



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 17, 2021 – 06:55 AM EDT

PDB ID : 1JRY  
Title : Crystal structure of Arg402Lys mutant flavocytochrome c3 from *Shewanella frigidimarina*  
Authors : Mowat, C.G.; Moysey, R.; Miles, C.S.; Leys, D.; Doherty, M.K.; Taylor, P.; Walkinshaw, M.D.; Reid, G.A.; Chapman, S.K.  
Deposited on : 2001-08-15  
Resolution : 2.00 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](mailto: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 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)	:	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)	:	2.23.2

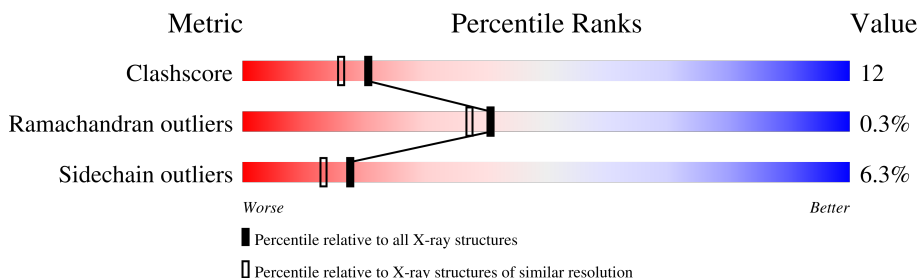
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	571	
1	B	571	

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
4	FAD	A	1805	X	-	-	-
4	FAD	B	2805	X	-	-	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10740 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 C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	568	Total	C	N	O	S	0	0	0
			4215	2615	742	833	25			
1	B	568	Total	C	N	O	S	0	0	0
			4215	2615	742	833	25			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	402	LYS	ARG	engineered mutation	UNP Q02469
B	402	LYS	ARG	engineered mutation	UNP Q02469

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C<sub>34</sub>H<sub>32</sub>FeN<sub>4</sub>O<sub>4</sub>).



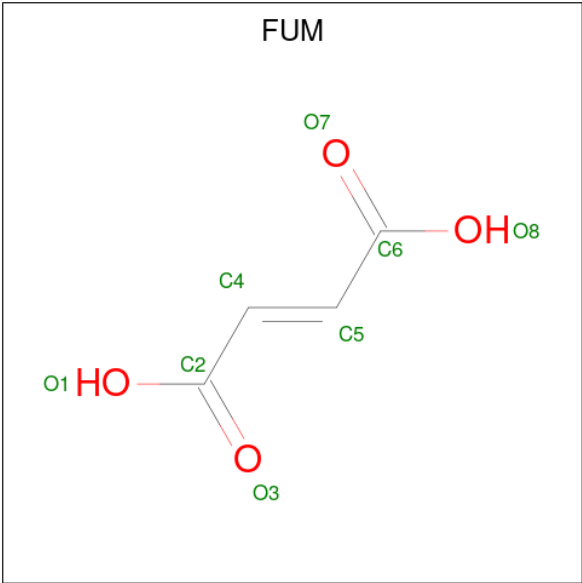
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0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

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



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

- Molecule 5 is FUMARIC ACID (three-letter code: FUM) (formula: C<sub>4</sub>H<sub>4</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			8	4	4		
5	B	1	Total	C	O	0	0
			8	4	4		

- Molecule 6 is water.

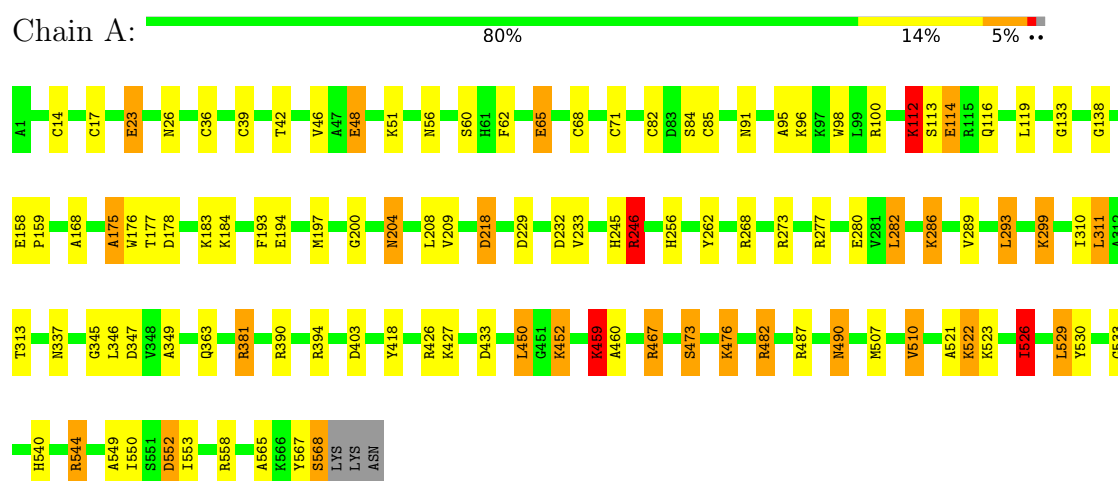
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	910	Total 910	O 910	0	0
6	B	932	Total 932	O 932	0	0

### 3 Residue-property plots

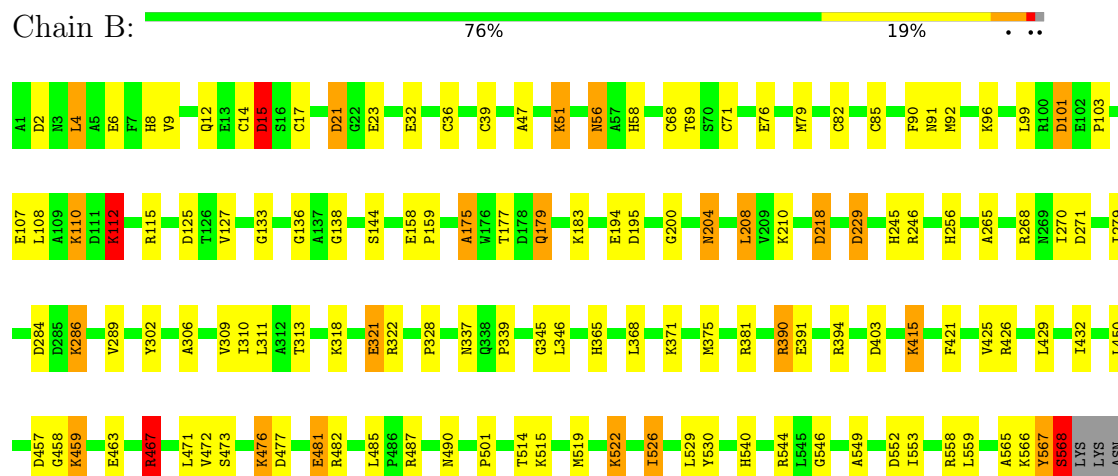
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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 C



#### • Molecule 1: FLAVOCYTOCHROME C



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.61Å 86.92Å 88.98Å 90.00° 104.48° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	99.9 (20.00-2.00)	Depositor
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.157 , 0.236	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10740	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FUM, FAD, NA, 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	0.69	0/4285	1.48	45/5792 (0.8%)
1	B	0.68	0/4285	1.48	42/5792 (0.7%)
All	All	0.68	0/8570	1.48	87/11584 (0.8%)

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	2
1	B	0	3
All	All	0	5

There are no bond length outliers.

All (87) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	487	ARG	CD-NE-CZ	24.28	157.60	123.60
1	A	487	ARG	NE-CZ-NH1	-15.64	112.48	120.30
1	B	381	ARG	NE-CZ-NH1	14.83	127.72	120.30
1	B	390	ARG	NE-CZ-NH2	-13.64	113.48	120.30
1	B	390	ARG	NE-CZ-NH1	12.80	126.70	120.30
1	A	487	ARG	NE-CZ-NH2	12.48	126.54	120.30
1	A	381	ARG	NE-CZ-NH1	12.45	126.53	120.30
1	B	175	ALA	O-C-N	-12.41	102.84	122.70
1	A	293	LEU	CA-CB-CG	12.36	143.72	115.30
1	A	218	ASP	CB-CG-OD1	-10.81	108.57	118.30
1	B	268	ARG	NE-CZ-NH2	-9.74	115.43	120.30
1	B	112	LYS	C-N-CA	9.66	145.86	121.70

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	112	LYS	C-N-CA	9.56	145.59	121.70
1	A	178	ASP	CB-CG-OD2	9.43	126.79	118.30
1	B	487	ARG	NE-CZ-NH1	9.19	124.89	120.30
1	B	394	ARG	NE-CZ-NH2	-9.12	115.74	120.30
1	A	544	ARG	NE-CZ-NH2	8.96	124.78	120.30
1	A	390	ARG	NE-CZ-NH2	-8.40	116.10	120.30
1	A	467	ARG	CD-NE-CZ	8.31	135.24	123.60
1	A	403	ASP	CB-CG-OD2	8.17	125.65	118.30
1	A	347	ASP	CB-CG-OD1	8.01	125.51	118.30
1	A	567	TYR	C-N-CA	7.81	141.22	121.70
1	B	15	ASP	CB-CG-OD2	7.32	124.88	118.30
1	B	544	ARG	NE-CZ-NH2	7.30	123.95	120.30
1	A	23	GLU	CA-CB-CG	7.29	129.45	113.40
1	A	246	ARG	NE-CZ-NH1	-7.26	116.67	120.30
1	A	394	ARG	NE-CZ-NH2	-7.24	116.68	120.30
1	A	526	ILE	CA-CB-CG2	7.18	125.27	110.90
1	B	15	ASP	CB-CG-OD1	-7.11	111.90	118.30
1	B	558	ARG	NE-CZ-NH2	-7.10	116.75	120.30
1	B	115	ARG	NE-CZ-NH1	7.06	123.83	120.30
1	B	175	ALA	CA-C-N	7.02	132.64	117.20
1	A	48	GLU	OE1-CD-OE2	6.90	131.57	123.30
1	A	175	ALA	N-CA-CB	6.87	119.72	110.10
1	A	567	TYR	CA-C-O	6.87	134.52	120.10
1	B	194	GLU	CA-CB-CG	6.82	128.41	113.40
1	A	390	ARG	NE-CZ-NH1	6.71	123.66	120.30
1	A	268	ARG	NE-CZ-NH2	-6.69	116.96	120.30
1	B	229	ASP	CB-CG-OD1	6.64	124.28	118.30
1	A	273	ARG	NE-CZ-NH1	-6.61	117.00	120.30
1	A	293	LEU	CB-CA-C	-6.57	97.71	110.20
1	B	467	ARG	CD-NE-CZ	6.51	132.71	123.60
1	B	482	ARG	NE-CZ-NH1	-6.50	117.05	120.30
1	A	175	ALA	C-N-CA	6.48	137.90	121.70
1	A	510	VAL	CA-CB-CG2	-6.46	101.22	110.90
1	A	62	PHE	CB-CG-CD2	-6.30	116.39	120.80
1	B	426	ARG	NE-CZ-NH1	-6.21	117.19	120.30
1	A	558	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	A	526	ILE	CB-CA-C	6.13	123.87	111.60
1	A	286	LYS	CA-CB-CG	6.12	126.87	113.40
1	B	286	LYS	CD-CE-NZ	6.11	125.76	111.70
1	B	218	ASP	CB-CG-OD1	-6.09	112.82	118.30
1	A	394	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	A	459	LYS	CB-CA-C	6.05	122.51	110.40

