



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:59 AM UTC

PDB ID : 1CCI / pdb_00001cci
Title : HOW FLEXIBLE ARE PROTEINS? TRAPPING OF A FLEXIBLE LOOP
Authors : Cao, Y.; Musah, R.A.; Wilcox, S.K.; Goodin, D.B.; Mcree, D.E.
Deposited on : 1996-12-18
Resolution : 2.40 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) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

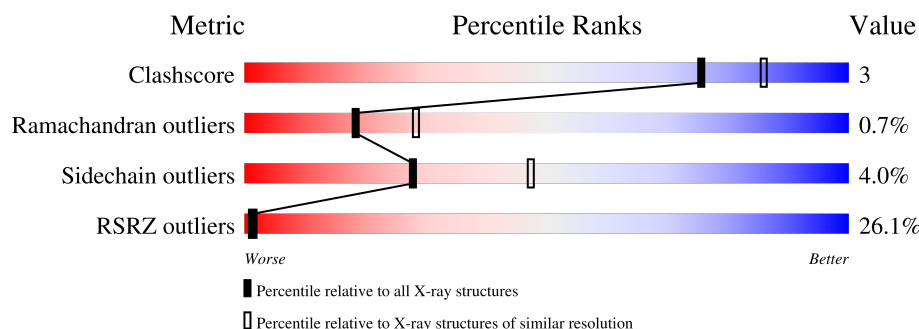
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	294	

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	DMI	A	499	-	X	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3003 atoms, of which 513 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.

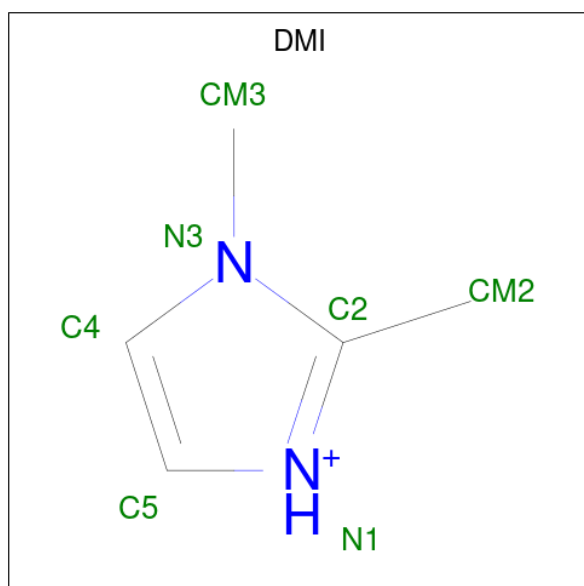
- Molecule 1 is a protein called CYTOCHROME C PEROXIDASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	291	2855	1494	512	392	451	6	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

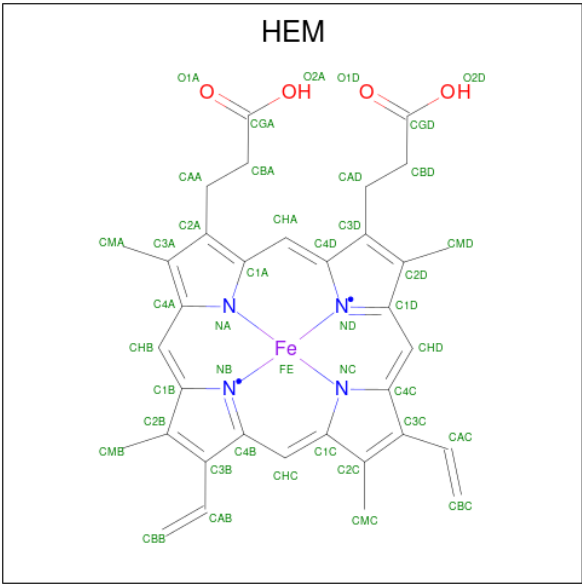
Chain	Residue	Modelled	Actual	Comment	Reference
A	53	ILE	THR	variant	UNP P00431
A	152	GLY	ASP	variant	UNP P00431
A	202	GLY	PHE	engineered mutation	UNP P00431

