Full wwPDB X-ray Structure Validation Report (i)

Aug 3, 2026 – 06:58 AM EDT

PDB ID	:	6NBL / pdb_00006nbl
Title	:	Cytochrome P450cam-putidaredoxin complex bound to camphor and cyanide
Authors	:	Follmer, A.H.; Tripathi, S.M.; Poulos, T.L.
Deposited on	:	2018-12-07
Resolution	:	2.15 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:

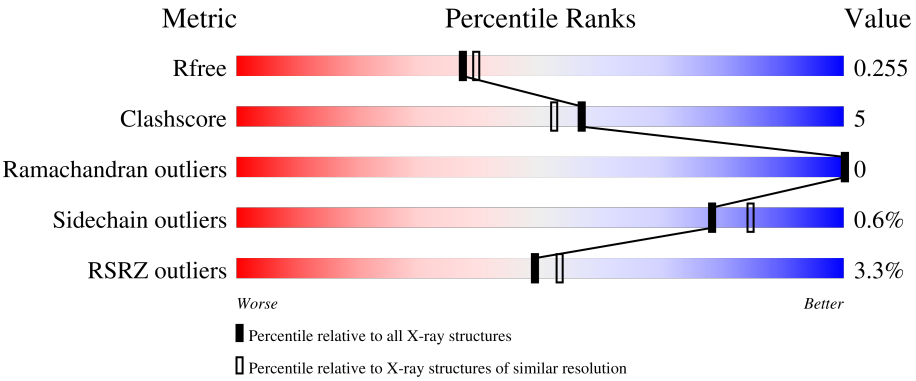
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	415	3% 86% 11% •
1	B	415	3% 87% 10% •
2	C	112	6% 82% 12% 5%
2	D	112	2% 84% 11% • •

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 8574 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 Camphor 5-monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	2	0
			3225	2049	559	603	14			
1	B	403	Total	C	N	O	S	0	1	0
			3198	2025	558	601	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	58	SER	CYS	engineered mutation	UNP P00183
A	85	SER	CYS	engineered mutation	UNP P00183
A	136	SER	CYS	engineered mutation	UNP P00183
A	285	SER	CYS	engineered mutation	UNP P00183
A	334	ALA	CYS	engineered mutation	UNP P00183
A	344	CYS	LYS	engineered mutation	UNP P00183
B	58	SER	CYS	engineered mutation	UNP P00183
B	85	SER	CYS	engineered mutation	UNP P00183
B	136	SER	CYS	engineered mutation	UNP P00183
B	285	SER	CYS	engineered mutation	UNP P00183
B	334	ALA	CYS	engineered mutation	UNP P00183
B	344	CYS	LYS	engineered mutation	UNP P00183

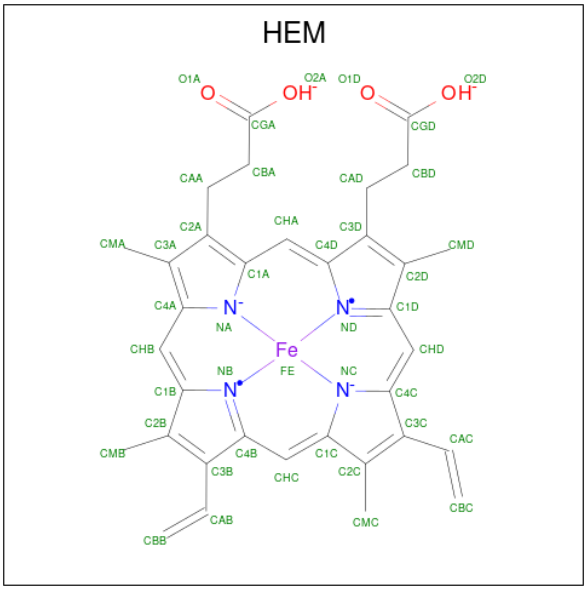
- Molecule 2 is a protein called Putidaredoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	106	Total	C	N	O	S	0	0	0
			792	487	136	160	9			
2	D	107	Total	C	N	O	S	0	0	0
			802	493	139	161	9			

There are 16 discrepancies between the modelled and reference sequences:

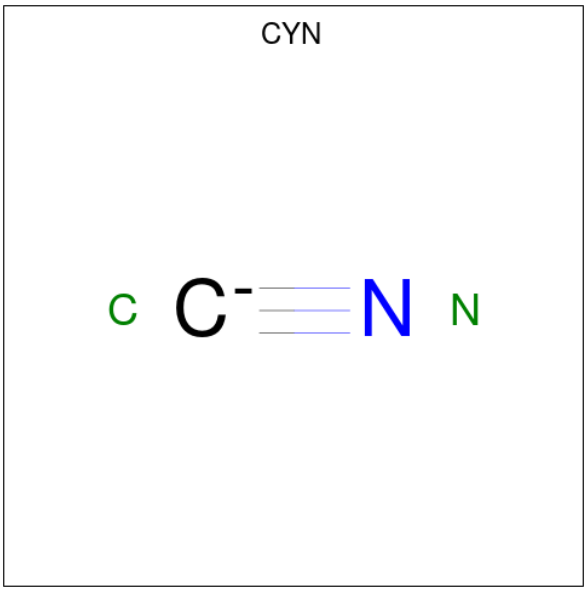
Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	HIS	-	expression tag	UNP P00259
C	-4	HIS	-	expression tag	UNP P00259
C	-3	HIS	-	expression tag	UNP P00259
C	-2	HIS	-	expression tag	UNP P00259
C	-1	HIS	-	expression tag	UNP P00259
C	0	HIS	-	expression tag	UNP P00259
C	19	CYS	ASP	engineered mutation	UNP P00259
C	73	SER	CYS	engineered mutation	UNP P00259
D	-5	HIS	-	expression tag	UNP P00259
D	-4	HIS	-	expression tag	UNP P00259
D	-3	HIS	-	expression tag	UNP P00259
D	-2	HIS	-	expression tag	UNP P00259
D	-1	HIS	-	expression tag	UNP P00259
D	0	HIS	-	expression tag	UNP P00259
D	19	CYS	ASP	engineered mutation	UNP P00259
D	73	SER	CYS	engineered mutation	UNP P00259

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



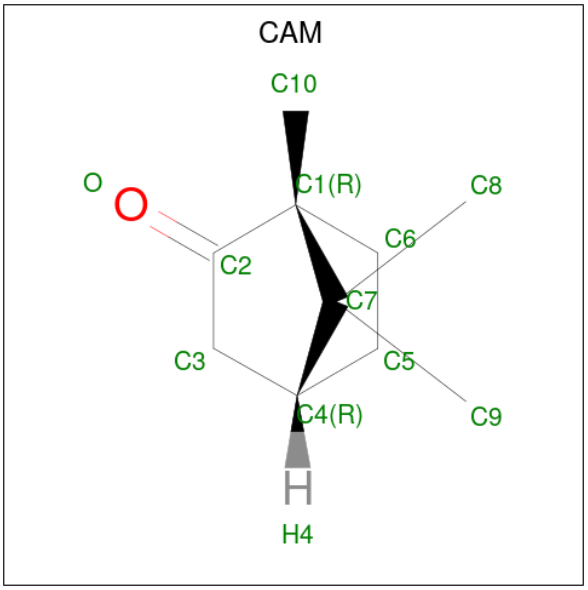
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 4 is CYANIDE ION (CCD ID: CYN) (formula: CN).