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	567	TYR	O-C-N	-6.05	113.01	122.70
1	B	403	ASP	CB-CG-OD2	6.01	123.71	118.30
1	A	487	ARG	CG-CD-NE	-5.98	99.25	111.80
1	A	433	ASP	CB-CG-OD1	5.93	123.64	118.30
1	A	544	ARG	NE-CZ-NH1	-5.92	117.34	120.30
1	A	552	ASP	CB-CG-OD1	5.82	123.54	118.30
1	B	2	ASP	CB-CG-OD1	-5.81	113.07	118.30
1	A	381	ARG	NH1-CZ-NH2	-5.71	113.12	119.40
1	B	381	ARG	NE-CZ-NH2	-5.63	117.49	120.30
1	A	482	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	B	284	ASP	CB-CG-OD1	5.59	123.33	118.30
1	B	568	SER	CA-C-O	-5.58	108.37	120.10
1	B	76	GLU	OE1-CD-OE2	-5.57	116.62	123.30
1	B	69	THR	CA-CB-CG2	-5.56	104.62	112.40
1	A	418	TYR	CB-CG-CD2	5.47	124.28	121.00
1	B	271	ASP	CB-CG-OD1	5.44	123.20	118.30
1	B	195	ASP	CB-CG-OD2	5.42	123.18	118.30
1	B	289	VAL	CA-CB-CG2	5.41	119.02	110.90
1	B	567	TYR	CB-CG-CD1	-5.39	117.77	121.00
1	B	568	SER	CB-CA-C	5.30	120.18	110.10
1	B	467	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	B	32	GLU	OE1-CD-OE2	-5.29	116.95	123.30
1	A	487	ARG	CD-NE-CZ	5.28	131.00	123.60
1	B	487	ARG	CG-CD-NE	-5.21	100.85	111.80
1	A	277	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	A	473	SER	N-CA-CB	5.18	118.27	110.50
1	B	125	ASP	CB-CG-OD1	5.17	122.95	118.30
1	B	391	GLU	OE1-CD-OE2	-5.14	117.13	123.30
1	A	100	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	A	450	LEU	CA-CB-CG	5.10	127.04	115.30
1	B	208	LEU	CB-CG-CD1	5.09	119.66	111.00
1	B	76	GLU	CG-CD-OE1	5.03	128.35	118.30
1	B	322	ARG	NE-CZ-NH2	-5.03	117.79	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	175	ALA	Mainchain,Peptide
1	B	101	ASP	Mainchain
1	B	175	ALA	Mainchain,Peptide

## 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	4215	0	4159	103	0
1	B	4215	0	4159	111	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	172	0	120	30	0
3	B	172	0	120	30	0
4	A	53	0	31	5	0
4	B	53	0	31	2	0
5	A	8	0	2	0	0
5	B	8	0	2	1	0
6	A	910	0	0	21	0
6	B	932	0	0	27	0
All	All	10740	0	8624	215	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 12.

All (215) 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:68:CYS:SG	3:B:803:HEM:CAB	2.42	1.07
1:B:36:CYS:SG	3:B:802:HEM:CAB	2.43	1.06
1:B:82:CYS:SG	3:B:804:HEM:CAB	2.44	1.05
1:A:36:CYS:SG	3:A:802:HEM:CAB	2.45	1.04
1:A:68:CYS:SG	3:A:803:HEM:CAB	2.49	1.00
1:B:14:CYS:SG	3:B:801:HEM:CAB	2.50	1.00
1:B:17:CYS:SG	3:B:801:HEM:CAC	2.48	1.00
1:A:85:CYS:SG	3:A:804:HEM:CAC	2.50	0.99
1:B:71:CYS:SG	3:B:803:HEM:CAC	2.50	0.99
1:B:39:CYS:HG	3:B:802:HEM:CAC	1.76	0.98
1:A:14:CYS:SG	3:A:801:HEM:CAB	2.51	0.98
1:B:68:CYS:HG	3:B:803:HEM:CAB	1.77	0.97
1:A:82:CYS:HG	3:A:804:HEM:CAB	1.76	0.97
1:B:39:CYS:SG	3:B:802:HEM:CAC	2.54	0.96
1:A:71:CYS:SG	3:A:803:HEM:CAC	2.54	0.96

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:CYS:SG	3:A:804:HEM:CAB	2.53	0.95
1:A:229:ASP:H	1:A:256:HIS:HE1	1.09	0.94
1:B:229:ASP:H	1:B:256:HIS:HE1	1.15	0.93
1:B:85:CYS:SG	3:B:804:HEM:CAC	2.56	0.93
1:A:14:CYS:HG	3:A:801:HEM:CAB	1.82	0.93
1:A:280:GLU:HB3	1:A:293:LEU:HD13	1.51	0.93
1:B:14:CYS:HG	3:B:801:HEM:CAB	1.82	0.92
1:A:39:CYS:SG	3:A:802:HEM:CAC	2.60	0.90
1:A:17:CYS:SG	3:A:801:HEM:CAC	2.59	0.89
1:A:282:LEU:HD11	1:A:293:LEU:HD12	1.56	0.88
1:B:71:CYS:HG	3:B:803:HEM:CAC	1.87	0.88
1:A:229:ASP:H	1:A:256:HIS:CE1	1.92	0.86
1:B:204:ASN:H	1:B:204:ASN:HD22	1.25	0.83
1:B:14:CYS:SG	3:B:801:HEM:HAB	2.20	0.82
1:B:82:CYS:HG	3:B:804:HEM:CAB	1.93	0.81
1:B:179:GLN:H	1:B:179:GLN:HE21	1.26	0.81
1:B:36:CYS:SG	3:B:802:HEM:HAB	2.21	0.81
1:A:218:ASP:HB3	6:A:1958:HOH:O	1.81	0.80
1:B:218:ASP:HB3	6:B:3344:HOH:O	1.80	0.79
1:B:526:ILE:HG21	6:B:3525:HOH:O	1.82	0.79
1:B:229:ASP:H	1:B:256:HIS:CE1	2.00	0.78
1:A:204:ASN:HD22	1:A:204:ASN:H	1.30	0.77
1:A:14:CYS:SG	3:A:801:HEM:HAB	2.22	0.77
1:A:427:LYS:HE3	1:B:328:PRO:HB3	1.66	0.76
1:B:522:LYS:HE2	6:B:3693:HOH:O	1.88	0.74
1:B:459:LYS:HE2	6:B:3373:HOH:O	1.89	0.72
1:B:68:CYS:SG	3:B:803:HEM:HAB	2.28	0.72
1:B:82:CYS:SG	3:B:804:HEM:HAB	2.28	0.71
1:B:183:LYS:HE2	6:B:2865:HOH:O	1.90	0.70
1:B:179:GLN:H	1:B:179:GLN:NE2	1.90	0.70
1:B:112:LYS:HG3	6:B:3624:HOH:O	1.92	0.69
1:A:36:CYS:SG	3:A:802:HEM:HAB	2.31	0.69
1:A:522:LYS:HD3	6:A:1972:HOH:O	1.93	0.68
1:B:415:LYS:HE2	6:B:3208:HOH:O	1.93	0.68
1:B:90:PHE:HB2	6:B:3736:HOH:O	1.94	0.67
1:A:200:GLY:HA3	1:A:204:ASN:HD21	1.59	0.67
1:A:459:LYS:HD2	1:A:460:ALA:N	2.10	0.66
1:B:200:GLY:HA3	1:B:204:ASN:HD21	1.61	0.65
1:A:71:CYS:SG	3:A:803:HEM:HAC	2.38	0.64
1:B:17:CYS:SG	3:B:801:HEM:HAC	2.38	0.63
1:A:299:LYS:HB3	6:A:1874:HOH:O	1.99	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:LEU:CD1	1:A:293:LEU:HD12	2.27	0.61
1:B:368:LEU:HB2	6:B:3605:HOH:O	1.98	0.61
1:B:39:CYS:SG	3:B:802:HEM:HAC	2.40	0.61
1:B:71:CYS:SG	3:B:803:HEM:HAC	2.41	0.61
1:A:293:LEU:HG	6:A:2336:HOH:O	2.02	0.60
1:A:183:LYS:CE	1:A:233:VAL:H	2.14	0.60
1:A:467:ARG:HD2	6:A:2301:HOH:O	2.01	0.59
1:B:459:LYS:HD2	6:B:3357:HOH:O	2.02	0.59
1:A:568:SER:HB3	6:A:1221:HOH:O	2.02	0.59
1:A:229:ASP:N	1:A:256:HIS:HE1	1.91	0.59
1:B:4:LEU:HD22	1:B:8:HIS:CE1	2.37	0.59
1:B:51:LYS:HG3	6:B:3043:HOH:O	2.03	0.58
1:B:39:CYS:SG	3:B:802:HEM:C3C	2.96	0.58
1:A:119:LEU:HD11	1:A:293:LEU:HD11	1.85	0.58
1:A:426:ARG:HH22	1:A:427:LYS:HD3	1.69	0.57
1:A:565:ALA:O	1:A:568:SER:HA	2.05	0.57
1:B:476:LYS:HB2	6:B:3215:HOH:O	2.04	0.57
1:B:136:GLY:HA3	1:B:553:ILE:HD12	1.86	0.56
1:B:467:ARG:HD2	6:B:3424:HOH:O	2.05	0.56
1:B:82:CYS:SG	3:B:804:HEM:C3B	2.98	0.56
1:A:158:GLU:HB3	1:A:159:PRO:HD2	1.87	0.56
1:B:56:ASN:HD22	1:B:58:HIS:H	1.53	0.56
1:A:177:THR:OG1	1:A:245:HIS:HE1	1.89	0.55
1:B:71:CYS:SG	3:B:803:HEM:C3C	2.99	0.55
1:A:68:CYS:SG	3:A:803:HEM:HAB	2.42	0.55
1:B:265:ALA:HA	1:B:270:ILE:HD12	1.87	0.55
1:A:204:ASN:H	1:A:204:ASN:ND2	2.03	0.55
1:A:282:LEU:HD11	1:A:293:LEU:CD1	2.35	0.55
1:B:567:TYR:O	1:B:568:SER:HB3	2.06	0.54
1:A:85:CYS:SG	3:A:804:HEM:CBC	2.96	0.54
1:B:17:CYS:SG	3:B:801:HEM:C3C	2.99	0.54
1:B:318:LYS:HD2	1:B:339:PRO:O	2.07	0.54
1:A:39:CYS:SG	3:A:802:HEM:C3C	3.00	0.54
1:A:183:LYS:O	1:A:184:LYS:HB2	2.08	0.54
1:A:349:ALA:CB	1:A:510:VAL:HG21	2.38	0.54
1:B:311:LEU:HD22	1:B:311:LEU:N	2.23	0.54
1:B:177:THR:OG1	1:B:245:HIS:HE1	1.91	0.54
1:B:107:GLU:O	1:B:110:LYS:HG2	2.07	0.53
1:B:549:ALA:HB3	4:B:2805:FAD:N1	2.23	0.53
1:A:82:CYS:SG	3:A:804:HEM:C3B	2.98	0.53
1:B:519:MET:HE3	6:B:3595:HOH:O	2.08	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:ALA:HB1	6:A:2876:HOH:O	2.08	0.53
1:B:467:ARG:HH11	1:B:467:ARG:CB	2.22	0.53
1:A:85:CYS:SG	3:A:804:HEM:C3C	3.03	0.52
1:A:533:GLY:HA2	1:A:553:ILE:HG22	1.90	0.52
1:B:68:CYS:SG	3:B:803:HEM:C3B	3.03	0.52
1:B:540:HIS:HE1	1:B:552:ASP:OD2	1.92	0.51
1:A:299:LYS:HG3	6:A:2877:HOH:O	2.11	0.51
1:A:65:GLU:HG2	1:A:262:TYR:OH	2.11	0.51
1:B:302:TYR:HA	6:B:3610:HOH:O	2.11	0.51
1:A:427:LYS:HD3	6:A:1670:HOH:O	2.11	0.50
1:A:522:LYS:HD2	6:A:2174:HOH:O	2.11	0.50
1:A:426:ARG:NH2	1:A:427:LYS:HD3	2.26	0.50
1:B:68:CYS:HG	3:B:803:HEM:CBB	2.23	0.50
1:A:133:GLY:O	1:A:138:GLY:HA3	2.12	0.50
1:A:17:CYS:SG	3:A:801:HEM:C3C	3.05	0.50
1:A:346:LEU:HD23	1:A:510:VAL:HG23	1.93	0.50
1:B:204:ASN:H	1:B:204:ASN:ND2	2.00	0.49
1:B:371:LYS:HE3	6:B:3685:HOH:O	2.12	0.49
1:B:546:GLY:HA2	5:B:2806:FUM:O7	2.13	0.49
1:B:365:HIS:O	1:B:501:PRO:HA	2.13	0.49
1:B:56:ASN:ND2	1:B:58:HIS:H	2.10	0.49
1:A:183:LYS:HZ1	1:A:233:VAL:H	1.61	0.49
1:A:540:HIS:HE1	1:A:552:ASP:OD2	1.95	0.49
1:A:549:ALA:HB3	4:A:1805:FAD:N1	2.27	0.49
1:A:91:ASN:HB2	6:A:2583:HOH:O	2.13	0.48
1:A:36:CYS:SG	3:A:802:HEM:CBB	3.00	0.48
1:B:210:LYS:HE2	6:B:3701:HOH:O	2.14	0.48
1:B:210:LYS:HE3	6:B:3585:HOH:O	2.13	0.48
1:B:565:ALA:O	1:B:568:SER:HA	2.14	0.48
1:A:112:LYS:HE3	1:A:112:LYS:HA	1.96	0.48
1:A:183:LYS:NZ	1:A:233:VAL:H	2.10	0.48
1:A:346:LEU:CD2	1:A:510:VAL:HG23	2.44	0.48
1:B:85:CYS:SG	3:B:804:HEM:CBC	3.01	0.48
1:A:459:LYS:HG2	6:A:2766:HOH:O	2.14	0.47
1:B:540:HIS:HD2	6:B:2848:HOH:O	1.96	0.47
1:A:26:ASN:HA	1:A:299:LYS:HE3	1.96	0.47
1:B:103:PRO:HB3	6:B:3264:HOH:O	2.14	0.47
1:A:232:ASP:HB3	1:A:246:ARG:HG2	1.96	0.47
1:A:311:LEU:HD23	1:A:349:ALA:HB2	1.97	0.47
1:B:309:VAL:HG12	1:B:311:LEU:HD22	1.98	0.46
1:B:313:THR:OG1	1:B:345:GLY:HA3	2.15	0.46