- Molecule 2 is 2,3-DIMETHYLIMIDAZOLIUM ION (CCD ID: DMI) (formula: C₅H₉N₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	N		
2	A	1	8	5	1	2	0	0

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

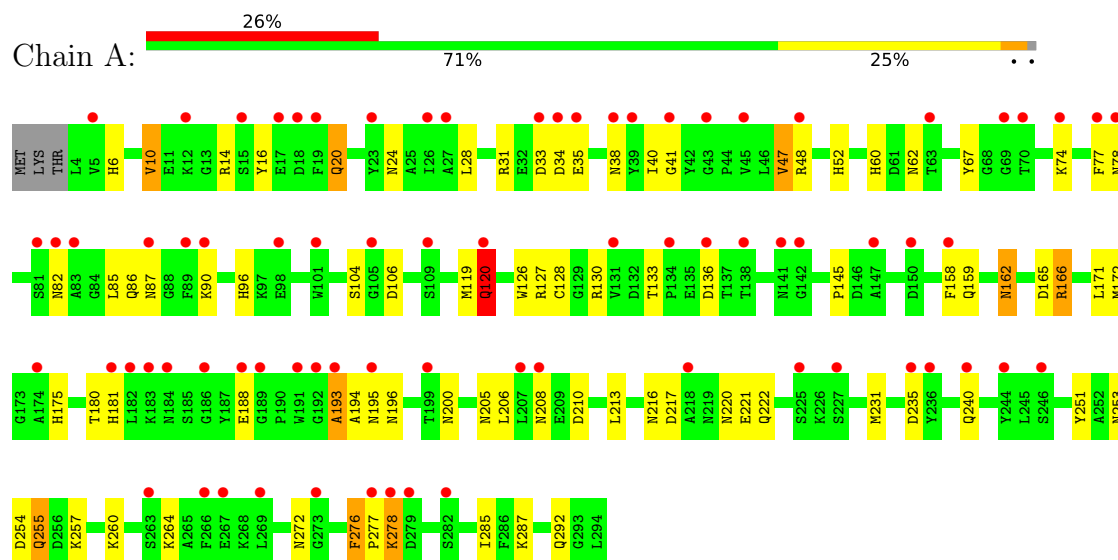
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	97	Total	O	0	0
			97	97		

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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: CYTOCHROME C PEROXIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	107.72Å 76.63Å 51.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 2.40 5.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	67.1 (5.00-2.40) 77.7 (5.00-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.01Å)	Xtriage
Refinement program	XTALVIEW, X-PLOR 3.1	Depositor
R, R_{free}	(Not available) , (Not available) 0.371 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	19.6	Xtriage
Anisotropy	0.297	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.50 , 80.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.70	EDS
Total number of atoms	3003	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DMI, 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	1.06	7/2408 (0.3%)	1.95	73/3259 (2.2%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	96	HIS	CD2-NE2	-7.40	1.29	1.37
1	A	47	VAL	CA-CB	7.37	1.64	1.54
1	A	6	HIS	CD2-NE2	-6.77	1.30	1.37
1	A	52	HIS	CD2-NE2	-6.67	1.30	1.37
1	A	60	HIS	CD2-NE2	-6.61	1.30	1.37
1	A	181	HIS	CD2-NE2	-6.61	1.30	1.37
1	A	175	HIS	CD2-NE2	-5.01	1.32	1.37

