



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:48 PM UTC

PDB ID : 1BJ9 / pdb_00001bj9
Title : EFFECT OF UNNATURAL HEME SUBSTITUTION ON KINETICS OF ELECTRON TRANSFER IN CYTOCHROME C PEROXIDASE
Authors : Miller, M.A.; Kraut, J.
Deposited on : 1998-07-03
Resolution : 2.20 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

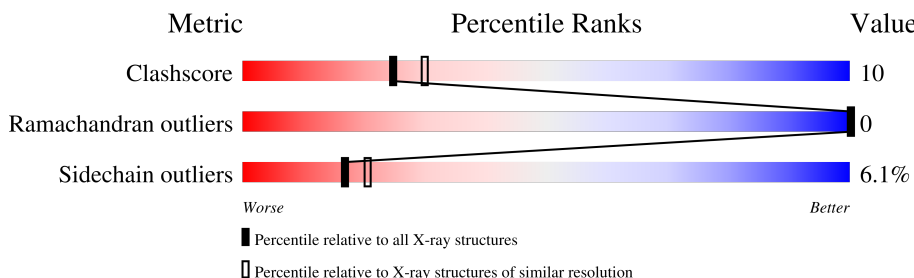
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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	66% 29% 5%

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
2	DDH	A	296	X	-	-	-

- Molecule 3 is water.

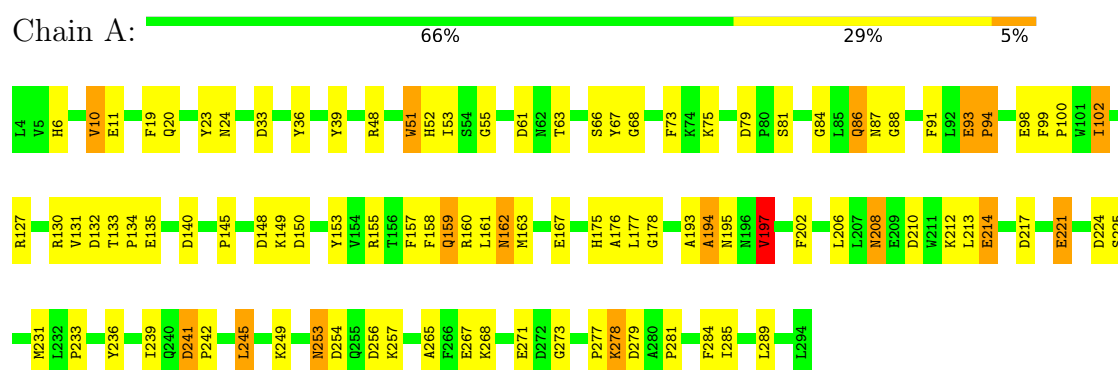
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	179	Total 179	O 179	0	0

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: CYTOCHROME C PEROXIDASE



4 Data and refinement statistics

Xtriage (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	105.20 Å 74.36 Å 45.40 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20	Depositor
% Data completeness (in resolution range)	99.4 (20.00-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	TNT 1	Depositor
R, R_{free}	0.179 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2516	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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: DDH

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	1.06	0/2357	1.82	54/3201 (1.7%)

There are no bond length outliers.

