



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:48 PM UTC

PDB ID : 3PI9 / pdb_00003pi9
Title : Site-specific Glycosylation of Hemoglobin Utilizing Oxime Ligation Chemistry as a Viable Alternative to PEGylation
Authors : Bhatt, V.S.; Styslinger, T.J.; Zhang, N.; Wang, P.G.; Palmer, A.F.
Deposited on : 2010-11-05
Resolution : 2.90 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

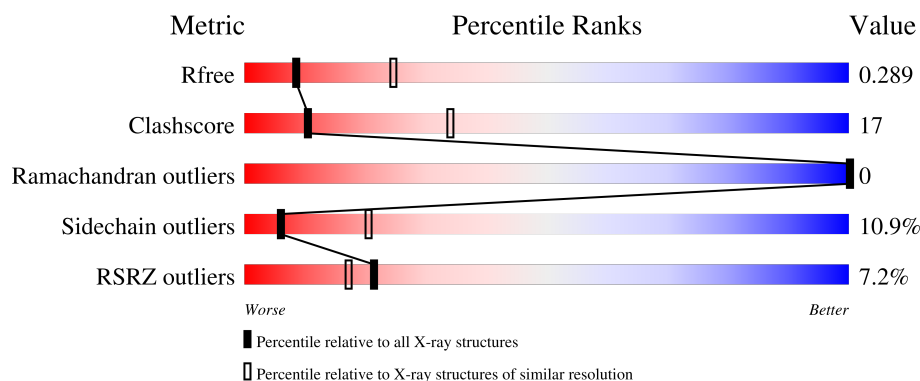
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	141	5% 70% 25% • •
1	C	141	2% 70% 26% • •
2	B	145	8% 59% 30% 12%
2	D	145	13% 57% 34% 7% •

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	CMO	B	148	-	-	X	-
4	CMO	D	148	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4578 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.

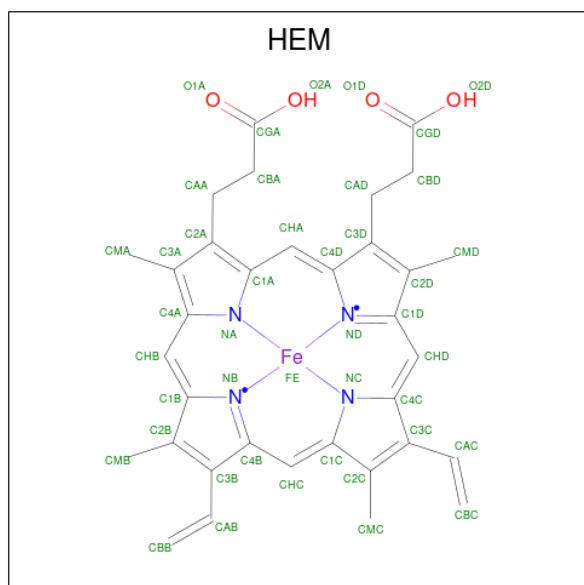
- Molecule 1 is a protein called Hemoglobin subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	10	0	0
			1066	683	186	196	1			
1	C	141	Total	C	N	O	S	1	0	0
			1066	683	186	196	1			

- Molecule 2 is a protein called Hemoglobin subunit beta.

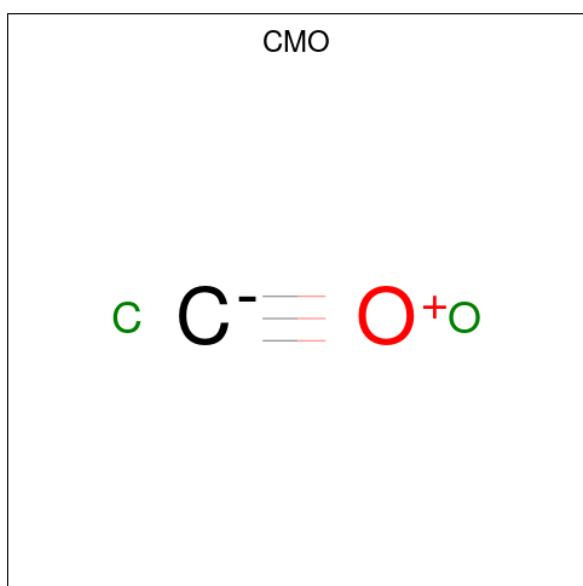
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	145	Total	C	N	O	S	3	0	0
			1127	726	194	203	4			
2	D	145	Total	C	N	O	S	6	0	0
			1127	726	194	203	4			

- 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		
3	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 4 is CARBON MONOXIDE (CCD ID: CMO) (formula: CO).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			2	1	1		
4	B	1	Total	C	O	0	0
			2	1	1		
4	C	1	Total	C	O	0	0
			2	1	1		
4	D	1	Total	C	O	0	0
			2	1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	O	0	0
			4	4		
5	B	2	Total	O	0	0
			2	2		

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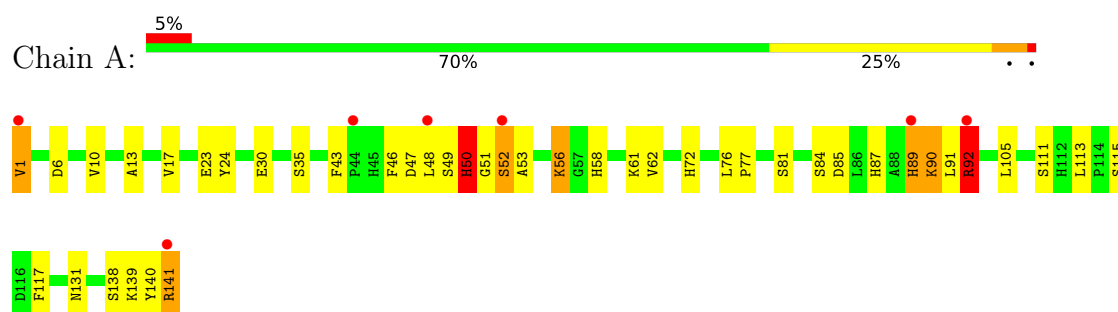
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total	O	0	0
			2	2		
5	D	4	Total	O	0	0
			4	4		

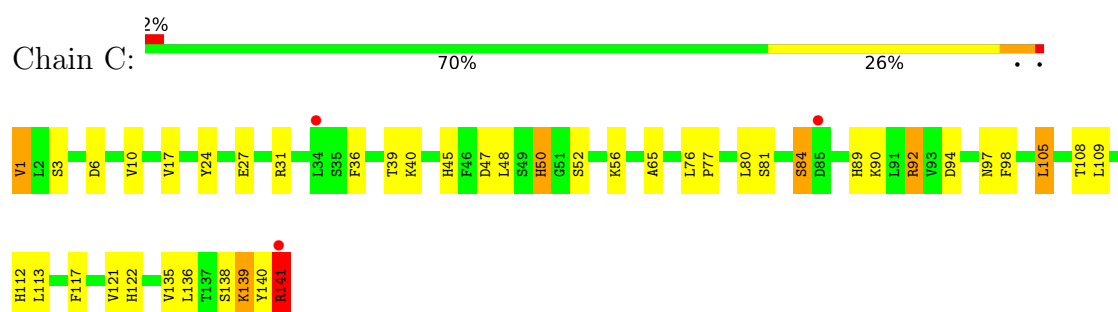
3 Residue-property plots

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.

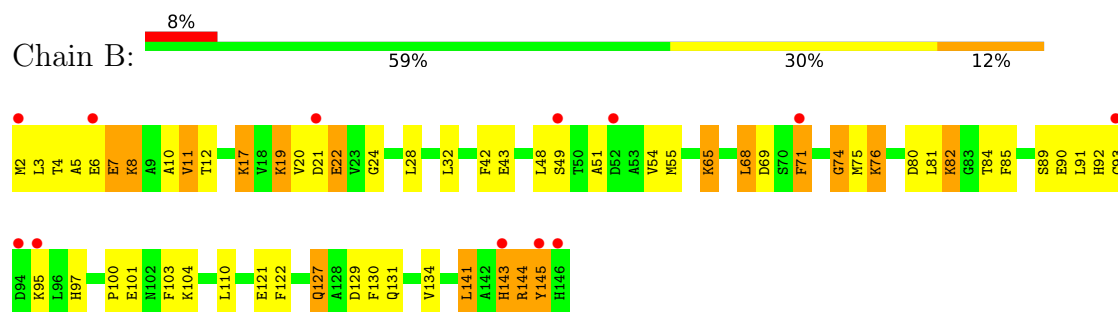
- Molecule 1: Hemoglobin subunit alpha



- Molecule 1: Hemoglobin subunit alpha

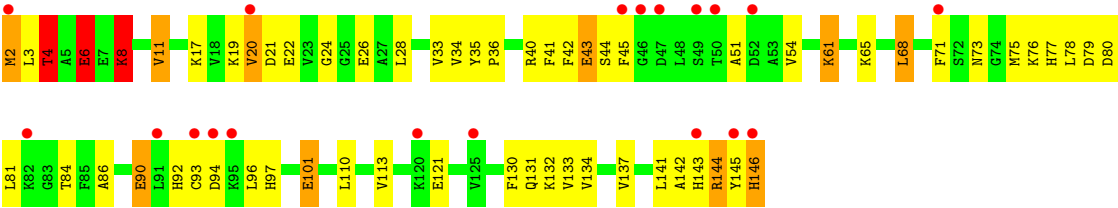


- Molecule 2: Hemoglobin subunit beta



- Molecule 2: Hemoglobin subunit beta





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.18Å 74.01Å 131.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.57 – 2.90 37.57 – 2.90	Depositor EDS
% Data completeness (in resolution range)	95.2 (37.57-2.90) 95.2 (37.57-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	12.09 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.261 , 0.293 0.255 , 0.289	Depositor DCC
R_{free} test set	614 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.453	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	4578	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, CMO

