



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 05:26 AM UTC

PDB ID : 2VXH / pdb_00002vxh
Title : The crystal structure of chlorite dismutase: a detox enzyme producing molecular oxygen
Authors : De Geus, D.C.; Thomassen, E.A.J.; Hagedoorn, P.L.; Pannu, N.S.; Abrahams, J.P.
Deposited on : 2008-07-04
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

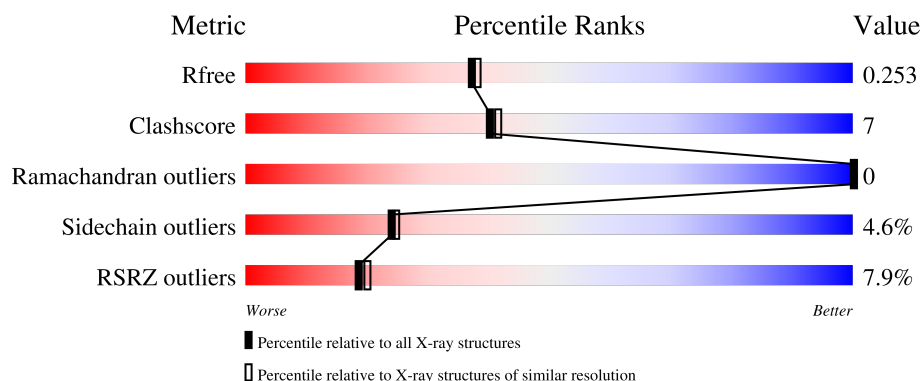
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	251	4% 78% 12% • 9%
1	B	251	6% 79% 11% • 8%
1	C	251	6% 80% 8% •• 9%
1	D	251	9% 80% 10% • 8%

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Mol	Chain	Length	Quality of chain
1	E	251	11% 80% 10% 8%
1	F	251	8% 80% 8% 9%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11790 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 CHLORITE DISMUTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	0	0
			1818	1167	303	342	6			
1	B	230	Total	C	N	O	S	0	0	0
			1826	1171	304	345	6			
1	C	228	Total	C	N	O	S	0	0	0
			1814	1163	302	343	6			
1	D	230	Total	C	N	O	S	0	0	0
			1830	1175	305	344	6			
1	E	230	Total	C	N	O	S	0	0	0
			1830	1175	305	344	6			
1	F	229	Total	C	N	O	S	0	0	0
			1821	1169	303	343	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q673K5
A	-1	SER	-	expression tag	UNP Q673K5
A	0	HIS	-	expression tag	UNP Q673K5
A	6	ALA	PRO	conflict	UNP Q673K5
B	-2	GLY	-	expression tag	UNP Q673K5
B	-1	SER	-	expression tag	UNP Q673K5
B	0	HIS	-	expression tag	UNP Q673K5
B	6	ALA	PRO	conflict	UNP Q673K5
C	-2	GLY	-	expression tag	UNP Q673K5
C	-1	SER	-	expression tag	UNP Q673K5
C	0	HIS	-	expression tag	UNP Q673K5
C	6	ALA	PRO	conflict	UNP Q673K5
D	-2	GLY	-	expression tag	UNP Q673K5
D	-1	SER	-	expression tag	UNP Q673K5
D	0	HIS	-	expression tag	UNP Q673K5
D	6	ALA	PRO	conflict	UNP Q673K5
E	-2	GLY	-	expression tag	UNP Q673K5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	SER	-	expression tag	UNP Q673K5
E	0	HIS	-	expression tag	UNP Q673K5
E	6	ALA	PRO	conflict	UNP Q673K5
F	-2	GLY	-	expression tag	UNP Q673K5
F	-1	SER	-	expression tag	UNP Q673K5
F	0	HIS	-	expression tag	UNP Q673K5
F	6	ALA	PRO	conflict	UNP Q673K5

- # HEM

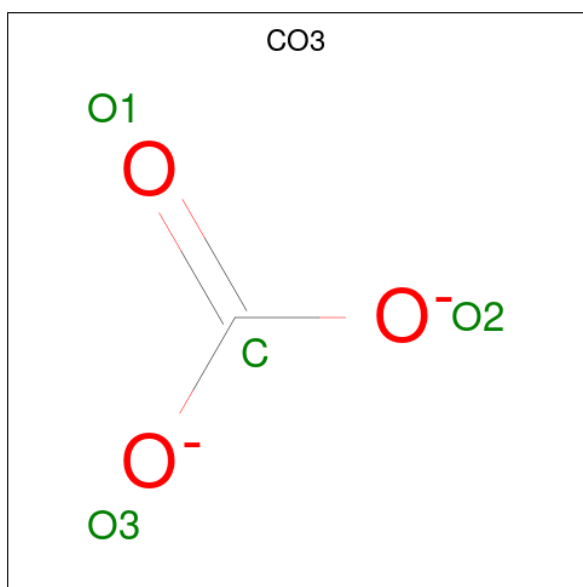
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	F	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	S	0	0
			3	1	1	1		
3	B	1	Total	C	N	S	0	0
			3	1	1	1		
3	C	1	Total	C	N	S	0	0
			3	1	1	1		
3	D	1	Total	C	N	S	0	0
			3	1	1	1		
3	E	1	Total	C	N	S	0	0
			3	1	1	1		
3	F	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 4 is CARBONATE ION (CCD ID: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	1	3		
4	B	1	Total	C	O	0	0
			4	1	3		
4	C	1	Total	C	O	0	0
			4	1	3		
4	E	1	Total	C	O	0	0
			4	1	3		
4	F	1	Total	C	O	0	0
			4	1	3		

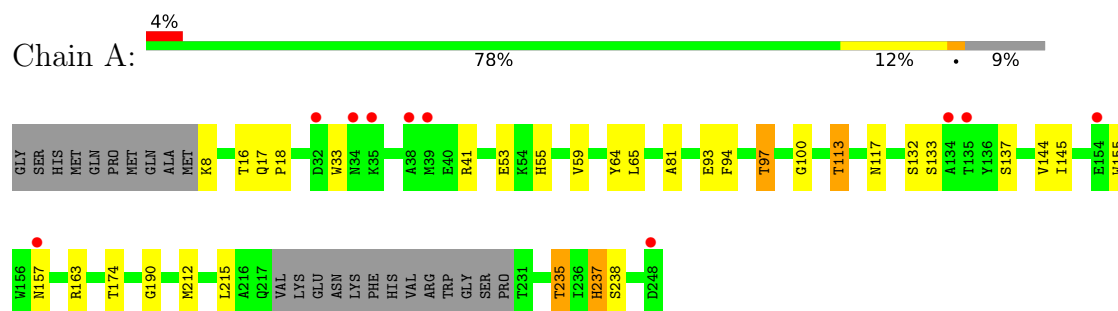
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	110	Total	O	0	0
			110	110		
5	B	98	Total	O	0	0
			98	98		
5	C	93	Total	O	0	0
			93	93		
5	D	66	Total	O	0	0
			66	66		
5	E	114	Total	O	0	0
			114	114		
5	F	74	Total	O	0	0
			74	74		

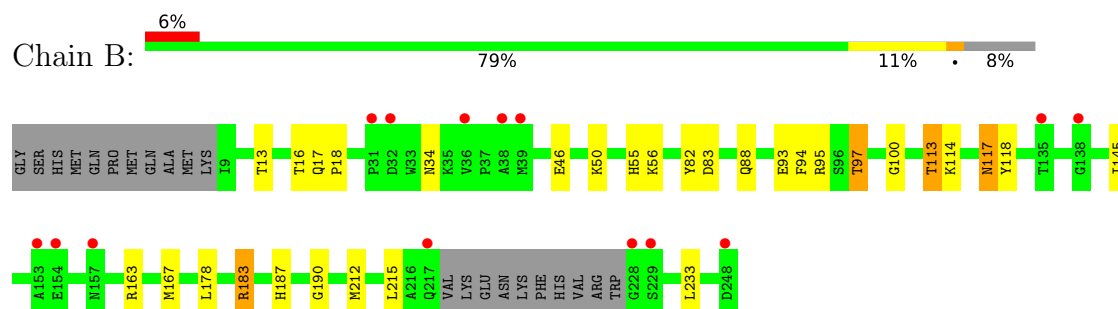
3 Residue-property plots [i](#)

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.

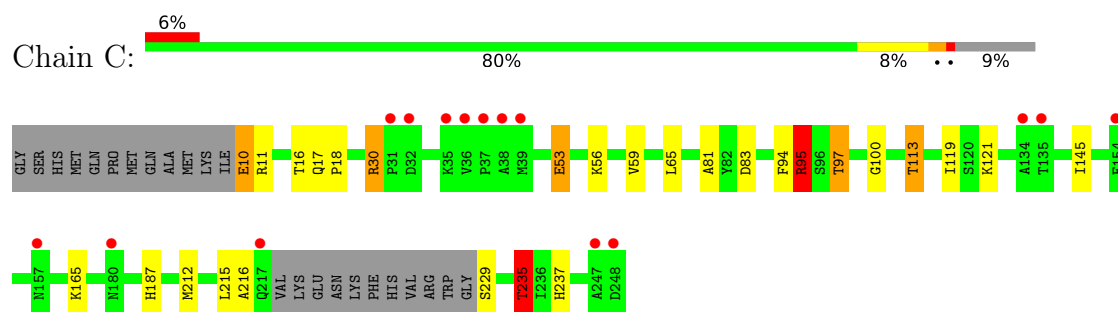
• Molecule 1: CHLORITE DISMUTASE



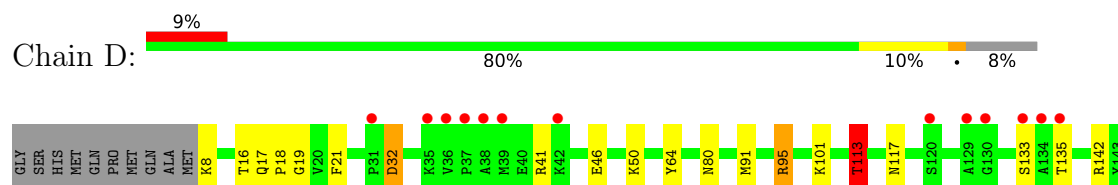
• Molecule 1: CHLORITE DISMUTASE

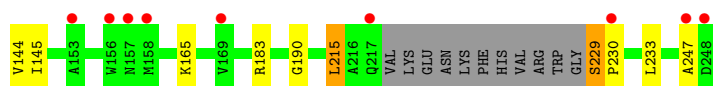


• Molecule 1: CHLORITE DISMUTASE

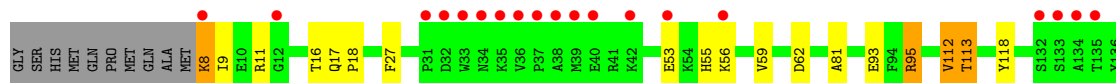
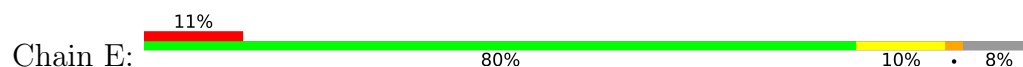


