Full wwPDB X-ray Structure Validation Report (i)

May 16, 2020 – 05:45 pm BST

PDB ID	:	2VE4
Title	:	Substrate free cyanobacterial CYP120A1
Authors	:	Kuhnel, K.; Ke, N.; Sligar, S.G.; Schuler, M.A.; Schlichting, I.
Deposited on	:	2007-10-16
Resolution	:	2.40 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 following versions of software and data (see references (i)) were used in the production of this report:

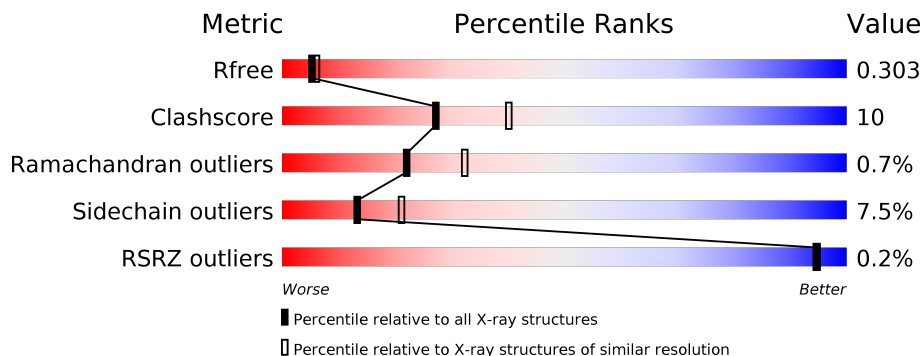|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.40 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	Percentile Ranks	Value
Rfree		0.303
Clashscore		10
Ramachandran outliers		0.7%
Sidechain outliers		7.5%
RSRZ outliers		0.2%

Worse — *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 on 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	444	72% · · · 22% · ·
1	B	444	71% · · · 24% · ·

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7144 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 PUTATIVE CYTOCHROME P450 120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	0	0
			3443	2231	590	613	9			
1	B	432	Total	C	N	O	S	0	0	0
			3454	2236	594	615	9			

- 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	77	Total 77	O 77	0	0
3	B	84	Total 84	O 84	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: PUTATIVE CYTOCHROME P450 120
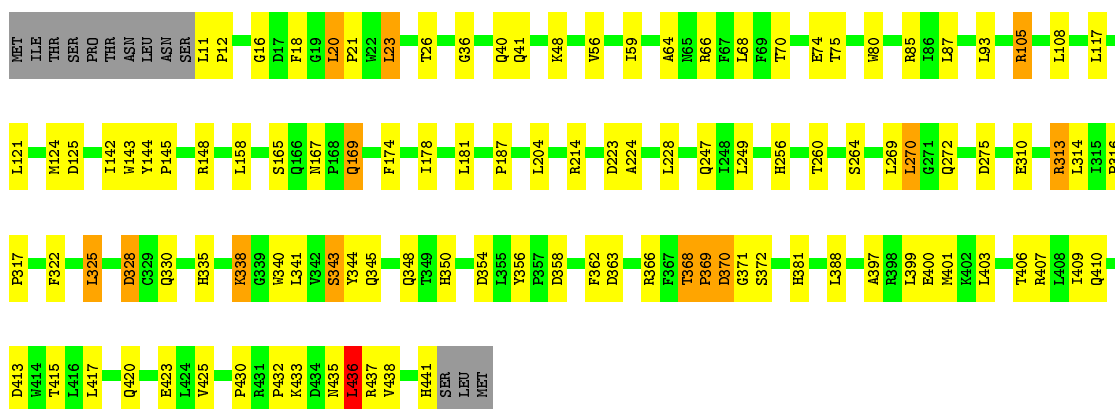
• Molecule 1: PUTATIVE CYTOCHROME P450 120
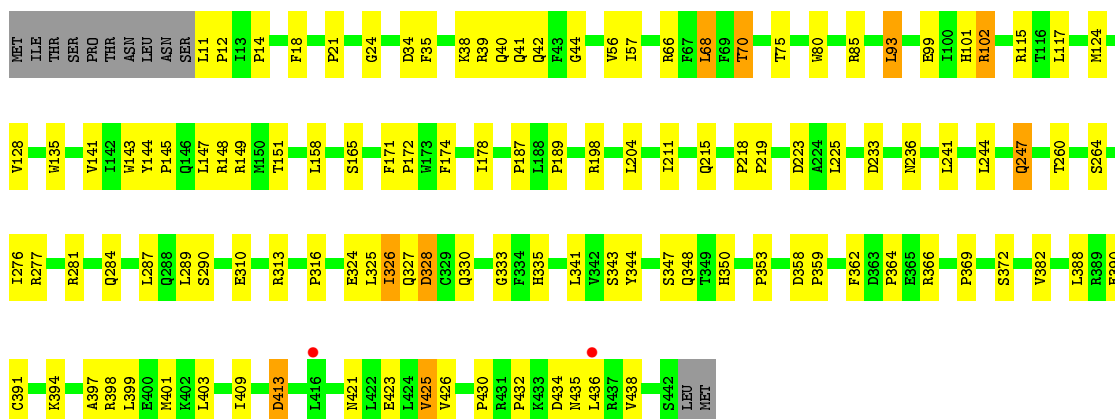
4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	153.64Å 122.17Å 64.92Å 90.00° 115.00° 90.00°	Depositor
Resolution (Å)	19.61 – 2.40 19.62 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.5 (19.61-2.40) 98.8 (19.62-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.72 (at 2.41Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.230 , 0.304 0.230 , 0.303	Depositor DCC
R_{free} test set	2093 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	49.8	Xtriage
Anisotropy	0.629	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 27.8	EDS
L-test for twinning[2]	$<|L|> = 0.49, <L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.480 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7144	wwPDB-VP
Average B, all atoms (Å^2)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.10% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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	0.57	0/3537	0.66	1/4807 (0.0%)
1	B	0.56	0/3548	0.68	0/4821
All	All	0.57	0/7085	0.67	1/9628 (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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	325	LEU	CA-CB-CG	5.15	127.14	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	437	ARG	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	3443	0	3425	82	0
1	B	3454	0	3439	57	0
2	A	43	0	30	4	0
2	B	43	0	30	0	0
3	A	77	0	0	1	0
3	B	84	0	0	0	0
All	All	7144	0	6924	140	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 10.

