



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:31 PM UTC

PDB ID : 5HY8 / pdb_00005hy8
Title : Glycation restrains allosteric transition in hemoglobin: The molecular basis of oxidative stress under hyperglycemic conditions in diabetes
Authors : Saraswathi, N.T.; Pannu, N.S.; Syakhovich, V.E.; Saurabh, A.; Bokut, S.B.; Moras, D.; Ruff, M.
Deposited on : 2016-02-01
Resolution : 2.30 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:

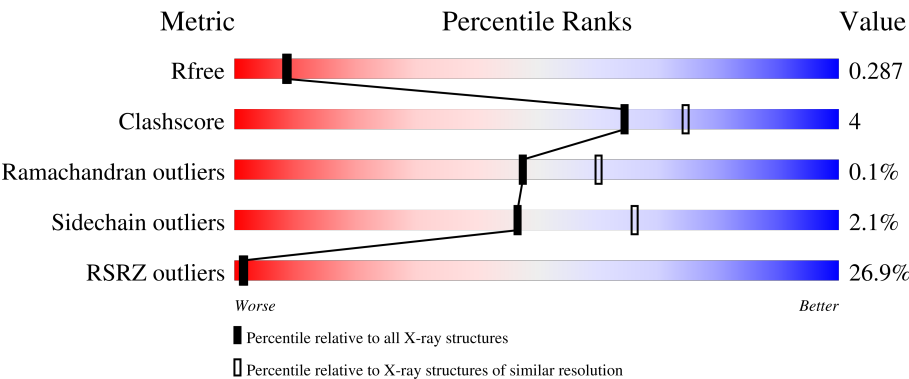
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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% 94% 5%
1	C	141	5% 94% 6%
1	E	141	81% 77% 16% ...
1	G	141	25% 88% 7% ...

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Mol	Chain	Length	Quality of chain
1	S	141	34% 94% 6%
2	B	146	% 95% 5%
2	D	146	6% 92% 8% .
2	F	146	16% 86% 12% ..
2	H	146	48% 88% 10% ..
2	T	146	48% 96% . .

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11609 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.

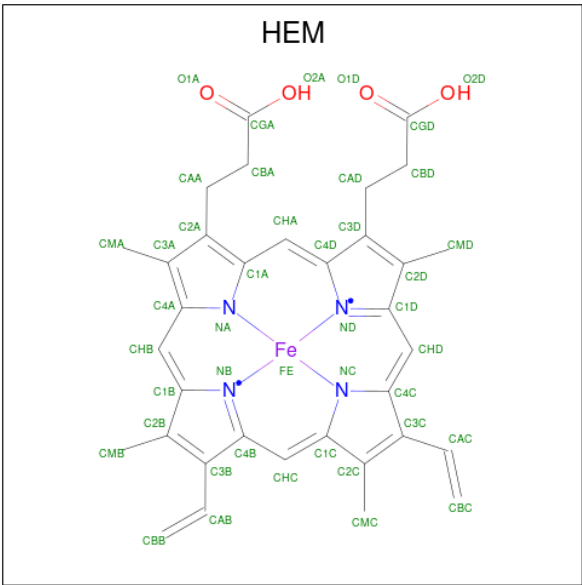
- Molecule 1 is a protein called Hemoglobin subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1068	685	187	193	3			
1	C	141	Total	C	N	O	S	0	0	0
			1068	685	187	193	3			
1	E	137	Total	C	N	O	S	0	0	0
			1030	659	180	188	3			
1	G	138	Total	C	N	O	S	0	0	0
			1042	668	181	190	3			
1	S	141	Total	C	N	O	S	0	0	0
			1068	685	187	193	3			

- Molecule 2 is a protein called Hemoglobin subunit beta.

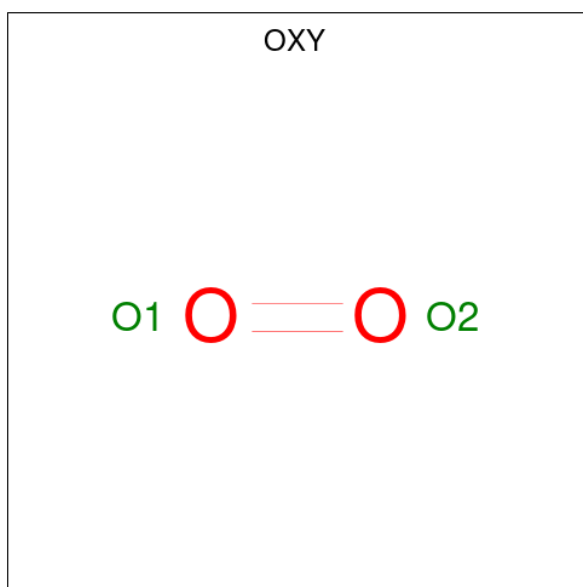
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1122	724	195	200	3			
2	D	146	Total	C	N	O	S	0	0	0
			1122	724	195	200	3			
2	F	146	Total	C	N	O	S	0	0	0
			1122	724	195	200	3			
2	H	146	Total	C	N	O	S	0	0	0
			1122	724	195	200	3			
2	T	146	Total	C	N	O	S	0	0	0
			1122	724	195	200	3			

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



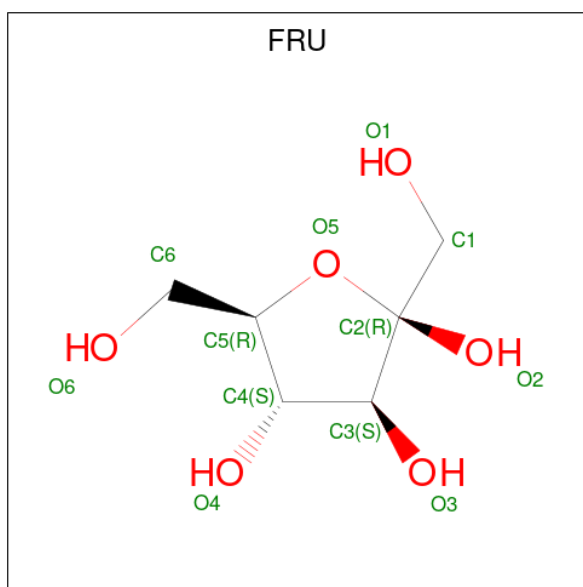
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	S	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	T	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 4 is OXYGEN MOLECULE (CCD ID: OXY) (formula: O₂).



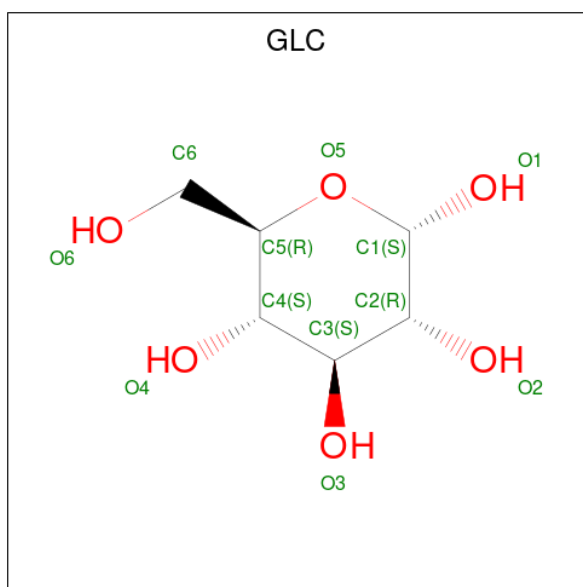
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O 2 2	0	0
4	B	1	Total O 2 2	0	0
4	C	1	Total O 2 2	0	0
4	D	1	Total O 2 2	0	0
4	F	1	Total O 2 2	0	0
4	G	1	Total O 2 2	0	0
4	S	1	Total O 2 2	0	0
4	T	1	Total O 2 2	0	0

- Molecule 5 is beta-D-fructofuranose (CCD ID: FRU) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		
5	C	1	Total	C	O	0	0
			11	6	5		
5	F	1	Total	C	O	0	0
			11	6	5		

- Molecule 6 is alpha-D-glucopyranose (CCD ID: GLC) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			12	6	6		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	30	Total 30	O 30	0	0
7	B	36	Total 36	O 36	0	0
7	C	39	Total 39	O 39	0	0
7	D	32	Total 32	O 32	0	0
7	E	12	Total 12	O 12	0	0
7	F	26	Total 26	O 26	0	0
7	G	18	Total 18	O 18	0	0
7	H	10	Total 10	O 10	0	0
7	S	15	Total 15	O 15	0	0
7	T	14	Total 14	O 14	0	0

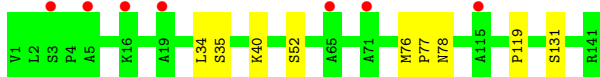
3 Residue-property plots [i](#)

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.

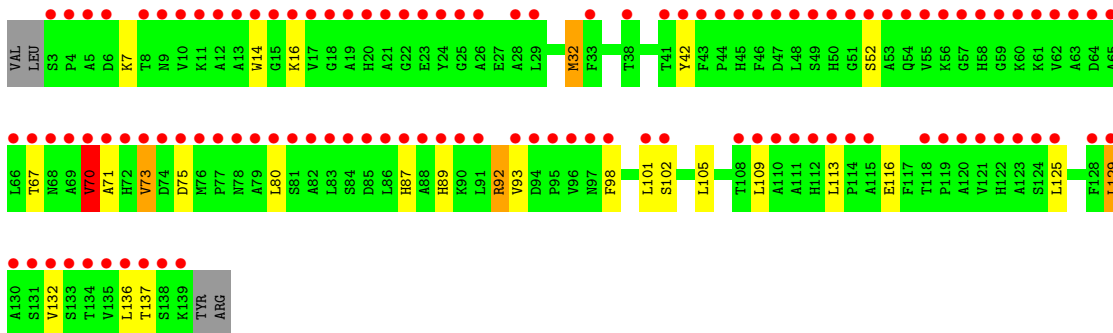
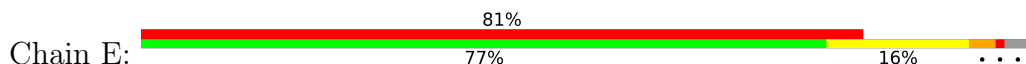
- Molecule 1: Hemoglobin subunit alpha



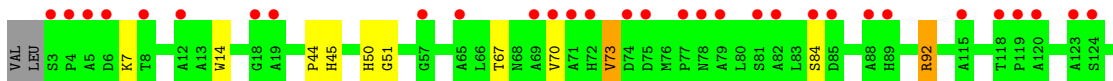
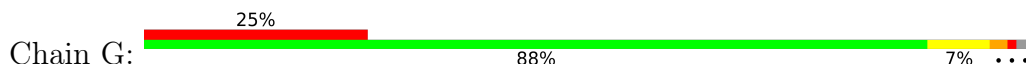
- Molecule 1: Hemoglobin subunit alpha

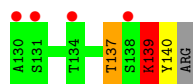


- Molecule 1: Hemoglobin subunit alpha

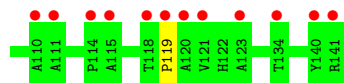
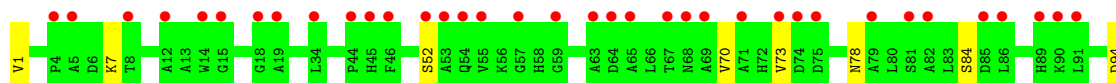
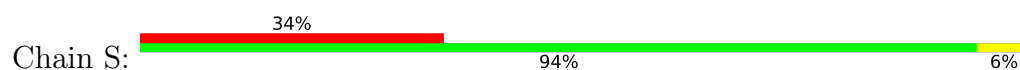


- Molecule 1: Hemoglobin subunit alpha

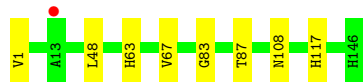




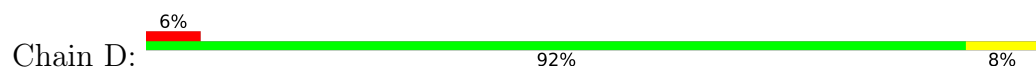
- Molecule 1: Hemoglobin subunit alpha



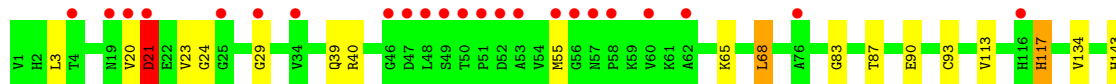
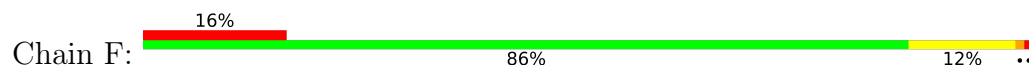
- Molecule 2: Hemoglobin subunit beta



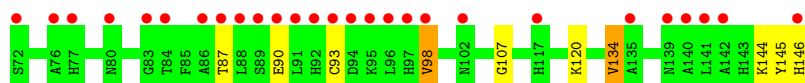
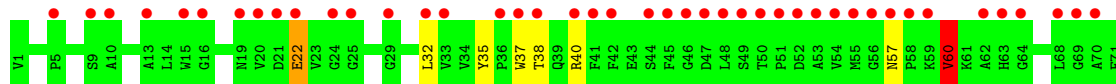
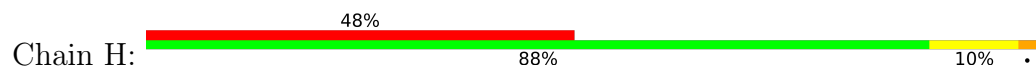
- Molecule 2: Hemoglobin subunit beta



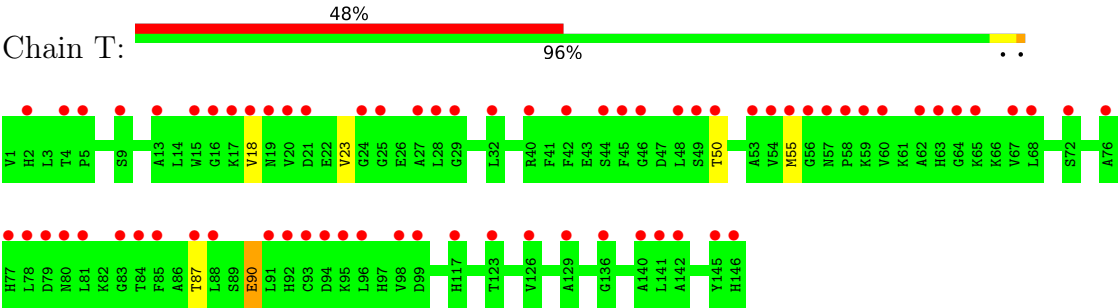
- Molecule 2: Hemoglobin subunit beta



- Molecule 2: Hemoglobin subunit beta



● Molecule 2: Hemoglobin subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	237.99Å 59.27Å 137.02Å 90.00° 125.36° 90.00°	Depositor
Resolution (Å)	112.13 – 2.30 112.13 – 2.30	Depositor EDS
% Data completeness (in resolution range)	87.0 (112.13-2.30) 87.0 (112.13-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.203 , 0.244 0.258 , 0.287	Depositor DCC
R_{free} test set	3020 reflections (4.33%)	wwPDB-VP
Wilson B-factor (Å ²)	41.0	Xtriage
Anisotropy	0.351	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 46.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11609	wwPDB-VP
Average B, all atoms (Å ²)	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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: GLC, HEM, FRU, OXY

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	1.39	3/1096 (0.3%)	1.14	2/1491 (0.1%)
1	C	1.34	3/1096 (0.3%)	1.11	1/1491 (0.1%)
1	E	1.09	1/1057 (0.1%)	1.26	12/1438 (0.8%)
1	G	1.25	2/1070 (0.2%)	1.27	8/1456 (0.5%)
1	S	1.11	2/1096 (0.2%)	1.04	1/1491 (0.1%)
2	B	1.46	3/1152 (0.3%)	1.14	2/1566 (0.1%)
2	D	1.33	2/1152 (0.2%)	1.13	4/1566 (0.3%)
2	F	1.28	2/1152 (0.2%)	1.23	7/1566 (0.4%)
2	H	1.10	0/1152	1.12	6/1566 (0.4%)
2	T	1.09	0/1152	1.06	1/1566 (0.1%)
All	All	1.25	18/11175 (0.2%)	1.15	44/15197 (0.3%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	139	LYS	CA-C	7.14	1.62	1.52
1	C	34	LEU	CA-C	-7.04	1.43	1.52
1	E	92	ARG	CA-CB	6.42	1.62	1.53
1	C	40	LYS	N-CA	6.19	1.54	1.46
1	G	45	HIS	N-CA	5.87	1.52	1.46
2	F	134	VAL	C-O	-5.76	1.16	1.24
1	S	84	SER	N-CA	-5.76	1.39	1.46
1	C	35	SER	N-CA	5.70	1.53	1.46
2	D	10	ALA	CA-C	5.45	1.60	1.52
2	B	67	VAL	N-CA	-5.44	1.40	1.46
1	A	49	SER	CA-CB	5.43	1.61	1.53
2	B	63	HIS	N-CA	-5.37	1.39	1.46
2	F	21	ASP	N-CA	5.34	1.53	1.46
1	A	28	ALA	N-CA	-5.17	1.40	1.46
2	B	117	HIS	C-O	-5.16	1.17	1.24
1	A	23	GLU	CA-C	5.14	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	S	94	ASP	CA-C	5.12	1.59	1.52
2	D	72	SER	N-CA	5.11	1.52	1.46

