



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:19 AM UTC

PDB ID : 1A2F / pdb_00001a2f
Title : PROBING THE STRENGTH AND CHARACTER OF AN ASP-HIS-X HYDROGEN BOND BY INTRODUCING BURIED CHARGES
Authors : Cao, Y.; Goodin, D.B.; Mcree, D.E.
Deposited on : 1998-01-02
Resolution : 2.10 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

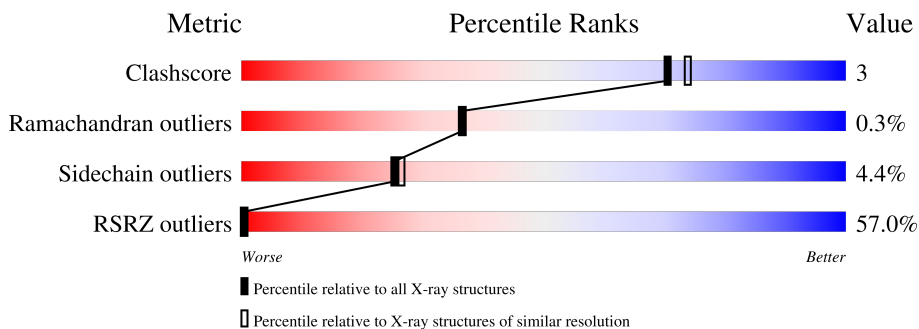
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	291	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3016 atoms, of which 515 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.

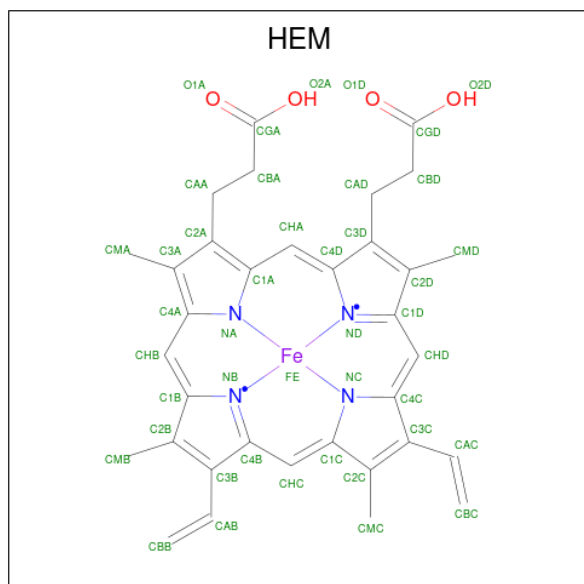
- Molecule 1 is a protein called CYTOCHROME C PEROXIDASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	291	Total	C	H	N	O	S	0	0	0
			2866	1502	515	393	451	5			

There are 3 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	172	LYS	MET	engineered mutation	UNP P00431