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	272	ASN	OD1-CG-ND2	-11.91	110.69	122.60
1	A	253	ASN	OD1-CG-ND2	-11.07	111.53	122.60
1	A	162	ASN	CA-CB-CG	9.28	121.88	112.60
1	A	255	GLN	OE1-CD-NE2	-9.13	113.47	122.60
1	A	127	ARG	CB-CG-CD	-9.10	90.38	111.30
1	A	205	ASN	OD1-CG-ND2	-9.06	113.54	122.60
1	A	78	ASN	OD1-CG-ND2	-8.48	114.12	122.60
1	A	162	ASN	N-CA-C	8.06	127.96	110.80
1	A	87	ASN	OD1-CG-ND2	-7.67	114.93	122.60
1	A	196	ASN	OD1-CG-ND2	-7.66	114.94	122.60
1	A	82	ASN	OD1-CG-ND2	-7.63	114.97	122.60
1	A	24	ASN	OD1-CG-ND2	-7.50	115.10	122.60
1	A	62	ASN	OD1-CG-ND2	-7.47	115.13	122.60
1	A	272	ASN	CA-CB-CG	7.41	120.01	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	ASN	CA-C-O	7.33	130.99	120.51
1	A	254	ASP	CA-CB-CG	7.31	119.91	112.60
1	A	240	GLN	OE1-CD-NE2	-7.20	115.40	122.60
1	A	31	ARG	NE-CZ-NH2	-7.13	112.78	119.20
1	A	38	ASN	OD1-CG-ND2	-7.07	115.53	122.60
1	A	120	GLN	N-CA-C	6.67	125.00	110.80
1	A	20	GLN	OE1-CD-NE2	-6.67	115.94	122.60
1	A	216	ASN	OD1-CG-ND2	-6.61	115.99	122.60
1	A	136	ASP	CA-CB-CG	6.50	119.09	112.60
1	A	159	GLN	OE1-CD-NE2	-6.45	116.15	122.60
1	A	38	ASN	CA-CB-CG	-6.36	106.24	112.60
1	A	292	GLN	OE1-CD-NE2	-6.33	116.27	122.60
1	A	195	ASN	N-CA-CB	-6.33	100.08	110.52
1	A	208	ASN	OD1-CG-ND2	-6.21	116.39	122.60
1	A	200	ASN	OD1-CG-ND2	-6.18	116.42	122.60
1	A	188	GLU	CB-CG-CD	6.10	122.97	112.60
1	A	165	ASP	N-CA-C	6.09	118.42	111.11
1	A	33	ASP	CA-CB-CG	6.04	118.64	112.60
1	A	220	ASN	OD1-CG-ND2	-6.02	116.58	122.60
1	A	145	PRO	N-CA-C	5.97	120.37	111.41
1	A	222	GLN	OE1-CD-NE2	-5.92	116.68	122.60
1	A	235	ASP	CA-CB-CG	5.89	118.49	112.60
1	A	104	SER	N-CA-C	5.84	118.12	111.11
1	A	41	GLY	O-C-N	-5.83	116.45	122.68
1	A	78	ASN	CB-CG-ND2	5.80	125.10	116.40
1	A	253	ASN	CB-CG-ND2	5.77	125.05	116.40
1	A	34	ASP	N-CA-C	5.71	120.08	113.18
1	A	210	ASP	CA-CB-CG	5.67	118.27	112.60
1	A	276	PHE	CA-C-N	5.66	125.59	119.76
1	A	276	PHE	C-N-CA	5.66	125.59	119.76
1	A	251	TYR	N-CA-C	5.66	118.38	111.82
1	A	133	THR	CA-C-N	5.62	125.53	119.85
1	A	133	THR	C-N-CA	5.62	125.53	119.85
1	A	180	THR	O-C-N	-5.60	116.70	123.03
1	A	216	ASN	N-CA-C	5.58	119.01	110.36
1	A	6	HIS	CB-CG-CD2	-5.58	123.95	131.20
1	A	106	ASP	CA-CB-CG	5.55	118.15	112.60
1	A	24	ASN	CB-CG-ND2	5.53	124.70	116.40
1	A	60	HIS	CB-CG-CD2	-5.52	124.02	131.20
1	A	195	ASN	N-CA-C	5.46	118.72	109.76
1	A	90	LYS	CA-CB-CG	-5.34	103.42	114.10
1	A	16	TYR	N-CA-C	5.34	117.52	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	96	HIS	CB-CG-CD2	-5.33	124.27	131.20
1	A	67	TYR	N-CA-C	5.30	116.74	111.07
1	A	120	GLN	OE1-CD-NE2	-5.28	117.33	122.60
1	A	255	GLN	CG-CD-NE2	5.26	124.28	116.40
1	A	166	ARG	CG-CD-NE	-5.20	100.57	112.00
1	A	210	ASP	O-C-N	-5.17	116.73	122.93
1	A	158	PHE	N-CA-C	5.17	118.84	112.54
1	A	166	ARG	NE-CZ-NH2	-5.16	114.55	119.20
1	A	175	HIS	CB-CG-CD2	-5.16	124.49	131.20
1	A	126	TRP	CG-CD2-CE3	5.14	139.04	133.90
1	A	78	ASN	N-CA-C	5.08	119.16	112.92
1	A	278	LYS	N-CA-C	5.05	118.55	112.38
1	A	120	GLN	CA-CB-CG	5.04	124.18	114.10
1	A	181	HIS	CB-CG-CD2	-5.03	124.66	131.20
1	A	193	ALA	CA-C-O	5.02	127.69	120.51
1	A	205	ASN	CB-CG-ND2	5.01	123.92	116.40
1	A	217	ASP	CA-CB-CG	-5.01	107.59	112.60