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

- Molecule 5 is CAMPHOR (CCD ID: CAM) (formula: $C_{10}H_{16}O$).

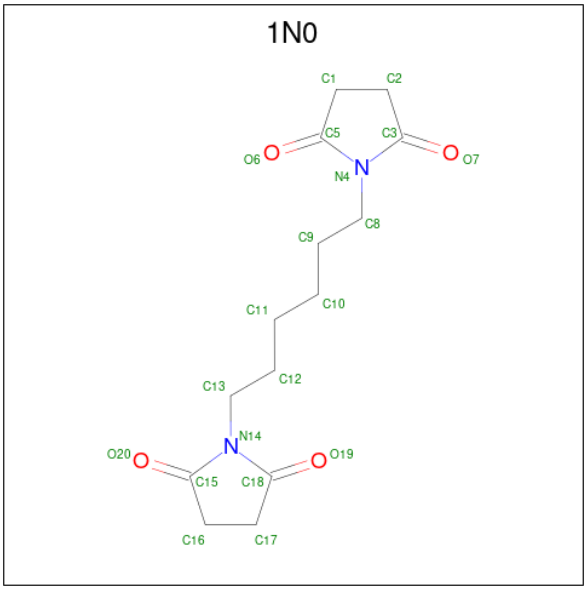


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 11 10 1	0	0
5	B	1	Total C O 11 10 1	0	0

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

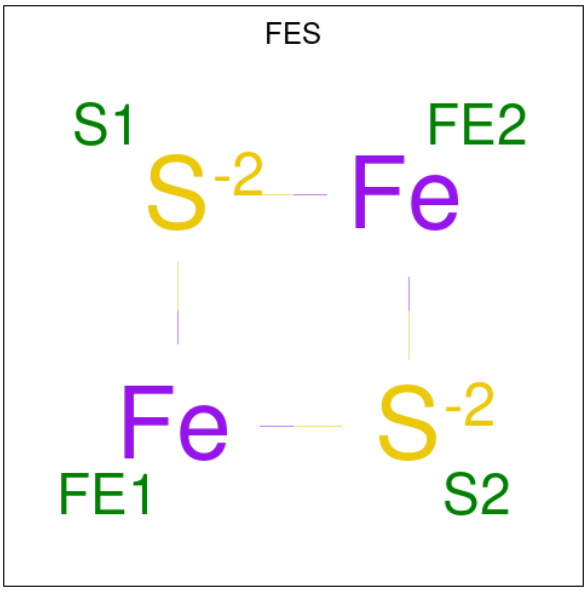
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Ca 1 1	0	0
6	B	1	Total Ca 1 1	0	0

- Molecule 7 is 1,1'-hexane-1,6-diyldipyrrolidine-2,5-dione (CCD ID: 1N0) (formula: $C_{14}H_{20}N_2O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total C N O 20 14 2 4	0	0
7	C	1	Total C N O 20 14 2 4	0	0

- Molecule 8 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	C	1	Total Fe S 4 2 2	0	0
8	D	1	Total Fe S 4 2 2	0	0

- Molecule 9 is water.

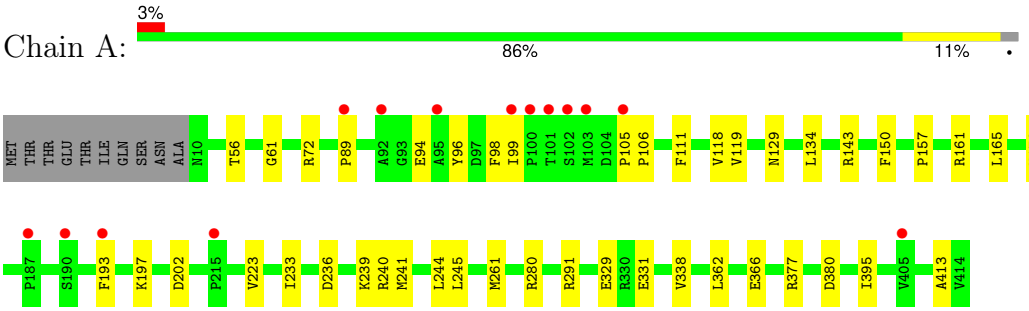
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	179	Total O 179 179	0	0
9	B	115	Total O 115 115	0	0
9	C	43	Total O 43 43	0	0
9	D	58	Total O 58 58	0	0

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.

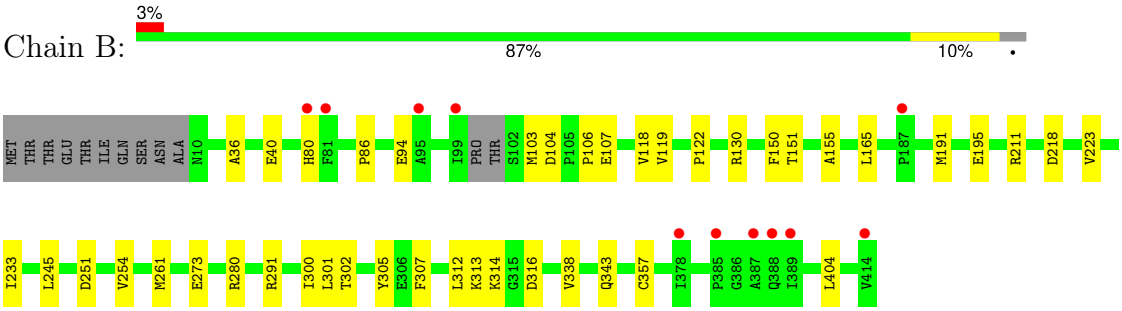
• Molecule 1: Camphor 5-monooxygenase

Chain A:



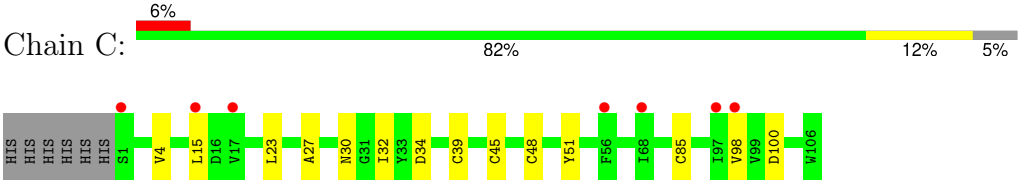
• Molecule 1: Camphor 5-monooxygenase

Chain B:



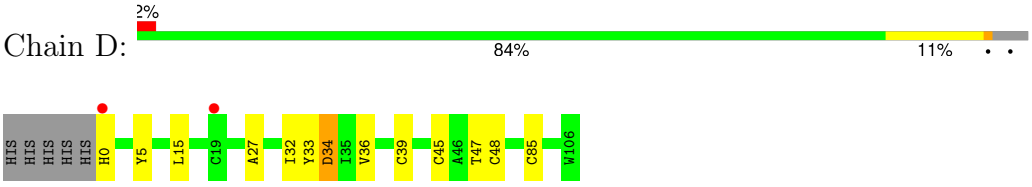
• Molecule 2: Putidaredoxin

Chain C:



• Molecule 2: Putidaredoxin

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	57.36Å 110.30Å 88.62Å 90.00° 107.67° 90.00°	Depositor
Resolution (Å)	40.60 – 2.15 40.60 – 2.15	Depositor EDS
% Data completeness (in resolution range)	96.3 (40.60-2.15) 93.1 (40.60-2.15)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.27 (at 2.16Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.195 , 0.254 0.196 , 0.255	Depositor DCC
R_{free} test set	2790 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å^2)	29.9	Xtriage
Anisotropy	0.205	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 40.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8574	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1N0, HEM, CAM, CYN, CA, FES

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	0.16	0/3315	0.36	0/4504
1	B	0.16	0/3275	0.35	0/4447
2	C	0.13	0/803	0.34	0/1090
2	D	0.15	0/814	0.36	0/1105
All	All	0.15	0/8207	0.36	0/11146

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

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	3225	0	3169	28	0
1	B	3198	0	3135	30	0
2	C	792	0	770	7	0
2	D	802	0	777	7	0
3	A	43	0	30	2	0
3	B	43	0	30	3	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	11	0	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	11	0	16	1	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	B	20	0	17	0	0
7	C	20	0	16	0	0
8	C	4	0	0	0	0
8	D	4	0	0	0	0
9	A	179	0	0	5	0
9	B	115	0	0	2	0
9	C	43	0	0	0	0
9	D	58	0	0	0	0
All	All	8574	0	7976	74	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.

All (74) 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)
3:B:501:HEM:HBC2	3:B:501:HEM:HHD	1.76	0.67
3:B:501:HEM:HHC	3:B:501:HEM:HBB2	1.76	0.67
1:A:197:LYS:NZ	9:A:605:HOH:O	2.28	0.66
1:A:380:ASP:OD2	9:A:601:HOH:O	2.14	0.65
3:A:501:HEM:HHD	3:A:501:HEM:HBC2	1.78	0.65
1:A:111[C]:PHE:HD1	1:A:241:MET:HE1	1.62	0.64
2:C:4:VAL:HB	2:C:98:VAL:HG22	1.79	0.63
1:B:103:MET:HE3	1:B:107:GLU:HB3	1.80	0.63
2:C:23:LEU:HB2	2:C:85:CYS:HB2	1.81	0.60
1:B:343:GLN:CD	1:B:343:GLN:H	2.10	0.60
3:A:501:HEM:HMB1	3:A:501:HEM:HBB2	1.85	0.58
2:D:34:ASP:OD1	2:D:34:ASP:N	2.35	0.57
2:C:39:CYS:HB3	2:C:45:CYS:HB3	1.88	0.55
1:B:130:ARG:HD2	1:B:165:LEU:HD11	1.91	0.52
2:D:39:CYS:HB3	2:D:45:CYS:HB3	1.91	0.52
1:A:129:ASN:OD1	9:A:602:HOH:O	2.18	0.52
1:B:357:CYS:HB2	3:B:501:HEM:NA	2.24	0.52
2:C:15:LEU:HD21	2:C:30:ASN:HD22	1.75	0.51
1:A:118:VAL:HG11	1:A:245:LEU:HD13	1.91	0.51
1:B:104:ASP:HB3	1:B:106:PRO:HD2	1.90	0.51
1:A:72:ARG:NH1	1:A:331:GLU:OE2	2.42	0.51
2:C:27:ALA:HA	2:C:32:ILE:HD12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ILE:HD13	1:A:244:LEU:HD22	1.93	0.50
1:B:40:GLU:OE2	1:B:291:ARG:NH2	2.44	0.50
1:A:143:ARG:NH2	1:A:413:ALA:HB2	2.26	0.50
1:A:150:PHE:CZ	1:A:261:MET:HG3	2.47	0.50
1:A:291:ARG:HG2	1:A:338:VAL:HG22	1.94	0.50
1:B:251[B]:ASP:OD1	1:B:251[B]:ASP:N	2.45	0.49
1:B:273:GLU:OE2	1:B:280:ARG:NH2	2.46	0.49
2:C:48:CYS:HB2	2:C:85:CYS:SG	2.52	0.49
2:D:27:ALA:HB1	2:D:32:ILE:HB	1.93	0.49
2:C:51:TYR:HB2	2:C:100:ASP:HB2	1.94	0.48
1:A:96:TYR:OH	1:A:240:ARG:NH1	2.46	0.48
1:B:155:ALA:O	1:B:254:VAL:HG22	2.14	0.48
1:A:157:PRO:HB3	1:A:178:LYS:NZ	2.29	0.47
1:B:80:HIS:O	1:B:302:THR:OG1	2.27	0.47
1:A:118:VAL:HG12	1:A:119:VAL:HG13	1.96	0.47
1:B:191:MET:HE2	1:B:195:GLU:HB3	1.96	0.47
1:A:184:MET:HB3	1:A:193:PHE:HE2	1.81	0.46
1:A:202:ASP:HB3	1:B:36:ALA:HB1	1.98	0.46
1:B:301:LEU:HD21	1:B:312:LEU:HD23	1.97	0.46
1:B:151:THR:HA	1:B:155:ALA:HB3	1.97	0.46
1:A:105:PRO:N	1:A:106:PRO:HD2	2.31	0.45
1:B:305:TYR:HE2	1:B:307:PHE:HD1	1.65	0.45
1:B:118:VAL:HG11	1:B:245:LEU:HD13	1.99	0.45
1:A:56:THR:O	1:A:61:GLY:HA2	2.17	0.44
1:A:223:VAL:O	1:A:233:ILE:HG21	2.18	0.44
1:A:89:PRO:HG2	1:A:94:GLU:O	2.18	0.44
1:A:362:LEU:O	1:A:366:GLU:HG3	2.17	0.44
1:A:280:ARG:HG2	9:A:673:HOH:O	2.18	0.43
2:D:36:VAL:HB	2:D:47:THR:HB	2.01	0.43
1:B:80:HIS:NE2	9:B:610:HOH:O	2.37	0.43
1:B:86:PRO:HG3	1:B:300:ILE:HB	2.01	0.43
1:A:236:ASP:HA	1:A:239:LYS:HE2	2.01	0.43
1:B:118:VAL:HG12	1:B:119:VAL:HG13	1.99	0.42
1:B:122:PRO:HG3	2:D:33:TYR:CD1	2.53	0.42
1:B:150:PHE:CZ	1:B:261:MET:HG3	2.54	0.42
1:A:89:PRO:HG3	1:A:395:ILE:HD12	2.01	0.42
1:A:134:LEU:HD21	1:A:161:ARG:HB2	2.01	0.42
1:B:313:LYS:HD2	1:B:314:LYS:O	2.19	0.42
1:A:179:TYR:O	1:A:183:GLN:HG2	2.19	0.41
1:B:313:LYS:HG3	1:B:316:ASP:CG	2.45	0.41
1:B:291:ARG:HG2	1:B:338:VAL:HG22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:301:LEU:HG	1:B:312:LEU:HB3	2.03	0.41
2:D:48:CYS:HB2	2:D:85:CYS:SG	2.61	0.41
1:B:211:ARG:NH1	1:B:218:ASP:OD2	2.52	0.41
1:A:178:LYS:NZ	9:A:623:HOH:O	2.53	0.41
1:B:150:PHE:HB2	1:B:404:LEU:HD13	2.03	0.41
1:B:191:MET:O	9:B:601:HOH:O	2.22	0.41
1:B:94:GLU:O	5:B:503:CAM:H81	2.20	0.41
1:A:98:PHE:HB2	1:A:244:LEU:HB2	2.03	0.41
2:D:5:TYR:CE2	2:D:15:LEU:HD12	2.56	0.41
1:B:223:VAL:O	1:B:233:ILE:HG21	2.21	0.40
1:A:143:ARG:HD3	1:A:377:ARG:HB3	2.03	0.40

