Full wwPDB X-ray Structure Validation Report ⓘ

Sep 17, 2023 – 09:34 PM EDT

PDB ID	:	4YBN
Title	:	Structure of the FAD and Heme binding protein msmeg_4975 from Mycobacterium smegmatis
Authors	:	Ahmed, F.H.; Carr, P.D.; Jackson, C.J.
Deposited on	:	2015-02-18
Resolution	:	1.90 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 ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

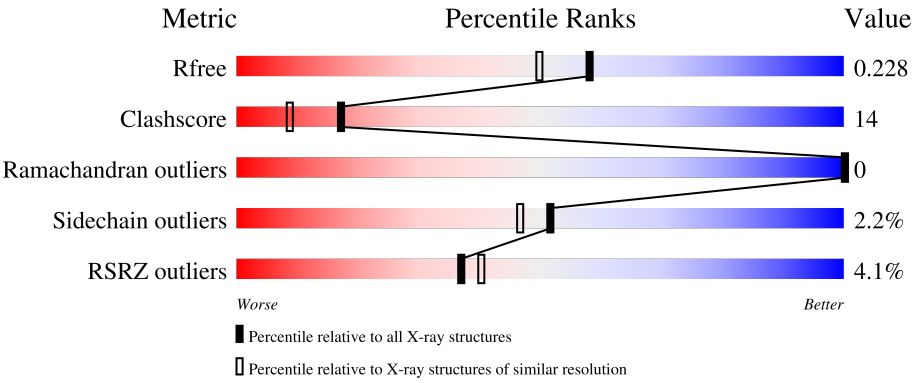
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh &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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	224	3% 84% 11% ·
1	B	224	4% 76% 13% · 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	HEM	A	304	-	-	-	X
6	FAD	B	302	-	-	X	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3805 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.

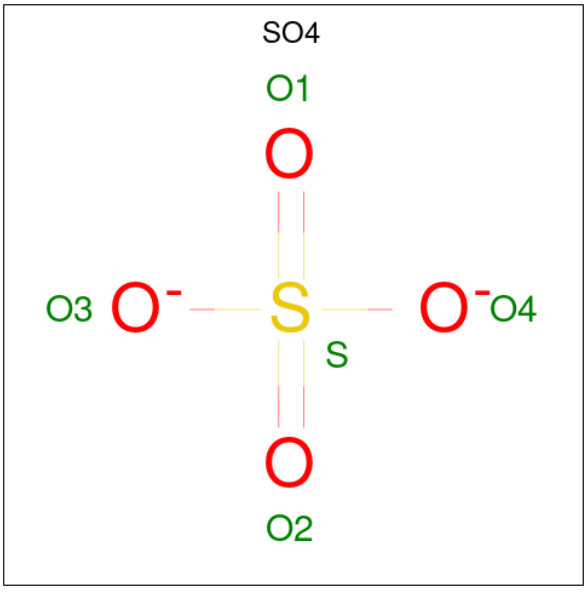
- Molecule 1 is a protein called Flavin-nucleotide-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	5	0
			1635	1026	288	320	1			
1	B	205	Total	C	N	O	S	0	12	0
			1636	1029	285	321	1			

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

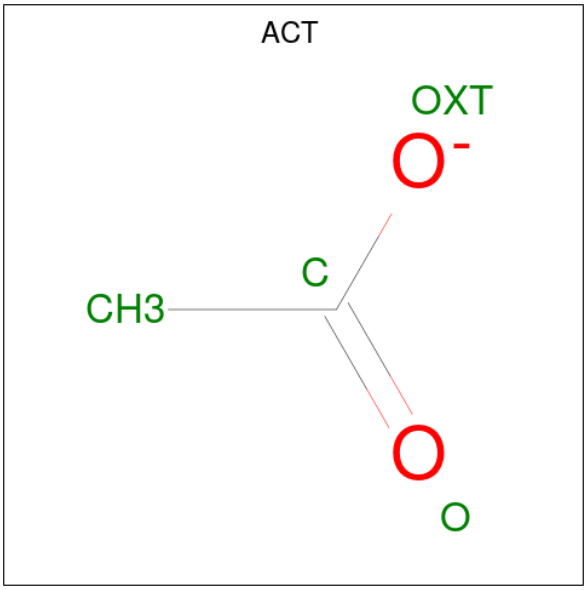
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ni	0	0
			1	1		
2	B	1	Total	Ni	0	0
			1	1		

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



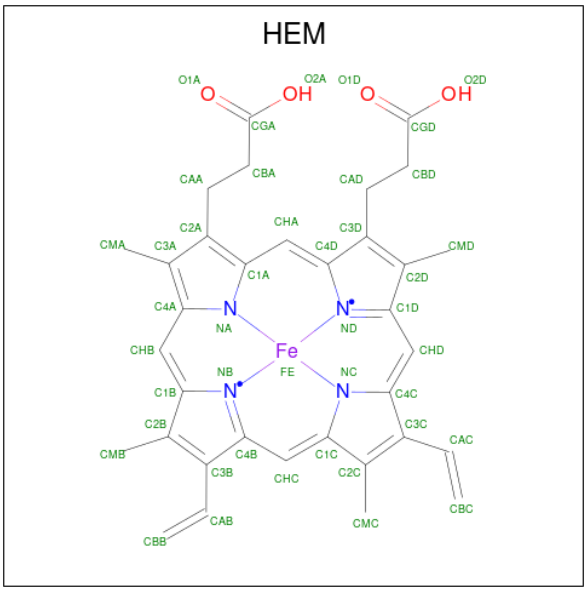
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



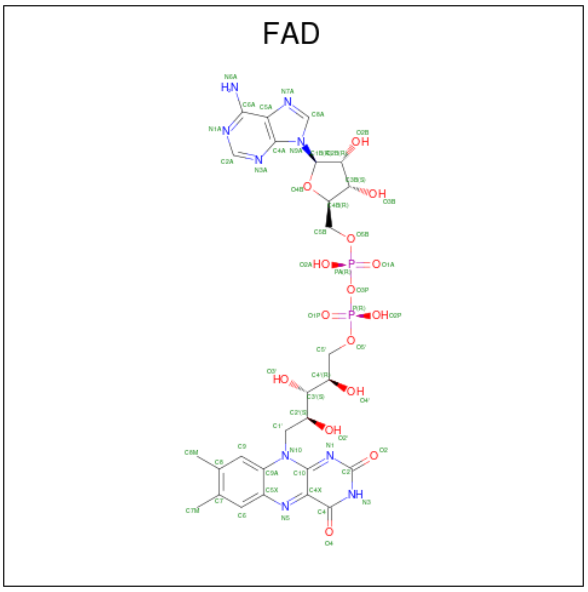
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 6 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 7 is water.

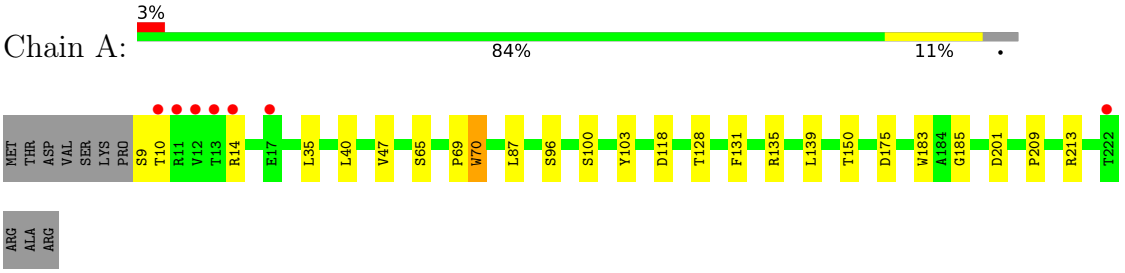
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	169	Total	O	0	0
			169	169		
7	B	155	Total	O	0	2
			157	157		

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.

