wwPDB X-ray Structure Validation Summary Report (i)

Feb 3, 2024 – 02:46 PM EST

PDB ID	:	1LTD
Title	:	THE 2.6 ANGSTROMS REFINED STRUCTURE OF THE ESCHERICHIA COLI RECOMBINANT SACCHAROMYCES CEREVISIAE FLAVOCYTOCHROME B2-SULPHITE COMPLEX
Authors	:	Tegoni, M.; Cambillau, C.
Deposited on	:	1994-01-14
Resolution	:	2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (1)) were used in the production of this report:

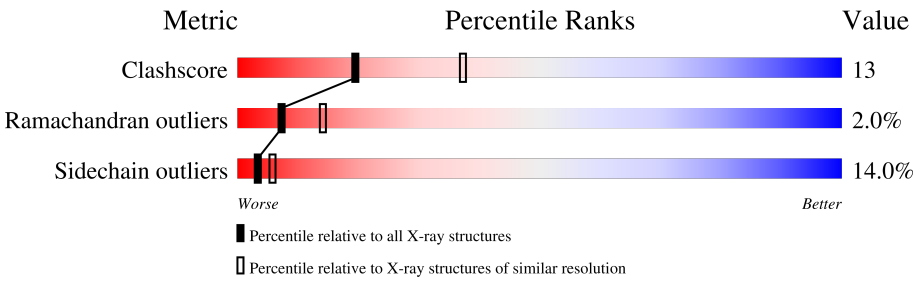
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.60 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))
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	506	57% 29% 8% • 5%
1	B	506	44% 23% 8% • 24%

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
3	FMN	A	570	X	-	-	-
3	FMN	B	570	X	-	-	-

2 Entry composition (i)

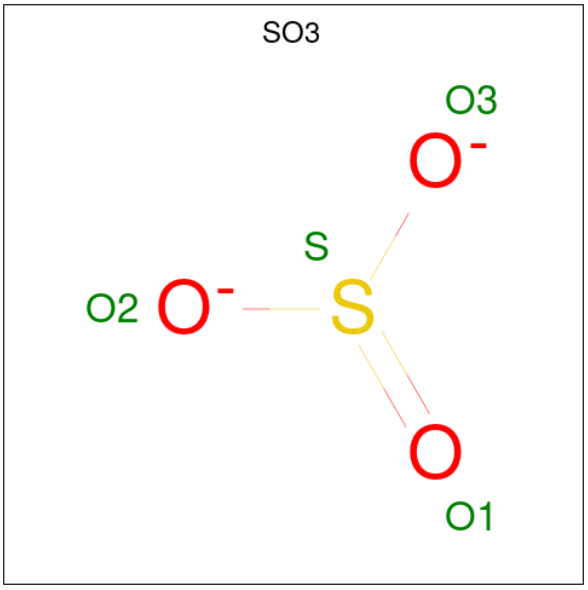
There are 5 unique types of molecules in this entry. The entry contains 7075 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FLAVOCYTOCHROME B2.

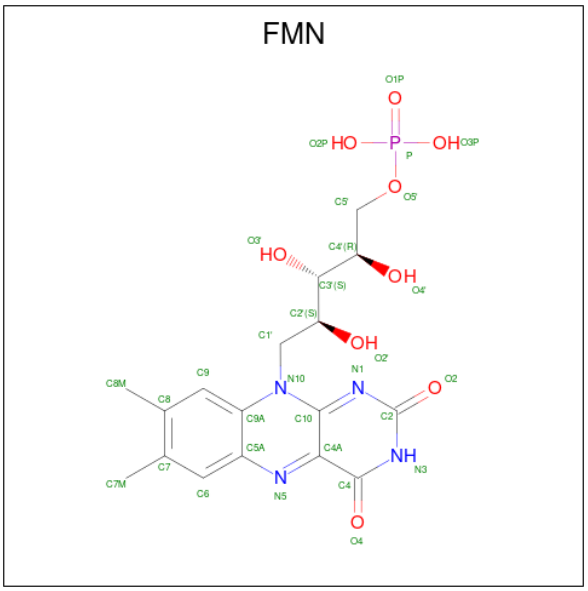
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	482	3742	2386	633	709	14	0	0	1
1	B	387	3014	1913	513	577	11	0	0	1

- Molecule 2 is SULFITE ION (three-letter code: SO3) (formula: O_3S).



