



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 27, 2024 – 09:04 AM EST

PDB ID : 1BES
Title : INTERACTION BETWEEN PROXIMAL AND DISTALS REGIONS OF
CYTOCHROME C PEROXIDASE
Authors : Miller, M.A.; Kraut, J.
Deposited on : 1998-05-16
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

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)
Xtrriage (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

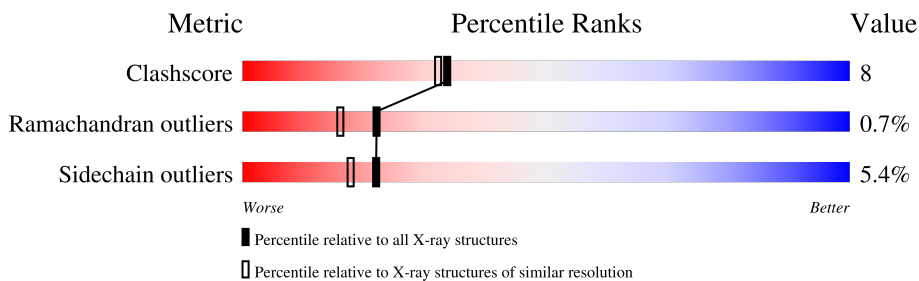
1 Overall quality at a glance

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 ≥ 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	291	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2549 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 CYTOCHROME C PEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	291	2324	1486	387	445	6	0	0	0

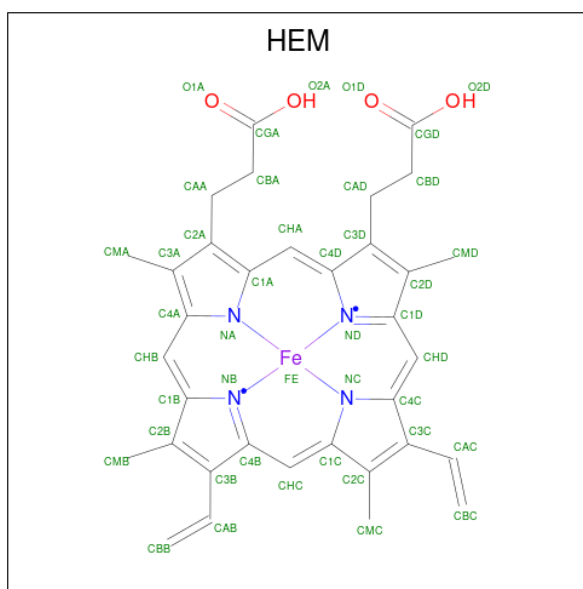
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	ILE	THR	engineered mutation	UNP P00431
A	152	GLY	ASP	engineered mutation	UNP P00431
A	191	TYR	TRP	engineered mutation	UNP P00431
A	272	ASP	ASN	engineered mutation	UNP P00431

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			S
4	A	1	12	6	1	4	1	0	0

- Molecule 5 is water.

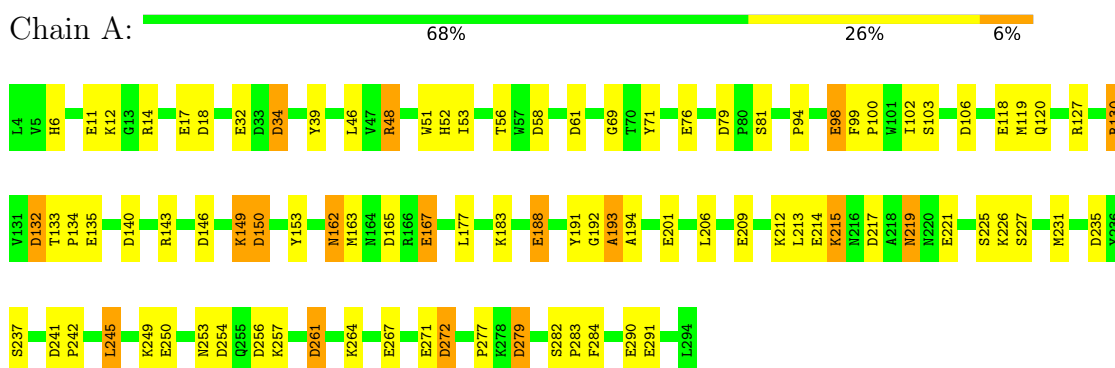
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	169	Total 169	O 169	0	0

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: CYTOCHROME C PEROXIDASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.30Å 74.26Å 45.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	90.0 (20.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	TNT 1	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	2549	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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: MES, HEM, CL

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	0.94	17/2388 (0.7%)	1.40	37/3232 (1.1%)