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:CYS:SG	3:A:803:HEM:C3B	3.08	0.46
1:B:108:LEU:CD1	1:B:279:ILE:HD12	2.45	0.46
1:B:90:PHE:HD1	6:B:3736:HOH:O	1.98	0.46
1:A:82:CYS:HG	3:A:804:HEM:CBB	2.27	0.46
1:B:375:MET:CE	4:B:2805:FAD:H6	2.45	0.46
1:B:68:CYS:SG	3:B:803:HEM:CBB	3.03	0.45
1:B:522:LYS:N	1:B:522:LYS:HE3	2.31	0.45
1:B:85:CYS:SG	3:B:804:HEM:C3C	3.09	0.45
1:A:23:GLU:HB3	6:A:2214:HOH:O	2.15	0.45
1:A:116:GLN:HB2	6:A:1608:HOH:O	2.17	0.45
1:A:427:LYS:HG3	6:A:1537:HOH:O	2.16	0.45
1:B:4:LEU:HD22	1:B:8:HIS:HE1	1.79	0.45
1:B:310:ILE:HG12	1:B:530:TYR:HB2	1.99	0.45
1:A:526:ILE:HG13	1:A:529:LEU:HB2	1.99	0.45
4:A:1805:FAD:H1'1	4:A:1805:FAD:H9	1.59	0.45
1:B:309:VAL:HG12	1:B:311:LEU:CD2	2.46	0.45
1:B:458:GLY:HA3	6:B:3342:HOH:O	2.17	0.45
1:A:427:LYS:HA	1:A:427:LYS:HD2	1.64	0.45
1:A:17:CYS:SG	3:A:801:HEM:CBC	3.03	0.45
1:B:47:ALA:HA	1:B:58:HIS:HB2	1.99	0.45
1:A:60:SER:HB3	3:A:804:HEM:HMB1	1.98	0.44
1:A:540:HIS:CD2	1:A:544:ARG:HG3	2.52	0.44
1:B:79:MET:HG2	1:B:96:LYS:HG3	1.99	0.44
1:A:36:CYS:SG	3:A:802:HEM:C3B	3.09	0.44
1:B:15:ASP:HB3	6:B:3282:HOH:O	2.16	0.44
1:B:133:GLY:O	1:B:138:GLY:HA3	2.18	0.44
1:A:476:LYS:N	1:A:476:LYS:HD3	2.33	0.44
1:A:459:LYS:HD2	1:A:459:LYS:C	2.33	0.44
1:A:71:CYS:SG	3:A:803:HEM:C3C	3.10	0.44
1:B:177:THR:HB	1:B:179:GLN:NE2	2.33	0.44
1:A:84:SER:HB3	1:A:98:TRP:CE2	2.53	0.43
1:B:421:PHE:HB2	1:B:425:VAL:HB	2.00	0.43
1:B:471:LEU:CD2	1:B:476:LYS:HZ1	2.32	0.43
1:A:42:THR:O	1:A:46:VAL:HG23	2.18	0.43
1:A:168:ALA:HA	4:A:1805:FAD:N5	2.34	0.43
1:A:193:PHE:CD2	1:A:209:VAL:HG12	2.53	0.43
1:A:490:ASN:N	1:A:490:ASN:HD22	2.16	0.43
1:A:168:ALA:HA	4:A:1805:FAD:C5X	2.49	0.43
1:B:158:GLU:HB3	1:B:159:PRO:HD2	2.00	0.43
1:A:550:ILE:HG12	4:A:1805:FAD:C2	2.49	0.43
1:B:101:ASP:HB3	6:B:3358:HOH:O	2.19	0.42

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:MET:HE2	6:A:2880:HOH:O	2.18	0.42
1:A:452:LYS:HE2	6:A:2148:HOH:O	2.18	0.42
1:A:521:ALA:HB3	6:A:2174:HOH:O	2.18	0.42
1:A:293:LEU:CG	6:A:2336:HOH:O	2.65	0.42
1:B:514:THR:O	1:B:559:LEU:HD21	2.19	0.42
1:B:321:GLU:HB2	6:B:3397:HOH:O	2.18	0.42
1:B:472:VAL:HG22	1:B:485:LEU:HB3	2.01	0.42
1:B:8:HIS:O	1:B:12:GLN:HG2	2.19	0.42
1:B:471:LEU:HD23	1:B:476:LYS:HZ1	1.84	0.42
3:A:804:HEM:HMC1	3:A:804:HEM:HBC2	2.01	0.42
1:A:183:LYS:HD3	6:A:1982:HOH:O	2.20	0.42
1:A:363:GLN:HB2	1:A:507:MET:SD	2.60	0.42
1:A:381:ARG:O	1:A:482:ARG:NH2	2.52	0.42
1:A:39:CYS:SG	3:A:802:HEM:CBC	3.05	0.42
1:A:313:THR:OG1	1:A:345:GLY:HA3	2.20	0.42
1:B:127:VAL:O	1:B:306:ALA:HA	2.19	0.42
1:B:21:ASP:HB3	1:B:23:GLU:OE1	2.20	0.41
1:A:48:GLU:HA	1:A:51:LYS:HD2	2.02	0.41
1:B:477:ASP:O	1:B:481:GLU:HA	2.20	0.41
1:A:194:GLU:O	1:A:194:GLU:HG2	2.17	0.41
1:A:310:ILE:HG12	1:A:530:TYR:HB2	2.03	0.41
1:B:457:ASP:OD1	1:B:459:LYS:HE3	2.21	0.41
1:A:82:CYS:SG	3:A:804:HEM:CBB	3.05	0.41
1:A:112:LYS:HE2	6:A:2881:HOH:O	2.20	0.41
1:B:522:LYS:HD2	6:B:3123:HOH:O	2.20	0.41
1:B:92:MET:HB2	3:B:803:HEM:HMD3	2.02	0.41
1:B:311:LEU:N	1:B:311:LEU:CD2	2.84	0.41
1:A:490:ASN:HD22	1:A:490:ASN:H	1.69	0.41
1:B:204:ASN:HD22	1:B:204:ASN:N	2.05	0.41
1:B:286:LYS:HE2	6:B:3450:HOH:O	2.21	0.41
1:B:346:LEU:HD23	1:B:346:LEU:HA	1.92	0.40
1:B:429:LEU:HD23	1:B:432:ILE:HG13	2.02	0.40
1:B:6:GLU:HA	1:B:9:VAL:HG22	2.04	0.40
1:A:14:CYS:SG	3:A:801:HEM:C3B	3.11	0.40
1:B:112:LYS:HD2	1:B:112:LYS:HA	1.86	0.40
1:B:311:LEU:CD2	1:B:529:LEU:HD11	2.52	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	566/571 (99%)	542 (96%)	21 (4%)	3 (0%)	29	23
1	B	566/571 (99%)	546 (96%)	20 (4%)	0	100	100
All	All	1132/1142 (99%)	1088 (96%)	41 (4%)	3 (0%)	41	37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	176	TRP
1	A	113	SER
1	A	114	GLU

### 5.3.2 Protein sidechains

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	442/445 (99%)	417 (94%)	25 (6%)	20	16
1	B	442/445 (99%)	411 (93%)	31 (7%)	15	10
All	All	884/890 (99%)	828 (94%)	56 (6%)	18	13

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	ASN
1	A	65	GLU
1	A	96	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	112	LYS
1	A	114	GLU
1	A	204	ASN
1	A	208	LEU
1	A	246	ARG
1	A	282	LEU
1	A	286	LYS
1	A	289	VAL
1	A	299	LYS
1	A	311	LEU
1	A	337	ASN
1	A	450	LEU
1	A	452	LYS
1	A	459	LYS
1	A	473	SER
1	A	476	LYS
1	A	490	ASN
1	A	522	LYS
1	A	523	LYS
1	A	526	ILE
1	A	529	LEU
1	A	568	SER
1	B	4	LEU
1	B	15	ASP
1	B	21	ASP
1	B	51	LYS
1	B	56	ASN
1	B	91	ASN
1	B	99	LEU
1	B	110	LYS
1	B	112	LYS
1	B	144	SER
1	B	179	GLN
1	B	204	ASN
1	B	208	LEU
1	B	246	ARG
1	B	321	GLU
1	B	337	ASN
1	B	390	ARG
1	B	415	LYS
1	B	450	LEU
1	B	459	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	463	GLU
1	B	467	ARG
1	B	473	SER
1	B	476	LYS
1	B	481	GLU
1	B	490	ASN
1	B	515	LYS
1	B	522	LYS
1	B	526	ILE
1	B	566	LYS
1	B	568	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	56	ASN
1	A	91	ASN
1	A	202	ASN
1	A	204	ASN
1	A	245	HIS
1	A	256	HIS
1	A	490	ASN
1	A	540	HIS
1	B	10	GLN
1	B	56	ASN
1	B	91	ASN
1	B	179	GLN
1	B	204	ASN
1	B	245	HIS
1	B	256	HIS
1	B	490	ASN
1	B	540	HIS