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	44	PRO	CA-C-N	-11.77	103.96	122.67
1	G	44	PRO	C-N-CA	-11.77	103.96	122.67
2	F	143	HIS	N-CA-C	8.71	120.39	111.07
2	H	60	VAL	N-CA-CB	8.12	120.06	110.55
2	F	113	VAL	N-CA-CB	8.06	122.67	110.58
2	T	90	GLU	N-CA-CB	7.66	121.35	109.94
2	F	117	HIS	CB-CA-C	-7.53	98.05	110.85
1	A	73	VAL	CB-CA-C	-7.02	102.67	112.14
2	D	124	PRO	N-CA-C	6.66	118.82	110.70
1	E	70	VAL	CB-CA-C	-6.57	103.56	111.97
2	F	21	ASP	N-CA-C	-6.31	97.36	110.80
2	F	90	GLU	N-CA-C	6.28	118.65	111.11
2	D	108	ASN	N-CA-C	6.15	118.06	111.36
2	H	134	VAL	N-CA-CB	-5.97	101.63	110.58
1	E	137	THR	CA-C-N	5.97	128.87	120.28
1	E	137	THR	C-N-CA	5.97	128.87	120.28
1	E	80	LEU	CB-CG-CD2	5.95	128.56	110.70
2	H	22	GLU	CB-CA-C	-5.86	100.76	110.37
1	E	70	VAL	N-CA-CB	5.79	117.32	110.55
1	E	16	LYS	CB-CA-C	5.61	120.11	110.01
1	G	73	VAL	CB-CA-C	-5.61	104.57	112.14
1	A	57	GLY	N-CA-C	-5.60	105.71	112.49
1	E	32	MET	CG-SD-CE	-5.54	88.72	100.90
2	F	68	LEU	CB-CA-C	5.50	120.80	110.63
2	D	9	SER	N-CA-CB	-5.46	101.89	110.30
2	H	87	THR	N-CA-CB	5.44	118.21	110.16
1	G	44	PRO	O-C-N	-5.39	115.27	122.22
1	G	51	GLY	N-CA-C	5.38	121.98	115.31
2	B	87	THR	N-CA-CB	5.37	118.60	110.28
1	E	116	GLU	CG-CD-OE2	5.28	130.54	118.40
1	E	129	LEU	CB-CG-CD2	5.27	126.50	110.70
1	E	89	HIS	CA-CB-CG	5.20	119.00	113.80
2	D	87	THR	N-CA-CB	5.19	117.84	110.16
1	G	137	THR	CA-C-N	5.17	128.88	120.60
1	G	137	THR	C-N-CA	5.17	128.88	120.60
2	H	98	VAL	CB-CA-C	5.14	117.84	111.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	116	GLU	CG-CD-OE1	-5.13	106.61	118.40
2	B	108	ASN	N-CA-C	5.08	117.72	111.82
2	H	98	VAL	N-CA-CB	5.08	116.06	110.53
1	G	50	HIS	N-CA-C	5.04	117.16	111.11
1	E	73	VAL	CB-CA-C	-5.03	105.35	112.14
1	S	78	ASN	N-CA-CB	5.03	117.60	110.16
1	C	131	SER	N-CA-C	5.01	116.82	111.36
2	F	21	ASP	N-CA-CB	5.00	118.95	110.49

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	1068	0	1071	2	0
1	C	1068	0	1070	2	0
1	E	1030	0	1028	26	0
1	G	1042	0	1037	7	0
1	S	1068	0	1073	3	0
2	B	1122	0	1118	2	0
2	D	1122	0	1118	4	0
2	F	1122	0	1116	18	0
2	H	1122	0	1118	16	0
2	T	1122	0	1118	3	0
3	A	43	0	30	0	0
3	B	43	0	30	1	0
3	C	43	0	30	1	0
3	D	43	0	30	1	0
3	E	43	0	30	3	0
3	F	43	0	30	2	0
3	G	43	0	30	0	0
3	H	43	0	30	1	0
3	S	43	0	30	1	0
3	T	43	0	30	2	0
4	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	F	2	0	0	0	0
4	G	2	0	0	0	0
4	S	2	0	0	0	0
4	T	2	0	0	0	0
5	A	11	0	9	1	0
5	C	11	0	9	1	0
5	F	11	0	9	2	0
6	C	12	0	12	0	0
7	A	30	0	0	0	0
7	B	36	0	0	0	0
7	C	39	0	0	0	0
7	D	32	0	0	1	0
7	E	12	0	0	0	0
7	F	26	0	0	1	0
7	G	18	0	0	0	0
7	H	10	0	0	0	0
7	S	15	0	0	0	0
7	T	14	0	0	0	0
All	All	11609	0	11206	87	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 4.

All (87) 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:H:93:CYS:SG	2:H:145:TYR:HE1	1.78	1.05
2:H:93:CYS:SG	2:H:145:TYR:CE1	2.49	1.04
2:H:35:TYR:O	2:H:38:THR:HG22	1.64	0.96
1:E:32:MET:HE1	1:E:101:LEU:HB2	1.52	0.89
2:F:24:GLY:N	2:F:68:LEU:HD12	1.97	0.80
1:G:139:LYS:HD2	1:G:139:LYS:O	1.85	0.77
1:E:32:MET:CE	1:E:101:LEU:HB2	2.14	0.77
2:H:32:LEU:HD23	2:H:38:THR:HG23	1.71	0.73
1:E:92:ARG:CG	2:H:37:TRP:HA	2.20	0.72
1:E:67:THR:O	1:E:70:VAL:HG12	1.91	0.70
1:E:92:ARG:HG2	2:H:37:TRP:HA	1.72	0.70
2:F:24:GLY:CA	2:F:68:LEU:HD12	2.22	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:102:SER:HA	1:E:129:LEU:HD23	1.74	0.69
2:H:93:CYS:SG	2:H:145:TYR:CD1	2.83	0.68
2:H:107:GLY:HA3	2:H:134:VAL:HG13	1.75	0.67
1:G:14:TRP:HE1	1:G:67:THR:HG22	1.61	0.65
1:E:14:TRP:HE1	1:E:67:THR:HG22	1.63	0.64
1:E:32:MET:CE	1:E:101:LEU:CB	2.77	0.63
3:E:201:HEM:HMB1	3:E:201:HEM:HBB2	1.82	0.61
2:F:24:GLY:HA2	2:F:68:LEU:CD1	2.30	0.61
2:H:57:ASN:HB3	2:H:60:VAL:HG13	1.81	0.61
1:E:14:TRP:HE1	1:E:67:THR:CG2	2.15	0.60
1:G:70:VAL:O	1:G:73:VAL:HG23	2.02	0.60
1:G:14:TRP:HE1	1:G:67:THR:CG2	2.15	0.60
1:S:70:VAL:O	1:S:73:VAL:HG23	2.03	0.59
1:A:70:VAL:O	1:A:73:VAL:HG23	2.03	0.59
2:F:93:CYS:HB2	2:F:145:TYR:CE1	2.38	0.58
1:E:70:VAL:O	1:E:73:VAL:HG23	2.03	0.58
2:F:40:ARG:NH2	7:F:302:HOH:O	2.35	0.58
2:F:24:GLY:CA	2:F:68:LEU:CD1	2.82	0.58
2:B:48:LEU:O	5:C:203:FRU:O3	2.22	0.57
1:E:32:MET:HE1	1:E:101:LEU:CB	2.31	0.57
3:S:201:HEM:HMB1	3:S:201:HEM:HBB2	1.84	0.57
1:E:101:LEU:HD23	1:E:101:LEU:O	2.05	0.56
1:E:93:VAL:HG23	1:E:98:PHE:HE1	1.71	0.56
1:A:7:LYS:HG2	1:A:73:VAL:HG11	1.87	0.56
2:F:21:ASP:HA	2:F:65:LYS:HG3	1.88	0.56
3:T:201:HEM:HBC2	3:T:201:HEM:HMC2	1.87	0.56
1:E:101:LEU:HD23	1:E:101:LEU:C	2.32	0.54
3:H:201:HEM:HBB2	3:H:201:HEM:HHC	1.89	0.54
2:F:20:VAL:HG23	2:F:20:VAL:O	2.07	0.54
3:C:201:HEM:HMB1	3:C:201:HEM:HBB2	1.90	0.52
1:G:7:LYS:HG2	1:G:73:VAL:HG11	1.90	0.52
2:H:107:GLY:HA3	2:H:134:VAL:CG1	2.39	0.52
1:E:7:LYS:HG2	1:E:73:VAL:HG11	1.90	0.52
2:H:35:TYR:O	2:H:38:THR:CG2	2.47	0.52
2:D:26:GLU:OE1	2:D:117:HIS:NE2	2.39	0.51
1:S:7:LYS:HG2	1:S:73:VAL:HG11	1.92	0.51
5:F:203:FRU:C6	2:H:146:HIS:HD2	2.24	0.50
2:T:87:THR:O	2:T:90:GLU:HG3	2.11	0.49
5:A:203:FRU:H61	2:D:33:VAL:HG13	1.94	0.49
2:F:93:CYS:HB2	2:F:145:TYR:CZ	2.47	0.49
2:F:20:VAL:O	2:F:21:ASP:CG	2.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:203:FRU:H62	2:H:146:HIS:HD2	1.78	0.49
2:H:32:LEU:HA	2:H:38:THR:CG2	2.44	0.48
2:F:24:GLY:N	2:F:68:LEU:CD1	2.75	0.48
3:D:201:HEM:HBC2	3:D:201:HEM:HMC1	1.96	0.47
2:H:93:CYS:CB	2:H:145:TYR:CE1	2.96	0.47
1:E:125:LEU:O	1:E:129:LEU:HD13	2.13	0.47
1:E:87:HIS:HE1	3:E:201:HEM:C4C	2.16	0.47
1:E:105:LEU:O	1:E:109:LEU:HD13	2.15	0.47
1:E:42:TYR:CD2	3:E:201:HEM:HBC1	2.50	0.46
2:H:90:GLU:HG3	2:H:144:LYS:HE2	1.96	0.46
1:E:93:VAL:CG2	1:E:98:PHE:HE1	2.28	0.46
1:E:125:LEU:O	1:E:129:LEU:CD1	2.63	0.46
1:C:119:PRO:HB3	2:D:55:MET:HE3	1.97	0.46
2:F:20:VAL:O	2:F:21:ASP:CB	2.64	0.45
2:D:87:THR:HG22	7:D:314:HOH:O	2.16	0.44
3:T:201:HEM:HHC	3:T:201:HEM:HBB2	2.00	0.44
2:T:18:VAL:HG13	2:T:23:VAL:HG21	2.00	0.43
1:E:32:MET:HE3	1:E:101:LEU:HA	1.99	0.43
1:E:70:VAL:CG1	1:E:71:ALA:N	2.80	0.43
1:G:137:THR:O	1:G:140:TYR:CD2	2.72	0.43
1:E:32:MET:HE3	1:E:101:LEU:CB	2.48	0.42
2:F:24:GLY:HA2	2:F:68:LEU:CG	2.48	0.42
2:F:39:GLN:OE1	1:G:92:ARG:NH2	2.52	0.42
1:E:32:MET:HE3	1:E:101:LEU:CA	2.50	0.41
3:F:201:HEM:HBB2	3:F:201:HEM:HHC	2.03	0.41
2:B:83:GLY:O	2:F:83:GLY:HA3	2.21	0.41
3:F:201:HEM:HMC1	3:F:201:HEM:HBC2	2.02	0.41
1:S:119:PRO:HB3	2:T:55:MET:HE3	2.01	0.41
2:F:20:VAL:O	2:F:20:VAL:CG2	2.68	0.41
3:B:201:HEM:HMC1	3:B:201:HEM:HBC2	2.03	0.41
1:E:132:VAL:HG12	1:E:136:LEU:HD12	2.02	0.41
2:F:29:GLY:C	2:F:55:MET:HE1	2.46	0.40
2:F:23:VAL:HG12	2:F:68:LEU:HD11	2.03	0.40
1:C:76:MET:N	1:C:77:PRO:CD	2.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	138 (99%)	1 (1%)	0	100	100
1	C	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
1	E	135/141 (96%)	133 (98%)	2 (2%)	0	100	100
1	G	136/141 (96%)	134 (98%)	2 (2%)	0	100	100
1	S	139/141 (99%)	137 (99%)	2 (1%)	0	100	100
2	B	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
2	D	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
2	F	144/146 (99%)	137 (95%)	6 (4%)	1 (1%)	18	23
2	H	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
2	T	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
All	All	1408/1435 (98%)	1379 (98%)	28 (2%)	1 (0%)	48	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	21	ASP

5.3.2 Protein sidechains

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	113/113 (100%)	112 (99%)	1 (1%)	70	84
1	C	113/113 (100%)	111 (98%)	2 (2%)	51	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	109/113 (96%)	105 (96%)	4 (4%)	30	45
1	G	110/113 (97%)	107 (97%)	3 (3%)	39	58
1	S	113/113 (100%)	111 (98%)	2 (2%)	51	70
2	B	118/118 (100%)	117 (99%)	1 (1%)	73	86
2	D	118/118 (100%)	116 (98%)	2 (2%)	53	72
2	F	118/118 (100%)	115 (98%)	3 (2%)	42	60
2	H	118/118 (100%)	113 (96%)	5 (4%)	26	40
2	T	118/118 (100%)	117 (99%)	1 (1%)	73	86
All	All	1148/1155 (99%)	1124 (98%)	24 (2%)	47	66

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	SER
2	B	1	VAL
1	C	52	SER
1	C	78	ASN
2	D	1	VAL
2	D	61	LYS
1	E	52	SER
1	E	70	VAL
1	E	75	ASP
1	E	113	LEU
2	F	3	LEU
2	F	87	THR
2	F	117	HIS
1	G	84	SER
1	G	92	ARG
1	G	139	LYS
2	H	22	GLU
2	H	40	ARG
2	H	60	VAL
2	H	98	VAL
2	H	120	LYS
1	S	1	VAL
1	S	52	SER
2	T	50	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13)

such sidechains are listed below:

Mol	Chain	Res	Type
2	B	80	ASN
2	B	97	HIS
2	D	97	HIS
2	D	143	HIS
1	E	87	HIS
2	F	77	HIS
1	G	97	ASN
2	H	63	HIS
2	H	143	HIS
2	H	146	HIS
2	T	80	ASN
2	T	97	HIS
2	T	139	ASN

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](#)

22 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	G	201	4,1	50,50,50	1.74	11 (22%)	67,82,82	1.80	14 (20%)
4	OXY	G	202	3	1,1,1	0.12	0	-		
3	HEM	F	201	4,2	50,50,50	1.73	11 (22%)	67,82,82	1.85	15 (22%)
3	HEM	T	201	4,2	50,50,50	1.65	6 (12%)	67,82,82	1.63	11 (16%)
5	FRU	A	203	-	11,11,12	0.87	0	15,17,18	3.35	2 (13%)
3	HEM	C	201	4,1	50,50,50	1.64	10 (20%)	67,82,82	1.64	16 (23%)
4	OXY	T	202	3	1,1,1	0.19	0	-		
4	OXY	F	202	3	1,1,1	0.15	0	-		
4	OXY	S	202	3	1,1,1	0.09	0	-		
3	HEM	H	201	2	50,50,50	1.71	10 (20%)	67,82,82	1.75	13 (19%)
4	OXY	D	202	3	1,1,1	0.18	0	-		
5	FRU	C	203	-	11,11,12	0.97	1 (9%)	15,17,18	1.44	3 (20%)
4	OXY	C	202	3	1,1,1	0.07	0	-		
5	FRU	F	203	-	11,11,12	0.78	0	15,17,18	1.23	2 (13%)
3	HEM	A	201	4,1	50,50,50	1.61	9 (18%)	67,82,82	1.69	14 (20%)
3	HEM	D	201	4,2	50,50,50	1.62	7 (14%)	67,82,82	1.59	14 (20%)
3	HEM	S	201	4,1	50,50,50	1.68	12 (24%)	67,82,82	1.68	12 (17%)
4	OXY	A	202	3	1,1,1	0.09	0	-		
3	HEM	E	201	1	50,50,50	1.72	7 (14%)	67,82,82	1.97	17 (25%)
4	OXY	B	202	3	1,1,1	0.27	0	-		
6	GLC	C	204	-	12,12,12	1.65	3 (25%)	17,17,17	1.78	5 (29%)
3	HEM	B	201	4,2	50,50,50	1.87	13 (26%)	67,82,82	1.85	16 (23%)