• Molecule 1: CHLORITE DISMUTASE

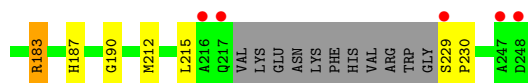
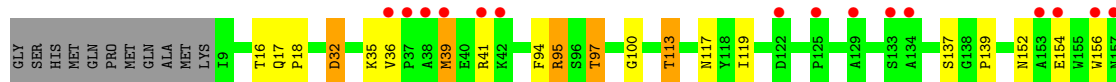
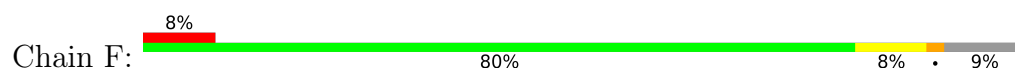




• Molecule 1: CHLORITE DISMUTASE



• Molecule 1: CHLORITE DISMUTASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	164.46Å 169.34Å 60.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.68 – 2.10 50.68 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (50.68-2.10) 100.0 (50.68-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.25 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.219 , 0.255 0.218 , 0.253	Depositor DCC
R_{free} test set	4994 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	25.7	Xtriage
Anisotropy	0.440	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 33.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11790	wwPDB-VP
Average B, all atoms (Å ²)	26.0	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: SCN, HEM, CO3

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	0.78	3/1857 (0.2%)	0.91	1/2516 (0.0%)
1	B	0.70	2/1866 (0.1%)	0.86	1/2530 (0.0%)
1	C	0.68	1/1854 (0.1%)	0.85	1/2514 (0.0%)
1	D	0.68	0/1870	0.82	1/2535 (0.0%)
1	E	0.73	1/1870 (0.1%)	0.87	1/2535 (0.0%)
1	F	0.74	0/1861	0.86	4/2524 (0.2%)
All	All	0.72	7/11178 (0.1%)	0.86	9/15154 (0.1%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	237	HIS	C-N	-7.38	1.22	1.33
1	B	82	TYR	C-N	-7.20	1.21	1.33
1	A	238	SER	C-N	-5.73	1.26	1.34
1	C	95	ARG	C-O	-5.34	1.17	1.24
1	E	95	ARG	C-O	-5.18	1.17	1.24
1	B	82	TYR	C-O	-5.12	1.17	1.24
1	A	137	SER	C-O	-5.01	1.17	1.23

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	137	SER	N-CA-C	6.29	123.52	114.39
1	A	133	SER	N-CA-C	5.93	120.58	113.23
1	F	139	PRO	CA-C-O	-5.72	114.76	122.08
1	B	82	TYR	O-C-N	5.56	129.11	122.27
1	C	235	THR	CB-CA-C	5.50	119.87	109.37
1	F	137	SER	CA-C-N	-5.36	113.46	121.87
1	F	137	SER	C-N-CA	-5.36	113.46	121.87
1	E	112	VAL	CB-CA-C	-5.35	102.26	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	113	THR	N-CA-CB	-5.31	102.17	109.97

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	1818	0	1829	24	0
1	B	1826	0	1831	28	0
1	C	1814	0	1817	33	0
1	D	1830	0	1841	23	0
1	E	1830	0	1841	30	0
1	F	1821	0	1828	23	0
2	A	43	0	30	1	0
2	B	43	0	30	1	0
2	C	43	0	30	1	0
2	D	43	0	30	0	0
2	E	43	0	30	0	0
2	F	43	0	30	2	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
4	E	4	0	0	0	0
4	F	4	0	0	0	0
5	A	110	0	0	2	0
5	B	98	0	0	8	0
5	C	93	0	0	5	0
5	D	66	0	0	1	0
5	E	114	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	74	0	0	4	0
All	All	11790	0	11167	148	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 7.