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

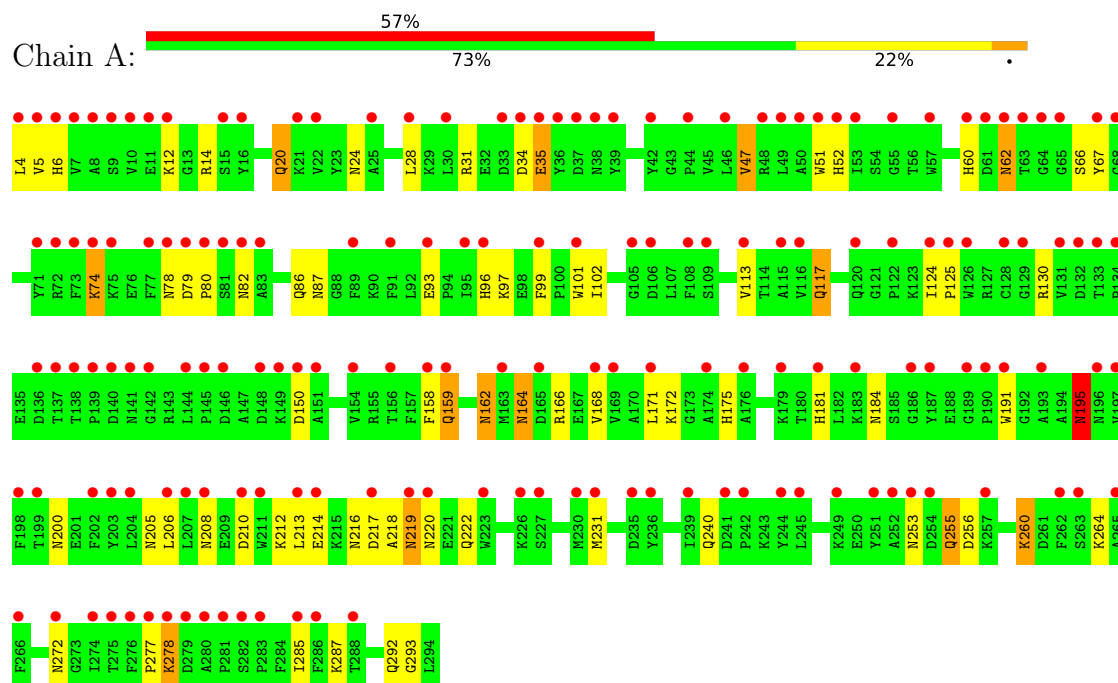
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	107	Total 107	O 107	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 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	103.80Å 73.50Å 44.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 2.10 5.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (5.00-2.10) 82.0 (5.00-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 1.91Å)	Xtriage
Refinement program	XTALVIEW, X-PLOR 3.1	Depositor
R, R_{free}	0.184 , (Not available) 0.484 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.644	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	3.23 , 166.0	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	0.57	EDS
Total number of atoms	3016	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.28% 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: 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	1.07	8/2417 (0.3%)	1.93	67/3271 (2.0%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	96	HIS	CD2-NE2	-7.52	1.29	1.37
1	A	6	HIS	CD2-NE2	-6.99	1.30	1.37
1	A	102	ILE	CA-CB	6.95	1.62	1.54
1	A	52	HIS	CD2-NE2	-6.93	1.30	1.37
1	A	60	HIS	CD2-NE2	-6.38	1.30	1.37
1	A	181	HIS	CD2-NE2	-6.16	1.31	1.37
1	A	175	HIS	CD2-NE2	-5.73	1.31	1.37
1	A	47	VAL	CA-CB	5.42	1.61	1.54