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	2343	512	2222	14	3
2	A	7	1	9	0	0
3	A	43	0	30	0	0
4	A	97	0	0	2	0
All	All	2490	513	2261	14	3

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 3.

All (14) 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:128:CYS:HA	4:A:326:HOH:O	1.81	0.81
1:A:130:ARG:NH1	4:A:326:HOH:O	2.37	0.56
1:A:206:LEU:HD13	1:A:231:MET:HE3	1.94	0.49
1:A:20:GLN:HE22	1:A:287:LYS:H	1.64	0.45
1:A:35:GLU:H	1:A:35:GLU:CD	2.25	0.45
1:A:276:PHE:HA	1:A:277:PRO:HD3	1.92	0.43
1:A:48:ARG:HG2	1:A:85:LEU:HD21	2.00	0.43
1:A:172:MET:HE2	1:A:172:MET:HB2	1.89	0.42
1:A:264:LYS:HB2	1:A:264:LYS:HZ2	1.84	0.42
1:A:119:MET:O	1:A:120:GLN:HG2	2.19	0.42
1:A:166:ARG:HH21	1:A:257:LYS:NZ	2.19	0.40
1:A:10:VAL:HG13	1:A:128:CYS:SG	2.61	0.40
1:A:40:ILE:HD11	1:A:194:ALA:HB3	2.03	0.40
1:A:77:PHE:CE1	1:A:86:GLN:HG3	2.57	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:ARG:HH21	1:A:213:LEU:O[4_477]	1.16	0.44
1:A:14:ARG:HH12	1:A:221:GLU:OE2[4_477]	1.31	0.29
1:A:14:ARG:NH2	1:A:213:LEU:O[4_477]	2.00	0.20

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	289/294 (98%)	278 (96%)	9 (3%)	2 (1%)	18 28

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	ASN

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Mol	Chain	Res	Type
1	A	193	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	248/251 (99%)	238 (96%)	10 (4%)	28	47

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	VAL
1	A	28	LEU
1	A	47	VAL
1	A	74	LYS
1	A	120	GLN
1	A	171	LEU
1	A	255	GLN
1	A	260	LYS
1	A	278	LYS
1	A	285	ILE

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	20	GLN
1	A	24	ASN
1	A	78	ASN
1	A	82	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	HEM	A	500	1,4	50,50,50	2.37	27 (54%)	67,82,82	1.16	4 (5%)
2	DMI	A	499	-	7,7,7	2.16	3 (42%)	8,9,9	3.74	5 (62%)

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	500	1,4	-	2/14/54/54	-
2	DMI	A	499	-	-	-	0/1/1/1