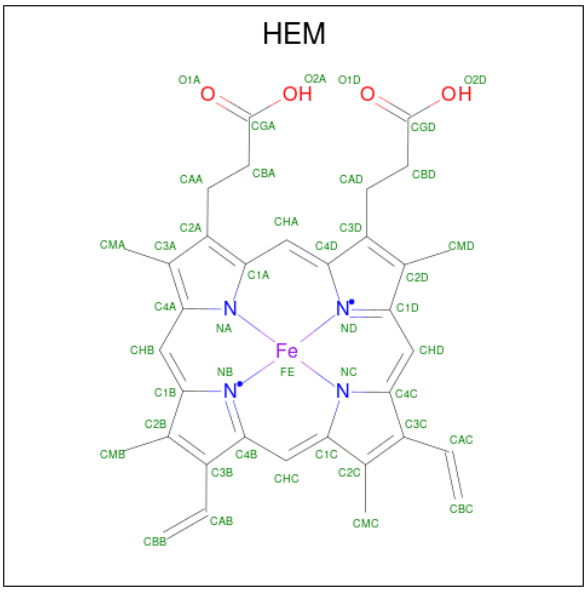
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	4	3	1	0	0
2	B	1	4	3	1	0	0

- Molecule 3 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	31	17	4	9	1	0	0
			Total	C	N	O	P		
3	B	1	31	17	4	9	1	0	0

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	145	145	145	0	0
			Total	O		
5	B	61	61	61	0	0

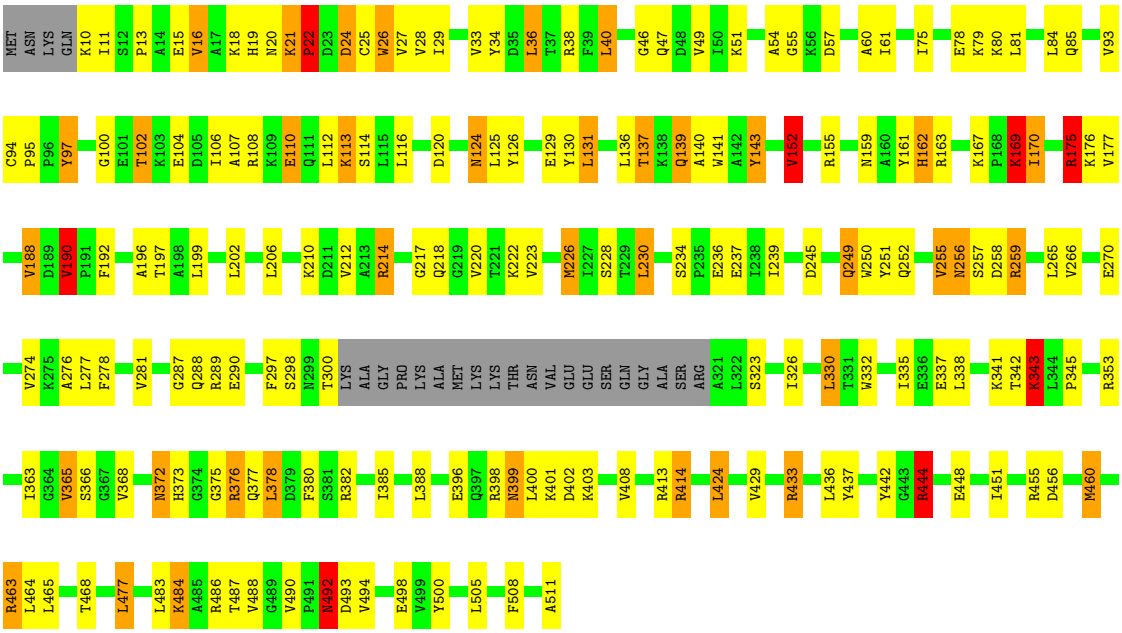
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