### 5.3.3 RNA ⓘ

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 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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	804	1	27,50,50	2.03	5 (18%)	17,82,82	2.12	8 (47%)
4	FAD	A	1805	-	51,58,58	1.82	13 (25%)	60,89,89	3.33	26 (43%)
5	FUM	A	1806	-	1,7,7	0.77	0	2,8,8	1.60	0
3	HEM	A	803	1	27,50,50	1.99	7 (25%)	17,82,82	1.95	7 (41%)
3	HEM	A	802	1	27,50,50	2.09	5 (18%)	17,82,82	1.96	6 (35%)
5	FUM	B	2806	-	1,7,7	0.78	0	2,8,8	1.94	1 (50%)
3	HEM	A	801	1	27,50,50	2.12	7 (25%)	17,82,82	1.93	5 (29%)
3	HEM	B	802	1	27,50,50	2.03	6 (22%)	17,82,82	2.13	8 (47%)
3	HEM	B	804	1	27,50,50	2.09	5 (18%)	17,82,82	2.07	5 (29%)
3	HEM	B	803	1	27,50,50	2.16	6 (22%)	17,82,82	2.06	7 (41%)
4	FAD	B	2805	-	51,58,58	1.95	12 (23%)	60,89,89	3.60	28 (46%)
3	HEM	B	801	1	27,50,50	2.14	7 (25%)	17,82,82	2.00	6 (35%)

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	804	1	-	1/6/54/54	-
4	FAD	A	1805	-	2/2/9/9	10/30/50/50	0/6/6/6
3	HEM	B	801	1	-	1/6/54/54	-
5	FUM	A	1806	-	-	0/0/5/5	-
3	HEM	A	803	1	-	1/6/54/54	-
3	HEM	A	802	1	-	0/6/54/54	-
5	FUM	B	2806	-	-	0/0/5/5	-
3	HEM	A	801	1	-	1/6/54/54	-
3	HEM	B	802	1	-	0/6/54/54	-
3	HEM	B	804	1	-	1/6/54/54	-
3	HEM	B	803	1	-	0/6/54/54	-
4	FAD	B	2805	-	2/2/9/9	9/30/50/50	0/6/6/6

All (73) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2805	FAD	C1'-N10	6.33	1.54	1.48
4	B	2805	FAD	C4-C4X	5.89	1.51	1.41
3	A	802	HEM	C3B-C2B	-5.54	1.32	1.40
3	B	804	HEM	C3B-C2B	-5.44	1.32	1.40
3	B	803	HEM	C3C-C2C	-5.43	1.32	1.40
3	B	803	HEM	C3B-C2B	-5.34	1.33	1.40
3	B	801	HEM	C3B-C2B	-5.14	1.33	1.40
4	A	1805	FAD	C4-C4X	5.07	1.50	1.41
3	A	802	HEM	C3C-C2C	-5.06	1.33	1.40
3	B	801	HEM	C3C-C2C	-5.05	1.33	1.40
3	A	803	HEM	C3B-C2B	-5.03	1.33	1.40
3	B	802	HEM	C3C-C2C	-5.00	1.33	1.40
3	A	801	HEM	C3C-C2C	-4.90	1.33	1.40
3	A	804	HEM	C3C-C2C	-4.65	1.33	1.40
3	B	802	HEM	C3B-C2B	-4.56	1.34	1.40
3	A	804	HEM	C3B-C2B	-4.54	1.34	1.40
3	A	801	HEM	C3B-C2B	-4.50	1.34	1.40
4	A	1805	FAD	C4X-C10	4.28	1.43	1.38
3	A	804	HEM	C3C-CAC	4.26	1.56	1.47
4	A	1805	FAD	C1'-N10	4.26	1.52	1.48
4	A	1805	FAD	C10-N1	-4.24	1.27	1.33
3	A	803	HEM	C3C-C2C	-4.21	1.34	1.40
3	B	802	HEM	C3C-CAC	4.14	1.56	1.47
3	B	804	HEM	CAA-C2A	4.03	1.58	1.52
4	B	2805	FAD	C5'-C4'	3.94	1.57	1.51
3	B	801	HEM	C3C-CAC	3.92	1.55	1.47
3	A	803	HEM	C3B-CAB	3.86	1.55	1.47

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	804	HEM	C3C-CAC	3.85	1.55	1.47
4	A	1805	FAD	C4-N3	3.84	1.39	1.33
3	A	801	HEM	C3C-CAC	3.81	1.55	1.47
3	B	804	HEM	C3C-C2C	-3.71	1.35	1.40
3	A	802	HEM	C3C-CAC	3.67	1.55	1.47
3	A	804	HEM	C3B-CAB	3.65	1.55	1.47
4	B	2805	FAD	C4-N3	3.63	1.39	1.33
4	B	2805	FAD	C2A-N3A	3.55	1.37	1.32
4	A	1805	FAD	C5'-C4'	3.50	1.56	1.51
3	B	803	HEM	C3C-CAC	3.50	1.55	1.47
3	A	801	HEM	C3B-CAB	3.49	1.55	1.47
3	B	803	HEM	C3B-CAB	3.47	1.55	1.47
3	B	801	HEM	C3B-CAB	3.42	1.54	1.47
3	A	803	HEM	C3C-CAC	3.41	1.54	1.47
3	B	804	HEM	C3B-CAB	3.38	1.54	1.47
4	B	2805	FAD	C4X-C10	3.36	1.42	1.38
4	B	2805	FAD	C10-N1	-3.24	1.29	1.33
3	A	802	HEM	C3B-CAB	3.22	1.54	1.47
3	B	802	HEM	CAA-C2A	3.08	1.56	1.52
3	A	804	HEM	CAA-C2A	3.08	1.56	1.52
3	B	802	HEM	C3B-CAB	3.07	1.54	1.47
3	A	802	HEM	CAA-C2A	2.88	1.56	1.52
4	A	1805	FAD	O4-C4	-2.84	1.17	1.24
3	A	801	HEM	CAA-C2A	2.82	1.56	1.52
3	B	803	HEM	CAA-C2A	2.80	1.56	1.52
3	B	801	HEM	CAA-C2A	2.77	1.56	1.52
3	A	803	HEM	CAA-C2A	2.67	1.56	1.52
4	B	2805	FAD	O4-C4	-2.61	1.18	1.24
4	B	2805	FAD	C9-C8	2.51	1.44	1.37
3	A	803	HEM	CAD-C3D	2.48	1.56	1.52
3	A	801	HEM	C4A-NA	2.35	1.41	1.36
4	A	1805	FAD	C2A-N3A	2.35	1.35	1.32
3	B	803	HEM	CAD-C3D	2.34	1.56	1.52
4	B	2805	FAD	O3'-C3'	-2.25	1.37	1.43
3	B	801	HEM	C4A-NA	2.18	1.40	1.36
4	A	1805	FAD	C2B-C1B	2.17	1.57	1.53
4	A	1805	FAD	PA-O1A	-2.16	1.43	1.50
3	B	802	HEM	CMA-C3A	2.14	1.56	1.51
3	A	801	HEM	CMD-C2D	2.12	1.56	1.51
4	A	1805	FAD	C4X-N5	-2.11	1.30	1.33
4	A	1805	FAD	C9-C8	2.08	1.43	1.37
3	A	803	HEM	CMD-C2D	2.07	1.55	1.51

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2805	FAD	P-O2P	-2.03	1.45	1.55
4	B	2805	FAD	PA-O1A	-2.02	1.43	1.50
4	A	1805	FAD	O4'-C4'	2.02	1.47	1.43
3	B	801	HEM	CAD-C3D	2.00	1.55	1.52

All (107) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2805	FAD	C4-N3-C2	15.44	128.18	115.14
4	A	1805	FAD	C4-N3-C2	14.30	127.21	115.14
4	B	2805	FAD	C4X-C4-N3	-10.35	109.27	123.43
4	A	1805	FAD	C4X-C4-N3	-9.80	110.03	123.43
4	A	1805	FAD	O4B-C1B-C2B	-7.43	96.07	106.93
4	B	2805	FAD	C10-C4X-N5	6.51	125.76	121.26
4	B	2805	FAD	C1'-N10-C10	6.42	124.16	118.41
4	B	2805	FAD	C5A-C6A-N6A	6.09	129.61	120.35
4	B	2805	FAD	C5'-C4'-C3'	-6.02	100.57	112.20
4	A	1805	FAD	C5'-C4'-C3'	-5.79	101.01	112.20
4	B	2805	FAD	O4B-C1B-C2B	-5.62	98.72	106.93
4	A	1805	FAD	C1'-N10-C9A	-4.87	114.46	118.29
4	B	2805	FAD	C1'-N10-C9A	-4.66	114.62	118.29
4	A	1805	FAD	C1'-N10-C10	4.66	122.58	118.41
4	A	1805	FAD	C10-C4X-N5	4.54	124.40	121.26
3	B	804	HEM	CMB-C2B-C3B	4.37	132.85	124.68
4	B	2805	FAD	O3'-C3'-C4'	4.35	119.32	108.81
4	A	1805	FAD	C5A-C6A-N6A	4.26	126.83	120.35
4	A	1805	FAD	C4X-C10-N10	-4.20	115.98	120.30
3	A	802	HEM	CMD-C2D-C1D	-4.19	122.03	128.46
3	B	803	HEM	CMC-C2C-C3C	4.08	132.31	124.68
3	A	801	HEM	CMD-C2D-C1D	-4.05	122.23	128.46
4	A	1805	FAD	C4-C4X-C10	-4.05	117.27	119.95
4	B	2805	FAD	C4X-C10-N10	-4.01	116.18	120.30
3	B	801	HEM	CMD-C2D-C1D	-3.87	122.52	128.46
4	B	2805	FAD	O4'-C4'-C3'	-3.85	99.75	109.10
3	A	803	HEM	CBD-CAD-C3D	-3.83	105.41	112.48
4	A	1805	FAD	C4'-C3'-C2'	3.79	121.25	113.36
3	B	802	HEM	CMA-C3A-C4A	-3.79	122.64	128.46
4	B	2805	FAD	C4-C4X-C10	-3.70	117.50	119.95
4	B	2805	FAD	C1'-C2'-C3'	3.66	120.02	109.79
3	A	804	HEM	CMA-C3A-C4A	-3.56	122.99	128.46
3	B	804	HEM	CBD-CAD-C3D	3.50	118.92	112.48
3	B	804	HEM	CMD-C2D-C1D	-3.47	123.14	128.46

