Full wwPDB X-ray Structure Validation Report (i)

Oct 25, 2023 – 12:51 PM EDT

PDB ID	:	3BNG
Title	:	W. succinogenes NrfA Y218F
Authors	:	Lukat, P.; Einsle, O.
Deposited on	:	2007-12-14
Resolution	:	1.50 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:

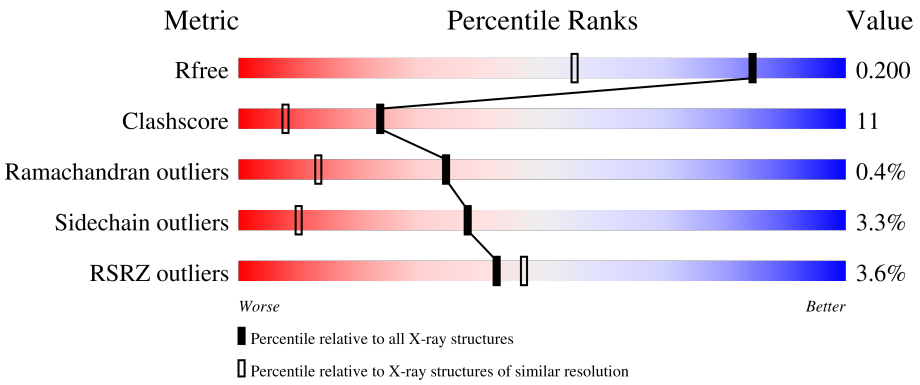
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.50 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	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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	485	4% 82% 14% • •

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 4698 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

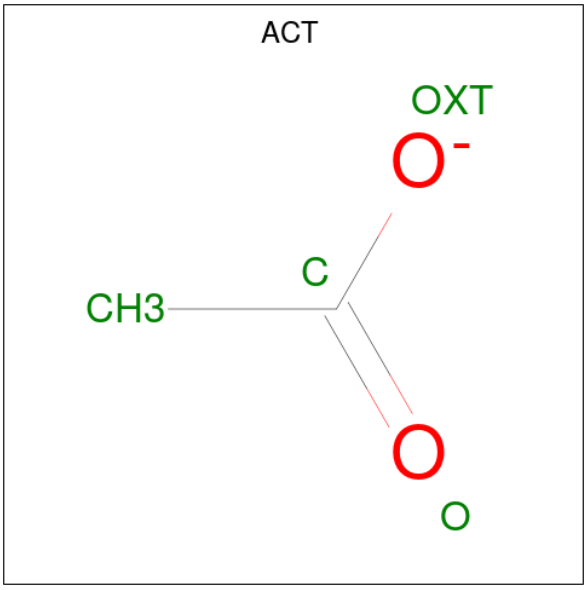
- Molecule 1 is a protein called Cytochrome c-552.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	471	3807	2412	654	720	21	19	6	0

There is a discrepancy between the modelled and reference sequences:

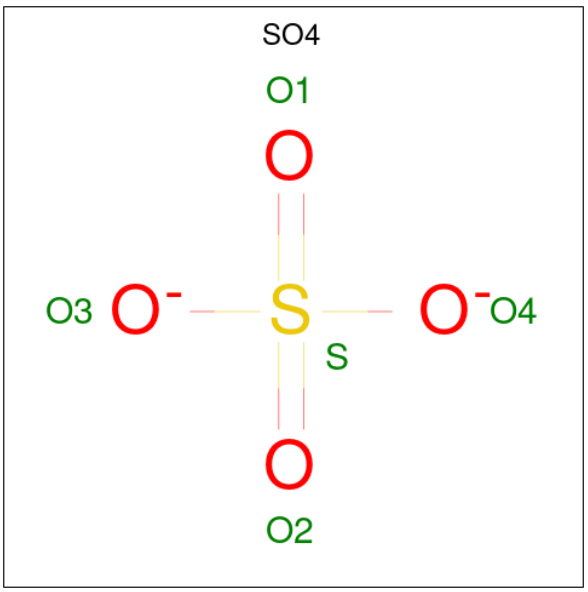
Chain	Residue	Modelled	Actual	Comment	Reference
A	218	PHE	TYR	engineered mutation	UNP Q9S1E5

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

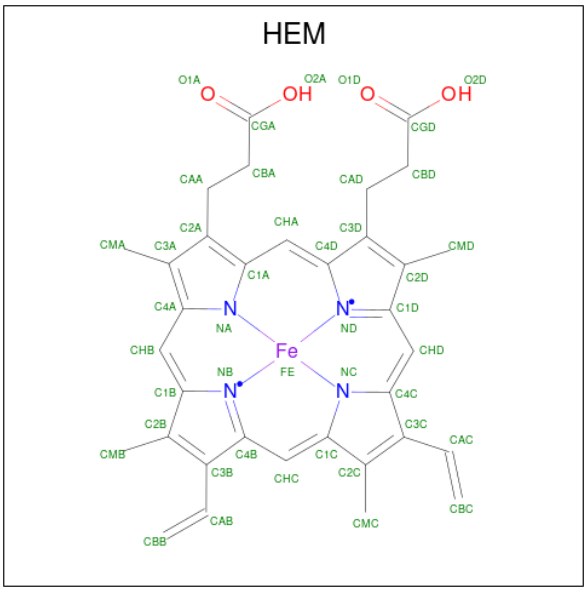
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Ca 1 1	0	0

- Molecule 5 is YTTRIUM ION (three-letter code: Y1) (formula: Y).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	4	Total Y 4 4	0	0

- Molecule 6 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 7 is water.

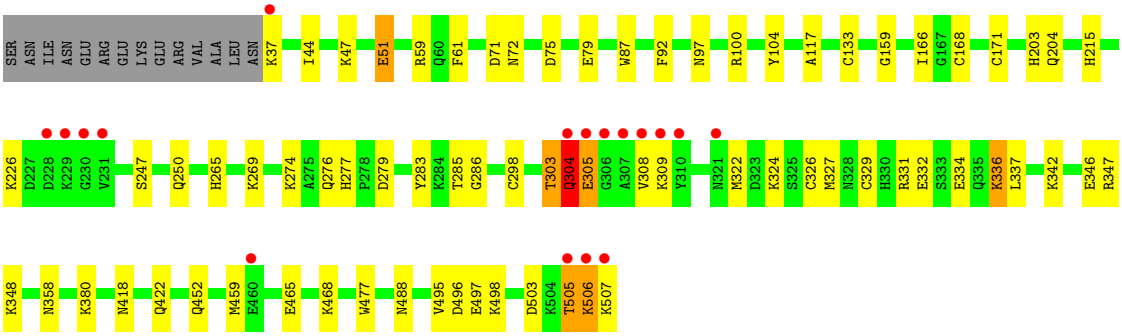
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	649	649	649	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Cytochrome c-552

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α, β, γ	120.03Å 120.03Å 186.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.45 – 1.50 24.18 – 1.40	Depositor EDS
% Data completeness (in resolution range)	98.7 (42.45-1.50) 98.1 (24.18-1.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.3.0008	Depositor
R, R_{free}	0.181 , 0.215 0.173 , 0.200	Depositor DCC
R_{free} test set	6593 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	17.8	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 48.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	4698	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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: ACT, SO4, Y1, CA, 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	0.71	3/3916 (0.1%)	0.72	2/5271 (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	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	342	LYS	CD-CE	-10.92	1.24	1.51
1	A	336	LYS	CB-CG	-6.17	1.35	1.52
1	A	331	ARG	CA-CB	-6.13	1.40	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	304	GLN	N-CA-C	7.19	130.42	111.00
1	A	305	GLU	N-CA-C	5.03	124.57	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	303	THR	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	3807	0	3739	87	2
2	A	12	0	9	0	0
3	A	10	0	0	1	0
4	A	1	0	0	0	0
5	A	4	0	0	0	0
6	A	215	0	150	23	0
7	A	649	0	0	16	2
All	All	4698	0	3898	89	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 11.