All (140) 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:B:99:GLU:HG2	1:B:102:ARG:HH21	1.10	1.16
1:A:345:GLN:HG3	1:A:348:GLN:HB2	1.50	0.92
1:B:99:GLU:HG2	1:B:102:ARG:NH2	1.84	0.92
1:A:407:ARG:HH11	1:A:410:GLN:HE22	1.16	0.92
1:A:345:GLN:HG3	1:A:348:GLN:CB	2.05	0.86
1:A:363:ASP:O	1:A:366:ARG:HG3	1.81	0.81
1:B:328:ASP:OD1	1:B:335:HIS:HE1	1.64	0.80
1:B:93:LEU:HD22	1:B:101:HIS:CD2	2.18	0.78
1:A:124:MET:CE	1:A:400:GLU:HA	2.15	0.77
1:A:93:LEU:H	1:A:247:GLN:HE22	1.33	0.76
1:A:124:MET:HE1	1:A:400:GLU:HA	1.68	0.76
1:A:59:ILE:HD12	1:A:64:ALA:HB1	1.67	0.76
1:A:80:TRP:O	1:A:85:ARG:NH1	2.19	0.74
1:A:423:GLU:HB2	3:A:2071:HOH:O	1.88	0.71
1:B:99:GLU:CG	1:B:102:ARG:HH21	1.96	0.71
1:B:284:GLN:O	1:B:289:LEU:HD22	1.91	0.70
1:A:397:ALA:O	1:A:401:MET:HG3	1.92	0.70
1:B:75:THR:O	1:B:326:ILE:HG13	1.91	0.69
1:A:345:GLN:CG	1:A:348:GLN:HB2	2.21	0.69
1:A:328:ASP:OD1	1:A:335:HIS:CE1	2.47	0.67
1:B:328:ASP:OD1	1:B:335:HIS:CE1	2.46	0.67
1:A:328:ASP:OD1	1:A:335:HIS:HE1	1.80	0.64
1:A:187:PRO:HB2	1:B:21:PRO:HG2	1.79	0.63
1:B:189:PRO:O	1:B:198:ARG:NH2	2.31	0.63
1:A:56:VAL:HG22	1:A:341:LEU:HB2	1.81	0.63
1:B:241:LEU:HA	1:B:244:LEU:HD12	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:124:MET:HE2	1:B:403:LEU:HD22	1.80	0.62
1:A:124:MET:HE1	1:A:400:GLU:CA	2.30	0.61
1:B:66:ARG:O	1:B:70:THR:OG1	2.18	0.61
1:A:415:THR:OG1	1:A:441:HIS:HE1	1.84	0.60
1:A:417:LEU:H	1:A:420:GLN:HE21	1.50	0.60
1:B:144:TYR:HB3	1:B:145:PRO:HD3	1.82	0.60
1:A:144:TYR:HB3	1:A:145:PRO:HD3	1.82	0.59
1:A:313:ARG:HG3	1:A:314:LEU:N	2.17	0.59
1:A:93:LEU:N	1:A:247:GLN:HE22	2.00	0.59
1:A:142:ILE:H	1:A:142:ILE:HD12	1.65	0.59
1:A:121:LEU:HD22	1:A:403:LEU:HD13	1.85	0.59
1:A:16:GLY:O	1:A:48:LYS:HE2	2.03	0.59
1:A:66:ARG:O	1:A:70:THR:HB	2.03	0.58
1:A:144:TYR:HB3	1:A:435:ASN:HB2	1.85	0.58
1:B:93:LEU:HD22	1:B:101:HIS:HD2	1.64	0.57
1:B:281:ARG:NH1	1:B:409:ILE:O	2.37	0.57
1:B:247:GLN:HA	1:B:247:GLN:HE21	1.69	0.57
1:A:345:GLN:HG3	1:A:348:GLN:HB3	1.87	0.56
1:A:407:ARG:HH11	1:A:410:GLN:NE2	1.95	0.55
1:A:66:ARG:O	1:A:70:THR:CB	2.54	0.55
2:A:1442:HEM:HHC	2:A:1442:HEM:HBB2	1.88	0.55
1:A:174:PHE:CE2	1:A:178:ILE:HD11	2.42	0.55
1:A:432:PRO:HG3	1:A:436:LEU:HD23	1.89	0.55
1:A:68:LEU:CD1	1:A:344:TYR:HB3	2.36	0.55
1:A:108:LEU:HD23	1:A:228:LEU:HD21	1.89	0.55
1:B:432:PRO:HG3	1:B:436:LEU:HG	1.89	0.54
1:A:425:VAL:O	1:A:430:PRO:HA	2.07	0.54
1:B:145:PRO:HD3	1:B:435:ASN:HB3	1.91	0.53
1:B:80:TRP:O	1:B:85:ARG:NH1	2.42	0.53
1:B:171:PHE:HB3	1:B:172:PRO:HD3	1.91	0.53
1:B:426:VAL:HG13	1:B:430:PRO:HD3	1.90	0.53
1:A:313:ARG:HA	1:A:350:HIS:HD1	1.74	0.52
1:B:330:GLN:HE21	1:B:333:GLY:HA2	1.74	0.52
1:B:135:TRP:CD1	1:B:141:VAL:HG11	2.46	0.51
1:A:124:MET:HE3	1:A:400:GLU:HA	1.92	0.51
1:A:310:GLU:HG3	1:A:362:PHE:CD1	2.46	0.51
1:B:397:ALA:O	1:B:401:MET:HG3	2.11	0.51
1:A:214:ARG:NH2	1:A:223:ASP:OD2	2.45	0.50
1:B:324:GLU:HG3	1:B:341:LEU:HD23	1.92	0.50
1:A:224:ALA:O	1:A:228:LEU:HG	2.11	0.50
1:B:277:ARG:NH1	1:B:413:ASP:OD2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:LEU:CD2	1:A:228:LEU:HD21	2.41	0.50
1:B:40:GLN:HG2	1:B:44:GLY:O	2.11	0.49
1:A:214:ARG:HH22	1:A:223:ASP:CG	2.16	0.49
1:B:211:ILE:O	1:B:215:GLN:HG3	2.13	0.49