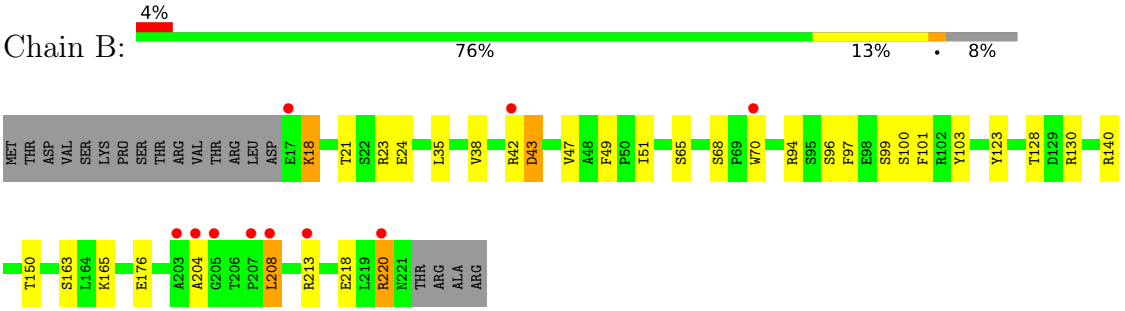
• Molecule 1: Flavin-nucleotide-binding protein

Chain A:



• Molecule 1: Flavin-nucleotide-binding protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	84.72Å 59.88Å 89.66Å 90.00° 93.83° 90.00°	Depositor
Resolution (Å)	44.73 – 1.90 43.60 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (44.73-1.90) 99.5 (43.60-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.39 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0049, PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.174 , 0.223 0.185 , 0.228	Depositor DCC
R_{free} test set	1749 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å^2)	27.0	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 41.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	3805	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.73% 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: ACT, HEM, NI, FAD, SO4

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	0.98	1/1668 (0.1%)	0.91	0/2279
1	B	0.96	1/1671 (0.1%)	0.96	4/2282 (0.2%)
All	All	0.97	2/3339 (0.1%)	0.94	4/4561 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	70	TRP	CB-CG	-8.14	1.35	1.50
1	B	24	GLU	CG-CD	5.11	1.59	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	130	ARG	NE-CZ-NH2	-8.42	116.09	120.30
1	B	130	ARG	NE-CZ-NH1	7.44	124.02	120.30
1	B	23	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	B	140	ARG	NE-CZ-NH1	5.34	122.97	120.30

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	1635	0	1617	42	0
1	B	1636	0	1592	46	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	4	0	3	0	0
5	A	43	0	30	20	0
5	B	43	0	30	10	0
6	B	106	0	62	41	0
7	A	169	0	0	1	1
7	B	157	0	0	5	1
All	All	3805	0	3334	95	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 14.