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	20	GLN	OE1-CD-NE2	-11.19	111.41	122.60
1	A	162	ASN	CA-CB-CG	11.00	123.60	112.60
1	A	240	GLN	OE1-CD-NE2	-10.88	111.72	122.60
1	A	208	ASN	OD1-CG-ND2	-10.24	112.36	122.60
1	A	195	ASN	N-CA-C	9.73	124.39	113.21
1	A	78	ASN	OD1-CG-ND2	-9.17	113.43	122.60
1	A	255	GLN	OE1-CD-NE2	-8.71	113.89	122.60
1	A	62	ASN	OD1-CG-ND2	-8.42	114.18	122.60
1	A	67	TYR	N-CA-C	8.06	120.78	111.11
1	A	222	GLN	OE1-CD-NE2	-8.00	114.60	122.60
1	A	164	ASN	CA-CB-CG	7.95	120.55	112.60
1	A	253	ASN	OD1-CG-ND2	-7.93	114.67	122.60
1	A	159	GLN	OE1-CD-NE2	-7.76	114.84	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	184	ASN	OD1-CG-ND2	-7.70	114.90	122.60
1	A	86	GLN	OE1-CD-NE2	-7.62	114.98	122.60
1	A	220	ASN	OD1-CG-ND2	-7.58	115.02	122.60
1	A	164	ASN	OD1-CG-ND2	-7.49	115.11	122.60
1	A	117	GLN	OE1-CD-NE2	-7.39	115.20	122.60
1	A	205	ASN	OD1-CG-ND2	-7.38	115.22	122.60
1	A	240	GLN	CG-CD-NE2	7.24	127.26	116.40
1	A	195	ASN	CA-CB-CG	7.16	119.76	112.60
1	A	278	LYS	CA-CB-CG	-7.13	99.84	114.10
1	A	82	ASN	OD1-CG-ND2	-6.88	115.72	122.60
1	A	87	ASN	OD1-CG-ND2	-6.87	115.73	122.60
1	A	24	ASN	OD1-CG-ND2	-6.86	115.74	122.60
1	A	195	ASN	OD1-CG-ND2	-6.80	115.80	122.60
1	A	277	PRO	CA-C-O	-6.80	113.38	121.67
1	A	79	ASP	CA-CB-CG	6.56	119.16	112.60
1	A	162	ASN	CA-C-O	6.30	129.53	120.51
1	A	162	ASN	N-CA-C	6.30	124.22	110.80
1	A	292	GLN	OE1-CD-NE2	-6.30	116.30	122.60
1	A	99	PHE	CA-C-N	6.24	125.86	119.56
1	A	99	PHE	C-N-CA	6.24	125.86	119.56
1	A	51	TRP	CB-CG-CD1	-6.21	117.59	126.90
1	A	272	ASN	OD1-CG-ND2	-6.16	116.44	122.60
1	A	62	ASN	CB-CG-ND2	5.97	125.36	116.40
1	A	51	TRP	CG-CD2-CE3	5.96	139.86	133.90
1	A	208	ASN	CB-CG-ND2	5.95	125.32	116.40
1	A	216	ASN	OD1-CG-ND2	-5.94	116.66	122.60
1	A	31	ARG	NE-CZ-NH2	-5.89	113.89	119.20
1	A	219	ASN	OD1-CG-ND2	-5.87	116.73	122.60
1	A	253	ASN	CB-CG-ND2	5.85	125.18	116.40
1	A	222	GLN	CG-CD-NE2	5.84	125.15	116.40
1	A	150	ASP	N-CA-C	5.83	119.18	109.96
1	A	210	ASP	CA-CB-CG	5.78	118.38	112.60
1	A	217	ASP	N-CA-C	5.74	119.38	112.38
1	A	181	HIS	CB-CG-CD2	-5.73	123.75	131.20
1	A	34	ASP	CA-CB-CG	5.70	118.30	112.60
1	A	219	ASN	CB-CG-ND2	5.64	124.87	116.40
1	A	5	VAL	O-C-N	-5.53	117.50	123.14
1	A	158	PHE	N-CA-C	5.52	119.27	112.54
1	A	124	ILE	O-C-N	-5.50	115.86	120.92
1	A	117	GLN	CG-CD-NE2	5.47	124.60	116.40
1	A	60	HIS	CB-CG-CD2	-5.46	124.11	131.20
1	A	51	TRP	CE2-CD2-CG	-5.41	100.71	107.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	164	ASN	CB-CG-ND2	5.40	124.50	116.40
1	A	93	GLU	N-CA-C	5.38	120.24	113.25
1	A	191	TRP	CE2-CD2-CG	-5.36	100.77	107.20
1	A	96	HIS	CB-CG-CD2	-5.16	124.49	131.20
1	A	93	GLU	CA-C-N	5.16	124.95	119.28
1	A	93	GLU	C-N-CA	5.16	124.95	119.28
1	A	66	SER	N-CA-C	5.11	118.78	112.54
1	A	51	TRP	CG-CD1-NE1	-5.09	103.58	110.20
1	A	52	HIS	CB-CG-CD2	-5.08	124.60	131.20
1	A	35	GLU	N-CA-C	5.05	119.29	113.18
1	A	78	ASN	CB-CG-ND2	5.05	123.97	116.40
1	A	97	LYS	CB-CA-C	-5.04	102.42	110.79

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	2351	515	2232	16	23
2	A	43	0	30	0	0
3	A	107	0	0	2	13
All	All	2501	515	2262	16	23

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 (16) 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:168:VAL:O	1:A:172:LYS:HG2	1.98	0.63
1:A:195:ASN:HD22	1:A:195:ASN:H	1.47	0.63
1:A:206:LEU:HD13	1:A:231:MET:SD	2.38	0.62
1:A:20:GLN:HE22	1:A:287:LYS:H	1.51	0.58
1:A:74:LYS:HD2	1:A:74:LYS:H	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:ASN:H	1:A:255:GLN:HE21	1.56	0.53
1:A:130:ARG:NE	3:A:326:HOH:O	2.43	0.51
1:A:256:ASP:O	1:A:260:LYS:HD2	2.17	0.44
1:A:164:ASN:O	1:A:168:VAL:HG23	2.17	0.44
1:A:20:GLN:HE22	1:A:287:LYS:N	2.13	0.44
1:A:218:ALA:O	1:A:219:ASN:HB2	2.18	0.44
1:A:125:PRO:HG3	1:A:285:ILE:HD11	2.01	0.42
1:A:113:VAL:O	1:A:117:GLN:HG3	2.20	0.41
1:A:195:ASN:HD22	1:A:195:ASN:N	2.18	0.41
1:A:4:LEU:HB2	1:A:62:ASN:HB3	2.02	0.41
1:A:130:ARG:CZ	3:A:326:HOH:O	2.69	0.40