1:B:316:PRO:HG2	1:B:347:SER:HB3	1.95	0.48
1:A:144:TYR:CB	1:A:435:ASN:HB2	2.43	0.48
1:A:87:LEU:HB2	1:A:181:LEU:HD23	1.96	0.48
1:A:425:VAL:HG22	1:A:433:LYS:HG2	1.96	0.48
1:B:425:VAL:O	1:B:430:PRO:HA	2.12	0.48
1:A:174:PHE:O	1:A:178:ILE:HG13	2.13	0.48
1:A:269:LEU:HD23	1:A:272:GLN:HE21	1.77	0.48
1:B:40:GLN:C	1:B:42:GLN:H	2.18	0.47
1:B:148:ARG:HG3	1:B:260:THR:HG21	1.97	0.47
1:A:36:GLY:O	1:A:40:GLN:HB2	2.14	0.47
1:B:117:LEU:HB3	1:B:399:LEU:HD22	1.96	0.47
1:B:313:ARG:O	1:B:350:HIS:HB3	2.15	0.47
1:A:322:PHE:CE2	1:A:343:SER:HB2	2.50	0.47
1:A:270:LEU:HD12	1:A:409:ILE:HD11	1.96	0.47
1:B:34:ASP:O	1:B:38:LYS:HD2	2.14	0.47
1:A:310:GLU:OE1	1:A:313:ARG:HG2	2.15	0.47
1:A:310:GLU:HG3	1:A:362:PHE:CE1	2.51	0.46
1:A:21:PRO:HG2	1:B:187:PRO:HB2	1.97	0.46
1:B:14:PRO:HG2	1:B:57:ILE:HG12	1.97	0.46
1:A:316:PRO:HA	1:A:317:PRO:HD3	1.71	0.46
1:B:68:LEU:HD12	1:B:344:TYR:CD1	2.51	0.46
1:B:35:PHE:O	1:B:39:ARG:HD2	2.16	0.46
1:B:421:ASN:OD1	1:B:423:GLU:HB2	2.16	0.46
1:A:415:THR:OG1	1:A:441:HIS:CE1	2.68	0.45
1:A:407:ARG:NH1	1:A:410:GLN:HE22	1.99	0.45
1:A:368:THR:O	1:A:370:ASP:N	2.49	0.45
1:A:417:LEU:H	1:A:420:GLN:NE2	2.12	0.45
1:A:18:PHE:HZ	1:A:340:TRP:CH2	2.35	0.45
1:A:313:ARG:HB3	1:A:381:HIS:CE1	2.52	0.45
1:B:353:PRO:HA	1:B:359:PRO:HG3	1.98	0.45
1:B:56:VAL:HG22	1:B:341:LEU:HB2	1.99	0.44
1:A:158:LEU:O	1:A:223:ASP:HB2	2.16	0.44
1:A:249:LEU:HD23	1:A:249:LEU:HA	1.87	0.44
1:A:344:TYR:OH	2:A:1442:HEM:O1A	2.25	0.44
1:B:11:LEU:HB3	1:B:12:PRO:HD3	2.00	0.44
1:B:158:LEU:O	1:B:223:ASP:HB2	2.18	0.43
1:A:406:THR:O	1:A:410:GLN:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:LEU:O	1:B:151:THR:HG23	2.19	0.43
1:A:275:ASP:OD1	1:A:275:ASP:N	2.51	0.43
1:B:174:PHE:O	1:B:178:ILE:HG12	2.18	0.43
1:B:218:PRO:HA	1:B:219:PRO:HD3	1.88	0.43
1:A:148:ARG:HG3	1:A:260:THR:HG21	2.01	0.43
1:B:310:GLU:HG3	1:B:362:PHE:CD1	2.54	0.43
1:B:276:ILE:HD13	1:B:364:PRO:HG2	2.02	0.42
1:A:313:ARG:HA	1:A:350:HIS:ND1	2.33	0.42
1:B:233:ASP:O	1:B:236:ASN:N	2.47	0.42
1:B:394:LYS:O	1:B:398:ARG:HG3	2.18	0.42
1:A:117:LEU:HB3	1:A:399:LEU:HD22	2.01	0.42
1:A:11:LEU:CB	1:A:12:PRO:HD3	2.49	0.42
1:A:11:LEU:HB2	1:A:12:PRO:HD3	2.02	0.42
1:A:124:MET:HE1	1:A:400:GLU:N	2.35	0.42
2:A:1442:HEM:HBC2	2:A:1442:HEM:HMC2	2.02	0.42
1:A:167:ASN:OD1	1:A:169:GLN:OE1	2.38	0.42
1:A:356:TYR:HB3	1:A:366:ARG:NH2	2.35	0.41
1:A:368:THR:HG22	1:A:369:PRO:HD2	2.02	0.41
1:A:66:ARG:O	1:A:70:THR:OG1	2.31	0.41
2:A:1442:HEM:HBC2	2:A:1442:HEM:CMC	2.51	0.41
1:A:310:GLU:OE1	1:A:310:GLU:HA	2.20	0.41
1:A:20:LEU:H	1:A:20:LEU:HG	1.62	0.41
1:A:121:LEU:O	1:A:125:ASP:HB2	2.20	0.41
1:B:390:GLU:O	1:B:391:CYS:C	2.59	0.41
1:A:93:LEU:HD21	1:A:105:ARG:HG3	2.03	0.41
1:B:326:ILE:HG13	1:B:326:ILE:H	1.74	0.40
1:A:368:THR:O	1:A:371:GLY:N	2.52	0.40
1:A:23:LEU:HD22	1:A:26:THR:HB	2.03	0.40
1:A:313:ARG:O	1:A:350:HIS:HB3	2.22	0.40
1:B:124:MET:O	1:B:128:VAL:HG23	2.21	0.40
1:B:211:ILE:HG12	1:B:225:LEU:HD11	2.04	0.40
1:B:18:PHE:O	1:B:24:GLY:HA2	2.22	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	429/444 (97%)	402 (94%)	23 (5%)	4 (1%)	17	25
1	B	430/444 (97%)	405 (94%)	23 (5%)	2 (0%)	29	41
All	All	859/888 (97%)	807 (94%)	46 (5%)	6 (1%)	22	32