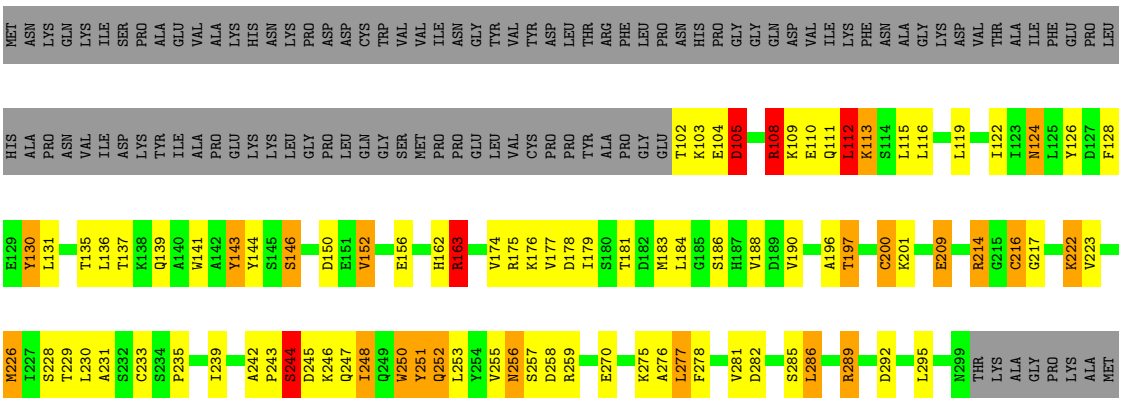
• Molecule 1: FLAVOCYTOCHROME B2

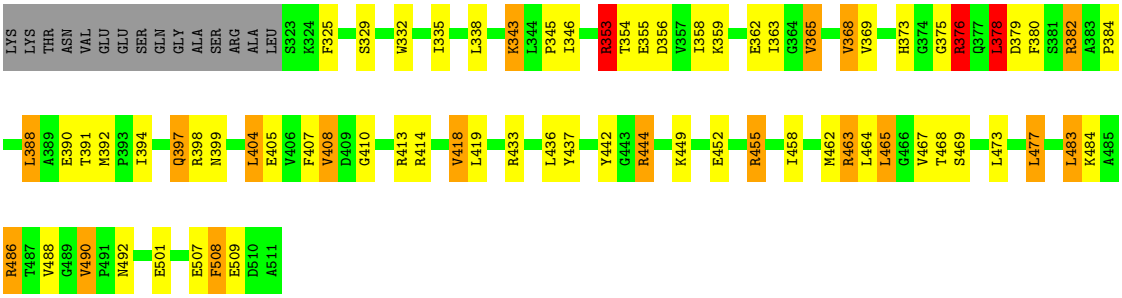
Chain A: 57% 29% 8% • 5%



• Molecule 1: FLAVOCYTOCHROME B2

Chain B: 44% 23% 8% • 24%




LYS
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K324
F325
S329
W332
I335
L338
K343
L344
P345
I346
R353
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D356
V357
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E362
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K484
A485
R486
T487
V488
G489
V490
P491
N492
E501
E507
F508
E509
D510
A511

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	164.50Å 164.50Å 114.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 2.60	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.173 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7075	wwPDB-VP
Average B, all atoms ($Å^2$)	27.0	wwPDB-VP

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: FMN, HEM, SO3

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	0.99	0/3816	1.86	80/5170 (1.5%)
1	B	1.00	0/3063	1.83	59/4138 (1.4%)
All	All	0.99	0/6879	1.84	139/9308 (1.5%)

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	3
1	B	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 139 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	376	ARG	NE-CZ-NH1	19.71	130.16	120.30
1	A	382	ARG	NE-CZ-NH2	-18.40	111.10	120.30
1	B	463	ARG	NE-CZ-NH2	-15.52	112.54	120.30
1	A	486	ARG	NE-CZ-NH2	-14.28	113.16	120.30
1	A	376	ARG	NE-CZ-NH2	-13.88	113.36	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	130	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	A	463	ARG	Sidechain
1	A	492	ASN	Mainchain
1	B	251	TYR	Sidechain

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	3742	0	3794	98	0
1	B	3014	0	3072	94	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
3	A	31	0	18	1	0
3	B	31	0	17	1	0
4	A	43	0	30	5	0
5	A	145	0	0	2	0
5	B	61	0	0	2	0
All	All	7075	0	6931	177	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 13.