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	ASN	CA-CB-CG	-9.90	102.70	112.60
1	A	140	ASP	CA-CB-CG	-8.98	103.61	112.60
1	A	210	ASP	CA-CB-CG	8.74	121.34	112.60
1	A	162	ASN	CB-CA-C	-7.83	99.14	111.51
1	A	208	ASN	N-CA-C	7.81	123.10	113.50
1	A	241	ASP	CA-C-N	7.64	127.18	119.24
1	A	241	ASP	C-N-CA	7.64	127.18	119.24
1	A	197	VAL	CB-CA-C	7.52	121.31	110.33
1	A	202	PHE	CA-CB-CG	7.32	121.12	113.80
1	A	177	LEU	N-CA-C	7.31	122.23	109.96
1	A	195	ASN	N-CA-C	6.82	121.26	113.15
1	A	67	TYR	N-CA-C	6.70	122.35	111.37
1	A	145	PRO	N-CA-C	6.51	121.73	111.38
1	A	265	ALA	N-CA-C	6.50	118.44	111.36
1	A	93	GLU	CA-C-O	6.45	124.50	118.44
1	A	66	SER	N-CA-C	6.38	120.32	112.54
1	A	208	ASN	CA-CB-CG	-6.26	106.34	112.60
1	A	281	PRO	CB-CA-C	-6.09	102.97	110.95
1	A	245	LEU	N-CA-C	6.06	118.67	111.33
1	A	210	ASP	CB-CA-C	6.05	121.63	111.22
1	A	273	GLY	CA-C-N	-5.99	115.37	123.10
1	A	273	GLY	C-N-CA	-5.99	115.37	123.10
1	A	93	GLU	CB-CA-C	5.98	126.71	111.77
1	A	91	PHE	CA-CB-CG	5.96	119.77	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	10	VAL	CB-CA-C	-5.81	101.93	111.51
1	A	253	ASN	N-CA-C	5.76	120.38	113.23
1	A	132	ASP	CA-CB-CG	-5.75	106.85	112.60
1	A	51	TRP	CB-CA-C	5.73	120.59	110.85
1	A	68	GLY	N-CA-C	5.64	122.71	115.32
1	A	79	ASP	CA-C-N	5.61	125.28	119.05
1	A	79	ASP	C-N-CA	5.61	125.28	119.05
1	A	150	ASP	N-CA-C	5.61	117.77	109.69
1	A	176	ALA	N-CA-C	-5.61	105.32	111.82
1	A	79	ASP	CA-C-O	5.49	124.91	119.75
1	A	162	ASN	N-CA-C	5.48	119.26	112.24
1	A	193	ALA	N-CA-C	5.47	120.06	112.45
1	A	6	HIS	CB-CA-C	-5.46	102.38	110.62
1	A	158	PHE	CA-CB-CG	-5.37	108.43	113.80
1	A	6	HIS	CA-CB-CG	-5.21	108.59	113.80
1	A	241	ASP	CA-CB-CG	5.21	117.81	112.60
1	A	39	TYR	N-CA-C	5.20	119.57	113.23
1	A	217	ASP	CA-CB-CG	-5.19	107.41	112.60
1	A	161	LEU	CB-CA-C	-5.18	101.96	110.72
1	A	256	ASP	CB-CA-C	5.18	119.02	110.88
1	A	131	VAL	N-CA-C	5.15	115.32	108.11
1	A	157	PHE	CA-CB-CG	-5.11	108.69	113.80
1	A	33	ASP	CA-CB-CG	5.10	117.70	112.60
1	A	19	PHE	CA-CB-CG	-5.10	108.70	113.80
1	A	194	ALA	CB-CA-C	-5.09	104.09	112.03
1	A	175	HIS	CA-CB-CG	-5.07	108.73	113.80
1	A	94	PRO	CB-CA-C	-5.03	104.77	112.11
1	A	102	ILE	N-CA-CB	5.02	117.14	110.26
1	A	284	PHE	CB-CA-C	-5.01	101.03	109.50
1	A	88	GLY	CA-C-O	5.01	125.81	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	2292	0	2113	41	0
2	A	45	0	29	4	0
3	A	179	0	0	1	0
All	All	2516	0	2142	44	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (44) 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:213:LEU:HD11	1:A:221:GLU:HB3	1.68	0.74
1:A:84:GLY:N	1:A:86:GLN:OE1	2.28	0.67
1:A:194:ALA:HB1	1:A:197:VAL:HG13	1.80	0.62
1:A:149:LYS:HG2	1:A:153:TYR:CG	2.34	0.62
1:A:133:THR:HB	1:A:134:PRO:HD2	1.83	0.59
1:A:133:THR:HB	1:A:134:PRO:CD	2.34	0.58
1:A:279:ASP:N	1:A:279:ASP:OD1	2.32	0.58
1:A:48:ARG:NH1	3:A:649:HOH:O	2.29	0.57
1:A:159:GLN:NE2	1:A:159:GLN:HA	2.19	0.57
1:A:254:ASP:OD2	1:A:257:LYS:HB2	2.05	0.57
1:A:213:LEU:HD21	1:A:221:GLU:OE1	2.04	0.57
1:A:127:ARG:O	1:A:130:ARG:NH1	2.39	0.56
2:A:296:DDH:CBC	2:A:296:DDH:HMC1	2.37	0.55
1:A:277:PRO:HB2	1:A:279:ASP:OD1	2.10	0.52
1:A:149:LYS:HG2	1:A:153:TYR:CD1	2.46	0.50
1:A:245:LEU:O	1:A:249:LYS:HG3	2.12	0.50
1:A:278:LYS:HG3	1:A:279:ASP:N	2.26	0.50
2:A:296:DDH:CMB	2:A:296:DDH:HBB1	2.41	0.49
1:A:267:GLU:OE2	1:A:271:GLU:OE2	2.30	0.49
1:A:98:GLU:C	1:A:100:PRO:HD3	2.38	0.48
1:A:214:GLU:OE2	1:A:224:ASP:OD2	2.31	0.48
1:A:52:HIS:HE1	1:A:81:SER:O	1.97	0.48
1:A:163:MET:HA	1:A:167:GLU:OE1	2.13	0.48
2:A:296:DDH:HMC1	2:A:296:DDH:HBC2	1.95	0.48
1:A:98:GLU:HB3	1:A:99:PHE:CD1	2.49	0.48
1:A:36:TYR:OH	1:A:87:ASN:ND2	2.47	0.47
1:A:73:PHE:CE2	1:A:135:GLU:HA	2.51	0.46
1:A:206:LEU:HD13	1:A:231:MET:SD	2.56	0.46
1:A:10:VAL:HG12	1:A:11:GLU:O	2.16	0.45
1:A:93:GLU:N	1:A:94:PRO:HD2	2.32	0.44
1:A:23:TYR:CD1	1:A:23:TYR:C	2.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:ARG:HH11	1:A:155:ARG:HD2	1.63	0.44
1:A:208:ASN:HD22	1:A:208:ASN:HA	1.50	0.43
1:A:241:ASP:HA	1:A:242:PRO:HD3	1.64	0.43
1:A:20:GLN:HE21	1:A:24:ASN:ND2	2.16	0.43
1:A:148:ASP:HA	1:A:233:PRO:HG2	2.01	0.43
1:A:178:GLY:HA3	2:A:296:DDH:O2D	2.19	0.42
1:A:241:ASP:CG	1:A:242:PRO:HD2	2.44	0.42
1:A:163:MET:HE1	1:A:268:LYS:HG2	2.01	0.42
1:A:236:TYR:O	1:A:239:ILE:HG12	2.20	0.42
1:A:61:ASP:CG	1:A:63:THR:HG1	2.28	0.42
1:A:99:PHE:O	1:A:102:ILE:HG22	2.19	0.41
1:A:289:LEU:HD23	1:A:289:LEU:HA	1.87	0.41
1:A:55:GLY:O	1:A:160:ARG:NH2	2.53	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%)	285 (99%)	4 (1%)	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	231/249 (93%)	217 (94%)	14 (6%)	17	20