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
5	FRU	C	203	-	-	0/2/21/24	0/1/1/1
5	FRU	F	203	-	-	2/2/21/24	0/1/1/1
3	HEM	A	201	4,1	-	2/14/54/54	-
3	HEM	D	201	4,2	-	2/14/54/54	-
3	HEM	E	201	1	-	4/14/54/54	-
3	HEM	G	201	4,1	-	4/14/54/54	-
3	HEM	H	201	2	-	6/14/54/54	-
3	HEM	F	201	4,2	-	4/14/54/54	-
3	HEM	T	201	4,2	-	5/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEM	B	201	4,2	-	2/14/54/54	-
6	GLC	C	204	-	-	0/2/22/22	0/1/1/1
5	FRU	A	203	-	-	2/2/21/24	0/1/1/1
3	HEM	C	201	4,1	-	7/14/54/54	-
3	HEM	S	201	4,1	-	2/14/54/54	-

All (100) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	201	HEM	FE-NC	6.01	2.15	1.95
3	D	201	HEM	FE-NB	5.94	2.13	1.94
3	E	201	HEM	FE-NC	5.70	2.14	1.95
3	E	201	HEM	C1B-NB	-5.64	1.30	1.40
3	T	201	HEM	FE-NB	5.50	2.11	1.94
3	T	201	HEM	FE-NC	5.30	2.12	1.95
3	H	201	HEM	FE-NB	5.11	2.10	1.94
3	A	201	HEM	FE-NC	4.93	2.11	1.95
3	D	201	HEM	FE-NC	4.65	2.10	1.95
3	S	201	HEM	C1B-NB	-4.63	1.32	1.40
3	F	201	HEM	FE-NB	4.48	2.08	1.94
3	C	201	HEM	FE-NB	4.38	2.08	1.94
3	B	201	HEM	FE-NB	4.28	2.08	1.94
3	B	201	HEM	FE-NC	4.27	2.09	1.95
3	B	201	HEM	C1B-NB	-4.21	1.33	1.40
3	A	201	HEM	C1B-NB	-4.21	1.33	1.40
3	D	201	HEM	C1B-NB	-4.18	1.33	1.40
3	A	201	HEM	FE-NB	4.16	2.07	1.94
3	C	201	HEM	FE-NC	3.90	2.08	1.95
3	S	201	HEM	FE-NC	3.80	2.07	1.95
3	H	201	HEM	FE-NC	3.68	2.07	1.95
3	C	201	HEM	C4D-ND	-3.66	1.33	1.40
3	S	201	HEM	FE-NB	3.59	2.06	1.94
3	F	201	HEM	C1D-ND	-3.58	1.31	1.38
3	B	201	HEM	C4D-ND	-3.55	1.34	1.40
3	E	201	HEM	FE-NB	3.53	2.05	1.94
3	H	201	HEM	C1B-NB	-3.47	1.34	1.40
3	F	201	HEM	C3C-C4C	-3.43	1.40	1.46
3	F	201	HEM	C1B-NB	-3.37	1.34	1.40
3	C	201	HEM	C1B-NB	-3.36	1.34	1.40
3	F	201	HEM	C4C-NC	-3.30	1.33	1.39
3	G	201	HEM	FE-NB	3.23	2.04	1.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	S	201	HEM	C4B-NB	-3.17	1.32	1.38
3	T	201	HEM	C1B-NB	-3.17	1.34	1.40
3	E	201	HEM	C1C-NC	-3.13	1.33	1.39
3	B	201	HEM	C4B-NB	-3.08	1.32	1.38
3	H	201	HEM	C4B-NB	-3.08	1.32	1.38
3	H	201	HEM	C1C-C2C	-3.07	1.39	1.45
3	A	201	HEM	C4D-ND	-3.06	1.34	1.40
3	C	201	HEM	C4B-NB	-3.04	1.32	1.38
3	F	201	HEM	FE-NC	3.03	2.05	1.95
3	T	201	HEM	C3B-C4B	3.02	1.50	1.44
3	H	201	HEM	CHD-C4C	-3.02	1.32	1.38
3	C	201	HEM	C3B-C4B	2.85	1.50	1.44
3	B	201	HEM	O2D-CGD	-2.79	1.21	1.30
3	F	201	HEM	C1C-C2C	-2.79	1.39	1.45
3	H	201	HEM	C4D-ND	-2.79	1.35	1.40
3	B	201	HEM	C4D-C3D	2.77	1.49	1.45
3	E	201	HEM	C1C-C2C	-2.77	1.39	1.45
3	S	201	HEM	C4D-ND	-2.76	1.35	1.40
3	G	201	HEM	FE-ND	-2.73	1.86	1.94
3	S	201	HEM	C1C-C2C	-2.69	1.40	1.45
6	C	204	GLC	O5-C1	2.67	1.49	1.42
3	S	201	HEM	C1C-NC	-2.66	1.34	1.39
3	G	201	HEM	C4D-C3D	2.66	1.49	1.45
3	E	201	HEM	C1D-ND	-2.65	1.33	1.38
3	G	201	HEM	FE-NA	2.63	2.03	1.95
3	G	201	HEM	C3B-C4B	2.63	1.50	1.44
3	B	201	HEM	C3B-C4B	2.51	1.49	1.44
3	G	201	HEM	C4D-ND	-2.50	1.35	1.40
3	T	201	HEM	C4D-ND	-2.49	1.35	1.40
3	B	201	HEM	FE-NA	2.44	2.03	1.95
3	S	201	HEM	C4C-NC	-2.43	1.35	1.39
3	A	201	HEM	FE-NA	2.43	2.03	1.95
3	C	201	HEM	FE-NA	2.42	2.03	1.95
6	C	204	GLC	O4-C4	2.40	1.48	1.43
3	G	201	HEM	C4C-NC	-2.39	1.35	1.39
3	S	201	HEM	FE-ND	-2.38	1.87	1.94
3	B	201	HEM	C3C-C4C	-2.37	1.41	1.46
3	D	201	HEM	C4C-NC	-2.37	1.35	1.39
3	F	201	HEM	C3B-C4B	2.36	1.49	1.44
3	B	201	HEM	CHB-C1B	2.36	1.43	1.38
3	E	201	HEM	C1D-C2D	2.35	1.49	1.44
3	F	201	HEM	C4B-NB	-2.34	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	201	HEM	C3B-C4B	2.32	1.49	1.44
3	F	201	HEM	C3C-C2C	2.32	1.41	1.37
3	A	201	HEM	C1C-NC	-2.31	1.35	1.39
3	H	201	HEM	C1D-C2D	2.31	1.49	1.44
5	C	203	FRU	C1-C2	2.30	1.55	1.52
3	B	201	HEM	C1B-C2B	-2.28	1.39	1.44
3	G	201	HEM	C1D-C2D	2.27	1.49	1.44
3	C	201	HEM	C1D-ND	-2.27	1.34	1.38
3	C	201	HEM	C1C-NC	-2.24	1.35	1.39
3	A	201	HEM	C3C-C4C	-2.23	1.42	1.46
3	D	201	HEM	C4D-ND	-2.22	1.36	1.40
3	B	201	HEM	O1A-CGA	2.19	1.29	1.22
3	S	201	HEM	C3C-C4C	-2.16	1.42	1.46
3	S	201	HEM	C1B-C2B	-2.15	1.40	1.44
3	D	201	HEM	C4B-NB	-2.11	1.34	1.38
3	A	201	HEM	C4C-NC	-2.11	1.35	1.39
3	S	201	HEM	C4A-NA	-2.10	1.35	1.39
3	C	201	HEM	C1A-NA	-2.09	1.35	1.39
3	G	201	HEM	CHB-C1B	2.08	1.42	1.38
3	F	201	HEM	C4D-ND	-2.08	1.36	1.40
3	H	201	HEM	C4D-C3D	2.08	1.48	1.45
6	C	204	GLC	O2-C2	2.07	1.48	1.43
3	D	201	HEM	C1D-ND	-2.06	1.34	1.38
3	T	201	HEM	C4D-C3D	2.05	1.48	1.45
3	A	201	HEM	C1D-ND	-2.02	1.34	1.38
3	G	201	HEM	C3C-C4C	-2.00	1.42	1.46

All (154) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	203	FRU	O5-C2-C1	9.32	113.70	107.46
5	A	203	FRU	O2-C2-O5	-8.34	104.51	109.99
3	E	201	HEM	CHC-C4B-NB	5.66	130.51	124.42
3	G	201	HEM	CHC-C4B-NB	5.27	130.09	124.42
3	E	201	HEM	C4B-C3B-C2B	-5.17	102.53	107.28
3	H	201	HEM	CAC-C3C-C4C	5.17	137.16	124.82
3	F	201	HEM	C3B-C4B-NB	-5.08	105.82	109.47
3	T	201	HEM	C3B-C4B-NB	-4.90	105.95	109.47
3	B	201	HEM	C3B-C4B-NB	-4.84	106.00	109.47
3	T	201	HEM	C1B-NB-C4B	4.82	110.92	105.21
3	B	201	HEM	CHD-C1D-ND	4.76	129.54	124.42
3	A	201	HEM	C1B-NB-C4B	4.74	110.82	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	S	201	HEM	CHD-C1D-ND	4.67	129.45	124.42
3	H	201	HEM	CHD-C1D-ND	4.62	129.39	124.42
3	D	201	HEM	C1B-NB-C4B	4.55	110.59	105.21
3	F	201	HEM	C1B-NB-C4B	4.46	110.49	105.21
3	G	201	HEM	C1B-NB-C4B	4.43	110.45	105.21
3	B	201	HEM	C1B-NB-C4B	4.41	110.43	105.21
3	B	201	HEM	CHC-C4B-NB	4.37	129.13	124.42
3	S	201	HEM	CHC-C4B-NB	4.32	129.08	124.42
3	F	201	HEM	CHD-C1D-C2D	-4.23	118.35	125.03
3	C	201	HEM	C1B-NB-C4B	4.23	110.21	105.21
3	B	201	HEM	CHD-C1D-C2D	-4.19	118.42	125.03
3	G	201	HEM	C3B-C4B-NB	-4.16	106.48	109.47
3	E	201	HEM	CAC-C3C-C4C	4.04	134.46	124.82
3	G	201	HEM	CHD-C1D-ND	3.98	128.70	124.42
3	A	201	HEM	CHC-C4B-NB	3.90	128.62	124.42
3	S	201	HEM	C1B-NB-C4B	3.86	109.78	105.21
3	S	201	HEM	CHD-C1D-C2D	-3.84	118.97	125.03
3	A	201	HEM	CHA-C4D-ND	3.83	129.11	124.37
3	T	201	HEM	CHD-C1D-ND	3.76	128.47	124.42
3	E	201	HEM	C1B-NB-C4B	3.75	109.65	105.21
3	E	201	HEM	CHA-C4D-C3D	-3.73	118.35	125.23
3	F	201	HEM	C2D-C1D-ND	3.71	114.19	109.90
3	D	201	HEM	CHC-C4B-NB	3.68	128.38	124.42
3	E	201	HEM	C3B-C2B-C1B	3.65	109.16	106.41
3	G	201	HEM	CHD-C1D-C2D	-3.65	119.27	125.03
3	E	201	HEM	CMD-C2D-C1D	3.65	130.73	125.03
3	D	201	HEM	CHD-C1D-ND	3.63	128.33	124.42
3	C	201	HEM	CHA-C4D-C3D	-3.61	118.58	125.23
3	A	201	HEM	CHA-C4D-C3D	-3.59	118.61	125.23
3	E	201	HEM	CHA-C4D-ND	3.55	128.76	124.37
3	C	201	HEM	CMD-C2D-C1D	3.54	130.57	125.03
3	E	201	HEM	CHD-C1D-ND	3.51	128.20	124.42
3	B	201	HEM	CAD-C3D-C4D	3.51	130.81	124.70
3	C	201	HEM	CHC-C4B-NB	3.50	128.19	124.42
3	A	201	HEM	CMD-C2D-C1D	3.50	130.51	125.03
3	G	201	HEM	CMD-C2D-C1D	3.50	130.50	125.03
3	H	201	HEM	C1B-NB-C4B	3.48	109.33	105.21
3	A	201	HEM	CHD-C1D-ND	3.48	128.17	124.42
3	T	201	HEM	CHC-C4B-NB	3.44	128.12	124.42
3	C	201	HEM	CHA-C4D-ND	3.43	128.61	124.37
3	B	201	HEM	CMD-C2D-C1D	3.41	130.36	125.03
3	G	201	HEM	CAA-CBA-CGA	-3.40	104.64	113.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	201	HEM	CAC-C3C-C2C	-3.40	117.38	128.43
6	C	204	GLC	O5-C1-C2	3.38	116.24	110.30
3	F	201	HEM	CMB-C2B-C1B	3.38	130.31	125.03
5	C	203	FRU	O2-C2-O5	3.37	112.20	109.99
3	B	201	HEM	C4C-CHD-C1D	-3.33	118.95	126.02
3	C	201	HEM	CBA-CAA-C2A	3.29	121.63	112.53
6	C	204	GLC	O2-C2-C1	3.28	116.83	109.25
3	G	201	HEM	CHA-C4D-C3D	-3.27	119.19	125.23
3	H	201	HEM	CHC-C1C-NC	3.25	127.99	124.45
3	G	201	HEM	CAD-C3D-C4D	3.23	130.32	124.70
3	H	201	HEM	CHA-C4D-ND	3.21	128.33	124.37
3	C	201	HEM	CAD-C3D-C4D	3.19	130.25	124.70
3	G	201	HEM	CHB-C1B-NB	3.17	128.29	124.37
3	F	201	HEM	CAD-C3D-C4D	3.16	130.21	124.70
3	T	201	HEM	CHD-C1D-C2D	-3.14	120.08	125.03
3	D	201	HEM	CBD-CAD-C3D	-3.13	103.87	112.53
3	S	201	HEM	C3B-C4B-NB	-3.06	107.27	109.47
3	H	201	HEM	CHD-C1D-C2D	-3.05	120.22	125.03
3	F	201	HEM	CHC-C4B-NB	3.00	127.65	124.42
3	G	201	HEM	CHA-C4D-ND	2.96	128.03	124.37
3	D	201	HEM	CHA-C4D-ND	2.95	128.02	124.37
3	S	201	HEM	CHA-C4D-ND	2.95	128.01	124.37
3	S	201	HEM	C4C-CHD-C1D	-2.92	119.82	126.02
3	D	201	HEM	C3B-C4B-NB	-2.88	107.40	109.47
3	A	201	HEM	C3B-C2B-C1B	2.88	108.57	106.41
3	T	201	HEM	CHA-C4D-ND	2.85	127.89	124.37
3	H	201	HEM	O2D-CGD-CBD	2.83	122.95	114.00
3	G	201	HEM	O2D-CGD-O1D	-2.83	116.06	123.33
3	E	201	HEM	CAC-C3C-C2C	-2.82	119.26	128.43
3	E	201	HEM	CAD-C3D-C4D	2.76	129.50	124.70
3	E	201	HEM	CHC-C4B-C3B	-2.75	119.58	125.07
3	D	201	HEM	CMD-C2D-C1D	2.74	129.32	125.03
6	C	204	GLC	O4-C4-C5	2.72	116.02	109.32
3	T	201	HEM	CHB-C1B-NB	2.71	127.72	124.37
6	C	204	GLC	C4-C3-C2	-2.70	106.08	110.83
3	A	201	HEM	C3B-C4B-NB	-2.70	107.53	109.47
3	A	201	HEM	CBD-CAD-C3D	-2.70	105.07	112.53
3	H	201	HEM	CAA-CBA-CGA	-2.67	106.59	113.67
3	F	201	HEM	CHD-C1D-ND	2.66	127.29	124.42
3	A	201	HEM	CHD-C1D-C2D	-2.65	120.84	125.03
3	A	201	HEM	CHB-C1B-NB	2.65	127.64	124.37
3	F	201	HEM	CAB-C3B-C2B	-2.61	119.93	128.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	201	HEM	C4B-C3B-C2B	-2.61	104.88	107.28
3	C	201	HEM	CHD-C1D-ND	2.59	127.21	124.42
3	B	201	HEM	CAD-C3D-C2D	-2.57	123.06	127.87
3	A	201	HEM	O2D-CGD-CBD	2.57	122.11	114.00
3	B	201	HEM	CHB-C1B-NB	2.56	127.54	124.37
3	F	201	HEM	C4C-C3C-C2C	-2.53	104.62	106.81
3	T	201	HEM	CMD-C2D-C1D	2.52	128.97	125.03
3	H	201	HEM	CHA-C4D-C3D	-2.50	120.62	125.23
3	F	201	HEM	CHB-C1B-NB	2.50	127.46	124.37
3	D	201	HEM	CHA-C4D-C3D	-2.49	120.64	125.23
3	C	201	HEM	CHB-C1B-NB	2.47	127.42	124.37
3	E	201	HEM	C3D-C4D-ND	2.47	112.88	110.17
3	F	201	HEM	CBD-CAD-C3D	-2.47	105.72	112.53
3	H	201	HEM	C4C-NC-C1C	2.46	109.82	105.82
3	S	201	HEM	CAA-C2A-C1A	2.45	129.73	124.94
3	C	201	HEM	O2A-CGA-CBA	2.45	121.75	114.00
3	D	201	HEM	CHD-C1D-C2D	-2.44	121.17	125.03
3	F	201	HEM	O1D-CGD-CBD	-2.42	115.43	123.09
3	C	201	HEM	C3D-C4D-ND	2.41	112.82	110.17
3	T	201	HEM	CHA-C4D-C3D	-2.40	120.79	125.23
3	T	201	HEM	CAB-C3B-C2B	-2.40	120.64	128.43
3	D	201	HEM	C1A-CHA-C4D	-2.38	120.65	126.25
3	E	201	HEM	CMB-C2B-C3B	-2.36	122.71	128.43
5	F	203	FRU	O5-C5-C6	2.36	115.31	108.89
3	G	201	HEM	C3D-C4D-ND	2.33	112.72	110.17
5	C	203	FRU	O2-C2-C1	-2.32	107.53	111.87
3	C	201	HEM	O2D-CGD-CBD	2.31	121.31	114.00
3	G	201	HEM	C1A-CHA-C4D	-2.31	120.83	126.25
3	B	201	HEM	CHD-C4C-NC	2.31	126.96	124.45
3	A	201	HEM	C4B-C3B-C2B	-2.30	105.16	107.28
3	E	201	HEM	CHD-C4C-C3C	2.28	129.06	125.21
3	B	201	HEM	C4C-NC-C1C	2.27	109.52	105.82
3	B	201	HEM	CHA-C4D-ND	2.25	127.16	124.37
3	B	201	HEM	O2D-CGD-O1D	-2.22	117.63	123.33
3	H	201	HEM	C4B-C3B-C2B	-2.21	105.25	107.28
3	D	201	HEM	C3B-C2B-C1B	2.20	108.07	106.41
3	S	201	HEM	CHB-C1B-NB	2.20	127.09	124.37
5	F	203	FRU	O2-C2-O5	2.20	111.43	109.99
3	E	201	HEM	C4D-C3D-C2D	-2.19	103.70	106.89
3	D	201	HEM	CAD-C3D-C4D	2.19	128.52	124.70
3	E	201	HEM	CHD-C1D-C2D	-2.19	121.58	125.03
6	C	204	GLC	C1-O5-C5	2.18	117.86	113.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	203	FRU	O2-C2-C3	-2.16	104.25	109.58
3	B	201	HEM	CAB-C3B-C2B	-2.16	121.42	128.43
3	B	201	HEM	CHA-C4D-C3D	-2.15	121.26	125.23
3	C	201	HEM	C4B-C3B-C2B	-2.12	105.33	107.28
3	S	201	HEM	CAD-C3D-C4D	2.09	128.33	124.70
3	C	201	HEM	C3B-C4B-NB	-2.08	107.97	109.47
3	D	201	HEM	O2A-CGA-CBA	2.07	120.55	114.00
3	F	201	HEM	CHD-C4C-NC	2.05	126.69	124.45
3	S	201	HEM	O2A-CGA-CBA	2.03	120.42	114.00
3	S	201	HEM	O1D-CGD-CBD	-2.03	116.65	123.09
3	H	201	HEM	O1D-CGD-CBD	-2.03	116.66	123.09
3	F	201	HEM	CHA-C4D-ND	2.02	126.87	124.37
3	T	201	HEM	CAD-C3D-C4D	2.02	128.22	124.70
3	C	201	HEM	CHD-C1D-C2D	-2.02	121.84	125.03
3	C	201	HEM	O2D-CGD-O1D	-2.01	118.17	123.33
3	A	201	HEM	CAD-CBD-CGD	-2.01	108.35	113.67