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	HEM	FE-ND	4.32	2.08	1.94
3	A	500	HEM	FE-NC	4.31	2.09	1.95
3	A	500	HEM	FE-NB	4.22	2.07	1.94
3	A	500	HEM	C4D-C3D	-3.76	1.38	1.45
3	A	500	HEM	C4D-ND	-3.74	1.33	1.40
2	A	499	DMI	C4-N3	-3.62	1.30	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	HEM	C1B-NB	-3.58	1.34	1.40
3	A	500	HEM	C3C-C4C	-3.51	1.39	1.46
3	A	500	HEM	CBC-CAC	3.43	1.46	1.30
3	A	500	HEM	CBB-CAB	3.35	1.46	1.30
3	A	500	HEM	FE-NA	3.24	2.05	1.95
3	A	500	HEM	C3B-C4B	-3.13	1.38	1.44
2	A	499	DMI	C5-N1	-3.09	1.32	1.38
3	A	500	HEM	C1A-NA	-2.96	1.34	1.39
3	A	500	HEM	C1C-C2C	-2.84	1.39	1.45
3	A	500	HEM	CAB-C3B	-2.77	1.40	1.47
3	A	500	HEM	C4A-NA	-2.73	1.34	1.39
3	A	500	HEM	C4C-NC	-2.62	1.34	1.39
3	A	500	HEM	C1A-C2A	-2.62	1.39	1.44
3	A	500	HEM	C3B-C2B	2.58	1.42	1.37
3	A	500	HEM	C1D-C2D	-2.47	1.39	1.44
3	A	500	HEM	CAC-C3C	-2.40	1.41	1.47
3	A	500	HEM	C4B-NB	-2.37	1.34	1.38
3	A	500	HEM	C3C-C2C	2.32	1.41	1.37
3	A	500	HEM	C1B-C2B	-2.28	1.39	1.44
3	A	500	HEM	C1C-NC	-2.26	1.35	1.39
3	A	500	HEM	C1D-ND	-2.22	1.34	1.38
3	A	500	HEM	O2D-CGD	-2.19	1.23	1.30
2	A	499	DMI	C2-N3	-2.14	1.33	1.38
3	A	500	HEM	O2A-CGA	-2.11	1.23	1.30

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	499	DMI	C4-N3-C2	8.09	112.11	106.83
2	A	499	DMI	CM2-C2-N3	4.13	128.72	122.25
3	A	500	HEM	C3C-C2C-C1C	-3.20	104.02	107.05
2	A	499	DMI	C5-N1-C2	3.11	110.04	105.86
2	A	499	DMI	C4-C5-N1	-2.52	107.44	110.74
3	A	500	HEM	O2A-CGA-CBA	2.52	121.95	114.00
2	A	499	DMI	CM3-N3-C2	-2.44	125.62	127.64
3	A	500	HEM	C3B-C4B-NB	2.27	111.10	109.47
3	A	500	HEM	O2D-CGD-CBD	2.17	120.85	114.00

There are no chirality outliers.

