



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 14, 2023 – 07:31 PM EDT

PDB ID : 7UVB  
Title : CRYSTAL STRUCTURE OF CARBONMONOXY HEMOGLOBIN S (LIG-  
ANDED SICKLE CELL HEMOGLOBIN) COMPLEXED WITH GBT021601  
Authors : Partridge, J.R.; Kaya, E.; Xu, Q.; Li, Z.; Strutt, S.C.; Cathers, B.E.  
Deposited on : 2022-04-29  
Resolution : 2.05 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

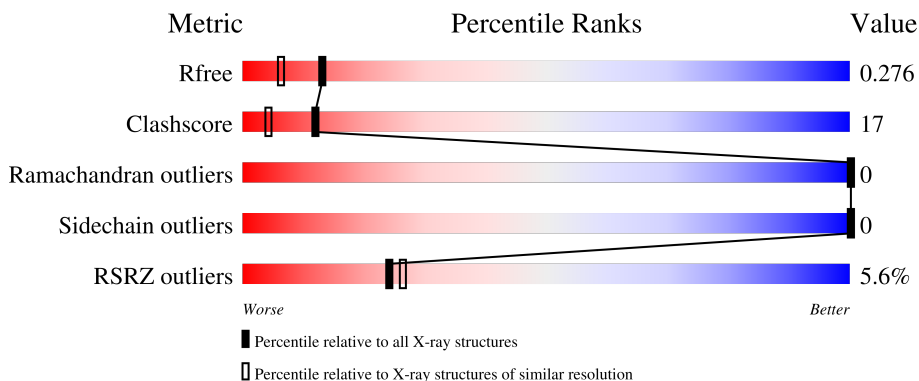
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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))
$R_{free}$	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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  $\geq 3$ , 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	 6% 67% 33%
1	C	141	 % 86% 14%
2	B	146	 5% 73% 27%
2	D	146	 10% 74% 25% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	FOR	B	202	-	-	X	-
5	OHF	A	203	-	-	X	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4732 atoms, of which 44 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
			Total	C	N	O	S			
1	A	141	1076	690	187	196	3	0	2	0
1	C	141	1075	689	187	196	3	0	2	0

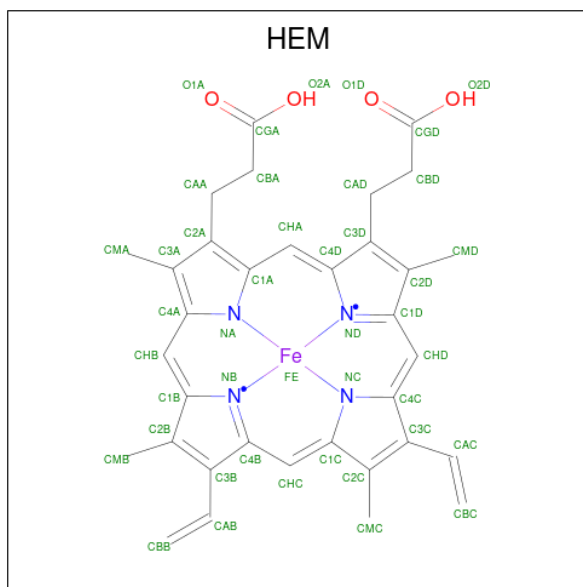
- Molecule 2 is a protein called Hemoglobin subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	146	1126	727	195	201	3	0	1	0
2	D	145	1114	719	194	198	3	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

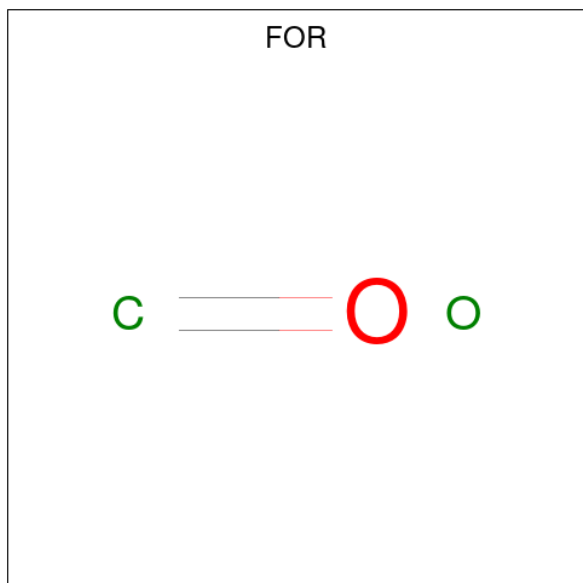
Chain	Residue	Modelled	Actual	Comment	Reference
B	6	VAL	GLU	engineered mutation	UNP P68871
D	6	VAL	GLU	engineered mutation	UNP P68871

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



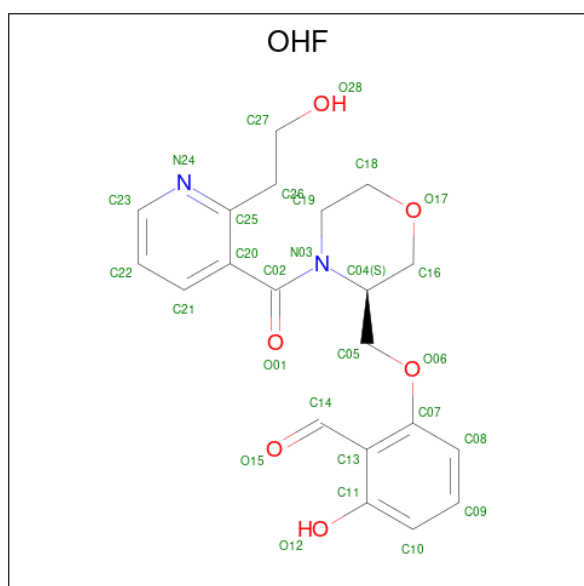
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Fe	N			O
3	A	1	43	34	1	4	4	0	0
3	B	1	43	34	1	4	4	0	0
3	C	1	43	34	1	4	4	0	0
3	D	1	43	34	1	4	4	0	0

- Molecule 4 is FORMYL GROUP (three-letter code: FOR) (formula: CH<sub>2</sub>O).



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

- Molecule 5 is 2-hydroxy-6-((3S)-4-[2-(2-hydroxyethyl)pyridine-3-carbonyl]morpholin-3-yl)methoxy)benzaldehyde (three-letter code: OHF) (formula: C<sub>20</sub>H<sub>22</sub>N<sub>2</sub>O<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C H N O 49 20 22 2 5	0	0
5	C	1	Total C H N O 49 20 22 2 5	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	19	Total O 19 19	0	0
6	B	12	Total O 12 12	0	0
6	C	26	Total O 26 26	0	0

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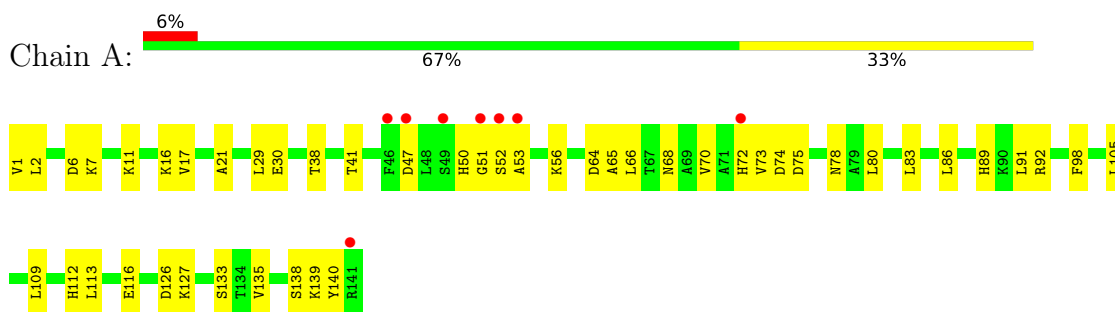
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
6	D	6	Total O 6 6	0	0

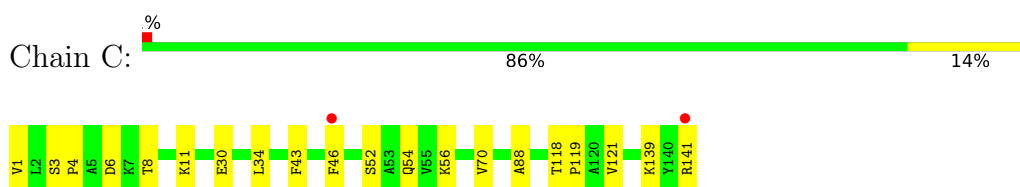
### 3 Residue-property plots [i](#)

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.