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	1.61	16/1093 (1.5%)	1.35	6/1483 (0.4%)
1	C	2.32	11/1093 (1.0%)	1.44	13/1483 (0.9%)
2	B	1.65	17/1152 (1.5%)	1.44	15/1556 (1.0%)
2	D	1.82	20/1152 (1.7%)	1.44	14/1556 (0.9%)
All	All	1.87	64/4490 (1.4%)	1.42	48/6078 (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	1
1	C	0	1
All	All	0	2

All (64) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	50	HIS	CD2-NE2	48.34	1.91	1.37
1	C	89	HIS	CG-ND1	26.19	1.67	1.38
1	C	89	HIS	CE1-NE2	21.73	1.54	1.32
2	D	6	GLU	CG-CD	16.94	1.94	1.52
2	B	97	HIS	CE1-NE2	16.88	1.49	1.32
1	A	92	ARG	CZ-NH1	16.75	1.56	1.32
1	C	50	HIS	CE1-NE2	-16.73	1.15	1.32
2	D	146	HIS	C-OXT	14.68	1.52	1.23
2	B	22	GLU	CG-CD	13.28	1.85	1.52
2	D	97	HIS	CE1-NE2	13.10	1.45	1.32
1	C	89	HIS	CD2-NE2	12.15	1.51	1.37
2	D	97	HIS	CG-ND1	11.54	1.50	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	97	HIS	CG-ND1	11.36	1.50	1.38
2	B	143	HIS	CD2-NE2	11.07	1.50	1.37
2	D	4	THR	CB-OG1	10.83	1.61	1.43
1	A	50	HIS	C-O	10.63	1.36	1.23
1	A	90	LYS	CE-NZ	10.55	1.80	1.49
2	D	144	ARG	CZ-NH1	10.06	1.46	1.32
2	D	44	SER	CB-OG	9.91	1.61	1.42
2	D	61	LYS	CE-NZ	9.73	1.78	1.49
2	B	80	ASP	CG-OD2	9.23	1.42	1.25
2	D	143	HIS	CE1-NE2	8.23	1.40	1.32
2	D	101	GLU	CD-OE1	8.01	1.40	1.25
1	A	58	HIS	CE1-NE2	7.68	1.40	1.32
2	B	76	LYS	CD-CE	7.56	1.75	1.52
1	C	50	HIS	CB-CG	7.44	1.60	1.50
1	A	50	HIS	CB-CG	-7.42	1.39	1.50
1	A	53	ALA	CA-CB	-7.41	1.41	1.53
1	C	141	ARG	CD-NE	7.39	1.56	1.46
2	D	143	HIS	ND1-CE1	-7.37	1.25	1.32
2	B	143	HIS	CG-ND1	7.37	1.46	1.38
2	B	10	ALA	CA-C	-7.18	1.43	1.52
1	A	72	HIS	CE1-NE2	-6.92	1.25	1.32
1	A	23	GLU	CD-OE2	6.81	1.38	1.25
1	C	141	ARG	NE-CZ	6.69	1.40	1.33
2	B	74	GLY	C-O	-6.68	1.14	1.23
2	D	43	GLU	CD-OE2	6.61	1.38	1.25
2	B	5	ALA	CA-C	-6.41	1.44	1.52
1	A	85	ASP	CG-OD1	-6.30	1.13	1.25
2	D	146	HIS	C-O	6.25	1.36	1.23
2	D	4	THR	CB-CG2	6.19	1.73	1.52
2	D	51	ALA	N-CA	6.14	1.53	1.46
1	C	141	ARG	CZ-NH1	5.95	1.41	1.32
1	A	89	HIS	ND1-CE1	-5.87	1.26	1.32
2	D	43	GLU	C-O	5.83	1.30	1.24
1	A	30	GLU	CD-OE1	5.63	1.36	1.25
1	A	52	SER	C-O	5.62	1.30	1.23
1	C	139	LYS	CE-NZ	5.51	1.65	1.49
1	C	50	HIS	ND1-CE1	5.48	1.38	1.32
2	B	10	ALA	N-CA	5.47	1.52	1.46
1	A	89	HIS	CE1-NE2	5.45	1.38	1.32
2	B	22	GLU	CA-C	5.42	1.59	1.52
2	D	101	GLU	CD-OE2	5.42	1.35	1.25
2	B	7	GLU	CB-CG	5.39	1.68	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	92	ARG	CG-CD	5.37	1.68	1.52
2	D	6	GLU	CB-CG	5.34	1.68	1.52
2	D	132	LYS	CE-NZ	5.26	1.65	1.49
2	B	8	LYS	CE-NZ	5.25	1.65	1.49
2	D	133	VAL	CA-CB	5.24	1.60	1.54
2	B	22	GLU	CA-CB	5.23	1.61	1.53
2	B	20	VAL	CA-CB	5.14	1.60	1.54
1	A	56	LYS	CE-NZ	5.10	1.64	1.49
1	A	92	ARG	CZ-NH2	5.08	1.40	1.33
2	B	82	LYS	CD-CE	5.05	1.67	1.52

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	50	HIS	CA-CB-CG	18.69	132.49	113.80
1	C	50	HIS	CE1-NE2-CD2	-16.39	92.61	109.00
1	C	50	HIS	CG-CD2-NE2	-14.06	93.14	107.20
2	D	43	GLU	CB-CG-CD	11.84	132.72	112.60
2	D	144	ARG	NE-CZ-NH1	11.01	132.51	121.50
1	C	89	HIS	CG-CD2-NE2	-11.00	96.20	107.20
2	D	144	ARG	NH1-CZ-NH2	-11.00	105.00	119.30
1	C	89	HIS	CE1-NE2-CD2	10.61	119.61	109.00
2	B	22	GLU	CG-CD-OE2	-8.09	99.81	118.40
1	C	89	HIS	CA-CB-CG	-7.97	105.83	113.80
2	D	6	GLU	CB-CA-C	-7.94	98.11	110.81
1	C	36	PHE	CA-C-N	7.43	127.79	119.32
1	C	36	PHE	C-N-CA	7.43	127.79	119.32
2	B	22	GLU	CG-CD-OE1	7.28	135.15	118.40
2	D	79	ASP	O-C-N	7.19	131.18	122.48
1	C	89	HIS	ND1-CG-CD2	7.04	113.14	106.10
2	B	145	TYR	CA-C-O	6.84	128.64	119.47
1	A	50	HIS	CB-CG-CD2	-6.83	122.32	131.20
1	A	50	HIS	N-CA-C	-6.76	99.82	109.96
2	B	12	THR	OG1-CB-CG2	6.70	122.70	109.30
2	D	8	LYS	CB-CG-CD	-6.67	95.95	111.30
2	D	43	GLU	CG-CD-OE1	-6.55	103.34	118.40
1	C	89	HIS	ND1-CE1-NE2	-6.40	102.00	108.40
2	B	129	ASP	N-CA-C	-6.37	104.34	111.28
2	B	127	GLN	OE1-CD-NE2	6.14	128.74	122.60
2	B	8	LYS	N-CA-C	6.13	117.76	111.14
2	D	97	HIS	ND1-CG-CD2	6.03	112.12	106.10
2	D	20	VAL	N-CA-C	6.02	116.68	110.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	7	GLU	CA-C-N	5.87	128.43	120.44
2	B	7	GLU	C-N-CA	5.87	128.43	120.44
2	D	35	TYR	CA-C-N	5.87	125.55	119.56
2	D	35	TYR	C-N-CA	5.87	125.55	119.56
1	C	94	ASP	CA-C-N	5.73	125.85	119.32
1	C	94	ASP	C-N-CA	5.73	125.85	119.32
2	D	143	HIS	N-CA-C	5.66	117.45	111.28
1	A	52	SER	O-C-N	5.61	129.85	123.12
2	B	49	SER	N-CA-C	5.61	118.93	111.75
2	B	97	HIS	CE1-NE2-CD2	-5.61	103.39	109.00
2	D	6	GLU	CG-CD-OE2	-5.60	105.53	118.40
1	C	89	HIS	CB-CG-CD2	-5.59	123.93	131.20
1	A	52	SER	CA-C-O	-5.50	115.13	121.07
2	B	80	ASP	CB-CG-OD2	-5.49	105.77	118.40
1	C	122	HIS	N-CA-C	-5.47	105.22	111.07
2	B	143	HIS	CG-CD2-NE2	-5.28	101.92	107.20
1	A	53	ALA	CB-CA-C	5.25	119.51	110.79
2	B	76	LYS	N-CA-C	-5.19	106.94	113.28
2	B	145	TYR	O-C-N	-5.19	116.12	122.25
2	D	6	GLU	CG-CD-OE1	5.09	130.11	118.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	50	HIS	Sidechain
1	C	50	HIS	Sidechain

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	1066	0	1069	33	0
1	C	1066	0	1069	30	0
2	B	1127	0	1129	36	0
2	D	1127	0	1129	43	0
3	A	43	0	30	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	43	0	30	7	0
3	C	43	0	30	8	0
3	D	43	0	30	7	0
4	A	2	0	0	0	0
4	B	2	0	0	5	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	4	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	4	0	0	3	0
All	All	4578	0	4516	153	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 17.