All (95) 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:35[B]:LEU:CD1	6:B:302:FAD:HM72	1.79	1.11
1:A:35[B]:LEU:HD11	6:B:302:FAD:C7M	1.90	1.01
1:B:103:TYR:CG	6:B:302:FAD:HM83	1.95	1.01
1:A:35[B]:LEU:CD2	6:B:302:FAD:HM72	1.90	0.99
5:A:304:HEM:CHB	1:B:100:SER:HA	1.99	0.93
1:A:128:THR:HG23	5:A:304:HEM:HBB1	1.50	0.92
1:A:35[B]:LEU:CD1	6:B:302:FAD:C7M	2.46	0.90
1:A:103:TYR:CD1	6:B:305:FAD:HM83	2.09	0.88
1:B:103:TYR:CD1	6:B:302:FAD:HM83	2.09	0.88
1:A:103:TYR:CG	6:B:305:FAD:HM83	2.13	0.83
1:A:35[B]:LEU:HD11	6:B:302:FAD:HM72	1.52	0.82
1:A:65:SER:HB2	5:A:304:HEM:HAD1	1.63	0.80
1:B:128:THR:HG23	5:B:301:HEM:HBB1	1.66	0.77
1:B:103:TYR:CD1	6:B:302:FAD:C8M	2.67	0.77
1:A:35[B]:LEU:HD21	6:B:302:FAD:HM72	1.67	0.76
1:B:42[A]:ARG:NH2	1:B:70[A]:TRP:HA	2.00	0.76
1:B:35[A]:LEU:CD1	6:B:305:FAD:HM72	2.19	0.72
1:A:35[B]:LEU:HD13	6:B:302:FAD:HM72	1.70	0.72
1:B:42[A]:ARG:HH22	1:B:70[A]:TRP:HA	1.55	0.71
1:B:35[A]:LEU:HD13	6:B:305:FAD:HM72	1.73	0.70
1:B:103:TYR:CG	6:B:302:FAD:C8M	2.73	0.70
1:A:103:TYR:CD1	6:B:305:FAD:C8M	2.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35[B]:LEU:CG	6:B:302:FAD:HM72	2.25	0.66
1:B:65:SER:HB2	5:B:301:HEM:HAD1	1.77	0.66
5:A:304:HEM:HMA3	1:B:100:SER:HB2	1.79	0.64
1:A:35[B]:LEU:HD21	6:B:302:FAD:C7M	2.27	0.64
1:B:49[B]:PHE:C	1:B:49[B]:PHE:CD1	2.69	0.63
1:A:70:TRP:CZ3	6:B:302:FAD:H3'	2.34	0.63
1:A:131:PHE:CD2	5:A:304:HEM:HMB2	2.34	0.62
1:A:35[B]:LEU:HD22	6:B:302:FAD:HM72	1.81	0.62
1:B:49[B]:PHE:CD1	1:B:49[B]:PHE:O	2.52	0.62
1:B:70[B]:TRP:CZ3	6:B:305:FAD:H3B	2.35	0.62
5:A:304:HEM:HHB	1:B:100:SER:HA	1.80	0.62
1:A:70:TRP:HZ3	6:B:302:FAD:H3'	1.66	0.60
5:A:304:HEM:HBB2	5:A:304:HEM:HHC	1.83	0.59
1:B:70[B]:TRP:CH2	6:B:305:FAD:C8A	2.86	0.59
5:A:304:HEM:HMC3	1:B:96:SER:OG	2.03	0.58
1:B:150:THR:OG1	5:B:301:HEM:HAC	2.04	0.57
1:A:201:ASP:OD1	1:B:94[B]:ARG:NH2	2.38	0.57
1:A:35[B]:LEU:CD2	6:B:302:FAD:C7M	2.75	0.55
1:B:123:TYR:OH	7:B:401:HOH:O	2.17	0.55
1:B:103:TYR:CB	6:B:302:FAD:HM83	2.37	0.55
1:A:100[A]:SER:HA	5:B:301:HEM:CHB	2.37	0.54
5:A:304:HEM:HMA3	1:B:101:PHE:H	1.73	0.53
1:A:70:TRP:CZ2	6:B:302:FAD:H3B	2.44	0.53
1:B:42[A]:ARG:O	1:B:43[A]:ASP:C	2.47	0.53
1:B:18:LYS:HG3	1:B:165:LYS:HE3	1.93	0.51
5:B:301:HEM:HHC	5:B:301:HEM:HBB2	1.93	0.51
1:B:208:LEU:O	1:B:213:ARG:NH1	2.44	0.51
1:B:218:GLU:O	1:B:220:ARG:HB2	2.11	0.51
1:A:35[B]:LEU:HD11	6:B:302:FAD:HM71	1.87	0.50
1:A:70:TRP:CH2	6:B:302:FAD:C8A	2.95	0.50
1:A:150:THR:OG1	5:A:304:HEM:HAC	2.11	0.50
5:A:304:HEM:CHC	1:B:96:SER:O	2.59	0.50
1:B:70[B]:TRP:HH2	6:B:305:FAD:C8A	2.25	0.50
1:A:69:PRO:HD2	6:B:302:FAD:O2P	2.11	0.49
1:B:18:LYS:HG3	1:B:165:LYS:CE	2.42	0.49
1:B:103:TYR:CD2	6:B:302:FAD:C8	2.96	0.49
1:B:42[A]:ARG:HD2	1:B:47:VAL:HG11	1.96	0.48
1:A:9:SER:O	6:B:305:FAD:O3B	2.26	0.48
5:A:304:HEM:O2D	7:B:405[B]:HOH:O	2.20	0.47
1:A:35[B]:LEU:CD1	6:B:302:FAD:HM71	2.43	0.47
1:A:35[B]:LEU:HD13	6:B:302:FAD:C7M	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:304:HEM:CMC	5:A:304:HEM:HBC2	2.46	0.46
5:A:304:HEM:HBC2	5:A:304:HEM:HMC2	1.96	0.46
1:A:10:THR:HG23	7:A:505:HOH:O	2.15	0.45
1:A:135:ARG:HG3	1:A:139:LEU:HD11	1.97	0.45
5:A:304:HEM:C1B	1:B:100:SER:HA	2.50	0.45
1:B:103:TYR:CD1	1:B:103:TYR:C	2.90	0.44
1:A:100[B]:SER:HA	5:B:301:HEM:CHB	2.47	0.44
1:B:35[B]:LEU:HD13	6:B:305:FAD:HM72	1.99	0.44
1:B:51:ILE:HG13	6:B:305:FAD:C4	2.47	0.44
6:B:305:FAD:H9	6:B:305:FAD:H1'1	1.75	0.44
1:A:128:THR:CG2	5:A:304:HEM:HBB1	2.36	0.43
1:A:87:LEU:HD13	1:B:35[A]:LEU:HD11	2.01	0.43
1:B:103:TYR:CE2	6:B:302:FAD:C9	3.02	0.43
1:A:103:TYR:CD1	1:A:103:TYR:C	2.92	0.43
1:B:38:VAL:HB	1:B:49[B]:PHE:CZ	2.54	0.42
1:B:163:SER:HA	7:B:439:HOH:O	2.19	0.42
5:B:301:HEM:CMC	5:B:301:HEM:HBC2	2.48	0.42
1:A:40:LEU:HG	1:A:47:VAL:HG22	2.02	0.42
1:A:183:TRP:CH2	1:A:185:GLY:HA3	2.55	0.42
1:A:209:PRO:O	1:A:213:ARG:HG3	2.20	0.42
1:A:70:TRP:HZ2	6:B:302:FAD:H3B	1.84	0.42
1:A:131:PHE:CD2	5:A:304:HEM:CMB	3.01	0.42
1:B:176:GLU:OE1	1:B:176:GLU:N	2.45	0.41
5:A:304:HEM:C3C	1:B:97:PHE:HA	2.55	0.41
1:B:103:TYR:CD1	6:B:302:FAD:HM81	2.50	0.41
1:A:96:SER:O	5:B:301:HEM:CHC	2.69	0.41
5:B:301:HEM:HMC1	7:B:522:HOH:O	2.21	0.41
1:B:21:THR:HG23	7:B:531:HOH:O	2.19	0.41
1:A:14:ARG:HB3	5:B:301:HEM:O2D	2.21	0.41
6:B:302:FAD:H9	6:B:302:FAD:H1'1	1.85	0.40
5:A:304:HEM:C1B	1:B:99:SER:O	2.74	0.40
5:A:304:HEM:C3A	1:B:100:SER:HB2	2.57	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:B:204:ALA:O	1:B:204:ALA:O[2_656]	1.94	0.26
7:A:496:HOH:O	7:B:444:HOH:O[3_445]	2.08	0.12

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	217/224 (97%)	212 (98%)	5 (2%)	0	100	100
1	B	215/224 (96%)	211 (98%)	4 (2%)	0	100	100
All	All	432/448 (96%)	423 (98%)	9 (2%)	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	170/174 (98%)	168 (99%)	2 (1%)	71	70
1	B	168/174 (97%)	162 (96%)	6 (4%)	35	26
All	All	338/348 (97%)	330 (98%)	8 (2%)	52	43

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

Mol	Chain	Res	Type
1	A	118	ASP
1	A	175	ASP
1	B	18	LYS
1	B	43[A]	ASP
1	B	43[B]	ASP
1	B	68	SER
1	B	208	LEU
1	B	220	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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	SO4	B	304	-	4,4,4	0.27	0	6,6,6	0.41	0
5	HEM	B	301	1,7	41,50,50	1.37	6 (14%)	45,82,82	2.02	12 (26%)
4	ACT	A	303	-	3,3,3	0.81	0	3,3,3	1.02	0
5	HEM	A	304	1,7	41,50,50	1.40	7 (17%)	45,82,82	1.74	11 (24%)
6	FAD	B	302	-	53,58,58	1.35	6 (11%)	68,89,89	1.67	13 (19%)
3	SO4	A	302	2	4,4,4	0.33	0	6,6,6	0.29	0
6	FAD	B	305	-	53,58,58	1.40	7 (13%)	68,89,89	1.72	11 (16%)

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
5	HEM	A	304	1,7	-	5/12/54/54	-
6	FAD	B	302	-	-	7/30/50/50	0/6/6/6
6	FAD	B	305	-	-	5/30/50/50	0/6/6/6
5	HEM	B	301	1,7	-	5/12/54/54	-

