2.8
1	A	244	GLU	2.8
1	B	383	SER	2.8
1	B	136	ASP	2.8
1	B	220	ILE	2.8
1	B	268	GLY	2.7
1	B	458	ILE	2.7
1	A	392	PRO	2.7
1	A	385	ILE	2.6
1	B	439	LEU	2.6
1	A	150	LEU	2.6
1	A	239	ASN	2.5
1	B	246	GLY	2.5
1	A	227	GLY	2.4
1	B	195	ASP	2.4
1	A	393	PHE	2.4
1	B	221	ALA	2.4
1	B	244	GLU	2.4
1	B	345	TYR	2.4
1	B	192	ASN	2.4
1	A	262	LEU	2.3
1	B	357	ILE	2.3
1	B	150	LEU	2.3
1	B	92	HIS	2.3
1	B	407	LEU	2.3
1	A	454	PRO	2.3
1	A	223	ARG	2.2
1	B	340	VAL	2.2
1	A	266	HIS	2.2
1	A	394	GLY	2.2
1	B	273	LEU	2.2
1	A	174	ILE	2.2
1	A	268	GLY	2.2
1	B	366	VAL	2.2
1	A	322	LEU	2.2
1	A	285[A]	HIS	2.2
1	B	269	THR	2.2
1	A	387	GLN	2.1
1	B	152	THR	2.1
1	A	326	PRO	2.1
1	A	229	GLN	2.0
1	B	199	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	224	LYS	2.0
1	B	240	GLY	2.0
1	B	329	PRO	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

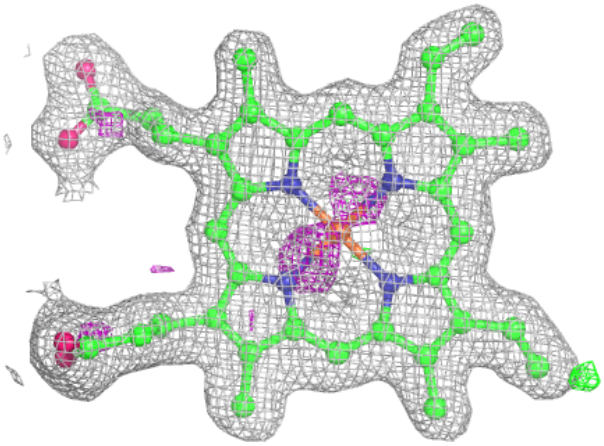
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

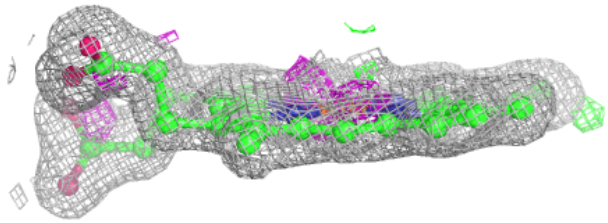
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	HEM	B	501	43/43	0.94	0.13	24,28,34,42	0
2	HEM	A	501	43/43	0.96	0.15	23,26,29,33	0

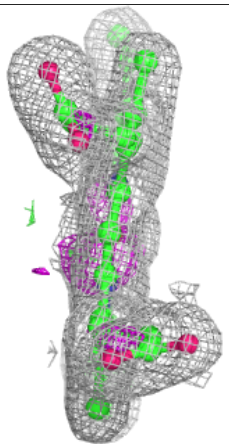
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HEM 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)

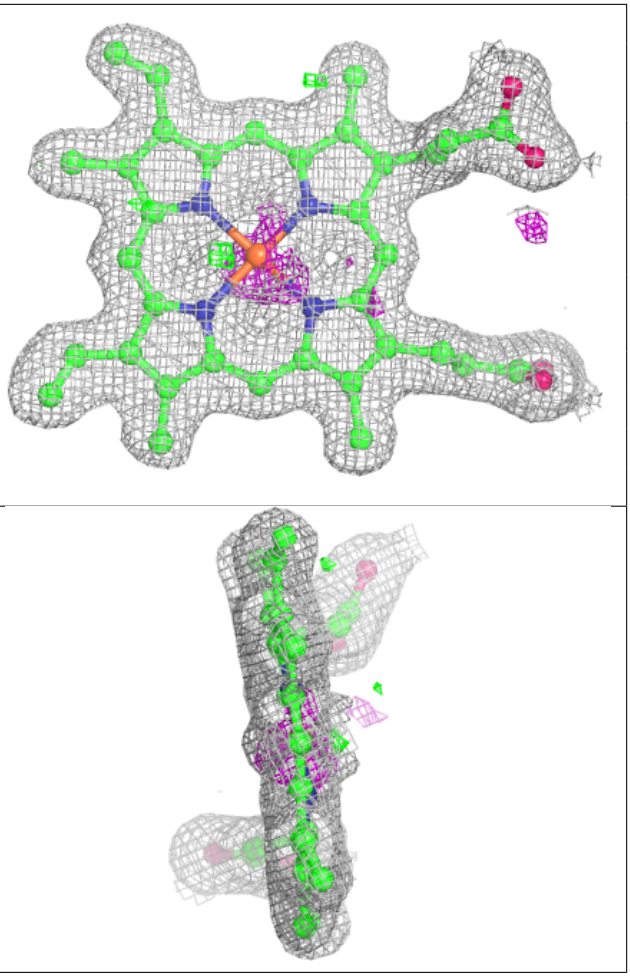






Electron density around HEM A 501:

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.