All (153) 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)
2:B:76:LYS:CD	2:B:76:LYS:CE	1.75	1.55
2:D:61:LYS:CE	2:D:61:LYS:NZ	1.78	1.45
1:A:90:LYS:CE	1:A:90:LYS:NZ	1.81	1.43
2:D:11:VAL:HG13	2:D:75:MET:HE1	1.21	1.11
1:A:140:TYR:O	1:A:141:ARG:OXT	1.69	1.11
1:A:92:ARG:HH22	1:A:139:LYS:NZ	1.70	0.90
2:B:11:VAL:HG13	2:B:75:MET:HE1	1.53	0.88
1:C:45:HIS:NE2	3:C:142:HEM:O1D	2.06	0.88
3:B:147:HEM:FE	4:B:148:CMO:C	1.61	0.81
3:B:147:HEM:NB	4:B:148:CMO:C	2.45	0.80
2:D:11:VAL:CG1	2:D:75:MET:HE1	2.08	0.80
2:D:19:LYS:HE2	5:D:149:HOH:O	1.80	0.79
2:B:76:LYS:CE	2:B:76:LYS:CG	2.62	0.78
1:C:40:LYS:HG2	1:C:48:LEU:HD13	1.68	0.76
2:D:11:VAL:HG22	2:D:130:PHE:CE2	2.23	0.74
3:B:147:HEM:NC	4:B:148:CMO:C	2.51	0.73
1:C:139:LYS:HA	1:C:141:ARG:HH22	1.56	0.71
2:D:19:LYS:CE	5:D:149:HOH:O	2.35	0.71
2:B:11:VAL:HG22	2:B:130:PHE:CE2	2.25	0.71
3:A:142:HEM:HMB2	3:A:142:HEM:HBB2	1.72	0.71
2:B:11:VAL:HG22	2:B:130:PHE:CD2	2.26	0.70
1:A:76:LEU:N	1:A:77:PRO:HD2	2.08	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2:MET:HG3	2:B:3:LEU:H	1.57	0.69
2:B:89:SER:OG	2:B:144:ARG:HG2	1.93	0.69
1:A:61:LYS:HE2	3:A:142:HEM:O1A	1.94	0.68
2:B:32:LEU:HD21	2:B:42:PHE:CD2	2.29	0.67
2:D:11:VAL:HG13	2:D:75:MET:CE	2.13	0.66
1:A:92:ARG:HH22	1:A:139:LYS:HZ3	1.41	0.66
1:C:92:ARG:HH22	1:C:139:LYS:HZ2	1.43	0.66
2:B:2:MET:HE2	2:B:3:LEU:HG	1.78	0.66
2:D:3:LEU:O	2:D:8:LYS:NZ	2.29	0.65
3:B:147:HEM:ND	4:B:148:CMO:C	2.60	0.64
1:A:140:TYR:O	1:A:141:ARG:C	2.39	0.64
2:D:81:LEU:HD22	2:D:137:VAL:HG22	1.79	0.64
2:D:2:MET:HG2	2:D:3:LEU:HD22	1.79	0.63
2:B:19:LYS:H	2:B:19:LYS:HE2	1.63	0.63
1:C:3:SER:HB2	1:C:6:ASP:H	1.64	0.63
1:C:98:PHE:HE2	1:C:136:LEU:HD12	1.65	0.62
2:B:4:THR:OG1	2:B:7:GLU:HG3	1.98	0.62
3:B:147:HEM:NA	4:B:148:CMO:C	2.64	0.61
1:A:6:ASP:O	1:A:10:VAL:HG23	2.01	0.60
2:B:81:LEU:HD22	2:B:85:PHE:HE2	1.67	0.60
1:C:105:LEU:O	1:C:109:LEU:HG	2.02	0.58
3:C:142:HEM:CMC	3:C:142:HEM:HBC2	2.34	0.58
2:D:11:VAL:HG22	2:D:130:PHE:CZ	2.39	0.57
1:A:47:ASP:OD2	1:A:49:SER:OG	2.17	0.57
2:B:11:VAL:CG1	2:B:75:MET:HE1	2.28	0.57
2:B:93:CYS:HA	2:B:145:TYR:OH	2.05	0.56
2:D:42:PHE:HA	5:D:150:HOH:O	2.04	0.56
2:B:6:GLU:O	2:B:7:GLU:C	2.48	0.56
1:C:76:LEU:N	1:C:77:PRO:HD2	2.19	0.56
1:A:140:TYR:HB3	1:C:1:VAL:HG22	1.86	0.56
2:D:92:HIS:HE1	3:D:147:HEM:C4A	2.24	0.56
2:D:92:HIS:HA	2:D:96:LEU:HD12	1.88	0.55
2:D:20:VAL:HG13	2:D:68:LEU:HB3	1.88	0.55
1:A:17:VAL:HG13	1:A:24:TYR:CD2	2.40	0.55
2:B:93:CYS:SG	2:B:141:LEU:O	2.64	0.55
3:C:142:HEM:HBD1	3:C:142:HEM:HMD2	1.88	0.55
2:B:71:PHE:CZ	2:B:134:VAL:HG12	2.42	0.54
2:B:92:HIS:CE1	3:B:147:HEM:NA	2.75	0.54
3:D:147:HEM:CBA	3:D:147:HEM:CMA	2.84	0.54
1:A:61:LYS:HE2	3:A:142:HEM:CGA	2.37	0.54
2:D:19:LYS:HZ2	2:D:22:GLU:HG3	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:LEU:N	1:A:77:PRO:CD	2.71	0.53
2:D:73:ASN:HA	2:D:76:LYS:HE3	1.90	0.52
3:D:147:HEM:HMA1	3:D:147:HEM:HBA1	1.92	0.52
3:D:147:HEM:CMA	3:D:147:HEM:HBA1	2.40	0.52
1:A:91:LEU:O	2:D:40:ARG:HD2	2.10	0.51
3:C:142:HEM:HHA	3:C:142:HEM:HBA2	1.93	0.51
2:D:86:ALA:HB1	2:D:144:ARG:HH22	1.76	0.51
1:A:90:LYS:NZ	1:A:90:LYS:CD	2.67	0.50
2:B:90:GLU:HG3	2:B:144:ARG:NH2	2.27	0.50
2:B:100:PRO:HD3	2:B:145:TYR:CE2	2.47	0.49
2:D:26:GLU:CD	2:D:113:VAL:HG13	2.37	0.49
2:B:71:PHE:HZ	2:B:134:VAL:HG12	1.78	0.49
3:C:142:HEM:HHA	3:C:142:HEM:CBA	2.42	0.49
2:D:4:THR:O	2:D:8:LYS:HB2	2.12	0.49
2:B:48:LEU:HD22	2:B:54:VAL:HG22	1.95	0.49
1:A:76:LEU:H	1:A:77:PRO:HD2	1.74	0.49
1:C:139:LYS:HA	1:C:141:ARG:NH2	2.27	0.48
2:D:24:GLY:CA	2:D:68:LEU:HG	2.43	0.48
2:D:86:ALA:O	2:D:144:ARG:NH2	2.47	0.48
2:B:3:LEU:HB3	2:B:7:GLU:HB2	1.95	0.48
2:D:61:LYS:NZ	2:D:61:LYS:CD	2.69	0.48
2:D:77:HIS:HB2	2:D:84:THR:OG1	2.14	0.48
2:B:91:LEU:HD12	2:B:95:LYS:HD2	1.96	0.47
1:C:6:ASP:O	1:C:10:VAL:HG23	2.14	0.47
1:C:76:LEU:N	1:C:77:PRO:CD	2.76	0.47
2:B:81:LEU:HD22	2:B:85:PHE:CE2	2.49	0.47
1:A:43:PHE:O	1:A:48:LEU:HD11	2.15	0.47
2:B:100:PRO:HA	2:B:103:PHE:CD2	2.50	0.47
1:C:17:VAL:HG13	1:C:24:TYR:CD2	2.50	0.47
2:D:142:ALA:HB3	2:D:146:HIS:HE1	1.80	0.47
1:A:113:LEU:O	1:A:117:PHE:HB2	2.15	0.47
3:C:142:HEM:HMC1	3:C:142:HEM:CBC	2.46	0.46
1:A:87:HIS:HE1	3:A:142:HEM:C4A	2.33	0.46
2:D:4:THR:OG1	2:D:6:GLU:HB3	2.15	0.46
1:A:140:TYR:CB	1:C:1:VAL:HG22	2.46	0.46
1:C:39:THR:HG22	1:C:97:ASN:HD22	1.80	0.46
1:A:1:VAL:HG22	1:C:140:TYR:CB	2.46	0.46
2:D:11:VAL:CG2	2:D:130:PHE:CE2	2.97	0.46
1:C:80:LEU:HB2	1:C:135:VAL:HG11	1.98	0.45
1:A:92:ARG:HH22	1:A:139:LYS:HZ2	1.61	0.45
1:C:108:THR:O	1:C:112:HIS:HD2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:47:ASP:CG	1:C:52:SER:HB2	2.42	0.45
2:D:90:GLU:HG2	2:D:94:ASP:OD2	2.17	0.45
2:D:42:PHE:O	2:D:45:PHE:HB2	2.16	0.45
2:B:6:GLU:C	2:B:8:LYS:N	2.71	0.44
2:D:19:LYS:HZ2	2:D:21:ASP:HB2	1.81	0.44
1:A:138:SER:CB	1:C:1:VAL:HG13	2.46	0.44
2:B:65:LYS:NZ	2:B:69:ASP:OD1	2.45	0.44
2:D:80:ASP:O	2:D:84:THR:OG1	2.30	0.44
2:D:75:MET:HA	2:D:78:LEU:HG	1.99	0.44
1:A:51:GLY:O	1:A:52:SER:C	2.61	0.44
1:A:62:VAL:HG22	3:A:142:HEM:CHB	2.48	0.43
2:B:76:LYS:CD	2:B:76:LYS:NZ	2.72	0.43
2:B:122:PHE:CZ	2:B:127:GLN:HA	2.52	0.43
1:C:138:SER:O	1:C:141:ARG:NH2	2.51	0.43
2:D:34:VAL:C	2:D:36:PRO:HD3	2.43	0.43
3:D:147:HEM:CMB	3:D:147:HEM:HBB2	2.49	0.43
2:D:90:GLU:HG3	2:D:144:ARG:HE	1.84	0.43
1:C:39:THR:HG22	1:C:97:ASN:ND2	2.34	0.43
1:A:46:PHE:CE1	3:A:142:HEM:O1D	2.72	0.43
1:A:13:ALA:O	1:A:17:VAL:HG23	2.18	0.43
1:C:113:LEU:O	1:C:117:PHE:HB2	2.19	0.42
1:A:35:SER:HB3	2:B:131:GLN:HG3	2.00	0.42
3:C:142:HEM:HBC2	3:C:142:HEM:HMC1	2.01	0.42
1:A:87:HIS:CE1	3:A:142:HEM:C4A	3.07	0.42
2:D:19:LYS:NZ	2:D:21:ASP:HB2	2.35	0.42
2:D:33:VAL:HG23	2:D:54:VAL:HG11	2.02	0.42
2:D:92:HIS:CE1	3:D:147:HEM:C4A	3.00	0.42
2:B:2:MET:CE	2:B:3:LEU:HG	2.47	0.42
1:C:65:ALA:HB2	3:C:142:HEM:HMA1	2.02	0.42
1:A:17:VAL:HG13	1:A:24:TYR:HD2	1.84	0.41
1:C:112:HIS:O	1:C:113:LEU:HD23	2.20	0.41
1:C:27:GLU:O	1:C:31:ARG:HG3	2.20	0.41
2:B:74:GLY:HA2	2:B:84:THR:HG21	2.02	0.41
2:D:17:LYS:HE3	2:D:121:GLU:OE2	2.20	0.41
2:D:41:PHE:HB3	3:D:147:HEM:HMD2	2.03	0.41
2:B:51:ALA:O	2:B:55:MET:HG2	2.20	0.41
2:B:24:GLY:HA2	2:B:68:LEU:HD23	2.02	0.41
3:A:142:HEM:HHA	3:A:142:HEM:HAA1	1.80	0.41
1:C:84:SER:HB2	1:C:141:ARG:HE	1.85	0.41
2:D:131:GLN:HA	2:D:134:VAL:HG22	2.03	0.41
2:B:17:LYS:NZ	2:B:121:GLU:OE2	2.27	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:SER:O	1:C:56:LYS:HD3	2.20	0.41
1:C:84:SER:HB2	1:C:141:ARG:HH21	1.86	0.41
1:A:1:VAL:HG22	1:C:140:TYR:CG	2.56	0.41
2:D:68:LEU:HD22	2:D:68:LEU:HA	1.83	0.41
1:A:131:ASN:N	1:A:131:ASN:HD22	2.19	0.40
2:D:93:CYS:HA	2:D:145:TYR:OH	2.20	0.40
1:A:62:VAL:HG13	3:A:142:HEM:CMB	2.51	0.40
3:B:147:HEM:HBB2	3:B:147:HEM:HMB2	2.02	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	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
1	C	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
2	B	143/145 (99%)	137 (96%)	6 (4%)	0	100	100
2	D	143/145 (99%)	134 (94%)	9 (6%)	0	100	100
All	All	564/572 (99%)	540 (96%)	24 (4%)	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	112/112 (100%)	101 (90%)	11 (10%)	7	25
1	C	112/112 (100%)	104 (93%)	8 (7%)	13	40
2	B	118/118 (100%)	101 (86%)	17 (14%)	3	11
2	D	118/118 (100%)	104 (88%)	14 (12%)	5	16
All	All	460/460 (100%)	410 (89%)	50 (11%)	6	20