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	406/415 (98%)	394 (97%)	12 (3%)	0	100	100
1	B	400/415 (96%)	385 (96%)	15 (4%)	0	100	100
2	C	104/112 (93%)	102 (98%)	2 (2%)	0	100	100
2	D	105/112 (94%)	103 (98%)	2 (2%)	0	100	100
All	All	1015/1054 (96%)	984 (97%)	31 (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	352/358 (98%)	350 (99%)	2 (1%)	78 84
1	B	348/358 (97%)	348 (100%)	0	100 100
2	C	89/95 (94%)	88 (99%)	1 (1%)	65 72
2	D	90/95 (95%)	88 (98%)	2 (2%)	45 51
All	All	879/906 (97%)	874 (99%)	5 (1%)	78 84

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	165	LEU
1	A	329	GLU
2	C	34	ASP
2	D	0	HIS
2	D	34	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	33	ASN
1	B	49	ASN
1	B	213	GLN
1	B	390	GLN
2	C	25	GLN
2	C	30	ASN
2	D	0	HIS
2	D	30	ASN

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)

Of 12 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
3	HEM	A	501	1	50,50,50	1.60	9 (18%)	67,82,82	1.69	16 (23%)
7	1N0	C	202	2,1	21,21,21	1.36	3 (14%)	28,28,28	2.51	10 (35%)
7	1N0	B	505	1	21,21,21	1.40	4 (19%)	28,28,28	2.50	10 (35%)
8	FES	C	201	2	0,4,4	-	-	-		
4	CYN	A	502	-	1,1,1	0.32	0	-		
4	CYN	B	502	-	1,1,1	0.25	0	-		
3	HEM	B	501	1	50,50,50	1.66	6 (12%)	67,82,82	1.81	16 (23%)
5	CAM	A	503	-	12,12,12	3.92	3 (25%)	20,21,21	0.86	1 (5%)
5	CAM	B	503	-	12,12,12	3.96	4 (33%)	20,21,21	0.88	0
8	FES	D	201	2	0,4,4	-	-	-		

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	HEM	A	501	1	-	2/14/54/54	-
7	1N0	C	202	2,1	-	3/9/35/35	0/2/2/2
7	1N0	B	505	1	-	1/9/35/35	0/2/2/2
8	FES	C	201	2	-	-	0/1/1/1
3	HEM	B	501	1	-	2/14/54/54	-
5	CAM	A	503	-	-	-	0/3/2/2
5	CAM	B	503	-	-	-	0/3/2/2
8	FES	D	201	2	-	-	0/1/1/1

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	503	CAM	O-C2	12.46	1.40	1.21
5	A	503	CAM	O-C2	12.20	1.40	1.21
3	B	501	HEM	FE-NB	5.21	2.10	1.94
3	B	501	HEM	FE-ND	4.76	2.09	1.94
3	A	501	HEM	FE-ND	4.66	2.09	1.94
3	A	501	HEM	FE-NC	4.39	2.09	1.95
3	A	501	HEM	FE-NA	4.15	2.08	1.95
3	B	501	HEM	FE-NA	4.15	2.08	1.95
7	B	505	1N0	C15-N14	-3.67	1.33	1.38
7	C	202	1N0	C15-N14	-3.63	1.33	1.38
5	A	503	CAM	C1-C2	-3.29	1.48	1.52
3	B	501	HEM	FE-NC	3.24	2.05	1.95
3	A	501	HEM	CAB-C3B	3.21	1.55	1.47
7	C	202	1N0	C17-C16	-3.02	1.45	1.52
3	B	501	HEM	CAC-C3C	3.00	1.55	1.47
3	B	501	HEM	CAB-C3B	2.99	1.55	1.47
7	B	505	1N0	C17-C16	-2.95	1.45	1.52
3	A	501	HEM	CAC-C3C	2.92	1.55	1.47
3	A	501	HEM	FE-NB	2.83	2.03	1.94
5	B	503	CAM	C1-C2	-2.77	1.49	1.52
5	B	503	CAM	C7-C1	-2.29	1.50	1.56
3	A	501	HEM	CMC-C2C	2.23	1.55	1.50
3	A	501	HEM	CMD-C2D	2.15	1.55	1.50
5	A	503	CAM	C7-C1	-2.12	1.50	1.56
7	B	505	1N0	C3-N4	-2.12	1.35	1.38
3	A	501	HEM	CMB-C2B	2.11	1.55	1.50
5	B	503	CAM	C3-C4	-2.07	1.48	1.53
7	B	505	1N0	C1-C2	-2.05	1.47	1.52
7	C	202	1N0	C1-C2	-2.05	1.47	1.52