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	369	PRO
1	B	369	PRO
1	A	256	HIS
1	A	338	LYS
1	A	436	LEU
1	B	41	GLN

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	368/390 (94%)	341 (93%)	27 (7%)	14	22
1	B	370/390 (95%)	342 (92%)	28 (8%)	13	20
All	All	738/780 (95%)	683 (92%)	55 (8%)	13	21

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LEU
1	A	23	LEU
1	A	41	GLN
1	A	74	GLU
1	A	75	THR
1	A	105	ARG

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Full wwPDB X-ray Structure Validation Report

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Mol	Chain	Res	Type
1	A	143	TRP
1	A	165	SER
1	A	169	GLN
1	A	204	LEU
1	A	264	SER
1	A	270	LEU
1	A	313	ARG
1	A	325	LEU
1	A	328	ASP
1	A	330	GLN
1	A	338	LYS
1	A	343	SER
1	A	354	ASP
1	A	358	ASP
1	A	368	THR
1	A	370	ASP
1	A	372	SER
1	A	388	LEU
1	A	413	ASP
1	A	436	LEU
1	A	438	VAL
1	B	68	LEU
1	B	70	THR
1	B	93	LEU
1	B	102	ARG
1	B	115	ARG
1	B	143	TRP
1	B	149	ARG
1	B	165	SER
1	B	204	LEU
1	B	247	GLN
1	B	264	SER
1	B	287	LEU
1	B	290	SER
1	B	325	LEU
1	B	326	ILE
1	B	327	GLN
1	B	328	ASP
1	B	343	SER
1	B	348	GLN
1	B	358	ASP
1	B	366	ARG

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Mol	Chain	Res	Type
1	B	372	SER
1	B	382	VAL
1	B	388	LEU
1	B	413	ASP
1	B	425	VAL
1	B	434	ASP
1	B	438	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	169	GLN
1	A	235	ASN
1	A	247	GLN
1	A	256	HIS
1	A	272	GLN
1	A	306	GLN
1	A	335	HIS
1	A	381	HIS
1	A	410	GLN
1	A	441	HIS
1	B	28	ASN
1	B	40	GLN
1	B	77	GLN
1	B	166	GLN
1	B	247	GLN
1	B	330	GLN
1	B	335	HIS
1	B	348	GLN
1	B	381	HIS
1	B	435	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 carbohydrates 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	B	1443	1	27,50,50	2.16	5 (18%)	17,82,82	1.77	3 (17%)
2	HEM	A	1442	1	27,50,50	2.18	5 (18%)	17,82,82	1.53	4 (23%)

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	B	1443	1	-	0/6/54/54	-
2	HEM	A	1442	1	-	0/6/54/54	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1443	HEM	C3D-C2D	5.31	1.53	1.37
2	A	1442	HEM	C3B-C2B	-5.14	1.33	1.40
2	B	1443	HEM	C3B-C2B	-4.99	1.33	1.40
2	A	1442	HEM	C3D-C2D	4.98	1.52	1.37
2	A	1442	HEM	C3C-CAC	3.99	1.56	1.47
2	A	1442	HEM	C3B-CAB	3.88	1.55	1.47
2	B	1443	HEM	C3B-CAB	3.83	1.55	1.47
2	B	1443	HEM	C3C-C2C	-3.78	1.35	1.40
2	A	1442	HEM	C3C-C2C	-3.74	1.35	1.40
2	B	1443	HEM	C3C-CAC	3.39	1.54	1.47

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1443	HEM	CBD-CAD-C3D	-3.99	105.12	112.48
2	B	1443	HEM	CAA-CBA-CGA	-3.85	106.21	112.67
2	A	1442	HEM	C1D-C2D-C3D	-2.81	105.04	107.00
2	A	1442	HEM	CBD-CAD-C3D	-2.69	107.52	112.48
2	A	1442	HEM	CAA-CBA-CGA	-2.50	108.48	112.67
2	B	1443	HEM	CMA-C3A-C4A	-2.19	125.09	128.46
2	A	1442	HEM	CMA-C3A-C4A	-2.18	125.11	128.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1442	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 B 1443