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	VAL
1	A	50	HIS
1	A	56	LYS
1	A	81	SER
1	A	84	SER
1	A	89	HIS
1	A	92	ARG
1	A	105	LEU
1	A	111	SER
1	A	115	SER
1	A	141	ARG
2	B	11	VAL
2	B	17	LYS
2	B	19	LYS
2	B	21	ASP
2	B	22	GLU
2	B	28	LEU
2	B	43	GLU
2	B	65	LYS
2	B	68	LEU
2	B	71	PHE
2	B	82	LYS
2	B	101	GLU
2	B	104	LYS
2	B	110	LEU
2	B	141	LEU
2	B	143	HIS
2	B	144	ARG
1	C	1	VAL
1	C	81	SER
1	C	84	SER
1	C	90	LYS
1	C	92	ARG

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Mol	Chain	Res	Type
1	C	105	LEU
1	C	121	VAL
1	C	141	ARG
2	D	2	MET
2	D	4	THR
2	D	6	GLU
2	D	8	LYS
2	D	11	VAL
2	D	28	LEU
2	D	43	GLU
2	D	65	LYS
2	D	68	LEU
2	D	71	PHE
2	D	90	GLU
2	D	101	GLU
2	D	110	LEU
2	D	141	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
2	B	39	GLN
2	B	108	ASN
1	C	89	HIS
1	C	97	ASN
2	D	97	HIS

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

8 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
4	CMO	B	148	3	0,1,1	-	-	-		
4	CMO	C	143	-	0,1,1	-	-	-		
3	HEM	B	147	2,4	50,50,50	2.17	17 (34%)	67,82,82	2.02	21 (31%)
3	HEM	A	142	1	50,50,50	2.29	17 (34%)	67,82,82	1.81	13 (19%)
4	CMO	A	143	-	0,1,1	-	-	-		
4	CMO	D	148	-	0,1,1	-	-	-		
3	HEM	C	142	1	50,50,50	2.07	18 (36%)	67,82,82	1.81	22 (32%)
3	HEM	D	147	2	50,50,50	1.91	15 (30%)	67,82,82	2.00	17 (25%)

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	C	142	1	-	8/14/54/54	-
3	HEM	B	147	2,4	-	6/14/54/54	-
3	HEM	A	142	1	-	9/14/54/54	-
3	HEM	D	147	2	-	7/14/54/54	-

All (67) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	142	HEM	FE-NA	-7.53	1.70	1.95
3	D	147	HEM	C3D-C2D	6.81	1.51	1.36
3	C	142	HEM	C3D-C2D	5.90	1.49	1.36
3	A	142	HEM	FE-NB	-5.87	1.76	1.94
3	A	142	HEM	C3D-C2D	5.83	1.49	1.36
3	C	142	HEM	FE-ND	-5.76	1.77	1.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	147	HEM	C3D-C2D	5.54	1.48	1.36
3	B	147	HEM	FE-NA	-5.28	1.77	1.95
3	B	147	HEM	FE-NB	-4.51	1.81	1.94
3	D	147	HEM	C2A-C3A	-3.71	1.29	1.38
3	B	147	HEM	C3B-C2B	-3.66	1.29	1.37
3	B	147	HEM	C3C-C2C	-3.65	1.29	1.37
3	C	142	HEM	C2A-C3A	-3.63	1.29	1.38
3	C	142	HEM	C3C-C2C	-3.59	1.29	1.37
3	B	147	HEM	CHC-C1C	-3.46	1.31	1.38
3	A	142	HEM	C3C-C2C	-3.45	1.30	1.37
3	D	147	HEM	C3C-C4C	-3.38	1.40	1.46
3	B	147	HEM	C1C-C2C	-3.22	1.39	1.45
3	D	147	HEM	C3C-C2C	-3.17	1.30	1.37
3	D	147	HEM	CHD-C1D	-3.16	1.32	1.39
3	C	142	HEM	CAB-C3B	3.09	1.55	1.47
3	B	147	HEM	C4D-C3D	-3.08	1.39	1.45
3	A	142	HEM	FE-ND	3.03	2.04	1.94
3	D	147	HEM	CHD-C4C	-3.00	1.32	1.38
3	C	142	HEM	C3B-C2B	-2.81	1.31	1.37
3	A	142	HEM	CHC-C4B	-2.75	1.32	1.39
3	B	147	HEM	CHC-C4B	-2.74	1.33	1.39
3	A	142	HEM	CHA-C4D	-2.73	1.33	1.38
3	A	142	HEM	C3B-C2B	-2.72	1.31	1.37
3	C	142	HEM	FE-NA	-2.71	1.86	1.95
3	B	147	HEM	C2A-C3A	-2.69	1.31	1.38
3	B	147	HEM	CAC-C3C	2.66	1.54	1.47
3	B	147	HEM	C3B-C4B	-2.63	1.39	1.44
3	D	147	HEM	C1D-C2D	-2.62	1.39	1.44
3	B	147	HEM	FE-ND	-2.60	1.86	1.94
3	A	142	HEM	C2A-C3A	-2.60	1.32	1.38
3	C	142	HEM	CHB-C4A	-2.54	1.33	1.39
3	D	147	HEM	FE-NB	-2.52	1.87	1.94
3	D	147	HEM	C3B-C2B	-2.49	1.32	1.37
3	C	142	HEM	CHB-C1B	-2.49	1.33	1.38
3	C	142	HEM	C1B-C2B	-2.45	1.39	1.44
3	A	142	HEM	CHC-C1C	-2.44	1.33	1.38
3	C	142	HEM	CHA-C1A	-2.42	1.34	1.39
3	A	142	HEM	C3B-C4B	-2.42	1.40	1.44
3	B	147	HEM	CHA-C1A	-2.37	1.34	1.39
3	A	142	HEM	CHA-C1A	-2.36	1.34	1.39
3	C	142	HEM	C4D-C3D	-2.35	1.41	1.45
3	A	142	HEM	C4D-C3D	-2.33	1.41	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	147	HEM	CHC-C4B	-2.32	1.33	1.39
3	C	142	HEM	CHC-C1C	-2.30	1.33	1.38
3	A	142	HEM	CHD-C1D	-2.29	1.34	1.39
3	A	142	HEM	CHD-C4C	-2.27	1.33	1.38
3	C	142	HEM	O2D-CGD	-2.27	1.23	1.30
3	A	142	HEM	CAB-C3B	2.27	1.53	1.47
3	C	142	HEM	CHD-C4C	-2.23	1.34	1.38
3	C	142	HEM	CHC-C4B	-2.21	1.34	1.39
3	D	147	HEM	C3B-C4B	-2.19	1.40	1.44
3	A	142	HEM	FE-NC	2.15	2.02	1.95
3	D	147	HEM	CAB-C3B	2.15	1.53	1.47
3	D	147	HEM	CHB-C1B	-2.13	1.34	1.38
3	B	147	HEM	CHD-C1D	-2.12	1.34	1.39
3	B	147	HEM	O2D-CGD	-2.09	1.23	1.30
3	C	142	HEM	CHA-C4D	-2.08	1.34	1.38
3	D	147	HEM	CHC-C1C	-2.07	1.34	1.38
3	B	147	HEM	CHA-C4D	-2.02	1.34	1.38
3	D	147	HEM	CAC-C3C	2.01	1.52	1.47
3	C	142	HEM	CMB-C2B	2.00	1.54	1.50