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	201	HEM	C1A-C2A-CAA-CBA
3	C	201	HEM	C3A-C2A-CAA-CBA
3	E	201	HEM	C1A-C2A-CAA-CBA
3	E	201	HEM	C3A-C2A-CAA-CBA
5	F	203	FRU	O5-C5-C6-O6
5	A	203	FRU	O5-C5-C6-O6
5	A	203	FRU	C4-C5-C6-O6
3	C	201	HEM	C2A-CAA-CBA-CGA
3	E	201	HEM	C2A-CAA-CBA-CGA
5	F	203	FRU	C4-C5-C6-O6
3	E	201	HEM	C4C-C3C-CAC-CBC
3	H	201	HEM	C4B-C3B-CAB-CBB
3	H	201	HEM	C4C-C3C-CAC-CBC
3	T	201	HEM	C4B-C3B-CAB-CBB
3	D	201	HEM	CAD-CBD-CGD-O2D
3	A	201	HEM	CAD-CBD-CGD-O1D
3	S	201	HEM	CAD-CBD-CGD-O1D
3	A	201	HEM	CAD-CBD-CGD-O2D
3	F	201	HEM	CAD-CBD-CGD-O1D
3	T	201	HEM	CAA-CBA-CGA-O1A
3	F	201	HEM	CAD-CBD-CGD-O2D

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Mol	Chain	Res	Type	Atoms
3	S	201	HEM	CAD-CBD-CGD-O2D
3	T	201	HEM	CAA-CBA-CGA-O2A
3	T	201	HEM	CAD-CBD-CGD-O1D
3	G	201	HEM	CAA-CBA-CGA-O1A
3	D	201	HEM	CAD-CBD-CGD-O1D
3	F	201	HEM	CAA-CBA-CGA-O2A
3	T	201	HEM	CAD-CBD-CGD-O2D
3	G	201	HEM	CAA-CBA-CGA-O2A
3	C	201	HEM	CAD-CBD-CGD-O1D
3	B	201	HEM	CAD-CBD-CGD-O1D
3	H	201	HEM	CAD-CBD-CGD-O2D
3	G	201	HEM	CAD-CBD-CGD-O1D
3	G	201	HEM	CAD-CBD-CGD-O2D
3	C	201	HEM	CAA-CBA-CGA-O2A
3	H	201	HEM	CAA-CBA-CGA-O2A
3	F	201	HEM	CAA-CBA-CGA-O1A
3	H	201	HEM	CAD-CBD-CGD-O1D
3	C	201	HEM	CAA-CBA-CGA-O1A
3	H	201	HEM	CAA-CBA-CGA-O1A
3	B	201	HEM	CAD-CBD-CGD-O2D
3	C	201	HEM	CAD-CBD-CGD-O2D

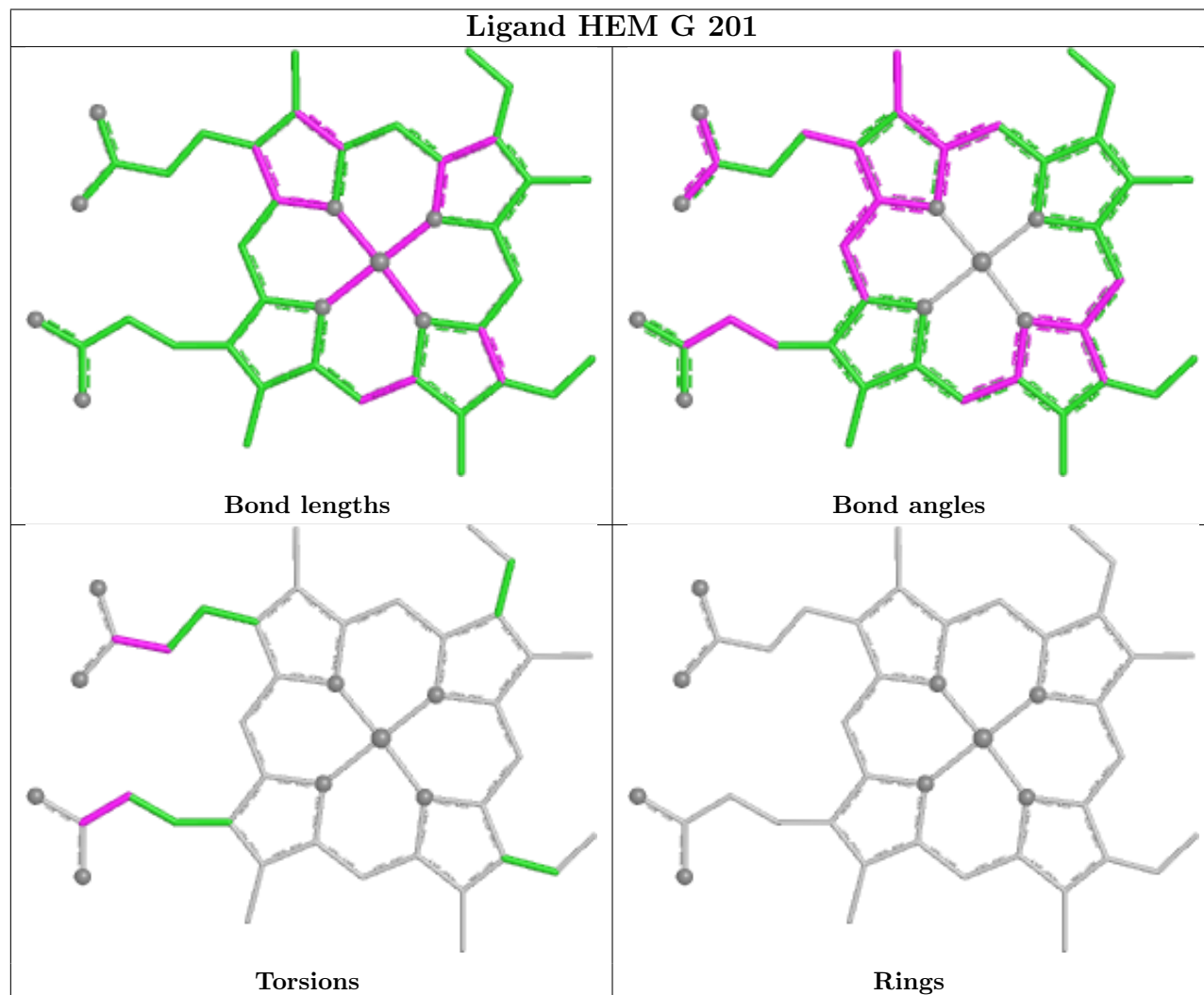
There are no ring outliers.

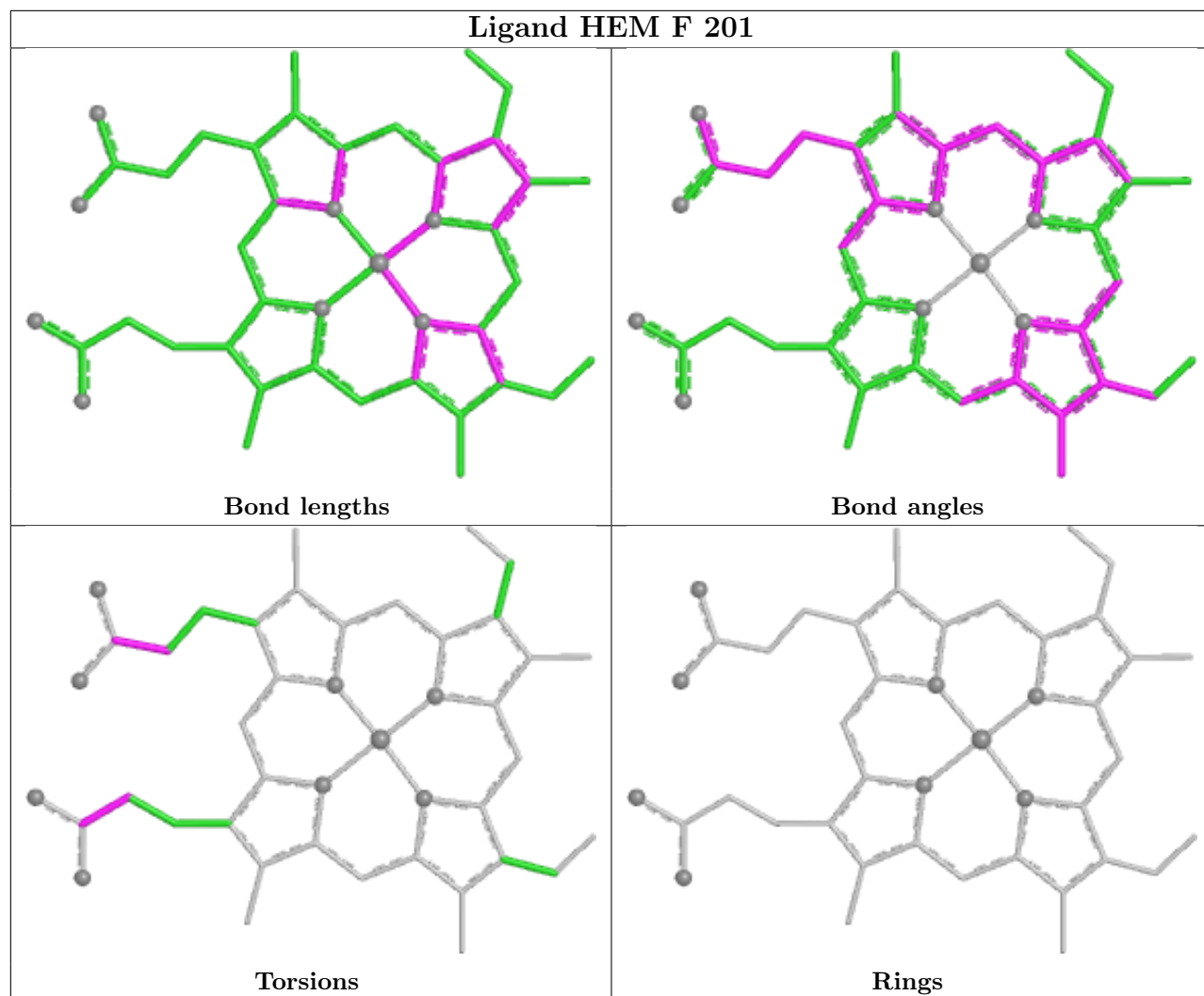
11 monomers are involved in 16 short contacts:

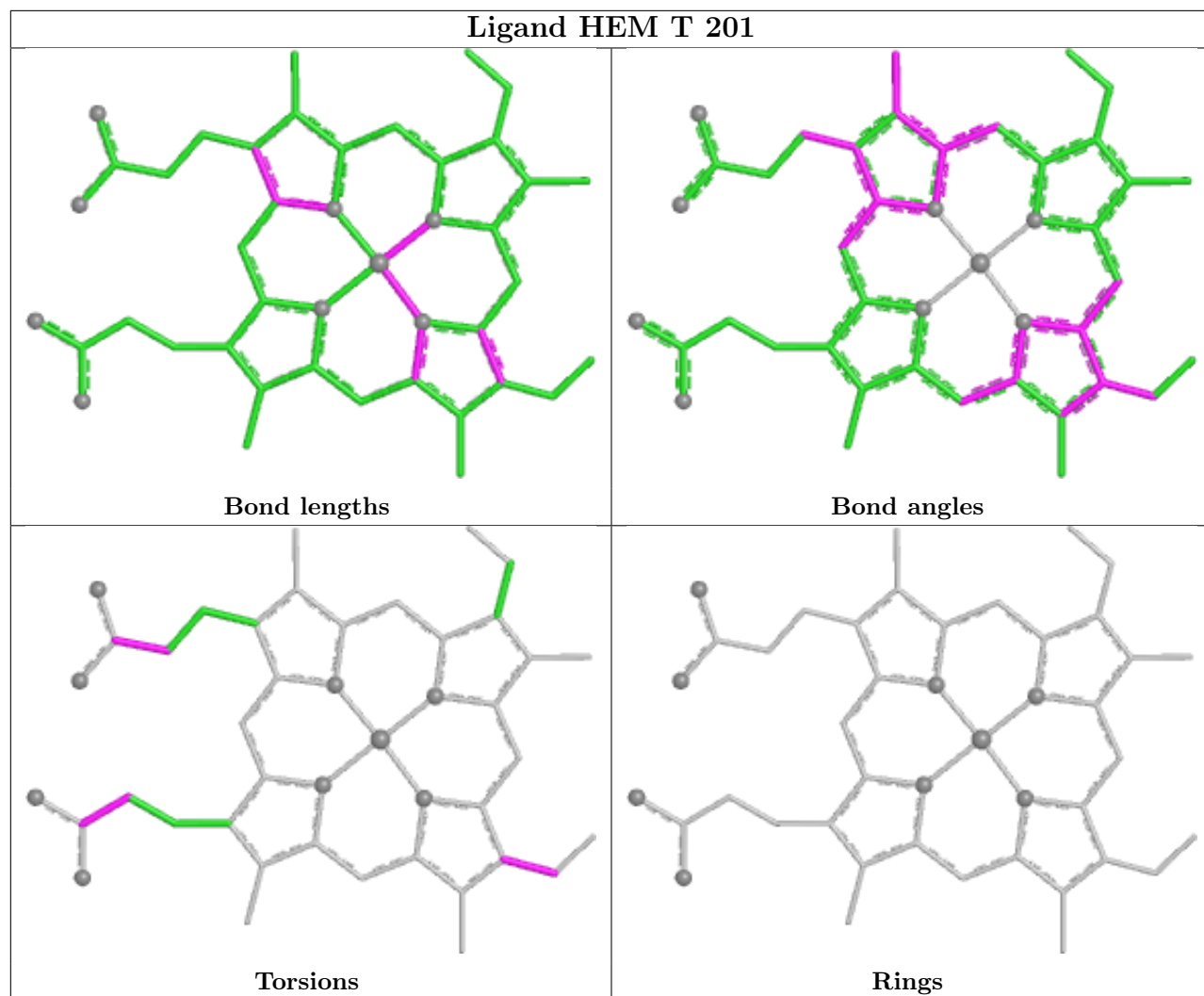
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	201	HEM	2	0
3	T	201	HEM	2	0
5	A	203	FRU	1	0
3	C	201	HEM	1	0
3	H	201	HEM	1	0
5	C	203	FRU	1	0
5	F	203	FRU	2	0
3	D	201	HEM	1	0
3	S	201	HEM	1	0
3	E	201	HEM	3	0
3	B	201	HEM	1	0

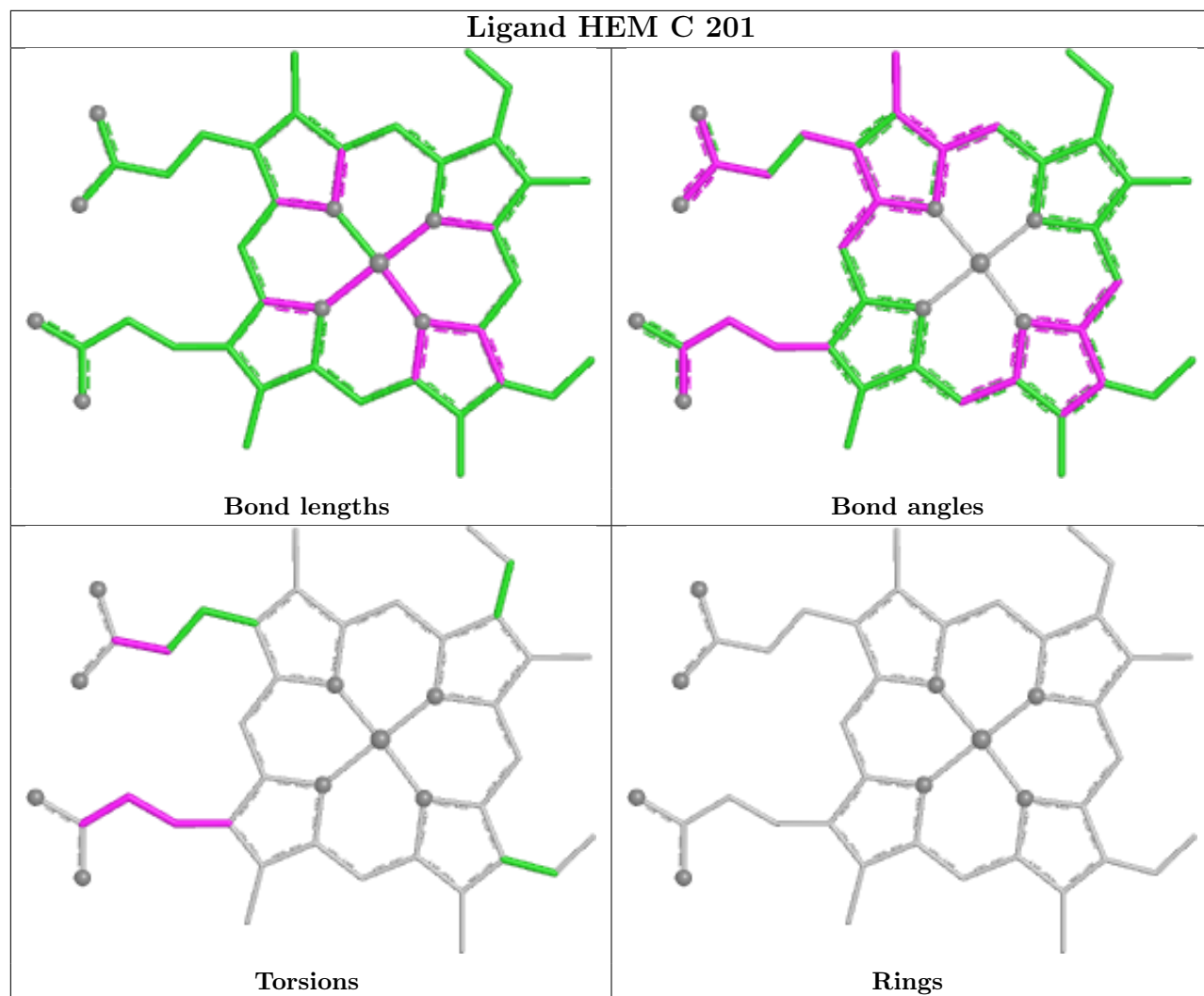
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

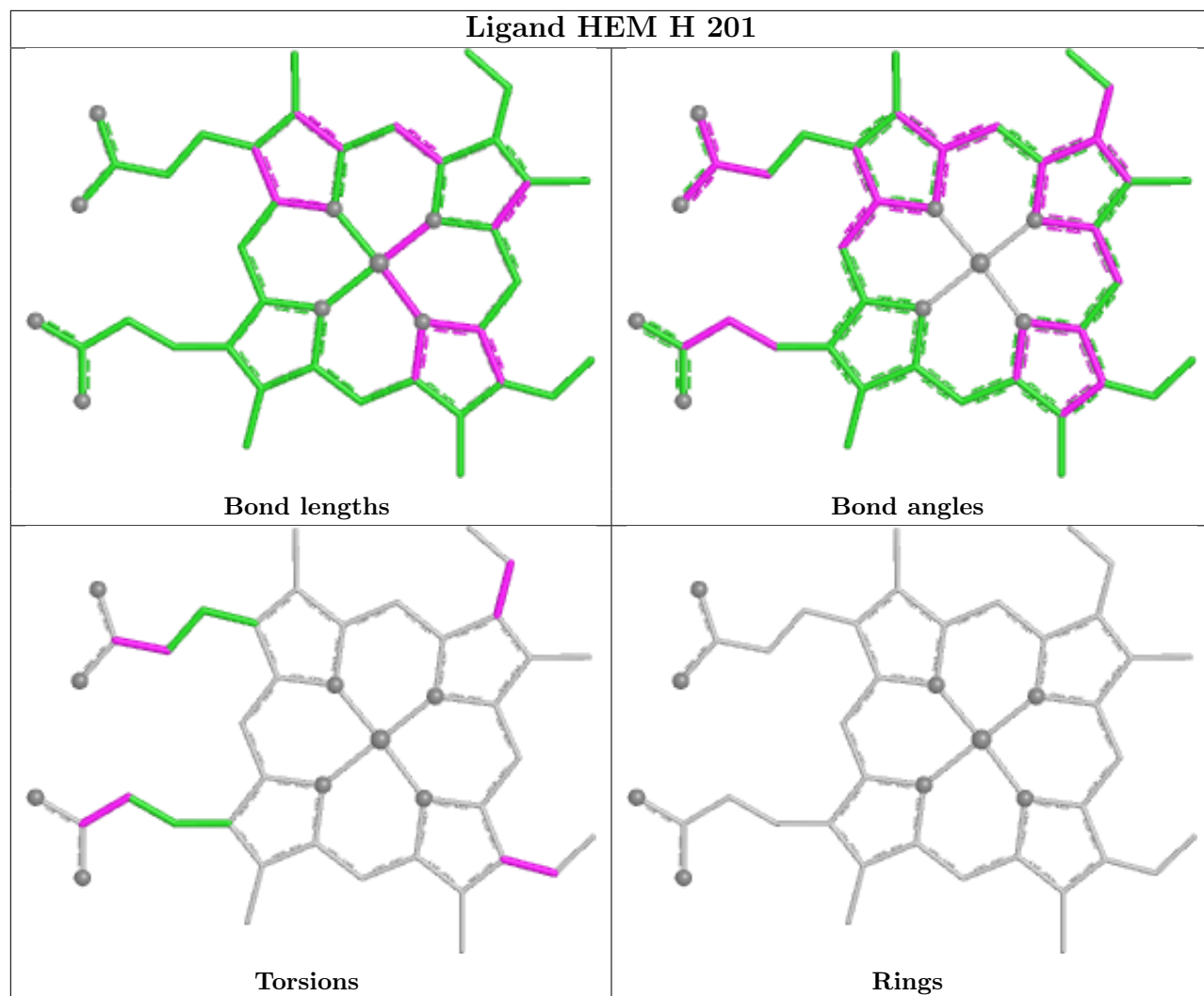
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