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

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	17	GLU	CD-OE1	7.31	1.33	1.25
1	A	98	GLU	CD-OE1	7.19	1.33	1.25
1	A	290	GLU	CD-OE1	6.62	1.32	1.25
1	A	188	GLU	CD-OE2	6.35	1.32	1.25
1	A	209	GLU	CD-OE2	6.32	1.32	1.25
1	A	76	GLU	CD-OE1	6.23	1.32	1.25
1	A	118	GLU	CD-OE1	6.21	1.32	1.25
1	A	250	GLU	CD-OE2	6.17	1.32	1.25
1	A	32	GLU	CD-OE1	5.72	1.31	1.25
1	A	167	GLU	CD-OE1	5.71	1.31	1.25
1	A	11	GLU	CD-OE1	5.68	1.31	1.25
1	A	267	GLU	CD-OE1	5.60	1.31	1.25
1	A	291	GLU	CD-OE1	5.39	1.31	1.25
1	A	271	GLU	CD-OE1	5.38	1.31	1.25
1	A	201	GLU	CD-OE2	5.25	1.31	1.25
1	A	214	GLU	CD-OE2	-5.14	1.20	1.25
1	A	135	GLU	CD-OE1	5.02	1.31	1.25

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	150	ASP	CB-CG-OD2	-8.49	110.66	118.30
1	A	127	ARG	NE-CZ-NH1	8.27	124.43	120.30
1	A	127	ARG	NE-CZ-NH2	-7.66	116.47	120.30
1	A	58	ASP	CB-CG-OD2	-7.55	111.50	118.30
1	A	150	ASP	CB-CG-OD1	7.54	125.08	118.30
1	A	272	ASP	CB-CG-OD1	7.52	125.07	118.30
1	A	235	ASP	CB-CG-OD2	-7.52	111.53	118.30
1	A	254	ASP	CB-CG-OD2	-7.43	111.61	118.30
1	A	272	ASP	CB-CG-OD2	-7.41	111.63	118.30
1	A	165	ASP	CB-CG-OD1	7.36	124.92	118.30
1	A	58	ASP	CB-CG-OD1	7.27	124.84	118.30
1	A	130	ARG	NE-CZ-NH1	7.15	123.87	120.30
1	A	132	ASP	CB-CG-OD1	7.14	124.73	118.30
1	A	165	ASP	CB-CG-OD2	-7.12	111.89	118.30
1	A	254	ASP	CB-CG-OD1	6.90	124.51	118.30
1	A	34	ASP	CB-CG-OD2	-6.72	112.26	118.30
1	A	279	ASP	CB-CG-OD1	-6.60	112.36	118.30
1	A	132	ASP	CB-CG-OD2	-6.51	112.44	118.30
1	A	261	ASP	CB-CG-OD2	-6.45	112.50	118.30
1	A	261	ASP	CB-CG-OD1	6.39	124.05	118.30
1	A	256	ASP	CB-CG-OD2	-6.25	112.68	118.30
1	A	34	ASP	CB-CG-OD1	6.18	123.86	118.30
1	A	284	PHE	CB-CA-C	-6.17	98.07	110.40
1	A	162	ASN	CA-CB-CG	-6.09	99.99	113.40
1	A	18	ASP	CB-CG-OD1	-5.92	112.97	118.30
1	A	279	ASP	CB-CG-OD2	5.88	123.59	118.30
1	A	146	ASP	CB-CG-OD1	-5.71	113.17	118.30
1	A	140	ASP	CB-CG-OD2	-5.64	113.22	118.30
1	A	256	ASP	CB-CG-OD1	5.57	123.31	118.30
1	A	61	ASP	CB-CG-OD2	-5.55	113.31	118.30
1	A	235	ASP	CB-CG-OD1	5.53	123.28	118.30
1	A	130	ARG	NE-CZ-NH2	-5.45	117.58	120.30
1	A	217	ASP	CB-CG-OD2	-5.45	113.39	118.30
1	A	48	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	A	79	ASP	CB-CG-OD1	5.25	123.02	118.30
1	A	14	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	A	162	ASN	CB-CA-C	-5.01	100.37	110.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	191	TYR	Peptide
1	A	192	GLY	Peptide
1	A	193	ALA	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	2324	0	2193	39	0
2	A	1	0	0	0	0
3	A	43	0	30	1	0
4	A	12	0	13	0	0
5	A	169	0	0	8	0
All	All	2549	0	2236	39	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 8.