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	147	HEM	C3B-C4B-NB	6.90	114.42	109.47
3	D	147	HEM	CAA-CBA-CGA	-5.26	99.71	113.67
3	D	147	HEM	CHC-C4B-NB	5.17	129.99	124.42
3	D	147	HEM	CHD-C1D-C2D	-4.80	117.45	125.03
3	A	142	HEM	CAA-CBA-CGA	-4.67	101.28	113.67
3	A	142	HEM	C3B-C4B-NB	4.67	112.82	109.47
3	B	147	HEM	CBD-CAD-C3D	-4.52	100.03	112.53
3	A	142	HEM	CBA-CAA-C2A	4.35	124.56	112.53
3	D	147	HEM	C1D-C2D-C3D	-4.26	102.50	106.98
3	B	147	HEM	C1B-NB-C4B	-4.24	100.19	105.21
3	D	147	HEM	C4A-CHB-C1B	-4.22	116.32	126.25
3	D	147	HEM	C2D-C1D-ND	4.19	114.75	109.90
3	D	147	HEM	C4C-CHD-C1D	-4.08	117.34	126.02
3	A	142	HEM	CAA-C2A-C3A	4.02	136.09	127.07
3	C	142	HEM	C3B-C4B-NB	3.52	112.00	109.47
3	C	142	HEM	C2B-C1B-NB	3.51	113.87	109.84
3	A	142	HEM	CAA-C2A-C1A	-3.48	118.15	124.94
3	B	147	HEM	C4A-CHB-C1B	-3.47	118.08	126.25
3	C	142	HEM	CHB-C1B-NB	3.44	128.63	124.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	147	HEM	CHC-C4B-C3B	-3.39	118.30	125.07
3	C	142	HEM	C1B-NB-C4B	-3.36	101.23	105.21
3	C	142	HEM	C3D-C4D-ND	3.35	113.84	110.17
3	C	142	HEM	CHD-C1D-C2D	-3.34	119.75	125.03
3	B	147	HEM	CHC-C4B-C3B	-3.33	118.43	125.07
3	C	142	HEM	CHB-C1B-C2B	-3.33	117.50	126.95
3	C	142	HEM	C1A-CHA-C4D	-3.19	118.74	126.25
3	D	147	HEM	CHD-C1D-ND	3.14	127.80	124.42
3	B	147	HEM	C4C-CHD-C1D	-3.12	119.38	126.02
3	C	142	HEM	CHD-C1D-ND	3.12	127.78	124.42
3	D	147	HEM	C3B-C4B-NB	3.12	111.71	109.47
3	B	147	HEM	CHA-C4D-C3D	-3.09	119.53	125.23
3	C	142	HEM	CAA-CBA-CGA	-3.09	105.48	113.67
3	C	142	HEM	C4A-NA-C1A	-2.99	100.94	105.82
3	A	142	HEM	C4A-CHB-C1B	-2.90	119.42	126.25
3	A	142	HEM	C1D-C2D-C3D	-2.88	103.95	106.98
3	C	142	HEM	CHA-C4D-C3D	-2.82	120.03	125.23
3	B	147	HEM	C1C-CHC-C4B	-2.79	120.10	126.02
3	C	142	HEM	C4D-C3D-C2D	-2.78	102.85	106.89
3	C	142	HEM	C1C-CHC-C4B	-2.74	120.19	126.02
3	A	142	HEM	C4C-NC-C1C	-2.72	101.38	105.82
3	B	147	HEM	C4C-NC-C1C	-2.72	101.39	105.82
3	B	147	HEM	CMD-C2D-C1D	2.70	129.26	125.03
3	B	147	HEM	CHA-C4D-ND	2.55	127.53	124.37
3	B	147	HEM	C2A-C1A-NA	2.55	112.98	110.15
3	B	147	HEM	CHC-C4B-NB	2.53	127.15	124.42
3	C	142	HEM	CMB-C2B-C1B	-2.53	121.08	125.03
3	A	142	HEM	CHA-C1A-C2A	-2.52	119.78	125.30
3	D	147	HEM	C1A-C2A-C3A	2.49	110.73	106.87
3	B	147	HEM	C3D-C4D-ND	2.48	112.89	110.17
3	B	147	HEM	C1A-CHA-C4D	-2.43	120.52	126.25
3	D	147	HEM	CMD-C2D-C3D	2.40	132.65	126.15
3	B	147	HEM	O1D-CGD-CBD	-2.40	115.48	123.09
3	A	142	HEM	C2A-C1A-NA	2.39	112.80	110.15
3	A	142	HEM	CHC-C4B-C3B	-2.36	120.35	125.07
3	B	147	HEM	C4A-NA-C1A	-2.36	101.98	105.82
3	B	147	HEM	O2D-CGD-CBD	2.31	121.29	114.00
3	B	147	HEM	C1D-C2D-C3D	-2.30	104.56	106.98
3	D	147	HEM	CHA-C1A-NA	2.29	128.02	123.86
3	B	147	HEM	CHD-C1D-C2D	-2.24	121.50	125.03
3	A	142	HEM	CHC-C4B-NB	2.23	126.83	124.42
3	D	147	HEM	C2A-C1A-NA	-2.22	107.69	110.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	142	HEM	C2D-C1D-ND	2.21	112.46	109.90
3	C	142	HEM	CHB-C4A-C3A	-2.18	121.11	127.43
3	C	142	HEM	CAA-C2A-C1A	2.17	129.18	124.94
3	C	142	HEM	C4C-NC-C1C	-2.17	102.29	105.82
3	A	142	HEM	C2D-C1D-ND	2.14	112.37	109.90
3	C	142	HEM	C4A-CHB-C1B	-2.08	121.35	126.25
3	B	147	HEM	C2B-C1B-NB	2.07	112.22	109.84
3	D	147	HEM	C4C-NC-C1C	-2.05	102.48	105.82
3	C	142	HEM	CBD-CAD-C3D	-2.04	106.89	112.53
3	C	142	HEM	C2A-C1A-NA	2.04	112.41	110.15
3	D	147	HEM	C1B-NB-C4B	-2.02	102.81	105.21
3	D	147	HEM	CHD-C4C-C3C	-2.00	121.83	125.21

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	142	HEM	C3A-C2A-CAA-CBA
3	C	142	HEM	C1A-C2A-CAA-CBA
3	A	142	HEM	C1A-C2A-CAA-CBA
3	A	142	HEM	C3D-CAD-CBD-CGD
3	C	142	HEM	C4D-C3D-CAD-CBD
3	C	142	HEM	C2D-C3D-CAD-CBD
3	C	142	HEM	C3A-C2A-CAA-CBA
3	D	147	HEM	C3A-C2A-CAA-CBA
3	D	147	HEM	C1A-C2A-CAA-CBA
3	B	147	HEM	C3A-C2A-CAA-CBA
3	B	147	HEM	C1A-C2A-CAA-CBA
3	A	142	HEM	C2C-C3C-CAC-CBC
3	A	142	HEM	C2A-CAA-CBA-CGA
3	A	142	HEM	C4C-C3C-CAC-CBC
3	D	147	HEM	C3D-CAD-CBD-CGD
3	C	142	HEM	CAD-CBD-CGD-O1D
3	D	147	HEM	CAD-CBD-CGD-O1D
3	C	142	HEM	CAA-CBA-CGA-O2A
3	B	147	HEM	CAD-CBD-CGD-O2D
3	D	147	HEM	CAD-CBD-CGD-O2D
3	B	147	HEM	CAD-CBD-CGD-O1D
3	C	142	HEM	CAA-CBA-CGA-O1A
3	B	147	HEM	CAA-CBA-CGA-O1A
3	C	142	HEM	CAD-CBD-CGD-O2D
3	A	142	HEM	CAA-CBA-CGA-O2A