The worst 5 of 177 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:488:VAL:HG22	1:B:490:VAL:HG21	1.49	0.95
1:A:199:LEU:HD21	4:A:560:HEM:HAA1	1.71	0.72
1:A:372:ASN:HD22	1:A:375:GLY:H	1.36	0.72
1:A:488:VAL:HG22	1:B:490:VAL:CG2	2.19	0.71
1:B:243:PRO:HD2	1:B:247:GLN:HE22	1.55	0.71

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	478/506 (94%)	440 (92%)	29 (6%)	9 (2%)	8 15
1	B	383/506 (76%)	341 (89%)	34 (9%)	8 (2%)	7 13
All	All	861/1012 (85%)	781 (91%)	63 (7%)	17 (2%)	7 14

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	245	ASP
1	A	46	GLY
1	A	114	SER
1	B	103	LYS
1	B	473	LEU

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	412/435 (95%)	358 (87%)	54 (13%)	4 7
1	B	333/435 (77%)	283 (85%)	50 (15%)	3 5
All	All	745/870 (86%)	641 (86%)	104 (14%)	3 6

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	112	LEU

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Mol	Chain	Res	Type
1	B	252	GLN
1	B	483	LEU
1	B	131	LEU
1	B	186	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	497	ASN
1	B	218	GLN
1	B	162	HIS
1	B	247	GLN
1	A	225	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

5 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	$\#\|Z\| > 2$
3	FMN	A	570	2	33,33,33	1.90	9 (27%)	48,50,50	2.39	14 (29%)
4	HEM	A	560	1	41,50,50	1.55	8 (19%)	45,82,82	1.27	4 (8%)
2	SO3	B	580	3	1,3,3	0.61	0	0,3,3	-	-
2	SO3	A	580	3	1,3,3	0.72	0	0,3,3	-	-
3	FMN	B	570	2	33,33,33	1.69	6 (18%)	48,50,50	2.47	21 (43%)

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
4	HEM	A	560	1	-	8/12/54/54	-
3	FMN	A	570	2	2/2/4/4	11/18/18/18	0/3/3/3
3	FMN	B	570	2	2/2/4/4	11/18/18/18	0/3/3/3

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	570	FMN	C1'-N10	-4.97	1.35	1.48
3	B	570	FMN	C9-C8	-4.41	1.33	1.39
4	A	560	HEM	C3C-CAC	-4.37	1.38	1.47
3	B	570	FMN	C1'-N10	-4.25	1.37	1.48
4	A	560	HEM	C3C-C2C	-4.21	1.34	1.40

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	570	FMN	C4'-C3'-C2'	7.02	127.97	113.36
3	B	570	FMN	C4A-C10-N1	-5.84	111.18	124.73
3	A	570	FMN	C4A-C10-N1	-5.61	111.72	124.73
3	A	570	FMN	C10-N1-C2	5.53	127.97	116.90
3	B	570	FMN	C4-C4A-C10	5.47	125.98	116.79

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	570	FMN	C4'
3	A	570	FMN	C2'
3	B	570	FMN	C4'

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Mol	Chain	Res	Type	Atom
3	B	570	FMN	C2'

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	570	FMN	N10-C1'-C2'-O2'
3	A	570	FMN	O2'-C2'-C3'-O3'
3	A	570	FMN	C2'-C3'-C4'-O4'
3	A	570	FMN	O3'-C3'-C4'-O4'
3	A	570	FMN	O3'-C3'-C4'-C5'

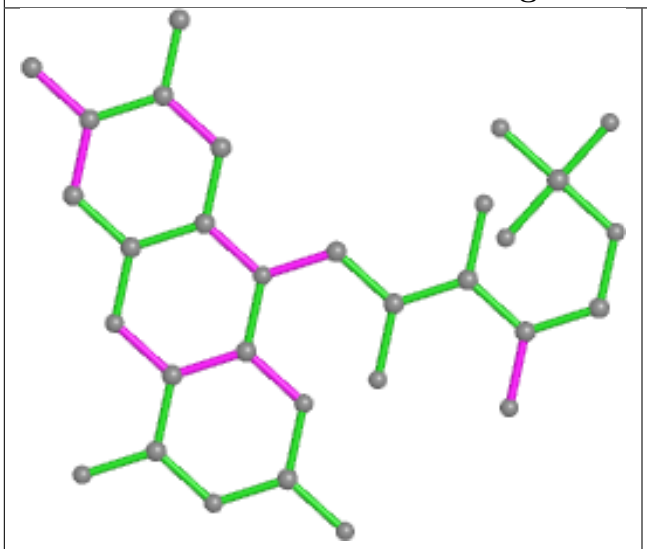
There are no ring outliers.