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	TRP
1	A	53	ILE
1	A	75	LYS
1	A	86	GLN
1	A	159	GLN
1	A	162	ASN
1	A	197	VAL
1	A	212	LYS
1	A	214	GLU
1	A	221	GLU
1	A	225	SER
1	A	253	ASN
1	A	278	LYS
1	A	285	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	HIS
1	A	24	ASN
1	A	87	ASN
1	A	141	ASN
1	A	159	GLN
1	A	208	ASN
1	A	292	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	DDH	A	296	3,1	52,52,52	1.88	10 (19%)	63,86,86	1.97	13 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DDH	A	296	3,1	1/1/5/9	2/14/58/58	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	296	DDH	CBC-CAC	-7.90	1.34	1.50
2	A	296	DDH	C3B-CAB	3.96	1.53	1.46
2	A	296	DDH	FE-ND	3.74	2.06	1.94
2	A	296	DDH	OCB-CAB	-3.29	1.23	1.33
2	A	296	DDH	FE-NA	-3.15	1.84	1.95
2	A	296	DDH	C3C-C2C	-3.09	1.32	1.42
2	A	296	DDH	FE-NB	3.07	2.04	1.94
2	A	296	DDH	C3C-C4C	2.56	1.46	1.41
2	A	296	DDH	C3C-CAC	2.18	1.53	1.46
2	A	296	DDH	CMC-C2C	2.06	1.55	1.50

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	296	DDH	CHA-C1A-NA	7.23	132.33	124.45
2	A	296	DDH	C4A-CHB-C1B	-6.37	112.47	126.02
2	A	296	DDH	CHB-C4A-NA	3.97	128.78	124.45
2	A	296	DDH	CHA-C1A-C2A	-3.97	118.60	124.86
2	A	296	DDH	O1D-CGD-O2D	3.43	132.16	123.33
2	A	296	DDH	OCC-CAC-C3C	-3.28	114.63	120.43
2	A	296	DDH	CHB-C1B-NB	3.18	127.85	124.42
2	A	296	DDH	CHB-C4A-C3A	-3.05	119.15	125.49
2	A	296	DDH	C1A-CHA-C4D	-2.53	120.64	126.02
2	A	296	DDH	CHC-C4B-C3B	-2.22	121.06	128.25
2	A	296	DDH	O2D-CGD-CBD	-2.04	116.61	123.09
2	A	296	DDH	CHB-C1B-C2B	-2.02	121.84	125.03
2	A	296	DDH	CMC-C2C-C1C	2.01	128.48	125.42