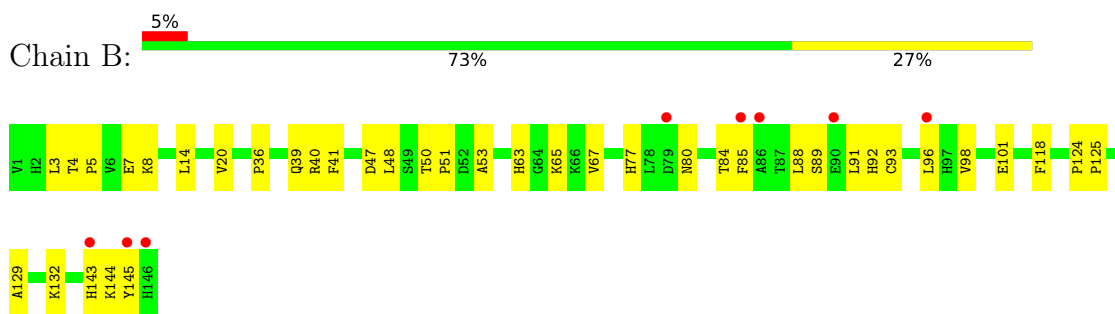
- Molecule 1: Hemoglobin subunit alpha



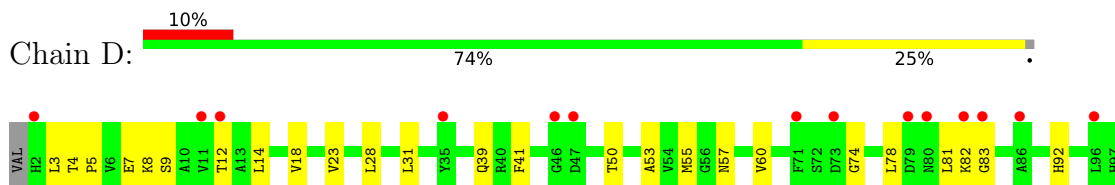
- Molecule 1: Hemoglobin subunit alpha



- Molecule 2: Hemoglobin subunit beta



- Molecule 2: Hemoglobin subunit beta







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.33Å 58.88Å 173.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.63 – 2.05 39.63 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.7 (39.63-2.05) 93.8 (39.63-2.05)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.20 (at 2.05Å)	Xtrriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, $R_{free}$	0.215 , 0.277 0.219 , 0.276	Depositor DCC
$R_{free}$ test set	1997 reflections (5.38%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.2	Xtrriage
Anisotropy	0.241	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 55.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.030 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4732	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.49	0/1110	0.61	0/1509
1	C	0.46	0/1109	0.58	0/1507
2	B	0.45	0/1159	0.54	0/1575
2	D	0.40	0/1144	0.50	0/1554
All	All	0.45	0/4522	0.56	0/6145

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1076	0	1085	49	0
1	C	1075	0	1083	25	0
2	B	1126	0	1125	31	0
2	D	1114	0	1109	39	0
3	A	43	0	30	8	0
3	B	43	0	30	13	0
3	C	43	0	30	1	0
3	D	43	0	30	5	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	6	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	27	22	0	10	0
5	C	27	22	0	6	0
6	A	19	0	0	1	0
6	B	12	0	0	1	0
6	C	26	0	0	0	0
6	D	6	0	0	0	0
All	All	4688	44	4522	157	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