3 monomers are involved in 7 short contacts:

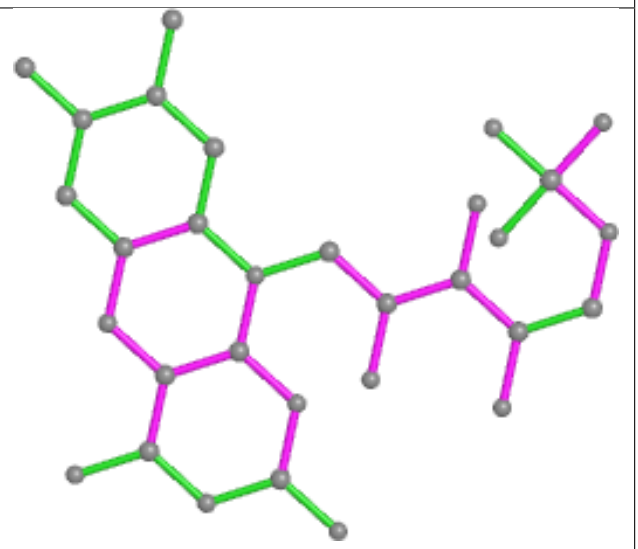
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	570	FMN	1	0
4	A	560	HEM	5	0
3	B	570	FMN	1	0

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.