All (39) 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:12:LYS:HA	5:A:313:HOH:O	1.86	0.76
1:A:69:GLY:HA2	5:A:652:HOH:O	1.92	0.68
1:A:215:LYS:HE2	1:A:219:ASN:ND2	2.09	0.68
1:A:133:THR:HB	1:A:134:PRO:HD2	1.79	0.65
1:A:282:SER:HB3	1:A:283:PRO:HD2	1.81	0.62
1:A:277:PRO:HB2	1:A:279:ASP:OD1	2.04	0.57
1:A:163:MET:HA	1:A:167:GLU:OE1	2.06	0.56
1:A:188:GLU:HG3	5:A:650:HOH:O	2.07	0.55
1:A:106:ASP:OD1	1:A:130:ARG:HG3	2.07	0.54
1:A:149:LYS:HG2	1:A:153:TYR:CG	2.42	0.54
1:A:257:LYS:HE3	1:A:261:ASP:OD2	2.08	0.54
1:A:98:GLU:HB3	1:A:99:PHE:CD1	2.44	0.53
1:A:215:LYS:HE2	1:A:219:ASN:HD21	1.73	0.53
1:A:53:ILE:HG22	1:A:71:TYR:HB2	1.91	0.53
1:A:279:ASP:OD1	1:A:279:ASP:N	2.41	0.53
1:A:206:LEU:HD13	1:A:231:MET:SD	2.49	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:HIS:ND1	5:A:433:HOH:O	2.34	0.52
1:A:226:LYS:HG3	1:A:227:SER:N	2.25	0.52
1:A:133:THR:HB	1:A:134:PRO:CD	2.41	0.50
1:A:99:PHE:O	1:A:102:ILE:HG22	2.12	0.49
1:A:226:LYS:HG2	5:A:624:HOH:O	2.11	0.48
1:A:103:SER:HB2	1:A:132:ASP:OD1	2.13	0.47
1:A:52:HIS:HE1	1:A:81:SER:O	1.98	0.47
1:A:56:THR:O	1:A:143:ARG:HD3	2.15	0.46
1:A:149:LYS:HG2	1:A:153:TYR:CD1	2.51	0.46
1:A:245:LEU:O	1:A:245:LEU:HD22	2.17	0.45
1:A:34:ASP:O	1:A:39:TYR:HA	2.17	0.45
1:A:245:LEU:O	1:A:249:LYS:HG3	2.17	0.44
1:A:272:ASP:HA	5:A:604:HOH:O	2.17	0.44
1:A:119:MET:O	1:A:120:GLN:HB2	2.17	0.44
1:A:226:LYS:CG	1:A:227:SER:N	2.80	0.44
1:A:48:ARG:HD2	3:A:296:HEM:C4D	2.53	0.43
1:A:98:GLU:C	1:A:100:PRO:HD3	2.39	0.43
1:A:213:LEU:HD11	1:A:221:GLU:HB3	2.01	0.43
1:A:282:SER:HB3	1:A:283:PRO:CD	2.48	0.41
1:A:150:ASP:HB2	5:A:539:HOH:O	2.20	0.40
1:A:183:LYS:HB2	5:A:488:HOH:O	2.20	0.40
1:A:46:LEU:HD23	1:A:46:LEU:HA	1.85	0.40
1:A:241:ASP:CG	1:A:242:PRO:HD2	2.42	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	289/291 (99%)	277 (96%)	10 (4%)	2 (1%)	22 16

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	ALA
1	A	194	ALA

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	242/249 (97%)	229 (95%)	13 (5%)	22 18

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	TRP
1	A	94	PRO
1	A	149	LYS
1	A	162	ASN
1	A	177	LEU
1	A	212	LYS
1	A	215	LYS
1	A	219	ASN
1	A	225	SER
1	A	237	SER
1	A	245	LEU
1	A	253	ASN
1	A	264	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	87	ASN
1	A	208	ASN
1	A	219	ASN
1	A	292	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](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	296	1,2	41,50,50	1.54	4 (9%)	45,82,82	1.74	10 (22%)
4	MES	A	975	-	12,12,12	0.81	0	14,16,16	0.92	1 (7%)

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	296	1,2	-	2/12/54/54	-
4	MES	A	975	-	-	0/6/14/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	296	HEM	C3C-C2C	-5.26	1.33	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	296	HEM	C3C-CAC	2.90	1.53	1.47
3	A	296	HEM	CAA-C2A	2.63	1.55	1.52
3	A	296	HEM	C1B-NB	-2.09	1.36	1.40