All (157) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:VAL:CA	5:A:203:OHF:C14	2.11	1.29
1:C:1:VAL:CA	5:C:203:OHF:C14	2.15	1.23
3:B:201:HEM:FE	4:B:202:FOR:C	1.16	1.16
3:B:201:HEM:ND	4:B:202:FOR:C	2.04	1.09
1:A:1:VAL:N	5:A:203:OHF:C13	2.16	1.08
3:D:201:HEM:HBB2	3:D:201:HEM:HHC	1.40	1.04
3:B:201:HEM:HBC2	3:B:201:HEM:HMC2	1.41	1.01
1:C:1:VAL:N	5:C:203:OHF:C13	2.24	1.00
3:B:201:HEM:NC	4:B:202:FOR:C	2.17	0.98
2:B:91:LEU:O	2:B:96:LEU:HD12	1.65	0.95
1:A:65:ALA:HB2	3:A:201:HEM:HMA2	1.59	0.85
1:C:1:VAL:N	5:C:203:OHF:C14	0.69	0.78
1:A:1:VAL:N	5:A:203:OHF:C14	0.65	0.78
1:C:141:ARG:HG3	1:C:141:ARG:OXT	1.86	0.76
1:A:51:GLY:HA2	1:A:56:LYS:HE3	1.69	0.75
1:A:65:ALA:HB2	3:A:201:HEM:CMA	2.17	0.74
2:D:81:LEU:H	2:D:81:LEU:HD12	1.52	0.74
3:D:201:HEM:HBB2	3:D:201:HEM:CHC	2.14	0.73
3:B:201:HEM:NB	4:B:202:FOR:C	2.41	0.73
3:B:201:HEM:NA	4:B:202:FOR:C	2.42	0.73
3:B:201:HEM:HBC2	3:B:201:HEM:CMC	2.16	0.72
3:D:201:HEM:HHC	3:D:201:HEM:CBB	2.17	0.72
2:B:63:HIS:O	2:B:67:VAL:HG23	1.90	0.70
1:A:138:SER:OG	1:C:1:VAL:HG23	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:201:HEM:HMB1	3:A:201:HEM:HBB2	1.73	0.70
2:B:80:ASN:O	2:B:84:THR:HG23	1.91	0.70
1:C:1:VAL:H1	5:C:203:OHF:C14	0.82	0.69
1:A:138:SER:OG	1:C:1:VAL:CG2	2.41	0.69
1:A:66:LEU:O	1:A:70:VAL:HG23	1.93	0.69
1:A:65:ALA:CB	3:A:201:HEM:HMA2	2.23	0.68
1:A:16:LYS:HG3	1:A:116:GLU:OE1	1.94	0.68
1:A:86:LEU:O	1:A:91:LEU:HG	1.94	0.68
2:D:8:LYS:O	2:D:12:THR:HG23	1.94	0.67
2:B:93:CYS:HB3	2:B:145:TYR:CE1	2.30	0.67
1:A:1:VAL:H3	5:A:203:OHF:C14	0.82	0.67
2:B:89:SER:OG	2:B:144:LYS:HG2	1.95	0.67
3:B:201:HEM:HBD2	3:B:201:HEM:CMD	2.25	0.66
1:C:1:VAL:H2	5:C:203:OHF:C14	0.94	0.64
1:C:52:SER:O	1:C:56:LYS:HG3	1.96	0.64
2:B:77:HIS:HB2	2:B:84:THR:HG21	1.79	0.64
1:A:7:LYS:O	1:A:11:LYS:HD2	1.99	0.63
1:A:140:TYR:CD2	1:C:1:VAL:HG21	2.33	0.63
1:A:1:VAL:H1	5:A:203:OHF:C13	1.94	0.63
2:B:4:THR:HG23	2:B:7:GLU:H	1.62	0.63
1:A:75:ASP:OD1	1:A:78:ASN:HB2	1.98	0.62
2:B:50:THR:HG23	2:B:53:ALA:H	1.65	0.62
1:A:80:LEU:CD2	1:A:83:LEU:HD12	2.29	0.61
3:B:201:HEM:HBB2	3:B:201:HEM:HHC	1.82	0.61
1:A:1:VAL:H1	5:A:203:OHF:C14	0.84	0.61
3:B:201:HEM:CBD	3:B:201:HEM:HMD1	2.30	0.61
2:D:57:ASN:HB3	2:D:60:VAL:CG2	2.30	0.61
2:D:82:LYS:HG3	2:D:83:GLY:N	2.16	0.60
3:A:201:HEM:HBB2	3:A:201:HEM:CMB	2.32	0.60
2:D:14:LEU:C	2:D:14:LEU:HD23	2.21	0.60
2:B:14:LEU:HD11	2:B:118:PHE:CG	2.37	0.59
1:A:2:LEU:HB3	1:A:6:ASP:HB2	1.85	0.59
2:D:92:HIS:HD2	2:D:141:LEU:HD21	1.68	0.59
1:C:1:VAL:HG23	1:C:1:VAL:O	2.02	0.58
1:C:1:VAL:H3	5:C:203:OHF:C14	1.02	0.58
2:D:123:THR:OG1	2:D:125:PRO:HD2	2.04	0.58
2:D:100:PRO:HG3	2:D:145:TYR:CD2	2.39	0.58
2:B:4:THR:OG1	2:B:5:PRO:HD2	2.03	0.57
2:D:31:LEU:HD22	2:D:106:LEU:HD13	1.85	0.57
2:D:100:PRO:HG3	2:D:145:TYR:CE2	2.39	0.57
2:D:78:LEU:HA	2:D:81:LEU:HD11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:201:HEM:HBD2	3:B:201:HEM:HMD1	1.87	0.56
2:D:92:HIS:CE1	3:D:201:HEM:NA	2.74	0.56
2:D:28:LEU:HD22	2:D:60:VAL:HG13	1.87	0.56
2:B:4:THR:O	2:B:8:LYS:HG3	2.06	0.56
3:A:201:HEM:HMC1	3:A:201:HEM:HBC2	1.87	0.55
1:A:47:ASP:HB3	1:A:52:SER:OG	2.05	0.55
2:B:50:THR:OG1	2:B:51:PRO:HD2	2.07	0.55
2:D:103:PHE:CD1	2:D:141:LEU:HD23	2.43	0.54
2:B:93:CYS:HB3	2:B:145:TYR:CZ	2.42	0.54
2:D:92:HIS:CD2	2:D:141:LEU:HD21	2.42	0.54
2:D:57:ASN:HB3	2:D:60:VAL:HG23	1.89	0.54
2:B:40:ARG:HD2	6:B:302:HOH:O	2.09	0.53
3:A:201:HEM:HBC2	3:A:201:HEM:CMC	2.39	0.53
2:D:82:LYS:CG	2:D:83:GLY:N	2.71	0.52
3:B:201:HEM:CMD	3:B:201:HEM:CBD	2.87	0.52
1:A:7:LYS:HD3	1:A:74:ASP:OD1	2.10	0.52
2:B:41:PHE:CE1	2:B:98:VAL:HG22	2.45	0.51
1:A:89:HIS:CD2	1:A:139:LYS:HG2	2.46	0.51
1:C:30:GLU:O	1:C:34:LEU:HD13	2.11	0.51
2:B:92:HIS:HA	2:B:96:LEU:HD12	1.92	0.50
2:B:124:PRO:HB2	2:B:125:PRO:HD3	1.93	0.50
1:A:38:THR:O	1:A:41[A]:THR:HG22	2.10	0.50
1:C:43:PHE:HB3	1:C:46:PHE:HB2	1.94	0.50
2:D:82:LYS:CG	2:D:83:GLY:H	2.25	0.50
2:D:28:LEU:HD23	2:D:28:LEU:O	2.11	0.50
2:D:4:THR:HB	2:D:5:PRO:HD2	1.95	0.49
2:D:105:LEU:O	2:D:109:VAL:HG23	2.13	0.49
2:B:65:LYS:O	2:B:65:LYS:HD3	2.12	0.49
2:D:103:PHE:CE1	2:D:141:LEU:HD23	2.48	0.48
1:A:98:PHE:HB3	1:A:133:SER:OG	2.13	0.48
3:B:201:HEM:C1D	4:B:202:FOR:C	2.84	0.48
2:D:41:PHE:CE1	2:D:98:VAL:HG22	2.48	0.48
2:B:47:ASP:O	2:B:48:LEU:HD23	2.14	0.48
2:B:3:LEU:O	2:B:8:LYS:HE3	2.14	0.47
2:B:101:GLU:HA	2:B:101:GLU:OE1	2.15	0.47
1:A:127:LYS:HG3	6:A:311:HOH:O	2.14	0.47
2:D:28:LEU:HD23	2:D:28:LEU:C	2.35	0.47
2:B:85:PHE:CD1	2:B:88:LEU:HD12	2.50	0.46
2:B:36:PRO:O	2:B:39:GLN:HG3	2.16	0.46
1:A:138:SER:CB	1:C:1:VAL:CG2	2.94	0.45
1:A:7:LYS:HG2	1:A:73:VAL:HG11	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:SER:CB	1:C:1:VAL:HG22	2.47	0.45
2:B:65:LYS:HD3	2:B:65:LYS:C	2.36	0.45
1:A:47:ASP:HB3	1:A:52:SER:HG	1.81	0.45
1:C:11:LYS:HE2	1:C:70:VAL:O	2.16	0.45
2:D:123:THR:CB	2:D:125:PRO:HD2	2.47	0.44
1:A:112:HIS:O	1:A:113:LEU:HD12	2.17	0.44
3:C:201:HEM:CMB	3:C:201:HEM:HBB2	2.48	0.44
2:D:78:LEU:HD23	2:D:81:LEU:HD21	2.00	0.44
1:A:29:LEU:O	1:A:30:GLU:C	2.55	0.44
2:B:129:ALA:O	2:B:132:LYS:HB2	2.18	0.44
1:A:68:ASN:OD1	1:A:72:HIS:ND1	2.51	0.43
2:B:3:LEU:HB2	2:B:8:LYS:HG2	2.00	0.43
1:C:3:SER:O	1:C:6:ASP:HB2	2.18	0.43
1:A:17:VAL:CG1	1:A:21:ALA:HA	2.48	0.43
2:D:18:VAL:HG13	2:D:23:VAL:HG11	1.99	0.43
1:A:92:ARG:HD3	2:D:39:GLN:HB2	2.01	0.43
1:A:1:VAL:H2	5:A:203:OHF:C13	2.08	0.43
1:C:118:THR:OG1	1:C:121:VAL:HG23	2.19	0.43
2:D:137:VAL:O	2:D:141:LEU:HB2	2.18	0.42
1:A:2:LEU:HB3	1:A:6:ASP:CB	2.49	0.42
1:A:53:ALA:HA	1:A:56:LYS:HB2	2.02	0.42
2:D:50:THR:H	2:D:53:ALA:HB3	1.84	0.42
1:A:1:VAL:H2	5:A:203:OHF:C14	1.07	0.42
2:B:143:HIS:O	2:B:144:LYS:C	2.57	0.42
1:A:105:LEU:O	1:A:109:LEU:HG	2.19	0.42
2:B:20:VAL:O	2:B:65:LYS:HG2	2.20	0.42
2:D:9:SER:HA	2:D:12:THR:OG1	2.20	0.42
2:B:91:LEU:HG	2:B:96:LEU:CD1	2.50	0.41
1:C:4:PRO:O	1:C:8:THR:HG23	2.20	0.41
1:C:46:PHE:CD1	1:C:54:GLN:NE2	2.88	0.41
2:D:82:LYS:HG3	2:D:83:GLY:H	1.83	0.41
2:D:124:PRO:N	2:D:125:PRO:CD	2.83	0.41
2:D:14:LEU:HD23	2:D:14:LEU:O	2.20	0.41
1:A:140:TYR:CD2	1:C:1:VAL:CG2	3.03	0.41
2:D:92:HIS:HE1	3:D:201:HEM:NA	2.16	0.41
1:A:1:VAL:CB	5:A:203:OHF:C14	2.91	0.41
1:A:64:ASP:O	1:A:68:ASN:N	2.37	0.41
1:A:80:LEU:HD23	1:A:83:LEU:HD12	2.03	0.41
3:A:201:HEM:HMC1	3:A:201:HEM:CBC	2.50	0.41
1:C:88:ALA:HB1	1:C:139:LYS:HG2	2.03	0.41
2:D:3:LEU:HA	2:D:7:GLU:OE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:TYR:HA	1:C:3:SER:HB3	2.03	0.41
2:D:74:GLY:O	2:D:78:LEU:HD23	2.21	0.41
1:C:119:PRO:HG2	2:D:55:MET:HG3	2.03	0.41
2:B:91:LEU:C	2:B:96:LEU:HD12	2.34	0.41
1:A:7:LYS:HG2	1:A:73:VAL:HG21	2.03	0.41
2:D:82:LYS:HE2	2:D:82:LYS:HB3	1.83	0.41
1:A:30:GLU:OE2	1:A:50:HIS:ND1	2.54	0.40
1:A:126:ASP:OD2	5:A:203:OHF:O28	2.40	0.40
2:B:4:THR:HG22	2:B:7:GLU:CG	2.52	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	141/141 (100%)	136 (96%)	5 (4%)	0	100	100
1	C	141/141 (100%)	139 (99%)	2 (1%)	0	100	100
2	B	145/146 (99%)	141 (97%)	4 (3%)	0	100	100
2	D	143/146 (98%)	136 (95%)	7 (5%)	0	100	100
All	All	570/574 (99%)	552 (97%)	18 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	115/113 (102%)	115 (100%)	0	100	100
1	C	115/113 (102%)	115 (100%)	0	100	100
2	B	119/118 (101%)	119 (100%)	0	100	100
2	D	117/118 (99%)	117 (100%)	0	100	100
All	All	466/462 (101%)	466 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	FOR	C	202	3	0,1,1	-	-	-		
4	FOR	D	202	3	0,1,1	-	-	-		
3	HEM	B	201	4,2	41,50,50	2.01	9 (21%)	45,82,82	2.23	17 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	HEM	A	201	4,1	41,50,50	2.57	16 (39%)	45,82,82	2.58	11 (24%)
4	FOR	B	202	3	0,1,1	-	-	-		
4	FOR	A	202	3	0,1,1	-	-	-		
3	HEM	D	201	4	41,50,50	2.19	13 (31%)	45,82,82	2.27	17 (37%)
5	OHF	C	203	-	29,29,30	2.80	15 (51%)	32,39,40	1.79	7 (21%)
5	OHF	A	203	-	29,29,30	2.74	12 (41%)	32,39,40	1.93	6 (18%)
3	HEM	C	201	4,1	41,50,50	2.55	15 (36%)	45,82,82	1.88	13 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEM	B	201	4,2	-	5/12/54/54	-
3	HEM	A	201	4,1	-	6/12/54/54	-
3	HEM	D	201	4	-	5/12/54/54	-
5	OHF	C	203	-	-	3/16/27/29	0/3/3/3
5	OHF	A	203	-	-	3/16/27/29	0/3/3/3
3	HEM	C	201	4,1	-	2/12/54/54	-