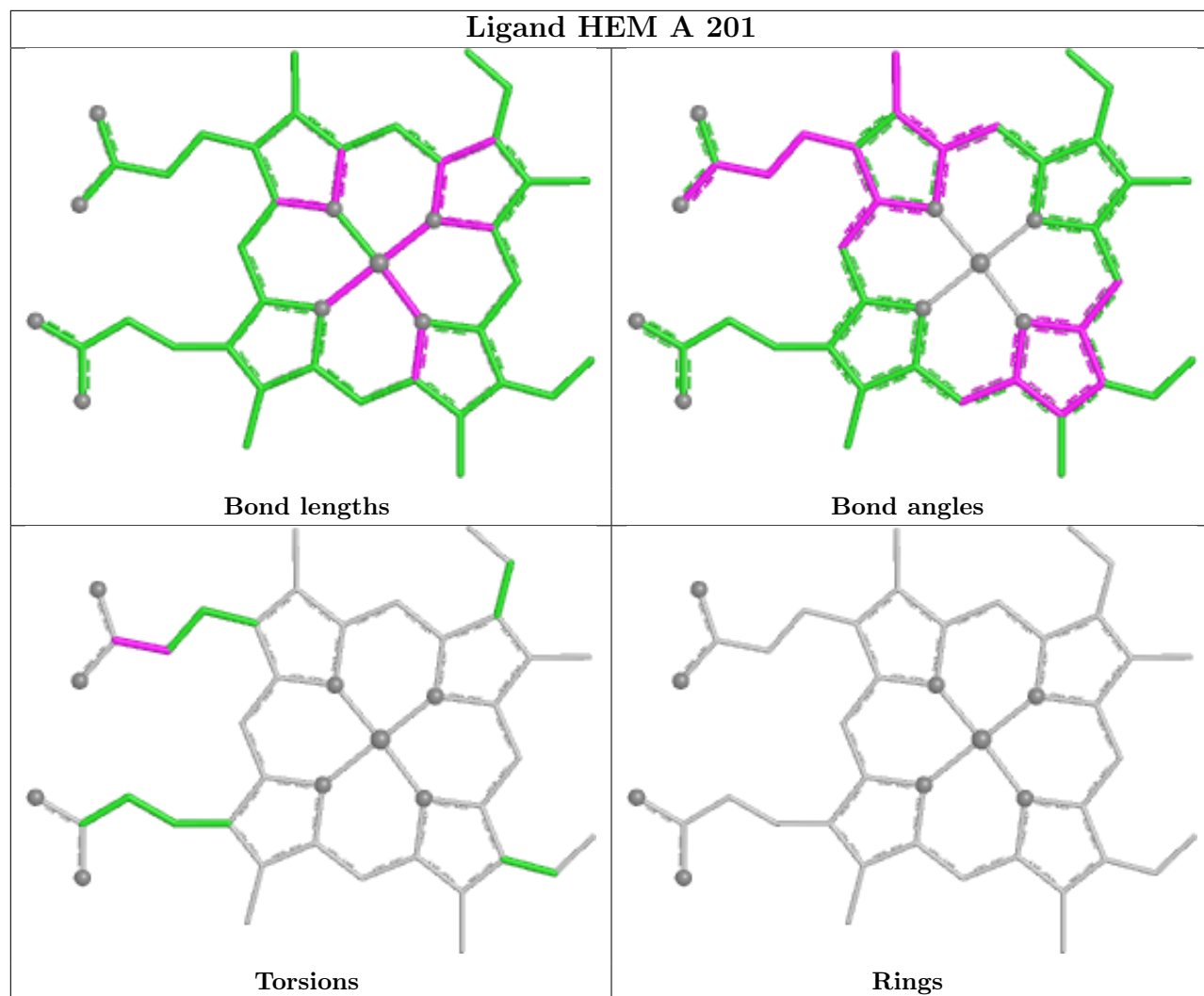


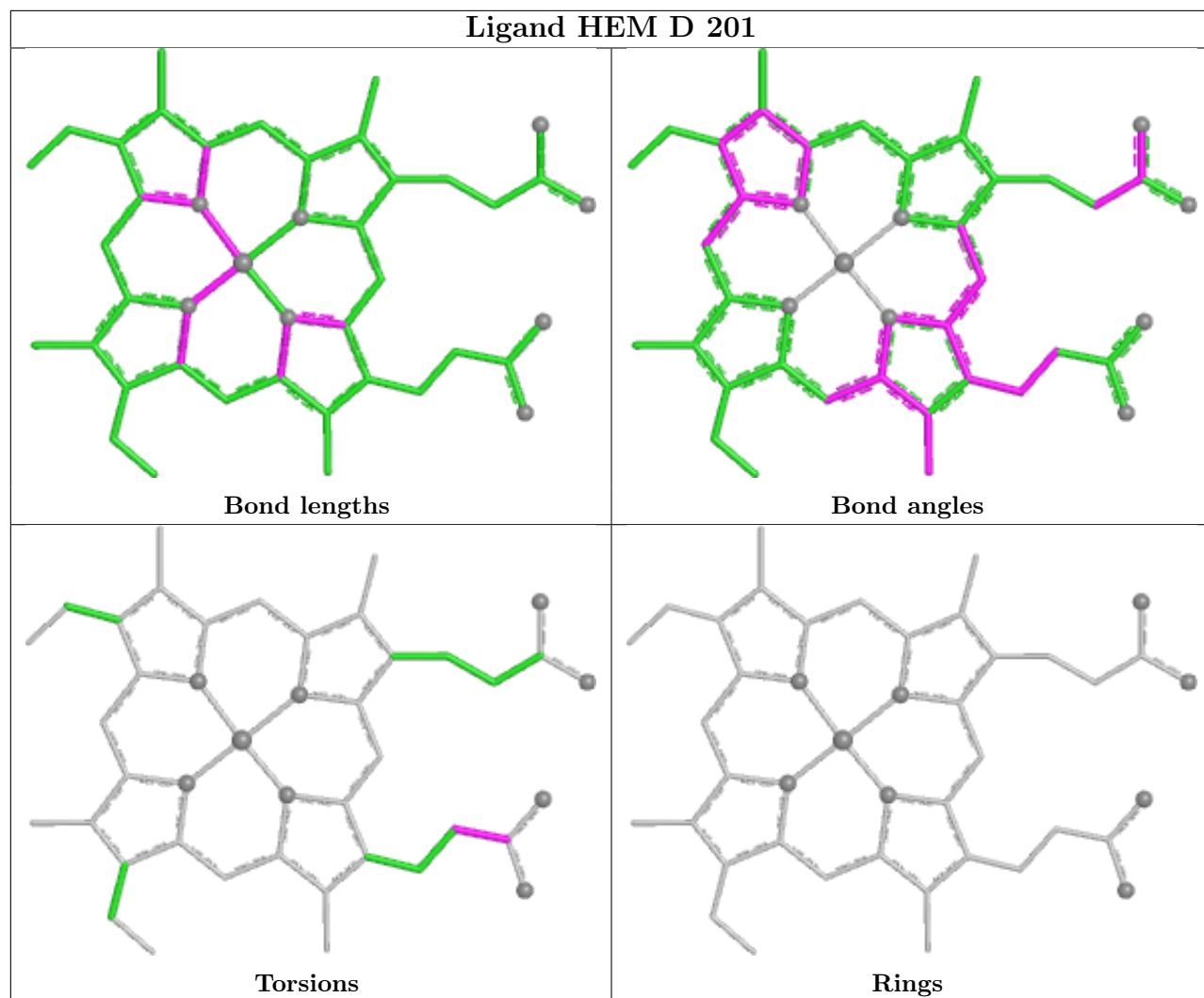


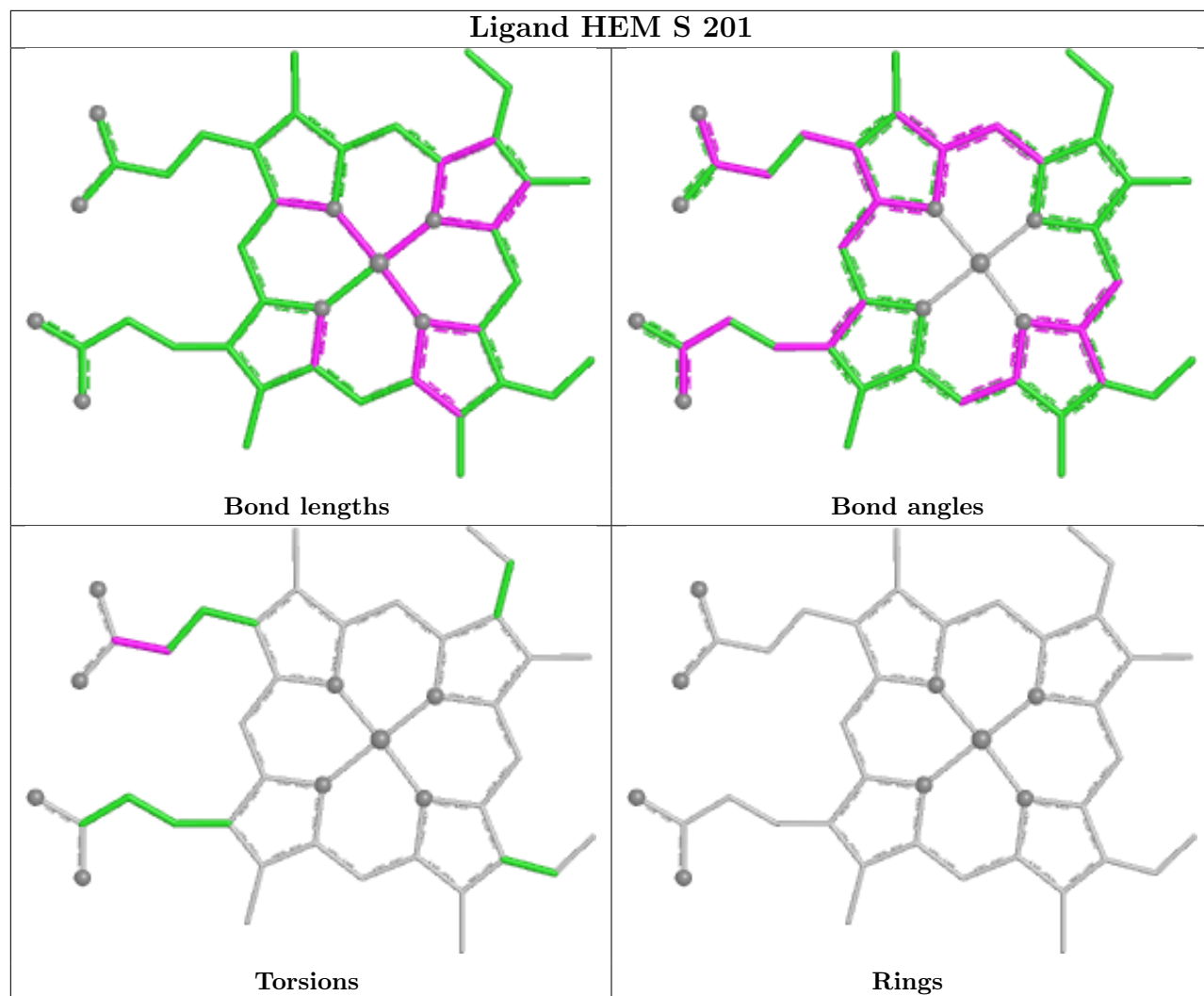


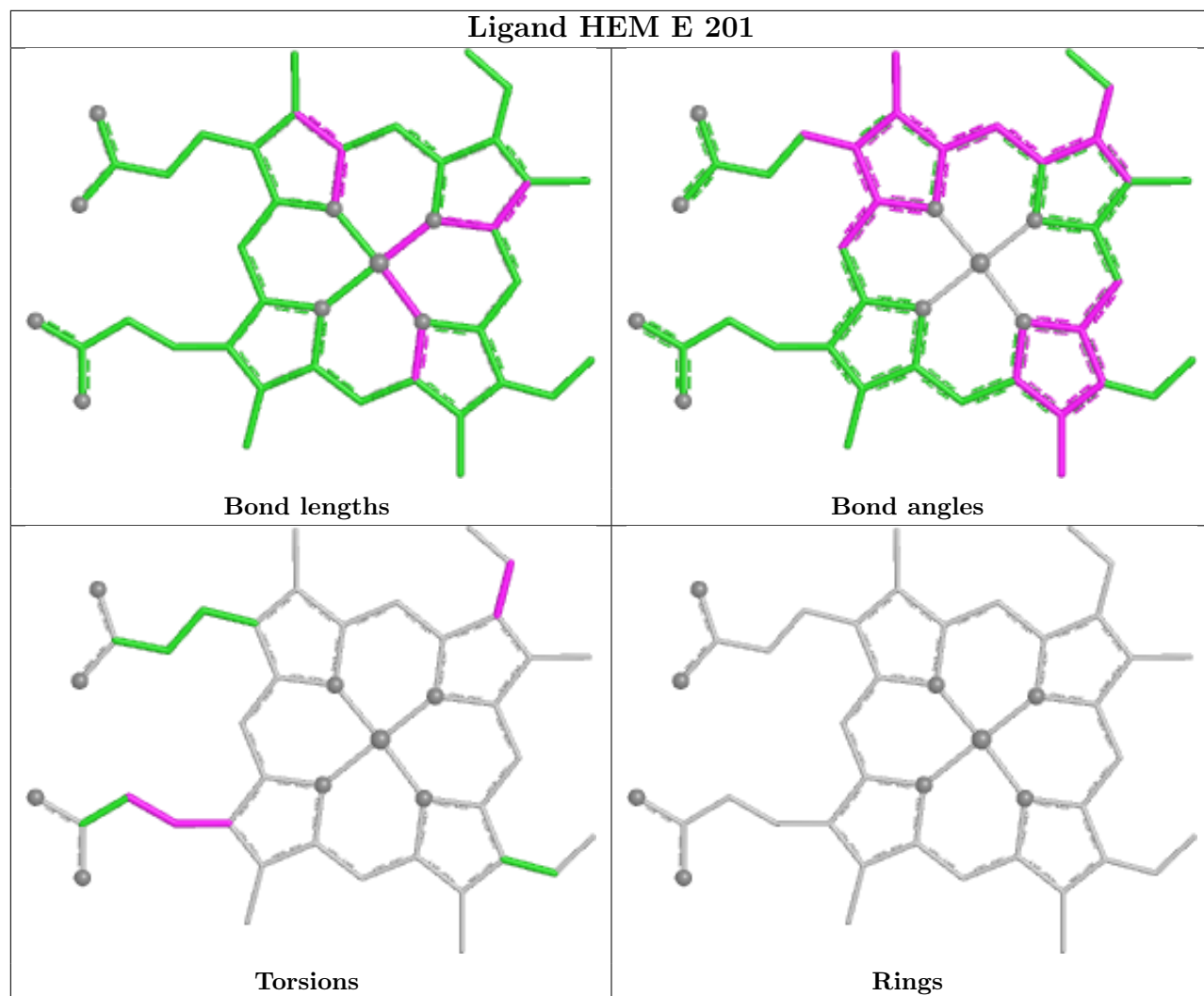


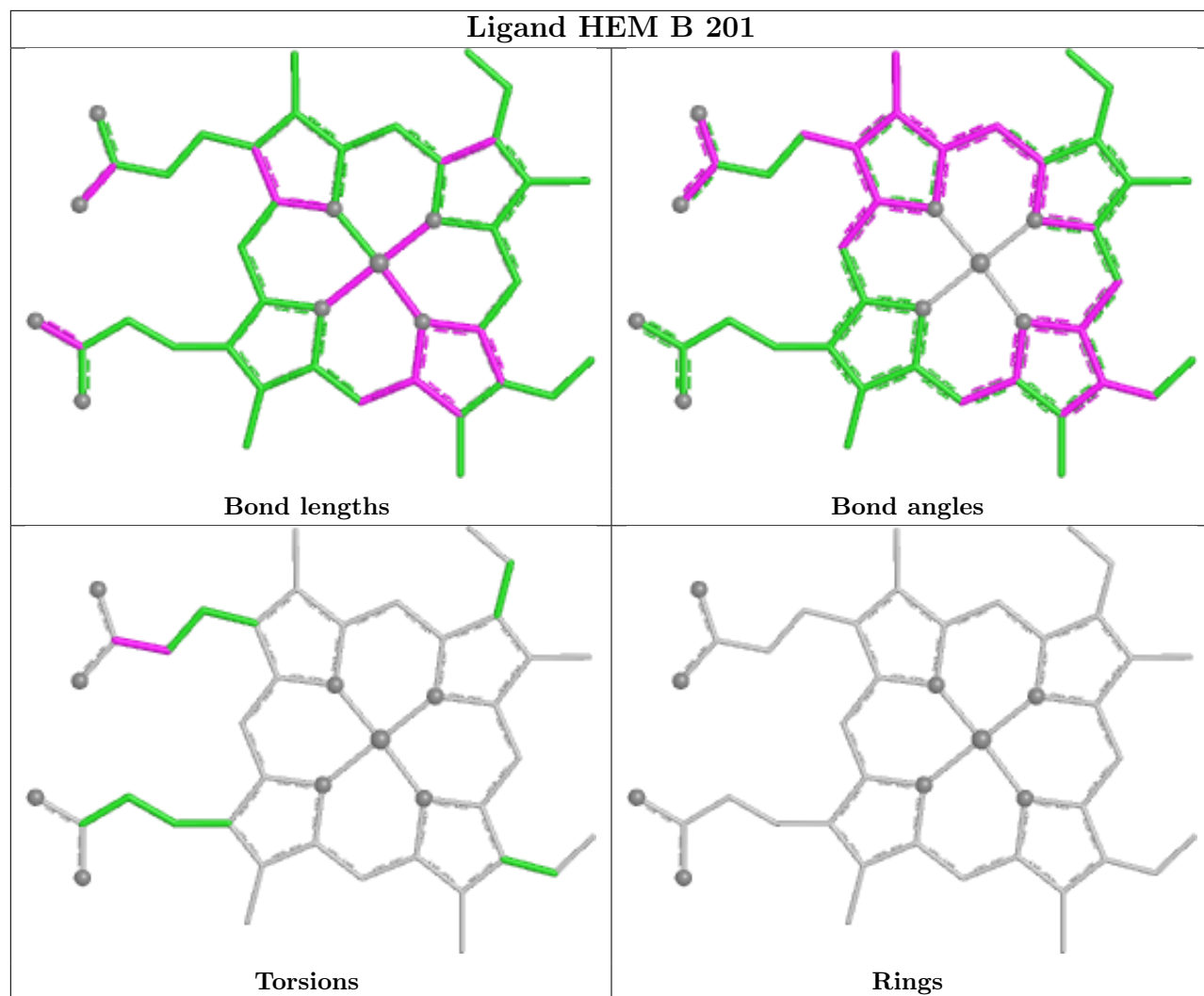












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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%)	0.35	7 (4%) 34 35	39, 70, 99, 119	0
1	C	141/141 (100%)	0.57	7 (4%) 34 35	36, 77, 119, 139	0
1	E	137/141 (97%)	3.17	114 (83%) 0 0	89, 209, 324, 372	0
1	G	138/141 (97%)	1.32	35 (25%) 1 2	47, 109, 194, 234	0
1	S	141/141 (100%)	1.64	48 (34%) 1 1	61, 116, 178, 193	0
2	B	146/146 (100%)	0.07	1 (0%) 84 85	28, 61, 109, 132	0
2	D	146/146 (100%)	0.52	9 (6%) 26 28	40, 80, 116, 137	0
2	F	146/146 (100%)	0.95	23 (15%) 5 5	35, 90, 185, 232	0
2	H	146/146 (100%)	2.10	70 (47%) 0 0	65, 155, 240, 273	0
2	T	146/146 (100%)	1.96	70 (47%) 0 0	69, 150, 211, 241	0
All	All	1428/1435 (99%)	1.26	384 (26%) 1 1	28, 98, 232, 372	0

All (384) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	T	16	GLY	6.8
1	E	59	GLY	6.0
1	E	132	VAL	5.9
1	E	84	SER	5.9
1	E	71	ALA	5.7
2	H	48	LEU	5.6
1	E	85	ASP	5.3
2	H	49	SER	5.3
2	H	16	GLY	5.3
2	T	46	GLY	5.2
2	H	58	PRO	5.2
1	E	48	LEU	5.2
1	E	79	ALA	5.2

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Mol	Chain	Res	Type	RSRZ
1	E	67	THR	5.1
1	E	63	ALA	5.1
1	E	82	ALA	5.1
1	E	57	GLY	5.1
1	E	108	THR	5.0
1	E	21	ALA	5.0
2	H	92	HIS	5.0
1	E	86	LEU	5.0
1	E	26	ALA	4.9
2	H	25	GLY	4.8
2	H	64	GLY	4.8
1	E	46	PHE	4.8
2	D	9	SER	4.8
2	H	32	LEU	4.7
2	H	46	GLY	4.6
1	S	115	ALA	4.6
1	E	53	ALA	4.6
1	E	88	ALA	4.6
2	H	62	ALA	4.6
1	E	47	ASP	4.6
2	H	21	ASP	4.5
2	F	50	THR	4.5
1	E	135	VAL	4.5
1	G	5	ALA	4.5
1	E	65	ALA	4.4
1	E	74	ASP	4.4
1	S	79	ALA	4.4
2	T	84	THR	4.4
1	G	3	SER	4.4
1	E	13	ALA	4.3
1	E	3	SER	4.3
2	T	44	SER	4.2
1	E	128	PHE	4.2
1	E	4	PRO	4.2
1	E	137	THR	4.1
1	E	93	VAL	4.1
1	E	68	ASN	4.1
1	E	62	VAL	4.1
1	E	121	VAL	4.1
1	S	82	ALA	4.1
1	E	41	THR	4.1
1	E	138	SER	4.0