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	B	505	1N0	C5-N4-C3	8.10	116.48	112.94
7	C	202	1N0	C5-N4-C3	8.00	116.43	112.94
7	B	505	1N0	C18-N14-C15	7.40	116.17	112.94
7	C	202	1N0	C18-N14-C15	7.14	116.05	112.94
3	B	501	HEM	C3B-C4B-NB	-4.70	106.09	109.47
3	B	501	HEM	C3B-C2B-C1B	3.82	109.28	106.41
3	A	501	HEM	C4D-ND-C1D	3.76	109.66	105.21
3	B	501	HEM	C1B-NB-C4B	3.72	109.61	105.21
3	A	501	HEM	CHD-C1D-ND	3.64	128.34	124.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	501	HEM	C2A-C1A-NA	-3.43	106.34	110.15
3	B	501	HEM	C4D-ND-C1D	3.41	109.25	105.21
3	A	501	HEM	C3D-C4D-ND	-3.41	106.43	110.17
3	A	501	HEM	C2D-C1D-ND	-3.32	106.07	109.90
3	B	501	HEM	CHC-C1C-NC	3.24	127.98	124.45
3	B	501	HEM	C3D-C4D-ND	-3.11	106.76	110.17
7	B	505	1N0	O19-C18-N14	3.01	127.17	123.94
3	A	501	HEM	CHC-C4B-NB	3.00	127.65	124.42
7	C	202	1N0	O20-C15-N14	2.97	127.13	123.94
7	C	202	1N0	O7-C3-N4	2.93	127.08	123.94
3	A	501	HEM	CHC-C1C-NC	2.92	127.63	124.45
3	B	501	HEM	C2D-C1D-ND	-2.85	106.61	109.90
3	A	501	HEM	CHA-C4D-ND	2.84	127.88	124.37
3	A	501	HEM	C3B-C2B-C1B	2.83	108.54	106.41
7	C	202	1N0	O6-C5-N4	2.82	126.97	123.94
7	C	202	1N0	O19-C18-N14	2.81	126.95	123.94
3	B	501	HEM	C2A-C1A-NA	-2.78	107.06	110.15
3	B	501	HEM	C2B-C1B-NB	-2.75	106.68	109.84
3	B	501	HEM	CHB-C1B-NB	2.71	127.72	124.37
3	B	501	HEM	CHA-C4D-ND	2.60	127.59	124.37
7	B	505	1N0	O20-C15-N14	2.60	126.73	123.94
7	B	505	1N0	O6-C5-N4	2.58	126.71	123.94
3	A	501	HEM	C1B-NB-C4B	2.56	108.23	105.21
3	B	501	HEM	CHB-C4A-NA	2.54	128.46	123.86
3	B	501	HEM	C3C-C2C-C1C	2.53	109.44	107.05
3	B	501	HEM	CHD-C1D-ND	2.53	127.14	124.42
7	C	202	1N0	C2-C3-N4	-2.51	105.85	108.03
7	B	505	1N0	C16-C15-N14	-2.38	105.96	108.03
7	B	505	1N0	C17-C18-N14	-2.35	105.98	108.03
7	C	202	1N0	C16-C15-N14	-2.33	106.00	108.03
7	C	202	1N0	C1-C5-N4	-2.31	106.03	108.03
7	B	505	1N0	O7-C3-N4	2.27	126.38	123.94
7	B	505	1N0	C1-C5-N4	-2.26	106.07	108.03
7	C	202	1N0	C17-C18-N14	-2.25	106.08	108.03
3	A	501	HEM	C3A-C4A-NA	-2.20	106.61	110.14
3	A	501	HEM	CHD-C4C-C3C	2.18	128.88	125.21
3	A	501	HEM	C2B-C1B-NB	-2.17	107.35	109.84
3	A	501	HEM	C4A-NA-C1A	2.15	109.33	105.82
3	B	501	HEM	C4C-NC-C1C	2.15	109.33	105.82
7	B	505	1N0	C2-C3-N4	-2.14	106.17	108.03
3	A	501	HEM	CBA-CAA-C2A	-2.11	106.69	112.53
3	A	501	HEM	CHA-C1A-NA	2.10	127.67	123.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	501	HEM	CAB-C3B-C2B	-2.09	121.63	128.43
5	A	503	CAM	C5-C4-C7	-2.02	99.00	102.83

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	202	1N0	N4-C8-C9-C10
7	B	505	1N0	C9-C10-C11-C12
7	C	202	1N0	C9-C10-C11-C12
7	C	202	1N0	C10-C11-C12-C13
3	A	501	HEM	C4C-C3C-CAC-CBC
3	B	501	HEM	C4B-C3B-CAB-CBB
3	B	501	HEM	C4C-C3C-CAC-CBC
3	A	501	HEM	CAD-CBD-CGD-O2D

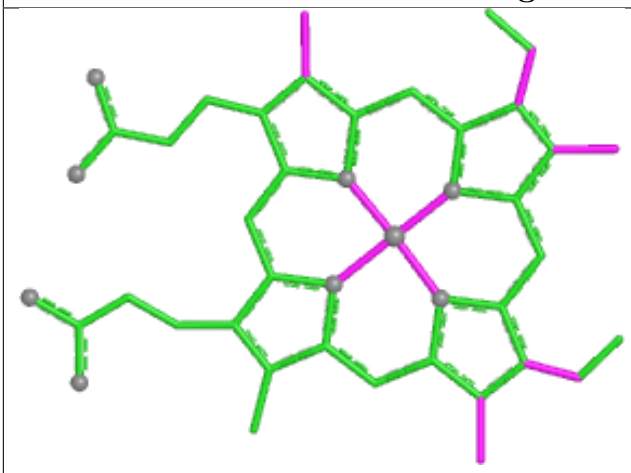
There are no ring outliers.

3 monomers are involved in 6 short contacts:

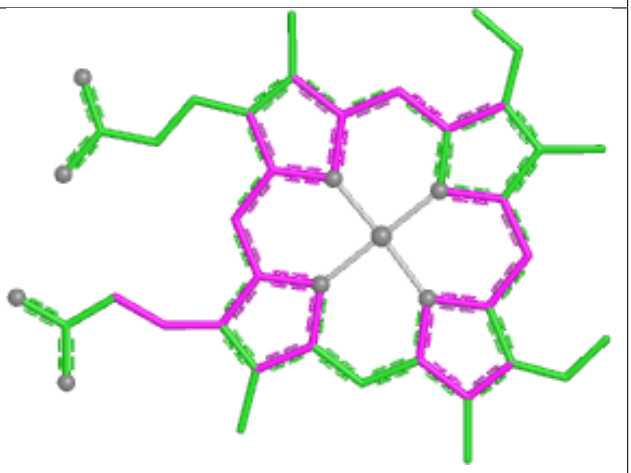
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	HEM	2	0
3	B	501	HEM	3	0
5	B	503	CAM	1	0

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 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.