All (80) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	201	HEM	C1B-NB	-7.22	1.27	1.40
3	D	201	HEM	C1B-NB	-7.09	1.28	1.40
3	A	201	HEM	C1B-NB	-7.05	1.28	1.40
5	A	203	OHF	C11-C13	-6.89	1.32	1.40
5	A	203	OHF	C25-N24	-6.38	1.26	1.34
5	C	203	OHF	C11-C13	-6.27	1.32	1.40
5	C	203	OHF	C25-N24	-5.86	1.26	1.34
3	B	201	HEM	C1B-NB	-5.77	1.30	1.40
3	C	201	HEM	C4B-NB	-5.50	1.27	1.38
3	A	201	HEM	C4D-ND	-5.40	1.31	1.40
3	A	201	HEM	C1D-ND	-5.17	1.28	1.38
3	B	201	HEM	C4D-ND	-5.17	1.31	1.40
3	C	201	HEM	C3C-C2C	-4.98	1.33	1.40
5	A	203	OHF	C02-N03	4.70	1.45	1.34
3	C	201	HEM	C4D-ND	-4.68	1.32	1.40
3	A	201	HEM	C4B-NB	-4.62	1.29	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	201	HEM	C1B-C2B	-4.53	1.35	1.44
3	A	201	HEM	FE-ND	-4.49	1.74	1.96
5	C	203	OHF	C02-N03	4.36	1.44	1.34
3	D	201	HEM	C1D-ND	-4.27	1.30	1.38
5	C	203	OHF	C04-N03	-4.13	1.43	1.47
5	C	203	OHF	C09-C08	-4.13	1.30	1.38
5	A	203	OHF	C09-C08	-4.02	1.30	1.38
3	C	201	HEM	C1D-ND	-4.01	1.30	1.38
3	D	201	HEM	C4D-ND	-3.88	1.33	1.40
3	A	201	HEM	C3C-C2C	-3.82	1.35	1.40
5	C	203	OHF	O01-C02	-3.80	1.15	1.22
3	B	201	HEM	C1D-ND	-3.77	1.31	1.38
3	D	201	HEM	C3C-C2C	-3.73	1.35	1.40
3	D	201	HEM	FE-ND	-3.69	1.78	1.96
3	C	201	HEM	C3D-C2D	-3.69	1.28	1.36
5	A	203	OHF	C04-N03	-3.67	1.43	1.47
3	B	201	HEM	FE-ND	-3.65	1.78	1.96
3	C	201	HEM	C1B-C2B	-3.63	1.37	1.44
3	D	201	HEM	C4B-NB	-3.60	1.31	1.38
3	B	201	HEM	C1B-C2B	-3.60	1.37	1.44
5	C	203	OHF	C20-C02	3.54	1.56	1.50
3	A	201	HEM	C3D-C2D	-3.34	1.29	1.36
5	A	203	OHF	C05-C04	3.33	1.60	1.52
5	A	203	OHF	C22-C21	-3.33	1.31	1.38
5	C	203	OHF	C23-N24	-3.22	1.27	1.34
5	C	203	OHF	C19-N03	-3.10	1.41	1.47
3	C	201	HEM	C1A-CHA	-3.05	1.32	1.41
3	D	201	HEM	C4A-CHB	-3.05	1.32	1.41
3	D	201	HEM	C1B-C2B	-3.03	1.38	1.44
3	A	201	HEM	CHD-C1D	-3.02	1.32	1.41
5	A	203	OHF	C19-N03	-3.02	1.41	1.47
5	C	203	OHF	C22-C21	-3.00	1.32	1.38
5	A	203	OHF	O01-C02	-3.00	1.16	1.22
3	C	201	HEM	C3B-C2B	-2.98	1.31	1.37
3	C	201	HEM	FE-ND	-2.95	1.82	1.96
3	C	201	HEM	O2A-CGA	-2.91	1.20	1.30
3	B	201	HEM	C3C-C2C	-2.89	1.36	1.40
5	C	203	OHF	C26-C25	2.86	1.59	1.51
3	B	201	HEM	C4B-NB	-2.85	1.32	1.38
5	A	203	OHF	C23-N24	-2.83	1.28	1.34
5	C	203	OHF	C05-C04	2.74	1.58	1.52
3	C	201	HEM	O2D-CGD	-2.71	1.21	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	201	HEM	C3B-C2B	-2.69	1.31	1.37
3	B	201	HEM	C1A-CHA	-2.67	1.33	1.41
3	A	201	HEM	CHC-C4B	-2.66	1.33	1.41
3	C	201	HEM	C2C-C1C	-2.64	1.36	1.42
3	A	201	HEM	C1A-CHA	-2.56	1.33	1.41
3	A	201	HEM	C2C-C1C	-2.51	1.36	1.42
3	A	201	HEM	C3B-C4B	-2.49	1.39	1.44
5	C	203	OHF	C21-C20	-2.48	1.35	1.39
3	A	201	HEM	C3B-C2B	-2.44	1.32	1.37
5	C	203	OHF	O17-C16	-2.38	1.38	1.42
5	A	203	OHF	C26-C25	2.33	1.57	1.51
3	D	201	HEM	C3D-C2D	-2.31	1.31	1.36
3	D	201	HEM	O2D-CGD	-2.31	1.23	1.30
3	C	201	HEM	C2A-C3A	-2.27	1.31	1.37
3	D	201	HEM	C1A-CHA	-2.25	1.34	1.41
5	A	203	OHF	O17-C16	-2.25	1.38	1.42
3	A	201	HEM	O2A-CGA	-2.14	1.23	1.30
3	C	201	HEM	FE-NB	2.12	2.07	1.96
3	A	201	HEM	O2D-CGD	-2.11	1.23	1.30
3	D	201	HEM	C2C-C1C	-2.10	1.37	1.42
3	B	201	HEM	C3C-CAC	-2.06	1.43	1.47
5	C	203	OHF	C14-C13	2.04	1.55	1.51