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	302	FAD	C9A-C5X	4.65	1.49	1.41
6	B	305	FAD	C9A-C5X	4.38	1.48	1.41
5	B	301	HEM	C1B-NB	-3.60	1.34	1.40
5	A	304	HEM	C4D-ND	-3.34	1.34	1.40
5	A	304	HEM	C1B-NB	-3.08	1.35	1.40
5	B	301	HEM	FE-NB	3.04	2.11	1.96
5	A	304	HEM	FE-NB	3.02	2.11	1.96
6	B	305	FAD	C8-C7	2.99	1.48	1.40
6	B	302	FAD	C8-C7	2.97	1.48	1.40
6	B	302	FAD	C5A-C4A	2.89	1.48	1.40
6	B	305	FAD	C4X-N5	2.74	1.36	1.30
5	B	301	HEM	C4D-ND	-2.74	1.35	1.40
5	B	301	HEM	C3B-C4B	2.72	1.50	1.44
5	A	304	HEM	C3B-C4B	2.63	1.50	1.44
6	B	305	FAD	C6-C5X	-2.53	1.36	1.40
5	B	301	HEM	CHA-C4D	2.52	1.41	1.35
6	B	302	FAD	C4X-N5	2.51	1.35	1.30
5	A	304	HEM	CHB-C1B	2.33	1.41	1.35
6	B	305	FAD	C4A-N3A	2.31	1.38	1.35
6	B	305	FAD	C5A-C4A	2.29	1.47	1.40
6	B	302	FAD	C4A-N3A	2.24	1.38	1.35
5	B	301	HEM	CHB-C1B	2.24	1.40	1.35
5	A	304	HEM	C1D-ND	-2.16	1.34	1.38
6	B	305	FAD	C2A-N3A	2.13	1.35	1.32
6	B	302	FAD	C10-N10	2.10	1.41	1.37
5	A	304	HEM	C1D-C2D	2.00	1.48	1.44

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	305	FAD	O2-C2-N1	-5.27	113.10	121.83
6	B	305	FAD	O4-C4-C4X	-4.85	113.72	126.60
6	B	302	FAD	N3A-C2A-N1A	-4.83	121.13	128.68
5	B	301	HEM	CHA-C4D-ND	4.80	130.31	124.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	305	FAD	N3A-C2A-N1A	-4.49	121.67	128.68
5	B	301	HEM	C1B-NB-C4B	4.44	109.66	105.07
6	B	302	FAD	O2-C2-N1	-4.41	114.51	121.83
5	B	301	HEM	CHD-C1D-ND	4.40	129.22	124.43
5	A	304	HEM	C1B-NB-C4B	4.28	109.49	105.07
6	B	305	FAD	O4-C4-N3	4.23	128.23	120.12
5	A	304	HEM	CHA-C4D-ND	4.07	129.41	124.38
6	B	302	FAD	O4-C4-C4X	-3.97	116.06	126.60
5	B	301	HEM	C4B-CHC-C1C	3.73	127.49	122.56
5	B	301	HEM	CMA-C3A-C4A	-3.39	123.26	128.46
6	B	302	FAD	P-O3P-PA	-3.38	121.24	132.83
6	B	302	FAD	C2A-N1A-C6A	3.34	124.47	118.75
6	B	302	FAD	N6A-C6A-N1A	3.26	125.35	118.57
5	B	301	HEM	CAB-C3B-C2B	-3.10	118.38	128.60
6	B	305	FAD	N6A-C6A-N1A	3.08	124.97	118.57
5	B	301	HEM	CHD-C1D-C2D	-3.04	120.22	124.98
5	A	304	HEM	CHD-C1D-ND	3.01	127.70	124.43
5	A	304	HEM	CHA-C4D-C3D	-2.97	119.75	125.33
6	B	305	FAD	O2-C2-N3	2.96	124.41	118.65
6	B	302	FAD	O4-C4-N3	2.91	125.70	120.12
5	B	301	HEM	CHA-C4D-C3D	-2.81	120.05	125.33
5	B	301	HEM	CMB-C2B-C1B	2.73	129.20	125.04
6	B	302	FAD	C4X-C10-N1	-2.70	118.47	124.73
5	A	304	HEM	C4B-CHC-C1C	2.68	126.10	122.56
5	B	301	HEM	CMA-C3A-C2A	2.67	129.99	124.94
5	A	304	HEM	CMD-C2D-C1D	2.65	129.07	125.04
5	A	304	HEM	C4C-CHD-C1D	2.57	125.95	122.56
5	A	304	HEM	CHC-C4B-NB	2.56	127.21	124.43
6	B	305	FAD	C4-C4X-N5	2.44	121.71	118.23
6	B	302	FAD	O3B-C3B-C4B	2.43	118.06	111.05
6	B	302	FAD	C4-N3-C2	-2.39	121.22	125.64
5	B	301	HEM	O2A-CGA-CBA	2.32	121.50	114.03
6	B	305	FAD	O4B-C4B-C3B	-2.22	100.72	105.11
5	A	304	HEM	CHD-C1D-C2D	-2.21	121.53	124.98
6	B	305	FAD	C5A-C6A-N6A	-2.20	117.01	120.35
5	A	304	HEM	O2A-CGA-CBA	2.16	120.98	114.03
6	B	302	FAD	C10-N1-C2	2.16	121.21	116.90
5	A	304	HEM	CHB-C1B-NB	2.15	127.04	124.38
5	B	301	HEM	CAB-C3B-C4B	2.15	134.47	124.47
6	B	302	FAD	C4A-C5A-N7A	-2.06	107.25	109.40
6	B	305	FAD	C3B-C2B-C1B	2.04	104.05	100.98
6	B	305	FAD	C4X-C10-N1	-2.00	120.08	124.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	302	FAD	N3-C2-N1	2.00	123.31	119.38

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	302	FAD	C5B-O5B-PA-O1A
6	B	302	FAD	N10-C1'-C2'-O2'
6	B	302	FAD	N10-C1'-C2'-C3'
6	B	302	FAD	C5'-O5'-P-O3P
6	B	305	FAD	C5B-O5B-PA-O1A
6	B	305	FAD	N10-C1'-C2'-O2'
5	A	304	HEM	C4B-C3B-CAB-CBB
5	B	301	HEM	C4B-C3B-CAB-CBB
6	B	302	FAD	C5B-O5B-PA-O2A
6	B	302	FAD	C5'-O5'-P-O2P
6	B	305	FAD	C5B-O5B-PA-O2A
5	A	304	HEM	CAA-CBA-CGA-O2A
5	A	304	HEM	CAA-CBA-CGA-O1A
5	A	304	HEM	CAD-CBD-CGD-O2D
5	B	301	HEM	CAD-CBD-CGD-O1D
5	B	301	HEM	CAD-CBD-CGD-O2D
5	A	304	HEM	CAD-CBD-CGD-O1D
5	B	301	HEM	CAA-CBA-CGA-O1A
5	B	301	HEM	CAA-CBA-CGA-O2A
6	B	302	FAD	C5B-O5B-PA-O3P
6	B	305	FAD	C5B-O5B-PA-O3P
6	B	305	FAD	N10-C1'-C2'-C3'

There are no ring outliers.