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1805	FAD	C6-C5X-N5	3.44	122.84	119.05
3	B	802	HEM	CMB-C2B-C3B	3.44	131.11	124.68
4	B	2805	FAD	O4B-C4B-C5B	3.42	120.61	109.37
3	B	803	HEM	CMD-C2D-C1D	-3.37	123.28	128.46
3	A	802	HEM	CMB-C2B-C3B	3.27	130.80	124.68
4	A	1805	FAD	O3'-C3'-C4'	3.27	116.71	108.81
4	A	1805	FAD	C3B-C2B-C1B	-3.25	96.09	100.98
3	A	804	HEM	CBD-CAD-C3D	3.22	118.42	112.48
4	B	2805	FAD	C6-C5X-N5	3.18	122.56	119.05
3	B	801	HEM	CMC-C2C-C3C	3.18	130.63	124.68
3	A	801	HEM	CMB-C2B-C3B	3.14	130.55	124.68
3	A	804	HEM	CMD-C2D-C1D	-3.13	123.65	128.46
3	A	804	HEM	CMC-C2C-C3C	3.12	130.51	124.68
3	B	802	HEM	CMC-C2C-C3C	3.07	130.43	124.68
3	A	801	HEM	CMA-C3A-C4A	-3.07	123.75	128.46
3	B	801	HEM	CMD-C2D-C3D	3.07	130.72	124.94
4	B	2805	FAD	C3B-C2B-C1B	-2.98	96.49	100.98
3	A	802	HEM	CMD-C2D-C3D	2.96	130.53	124.94
4	A	1805	FAD	O5B-C5B-C4B	2.96	119.19	108.99
3	B	801	HEM	CMB-C2B-C3B	2.96	130.21	124.68
3	B	802	HEM	CMD-C2D-C1D	-2.93	123.96	128.46
3	B	803	HEM	CMA-C3A-C4A	-2.93	123.97	128.46
3	A	801	HEM	CMD-C2D-C3D	2.91	130.42	124.94
3	A	804	HEM	CMB-C2B-C3B	2.78	129.88	124.68
4	B	2805	FAD	C4'-C3'-C2'	2.73	119.04	113.36
4	B	2805	FAD	C7M-C7-C8	-2.71	115.17	120.74
3	B	804	HEM	CMD-C2D-C3D	2.70	130.03	124.94
3	A	803	HEM	CAD-CBD-CGD	2.67	117.15	112.67
3	A	804	HEM	C4C-C3C-C2C	2.64	108.74	106.90
4	A	1805	FAD	O4B-C4B-C5B	2.60	117.93	109.37
4	B	2805	FAD	O5B-C5B-C4B	2.58	117.86	108.99
3	B	801	HEM	CAD-CBD-CGD	2.55	116.95	112.67
4	A	1805	FAD	C7M-C7-C8	-2.52	115.56	120.74
4	A	1805	FAD	C7M-C7-C6	2.50	126.33	120.34
3	A	804	HEM	CMD-C2D-C3D	2.50	129.65	124.94
4	B	2805	FAD	O2'-C2'-C1'	2.48	115.57	109.59
3	A	803	HEM	CMB-C2B-C3B	2.48	129.32	124.68
3	B	802	HEM	C3B-C4B-NB	-2.48	106.01	109.21
3	B	803	HEM	CMD-C2D-C3D	2.47	129.60	124.94
3	B	803	HEM	C4C-C3C-C2C	2.46	108.61	106.90
4	B	2805	FAD	C7M-C7-C6	2.46	126.22	120.34
4	A	1805	FAD	O2A-PA-O1A	2.44	124.29	112.24

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1805	FAD	C5X-C9A-N10	2.43	119.48	117.72
3	A	802	HEM	CMC-C2C-C3C	2.43	129.22	124.68
4	B	2805	FAD	C5X-C9A-N10	2.43	119.47	117.72
4	B	2805	FAD	O2A-PA-O1A	2.41	124.16	112.24
3	B	802	HEM	CBD-CAD-C3D	2.39	116.89	112.48
3	A	802	HEM	CAA-CBA-CGA	2.38	116.66	112.67
3	A	803	HEM	CMC-C2C-C3C	2.37	129.11	124.68
4	B	2805	FAD	C5B-C4B-C3B	-2.35	106.37	115.18
3	B	803	HEM	CMA-C3A-C2A	2.30	129.28	124.94
3	B	803	HEM	CMB-C2B-C3B	2.29	128.97	124.68
3	B	804	HEM	CAD-CBD-CGD	-2.29	108.84	112.67
4	B	2805	FAD	C1B-N9A-C4A	2.28	130.65	126.64
3	B	801	HEM	CMA-C3A-C4A	-2.28	124.96	128.46
3	A	803	HEM	CMD-C2D-C1D	-2.27	124.97	128.46
4	A	1805	FAD	C5A-C6A-N1A	-2.26	115.23	120.35
3	A	802	HEM	CMA-C3A-C4A	-2.26	125.00	128.46
3	A	804	HEM	CMA-C3A-C2A	2.20	129.09	124.94
3	B	802	HEM	CMA-C3A-C2A	2.20	129.09	124.94
4	A	1805	FAD	C5B-C4B-C3B	-2.19	106.96	115.18
4	A	1805	FAD	O4'-C4'-C3'	-2.17	103.83	109.10
4	B	2805	FAD	O5'-C5'-C4'	-2.16	103.61	109.36
3	A	803	HEM	CBA-CAA-C2A	-2.14	108.54	112.49
3	A	803	HEM	C4C-C3C-C2C	2.09	108.36	106.90
4	B	2805	FAD	O4'-C4'-C5'	-2.06	105.29	109.92
5	B	2806	FUM	C6-C5-C4	-2.05	119.31	123.69
4	A	1805	FAD	O2'-C2'-C3'	-2.04	104.14	109.10
3	B	802	HEM	CMD-C2D-C3D	2.03	128.77	124.94
3	A	801	HEM	CMA-C3A-C2A	2.02	128.75	124.94
4	A	1805	FAD	O3'-C3'-C2'	2.01	113.68	108.81
4	A	1805	FAD	O2P-P-O1P	2.01	122.19	112.24
4	B	2805	FAD	O3'-C3'-C2'	2.01	113.67	108.81

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1805	FAD	C3'
4	A	1805	FAD	C4'
4	B	2805	FAD	C3'
4	B	2805	FAD	C4'

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	803	HEM	C2A-CAA-CBA-CGA
4	A	1805	FAD	C1'-C2'-C3'-O3'
4	A	1805	FAD	C1'-C2'-C3'-C4'
4	A	1805	FAD	O2'-C2'-C3'-O3'
4	A	1805	FAD	O2'-C2'-C3'-C4'
4	A	1805	FAD	C3'-C4'-C5'-O5'
4	A	1805	FAD	O4'-C4'-C5'-O5'
4	A	1805	FAD	PA-O3P-P-O5'
4	B	2805	FAD	C1'-C2'-C3'-O3'
4	B	2805	FAD	C1'-C2'-C3'-C4'
4	B	2805	FAD	O2'-C2'-C3'-O3'
4	B	2805	FAD	O2'-C2'-C3'-C4'
4	B	2805	FAD	PA-O3P-P-O5'
4	B	2805	FAD	C3'-C4'-C5'-O5'
4	B	2805	FAD	P-O3P-PA-O1A
4	B	2805	FAD	P-O3P-PA-O2A
3	A	804	HEM	C2A-CAA-CBA-CGA
3	B	804	HEM	C2D-C3D-CAD-CBD
4	A	1805	FAD	P-O3P-PA-O1A
4	A	1805	FAD	P-O3P-PA-O2A
3	A	801	HEM	C3D-CAD-CBD-CGD
3	B	801	HEM	C3D-CAD-CBD-CGD
4	A	1805	FAD	O4B-C4B-C5B-O5B
4	B	2805	FAD	O4B-C4B-C5B-O5B

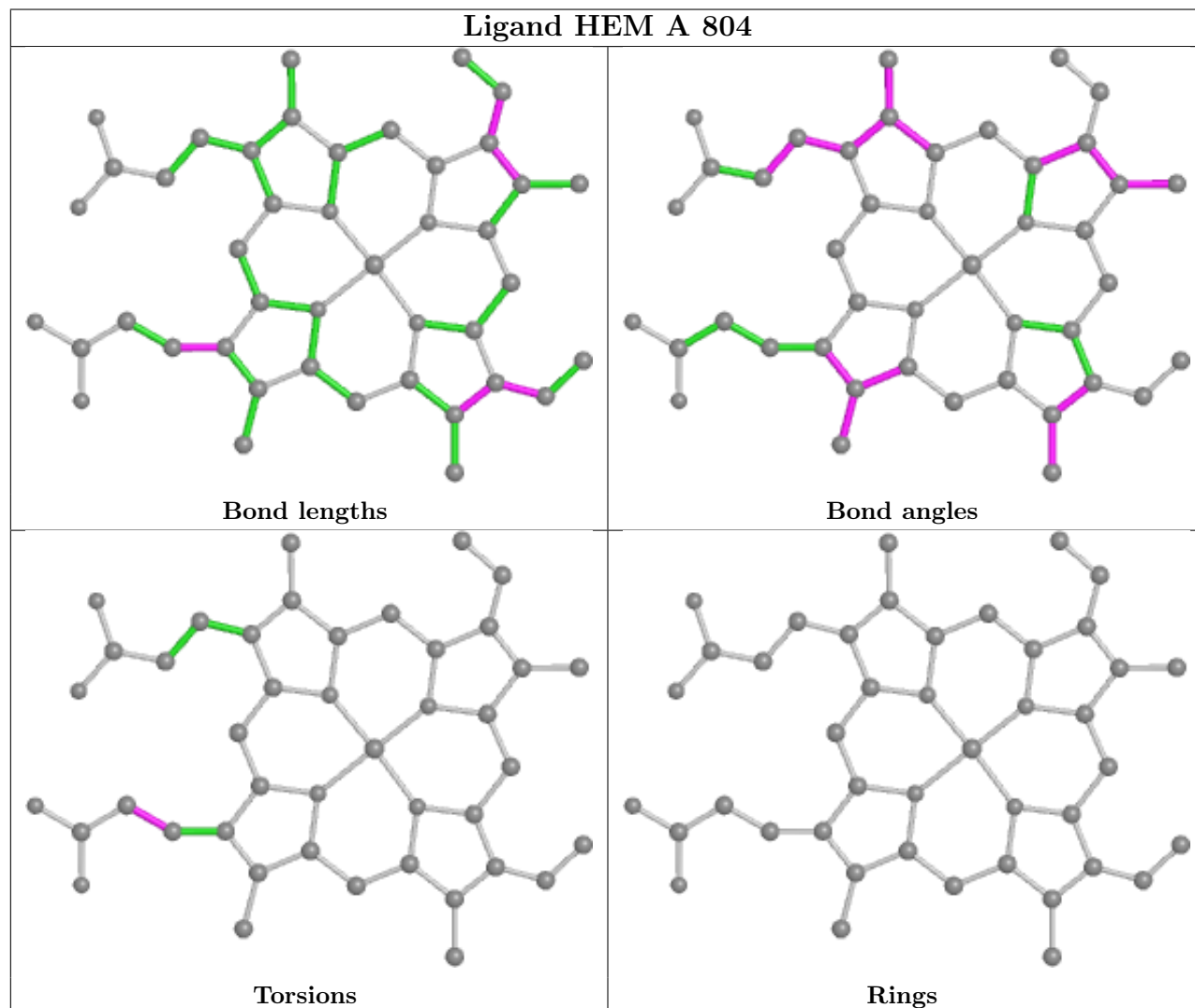
There are no ring outliers.