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	201	HEM	CHC-C4B-NB	8.73	133.91	124.43
3	A	201	HEM	CHD-C1D-ND	6.67	131.68	124.43
3	D	201	HEM	CHC-C4B-NB	6.48	131.47	124.43
3	B	201	HEM	CHA-C4D-ND	5.73	131.47	124.38
5	A	203	OHF	C18-C19-N03	5.61	114.75	109.36
3	A	201	HEM	CHD-C1D-C2D	-5.34	116.63	124.98
3	C	201	HEM	C1B-NB-C4B	5.26	110.51	105.07
3	B	201	HEM	CHA-C4D-C3D	-5.04	115.86	125.33
3	A	201	HEM	C1B-NB-C4B	4.80	110.03	105.07
3	D	201	HEM	CHB-C1B-NB	4.52	129.97	124.38
3	B	201	HEM	CHB-C1B-NB	4.39	129.81	124.38
3	D	201	HEM	C1B-NB-C4B	4.35	109.57	105.07
5	A	203	OHF	C18-O17-C16	4.22	115.81	109.97
3	C	201	HEM	CHC-C4B-NB	4.17	128.96	124.43
5	C	203	OHF	C18-O17-C16	4.14	115.70	109.97
3	B	201	HEM	C1B-NB-C4B	4.08	109.29	105.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	201	HEM	CMA-C3A-C4A	-4.04	122.26	128.46
3	D	201	HEM	CHA-C4D-C3D	-3.99	117.83	125.33
3	A	201	HEM	CHC-C4B-C3B	-3.94	118.54	124.57
3	D	201	HEM	CHA-C4D-ND	3.90	129.20	124.38
3	D	201	HEM	CHD-C1D-ND	3.86	128.62	124.43
3	B	201	HEM	CBA-CAA-C2A	3.85	119.20	112.62
5	A	203	OHF	O17-C16-C04	-3.77	105.92	110.99
3	A	201	HEM	CHB-C1B-NB	3.74	129.01	124.38
3	B	201	HEM	CHC-C4B-NB	3.74	128.49	124.43
5	A	203	OHF	O06-C07-C13	3.70	119.15	115.33
3	C	201	HEM	CHA-C4D-C3D	-3.70	118.39	125.33
3	A	201	HEM	CHA-C4D-ND	3.69	128.94	124.38
3	C	201	HEM	CHA-C4D-ND	3.67	128.91	124.38
5	C	203	OHF	O01-C02-N03	-3.65	115.68	121.59
5	A	203	OHF	C23-N24-C25	3.63	122.38	117.81
3	B	201	HEM	CHD-C1D-ND	3.42	128.15	124.43
5	C	203	OHF	O06-C07-C13	3.26	118.70	115.33
5	C	203	OHF	C20-C02-N03	3.23	122.39	117.92
3	D	201	HEM	CHD-C1D-C2D	-3.21	119.97	124.98
3	C	201	HEM	C4B-CHC-C1C	3.05	126.58	122.56
3	C	201	HEM	O2A-CGA-CBA	3.02	123.74	114.03
5	C	203	OHF	C23-N24-C25	2.94	121.51	117.81
3	A	201	HEM	CHA-C4D-C3D	-2.91	119.87	125.33
3	B	201	HEM	C4B-C3B-C2B	-2.80	104.89	107.11
5	C	203	OHF	C16-C04-C05	-2.71	108.25	112.28
3	C	201	HEM	O2D-CGD-CBD	2.70	122.70	114.03
3	C	201	HEM	CHB-C1B-NB	2.68	127.69	124.38
3	B	201	HEM	CMD-C2D-C1D	2.67	129.10	125.04
3	D	201	HEM	CMB-C2B-C1B	2.66	129.08	125.04
3	B	201	HEM	CHB-C1B-C2B	-2.54	119.69	126.72
3	D	201	HEM	O2A-CGA-CBA	2.54	122.19	114.03
3	B	201	HEM	C3B-C2B-C1B	2.52	108.36	106.49
3	C	201	HEM	O2A-CGA-O1A	-2.50	117.06	123.30
3	D	201	HEM	CHB-C1B-C2B	-2.49	119.84	126.72
3	D	201	HEM	C3D-C4D-ND	2.43	112.88	110.17
3	C	201	HEM	CHD-C1D-ND	2.37	127.01	124.43
3	A	201	HEM	CMA-C3A-C2A	2.36	129.39	124.94
3	B	201	HEM	O2A-CGA-CBA	2.34	121.55	114.03
3	C	201	HEM	C3D-C4D-ND	2.28	112.70	110.17
3	B	201	HEM	O2D-CGD-CBD	2.26	121.30	114.03
3	D	201	HEM	CAA-CBA-CGA	-2.26	107.43	113.76
3	A	201	HEM	CBA-CAA-C2A	2.24	116.44	112.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	201	HEM	CAD-C3D-C2D	2.24	132.04	127.88
3	C	201	HEM	O2D-CGD-O1D	-2.24	117.73	123.30
3	D	201	HEM	CHC-C4B-C3B	-2.23	121.15	124.57
3	C	201	HEM	C4A-C3A-C2A	2.21	108.54	107.00
3	B	201	HEM	C3D-C4D-ND	2.21	112.63	110.17
3	D	201	HEM	CBB-CAB-C3B	-2.16	116.88	127.62
3	D	201	HEM	O1A-CGA-CBA	-2.15	116.16	123.08
5	A	203	OHF	O06-C07-C08	-2.15	119.32	123.97
3	B	201	HEM	O2A-CGA-O1A	-2.13	117.98	123.30
3	D	201	HEM	C4B-C3B-C2B	-2.10	105.44	107.11
3	B	201	HEM	CAB-C3B-C2B	-2.05	121.84	128.60
3	D	201	HEM	CMD-C2D-C1D	2.02	128.11	125.04
5	C	203	OHF	C05-C04-N03	-2.02	106.41	110.47