Bond lengths

Bond angles

Torsions

Rings

Ligand HEM A 1442

Bond lengths

Bond angles

Torsions

Rings
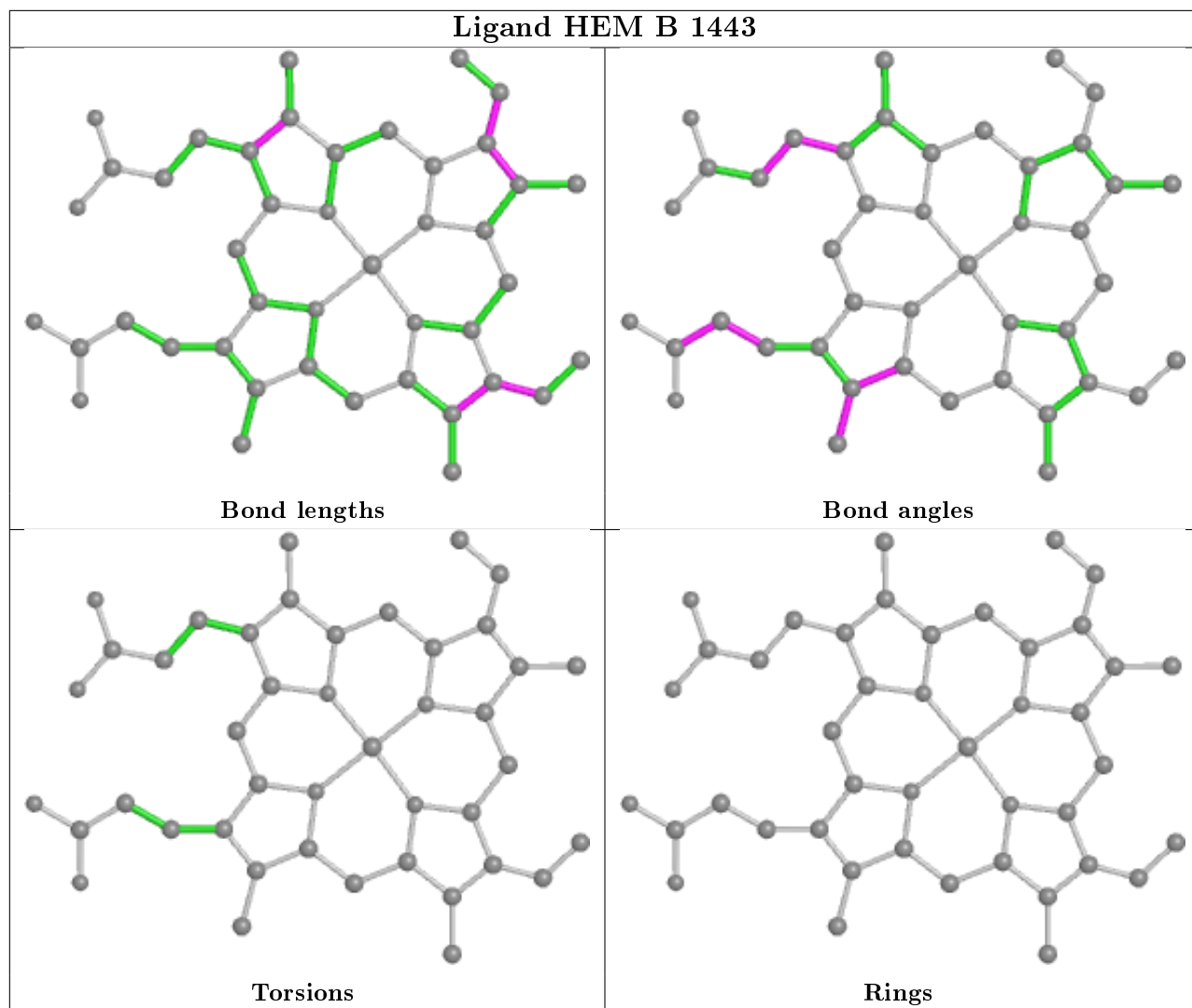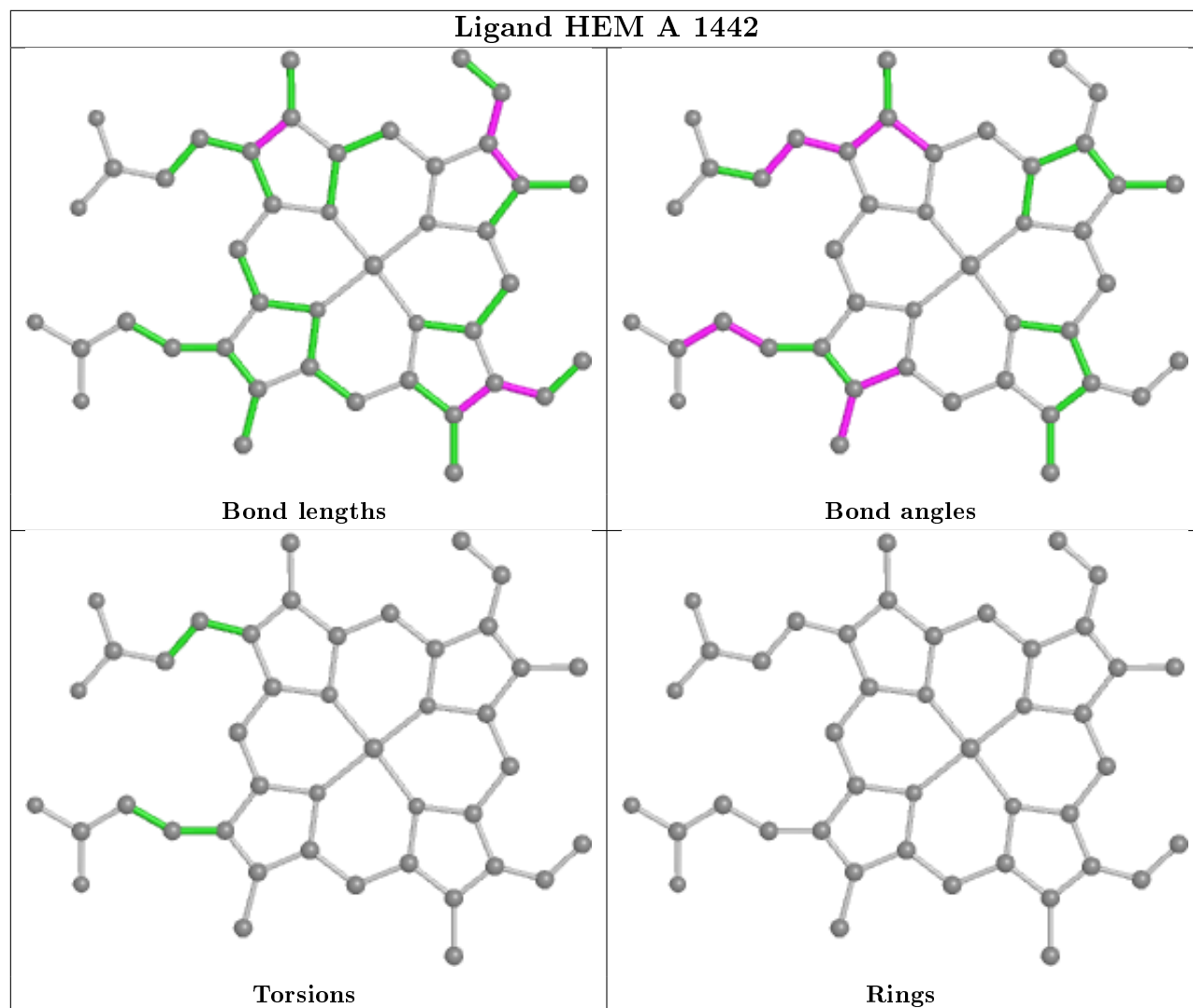
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	431/444 (97%)	-0.30	0	100	100	31, 57, 77, 84	0
1	B	432/444 (97%)	-0.32	2 (0%)	91	89	30, 57, 75, 83	0
All	All	863/888 (97%)	-0.31	2 (0%)	95	94	30, 57, 75, 84	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	416	LEU	2.4
1	B	436	LEU	2.3