All (148) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:138:GLY:HA3	5:E:2066:HOH:O	1.42	1.19
1:E:229:SER:HB3	1:E:230:PRO:CD	1.75	1.17
1:C:10:GLU:HA	1:C:10:GLU:OE2	1.43	1.09
1:E:229:SER:HB3	1:E:230:PRO:HD2	1.42	0.97
1:A:235:THR:HG23	1:A:237:HIS:NE2	1.82	0.94
1:D:229:SER:HB2	1:D:230:PRO:HD3	1.50	0.94
1:D:229:SER:HB2	1:D:230:PRO:CD	2.00	0.92
1:A:97:THR:HG22	1:A:100:GLY:H	1.34	0.92
1:B:17:GLN:O	1:B:113:THR:HG21	1.71	0.91
1:A:17:GLN:O	1:A:113:THR:HG21	1.71	0.91
1:D:17:GLN:O	1:D:113:THR:HG21	1.71	0.90
1:E:17:GLN:O	1:E:113:THR:HG21	1.72	0.89
1:C:97:THR:HG22	1:C:100:GLY:H	1.38	0.89
1:E:18:PRO:HA	1:E:113:THR:HG22	1.55	0.89
1:C:18:PRO:HA	1:C:113:THR:HG22	1.54	0.88
1:F:18:PRO:HA	1:F:113:THR:HG22	1.59	0.85
1:E:229:SER:HB3	1:E:230:PRO:HD3	1.59	0.84
1:F:17:GLN:O	1:F:113:THR:HG21	1.77	0.84
1:E:229:SER:CB	1:E:230:PRO:CD	2.56	0.83
1:E:235:THR:HG23	1:E:237:HIS:CE1	2.13	0.83
1:C:17:GLN:O	1:C:113:THR:HG21	1.78	0.83
1:B:97:THR:HG22	1:B:100:GLY:H	1.41	0.82
1:E:229:SER:CB	1:E:230:PRO:HD2	2.11	0.81
1:D:145:ILE:HD11	1:D:233:LEU:HD13	1.64	0.79
1:C:235:THR:HG23	1:C:237:HIS:NE2	1.96	0.79
1:E:235:THR:CG2	1:E:237:HIS:HE1	1.99	0.76
1:F:18:PRO:HA	1:F:113:THR:CG2	2.17	0.75
1:A:18:PRO:HA	1:A:113:THR:HG22	1.68	0.75
1:F:97:THR:HG22	1:F:100:GLY:H	1.50	0.75
1:D:18:PRO:HA	1:D:113:THR:CG2	2.17	0.73
1:C:18:PRO:HA	1:C:113:THR:CG2	2.19	0.72
1:E:235:THR:HG23	1:E:237:HIS:HE1	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:THR:CG2	1:A:237:HIS:NE2	2.54	0.71
1:C:235:THR:HG23	1:C:237:HIS:CD2	2.27	0.70
1:A:163:ARG:NH2	5:A:2073:HOH:O	2.25	0.69
1:C:83:ASP:OD1	1:D:142:ARG:NH1	2.26	0.68
1:C:187:HIS:HD2	5:C:2071:HOH:O	1.77	0.68
1:A:235:THR:HG23	1:A:237:HIS:CD2	2.31	0.66
1:B:18:PRO:HA	1:B:113:THR:HG22	1.77	0.64
1:D:46:GLU:HG3	1:D:50:LYS:HE2	1.78	0.64
1:B:18:PRO:HA	1:B:113:THR:CG2	2.26	0.64
1:E:55:HIS:HE1	1:E:93:GLU:OE1	1.82	0.63
1:D:95:ARG:NH1	5:D:2035:HOH:O	2.24	0.63
1:C:30:ARG:CG	1:C:30:ARG:HH11	2.11	0.62
1:B:187:HIS:HD2	5:B:2033:HOH:O	1.82	0.62
1:B:55:HIS:HE1	1:B:93:GLU:OE1	1.82	0.62
1:C:94:PHE:O	1:C:97:THR:HB	2.00	0.61
1:B:46:GLU:HG3	1:B:50:LYS:HE2	1.80	0.61
1:A:18:PRO:HA	1:A:113:THR:CG2	2.31	0.61
1:B:94:PHE:O	1:B:97:THR:HB	2.01	0.60
1:F:229:SER:CB	1:F:230:PRO:HD2	2.31	0.60
1:A:94:PHE:O	1:A:97:THR:HB	2.01	0.59
1:C:30:ARG:HH11	1:C:30:ARG:HG2	1.67	0.59
1:B:117:ASN:ND2	5:B:2047:HOH:O	2.36	0.58
1:C:83:ASP:HB2	5:C:2034:HOH:O	2.02	0.58
1:C:65:LEU:HB3	1:C:235:THR:HG22	1.85	0.57
1:D:229:SER:CB	1:D:230:PRO:CD	2.78	0.57
1:A:65:LEU:HB3	1:A:235:THR:HG22	1.85	0.57
1:E:18:PRO:HA	1:E:113:THR:CG2	2.33	0.56
1:D:17:GLN:O	1:D:113:THR:CG2	2.51	0.56
1:B:13:THR:O	1:B:17:GLN:HG3	2.05	0.56
1:A:212:MET:HG3	1:E:190:GLY:HA3	1.87	0.56
1:E:17:GLN:O	1:E:113:THR:CG2	2.50	0.56
1:A:17:GLN:O	1:A:113:THR:CG2	2.51	0.56
1:F:229:SER:CB	1:F:230:PRO:CD	2.84	0.56
1:C:95:ARG:HD2	5:C:2037:HOH:O	2.05	0.55
1:D:18:PRO:HA	1:D:113:THR:HG22	1.88	0.55
1:D:19:GLY:N	1:D:113:THR:HG22	2.23	0.54
1:F:229:SER:HB2	1:F:230:PRO:HD2	1.89	0.54
1:C:30:ARG:HG2	1:C:30:ARG:NH1	2.24	0.53
1:B:17:GLN:O	1:B:113:THR:CG2	2.51	0.53
1:A:64:TYR:CD1	1:A:144:VAL:HG11	2.44	0.53
1:C:10:GLU:OE2	1:C:10:GLU:CA	2.28	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:229:SER:N	5:C:2084:HOH:O	2.41	0.53
1:F:152:ASN:OD1	1:F:154:GLU:HB2	2.07	0.53
1:B:163:ARG:NH2	5:B:2065:HOH:O	2.42	0.53
1:E:235:THR:CG2	1:E:237:HIS:CE1	2.80	0.52
1:A:97:THR:HG22	1:A:100:GLY:N	2.16	0.52
1:A:212:MET:HG3	1:E:190:GLY:CA	2.40	0.52
1:C:235:THR:HG21	5:F:2030:HOH:O	2.09	0.52
1:D:145:ILE:CD1	1:D:233:LEU:HD13	2.36	0.52
1:F:97:THR:CG2	1:F:100:GLY:H	2.19	0.52
1:F:119:ILE:HG13	2:F:1001:HEM:HMA3	1.91	0.51
1:B:55:HIS:CE1	1:B:93:GLU:OE1	2.62	0.51
1:F:187:HIS:HE1	5:F:2054:HOH:O	1.91	0.51
1:B:178:LEU:HD21	2:B:1001:HEM:HMB3	1.93	0.51
1:C:30:ARG:HH11	1:C:30:ARG:HB3	1.76	0.50
1:A:55:HIS:HE1	1:A:93:GLU:OE1	1.93	0.50
1:D:18:PRO:HA	1:D:113:THR:HG23	1.92	0.50
1:A:59:VAL:HG12	1:A:81:ALA:HB2	1.94	0.49
1:D:32:ASP:OD1	1:D:32:ASP:N	2.41	0.48
1:C:97:THR:HG22	1:C:100:GLY:N	2.18	0.48
1:C:59:VAL:HG12	1:C:81:ALA:HB2	1.96	0.48
1:A:157:ASN:HB3	5:A:2071:HOH:O	2.14	0.47
1:F:39:MET:HE2	1:F:39:MET:HB2	1.83	0.47
1:B:17:GLN:HG2	5:B:2004:HOH:O	2.14	0.47
1:C:235:THR:CG2	1:C:237:HIS:NE2	2.72	0.47
1:A:190:GLY:HA3	1:F:212:MET:HG3	1.97	0.47
1:C:212:MET:HG3	1:F:190:GLY:HA3	1.95	0.47
1:E:53:GLU:O	1:E:56:LYS:HB2	2.15	0.47
1:C:119:ILE:HG13	2:C:1001:HEM:HMA3	1.95	0.47
1:B:34:ASN:HD21	1:D:101:LYS:HG2	1.78	0.47
1:B:183:ARG:NH2	5:B:2076:HOH:O	2.47	0.46
1:B:95:ARG:HD2	5:B:2042:HOH:O	2.15	0.46
1:E:8:LYS:HD3	1:E:9:ILE:H	1.81	0.46
1:F:32:ASP:HB3	1:F:35:LYS:HE3	1.98	0.45
1:C:53:GLU:O	1:C:56:LYS:HB2	2.17	0.45
1:C:30:ARG:CG	1:C:30:ARG:NH1	2.77	0.44
1:D:91:MET:O	1:D:95:ARG:HG2	2.17	0.44
1:F:95:ARG:HG3	5:F:2034:HOH:O	2.17	0.44
1:C:17:GLN:O	1:C:113:THR:CG2	2.59	0.44
1:A:235:THR:HG21	5:E:2045:HOH:O	2.17	0.44
1:C:30:ARG:HH11	1:C:30:ARG:CB	2.29	0.44
1:E:27:PHE:HE1	1:E:95:ARG:HD3	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:95:ARG:CD	5:B:2042:HOH:O	2.66	0.44
1:F:183:ARG:HD3	2:F:1001:HEM:C2B	2.53	0.44
1:C:212:MET:HG3	1:F:190:GLY:CA	2.48	0.44
1:B:83:ASP:CG	1:E:142:ARG:HH12	2.25	0.43
1:B:88:GLN:OE1	1:E:235:THR:HG21	2.18	0.43
1:B:114:LYS:NZ	1:E:210:ASN:ND2	2.66	0.43
1:C:216:ALA:O	1:F:156:TRP:HB3	2.18	0.43
1:F:97:THR:HG22	1:F:100:GLY:N	2.25	0.43
1:B:212:MET:HG3	1:D:190:GLY:HA3	1.99	0.43
1:D:41:ARG:NH2	1:D:247:ALA:O	2.52	0.43
1:A:174:THR:HB	2:A:1001:HEM:C3B	2.54	0.43
1:D:64:TYR:CD1	1:D:144:VAL:HG11	2.54	0.43
1:E:235:THR:HG21	1:E:237:HIS:HE1	1.80	0.43
1:D:215:LEU:HD12	1:D:215:LEU:HA	1.86	0.43
1:B:83:ASP:OD2	5:B:2036:HOH:O	2.21	0.42
1:B:118:TYR:CD2	1:B:167:MET:HG3	2.54	0.42
1:C:10:GLU:HB3	1:C:11:ARG:H	1.69	0.42
1:E:59:VAL:HG12	1:E:81:ALA:HB2	2.01	0.42
1:E:11:ARG:HH22	1:E:62:ASP:CG	2.26	0.42
1:B:145:ILE:HD11	1:B:233:LEU:HD13	2.02	0.41
1:E:55:HIS:CE1	1:E:93:GLU:OE1	2.67	0.41
1:F:187:HIS:CE1	5:F:2054:HOH:O	2.70	0.41
1:B:190:GLY:HA3	1:E:212:MET:HG3	2.01	0.41
1:A:155:TRP:CE2	1:A:163:ARG:HD2	2.55	0.41
1:E:118:TYR:CD2	1:E:167:MET:HG3	2.56	0.41
1:E:8:LYS:CD	1:E:9:ILE:H	2.34	0.41
1:F:94:PHE:O	1:F:97:THR:HB	2.21	0.41
1:A:33:TRP:CH2	1:A:41:ARG:HG2	2.56	0.41
1:B:212:MET:HE3	1:B:212:MET:HB3	1.97	0.41
1:D:21:PHE:O	1:D:80:ASN:HA	2.21	0.41
1:C:187:HIS:CD2	5:C:2071:HOH:O	2.61	0.40
1:F:36:VAL:O	1:F:41:ARG:HD2	2.22	0.40
1:A:97:THR:CG2	1:A:100:GLY:H	2.19	0.40
1:D:145:ILE:HD11	1:D:233:LEU:CD1	2.43	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	224/251 (89%)	221 (99%)	3 (1%)	0	100	100
1	B	226/251 (90%)	223 (99%)	3 (1%)	0	100	100
1	C	224/251 (89%)	221 (99%)	3 (1%)	0	100	100
1	D	226/251 (90%)	223 (99%)	3 (1%)	0	100	100
1	E	226/251 (90%)	223 (99%)	3 (1%)	0	100	100
1	F	225/251 (90%)	221 (98%)	4 (2%)	0	100	100
All	All	1351/1506 (90%)	1332 (99%)	19 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	200/220 (91%)	190 (95%)	10 (5%)	22	22
1	B	201/220 (91%)	194 (96%)	7 (4%)	32	35
1	C	200/220 (91%)	188 (94%)	12 (6%)	17	15
1	D	202/220 (92%)	190 (94%)	12 (6%)	18	16
1	E	202/220 (92%)	196 (97%)	6 (3%)	36	41
1	F	201/220 (91%)	192 (96%)	9 (4%)	24	25
All	All	1206/1320 (91%)	1150 (95%)	56 (5%)	24	25

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LYS
1	A	16	THR
1	A	53	GLU
1	A	97	THR
1	A	113	THR
1	A	117	ASN
1	A	132	SER
1	A	145	ILE
1	A	215	LEU
1	A	235	THR
1	B	16	THR
1	B	56	LYS
1	B	97	THR
1	B	113	THR
1	B	117	ASN
1	B	183	ARG
1	B	215	LEU
1	C	10	GLU
1	C	16	THR
1	C	30	ARG
1	C	53	GLU
1	C	95	ARG
1	C	97	THR
1	C	113	THR
1	C	121	LYS
1	C	145	ILE
1	C	165	LYS
1	C	215	LEU
1	C	235	THR
1	D	8	LYS
1	D	16	THR
1	D	32	ASP
1	D	95	ARG
1	D	113	THR
1	D	117	ASN
1	D	133	SER
1	D	135	THR
1	D	165	LYS
1	D	183	ARG
1	D	215	LEU
1	D	229	SER
1	E	8	LYS

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Mol	Chain	Res	Type
1	E	16	THR
1	E	112	VAL
1	E	113	THR
1	E	145	ILE
1	E	215	LEU
1	F	16	THR
1	F	32	ASP
1	F	39	MET
1	F	95	ARG
1	F	97	THR
1	F	113	THR
1	F	117	ASN
1	F	183	ARG
1	F	215	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	HIS
1	A	58	ASN
1	A	217	GLN
1	B	34	ASN
1	B	55	HIS
1	B	80	ASN
1	B	117	ASN
1	B	157	ASN
1	B	187	HIS
1	B	237	HIS
1	C	80	ASN
1	C	157	ASN
1	C	187	HIS
1	D	157	ASN
1	D	209	ASN
1	E	55	HIS
1	E	58	ASN
1	E	72	ASN
1	E	157	ASN
1	E	210	ASN
1	E	217	GLN
1	E	237	HIS
1	F	80	ASN
1	F	157	ASN

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Mol	Chain	Res	Type
1	F	187	HIS
1	F	209	ASN
1	F	210	ASN
1	F	217	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

17 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	SCN	F	1002	2	1,2,2	0.59	0	0,1,1	-	-
2	HEM	E	1001	3,1	50,50,50	2.05	10 (20%)	67,82,82	1.66	14 (20%)
3	SCN	A	1002	2	1,2,2	1.03	0	0,1,1	-	-
3	SCN	B	1002	2	1,2,2	1.26	0	0,1,1	-	-
2	HEM	F	1001	3,1	50,50,50	2.07	10 (20%)	67,82,82	1.60	13 (19%)
2	HEM	C	1001	3,1	50,50,50	2.04	10 (20%)	67,82,82	1.71	11 (16%)
2	HEM	B	1001	3,1	50,50,50	2.07	9 (18%)	67,82,82	1.62	11 (16%)
4	CO3	A	1003	-	3,3,3	0.93	0	2,3,3	1.07	0
3	SCN	C	1002	2	1,2,2	0.72	0	0,1,1	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SCN	E	1002	2	1,2,2	0.71	0	0,1,1	-	-
4	CO3	C	1003	-	3,3,3	0.83	0	2,3,3	1.16	0
4	CO3	E	1003	-	3,3,3	1.08	0	2,3,3	0.34	0
4	CO3	B	1003	-	3,3,3	0.88	0	2,3,3	0.40	0
2	HEM	D	1001	3,1	50,50,50	1.89	9 (18%)	67,82,82	1.36	7 (10%)
4	CO3	F	1003	-	3,3,3	0.78	0	2,3,3	0.35	0
2	HEM	A	1001	3,1	50,50,50	2.06	10 (20%)	67,82,82	1.67	13 (19%)
3	SCN	D	1002	2	1,2,2	0.39	0	0,1,1	-	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	E	1001	3,1	-	6/14/54/54	-
2	HEM	F	1001	3,1	-	8/14/54/54	-
2	HEM	C	1001	3,1	-	8/14/54/54	-
2	HEM	B	1001	3,1	-	8/14/54/54	-
2	HEM	D	1001	3,1	-	8/14/54/54	-
2	HEM	A	1001	3,1	-	8/14/54/54	-