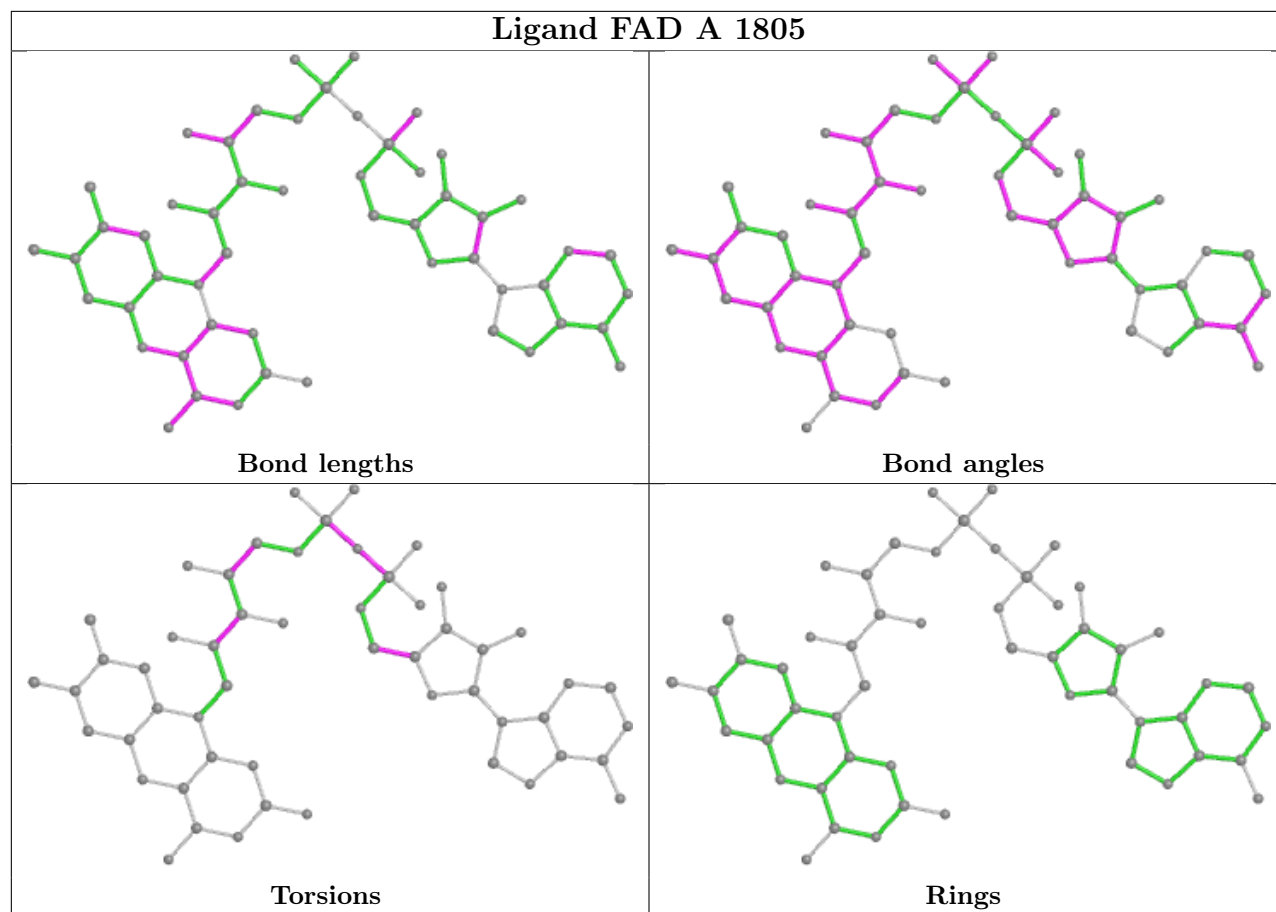
11 monomers are involved in 68 short contacts:

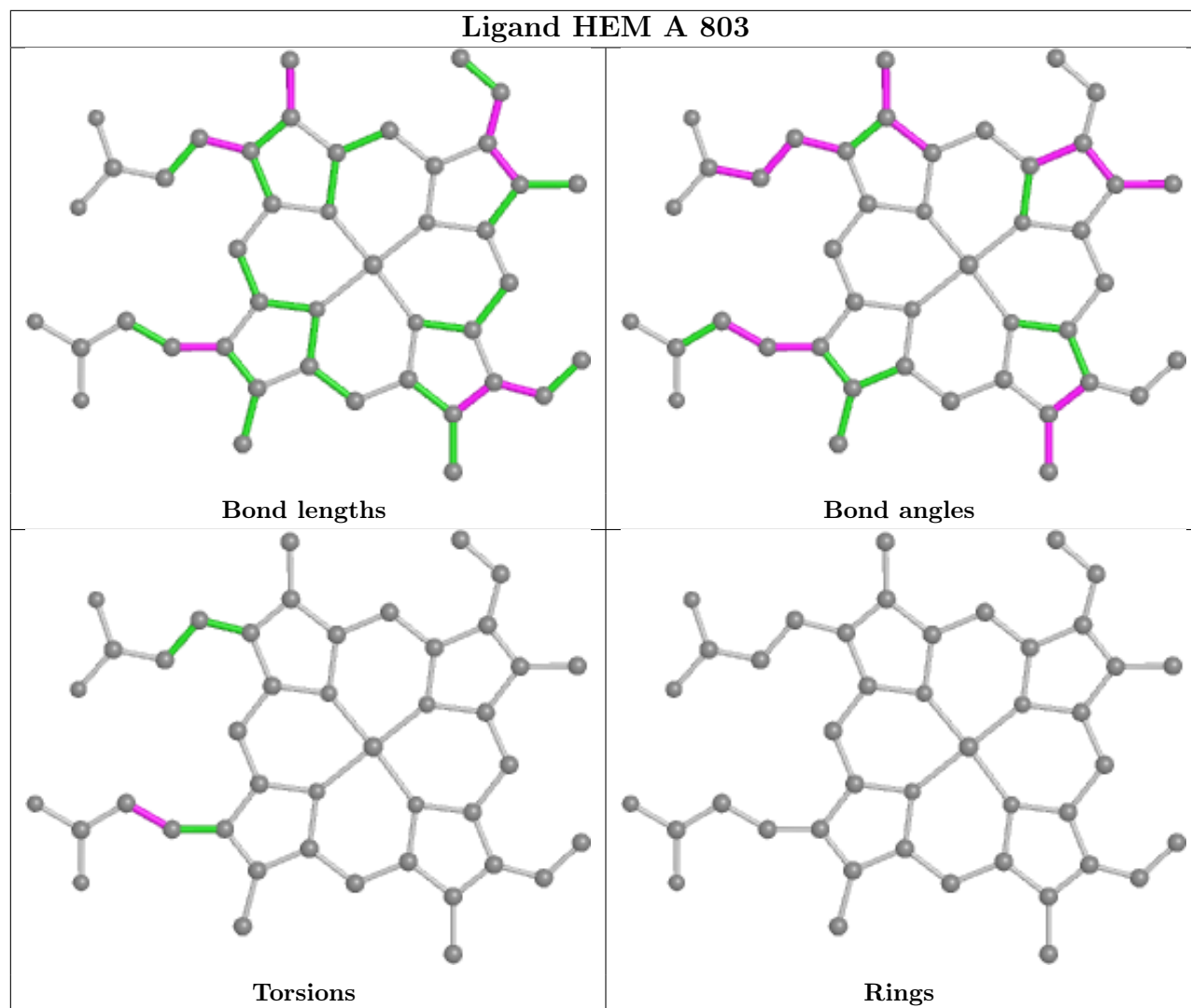
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	804	HEM	10	0
4	A	1805	FAD	5	0
3	A	803	HEM	6	0
3	A	802	HEM	7	0
5	B	2806	FUM	1	0
3	A	801	HEM	7	0
3	B	802	HEM	6	0
3	B	804	HEM	7	0
3	B	803	HEM	11	0
4	B	2805	FAD	2	0
3	B	801	HEM	6	0

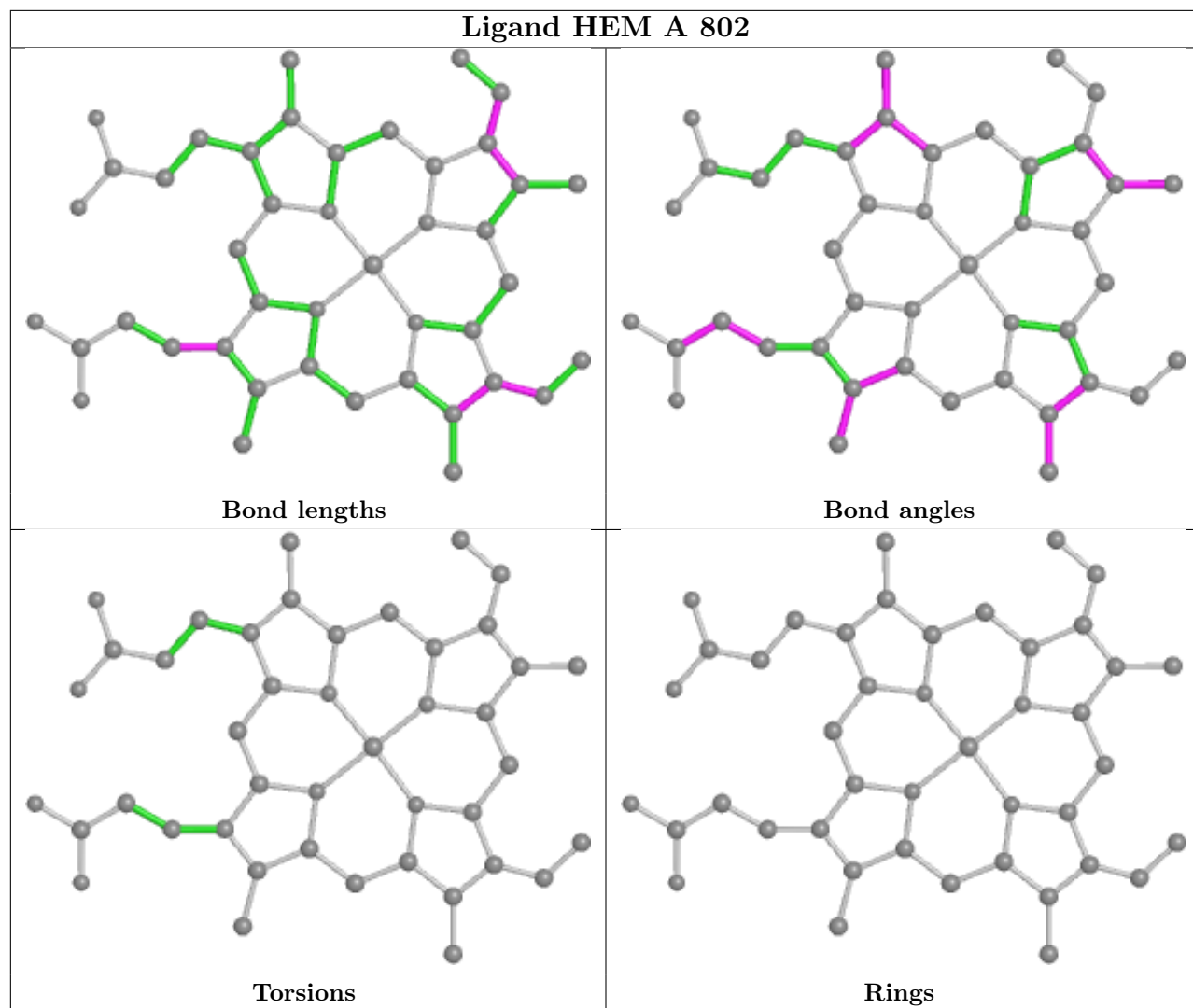
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