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	296	DDH	NA

All (2) torsion outliers are listed below:

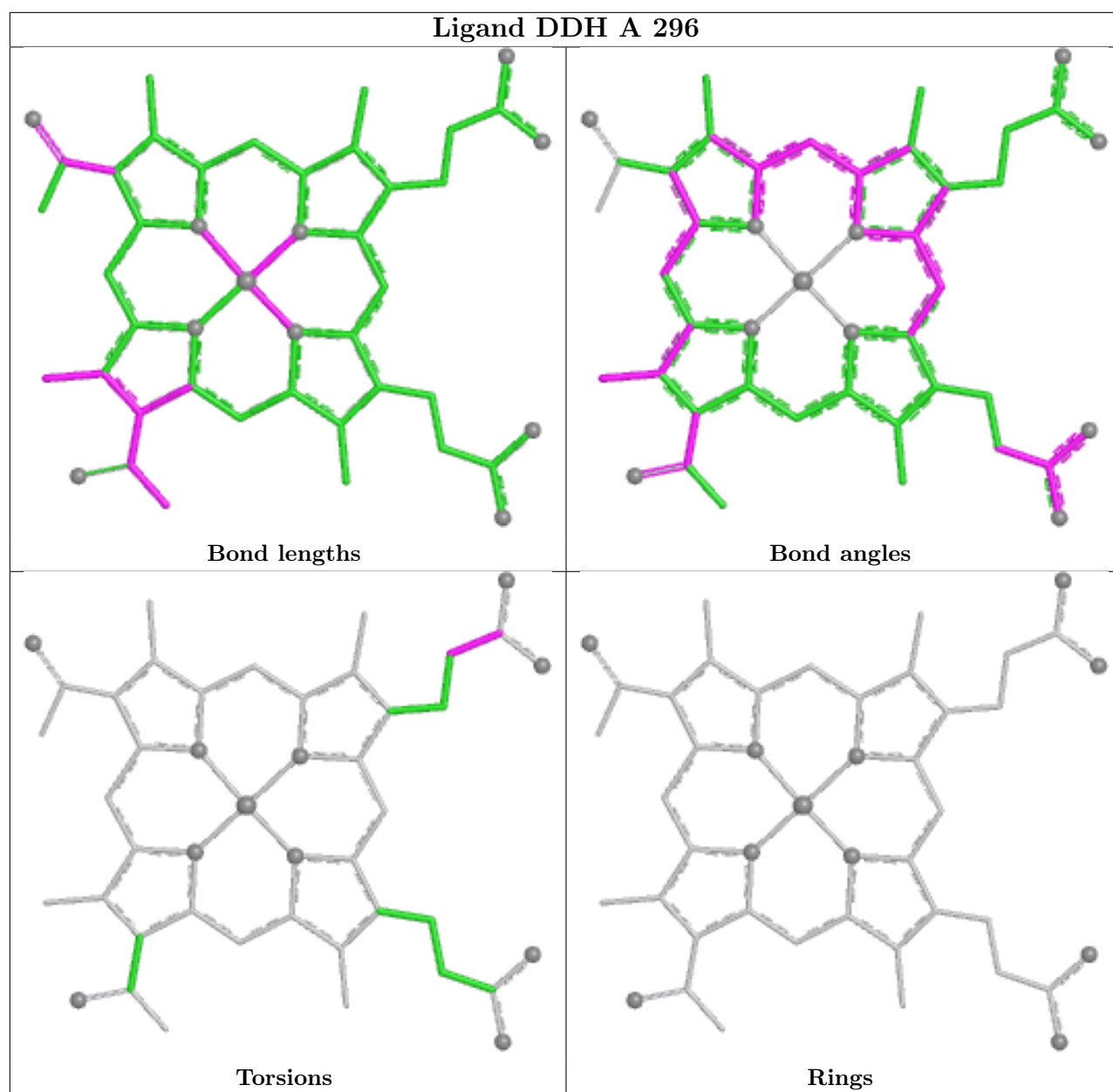
Mol	Chain	Res	Type	Atoms
2	A	296	DDH	CAA-CBA-CGA-O2A
2	A	296	DDH	CAA-CBA-CGA-O1A

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	296	DDH	4	0

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