All (58) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1001	HEM	C3D-C2D	8.30	1.54	1.36
2	E	1001	HEM	C3D-C2D	7.69	1.53	1.36
2	B	1001	HEM	C3D-C2D	7.58	1.53	1.36
2	D	1001	HEM	C3D-C2D	7.47	1.52	1.36
2	C	1001	HEM	C3D-C2D	7.44	1.52	1.36
2	A	1001	HEM	C3D-C2D	7.21	1.52	1.36
2	E	1001	HEM	FE-NA	6.03	2.15	1.95
2	C	1001	HEM	FE-ND	5.73	2.12	1.94
2	A	1001	HEM	FE-NB	5.71	2.12	1.94
2	F	1001	HEM	FE-NC	5.67	2.13	1.95
2	A	1001	HEM	FE-ND	5.66	2.12	1.94
2	B	1001	HEM	FE-NB	5.63	2.12	1.94
2	B	1001	HEM	FE-ND	5.46	2.11	1.94
2	F	1001	HEM	FE-ND	5.36	2.11	1.94
2	C	1001	HEM	FE-NB	4.79	2.09	1.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1001	HEM	FE-ND	4.73	2.09	1.94
2	A	1001	HEM	FE-NC	4.73	2.10	1.95
2	E	1001	HEM	FE-NC	4.64	2.10	1.95
2	F	1001	HEM	FE-NA	4.64	2.10	1.95
2	B	1001	HEM	FE-NC	4.48	2.09	1.95
2	C	1001	HEM	FE-NC	4.47	2.09	1.95
2	E	1001	HEM	FE-ND	4.43	2.08	1.94
2	B	1001	HEM	FE-NA	4.27	2.09	1.95
2	D	1001	HEM	FE-NA	4.13	2.08	1.95
2	D	1001	HEM	FE-NC	3.99	2.08	1.95
2	C	1001	HEM	FE-NA	3.98	2.08	1.95
2	E	1001	HEM	FE-NB	3.55	2.05	1.94
2	A	1001	HEM	FE-NA	3.54	2.06	1.95
2	E	1001	HEM	CAC-C3C	3.27	1.56	1.47
2	B	1001	HEM	CAC-C3C	3.13	1.55	1.47
2	C	1001	HEM	CAC-C3C	3.12	1.55	1.47
2	C	1001	HEM	CAB-C3B	3.05	1.55	1.47
2	F	1001	HEM	CAB-C3B	3.02	1.55	1.47
2	B	1001	HEM	CAB-C3B	3.01	1.55	1.47
2	D	1001	HEM	FE-NB	3.00	2.04	1.94
2	D	1001	HEM	CAB-C3B	2.97	1.55	1.47
2	A	1001	HEM	CAB-C3B	2.97	1.55	1.47
2	A	1001	HEM	CAC-C3C	2.86	1.55	1.47
2	D	1001	HEM	CAC-C3C	2.85	1.55	1.47
2	F	1001	HEM	CAC-C3C	2.70	1.54	1.47
2	E	1001	HEM	CAB-C3B	2.69	1.54	1.47
2	A	1001	HEM	CMD-C2D	2.36	1.55	1.50
2	C	1001	HEM	CMA-C3A	2.33	1.55	1.50
2	F	1001	HEM	CMB-C2B	2.31	1.55	1.50
2	E	1001	HEM	CMB-C2B	2.24	1.55	1.50
2	C	1001	HEM	CMB-C2B	2.23	1.55	1.50
2	F	1001	HEM	FE-NB	2.23	2.01	1.94
2	B	1001	HEM	CMC-C2C	2.21	1.55	1.50
2	B	1001	HEM	CMA-C3A	2.20	1.55	1.50
2	E	1001	HEM	CMA-C3A	2.19	1.55	1.50
2	F	1001	HEM	CMC-C2C	2.19	1.55	1.50
2	C	1001	HEM	CMC-C2C	2.18	1.55	1.50
2	A	1001	HEM	CMC-C2C	2.18	1.55	1.50
2	A	1001	HEM	CMA-C3A	2.11	1.55	1.50
2	E	1001	HEM	CMC-C2C	2.09	1.55	1.50
2	D	1001	HEM	CMB-C2B	2.08	1.55	1.50
2	F	1001	HEM	CMD-C2D	2.08	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1001	HEM	CMC-C2C	2.01	1.54	1.50

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1001	HEM	C4D-ND-C1D	7.28	113.83	105.21
2	F	1001	HEM	C4D-ND-C1D	6.61	113.03	105.21
2	B	1001	HEM	C4D-ND-C1D	6.49	112.89	105.21
2	E	1001	HEM	C4D-ND-C1D	6.14	112.47	105.21
2	A	1001	HEM	C4D-ND-C1D	5.70	111.95	105.21
2	D	1001	HEM	C4D-ND-C1D	4.85	110.95	105.21
2	C	1001	HEM	C3B-C4B-NB	-4.39	106.31	109.47
2	E	1001	HEM	C3B-C4B-NB	-4.09	106.53	109.47
2	B	1001	HEM	C1B-NB-C4B	3.66	109.54	105.21
2	B	1001	HEM	C3B-C4B-NB	-3.65	106.85	109.47
2	A	1001	HEM	C3B-C4B-NB	-3.62	106.87	109.47
2	A	1001	HEM	C2A-C1A-NA	-3.60	106.15	110.15
2	C	1001	HEM	C1B-NB-C4B	3.48	109.32	105.21
2	E	1001	HEM	C1B-NB-C4B	3.37	109.20	105.21
2	A	1001	HEM	C1B-NB-C4B	3.18	108.98	105.21
2	C	1001	HEM	CBD-CAD-C3D	-3.07	104.04	112.53
2	F	1001	HEM	C3B-C4B-NB	-3.05	107.28	109.47
2	A	1001	HEM	CBD-CAD-C3D	-3.01	104.20	112.53
2	F	1001	HEM	CHA-C4D-ND	2.97	128.04	124.37
2	F	1001	HEM	C1B-NB-C4B	2.87	108.60	105.21
2	C	1001	HEM	C2D-C1D-ND	-2.85	106.61	109.90
2	E	1001	HEM	CHD-C1D-ND	2.84	127.48	124.42
2	E	1001	HEM	C2A-C1A-NA	-2.82	107.02	110.15
2	B	1001	HEM	C3B-C2B-C1B	2.81	108.52	106.41
2	F	1001	HEM	CBD-CAD-C3D	-2.81	104.77	112.53
2	E	1001	HEM	CBD-CAD-C3D	-2.80	104.78	112.53
2	B	1001	HEM	C2B-C1B-NB	-2.76	106.67	109.84
2	A	1001	HEM	C4C-NC-C1C	2.74	110.29	105.82
2	B	1001	HEM	CBD-CAD-C3D	-2.66	105.17	112.53
2	A	1001	HEM	CAA-CBA-CGA	-2.65	106.63	113.67
2	E	1001	HEM	CHB-C1B-NB	2.57	127.55	124.37
2	A	1001	HEM	C3B-C2B-C1B	2.57	108.34	106.41
2	F	1001	HEM	C2A-C1A-NA	-2.48	107.39	110.15
2	F	1001	HEM	C3B-C2B-C1B	2.45	108.25	106.41
2	F	1001	HEM	CHB-C1B-NB	2.44	127.39	124.37
2	F	1001	HEM	CAA-CBA-CGA	-2.44	107.20	113.67
2	A	1001	HEM	C4A-NA-C1A	2.38	109.70	105.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1001	HEM	C2A-C1A-NA	-2.38	107.51	110.15
2	D	1001	HEM	C3B-C4B-NB	-2.38	107.76	109.47
2	E	1001	HEM	C3D-C4D-ND	-2.38	107.56	110.17
2	C	1001	HEM	C3D-C4D-ND	-2.35	107.60	110.17
2	E	1001	HEM	O2D-CGD-CBD	2.34	121.40	114.00
2	E	1001	HEM	C4C-NC-C1C	2.34	109.63	105.82
2	F	1001	HEM	C3D-C4D-ND	-2.33	107.61	110.17
2	D	1001	HEM	C2A-C1A-NA	-2.32	107.58	110.15
2	F	1001	HEM	C4C-NC-C1C	2.32	109.60	105.82
2	D	1001	HEM	CBD-CAD-C3D	-2.31	106.14	112.53
2	B	1001	HEM	C2D-C1D-ND	-2.30	107.24	109.90
2	C	1001	HEM	C4C-NC-C1C	2.29	109.55	105.82
2	D	1001	HEM	C1B-NB-C4B	2.26	107.88	105.21
2	E	1001	HEM	O1D-CGD-CBD	-2.26	115.93	123.09
2	F	1001	HEM	CHD-C1D-ND	2.25	126.85	124.42
2	C	1001	HEM	CHC-C4B-NB	2.22	126.81	124.42
2	E	1001	HEM	CHA-C4D-ND	2.20	127.09	124.37
2	B	1001	HEM	C2A-C1A-NA	-2.20	107.72	110.15
2	E	1001	HEM	CBB-CAB-C3B	-2.19	116.56	127.53
2	C	1001	HEM	CHA-C4D-ND	2.19	127.08	124.37
2	A	1001	HEM	CBB-CAB-C3B	-2.18	116.61	127.53
2	D	1001	HEM	C4C-NC-C1C	2.16	109.35	105.82
2	C	1001	HEM	CMD-C2D-C1D	2.16	128.40	125.03
2	B	1001	HEM	C3C-C2C-C1C	2.12	109.05	107.05
2	A	1001	HEM	CMD-C2D-C1D	2.11	128.33	125.03
2	E	1001	HEM	C4A-NA-C1A	2.11	109.25	105.82
2	A	1001	HEM	CAD-C3D-C4D	2.10	128.36	124.70
2	B	1001	HEM	C4C-NC-C1C	2.09	109.22	105.82
2	B	1001	HEM	C3D-C4D-ND	-2.04	107.94	110.17
2	F	1001	HEM	C2D-C1D-ND	-2.04	107.55	109.90
2	D	1001	HEM	C4A-NA-C1A	2.02	109.11	105.82
2	A	1001	HEM	CHD-C4C-NC	2.01	126.64	124.45

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	HEM	C2C-C3C-CAC-CBC
2	B	1001	HEM	C2C-C3C-CAC-CBC
2	C	1001	HEM	C2B-C3B-CAB-CBB
2	C	1001	HEM	C2C-C3C-CAC-CBC
2	D	1001	HEM	C2B-C3B-CAB-CBB