All (89) 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:168:CYS:SG	6:A:514:HEM:CAB	2.04	1.46
1:A:171:CYS:SG	6:A:514:HEM:CAC	2.05	1.43
1:A:298:CYS:SG	6:A:516:HEM:CAC	2.07	1.42
1:A:329:CYS:SG	6:A:517:HEM:CAC	2.14	1.34
1:A:168:CYS:SG	6:A:514:HEM:HAB	1.67	1.33
1:A:171:CYS:SG	6:A:514:HEM:HAC	1.67	1.25
1:A:298:CYS:SG	6:A:516:HEM:HAC	1.89	1.08
1:A:329:CYS:SG	6:A:517:HEM:HAC	1.93	1.06
1:A:285:THR:HG21	7:A:906:HOH:O	1.58	1.02
1:A:329:CYS:HG	6:A:517:HEM:CAC	1.74	0.97
1:A:498:LYS:H	1:A:507:LYS:HE2	1.31	0.95
1:A:358:ASN:HD22	1:A:418:ASN:HD21	1.15	0.92
1:A:332:GLU:HG3	1:A:337:LEU:HD13	1.56	0.86
1:A:498:LYS:N	1:A:507:LYS:HE2	1.91	0.85
1:A:71:ASP:HB2	1:A:507:LYS:HB2	1.63	0.80
1:A:298:CYS:SG	6:A:516:HEM:CBC	2.71	0.77
1:A:329:CYS:SG	6:A:517:HEM:C3C	2.81	0.73
1:A:322:MET:HB3	1:A:327:MET:HE2	1.70	0.73
1:A:305:GLU:HB2	7:A:1075:HOH:O	1.88	0.73
1:A:100:ARG:HH12	1:A:507:LYS:HE3	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:ALA:CB	1:A:465:GLU:HG2	2.18	0.72
1:A:497:GLU:HG3	1:A:507:LYS:HA	1.72	0.71
1:A:298:CYS:SG	6:A:516:HEM:C3C	2.83	0.71
1:A:171:CYS:SG	6:A:514:HEM:C3C	2.82	0.71
1:A:168:CYS:SG	6:A:514:HEM:CBB	2.79	0.70
6:A:514:HEM:HBC1	6:A:515:HEM:HHC	1.75	0.68
1:A:488[B]:ASN:ND2	7:A:938:HOH:O	2.25	0.67
1:A:51[A]:GLU:HG2	7:A:938:HOH:O	1.93	0.67
1:A:329:CYS:SG	6:A:517:HEM:CBC	2.83	0.66
1:A:100:ARG:HH22	1:A:507:LYS:HE3	1.60	0.66
1:A:168:CYS:SG	6:A:514:HEM:C3B	2.88	0.64
1:A:327:MET:HE3	1:A:334:GLU:HG2	1.79	0.64
1:A:104:TYR:CE1	1:A:507:LYS:HD2	2.34	0.63
1:A:71:ASP:CB	1:A:507:LYS:HB2	2.28	0.63
1:A:117:ALA:HB3	1:A:465:GLU:HG2	1.80	0.62
1:A:171:CYS:SG	6:A:514:HEM:CBC	2.82	0.62
1:A:100:ARG:HH12	1:A:507:LYS:HG3	1.64	0.62
6:A:516:HEM:HBD2	7:A:1024:HOH:O	1.99	0.61
1:A:286:GLY:HA2	3:A:1:SO4:O4	2.01	0.61
1:A:322:MET:HB3	1:A:327:MET:CE	2.30	0.60
1:A:100:ARG:HH22	1:A:507:LYS:CE	2.14	0.60
1:A:332:GLU:CG	1:A:337:LEU:HD13	2.29	0.60
1:A:100:ARG:HH22	1:A:507:LYS:NZ	2.01	0.59
1:A:100:ARG:NH1	1:A:507:LYS:HE3	2.18	0.59
1:A:100:ARG:HH22	1:A:507:LYS:HZ1	1.50	0.57
1:A:422:GLN:HE21	1:A:422:GLN:HA	1.69	0.57
1:A:346:GLU:HG2	7:A:1157:HOH:O	2.05	0.56
1:A:322:MET:CE	1:A:327:MET:CE	2.83	0.56
1:A:44:ILE:O	1:A:47[B]:LYS:HG3	2.06	0.56
1:A:285:THR:HB	7:A:835:HOH:O	2.06	0.55
1:A:495:VAL:O	1:A:507:LYS:NZ	2.32	0.55
1:A:452:GLN:HE22	1:A:459:MET:HG3	1.72	0.55
1:A:498:LYS:H	1:A:507:LYS:CE	2.12	0.55
1:A:380:LYS:HE3	7:A:997:HOH:O	2.06	0.54
1:A:247:SER:H	1:A:250:GLN:HE21	1.56	0.54
1:A:79:GLU:HG2	7:A:950:HOH:O	2.07	0.53
1:A:71:ASP:HB2	1:A:507:LYS:CB	2.38	0.53
1:A:71:ASP:OD2	1:A:506:LYS:HE2	2.09	0.52
1:A:100:ARG:NH2	1:A:507:LYS:HE3	2.23	0.52
1:A:503:ASP:OD1	1:A:505:THR:HA	2.09	0.52
1:A:322:MET:HE1	1:A:327:MET:CE	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ILE:HB	1:A:47[B]:LYS:HB3	1.92	0.51
1:A:285:THR:HA	7:A:1155:HOH:O	2.11	0.50
1:A:322:MET:HE1	1:A:327:MET:HE1	1.92	0.50
1:A:87:TRP:CE3	1:A:92:PHE:HB3	2.47	0.50
1:A:452:GLN:NE2	1:A:459:MET:HG3	2.26	0.50
1:A:322:MET:CE	1:A:327:MET:HE1	2.42	0.49
1:A:347[A]:ARG:NH2	7:A:985:HOH:O	2.19	0.49
1:A:215:HIS:HB3	1:A:279:ASP:HB2	1.96	0.48
1:A:87:TRP:CE2	1:A:274:LYS:HE2	2.49	0.48
1:A:327:MET:HE1	1:A:337:LEU:HD23	1.96	0.47
1:A:203:HIS:HE2	6:A:514:HEM:CGD	2.28	0.47
1:A:265:HIS:O	1:A:269:LYS:HD3	2.14	0.47
1:A:326:CYS:HB2	1:A:327:MET:HE2	1.98	0.46
1:A:75:ASP:HA	1:A:97:ASN:HD22	1.80	0.46
1:A:51[A]:GLU:CG	7:A:938:HOH:O	2.56	0.45
1:A:247:SER:H	1:A:250:GLN:NE2	2.14	0.45
1:A:276:GLN:O	1:A:277:HIS:C	2.54	0.44
1:A:159:GLY:HA3	1:A:477:TRP:CE2	2.53	0.44
1:A:285:THR:CB	7:A:835:HOH:O	2.64	0.44
1:A:305:GLU:HB3	1:A:308:VAL:O	2.19	0.43
1:A:61:PHE:HA	6:A:514:HEM:HBB2	2.00	0.42
1:A:496:ASP:HA	1:A:507:LYS:HZ3	1.85	0.42
1:A:203:HIS:NE2	6:A:514:HEM:O2D	2.49	0.42
1:A:133:CYS:HB2	6:A:513:HEM:C4C	2.54	0.41
1:A:346:GLU:CD	7:A:1156:HOH:O	2.58	0.41
1:A:72:ASN:ND2	7:A:798:HOH:O	2.50	0.40
1:A:104:TYR:HE1	1:A:507:LYS:HD2	1.83	0.40
1:A:309:LYS:HB2	7:A:1049:HOH:O	2.22	0.40