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	296	HEM	CHD-C1D-ND	4.81	129.65	124.43
3	A	296	HEM	O1D-CGD-CBD	-3.21	112.78	123.08
3	A	296	HEM	CHA-C4D-ND	-3.16	120.47	124.38
3	A	296	HEM	CMA-C3A-C4A	-3.16	123.60	128.46
3	A	296	HEM	O2D-CGD-O1D	2.94	130.63	123.30
3	A	296	HEM	C4B-CHC-C1C	-2.90	118.73	122.56
3	A	296	HEM	C4C-CHD-C1D	-2.83	118.82	122.56
3	A	296	HEM	CHD-C1D-C2D	-2.48	121.10	124.98
4	A	975	MES	O1S-S-C8	-2.40	104.02	106.92
3	A	296	HEM	C2C-C3C-C4C	2.24	108.47	106.90
3	A	296	HEM	CHC-C4B-C3B	-2.07	121.41	124.57

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	296	HEM	CAA-CBA-CGA-O2A
3	A	296	HEM	CAA-CBA-CGA-O1A

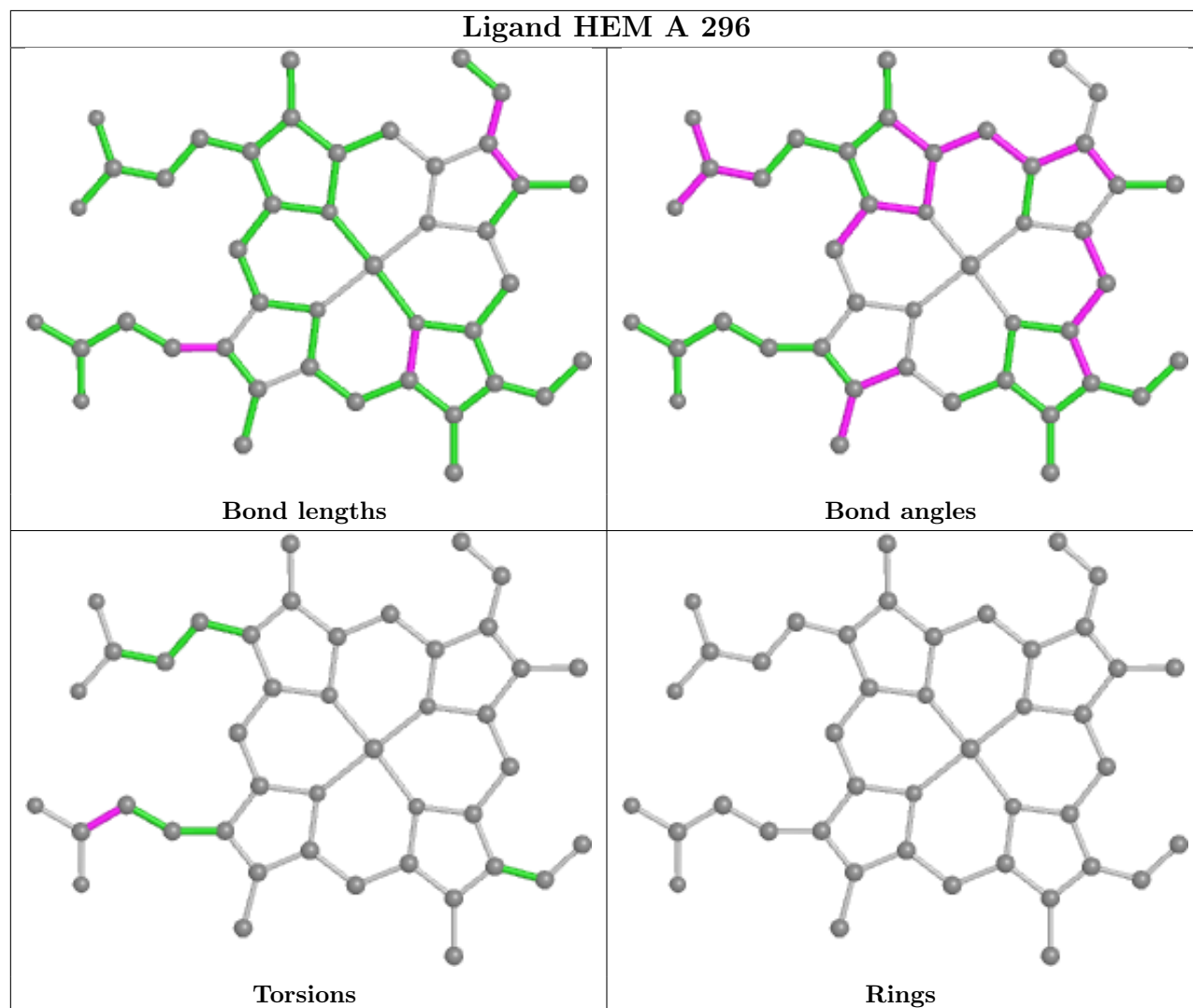
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	296	HEM	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 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.