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Mol	Chain	Res	Type	Atoms
2	D	1001	HEM	C2C-C3C-CAC-CBC
2	E	1001	HEM	C2B-C3B-CAB-CBB
2	E	1001	HEM	C2C-C3C-CAC-CBC
2	E	1001	HEM	C4C-C3C-CAC-CBC
2	F	1001	HEM	C2B-C3B-CAB-CBB
2	F	1001	HEM	C2C-C3C-CAC-CBC
2	A	1001	HEM	C2B-C3B-CAB-CBB
2	B	1001	HEM	C2B-C3B-CAB-CBB
2	A	1001	HEM	C4C-C3C-CAC-CBC
2	B	1001	HEM	C4C-C3C-CAC-CBC
2	D	1001	HEM	C4B-C3B-CAB-CBB
2	D	1001	HEM	C4C-C3C-CAC-CBC
2	B	1001	HEM	C4B-C3B-CAB-CBB
2	C	1001	HEM	C4B-C3B-CAB-CBB
2	C	1001	HEM	C4C-C3C-CAC-CBC
2	E	1001	HEM	C4B-C3B-CAB-CBB
2	F	1001	HEM	C4B-C3B-CAB-CBB
2	F	1001	HEM	C4C-C3C-CAC-CBC
2	A	1001	HEM	C4B-C3B-CAB-CBB
2	D	1001	HEM	CAD-CBD-CGD-O2D
2	D	1001	HEM	CAA-CBA-CGA-O1A
2	D	1001	HEM	CAD-CBD-CGD-O1D
2	D	1001	HEM	CAA-CBA-CGA-O2A
2	A	1001	HEM	CAD-CBD-CGD-O2D
2	B	1001	HEM	CAD-CBD-CGD-O2D
2	A	1001	HEM	CAD-CBD-CGD-O1D
2	B	1001	HEM	CAD-CBD-CGD-O1D
2	E	1001	HEM	CAD-CBD-CGD-O1D
2	F	1001	HEM	CAD-CBD-CGD-O2D
2	B	1001	HEM	CAA-CBA-CGA-O2A
2	A	1001	HEM	CAA-CBA-CGA-O2A
2	F	1001	HEM	CAA-CBA-CGA-O2A
2	E	1001	HEM	CAD-CBD-CGD-O2D
2	A	1001	HEM	CAA-CBA-CGA-O1A
2	C	1001	HEM	CAA-CBA-CGA-O2A
2	F	1001	HEM	CAA-CBA-CGA-O1A
2	C	1001	HEM	CAD-CBD-CGD-O2D
2	F	1001	HEM	CAD-CBD-CGD-O1D
2	B	1001	HEM	CAA-CBA-CGA-O1A
2	C	1001	HEM	CAD-CBD-CGD-O1D
2	C	1001	HEM	CAA-CBA-CGA-O1A

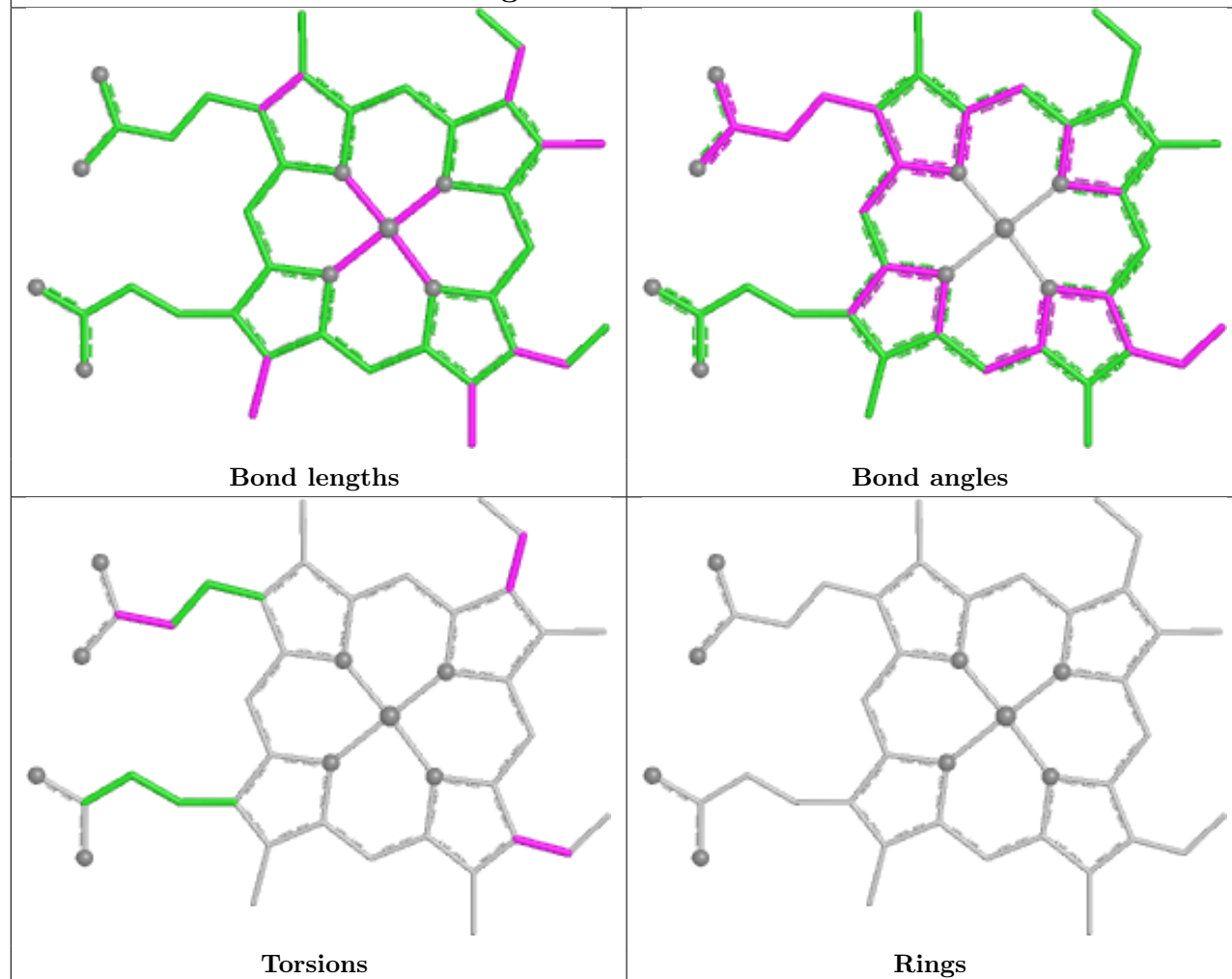
There are no ring outliers.

4 monomers are involved in 5 short contacts:

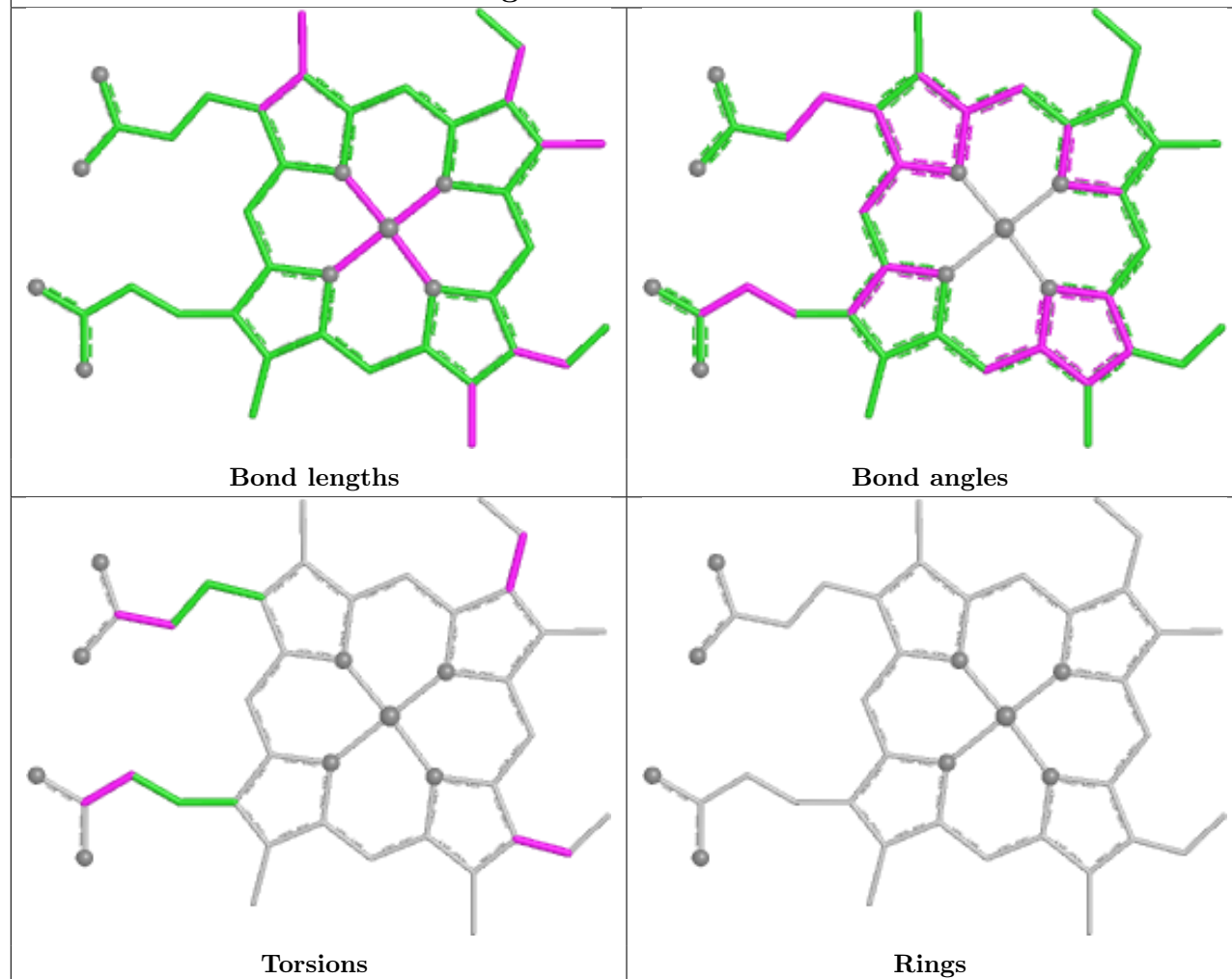
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1001	HEM	2	0
2	C	1001	HEM	1	0
2	B	1001	HEM	1	0
2	A	1001	HEM	1	0

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.