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)
1:A:304:GLN:O	7:A:1116:HOH:O[16_555]	2.06	0.14
1:A:347[B]:ARG:NH1	7:A:773:HOH:O[10_565]	2.10	0.10

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	475/485 (98%)	463 (98%)	10 (2%)	2 (0%)	34 13

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	166	ILE
1	A	505	THR

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	403/410 (98%)	389 (96%)	14 (4%)	36 9

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	LYS
1	A	51[A]	GLU
1	A	51[B]	GLU
1	A	59	ARG
1	A	204	GLN
1	A	226	LYS
1	A	283	TYR
1	A	303	THR
1	A	304	GLN

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Mol	Chain	Res	Type
1	A	324	LYS
1	A	336	LYS
1	A	348	LYS
1	A	468	LYS
1	A	506	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	97	ASN
1	A	144	GLN
1	A	204	GLN
1	A	250	GLN
1	A	328	ASN
1	A	352	GLN
1	A	418	ASN
1	A	422	GLN
1	A	452	GLN
1	A	480	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)

Of 15 ligands modelled in this entry, 5 are monoatomic - leaving 10 for Mogul analysis.

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	ACT	A	3	-	3,3,3	0.80	0	3,3,3	0.98	0
2	ACT	A	5	-	3,3,3	0.79	0	3,3,3	1.28	0
3	SO4	A	1	-	4,4,4	0.39	0	6,6,6	0.70	0
6	HEM	A	513	7,1	41,50,50	1.84	6 (14%)	45,82,82	1.58	8 (17%)
6	HEM	A	517	1	41,50,50	1.95	5 (12%)	45,82,82	1.60	8 (17%)
6	HEM	A	516	1	41,50,50	1.79	7 (17%)	45,82,82	1.60	10 (22%)
3	SO4	A	2	-	4,4,4	0.15	0	6,6,6	0.08	0
6	HEM	A	515	1	41,50,50	1.80	5 (12%)	45,82,82	1.59	9 (20%)
6	HEM	A	514	1	41,50,50	1.89	7 (17%)	45,82,82	1.53	8 (17%)
2	ACT	A	4	-	3,3,3	0.66	0	3,3,3	1.49	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
6	HEM	A	513	7,1	-	4/12/54/54	-
6	HEM	A	517	1	-	7/12/54/54	-
6	HEM	A	516	1	-	1/12/54/54	-
6	HEM	A	515	1	-	2/12/54/54	-
6	HEM	A	514	1	-	4/12/54/54	-

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	517	HEM	C3D-C2D	7.67	1.53	1.36
6	A	513	HEM	C3D-C2D	6.97	1.51	1.36
6	A	514	HEM	C3D-C2D	6.71	1.51	1.36
6	A	515	HEM	C3D-C2D	6.43	1.50	1.36
6	A	516	HEM	C3D-C2D	6.42	1.50	1.36
6	A	514	HEM	C3C-C2C	-4.62	1.34	1.40
6	A	515	HEM	C3C-CAC	4.44	1.56	1.47
6	A	517	HEM	C3C-CAC	4.42	1.56	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	513	HEM	C3C-C2C	-4.17	1.34	1.40
6	A	516	HEM	C3C-CAC	3.93	1.55	1.47
6	A	517	HEM	C3C-C2C	-3.89	1.35	1.40
6	A	514	HEM	C3C-CAC	3.85	1.55	1.47
6	A	516	HEM	C3C-C2C	-3.77	1.35	1.40
6	A	515	HEM	C3C-C2C	-3.76	1.35	1.40
6	A	513	HEM	C3C-CAC	3.74	1.55	1.47
6	A	514	HEM	CAB-C3B	3.19	1.56	1.47
6	A	517	HEM	CAB-C3B	3.17	1.56	1.47
6	A	514	HEM	CMB-C2B	3.03	1.57	1.50
6	A	514	HEM	CAA-C2A	2.95	1.56	1.52
6	A	513	HEM	CAB-C3B	2.91	1.55	1.47
6	A	515	HEM	CMB-C2B	2.91	1.56	1.50
6	A	517	HEM	CAA-C2A	2.57	1.55	1.52
6	A	516	HEM	CAA-C2A	2.47	1.55	1.52
6	A	515	HEM	CAB-C3B	2.41	1.54	1.47
6	A	516	HEM	CMB-C2B	2.29	1.55	1.50
6	A	516	HEM	CMA-C3A	2.26	1.56	1.51
6	A	513	HEM	CAA-C2A	2.15	1.55	1.52
6	A	516	HEM	CAB-C3B	2.07	1.53	1.47
6	A	514	HEM	CMD-C2D	2.04	1.55	1.50
6	A	513	HEM	O1D-CGD	2.02	1.28	1.22

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	517	HEM	C4D-ND-C1D	5.63	110.89	105.07
6	A	513	HEM	C4D-ND-C1D	5.35	110.60	105.07
6	A	514	HEM	C4D-ND-C1D	4.54	109.77	105.07
6	A	515	HEM	C4D-ND-C1D	4.37	109.59	105.07
6	A	516	HEM	C4D-ND-C1D	4.18	109.39	105.07
6	A	514	HEM	C1B-NB-C4B	3.59	108.79	105.07
6	A	515	HEM	CBA-CAA-C2A	-3.49	106.67	112.62
6	A	517	HEM	CMA-C3A-C4A	-3.49	123.10	128.46
6	A	514	HEM	CBD-CAD-C3D	-3.19	103.77	112.63
6	A	516	HEM	CAD-CBD-CGD	-3.06	107.02	113.60
6	A	516	HEM	CBB-CAB-C3B	-2.91	113.12	127.62
6	A	517	HEM	CAD-CBD-CGD	-2.75	107.67	113.60
6	A	514	HEM	CHC-C4B-NB	2.74	127.41	124.43
6	A	513	HEM	CMA-C3A-C4A	-2.73	124.27	128.46
6	A	516	HEM	C2C-C3C-C4C	2.72	108.80	106.90
6	A	513	HEM	CHD-C1D-ND	2.66	127.32	124.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	517	HEM	C4C-CHD-C1D	2.62	126.01	122.56
6	A	515	HEM	C4B-C3B-C2B	2.61	109.19	107.11
6	A	515	HEM	CHD-C1D-ND	2.61	127.27	124.43
6	A	516	HEM	CMC-C2C-C3C	2.61	129.56	124.68
6	A	517	HEM	C1B-NB-C4B	2.60	107.76	105.07
6	A	516	HEM	CBA-CAA-C2A	-2.54	108.28	112.62
6	A	515	HEM	C1B-NB-C4B	2.54	107.69	105.07
6	A	515	HEM	C1D-C2D-C3D	-2.54	104.29	106.96
6	A	516	HEM	CMA-C3A-C4A	-2.47	124.67	128.46
6	A	516	HEM	CHD-C1D-ND	2.45	127.09	124.43
6	A	515	HEM	CMA-C3A-C4A	-2.45	124.70	128.46
6	A	517	HEM	CBA-CAA-C2A	-2.40	108.53	112.62
6	A	516	HEM	CMD-C2D-C1D	2.38	128.66	125.04
6	A	514	HEM	CMC-C2C-C3C	2.34	129.05	124.68
6	A	513	HEM	C1B-NB-C4B	2.34	107.49	105.07
6	A	513	HEM	CBB-CAB-C3B	-2.28	116.25	127.62
6	A	513	HEM	CAD-C3D-C4D	2.26	128.61	124.66
6	A	516	HEM	CHC-C4B-NB	2.25	126.88	124.43
6	A	513	HEM	CMC-C2C-C3C	2.23	128.86	124.68
6	A	514	HEM	C4A-C3A-C2A	2.22	108.54	107.00
6	A	514	HEM	CHD-C1D-ND	2.19	126.81	124.43
6	A	515	HEM	CHB-C1B-NB	2.18	127.07	124.38
6	A	517	HEM	C4B-CHC-C1C	2.18	125.43	122.56
6	A	517	HEM	CMA-C3A-C2A	2.17	129.03	124.94
6	A	515	HEM	CAD-CBD-CGD	-2.14	108.99	113.60
6	A	514	HEM	CBA-CAA-C2A	-2.10	109.04	112.62
6	A	513	HEM	C4C-CHD-C1D	2.10	125.33	122.56