There are no chirality outliers.

All (24) torsion outliers are listed below:

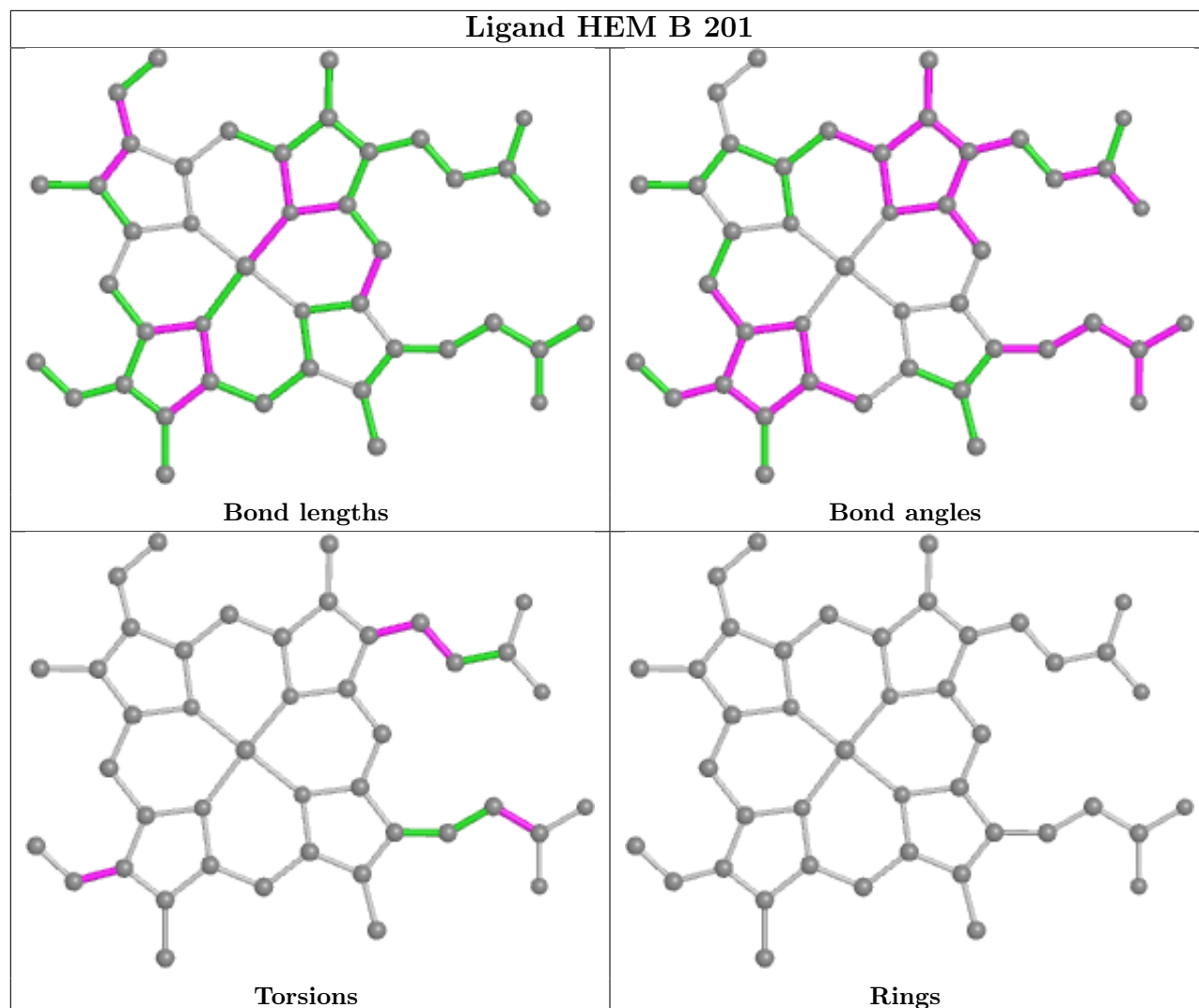
Mol	Chain	Res	Type	Atoms
3	A	201	HEM	C1A-C2A-CAA-CBA
3	A	201	HEM	C3A-C2A-CAA-CBA
3	B	201	HEM	C4D-C3D-CAD-CBD
5	A	203	OHF	C25-C26-C27-O28
5	A	203	OHF	N24-C25-C26-C27
5	A	203	OHF	C04-C05-O06-C07
5	C	203	OHF	N03-C04-C05-O06
5	C	203	OHF	C16-C04-C05-O06
3	B	201	HEM	C2D-C3D-CAD-CBD
3	D	201	HEM	C2D-C3D-CAD-CBD
3	D	201	HEM	C4D-C3D-CAD-CBD
3	D	201	HEM	C2A-CAA-CBA-CGA
5	C	203	OHF	C25-C26-C27-O28
3	B	201	HEM	C4B-C3B-CAB-CBB
3	B	201	HEM	C3D-CAD-CBD-CGD
3	D	201	HEM	CAA-CBA-CGA-O1A
3	A	201	HEM	CAA-CBA-CGA-O2A
3	C	201	HEM	CAD-CBD-CGD-O1D
3	A	201	HEM	CAA-CBA-CGA-O1A
3	A	201	HEM	CAD-CBD-CGD-O1D
3	C	201	HEM	CAD-CBD-CGD-O2D
3	A	201	HEM	CAD-CBD-CGD-O2D
3	D	201	HEM	CAA-CBA-CGA-O2A
3	B	201	HEM	CAA-CBA-CGA-O2A

There are no ring outliers.