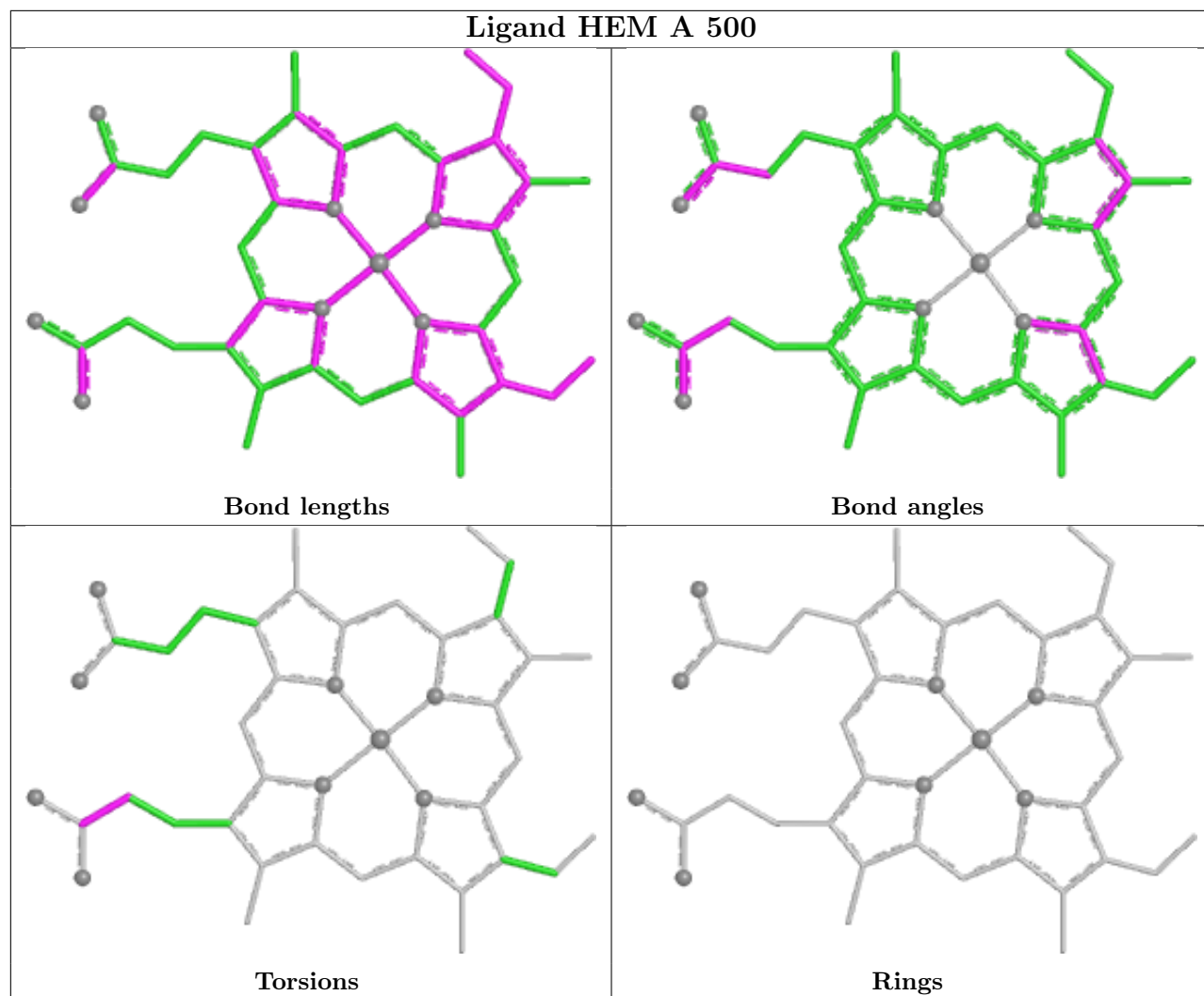
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	500	HEM	CAA-CBA-CGA-O2A
3	A	500	HEM	CAA-CBA-CGA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	291/294 (98%)	1.49	76 (26%) ⓘ ⓘ	7, 20, 37, 47	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	38	ASN	4.6
1	A	183	LYS	4.4
1	A	35	GLU	4.2
1	A	78	ASN	4.1
1	A	15	SER	3.9
1	A	189	GLY	3.7
1	A	134	PRO	3.7
1	A	192	GLY	3.6
1	A	17	GLU	3.5
1	A	195	ASN	3.4
1	A	39	TYR	3.3
1	A	266	PHE	3.3
1	A	181	HIS	3.3
1	A	63	THR	3.2
1	A	136	ASP	3.2
1	A	188	GLU	3.1
1	A	70	THR	3.1
1	A	277	PRO	3.1
1	A	5	VAL	3.0
1	A	101	TRP	2.9
1	A	33	ASP	2.9
1	A	142	GLY	2.9
1	A	138	THR	2.8
1	A	105	GLY	2.8
1	A	23	TYR	2.7
1	A	43	GLY	2.7
1	A	69	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	74	LYS	2.7
1	A	87	ASN	2.7
1	A	141	ASN	2.7
1	A	225	SER	2.7
1	A	77	PHE	2.7
1	A	208	ASN	2.7
1	A	244	TYR	2.7
1	A	34	ASP	2.6
1	A	184	ASN	2.6
1	A	218	ALA	2.6
1	A	278	LYS	2.6
1	A	279	ASP	2.5
1	A	207	LEU	2.5
1	A	199	THR	2.5
1	A	109	SER	2.5
1	A	186	GLY	2.4
1	A	191	TRP	2.4
1	A	131	VAL	2.4
1	A	182	LEU	2.4
1	A	19	PHE	2.4
1	A	246	SER	2.3
1	A	48	ARG	2.3
1	A	89	PHE	2.3
1	A	120	GLN	2.3
1	A	263	SER	2.3
1	A	282	SER	2.3
1	A	150	ASP	2.3
1	A	158	PHE	2.3
1	A	236	TYR	2.3
1	A	273	GLY	2.3
1	A	235	ASP	2.3
1	A	147	ALA	2.2
1	A	45	VAL	2.2
1	A	174	ALA	2.2
1	A	240	GLN	2.2
1	A	81	SER	2.2
1	A	83	ALA	2.2
1	A	90	LYS	2.2
1	A	82	ASN	2.2
1	A	18	ASP	2.2
1	A	267	GLU	2.2
1	A	41	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	269	LEU	2.1
1	A	193	ALA	2.1
1	A	98	GLU	2.1
1	A	12	LYS	2.1
1	A	227	SER	2.1
1	A	26	ILE	2.0
1	A	27	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