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	513	HEM	C2B-C3B-CAB-CBB
6	A	513	HEM	C4B-C3B-CAB-CBB
6	A	517	HEM	C2A-CAA-CBA-CGA
6	A	515	HEM	C2B-C3B-CAB-CBB
6	A	515	HEM	C4B-C3B-CAB-CBB
6	A	514	HEM	C2B-C3B-CAB-CBB
6	A	517	HEM	C2B-C3B-CAB-CBB
6	A	514	HEM	CAA-CBA-CGA-O1A
6	A	513	HEM	CAA-CBA-CGA-O1A
6	A	514	HEM	CAA-CBA-CGA-O2A

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Mol	Chain	Res	Type	Atoms
6	A	517	HEM	CAA-CBA-CGA-O2A
6	A	513	HEM	CAA-CBA-CGA-O2A
6	A	517	HEM	CAD-CBD-CGD-O2D
6	A	517	HEM	CAA-CBA-CGA-O1A
6	A	517	HEM	CAD-CBD-CGD-O1D
6	A	514	HEM	C4B-C3B-CAB-CBB
6	A	516	HEM	C4B-C3B-CAB-CBB
6	A	517	HEM	C4B-C3B-CAB-CBB

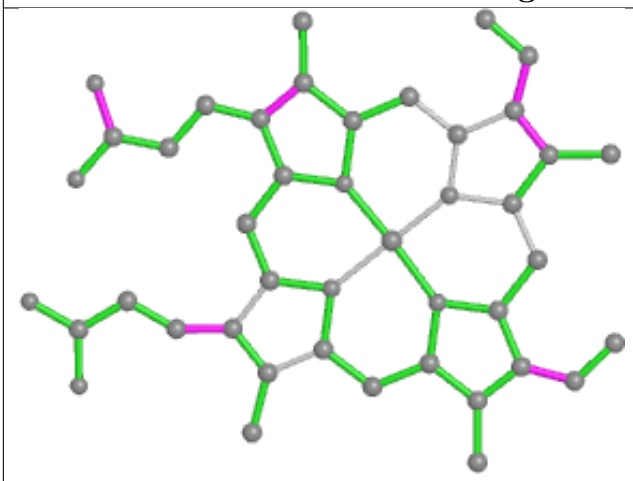
There are no ring outliers.

6 monomers are involved in 24 short contacts:

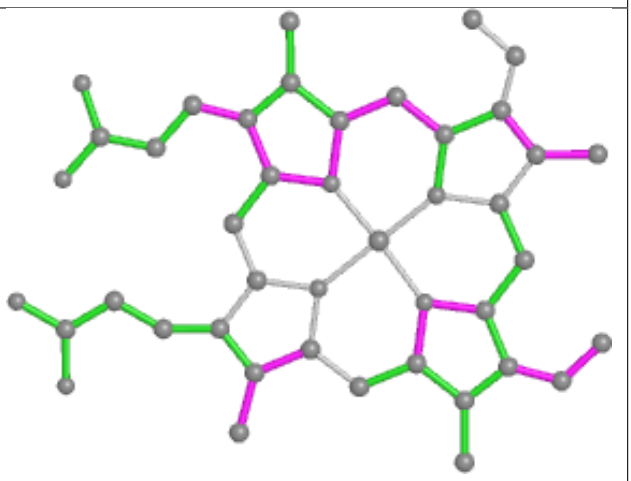
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	SO4	1	0
6	A	513	HEM	1	0
6	A	517	HEM	5	0
6	A	516	HEM	5	0
6	A	515	HEM	1	0
6	A	514	HEM	12	0

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.