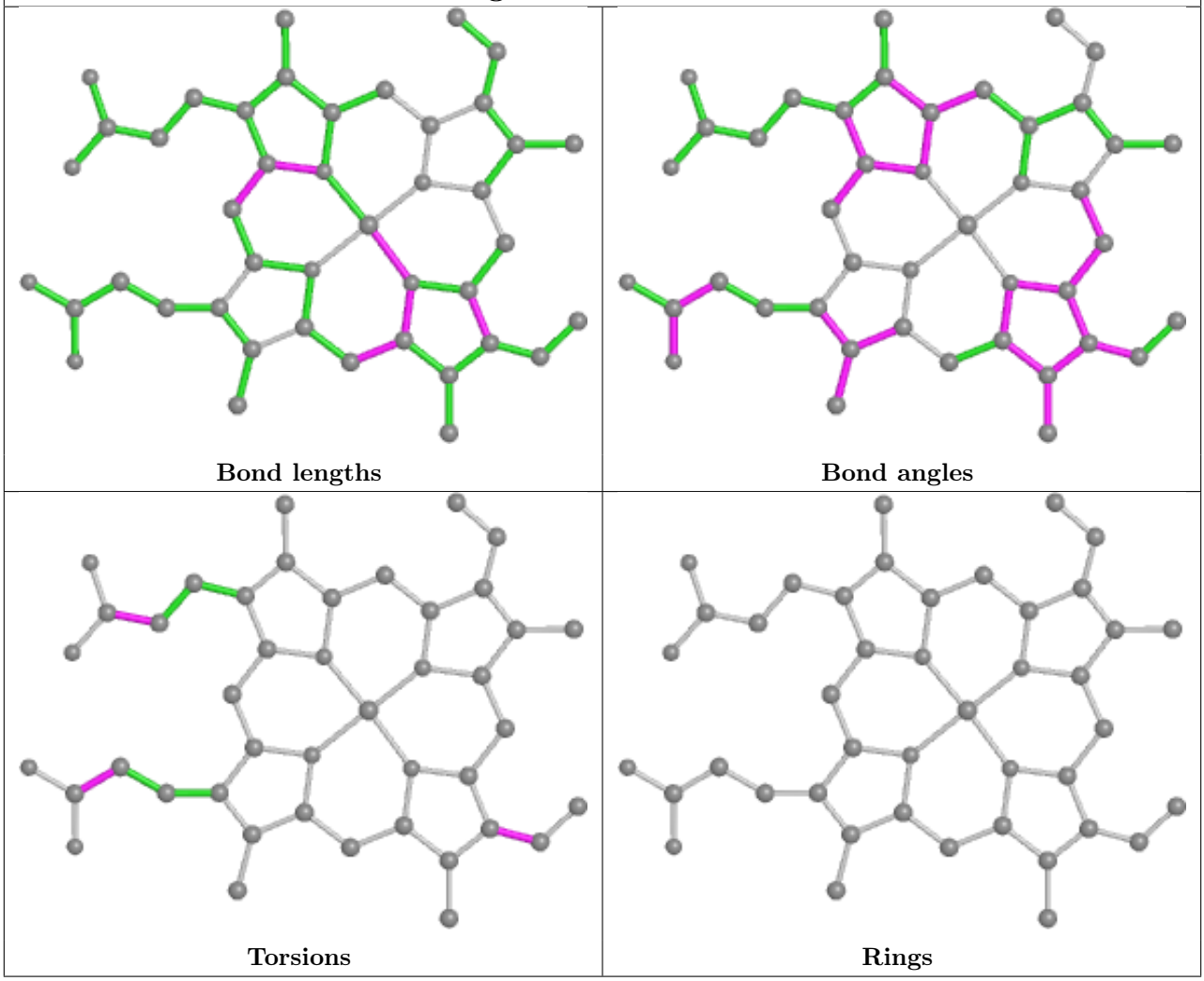
4 monomers are involved in 71 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	301	HEM	10	0
5	A	304	HEM	20	0
6	B	302	FAD	29	0
6	B	305	FAD	12	0

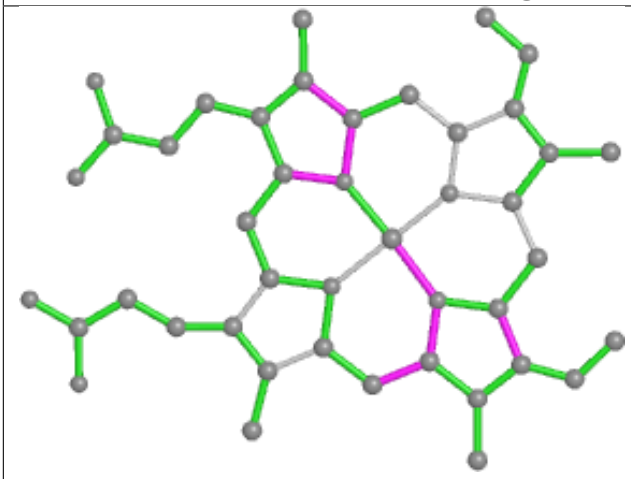
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

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.