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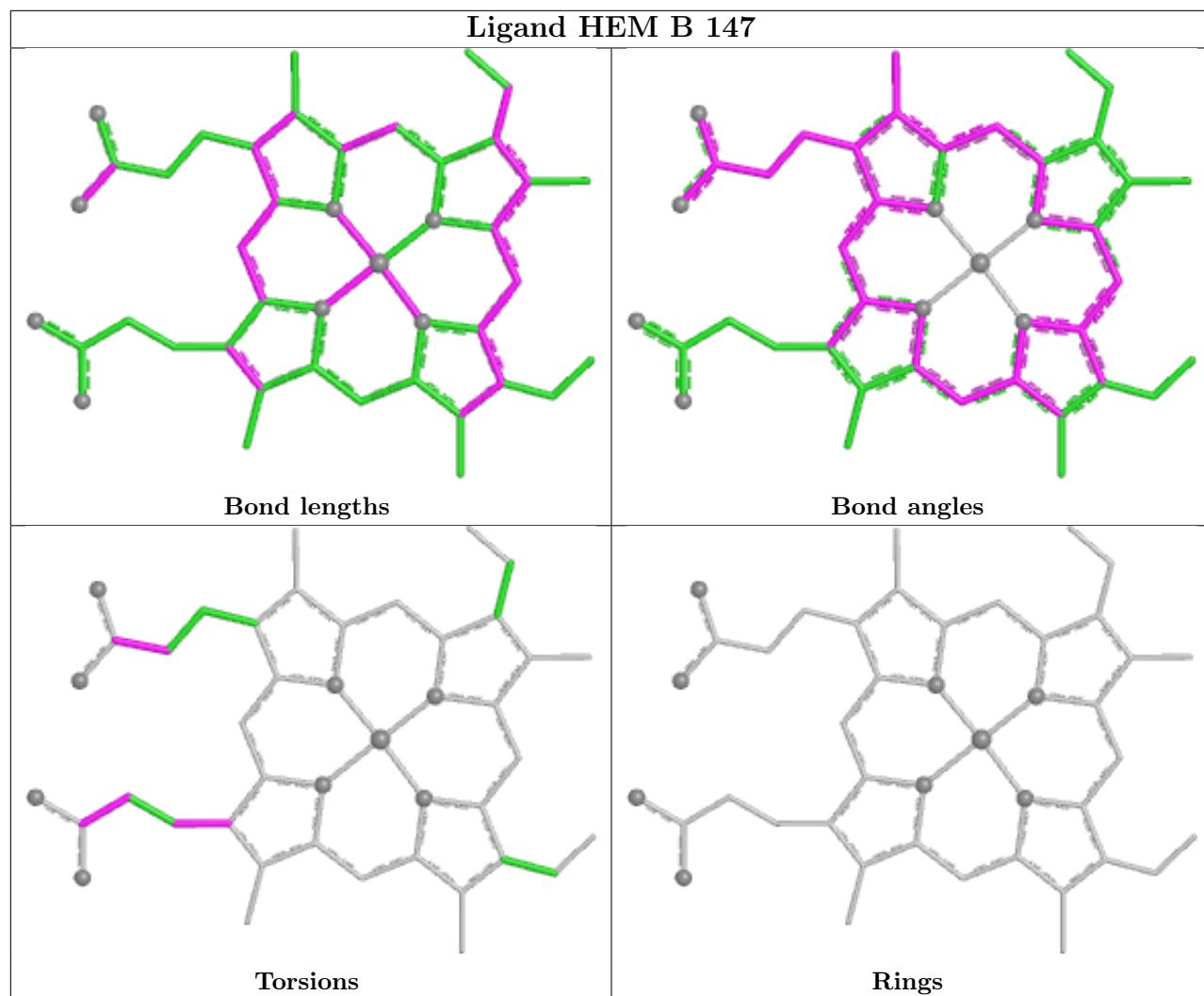
Mol	Chain	Res	Type	Atoms
3	A	142	HEM	CAA-CBA-CGA-O1A
3	B	147	HEM	CAA-CBA-CGA-O2A
3	A	142	HEM	C2D-C3D-CAD-CBD
3	D	147	HEM	CAA-CBA-CGA-O2A
3	D	147	HEM	CAA-CBA-CGA-O1A

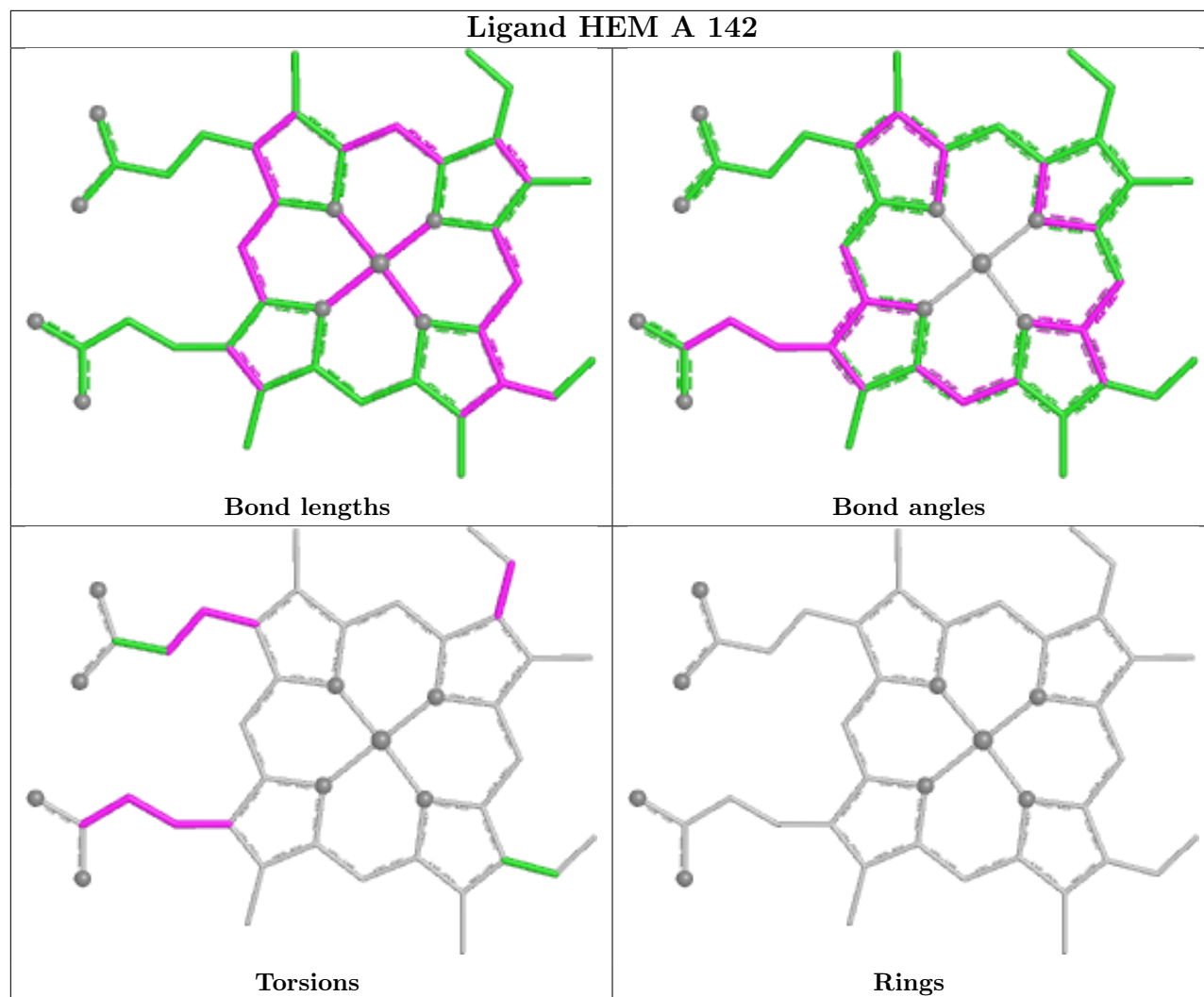
There are no ring outliers.

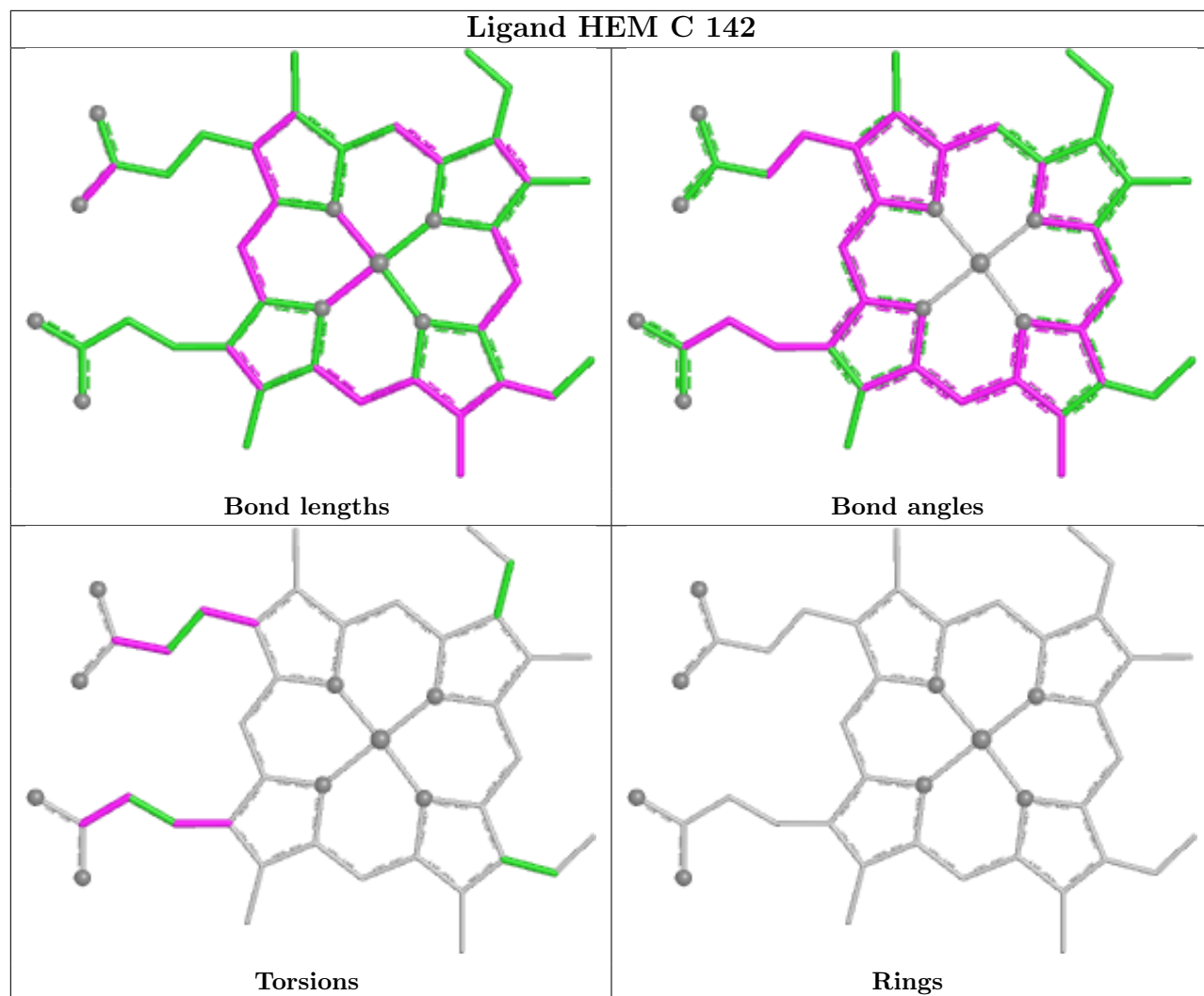
5 monomers are involved in 31 short contacts:

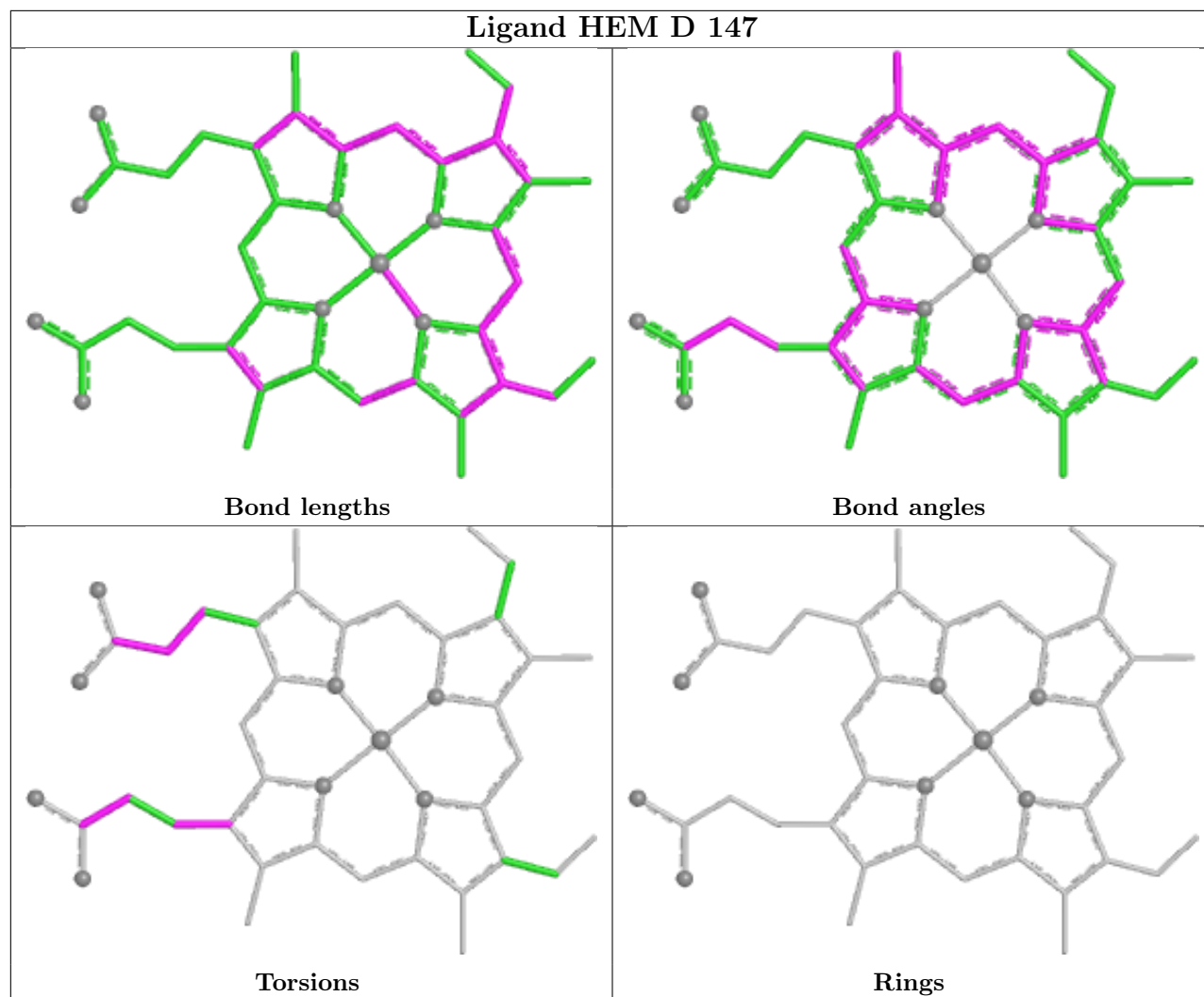
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	148	CMO	5	0
3	B	147	HEM	7	0
3	A	142	HEM	9	0
3	C	142	HEM	8	0
3	D	147	HEM	7	0

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

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	141/141 (100%)	0.39	7 (4%) 34 27	16, 28, 44, 48	2 (1%)
1	C	141/141 (100%)	0.35	3 (2%) 63 54	20, 34, 46, 57	0
2	B	145/145 (100%)	0.54	12 (8%) 17 14	15, 31, 62, 79	1 (0%)
2	D	145/145 (100%)	0.86	19 (13%) 7 6	19, 43, 68, 91	2 (1%)
All	All	572/572 (100%)	0.54	41 (7%) 21 17	15, 33, 59, 91	5 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	141	ARG	6.4
2	B	93	CYS	6.4
2	D	93	CYS	5.2
2	B	2	MET	4.2
2	D	47	ASP	4.1
2	D	145	TYR	3.9
2	B	143	HIS	3.5
2	B	146	HIS	3.5
2	B	145	TYR	3.4
2	D	146	HIS	3.3
2	D	52	ASP	3.3
1	C	141	ARG	3.2
2	D	2	MET	3.2
1	A	1	VAL	3.1
2	D	91	LEU	3.0
2	D	71	PHE	2.9
2	B	71	PHE	2.8
2	B	95	LYS	2.6
2	B	94	ASP	2.5
2	D	50	THR	2.5
2	D	120	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
2	D	143	HIS	2.4
2	D	20	VAL	2.4
2	D	125	VAL	2.4
2	D	49	SER	2.4
1	A	52	SER	2.3
2	D	94	ASP	2.3
2	D	82	LYS	2.3
2	D	46	GLY	2.3
1	A	44	PRO	2.3
1	A	48	LEU	2.2
1	A	92	ARG	2.2
1	A	89	HIS	2.2
1	C	85	ASP	2.2
2	B	6	GLU	2.2
2	B	52	ASP	2.2
2	D	95	LYS	2.2
2	B	21	ASP	2.1
1	C	34	LEU	2.1
2	B	49	SER	2.0
2	D	45	PHE	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.

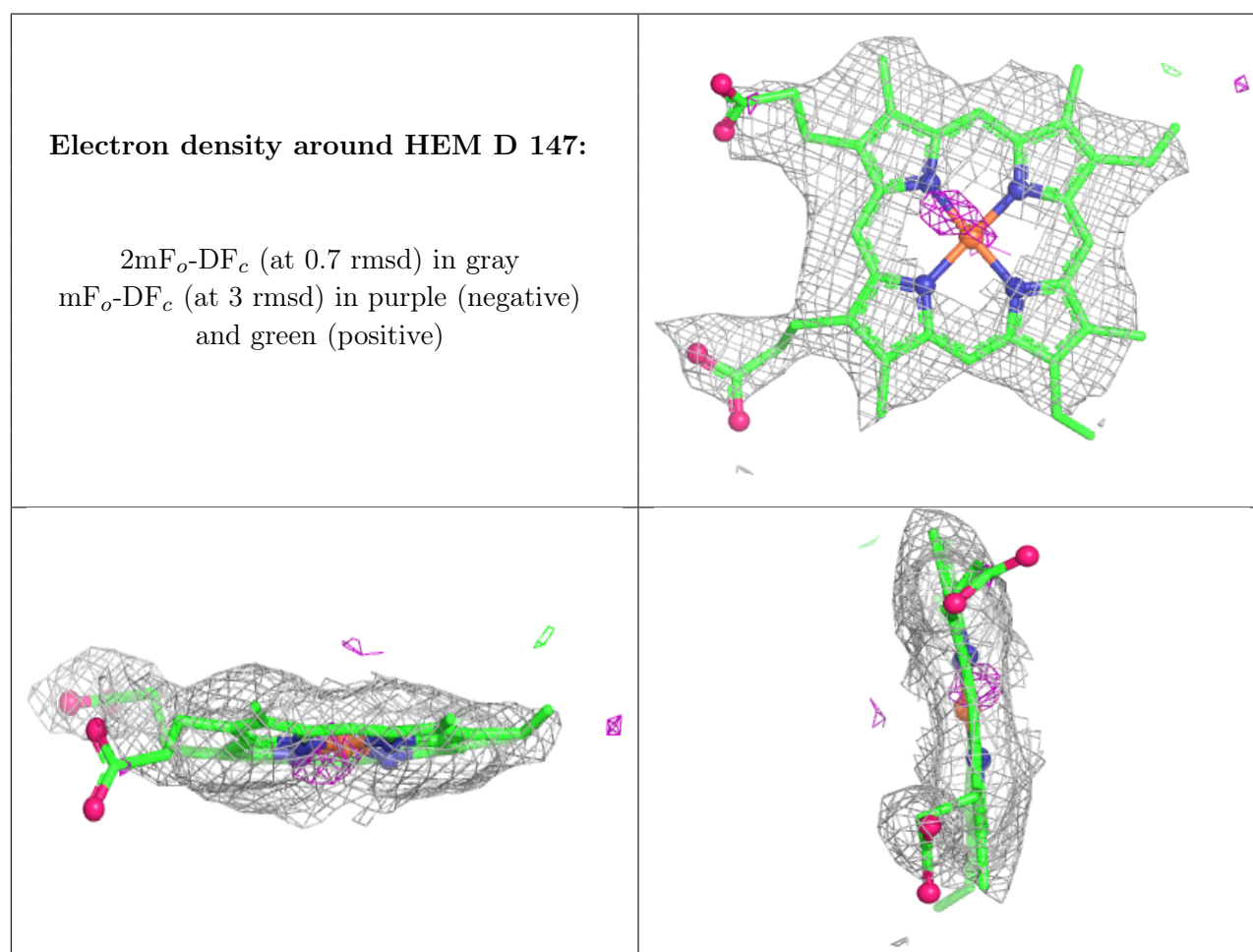
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CMO	D	148	2/2	0.64	0.41	17,17,17,18	0
4	CMO	A	143	2/2	0.66	0.25	7,7,7,10	0
4	CMO	C	143	2/2	0.70	0.20	11,11,11,15	0