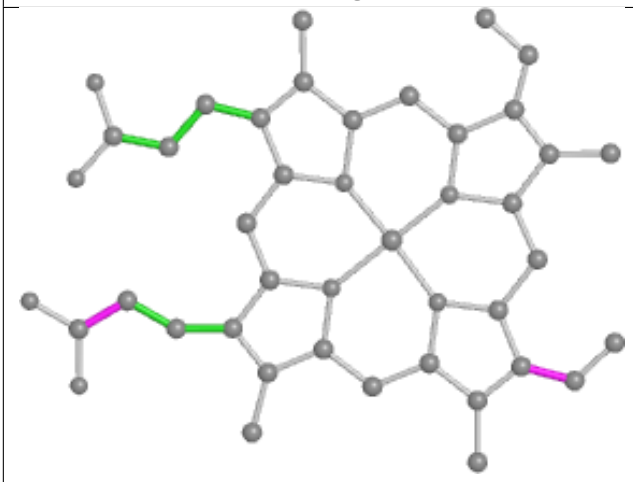
Ligand HEM A 513



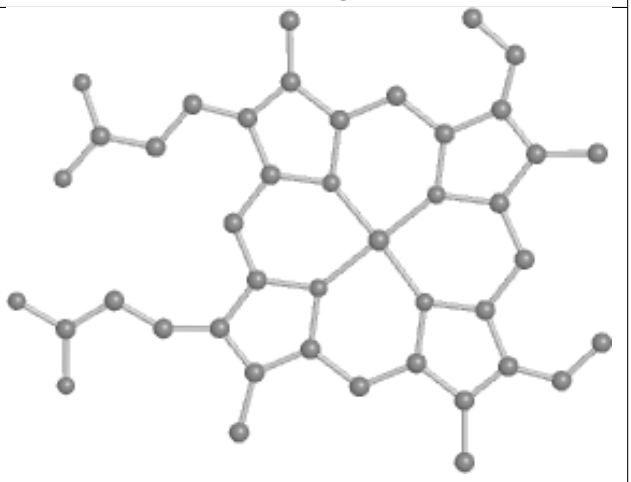
Bond lengths



Bond angles

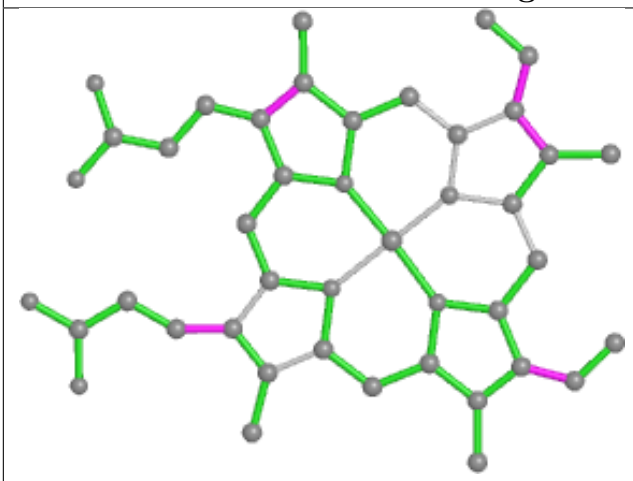


Torsions

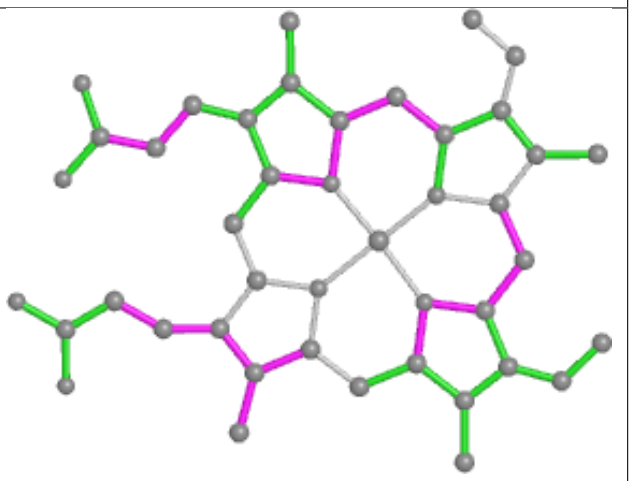


Rings

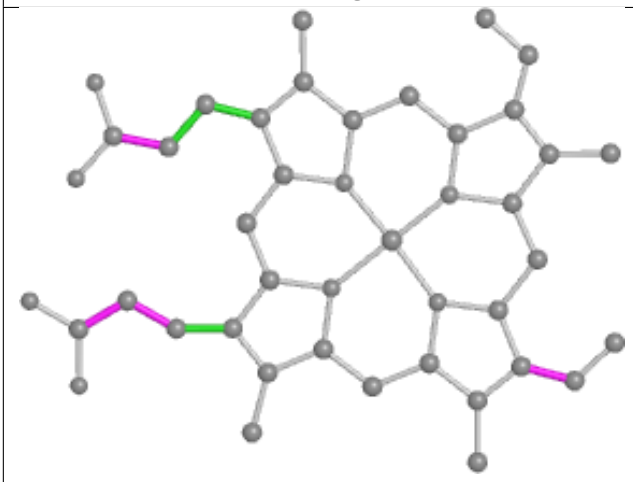
Ligand HEM A 517



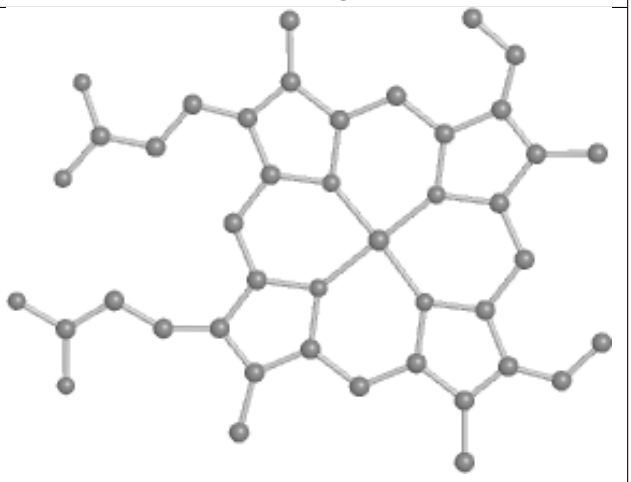
Bond lengths



Bond angles

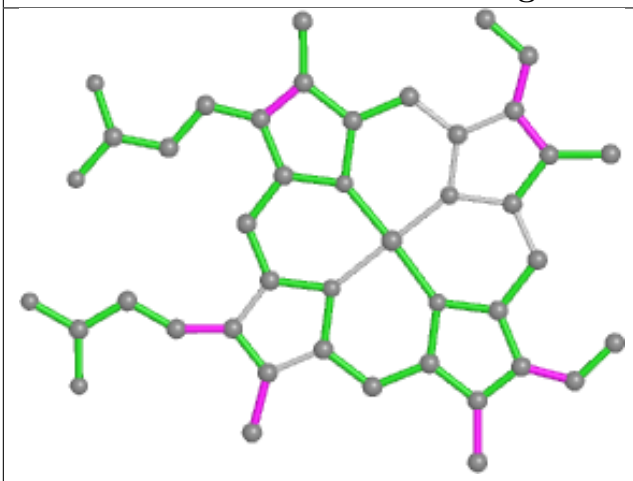


Torsions

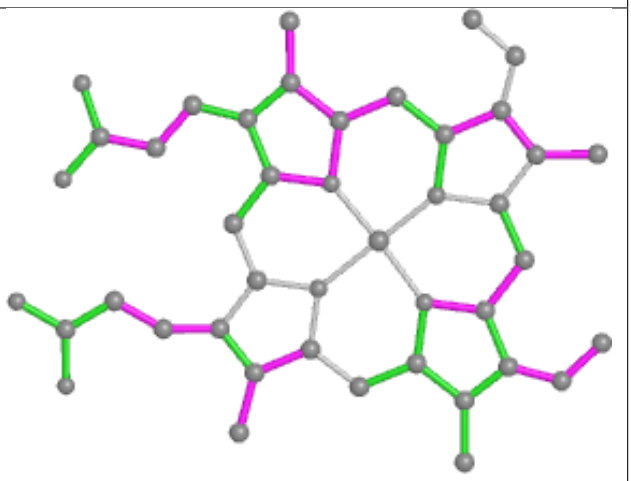


Rings

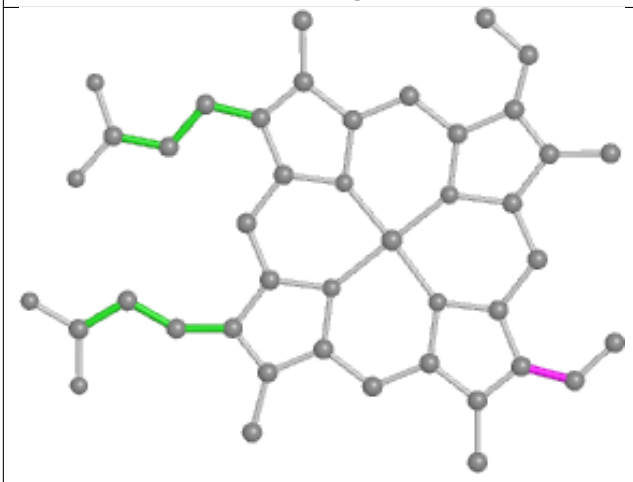
Ligand HEM A 516



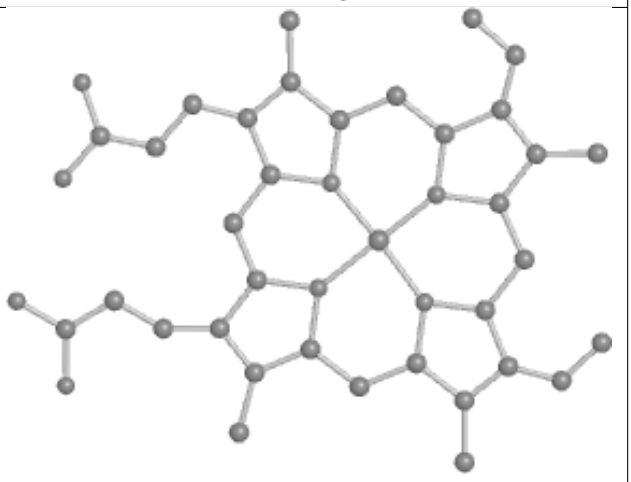
Bond lengths



Bond angles

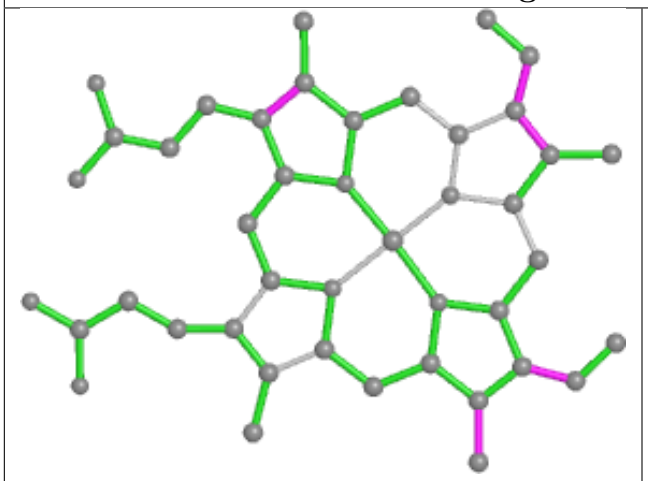


Torsions

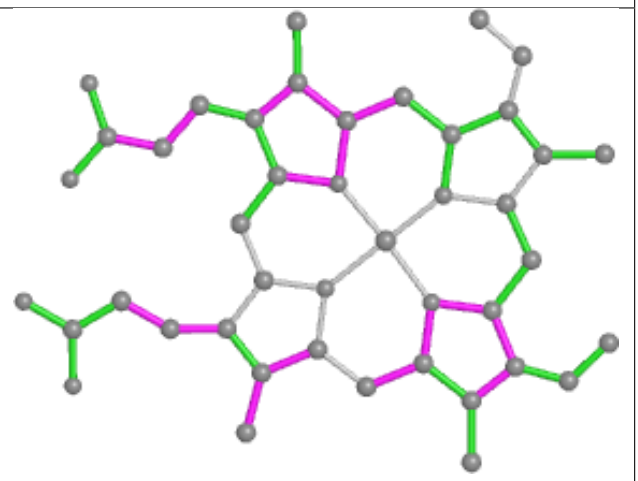


Rings

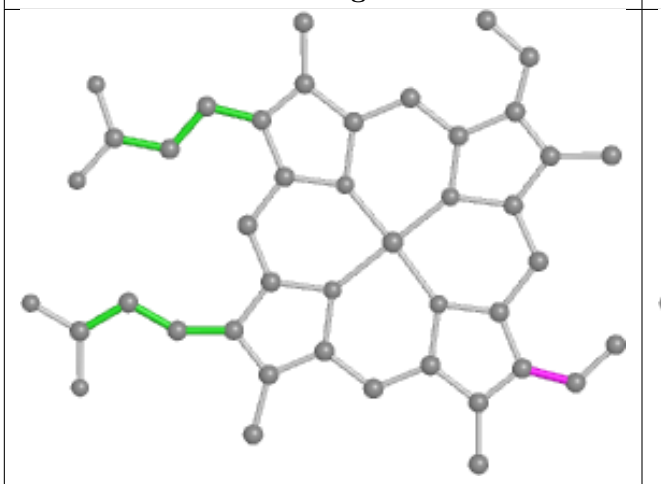
Ligand HEM A 515



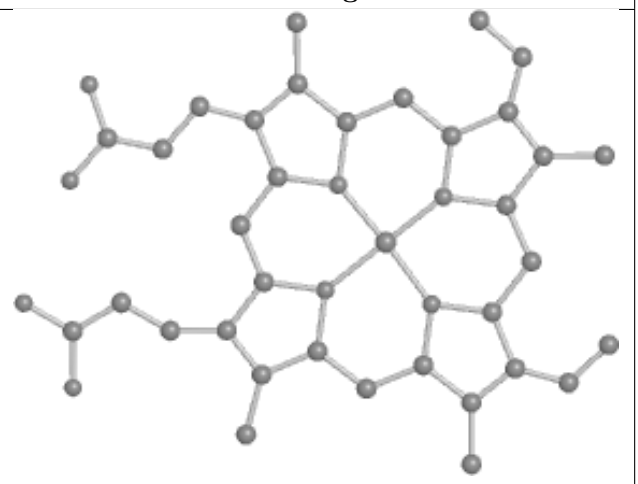
Bond lengths



Bond angles

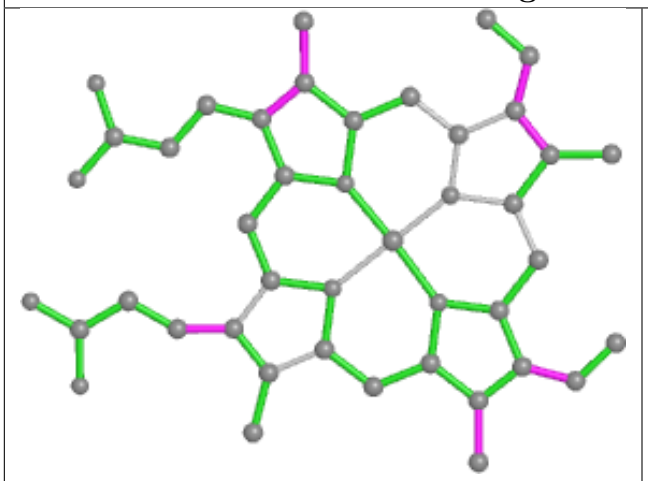


Torsions