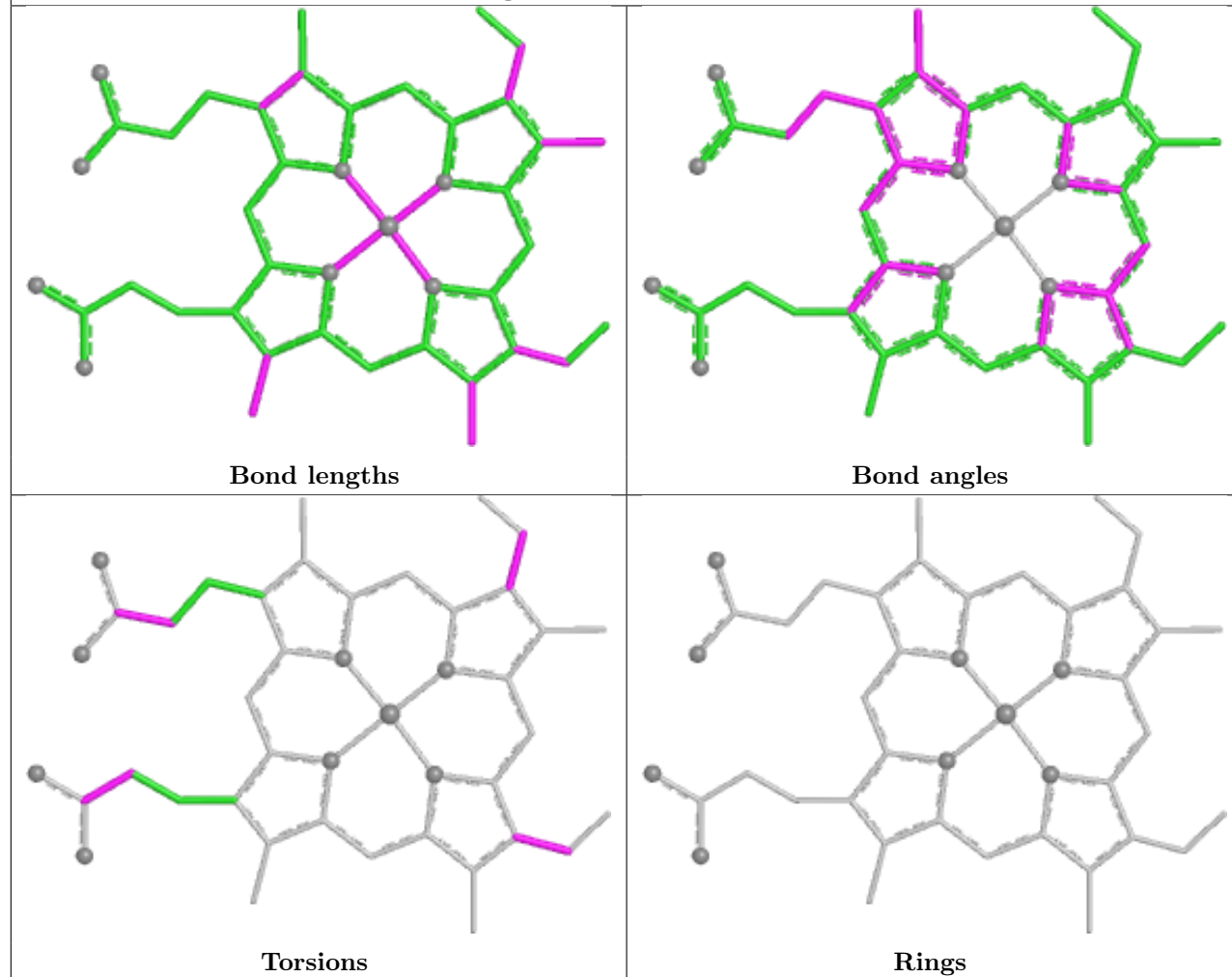
Ligand HEM E 1001



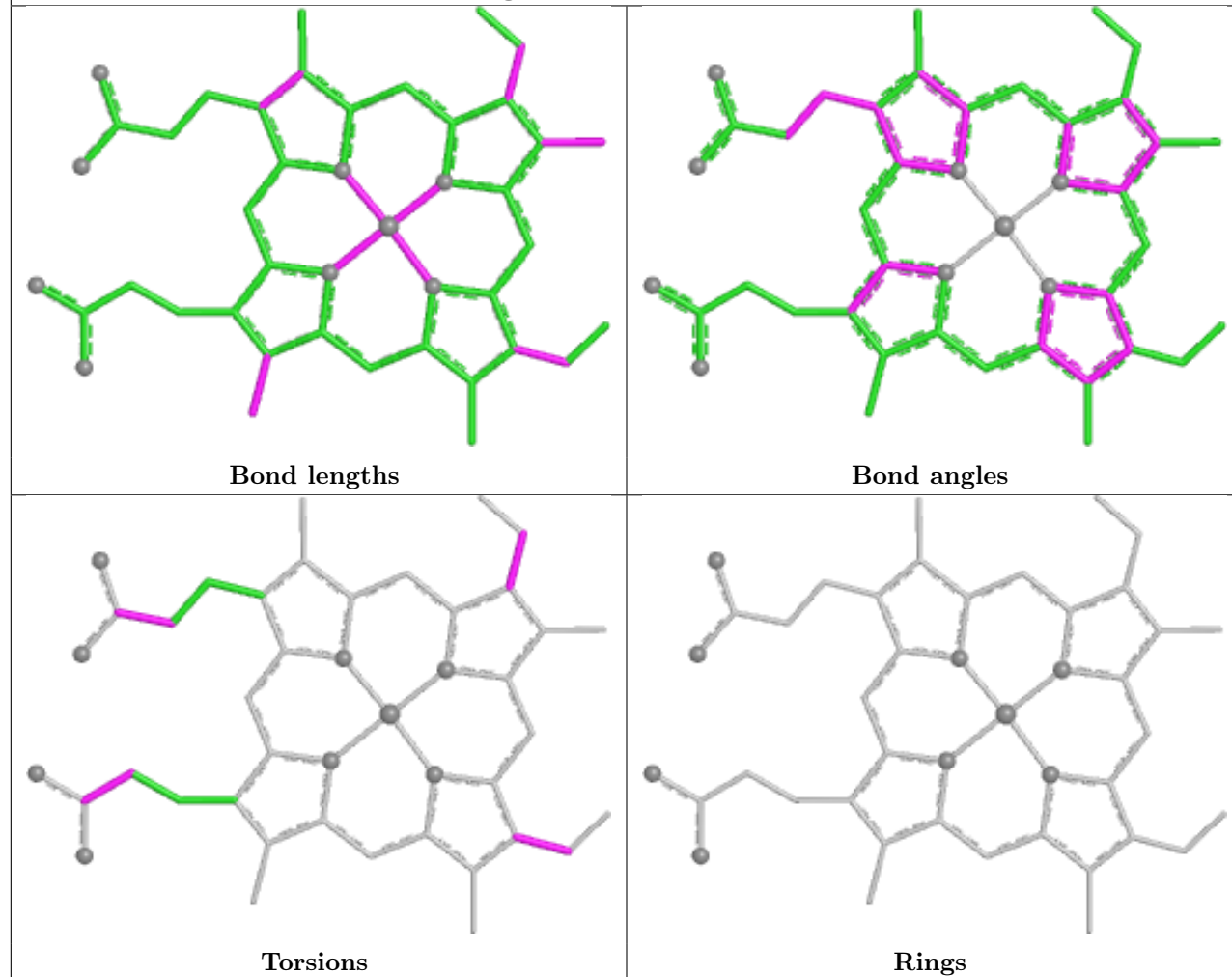
Ligand HEM F 1001



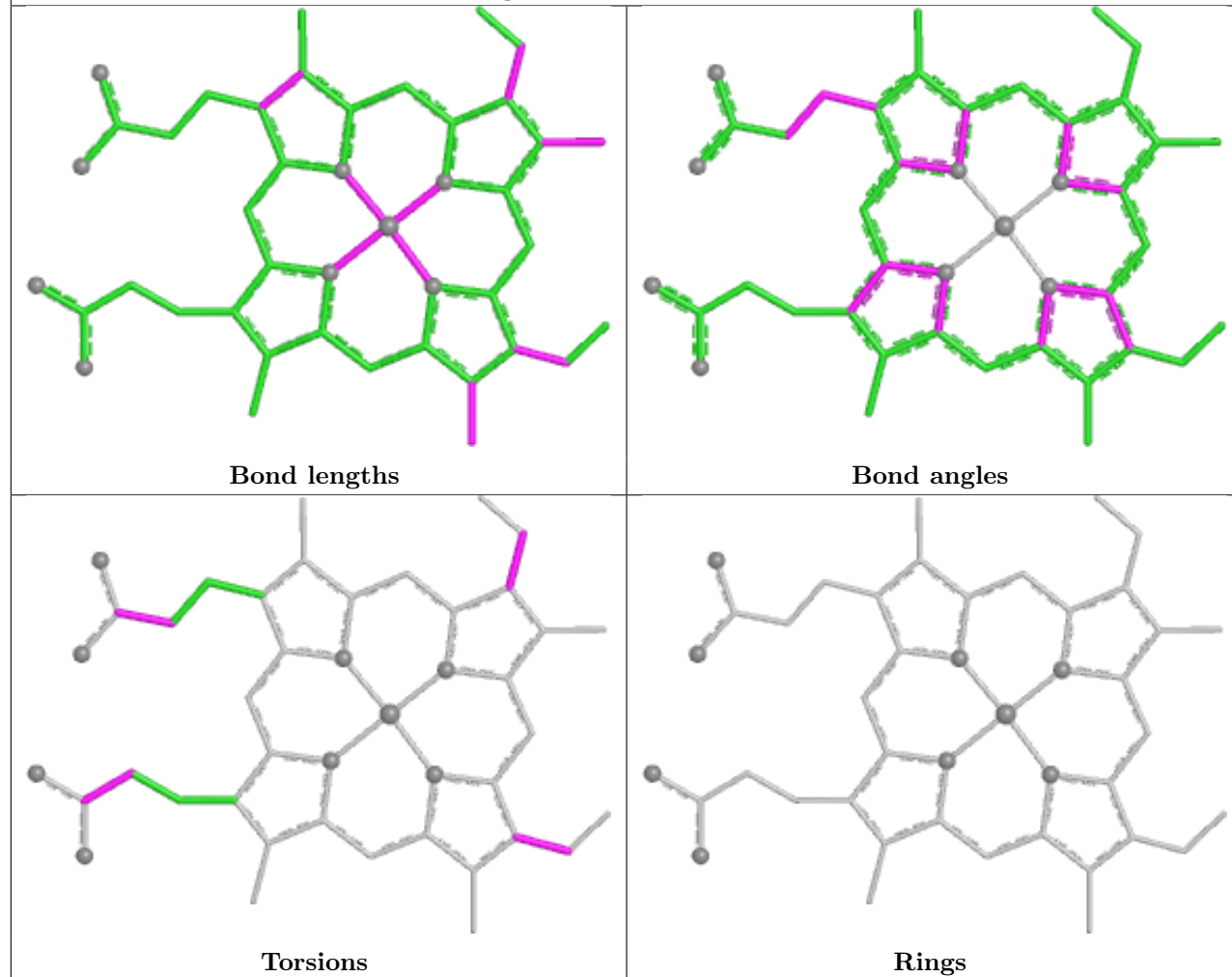
Ligand HEM C 1001

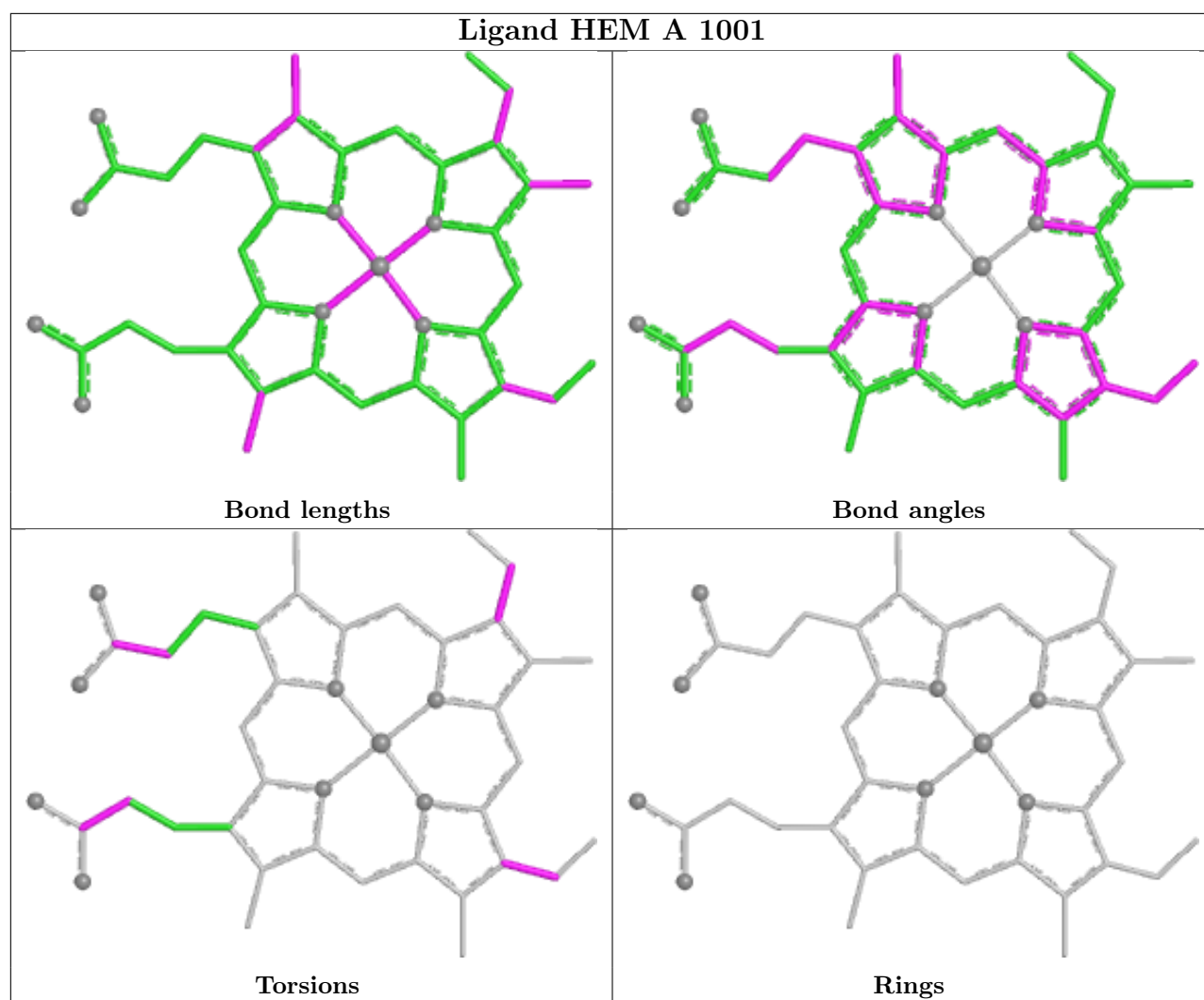


Ligand HEM B 1001



Ligand HEM D 1001





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	228/251 (90%)	0.28	10 (4%)	39 41	15, 24, 44, 53	0
1	B	230/251 (91%)	0.26	14 (6%)	27 29	15, 24, 44, 53	0
1	C	228/251 (90%)	0.35	15 (6%)	24 26	15, 25, 44, 53	0
1	D	230/251 (91%)	0.40	22 (9%)	13 14	15, 25, 44, 53	0
1	E	230/251 (91%)	0.44	27 (11%)	9 9	15, 24, 44, 52	0
1	F	229/251 (91%)	0.44	20 (8%)	16 16	15, 24, 44, 53	0
All	All	1375/1506 (91%)	0.36	108 (7%)	18 20	15, 24, 45, 53	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	39	MET	6.1
1	E	217	GLN	5.3
1	F	153	ALA	5.2
1	E	138	GLY	5.0
1	E	134	ALA	4.9
1	F	133	SER	4.8
1	A	157	ASN	4.7
1	F	157	ASN	4.4
1	F	217	GLN	4.3
1	C	135	THR	4.3
1	D	217	GLN	4.2
1	C	39	MET	4.1
1	F	248	ASP	4.0
1	F	39	MET	3.9
1	E	154	GLU	3.8
1	E	248	ASP	3.7
1	F	134	ALA	3.7
1	B	39	MET	3.7
1	E	38	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	133	SER	3.6
1	F	229	SER	3.6
1	D	157	ASN	3.6
1	B	248	ASP	3.4
1	D	153	ALA	3.4
1	D	156	TRP	3.3
1	A	248	ASP	3.3
1	B	138	GLY	3.3
1	F	36	VAL	3.3
1	E	8	LYS	3.3
1	E	157	ASN	3.2
1	D	38	ALA	3.2
1	E	39	MET	3.1
1	C	38	ALA	3.1
1	C	247	ALA	2.9
1	B	157	ASN	2.9
1	A	134	ALA	2.9
1	A	32	ASP	2.9
1	F	129	ALA	2.9
1	D	248	ASP	2.9
1	E	135	THR	2.9
1	A	38	ALA	2.9
1	C	248	ASP	2.8
1	B	31	PRO	2.8
1	E	42	LYS	2.8
1	D	135	THR	2.8
1	A	39	MET	2.6
1	B	32	ASP	2.6
1	D	36	VAL	2.6
1	A	35	LYS	2.6
1	F	125	PRO	2.6
1	D	158	MET	2.6
1	D	134	ALA	2.6
1	B	36	VAL	2.5
1	D	130	GLY	2.5
1	D	37	PRO	2.5
1	F	42	LYS	2.5
1	E	165	LYS	2.5
1	E	36	VAL	2.5
1	C	32	ASP	2.5
1	E	132	SER	2.5
1	B	38	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	153	ALA	2.5