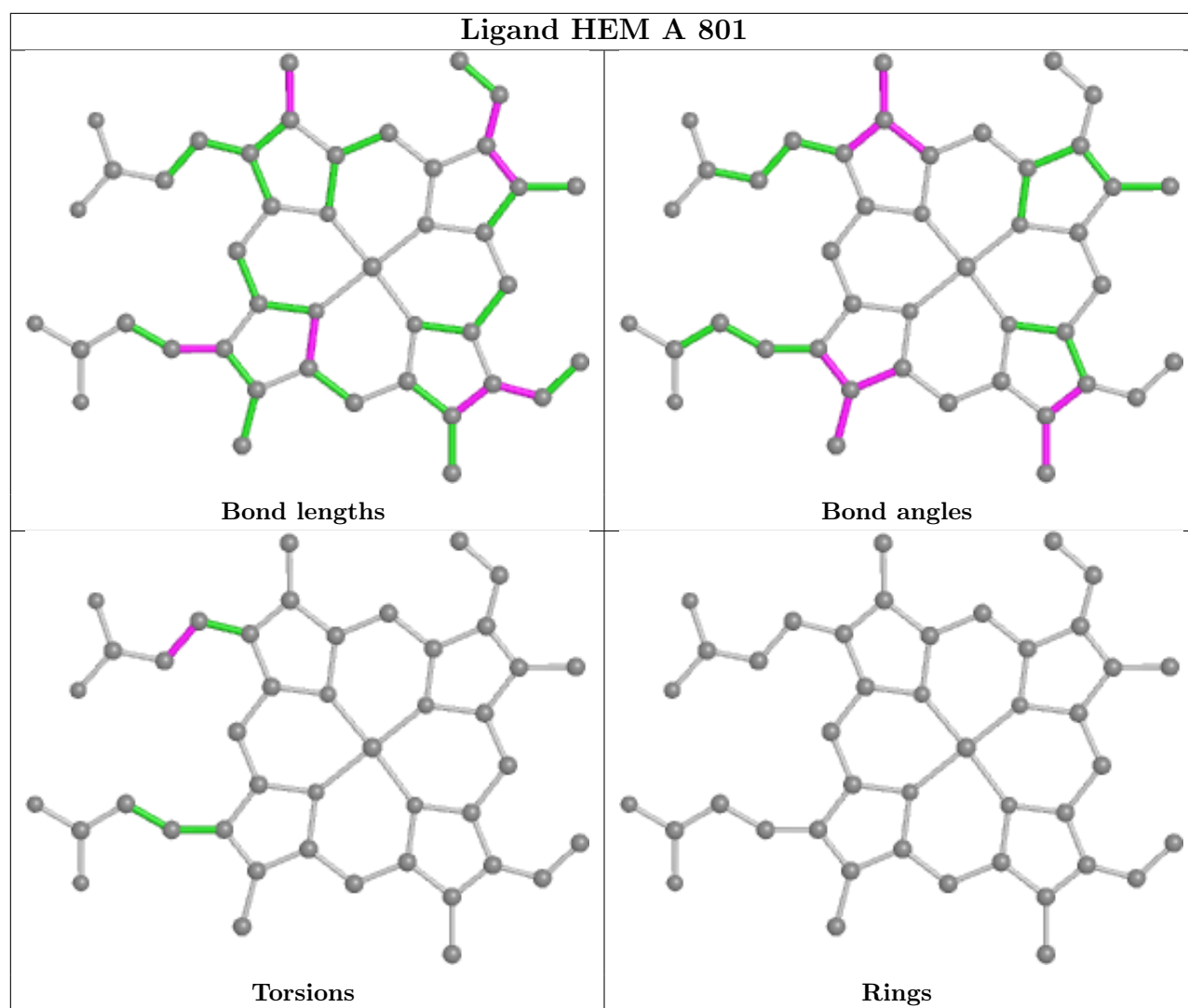
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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.