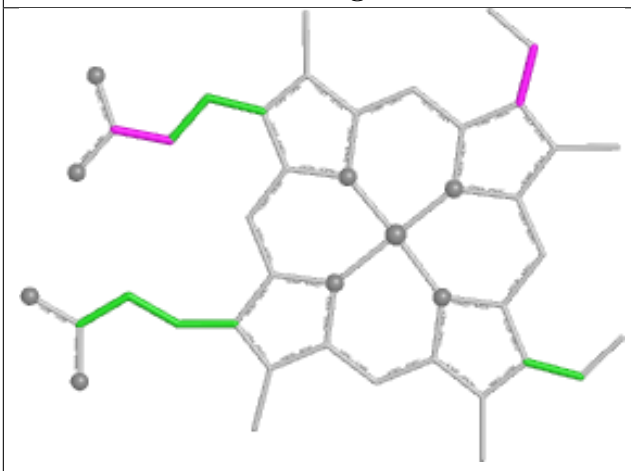
Ligand HEM A 501



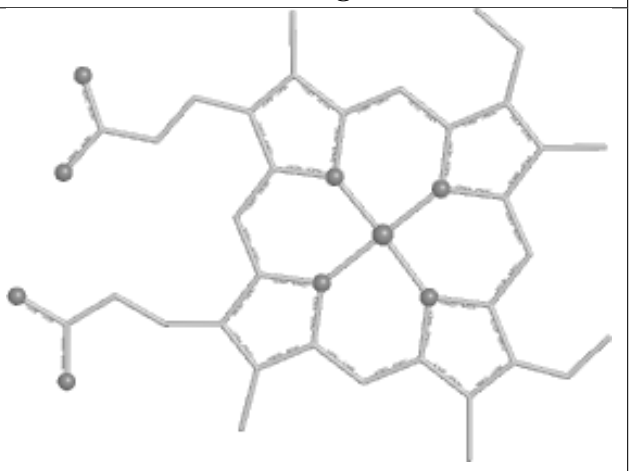
Bond lengths



Bond angles

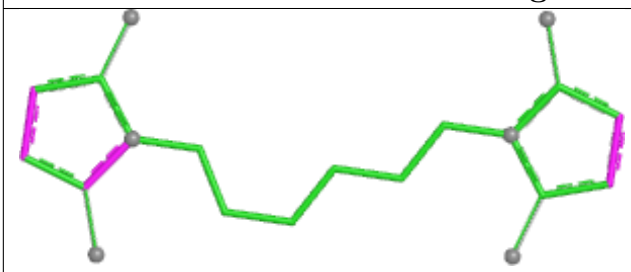


Torsions

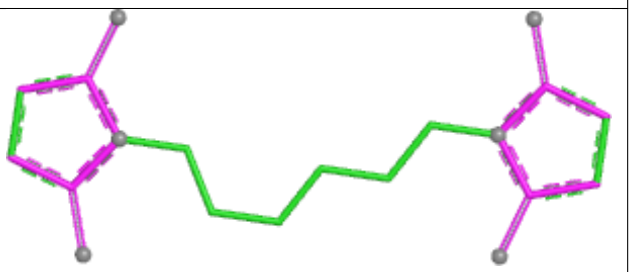


Rings

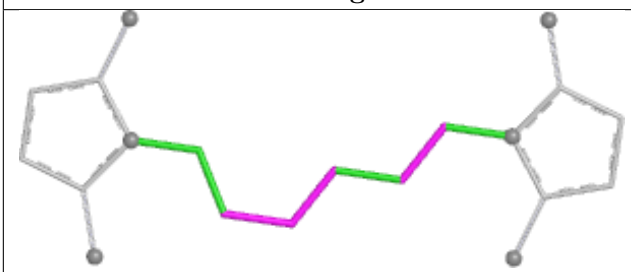
Ligand 1N0 C 202



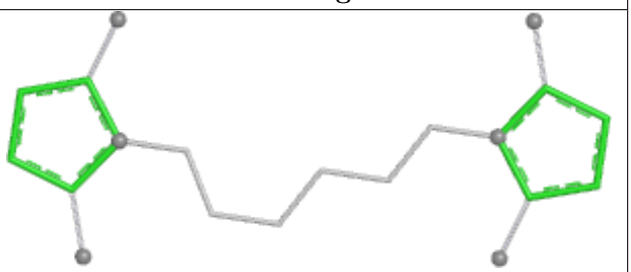
Bond lengths



Bond angles

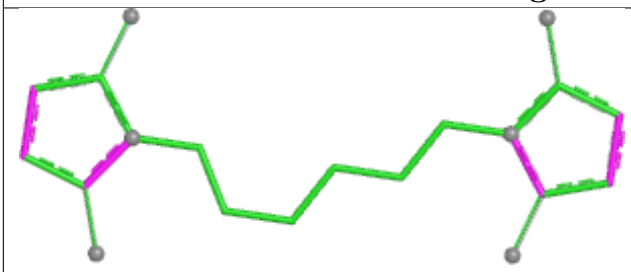


Torsions

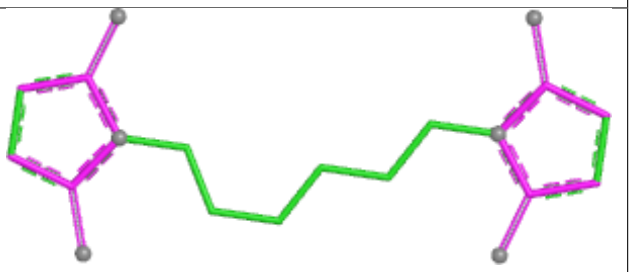


Rings

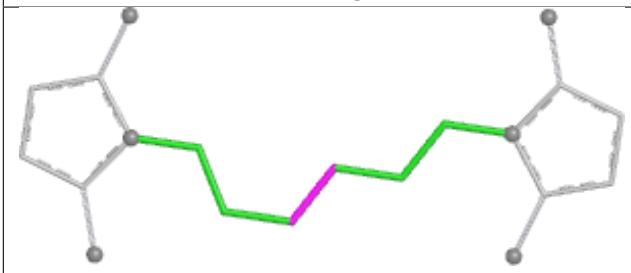
Ligand 1N0 B 505



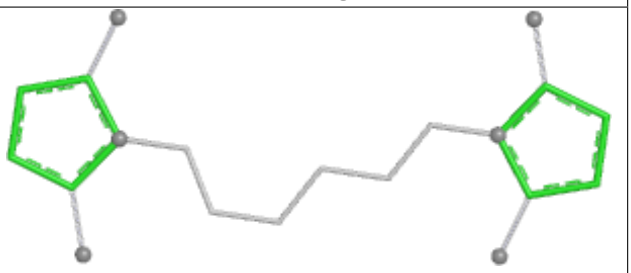
Bond lengths



Bond angles

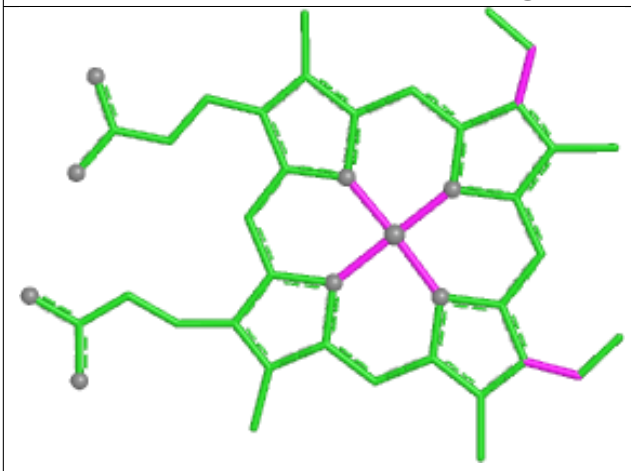


Torsions

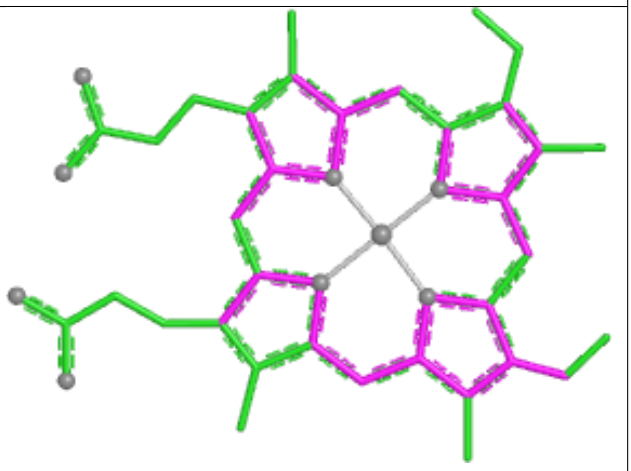


Rings

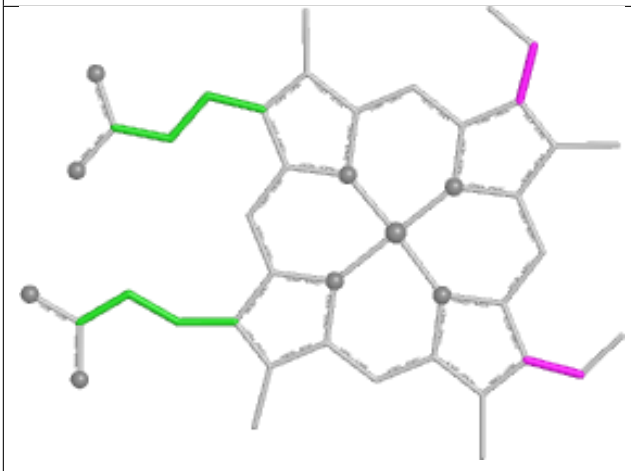
Ligand HEM B 501



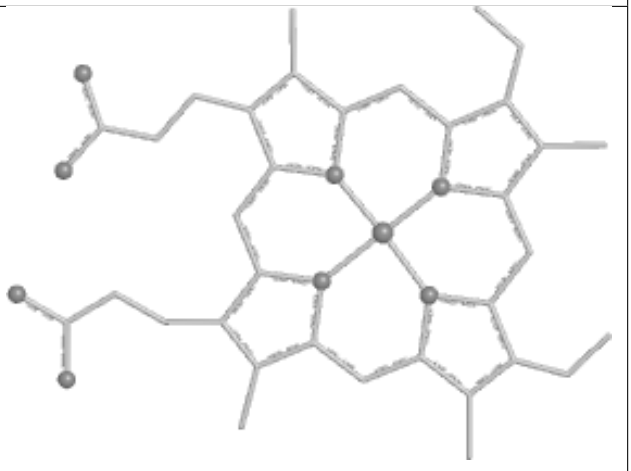
Bond lengths



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

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	405/415 (97%)	0.17	14 (3%) 47 51	13, 33, 69, 99	2 (0%)
1	B	403/415 (97%)	0.34	11 (2%) 56 60	21, 40, 65, 80	1 (0%)
2	C	106/112 (94%)	0.65	7 (6%) 24 27	22, 44, 68, 78	0
2	D	107/112 (95%)	0.08	2 (1%) 66 70	24, 34, 50, 65	0
All	All	1021/1054 (96%)	0.28	34 (3%) 49 53	13, 37, 67, 99	3 (0%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	103	MET	4.4
1	B	414	VAL	4.2
1	A	102	SER	4.1
1	A	99	ILE	3.7
1	B	99	ILE	3.6
1	A	101	THR	3.5
1	A	193	PHE	3.3
1	B	387	ALA	2.9
2	C	17	VAL	2.8
1	B	385	PRO	2.8