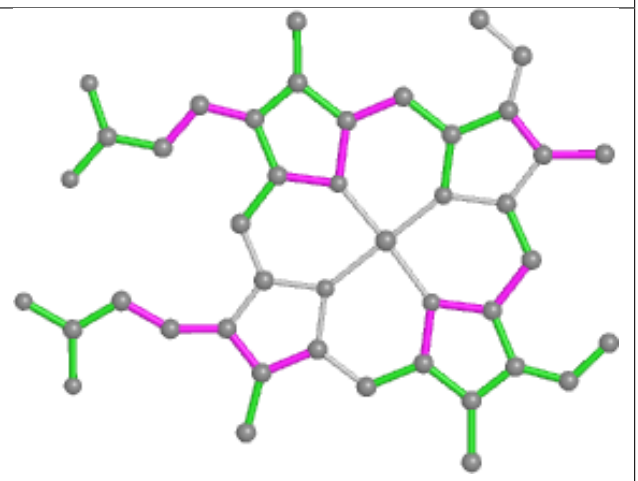


Rings

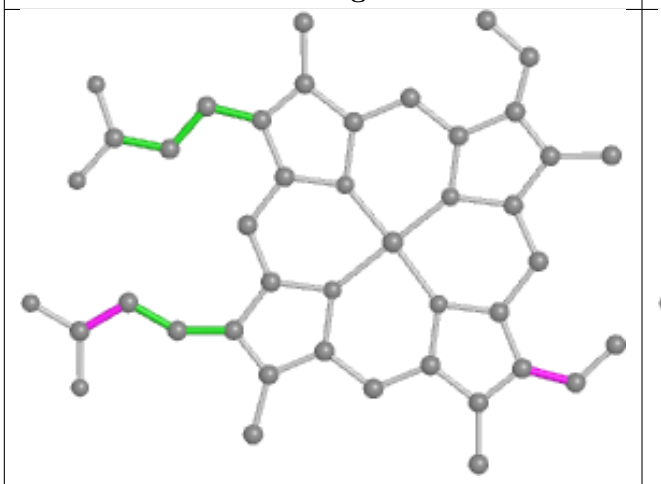
Ligand HEM A 514



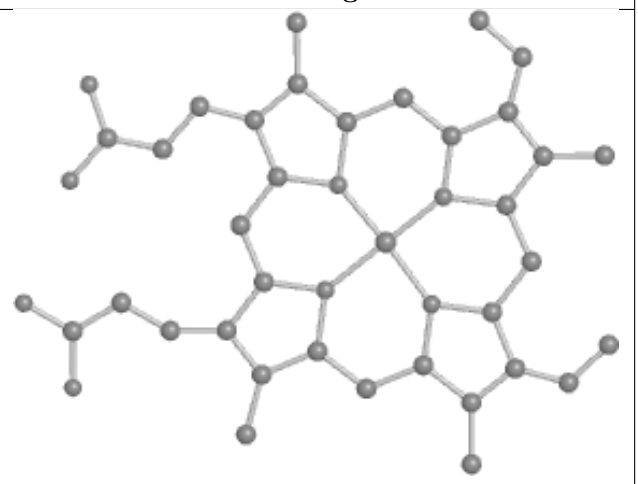
Bond lengths



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	471/485 (97%)	-0.19	17 (3%) 42 47	15, 21, 36, 53	5 (1%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	308	VAL	16.8
1	A	307	ALA	12.1
1	A	506	LYS	9.1
1	A	306	GLY	8.1
1	A	231	VAL	5.3
1	A	228	ASP	4.9
1	A	305	GLU	4.6
1	A	507	LYS	4.4
1	A	304	GLN	4.1
1	A	37	LYS	3.4
1	A	230	GLY	3.2
1	A	229	LYS	2.9
1	A	321	ASN	2.8
1	A	309	LYS	2.7
1	A	505	THR	2.3
1	A	460	GLU	2.1
1	A	310	TYR	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)

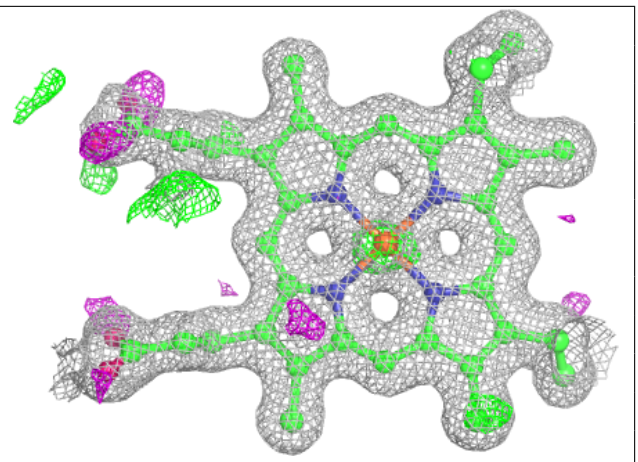
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

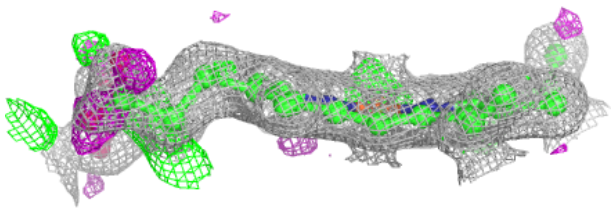
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	ACT	A	5	4/4	0.75	0.13	57,57,57,57	0