All (23) 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_5610]	1.01	0.59
1:A:14:ARG:HH21	1:A:213:LEU:C[4_5610]	1.01	0.59
1:A:212:LYS:NZ	3:A:374:HOH:O[4_4610]	1.70	0.50
1:A:212:LYS:CG	3:A:372:HOH:O[4_4610]	1.70	0.50
1:A:212:LYS:CD	3:A:372:HOH:O[4_4610]	1.74	0.46
1:A:14:ARG:NH2	1:A:213:LEU:C[4_5610]	1.81	0.39
1:A:264:LYS:HZ1	3:A:389:HOH:O[3_559]	1.22	0.38
1:A:264:LYS:NZ	3:A:389:HOH:O[3_559]	1.83	0.37
1:A:14:ARG:NH2	1:A:213:LEU:O[4_5610]	1.86	0.34
1:A:212:LYS:CE	3:A:374:HOH:O[4_4610]	1.86	0.34
1:A:12:LYS:CB	1:A:214:GLU:OE2[4_5610]	1.87	0.33
1:A:214:GLU:OE2	3:A:374:HOH:O[4_4610]	1.89	0.31
1:A:212:LYS:HZ3	3:A:374:HOH:O[4_4610]	1.35	0.25
1:A:212:LYS:CE	3:A:372:HOH:O[4_4610]	1.97	0.23
1:A:14:ARG:NH2	1:A:214:GLU:N[4_5610]	2.02	0.18
1:A:214:GLU:CG	3:A:373:HOH:O[4_4610]	2.05	0.15
1:A:101:TRP:CB	1:A:213:LEU:O[4_5610]	2.07	0.13
1:A:14:ARG:HH21	1:A:214:GLU:N[4_5610]	1.54	0.06
1:A:12:LYS:N	1:A:214:GLU:OE2[4_5610]	2.15	0.05
1:A:12:LYS:H	1:A:214:GLU:OE2[4_5610]	1.56	0.04
1:A:214:GLU:CB	3:A:373:HOH:O[4_4610]	2.17	0.03
1:A:213:LEU:O	3:A:373:HOH:O[4_4610]	2.18	0.02
1:A:293:GLY:O	3:A:330:HOH:O[3_549]	2.18	0.02

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%)	282 (98%)	6 (2%)	1 (0%)	36	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	ASN

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	249/249 (100%)	238 (96%)	11 (4%)	25	26

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	35	GLU
1	A	47	VAL
1	A	74	LYS
1	A	80	PRO
1	A	159	GLN
1	A	166	ARG
1	A	171	LEU
1	A	195	ASN
1	A	260	LYS

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Mol	Chain	Res	Type
1	A	278	LYS

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	20	GLN
1	A	24	ASN
1	A	87	ASN
1	A	159	GLN
1	A	195	ASN
1	A	255	GLN
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](#)

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	HEM	A	1	3,1	50,50,50	2.29	26 (52%)	67,82,82	1.11	3 (4%)

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	HEM	A	1	3,1	-	3/14/54/54	-

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	HEM	FE-ND	4.58	2.09	1.94
2	A	1	HEM	C4D-ND	-4.11	1.33	1.40
2	A	1	HEM	C4D-C3D	-3.89	1.38	1.45
2	A	1	HEM	FE-NB	3.59	2.05	1.94
2	A	1	HEM	CBC-CAC	3.38	1.46	1.30
2	A	1	HEM	C4C-NC	-3.38	1.33	1.39
2	A	1	HEM	C3C-C4C	-3.36	1.40	1.46
2	A	1	HEM	C1A-C2A	-3.36	1.37	1.44
2	A	1	HEM	C1B-NB	-3.23	1.34	1.40
2	A	1	HEM	C1D-C2D	-3.14	1.38	1.44
2	A	1	HEM	FE-NC	3.09	2.05	1.95
2	A	1	HEM	CAB-C3B	-3.04	1.39	1.47
2	A	1	HEM	C3B-C4B	-3.01	1.39	1.44
2	A	1	HEM	C1D-ND	-2.87	1.33	1.38
2	A	1	HEM	C4B-NB	-2.72	1.33	1.38
2	A	1	HEM	CBB-CAB	2.66	1.43	1.30
2	A	1	HEM	FE-NA	2.64	2.03	1.95
2	A	1	HEM	C1A-NA	-2.61	1.34	1.39
2	A	1	HEM	C1B-C2B	-2.61	1.39	1.44
2	A	1	HEM	C1C-NC	-2.60	1.34	1.39
2	A	1	HEM	C4A-C3A	-2.42	1.37	1.43
2	A	1	HEM	C1C-C2C	-2.38	1.40	1.45
2	A	1	HEM	C4A-NA	-2.36	1.35	1.39
2	A	1	HEM	CAC-C3C	-2.28	1.41	1.47
2	A	1	HEM	O2A-CGA	-2.18	1.23	1.30
2	A	1	HEM	O2D-CGD	-2.16	1.23	1.30