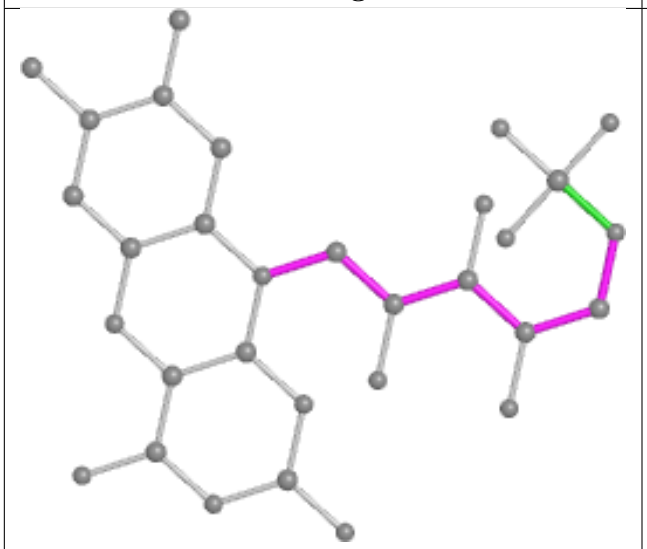
Ligand FMN A 570



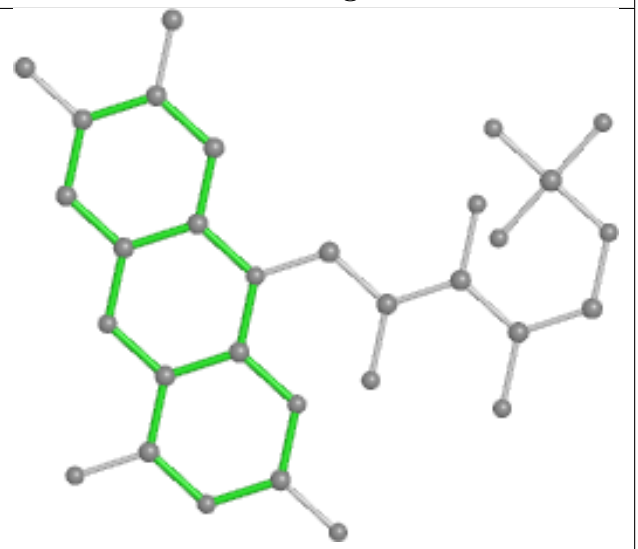
Bond lengths



Bond angles

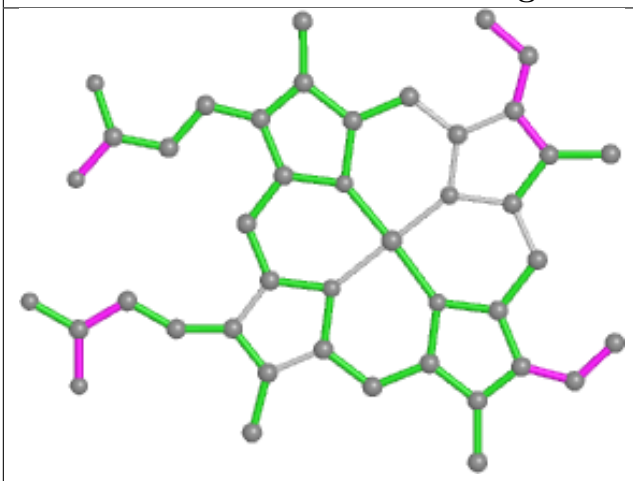


Torsions

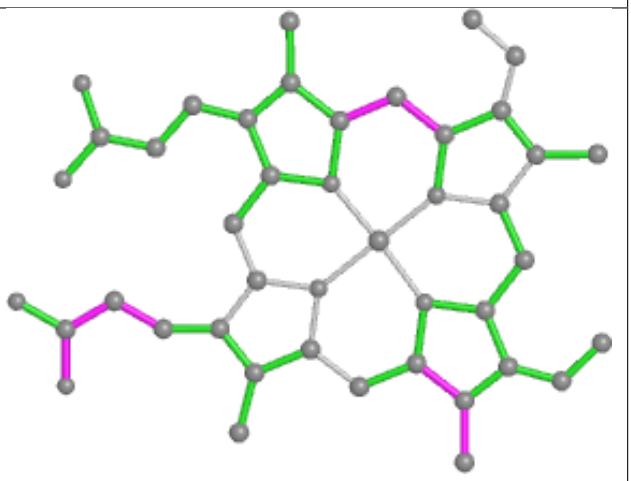


Rings