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

There are no non-standard protein/DNA/RNA residues in this entry.
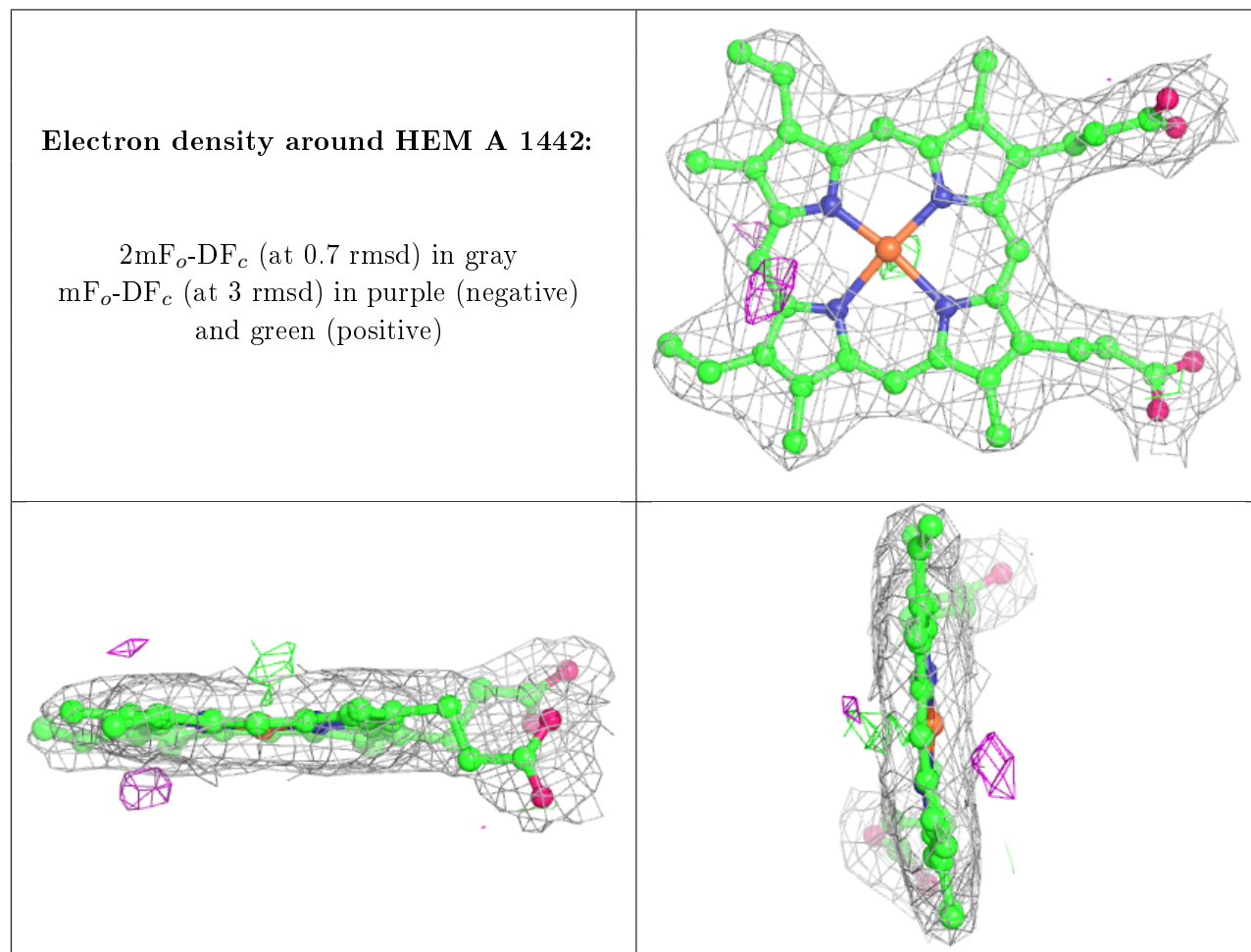
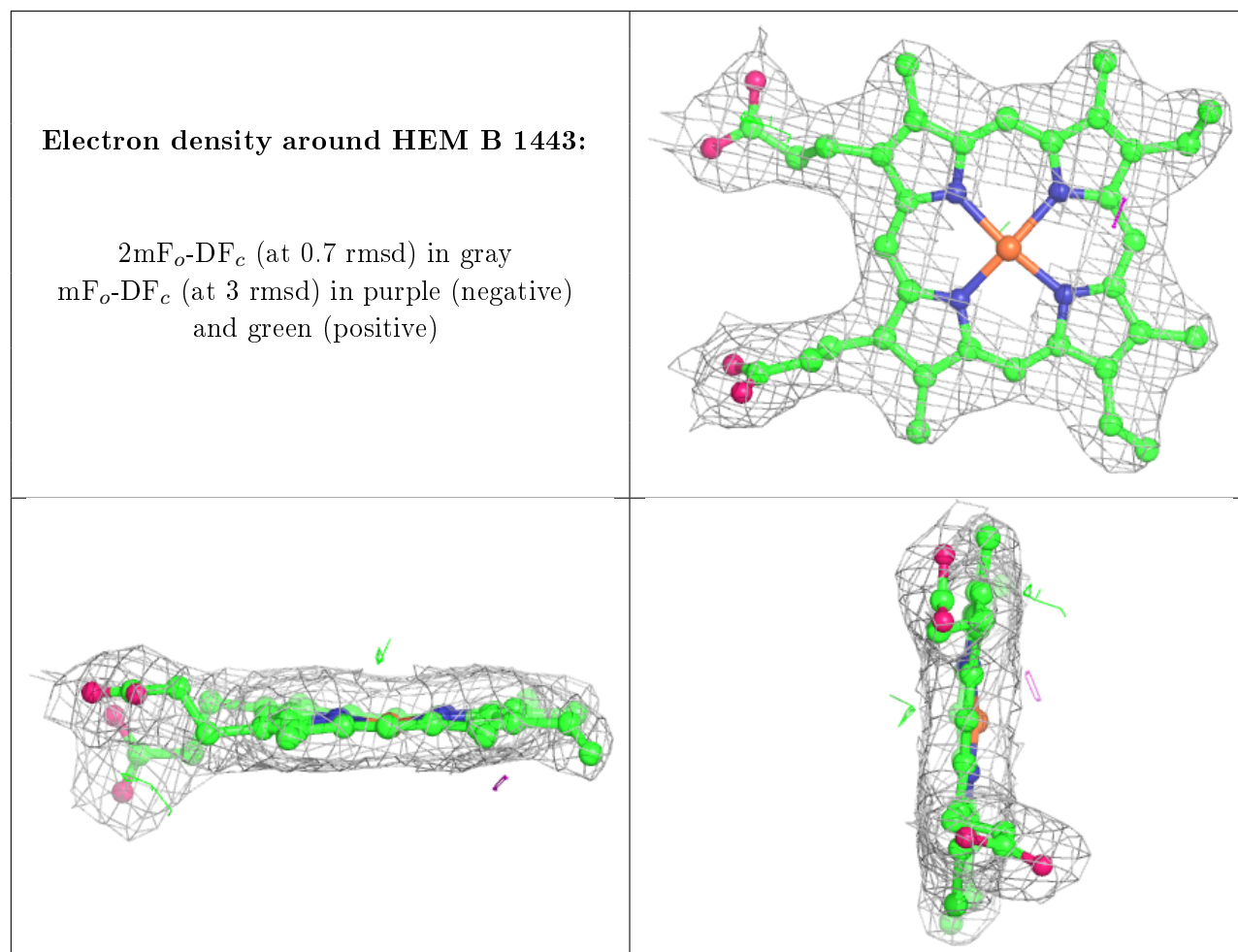## 6.3 Carbohydrates (i)

There are no carbohydrates 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	A	1442	43/43	0.98	0.14	35,39,48,53	0
2	HEM	B	1443	43/43	0.99	0.15	34,38,47,52	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 1442:

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

Electron density around HEM B 1443:

$2mF_o-DF_c$ (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.