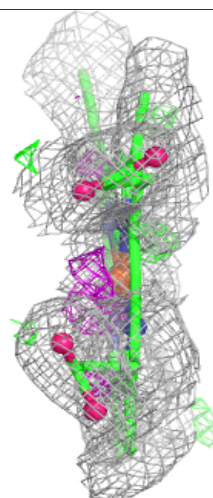
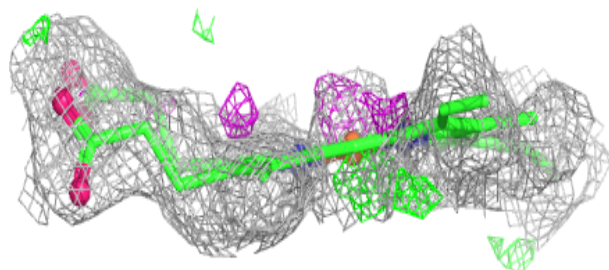
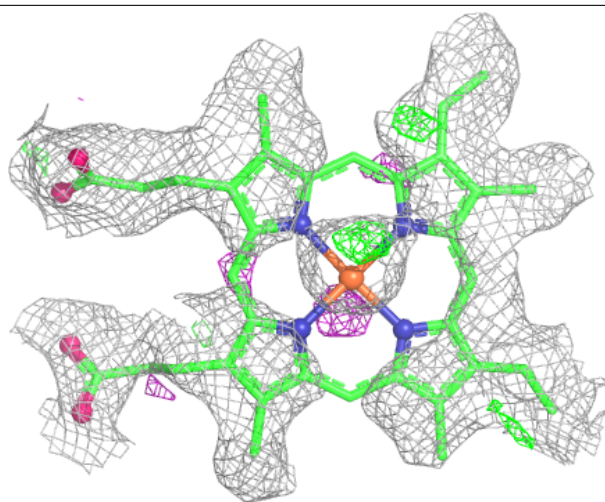
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	DMI	A	499	7/7	0.75	0.11	20,35,36,36	0
3	HEM	A	500	43/43	0.78	0.19	10,20,24,25	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around HEM A 500:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.