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	HEM	C3C-C2C-C1C	-3.56	103.68	107.05
2	A	1	HEM	C3B-C4B-NB	2.20	111.05	109.47
2	A	1	HEM	O2A-CGA-CBA	2.19	120.94	114.00

There are no chirality outliers.

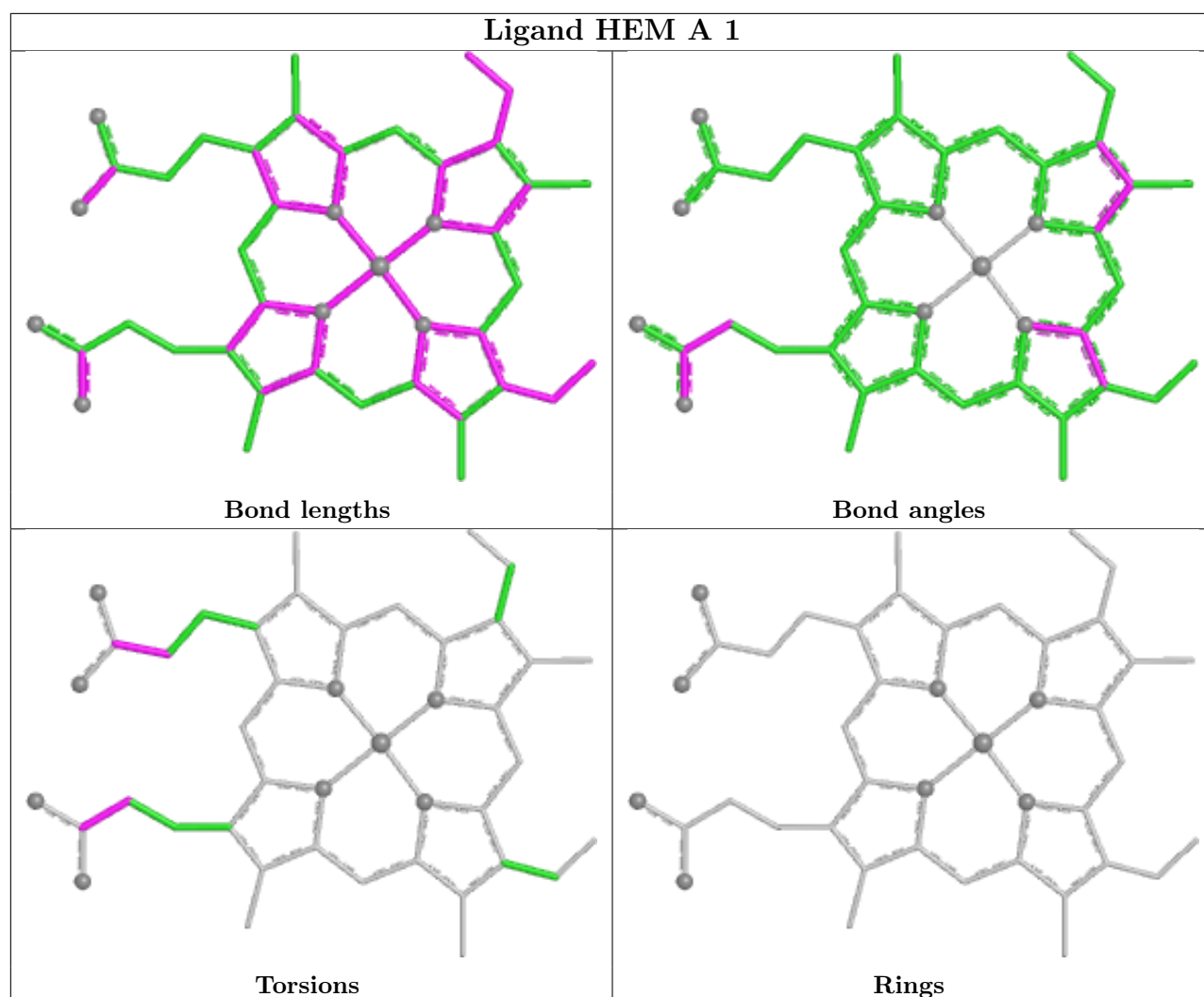
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	HEM	CAA-CBA-CGA-O2A
2	A	1	HEM	CAA-CBA-CGA-O1A
2	A	1	HEM	CAD-CBD-CGD-O2D