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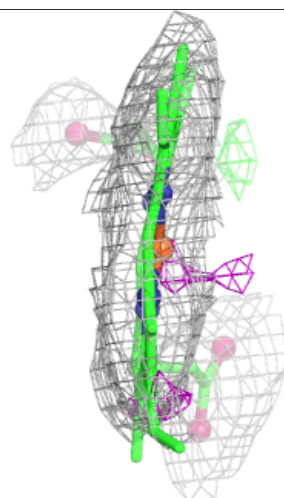
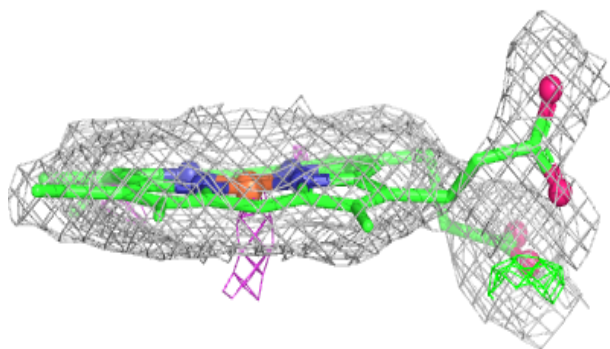
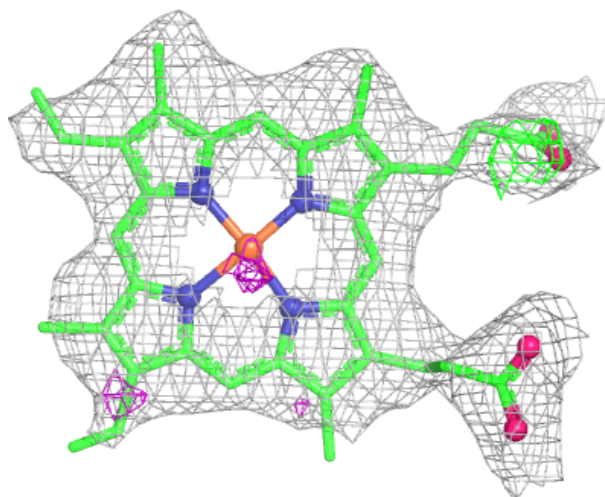
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CMO	B	148	2/2	0.84	0.27	13,13,13,15	0
3	HEM	D	147	43/43	0.92	0.12	16,27,54,59	0
3	HEM	B	147	43/43	0.93	0.10	7,15,44,48	0
3	HEM	C	142	43/43	0.94	0.10	3,13,29,40	0
3	HEM	A	142	43/43	0.94	0.09	3,13,29,43	0

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.



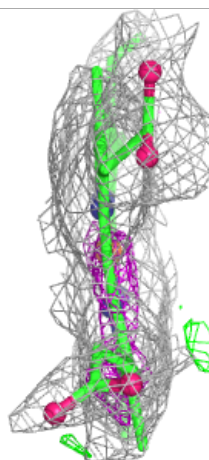
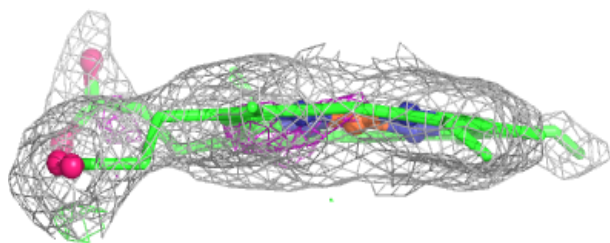
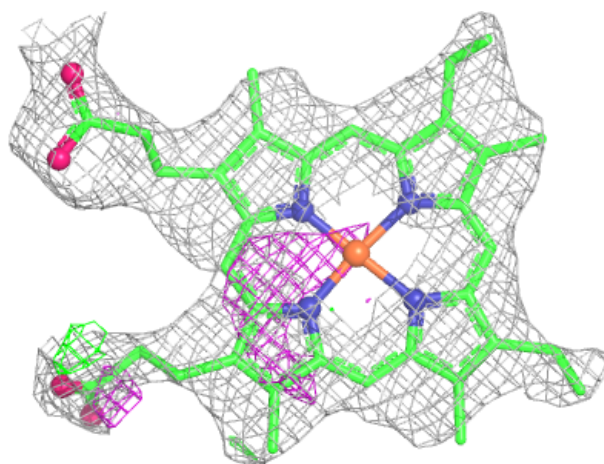
Electron density around HEM B 147:

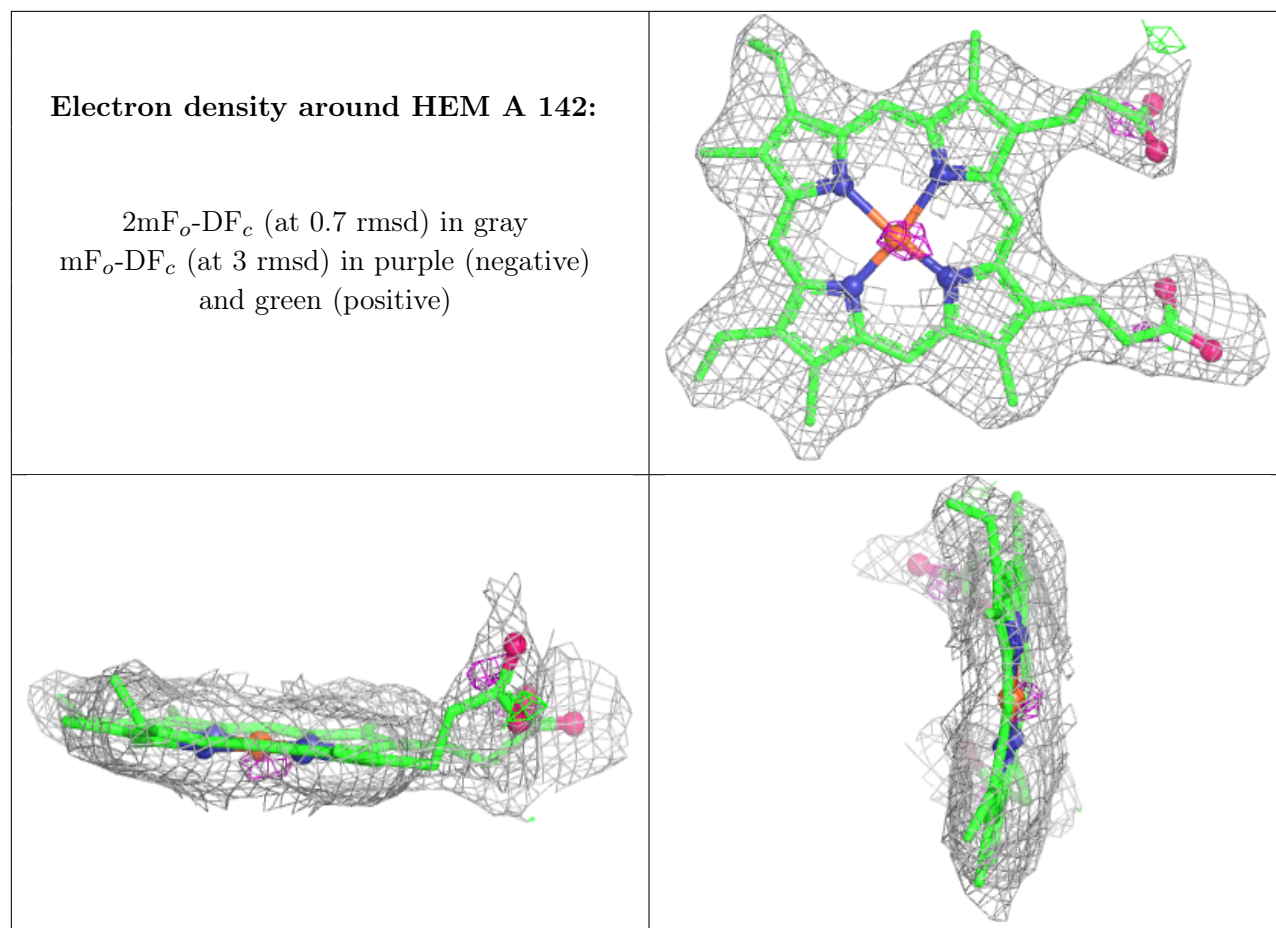
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM C 142:

$2mF_o-DF_c$ (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.