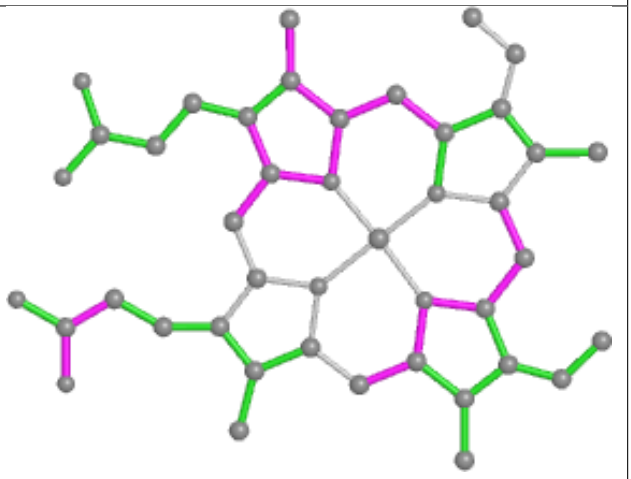
Ligand HEM B 301



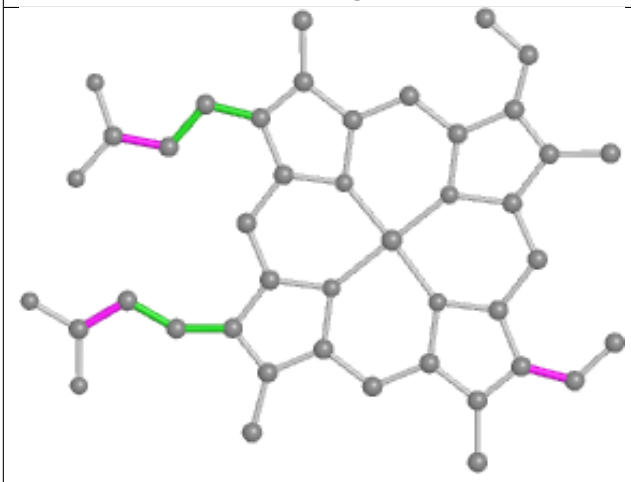
Ligand HEM A 304



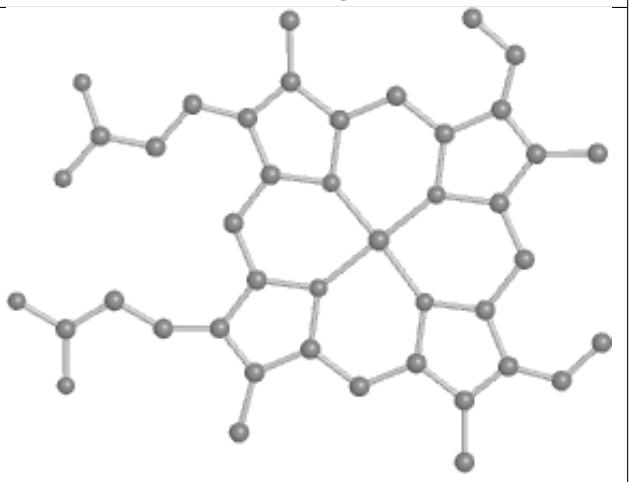
Bond lengths



Bond angles

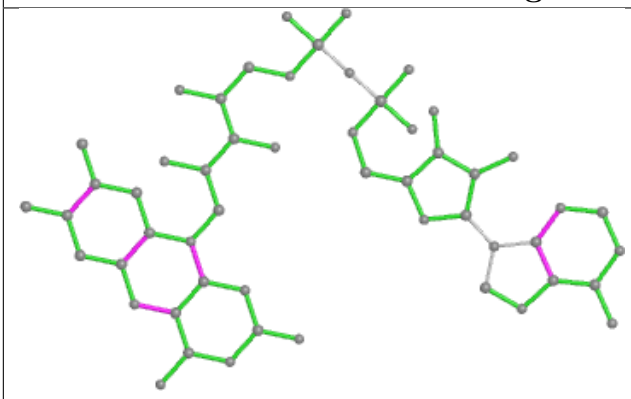


Torsions

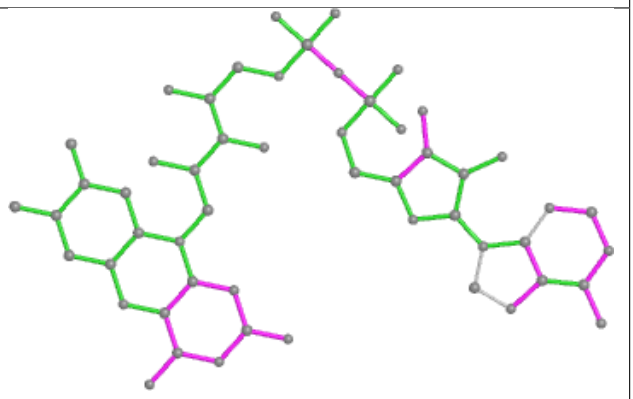


Rings

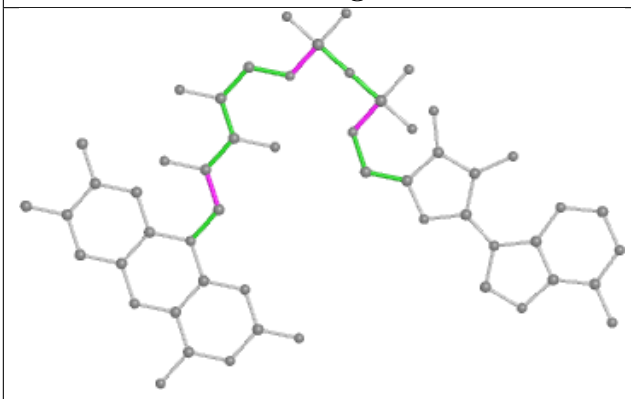
Ligand FAD B 302



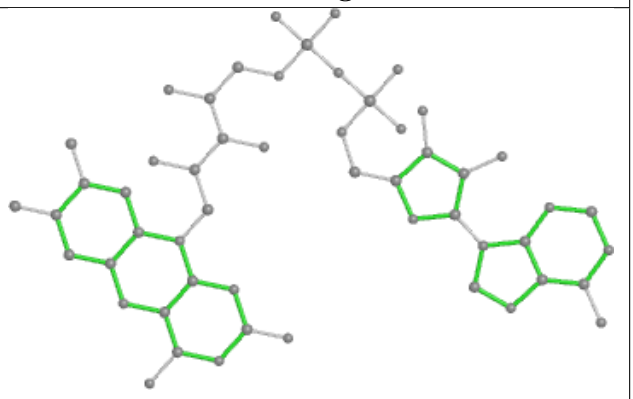
Bond lengths



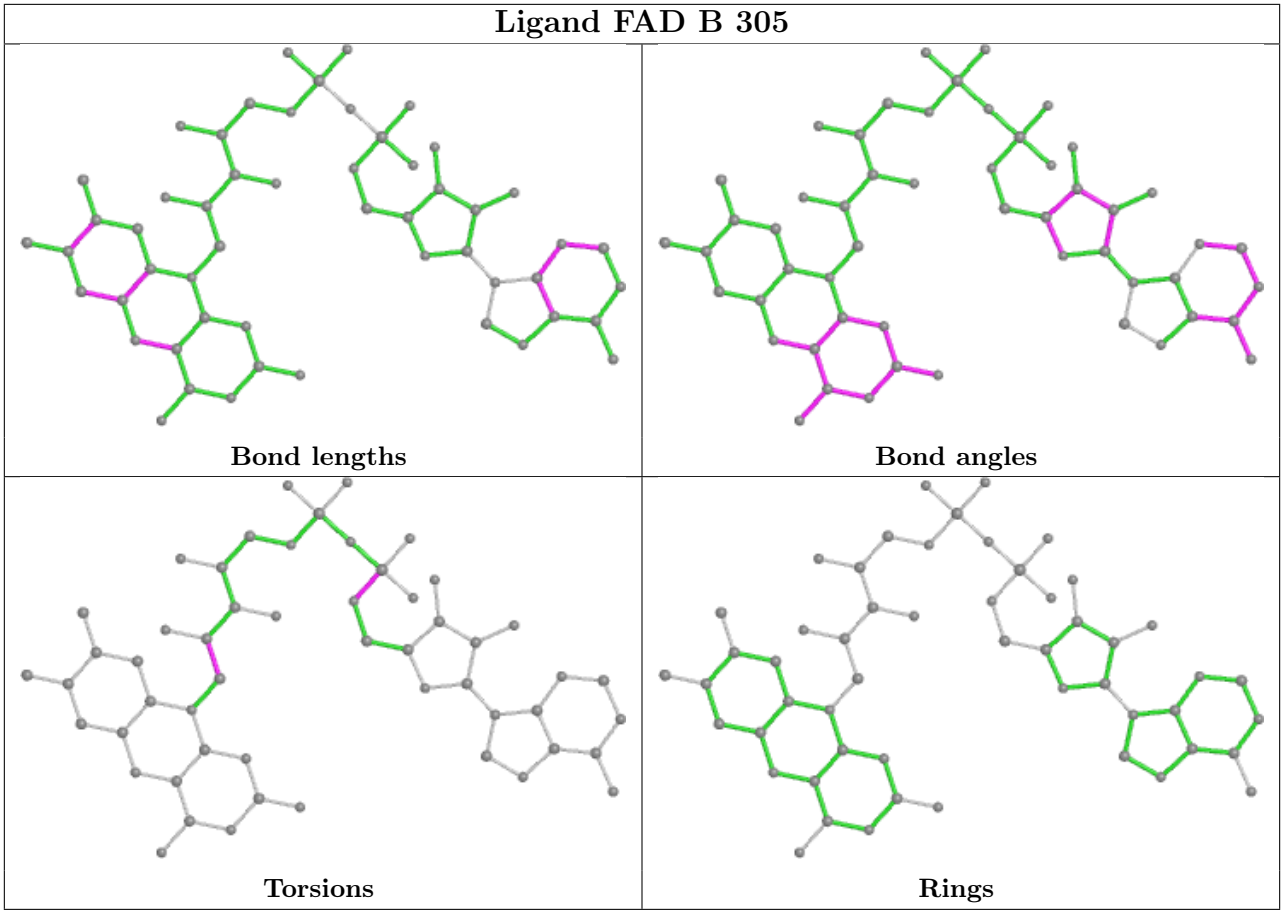
Bond angles



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	214/224 (95%)	0.02	7 (3%)	46	49	18, 29, 55, 77	0
1	B	205/224 (91%)	-0.03	10 (4%)	29	33	17, 30, 50, 85	0
All	All	419/448 (93%)	-0.00	17 (4%)	37	40	17, 29, 53, 85	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	205	GLY	4.6
1	A	11	ARG	4.5
1	B	203	ALA	3.8
1	B	204	ALA	3.7
1	B	220	ARG	3.6
1	B	17	GLU	3.4
1	B	207	PRO	3.3
1	B	70[A]	TRP	3.0
1	B	208	LEU	2.9
1	A	13	THR	2.8
1	B	42[A]	ARG	2.5
1	A	10	THR	2.4
1	A	14	ARG	2.2
1	A	17	GLU	2.2
1	A	12	VAL	2.1
1	A	222	THR	2.0
1	B	213	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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)