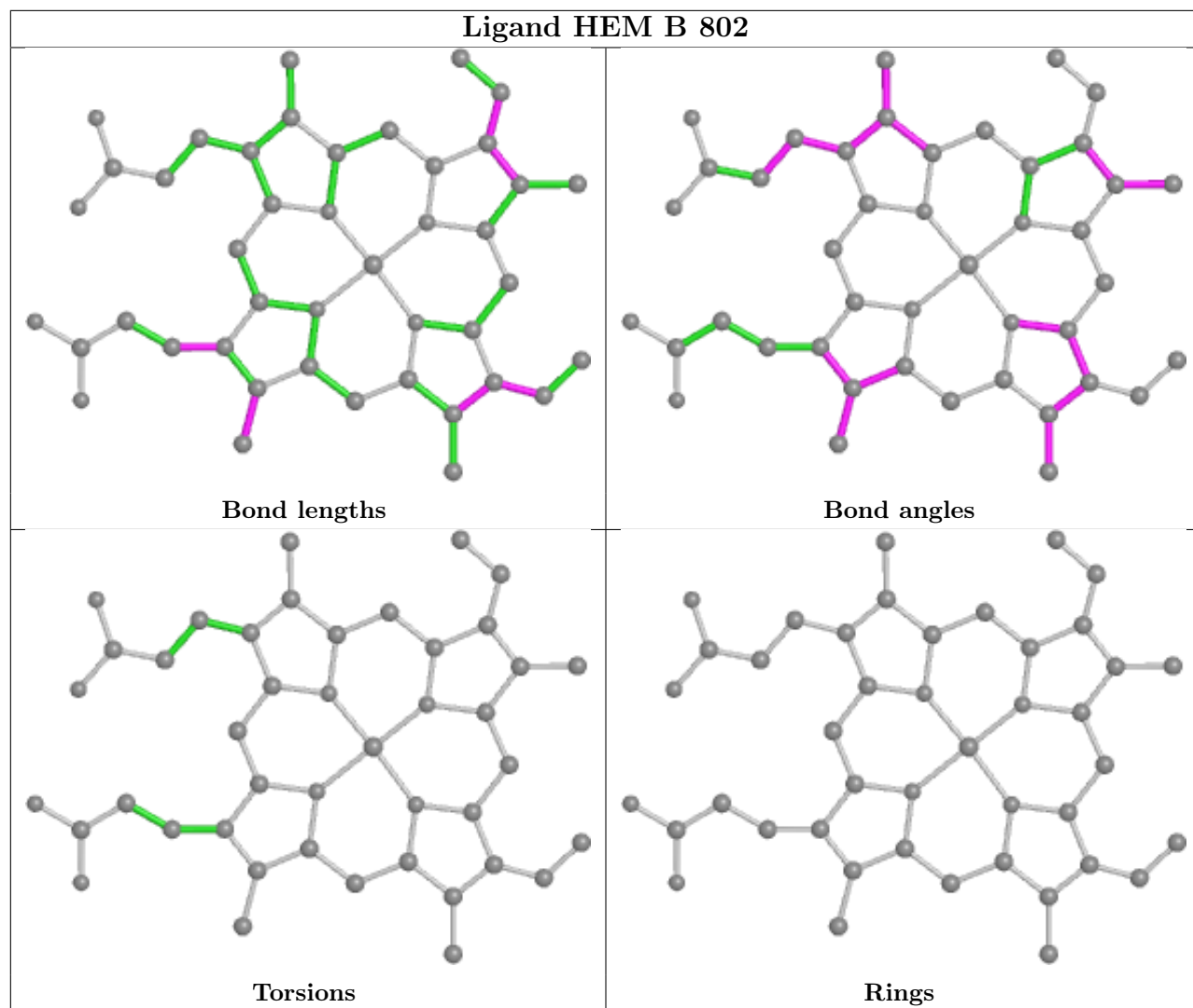


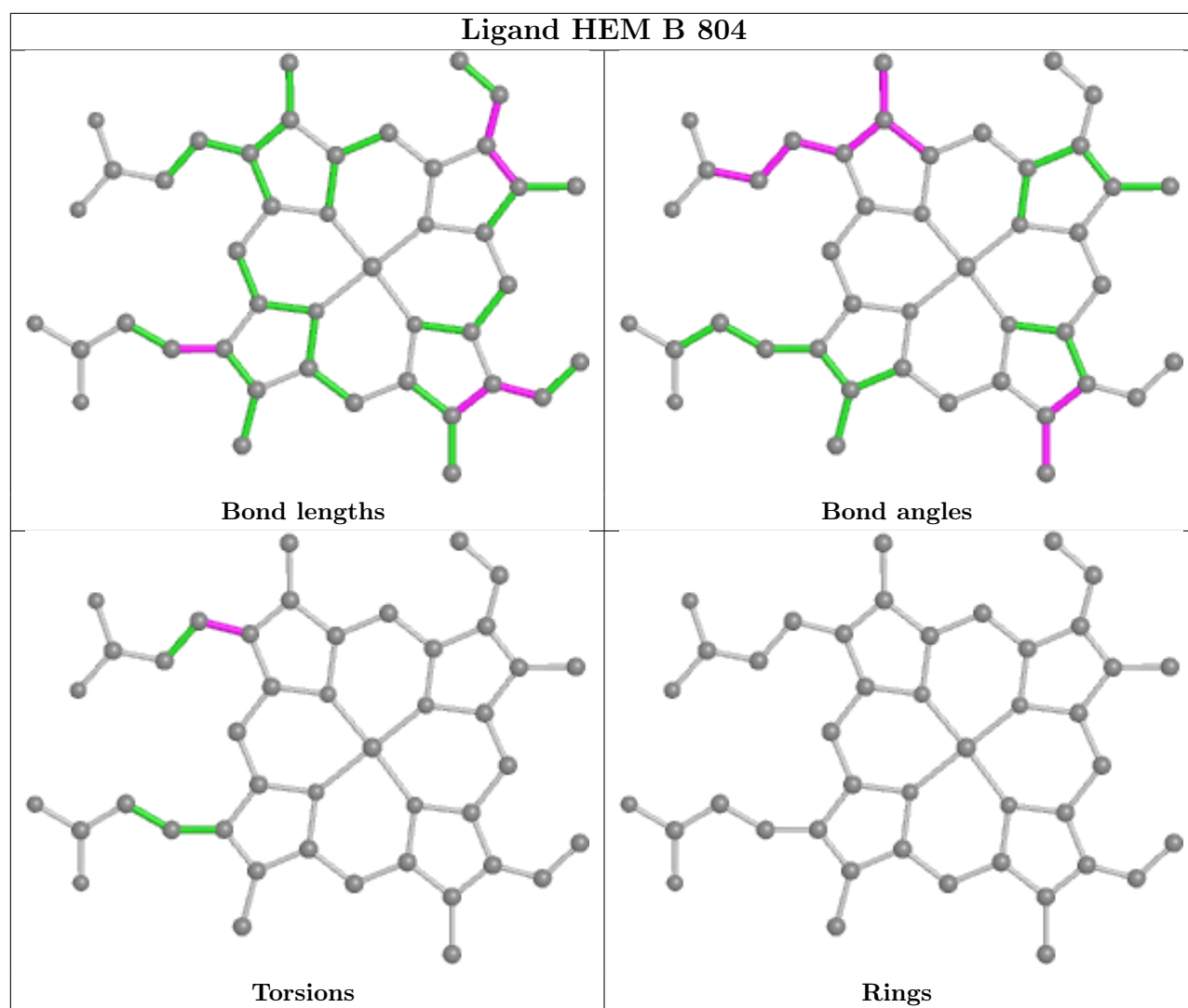


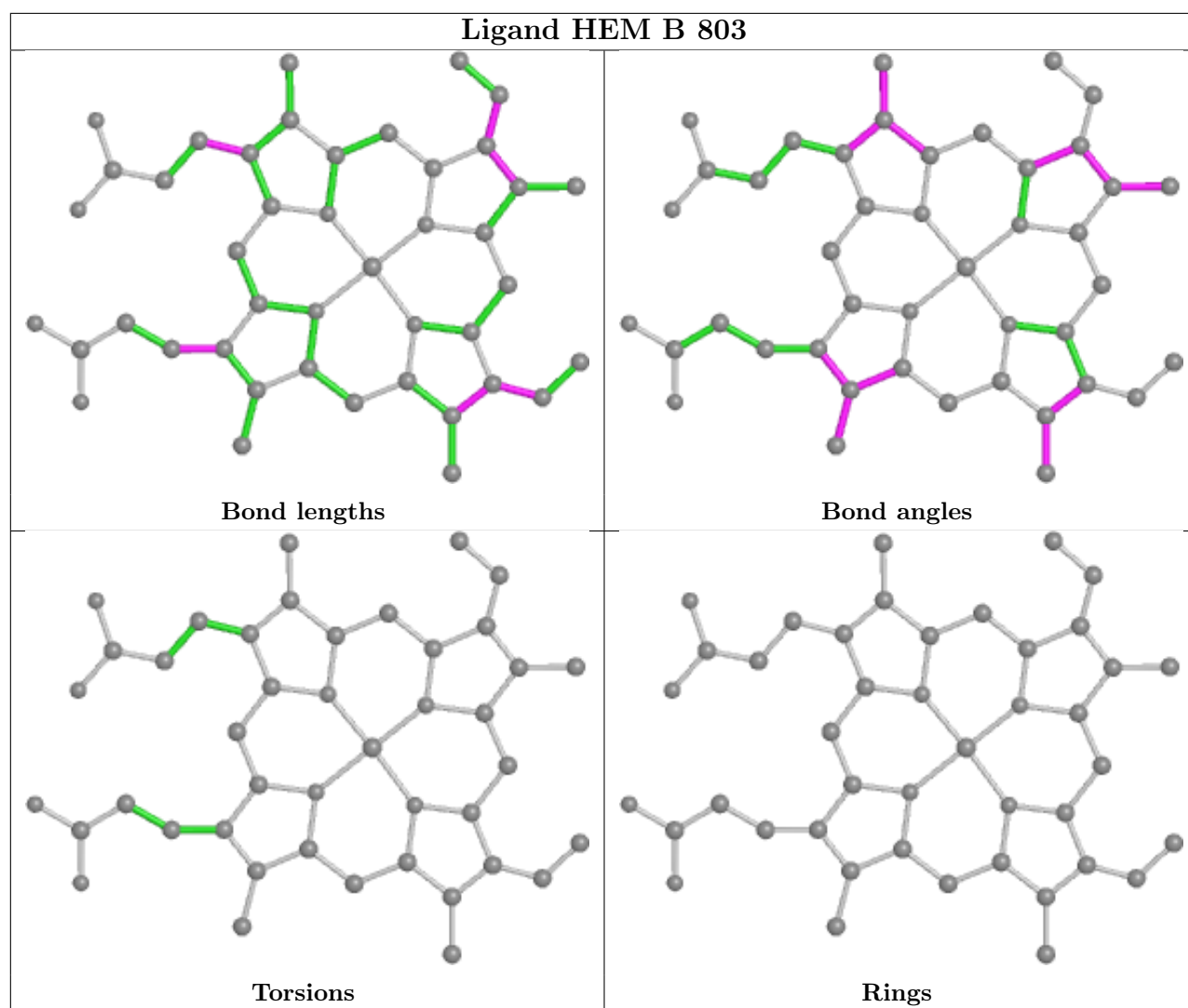


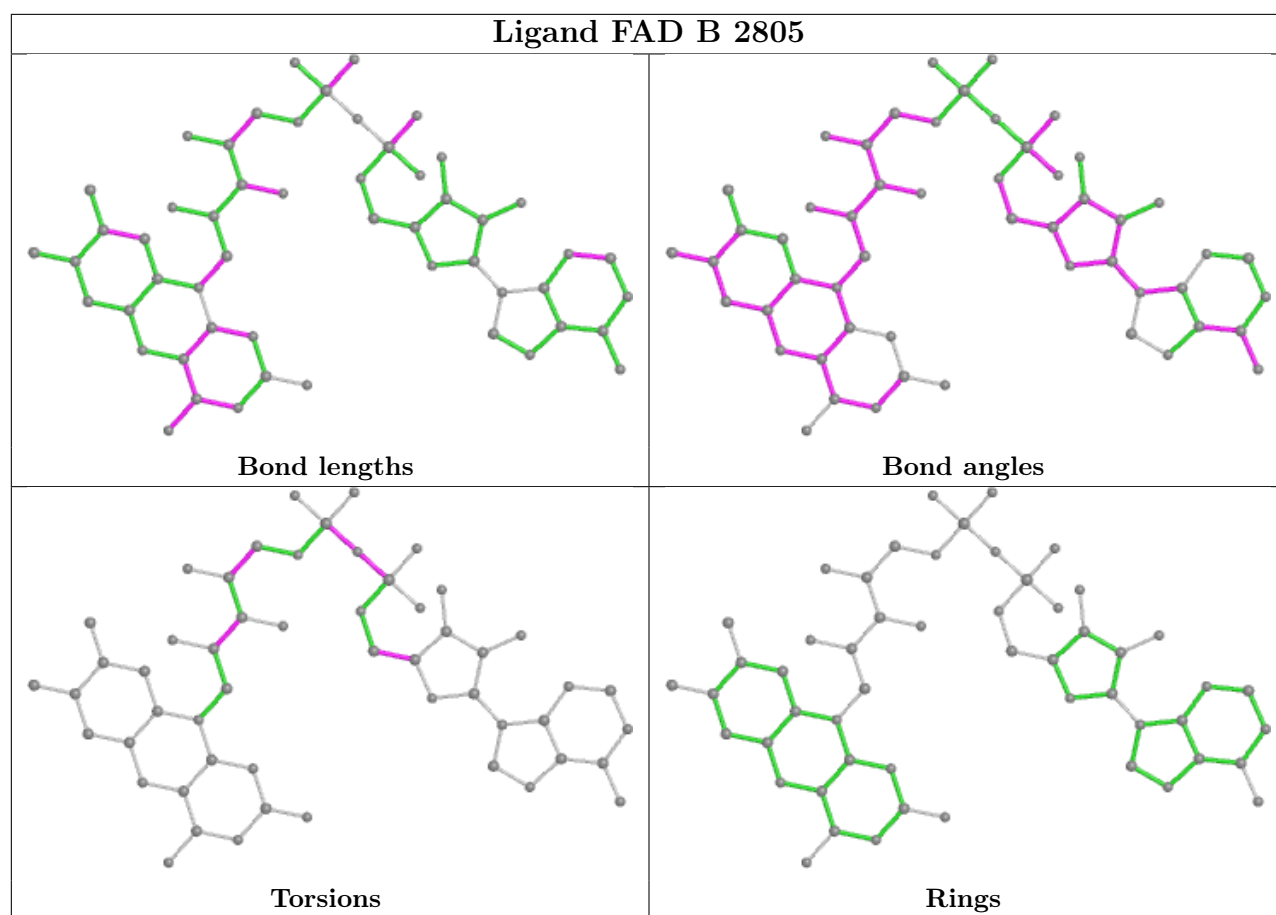


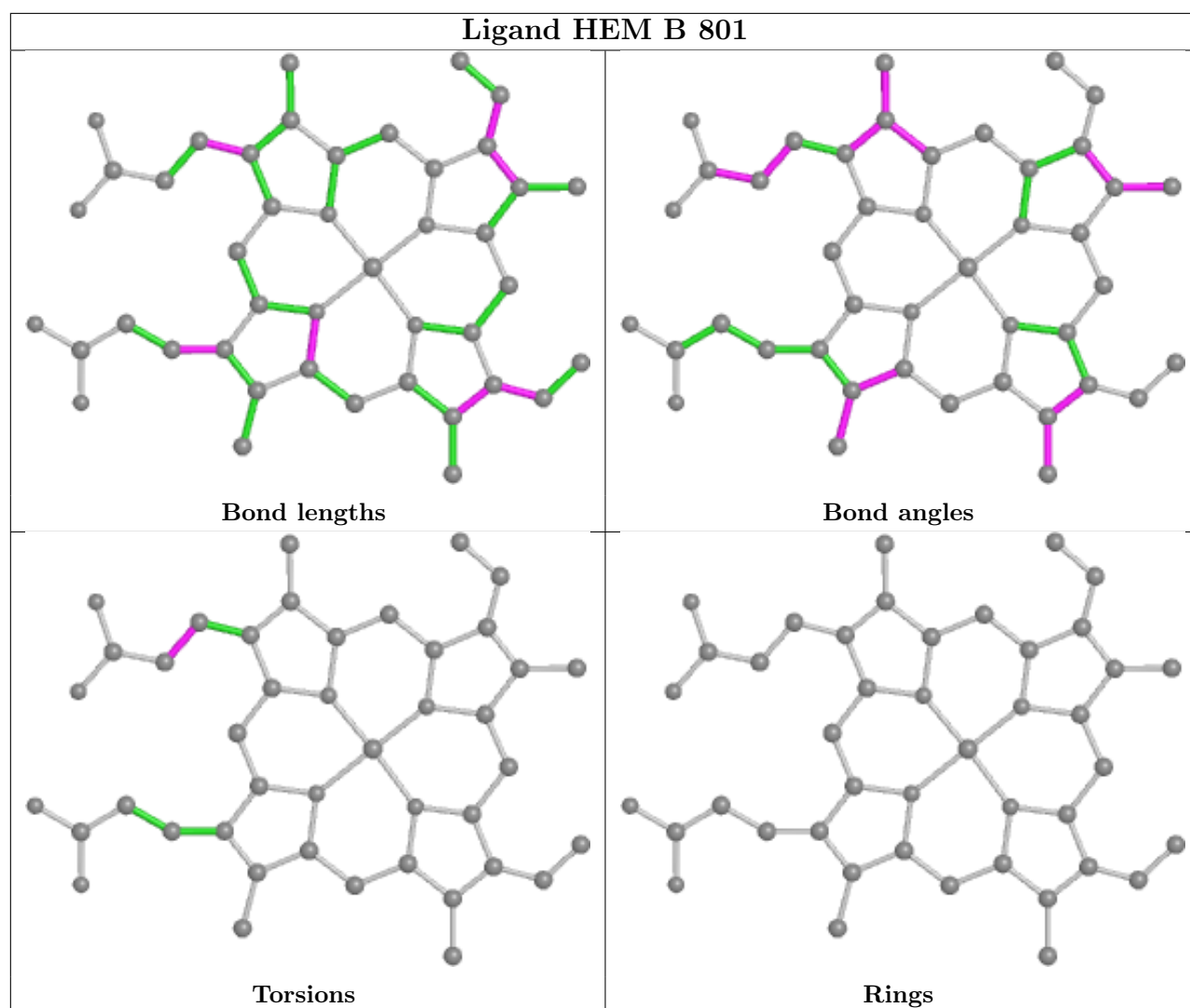












## 5.7 Other polymers [i](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.