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	291/291 (100%)	2.30	166 (57%) 0 0	9, 17, 28, 40	0

All (166) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	78	ASN	7.5
1	A	5	VAL	6.8
1	A	171	LEU	6.0
1	A	145	PRO	5.2
1	A	204	LEU	5.0
1	A	136	ASP	4.8
1	A	154	VAL	4.8
1	A	4	LEU	4.8
1	A	283	PRO	4.7
1	A	174	ALA	4.7
1	A	25	ALA	4.5
1	A	156	THR	4.5
1	A	39	TYR	4.3
1	A	10	VAL	4.3
1	A	236	TYR	4.3
1	A	73	PHE	4.2
1	A	80	PRO	4.1
1	A	65	GLY	4.0
1	A	262	PHE	4.0
1	A	282	SER	3.9
1	A	62	ASN	3.9
1	A	28	LEU	3.9
1	A	133	THR	3.9
1	A	223	TRP	3.8
1	A	42	TYR	3.8
1	A	277	PRO	3.8
1	A	38	ASN	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	50	ALA	3.8
1	A	8	ALA	3.7
1	A	275	THR	3.7
1	A	140	ASP	3.7
1	A	251	TYR	3.7
1	A	75	LYS	3.7
1	A	67	TYR	3.7
1	A	210	ASP	3.7
1	A	51	TRP	3.6
1	A	36	TYR	3.6
1	A	211	TRP	3.5
1	A	285	ILE	3.5
1	A	202	PHE	3.4
1	A	71	TYR	3.4
1	A	68	GLY	3.4
1	A	9	SER	3.4
1	A	49	LEU	3.4
1	A	63	THR	3.3
1	A	79	ASP	3.3
1	A	150	ASP	3.3
1	A	44	PRO	3.3
1	A	280	ALA	3.3
1	A	183	LYS	3.3
1	A	116	VAL	3.2
1	A	241	ASP	3.2
1	A	266	PHE	3.2
1	A	61	ASP	3.1
1	A	60	HIS	3.1
1	A	77	PHE	3.1
1	A	276	PHE	3.1
1	A	278	LYS	3.1
1	A	46	LEU	3.1
1	A	93	GLU	3.1
1	A	16	TYR	3.1
1	A	21	LYS	3.1
1	A	193	ALA	3.1
1	A	99	PHE	3.0
1	A	7	VAL	3.0
1	A	239	ILE	3.0
1	A	82	ASN	3.0
1	A	254	ASP	3.0
1	A	263	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	35	GLU	2.9
1	A	198	PHE	2.9
1	A	203	TYR	2.9
1	A	244	TYR	2.9
1	A	219	ASN	2.9
1	A	72	ARG	2.9
1	A	187	TYR	2.9
1	A	186	GLY	2.9
1	A	207	LEU	2.8
1	A	169	VAL	2.8
1	A	249	LYS	2.8
1	A	81	SER	2.8
1	A	138	THR	2.8
1	A	6	HIS	2.8
1	A	30	LEU	2.8
1	A	12	LYS	2.8
1	A	64	GLY	2.8
1	A	231	MET	2.7
1	A	148	ASP	2.7
1	A	158	PHE	2.7
1	A	131	VAL	2.7
1	A	265	ALA	2.7
1	A	208	ASN	2.7
1	A	57	TRP	2.7
1	A	257	LYS	2.7
1	A	213	LEU	2.7
1	A	272	ASN	2.7
1	A	217	ASP	2.7
1	A	279	ASP	2.7
1	A	129	GLY	2.7
1	A	253	ASN	2.6
1	A	83	ALA	2.6
1	A	226	LYS	2.6
1	A	53	ILE	2.6
1	A	230	MET	2.6
1	A	274	ILE	2.6
1	A	189	GLY	2.6
1	A	181	HIS	2.6
1	A	196	ASN	2.6
1	A	199	THR	2.6
1	A	113	VAL	2.5
1	A	124	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	235	ASP	2.5
1	A	139	PRO	2.5
1	A	252	ALA	2.5
1	A	15	SER	2.4
1	A	149	LYS	2.4
1	A	151	ALA	2.4
1	A	37	ASP	2.4
1	A	165	ASP	2.4
1	A	95	ILE	2.4
1	A	179	LYS	2.4
1	A	34	ASP	2.4
1	A	132	ASP	2.4
1	A	22	VAL	2.4
1	A	163	MET	2.4
1	A	134	PRO	2.3
1	A	176	ALA	2.3
1	A	74	LYS	2.3
1	A	89	PHE	2.3
1	A	286	PHE	2.3
1	A	101	TRP	2.3
1	A	227	SER	2.3
1	A	288	THR	2.3
1	A	55	GLY	2.3
1	A	105	GLY	2.3
1	A	144	LEU	2.3
1	A	91	PHE	2.2
1	A	108	PHE	2.2
1	A	122	PRO	2.2
1	A	190	PRO	2.2
1	A	128	CYS	2.2
1	A	106	ASP	2.2
1	A	115	ALA	2.2
1	A	109	SER	2.2
1	A	242	PRO	2.1
1	A	120	GLN	2.1
1	A	48	ARG	2.1
1	A	245	LEU	2.1
1	A	214	GLU	2.1
1	A	137	THR	2.1
1	A	159	GLN	2.1
1	A	141	ASN	2.1
1	A	125	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	281	PRO	2.1
1	A	126	TRP	2.1
1	A	168	VAL	2.1
1	A	206	LEU	2.1
1	A	33	ASP	2.1
1	A	96	HIS	2.1
1	A	197	VAL	2.1
1	A	142	GLY	2.0
1	A	11	GLU	2.0
1	A	191	TRP	2.0
1	A	220	ASN	2.0
1	A	146	ASP	2.0
1	A	52	HIS	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](#)