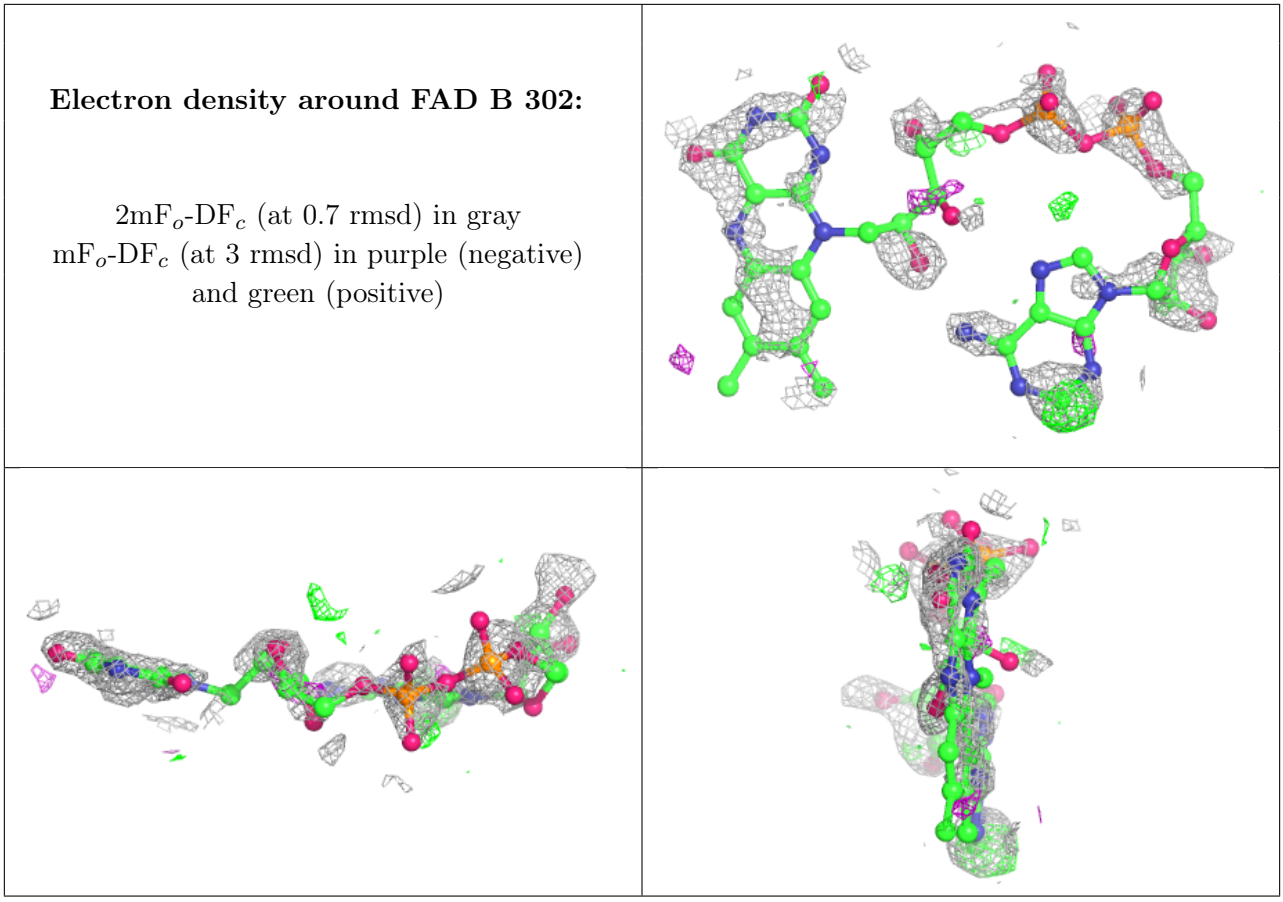
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
6	FAD	B	302	53/53	0.68	0.41	30,46,54,58	53
5	HEM	A	304	43/43	0.76	0.41	30,38,43,45	43
5	HEM	B	301	43/43	0.91	0.19	25,31,36,41	43
4	ACT	A	303	4/4	0.92	0.12	35,35,37,38	0
6	FAD	B	305	53/53	0.94	0.16	25,32,40,42	53
2	NI	B	303	1/1	0.95	0.23	37,37,37,37	1
3	SO4	A	302	5/5	0.96	0.08	64,65,66,73	0
2	NI	A	301	1/1	0.96	0.10	26,26,26,26	1
3	SO4	B	304	5/5	0.97	0.11	56,61,65,71	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.

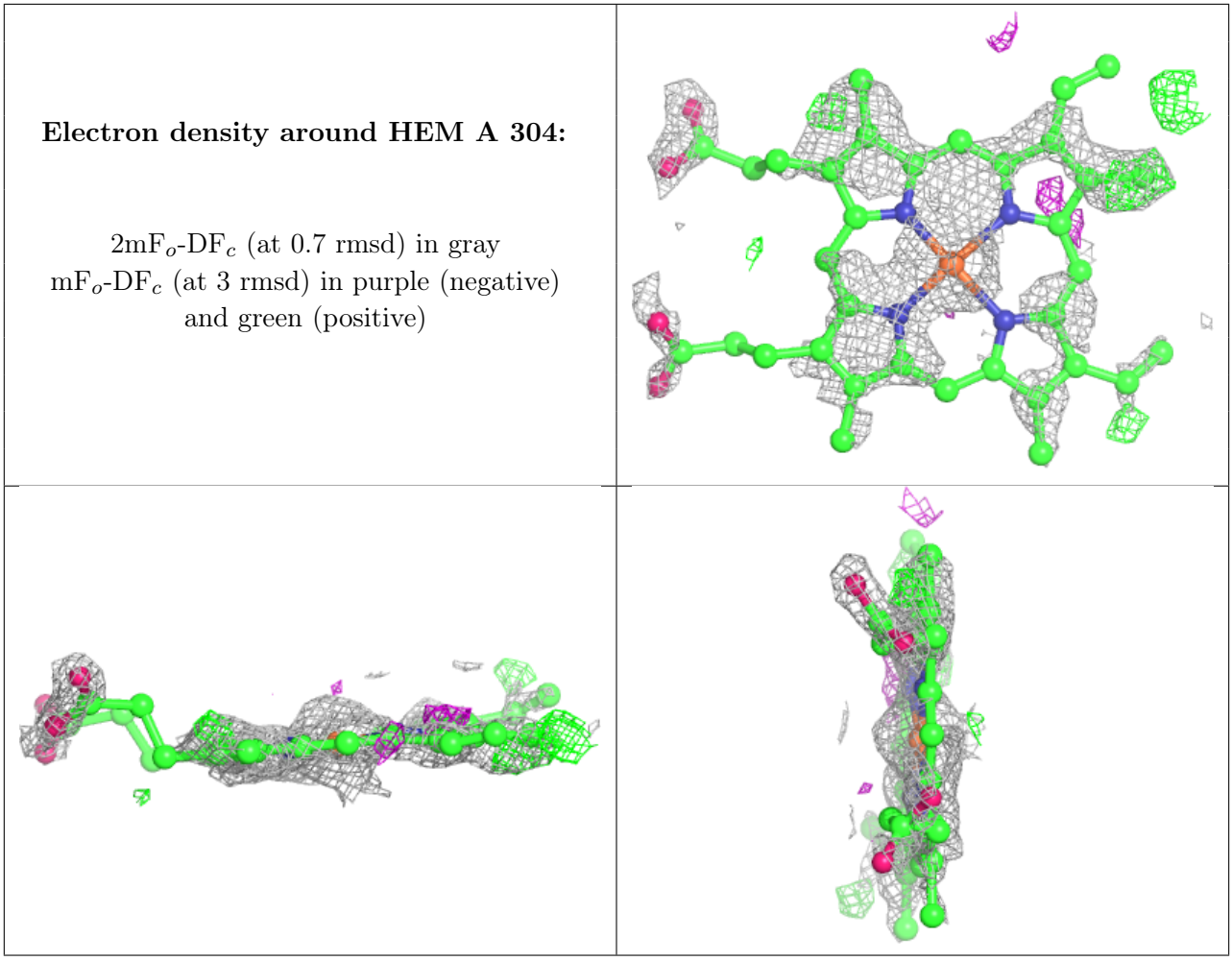
Electron density around FAD B 302:

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



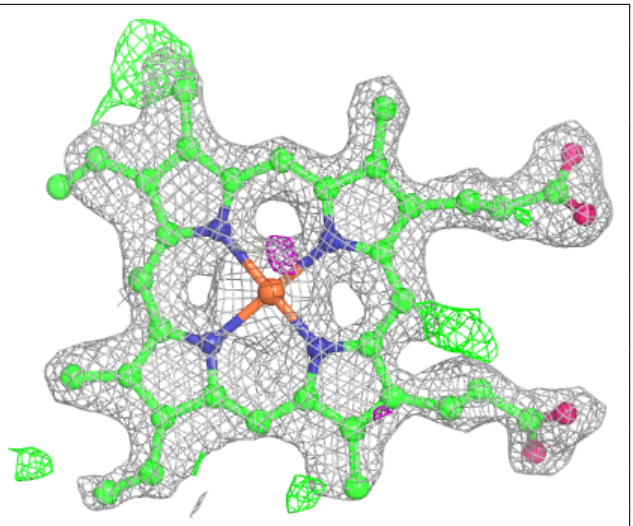
Electron density around HEM A 304:

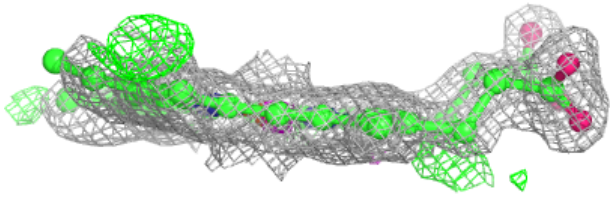
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

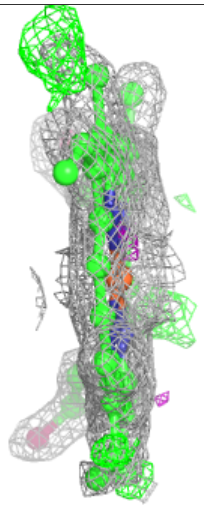


Electron density around HEM B 301:

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

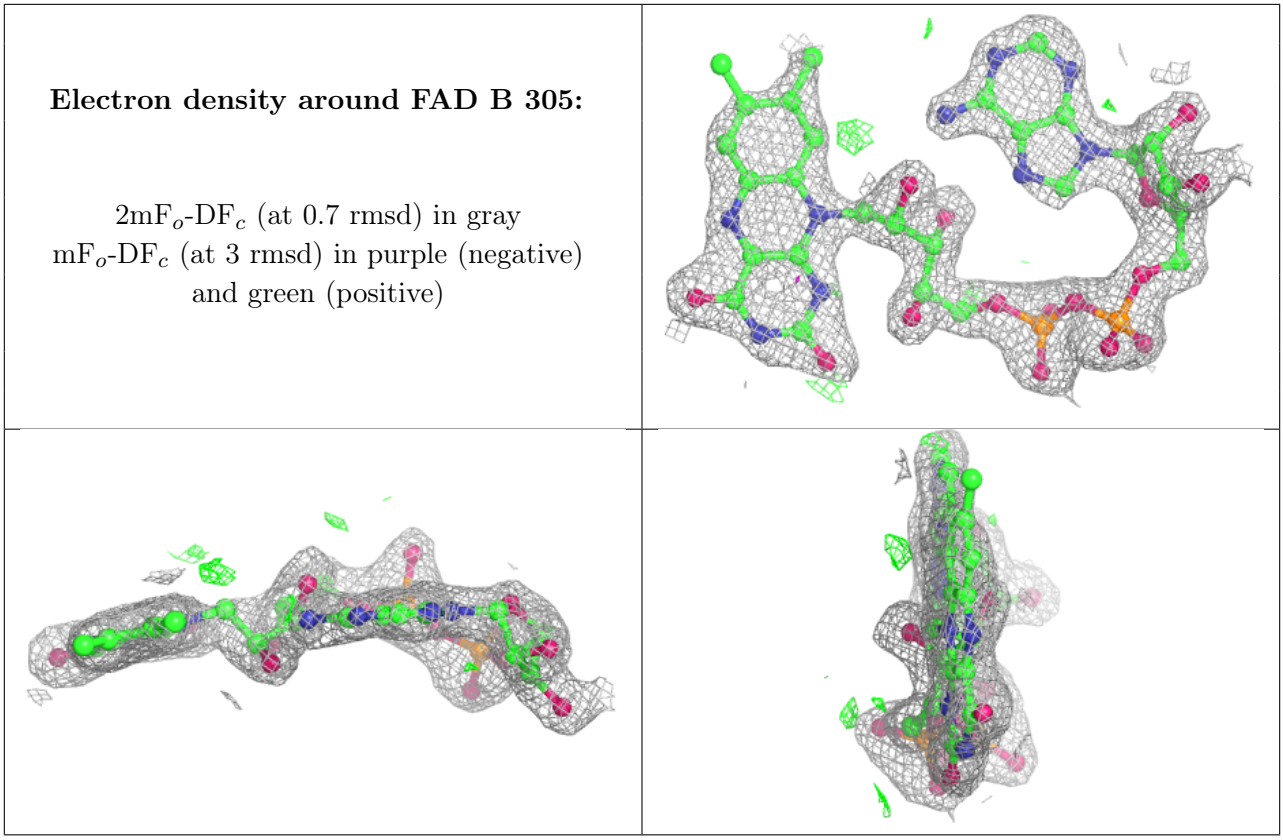






Electron density around FAD B 305:

$2mF_o$-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.