2	ACT	A	4	4/4	0.79	0.15	53,53,53,53	0
2	ACT	A	3	4/4	0.82	0.20	31,33,33,33	0
3	SO4	A	2	5/5	0.85	0.17	84,95,96,96	0
3	SO4	A	1	5/5	0.91	0.15	15,18,21,23	5
6	HEM	A	516	43/43	0.97	0.09	13,16,29,39	0
6	HEM	A	517	43/43	0.97	0.08	19,21,35,37	0
6	HEM	A	514	43/43	0.98	0.08	16,19,26,33	0
6	HEM	A	515	43/43	0.98	0.08	14,16,19,26	0
5	Y1	A	512	1/1	0.99	0.09	35,35,35,35	1
6	HEM	A	513	43/43	0.99	0.07	14,15,17,19	0
5	Y1	A	510	1/1	1.00	0.01	20,20,20,20	1
5	Y1	A	511	1/1	1.00	0.04	21,21,21,21	1
4	CA	A	508	1/1	1.00	0.01	18,18,18,18	0
5	Y1	A	509	1/1	1.00	0.04	22,22,22,22	0

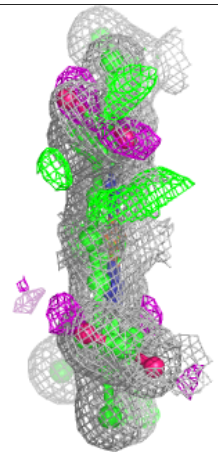
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HEM A 516:

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

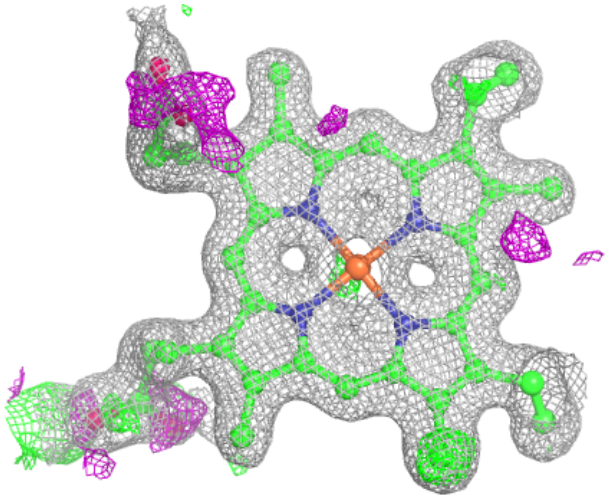


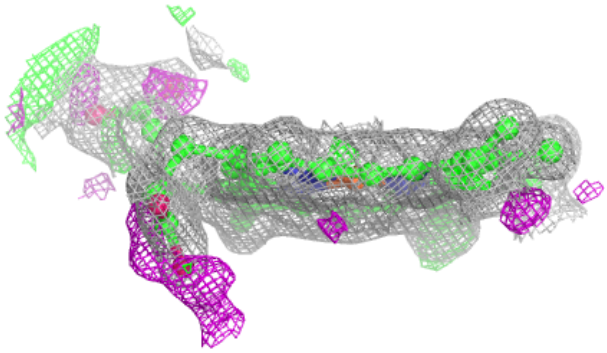


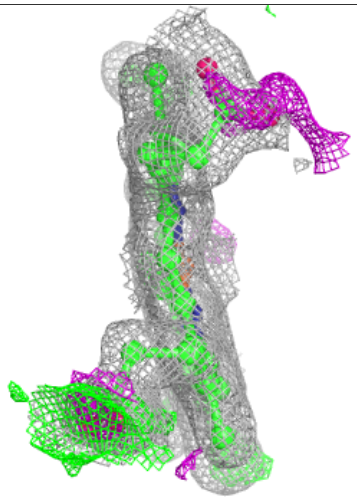


Electron density around HEM A 517:

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

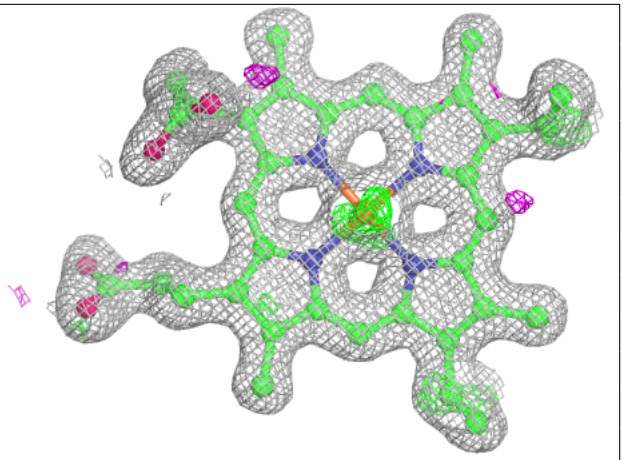


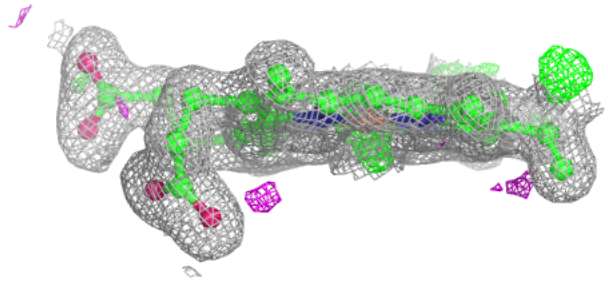


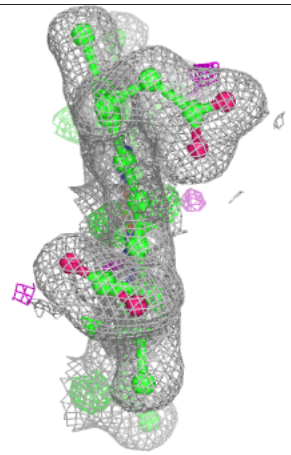


Electron density around HEM A 514:

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

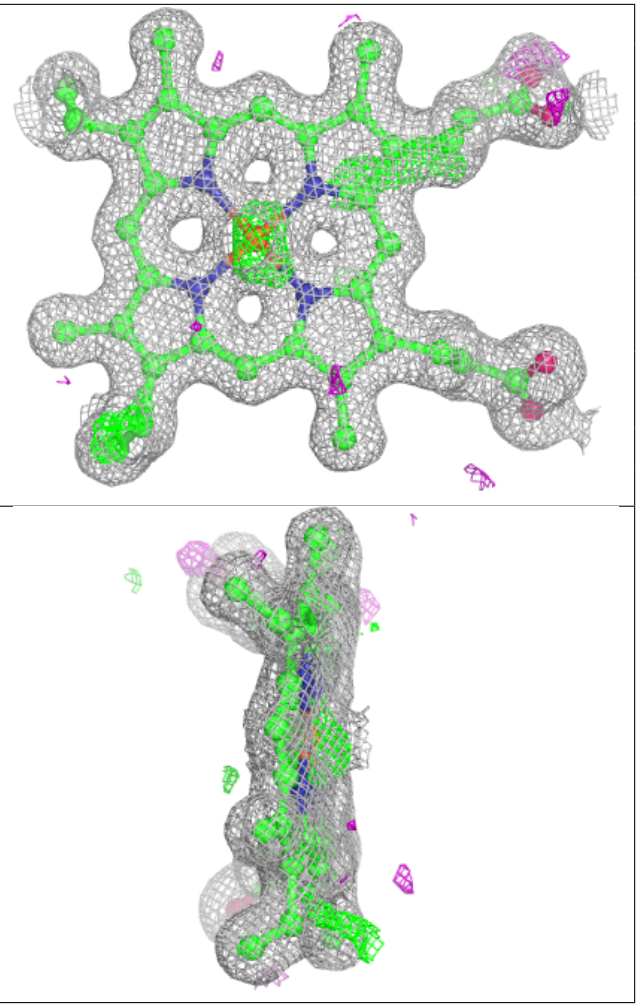






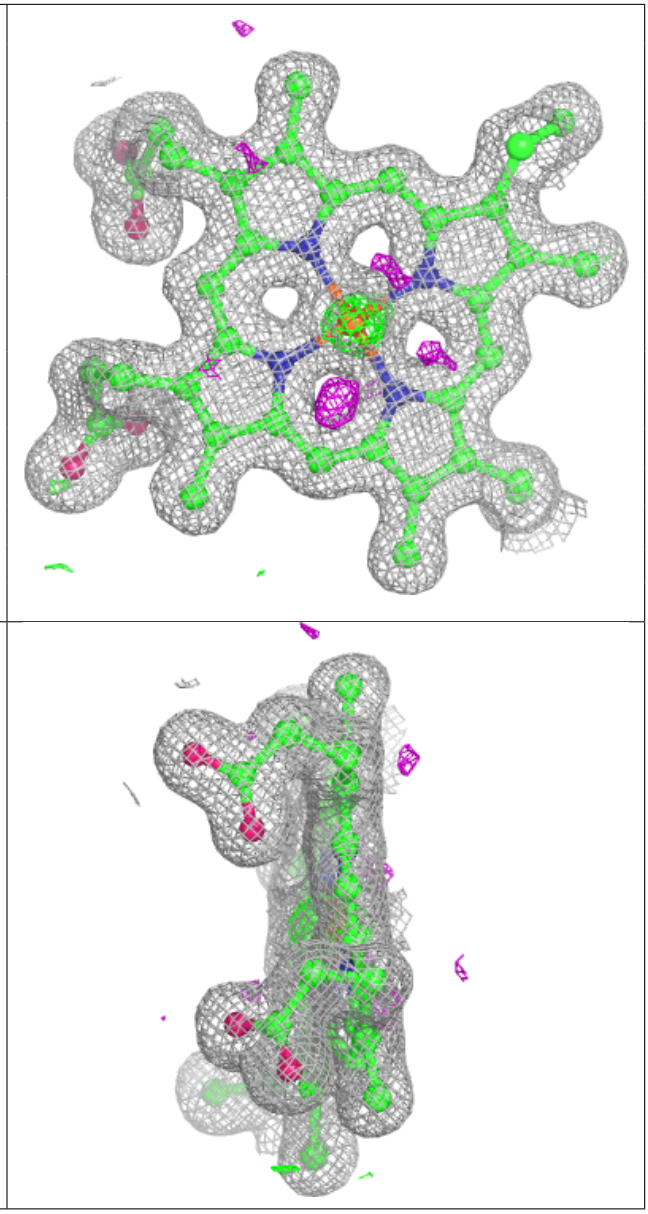
Electron density around HEM A 515:

$2mF_o$-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 513:

$2mF_o$-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.