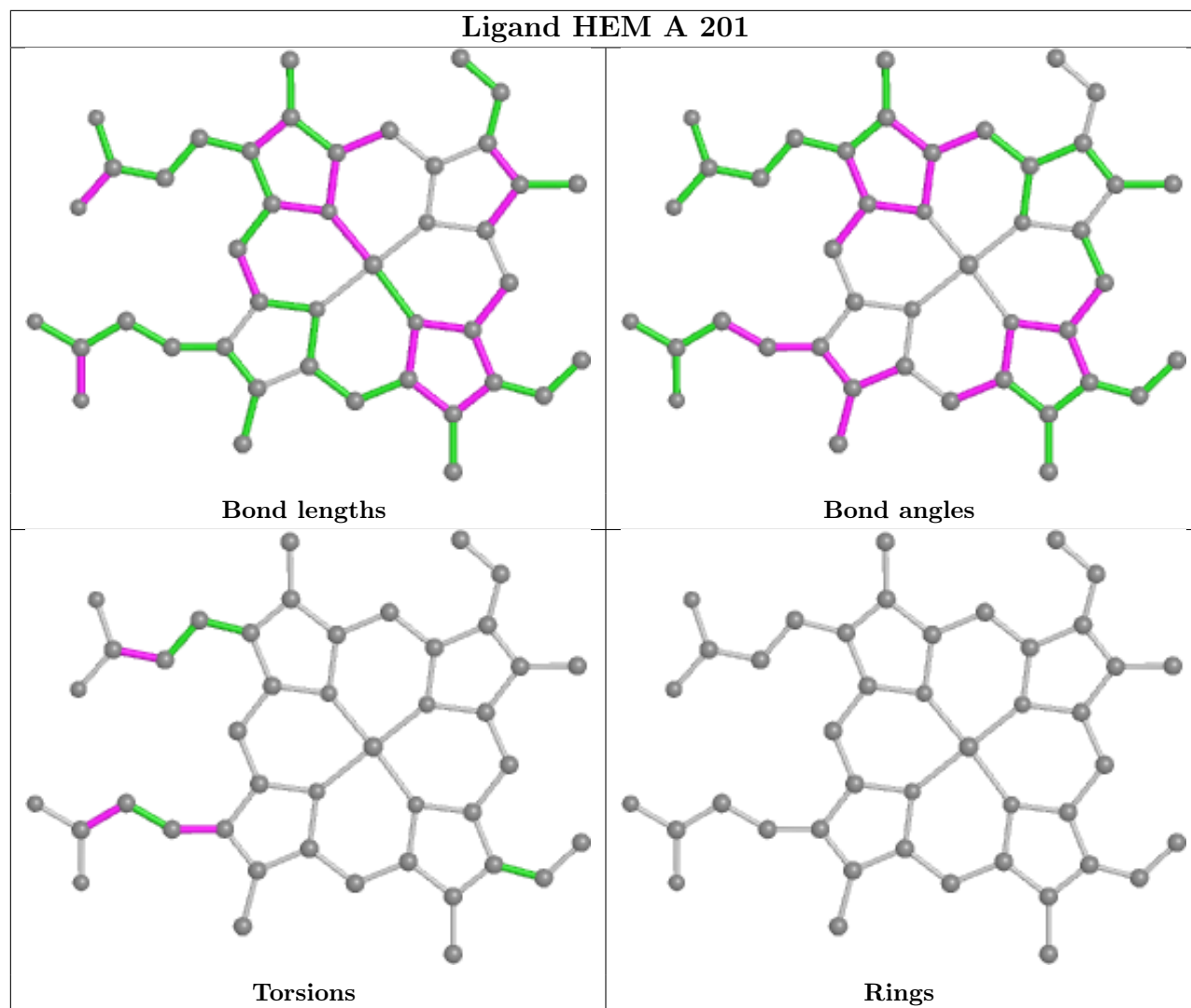
7 monomers are involved in 43 short contacts:

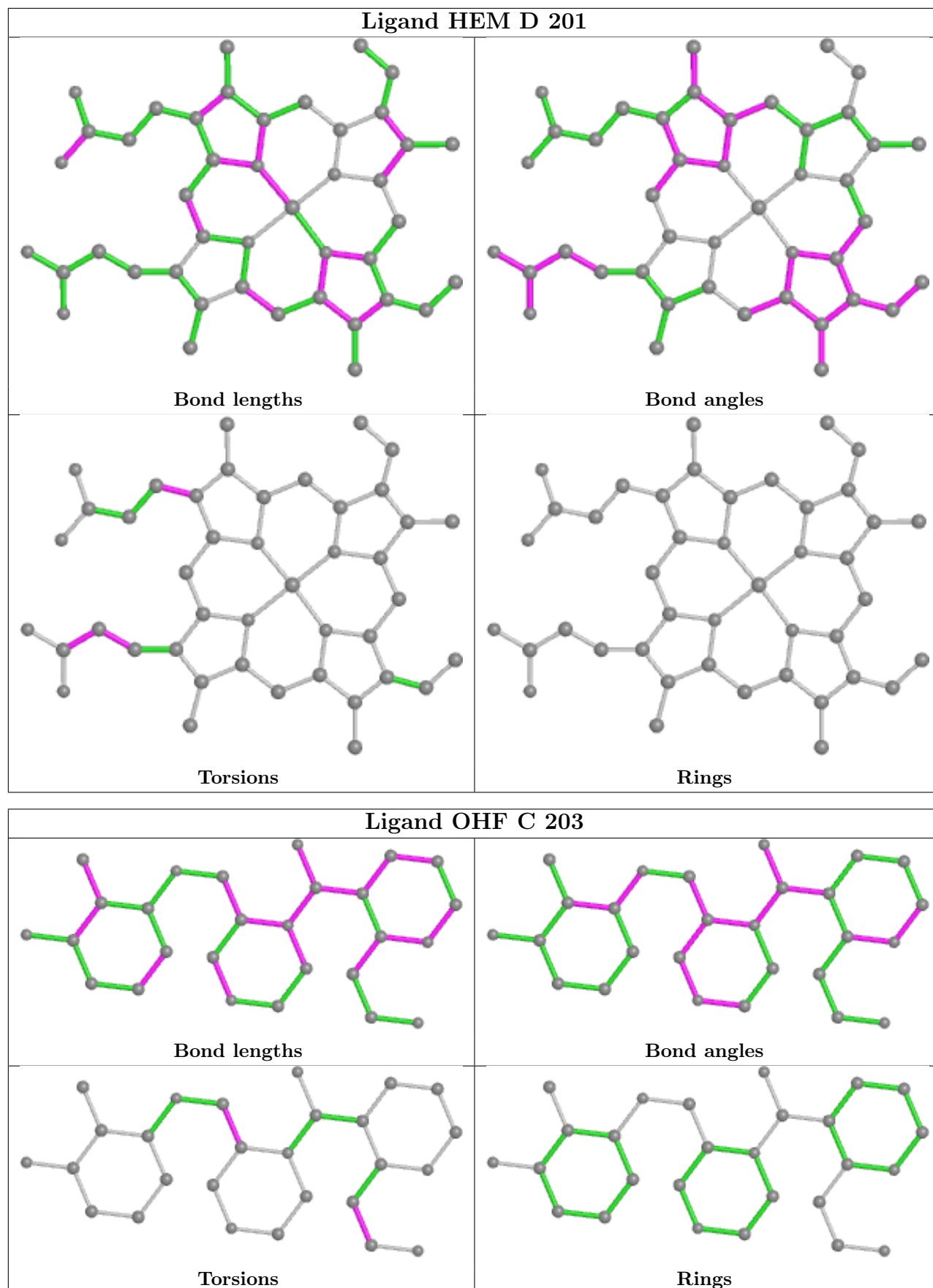
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	201	HEM	13	0
3	A	201	HEM	8	0
4	B	202	FOR	6	0
3	D	201	HEM	5	0
5	C	203	OHF	6	0
5	A	203	OHF	10	0
3	C	201	HEM	1	0