1	B	81	PHE	2.7
1	A	215	PRO	2.7
1	A	89	PRO	2.6
2	C	1	SER	2.6
1	B	80	HIS	2.5
1	B	388	GLN	2.5
1	A	105	PRO	2.5
2	C	98	VAL	2.4
1	A	100	PRO	2.4
2	C	56	PHE	2.4
2	D	19	CYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	187	PRO	2.3
1	B	389	ILE	2.3
1	A	405	VAL	2.2
2	C	68	ILE	2.2
1	B	378	ILE	2.2
1	B	187	PRO	2.1
2	D	0	HIS	2.1
1	B	95	ALA	2.1
1	A	190	SER	2.1
2	C	97	ILE	2.1
2	C	15	LEU	2.0
1	A	92	ALA	2.0
1	A	95	ALA	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 oligosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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
7	1N0	B	505	20/20	0.55	0.19	70,79,91,93	0
7	1N0	C	202	20/20	0.59	0.18	69,86,89,93	0
5	CAM	A	503	11/11	0.61	0.21	48,62,67,71	0
5	CAM	B	503	11/11	0.63	0.25	54,69,75,76	0
4	CYN	B	502	2/2	0.95	0.07	34,34,34,36	0
6	CA	A	504	1/1	0.95	0.07	56,56,56,56	0
3	HEM	B	501	43/43	0.96	0.09	21,29,39,47	0
4	CYN	A	502	2/2	0.97	0.09	18,18,18,24	0
3	HEM	A	501	43/43	0.98	0.08	15,22,32,44	0
6	CA	B	504	1/1	0.98	0.17	16,16,16,16	1

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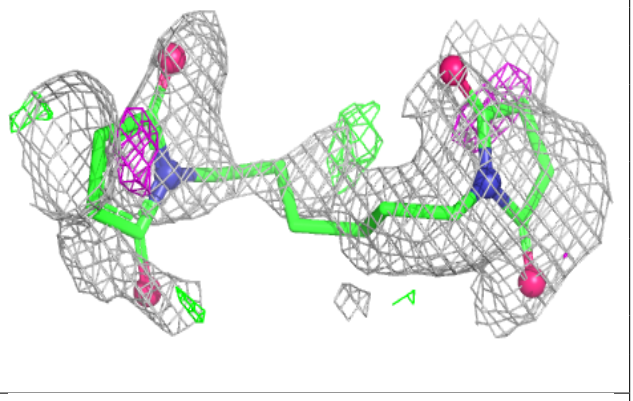
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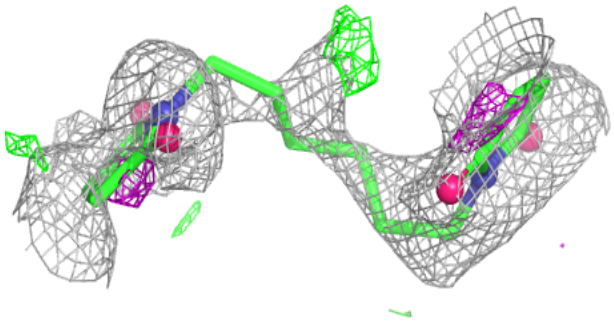
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
8	FES	C	201	4/4	0.99	0.04	24,24,29,30	0
8	FES	D	201	4/4	0.99	0.04	23,24,24,30	0

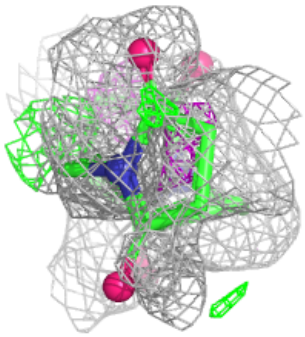
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 1N0 B 505:

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

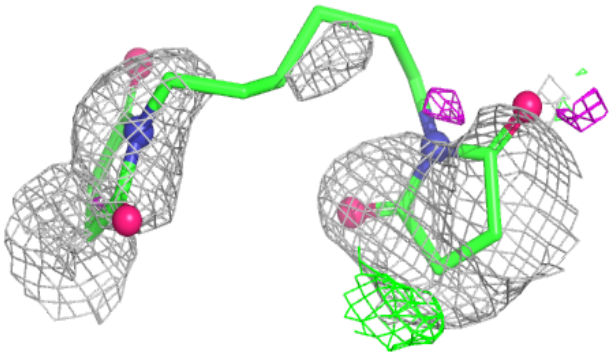


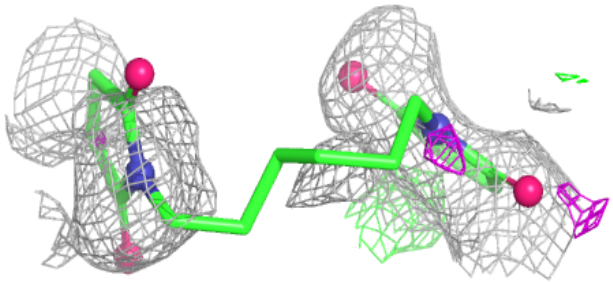


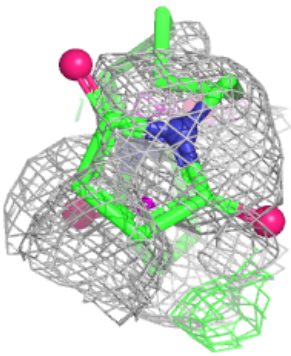


Electron density around 1N0 C 202:

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

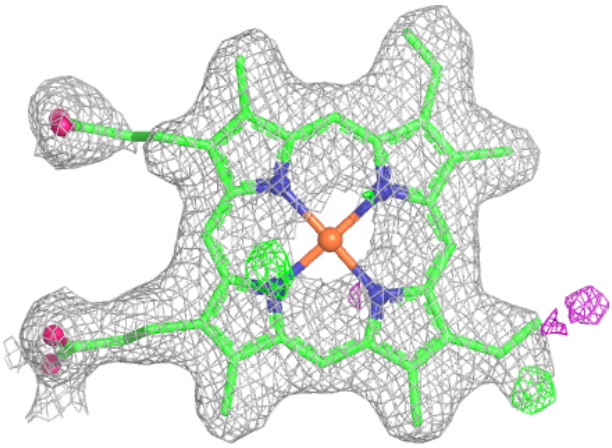


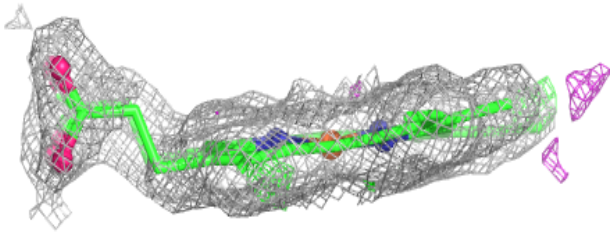




Electron density around HEM B 501:

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

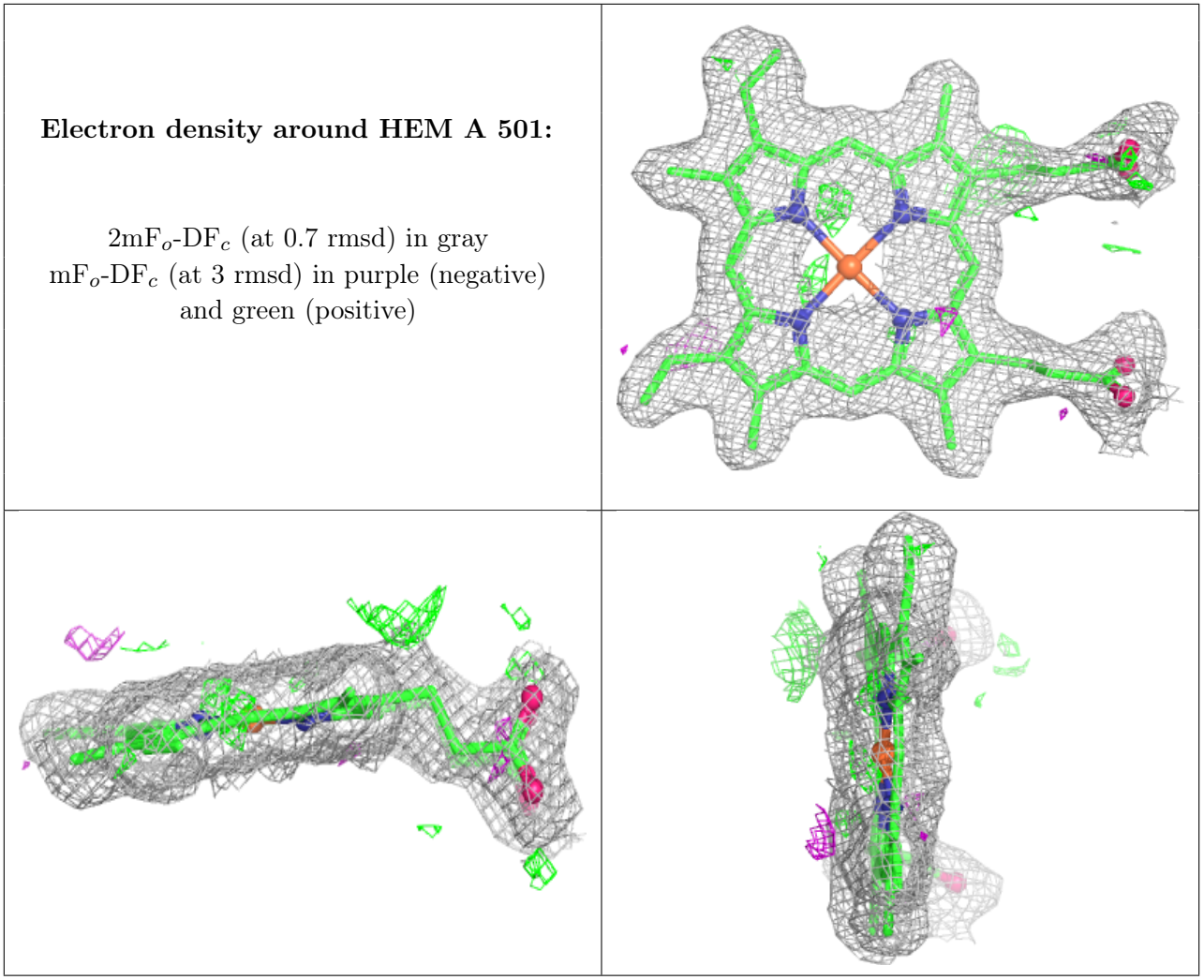






Electron density around HEM A 501:

$2mF_o$-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

There are no such residues in this entry.