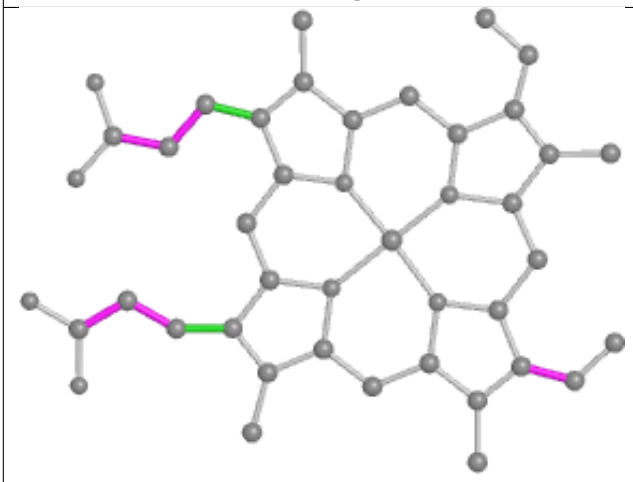
Ligand HEM A 560



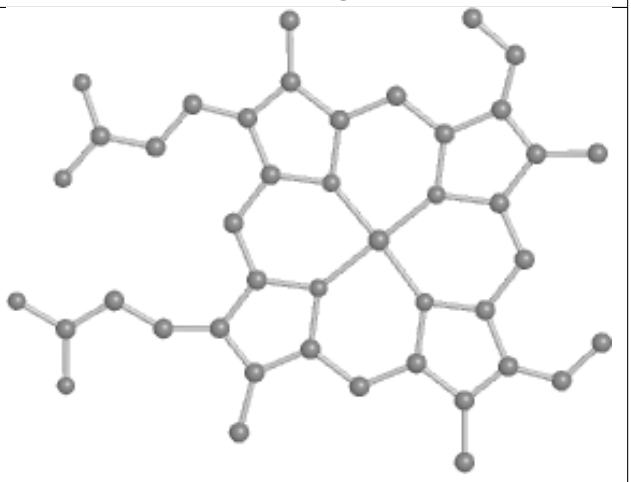
Bond lengths



Bond angles

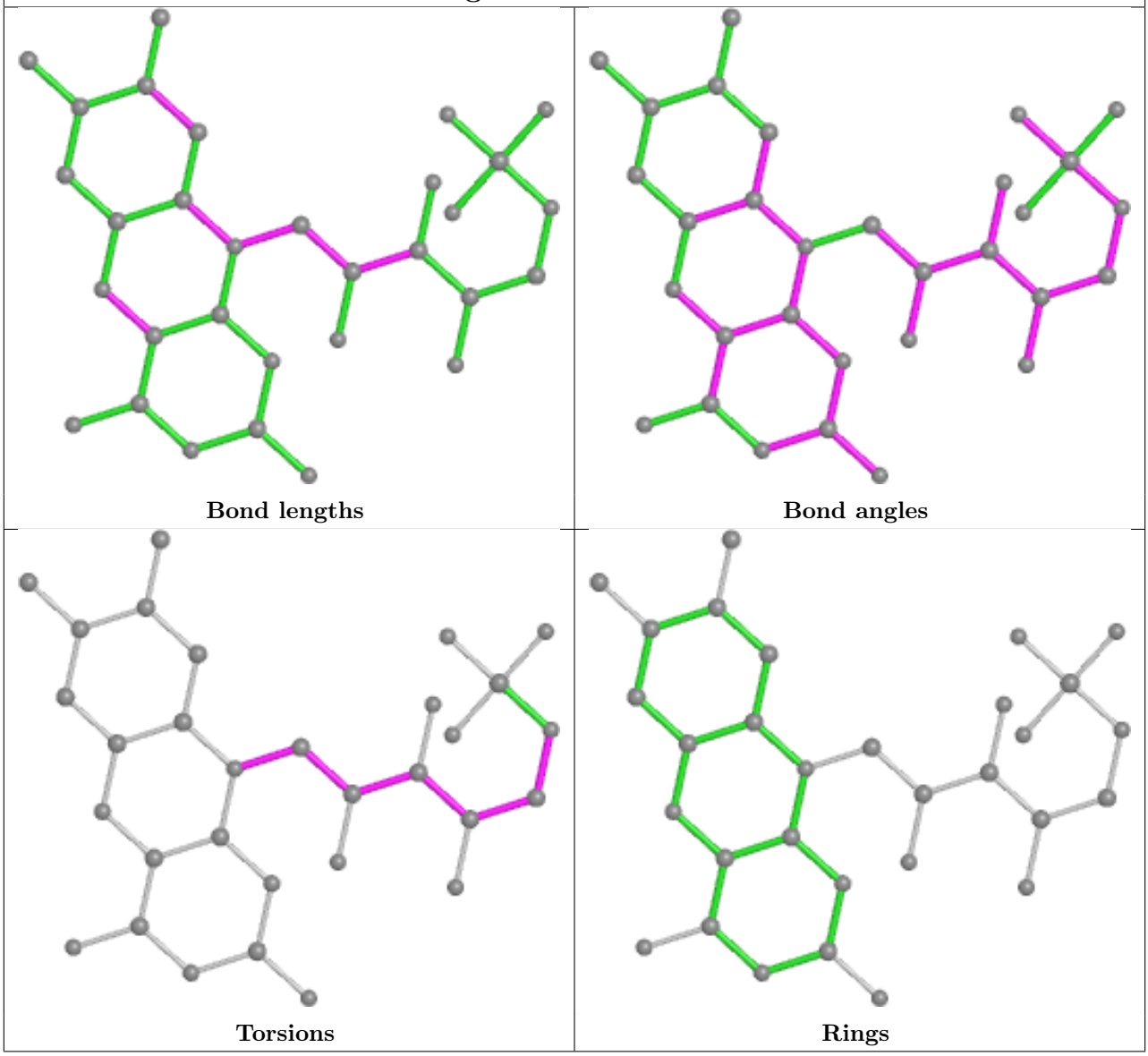


Torsions



Rings

Ligand FMN B 570



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.