1	C	217	GLN	2.4
1	F	154	GLU	2.4
1	E	37	PRO	2.4
1	E	33	TRP	2.4
1	B	228	GLY	2.4
1	F	122	ASP	2.4
1	C	134	ALA	2.3
1	B	135	THR	2.3
1	F	38	ALA	2.3
1	E	32	ASP	2.3
1	E	137	SER	2.3
1	F	216	ALA	2.3
1	B	154	GLU	2.2
1	D	31	PRO	2.2
1	C	157	ASN	2.2
1	D	42	LYS	2.2
1	F	41	ARG	2.2
1	A	34	ASN	2.2
1	E	158	MET	2.2
1	E	53	GLU	2.2
1	B	229	SER	2.2
1	F	156	TRP	2.2
1	E	35	LYS	2.2
1	F	37	PRO	2.2
1	D	247	ALA	2.2
1	E	133	SER	2.2
1	C	180	ASN	2.2
1	E	34	ASN	2.2
1	C	31	PRO	2.1
1	D	230	PRO	2.1
1	B	217	GLN	2.1
1	D	120	SER	2.1
1	A	154	GLU	2.1
1	D	169	VAL	2.1
1	C	36	VAL	2.1
1	E	56	LYS	2.1
1	F	247	ALA	2.1
1	A	135	THR	2.1
1	C	37	PRO	2.1
1	E	31	PRO	2.1
1	D	35	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	154	GLU	2.0
1	E	40	GLU	2.0
1	E	12	GLY	2.0
1	D	129	ALA	2.0
1	C	35	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

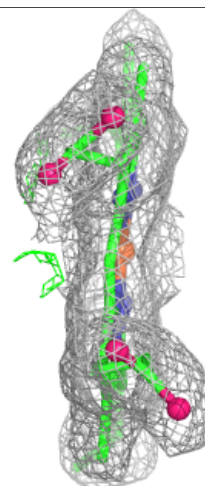
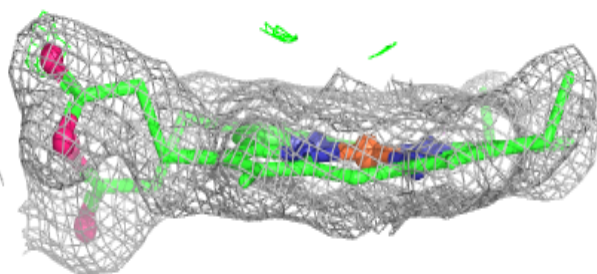
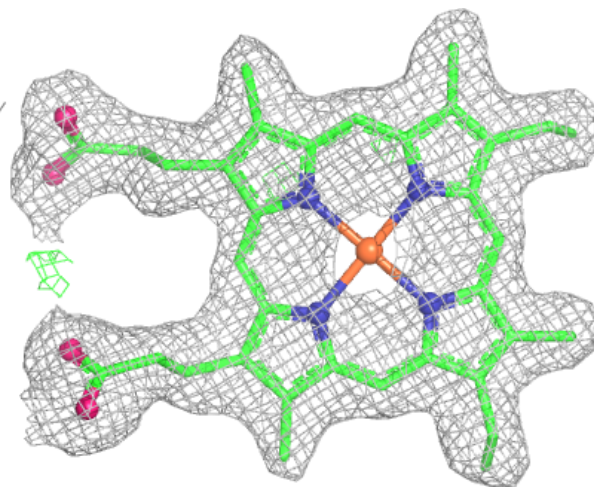
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CO3	A	1003	4/4	0.67	0.16	38,38,39,40	0
4	CO3	C	1003	4/4	0.75	0.16	40,41,41,42	0
4	CO3	B	1003	4/4	0.84	0.12	45,45,45,45	0
4	CO3	F	1003	4/4	0.84	0.12	48,49,49,49	0
4	CO3	E	1003	4/4	0.86	0.12	33,35,35,35	0
3	SCN	C	1002	3/3	0.95	0.09	20,20,20,22	0
3	SCN	D	1002	3/3	0.96	0.07	18,18,18,20	0
2	HEM	D	1001	43/43	0.97	0.07	20,24,26,28	0
2	HEM	A	1001	43/43	0.97	0.06	14,17,20,22	0
3	SCN	F	1002	3/3	0.98	0.06	21,21,22,22	0
2	HEM	F	1001	43/43	0.98	0.07	23,25,28,30	0
3	SCN	A	1002	3/3	0.98	0.06	19,19,20,22	0
3	SCN	B	1002	3/3	0.98	0.06	18,18,19,20	0
2	HEM	C	1001	43/43	0.98	0.06	17,19,21,23	0
2	HEM	E	1001	43/43	0.98	0.06	14,17,20,22	0
2	HEM	B	1001	43/43	0.99	0.05	15,18,24,25	0
3	SCN	E	1002	3/3	0.99	0.04	16,16,17,17	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.