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Mol	Chain	Res	Type	RSRZ
1	G	123	ALA	4.0
1	E	25	GLY	4.0
1	E	134	THR	4.0
1	E	43	PHE	4.0
1	C	71	ALA	4.0
1	E	54	GLN	4.0
1	G	69	ALA	4.0
2	T	142	ALA	4.0
2	T	21	ASP	4.0
2	F	49	SER	4.0
1	E	80	LEU	3.9
1	E	51	GLY	3.9
2	T	53	ALA	3.9
1	S	73	VAL	3.9
2	F	20	VAL	3.9
1	A	82	ALA	3.9
1	E	87	HIS	3.9
1	E	136	LEU	3.9
2	H	42	PHE	3.8
1	E	22	GLY	3.8
1	E	72	HIS	3.8
1	G	79	ALA	3.8
2	T	94	ASP	3.8
1	A	51	GLY	3.8
2	T	146	HIS	3.8
1	S	5	ALA	3.8
1	S	12	ALA	3.8
2	F	53	ALA	3.8
1	E	49	SER	3.8
2	H	45	PHE	3.7
1	E	24	TYR	3.7
1	S	54	GLN	3.7
2	T	79	ASP	3.7
1	S	110	ALA	3.7
2	D	16	GLY	3.7
1	E	76	MET	3.7
1	E	38	THR	3.7
2	H	36	PRO	3.7
1	G	81	SER	3.7
1	S	53	ALA	3.6
2	H	53	ALA	3.6
1	E	94	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
2	H	41	PHE	3.6
2	H	19	ASN	3.6
1	E	89	HIS	3.6
2	H	50	THR	3.6
1	S	57	GLY	3.5
1	C	115	ALA	3.5
1	E	110	ALA	3.5
1	S	71	ALA	3.5
2	H	55	MET	3.5
1	E	114	PRO	3.5
2	T	72	SER	3.5
1	G	119	PRO	3.5
1	E	55	VAL	3.5
2	D	13	ALA	3.5
2	T	93	CYS	3.5
1	S	46	PHE	3.5
1	E	19	ALA	3.4
1	G	71	ALA	3.4
1	E	91	LEU	3.4
1	E	69	ALA	3.4
2	H	56	GLY	3.4
2	T	83	GLY	3.4
2	H	15	TRP	3.4
2	H	96	LEU	3.3
2	T	68	LEU	3.3
1	E	90	LYS	3.3
2	F	56	GLY	3.3
2	T	56	GLY	3.3
1	G	78	ASN	3.3
1	E	44	PRO	3.3
1	G	77	PRO	3.3
2	T	91	LEU	3.3
1	E	20	HIS	3.3
1	E	118	THR	3.3
2	T	45	PHE	3.3
1	E	124	SER	3.3
1	E	52	SER	3.3
1	E	64	ASP	3.2
1	E	73	VAL	3.2
2	F	19	ASN	3.2
1	E	45	HIS	3.2
1	S	134	THR	3.2

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Mol	Chain	Res	Type	RSRZ
2	D	4	THR	3.2
2	T	87	THR	3.2
1	G	70	VAL	3.2
1	S	140	TYR	3.2
1	S	4	PRO	3.2
2	F	51	PRO	3.2
2	H	88	LEU	3.2
2	T	58	PRO	3.2
2	T	29	GLY	3.1
1	S	8	THR	3.1
2	T	25	GLY	3.1
1	E	5	ALA	3.1
2	T	129	ALA	3.1
2	H	98	VAL	3.1
1	S	52	SER	3.1
2	H	63	HIS	3.1
2	H	77	HIS	3.1
1	S	74	ASP	3.1
2	T	57	ASN	3.1
1	G	82	ALA	3.1
2	T	13	ALA	3.1
1	E	17	VAL	3.1
2	T	18	VAL	3.1
2	H	5	PRO	3.1
2	H	84	THR	3.1
2	H	20	VAL	3.1
2	H	54	VAL	3.1
2	T	67	VAL	3.1
2	H	89	SER	3.0
1	E	6	ASP	3.0
2	H	47	ASP	3.0
1	E	28	ALA	3.0
2	H	70	ALA	3.0
2	T	62	ALA	3.0
1	E	95	PRO	3.0
1	E	29	LEU	3.0
1	E	77	PRO	3.0
1	E	58	HIS	3.0
1	G	8	THR	3.0
2	F	4	THR	3.0
2	H	44	SER	3.0
1	E	66	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
2	F	60	VAL	3.0
1	E	8	THR	3.0
1	E	131	SER	3.0
2	H	72	SER	3.0
2	T	49	SER	3.0
2	T	76	ALA	2.9
1	E	9	ASN	2.9
1	E	15	GLY	2.9
1	E	10	VAL	2.9
1	G	6	ASP	2.9
1	E	23	GLU	2.9
1	S	81	SER	2.9
2	D	73	ASP	2.9
2	H	29	GLY	2.9
2	F	62	ALA	2.9
2	T	140	ALA	2.9
2	H	37	TRP	2.9
2	H	90	GLU	2.9
2	H	57	ASN	2.9
1	E	16	LYS	2.8
1	G	84	SER	2.8
1	E	14	TRP	2.8
2	D	5	PRO	2.8
1	E	33	PHE	2.8
1	G	12	ALA	2.8
2	H	10	ALA	2.8
2	H	22	GLU	2.8
1	E	70	VAL	2.8
2	H	93	CYS	2.8
1	S	68	ASN	2.8
1	E	81	SER	2.8
2	F	46	GLY	2.8
2	H	38	THR	2.8
2	T	2	HIS	2.8
2	T	9	SER	2.8
1	E	83	LEU	2.8
2	H	142	ALA	2.8
1	G	138	SER	2.7
1	G	4	PRO	2.7
2	T	65	LYS	2.7
1	G	120	ALA	2.7
2	B	13	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	75	ASP	2.7
1	E	101	LEU	2.7
1	A	12	ALA	2.7
2	H	13	ALA	2.7
1	S	75	ASP	2.7
1	E	60	LYS	2.7
2	T	55	MET	2.7
2	H	91	LEU	2.7
2	T	141	LEU	2.7
1	E	12	ALA	2.7
1	E	111	ALA	2.7
1	E	123	ALA	2.7
1	E	130	ALA	2.7
1	S	65	ALA	2.7
1	E	119	PRO	2.7
2	T	63	HIS	2.6
2	F	47	ASP	2.6
1	G	134	THR	2.6
2	H	117	HIS	2.6
1	S	14	TRP	2.6
2	T	19	ASN	2.6
2	T	85	PHE	2.6
1	G	57	GLY	2.6
1	S	18	GLY	2.6
1	S	34	LEU	2.6
2	H	24	GLY	2.6
1	E	115	ALA	2.6
2	H	139	ASN	2.6
2	H	69	GLY	2.6
1	E	113	LEU	2.5
1	G	130	ALA	2.5
2	T	54	VAL	2.5
2	T	48	LEU	2.5
1	A	75	ASP	2.5
1	E	120	ALA	2.5
1	S	111	ALA	2.5
2	H	51	PRO	2.5
2	T	59	LYS	2.5
2	T	95	LYS	2.5
1	E	133	SER	2.5
1	E	42	TYR	2.5
1	S	86	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
2	T	78	LEU	2.5
2	F	52	ASP	2.5
1	G	89	HIS	2.5
2	H	146	HIS	2.5
2	T	64	GLY	2.5
2	H	87	THR	2.5
1	C	3	SER	2.5
2	T	98	VAL	2.5
2	T	81	LEU	2.5
2	T	17	LYS	2.5
1	G	75	ASP	2.5
1	E	50	HIS	2.5
1	G	88	ALA	2.5
2	T	27	ALA	2.5
1	S	114	PRO	2.5
2	F	29	GLY	2.5
1	E	109	LEU	2.4
2	F	21	ASP	2.4
1	E	18	GLY	2.4
2	F	25	GLY	2.4
2	H	33	VAL	2.4
2	T	42	PHE	2.4
1	S	63	ALA	2.4
1	S	69	ALA	2.4
2	H	83	GLY	2.4
1	G	124	SER	2.4
1	E	125	LEU	2.4
2	D	80	ASN	2.4
2	F	57	ASN	2.4
2	T	24	GLY	2.4
1	E	96	VAL	2.4
2	T	20	VAL	2.4
1	G	18	GLY	2.3
1	S	67	THR	2.3
1	S	121	VAL	2.3
2	T	92	HIS	2.3
2	H	52	ASP	2.3
1	G	131	SER	2.3
1	S	141	ARG	2.3
2	T	40	ARG	2.3
1	S	89	HIS	2.3
2	T	117	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	98	PHE	2.3
2	T	5	PRO	2.3
2	T	77	HIS	2.3
2	D	6	GLU	2.3
1	A	73	VAL	2.3
2	F	34	VAL	2.3
1	C	5	ALA	2.3
2	D	12	THR	2.3
1	E	78	ASN	2.2
1	E	122	HIS	2.2
1	G	115	ALA	2.2
2	H	140	ALA	2.2
1	E	102	SER	2.2
2	F	48	LEU	2.2
2	T	96	LEU	2.2
2	H	102	ASN	2.2
1	S	119	PRO	2.2
2	F	55	MET	2.2
1	S	59	GLY	2.2
2	H	97	HIS	2.2
1	G	118	THR	2.2
2	T	145	TYR	2.2
2	H	68	LEU	2.2
2	H	40	ARG	2.2
2	H	94	ASP	2.2
2	T	99	ASP	2.2
1	S	44	PRO	2.2
2	F	58	PRO	2.2
1	E	11	LYS	2.2
1	G	72	HIS	2.2
1	G	19	ALA	2.2
2	H	9	SER	2.2
2	T	32	LEU	2.2
2	H	95	LYS	2.2
2	T	136	GLY	2.2
1	S	118	THR	2.2
1	S	123	ALA	2.2
1	S	91	LEU	2.1
2	T	15	TRP	2.1
1	C	16	LYS	2.1
2	H	59	LYS	2.1
2	H	135	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
2	T	4	THR	2.1
2	T	50	THR	2.1
1	E	61	LYS	2.1
2	H	141	LEU	2.1
2	T	28	LEU	2.1
2	T	88	LEU	2.1
1	G	74	ASP	2.1
1	S	85	ASP	2.1
2	T	80	ASN	2.1
1	S	45	HIS	2.1
2	T	60	VAL	2.1
1	E	129	LEU	2.1
1	S	15	GLY	2.1
1	A	52	SER	2.1
2	T	123	THR	2.1
1	S	19	ALA	2.1
1	S	90	LYS	2.1
1	A	85	ASP	2.1
1	E	97	ASN	2.1
1	E	112	HIS	2.1
1	S	64	ASP	2.1
2	H	80	ASN	2.1
1	C	19	ALA	2.0
1	C	65	ALA	2.0
1	S	120	ALA	2.0
2	F	116	HIS	2.0
1	S	55	VAL	2.0
2	T	126	VAL	2.0
1	E	139	LYS	2.0
1	G	65	ALA	2.0
2	F	76	ALA	2.0
2	H	76	ALA	2.0
2	H	86	ALA	2.0
1	G	85	ASP	2.0
1	E	56	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

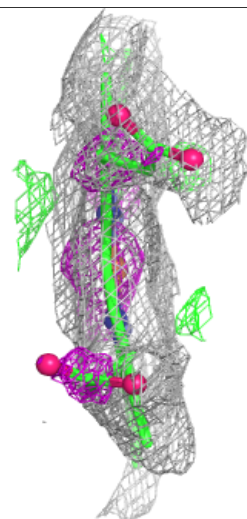
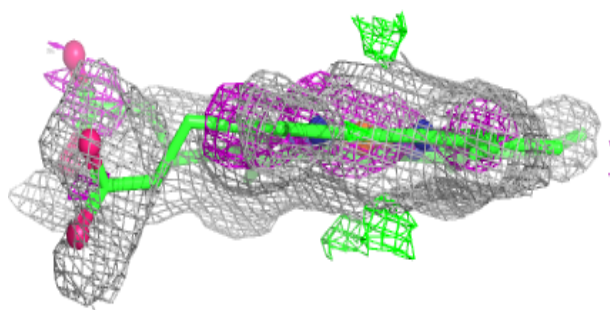
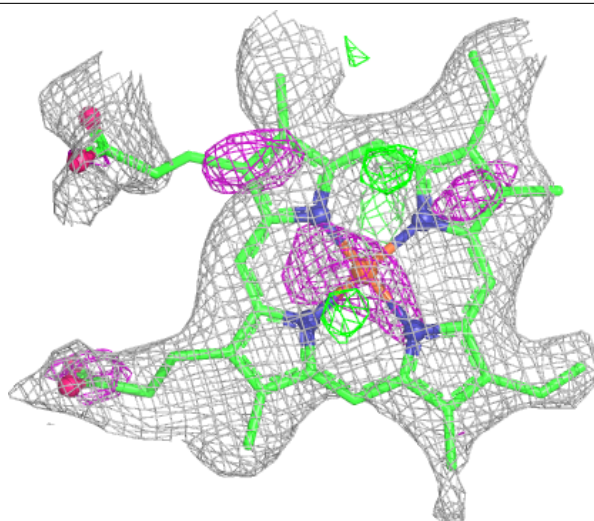
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
5	FRU	F	203	11/12	0.49	0.13	99,107,119,123	0
6	GLC	C	204	12/12	0.69	0.13	47,56,60,62	0
5	FRU	A	203	11/12	0.79	0.12	77,89,100,105	0
3	HEM	H	201	43/43	0.80	0.12	52,71,99,110	0
5	FRU	C	203	11/12	0.84	0.12	79,83,95,115	0
3	HEM	E	201	43/43	0.85	0.11	52,64,87,92	0
4	OXY	G	202	2/2	0.85	0.36	80,80,80,117	0
3	HEM	T	201	43/43	0.86	0.13	71,98,114,124	0
4	OXY	D	202	2/2	0.89	0.21	44,44,44,76	0
4	OXY	A	202	2/2	0.90	0.30	46,46,46,72	0
4	OXY	C	202	2/2	0.91	0.28	45,45,45,71	0
4	OXY	T	202	2/2	0.92	0.20	56,56,56,84	0
4	OXY	S	202	2/2	0.93	0.23	63,63,63,88	0
3	HEM	S	201	43/43	0.93	0.08	33,45,66,70	0
3	HEM	G	201	43/43	0.93	0.09	33,48,79,84	0
4	OXY	F	202	2/2	0.95	0.19	78,78,78,81	0
3	HEM	A	201	43/43	0.95	0.09	30,40,53,59	0
3	HEM	F	201	43/43	0.95	0.08	28,35,60,71	0
3	HEM	D	201	43/43	0.95	0.08	36,47,66,70	0
3	HEM	B	201	43/43	0.96	0.08	23,28,44,55	0
3	HEM	C	201	43/43	0.96	0.07	23,39,82,100	0
4	OXY	B	202	2/2	0.97	0.21	35,35,35,56	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.

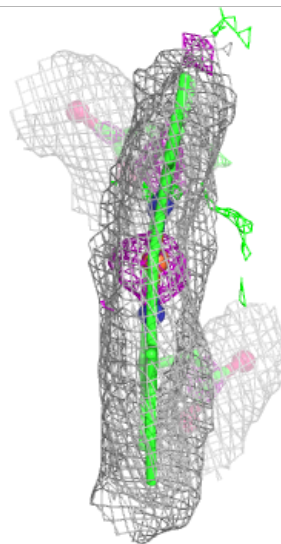
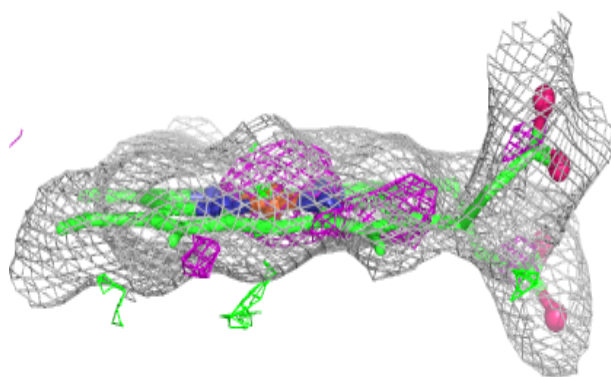
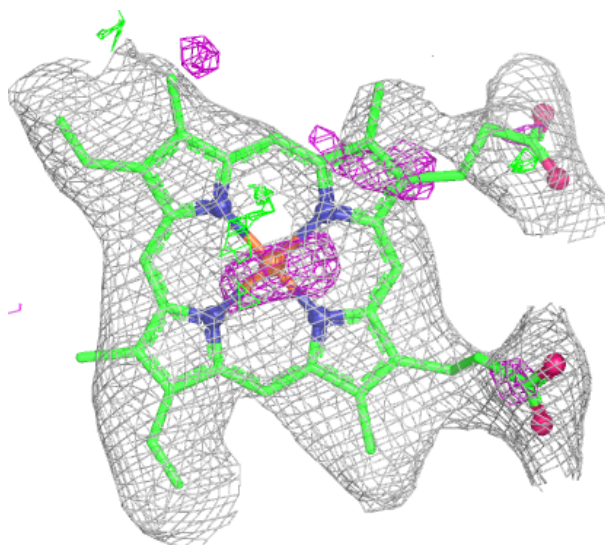
Electron density around HEM H 201:

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



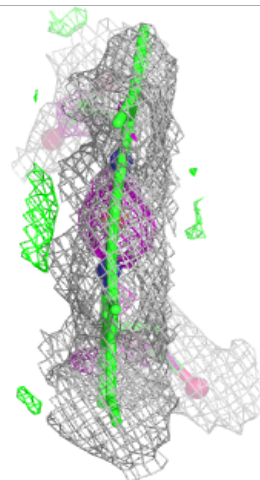
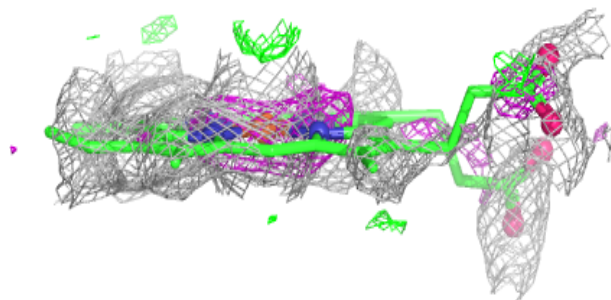
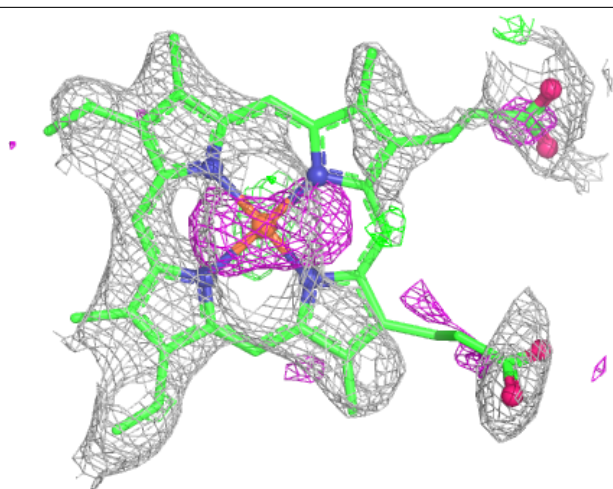
Electron density around HEM E 201:

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



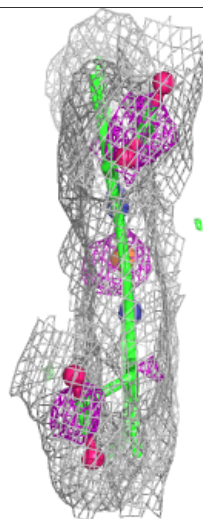
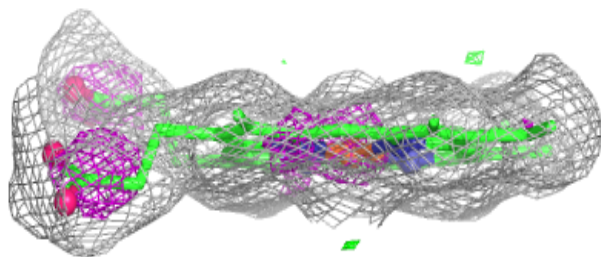
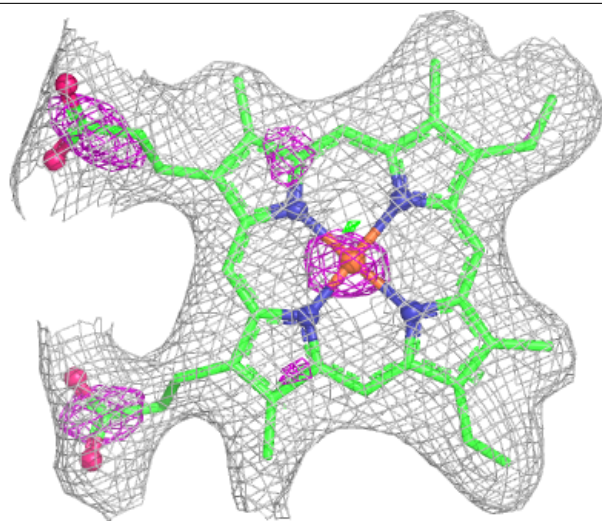
Electron density around HEM T 201:

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



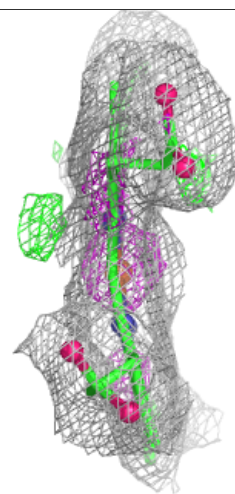
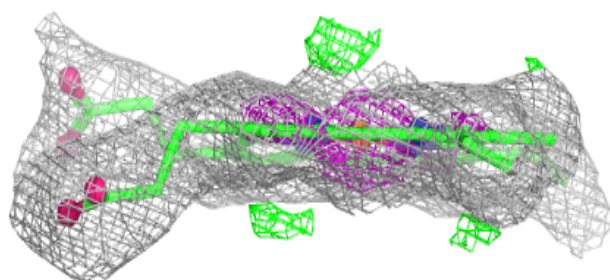
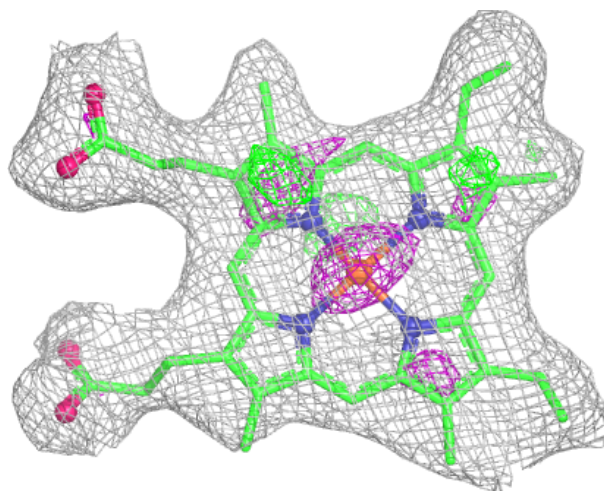
Electron density around HEM S 201:

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



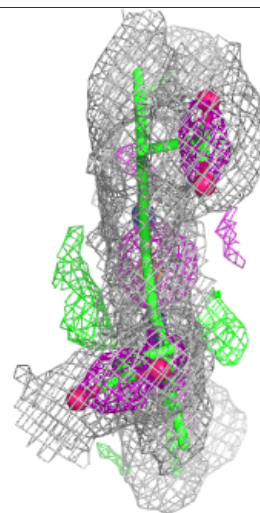
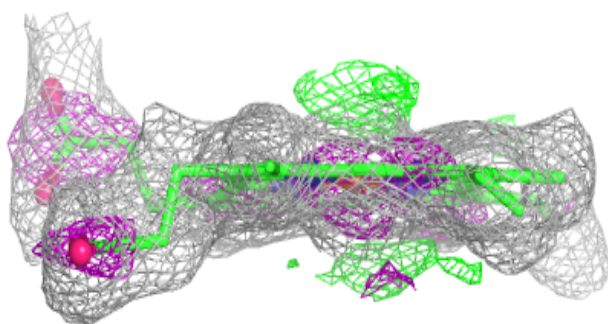
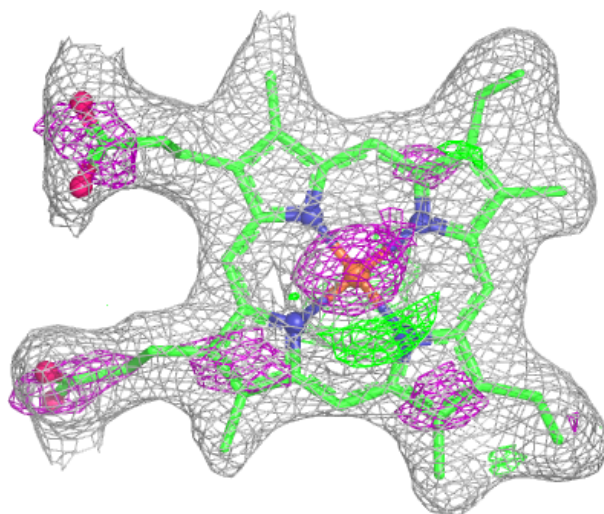
Electron density around HEM G 201:

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



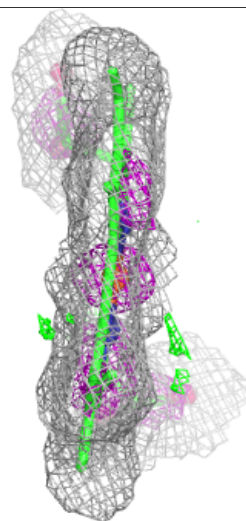
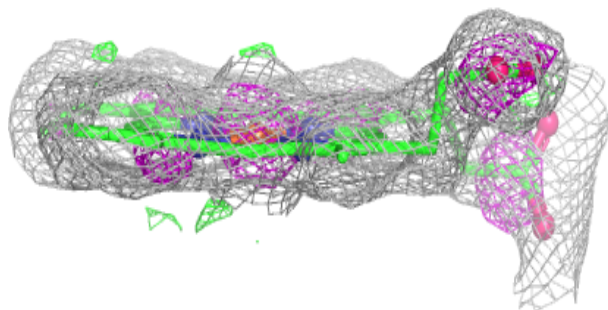
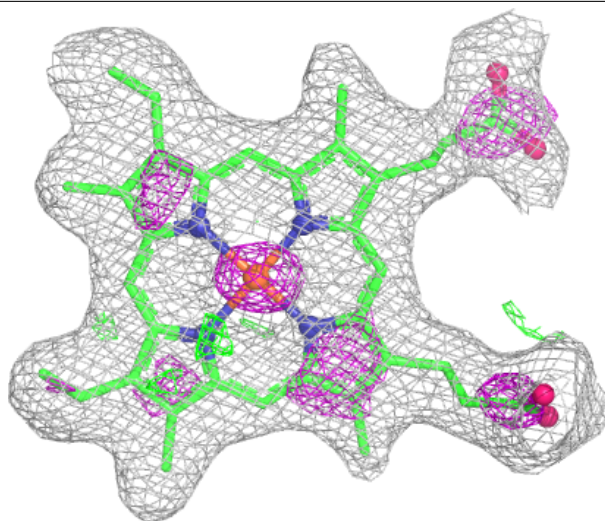
Electron density around HEM A 201:

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



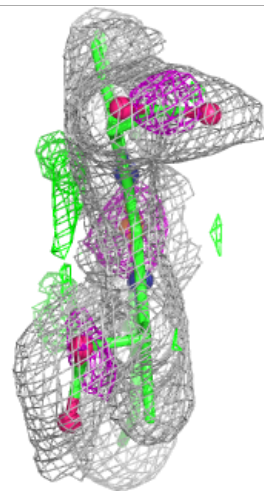
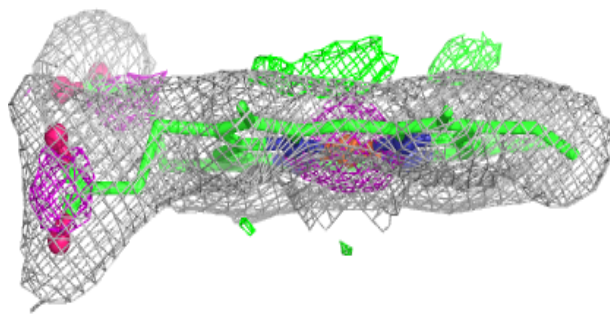
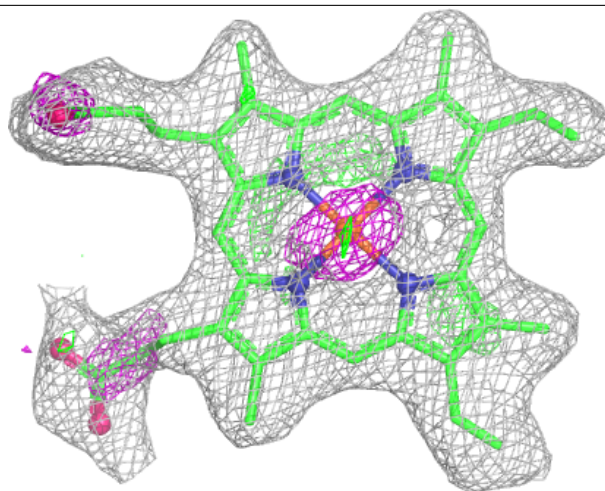
Electron density around HEM F 201:

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



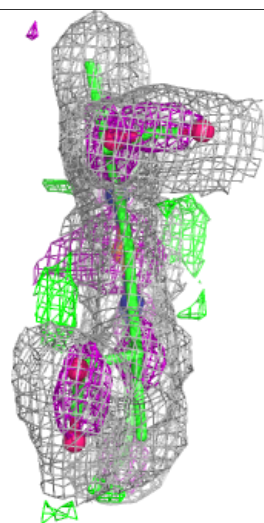
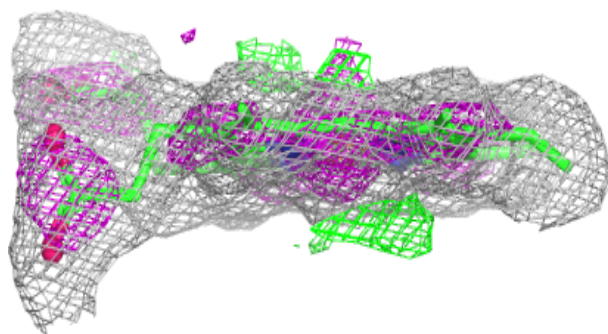
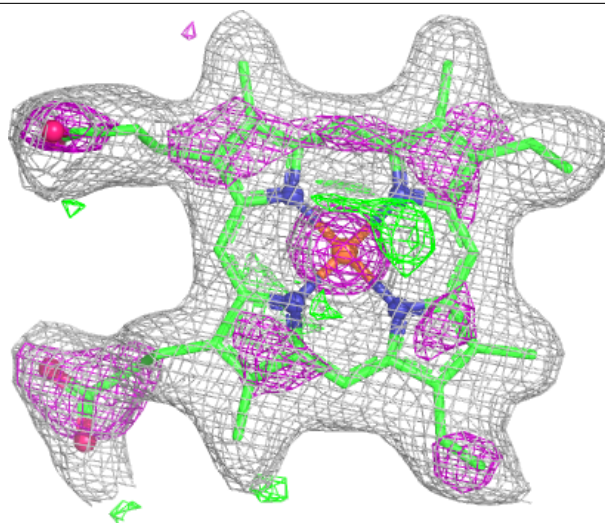
Electron density around HEM D 201:

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



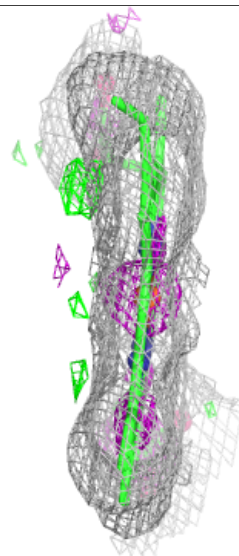
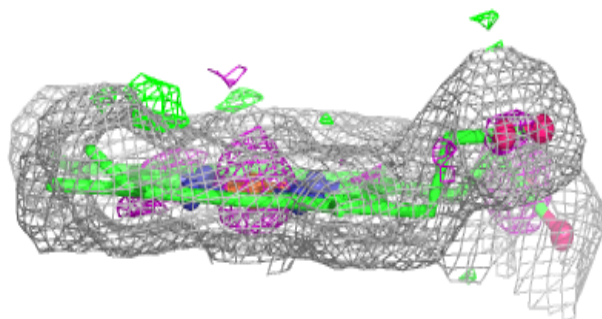
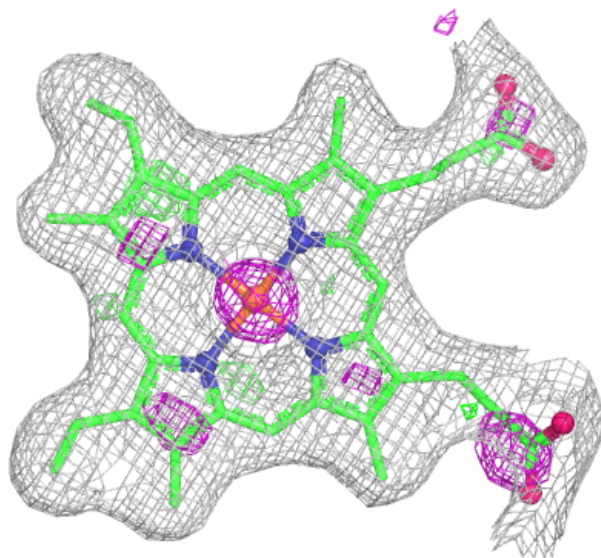
Electron density around HEM B 201:

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



Electron density around HEM C 201:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.