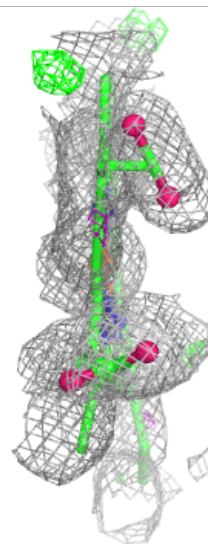
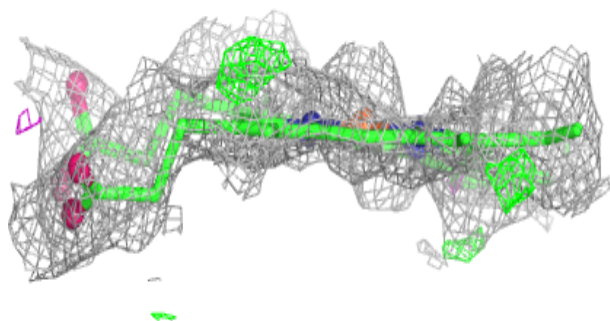
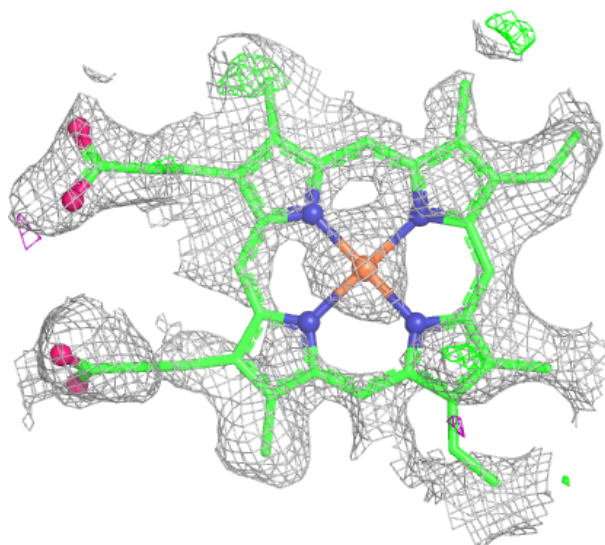
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	HEM	A	1	43/43	0.74	0.12	10,14,18,23	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 1:

$2mF_o-DF_c$ (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.