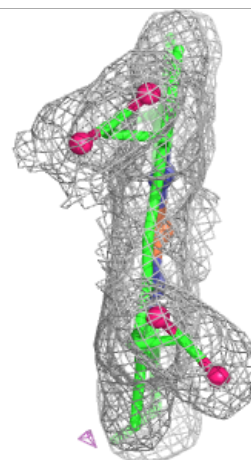
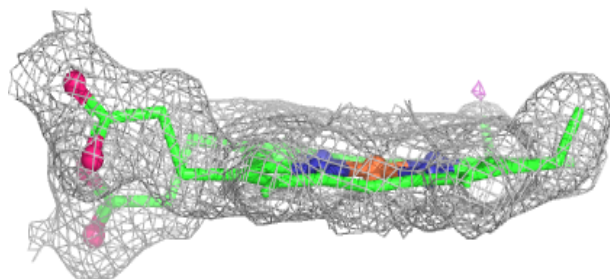
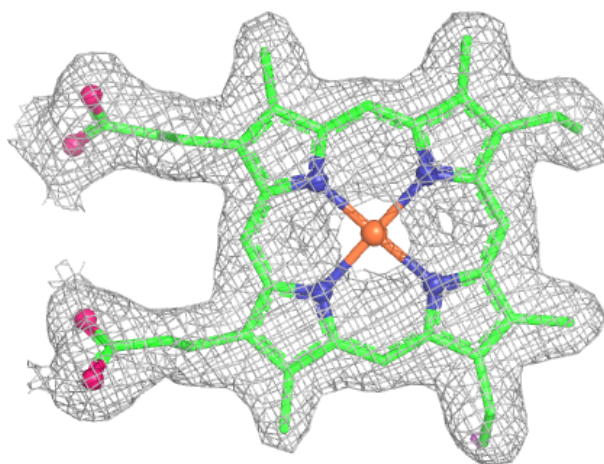
Electron density around HEM D 1001:

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



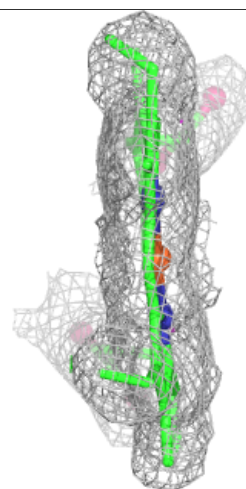
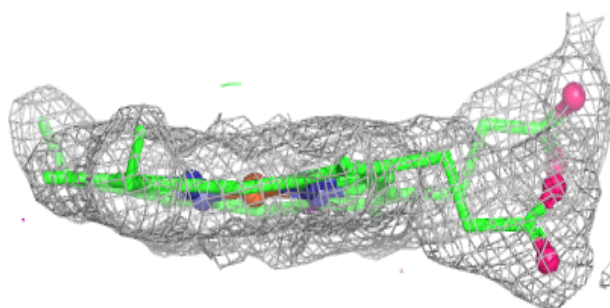
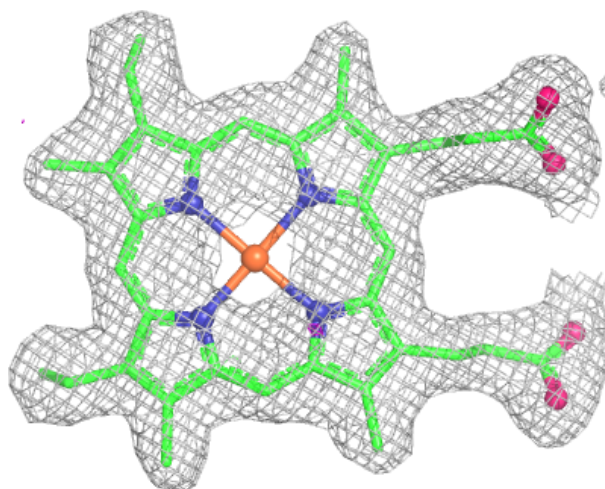
Electron density around HEM A 1001:

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



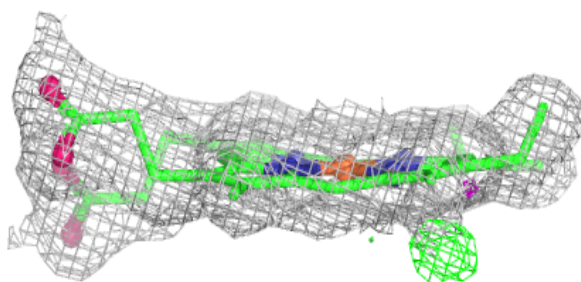
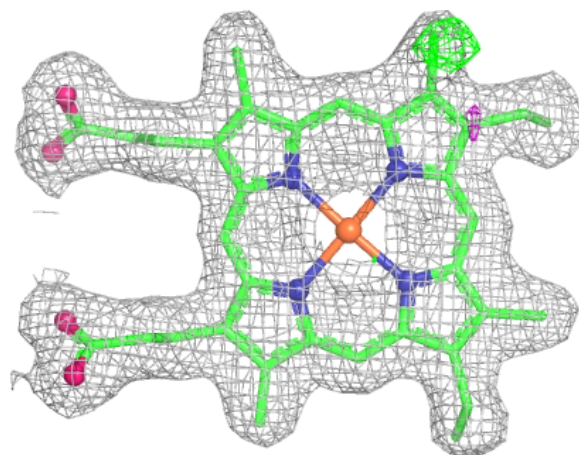
Electron density around HEM F 1001:

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



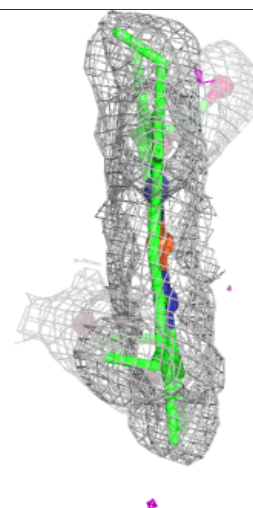
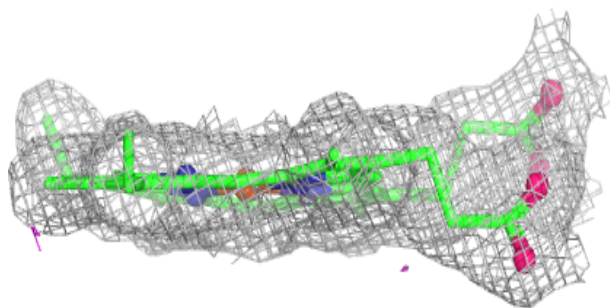
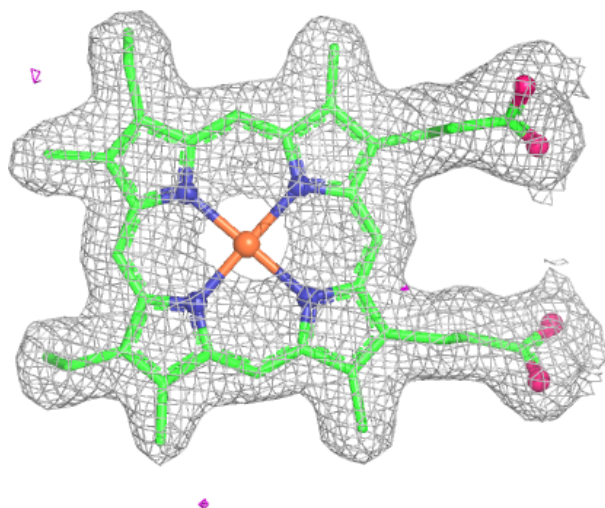
Electron density around HEM C 1001:

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



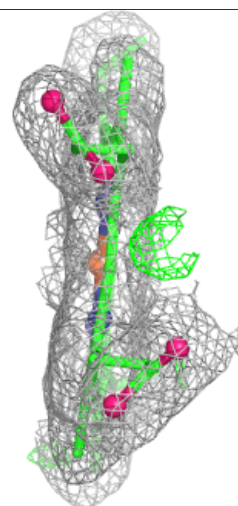
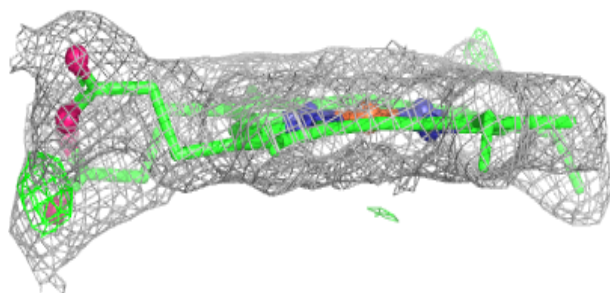
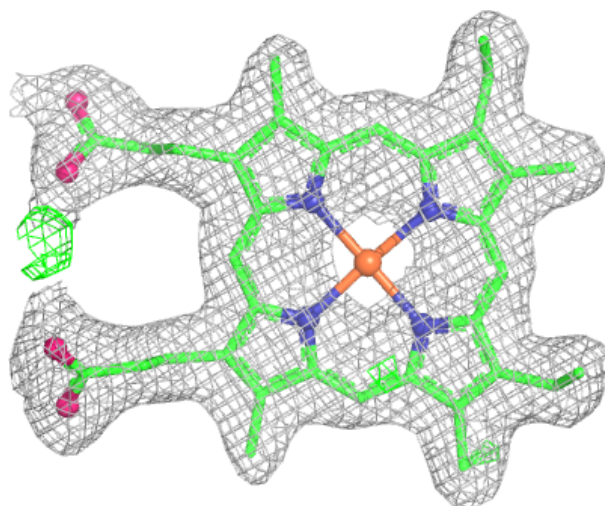
Electron density around HEM E 1001:

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



Electron density around HEM B 1001:

$2mF_o-DF_c$ (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.