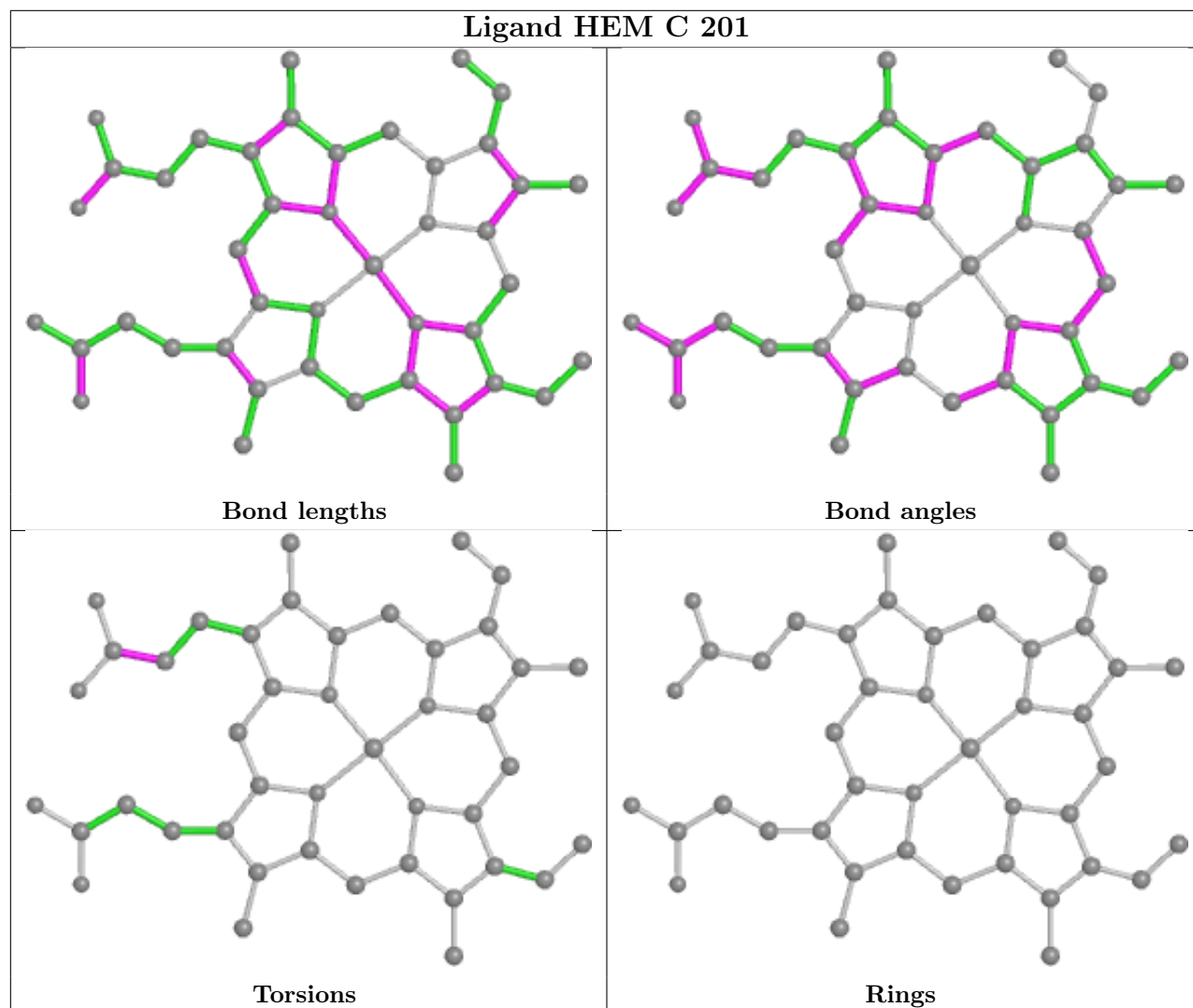
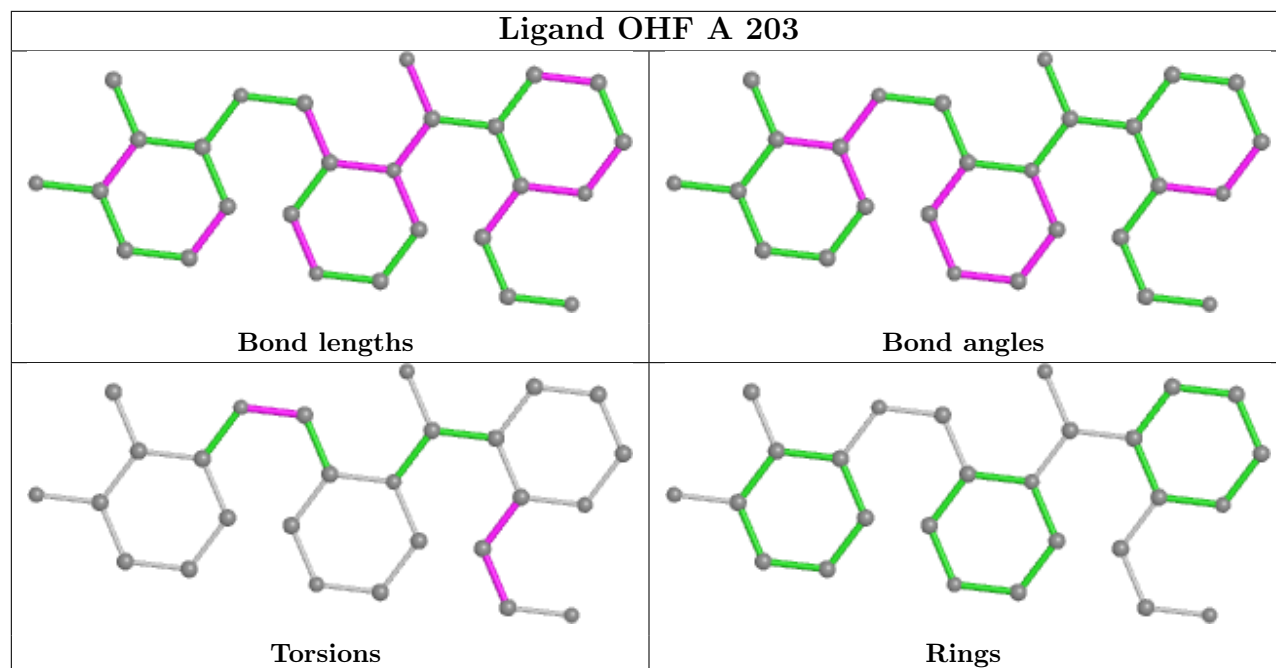
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	141/141 (100%)	0.72	8 (5%) 23 25	34, 67, 100, 124	0
1	C	141/141 (100%)	0.18	2 (1%) 75 78	31, 52, 76, 114	0
2	B	146/146 (100%)	0.43	8 (5%) 25 27	36, 69, 104, 138	0
2	D	145/146 (99%)	0.71	14 (9%) 7 8	48, 87, 125, 140	0
All	All	573/574 (99%)	0.51	32 (5%) 24 26	31, 65, 114, 140	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	85	PHE	4.9
1	A	52	SER	4.8
2	B	146	HIS	4.2
2	D	82	LYS	3.8
2	D	83	GLY	3.6
2	D	96	LEU	3.4
1	A	49	SER	3.3
1	A	72	HIS	3.2
1	C	141	ARG	3.1
2	B	90	GLU	3.0
2	D	2	HIS	2.9
2	B	79	ASP	2.9
2	B	86	ALA	2.7
1	A	51	GLY	2.7
1	C	46	PHE	2.7
1	A	53	ALA	2.6
2	D	12	THR	2.5
2	D	11	VAL	2.5
1	A	47	ASP	2.5
2	D	71	PHE	2.4
2	B	143	HIS	2.4

*Continued on next page...*

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Mol	Chain	Res	Type	RSRZ
2	D	47	ASP	2.3
2	D	79	ASP	2.3
2	D	80	ASN	2.3
1	A	46	PHE	2.3
2	D	73	ASP	2.2
2	B	145	TYR	2.2
2	D	35	TYR	2.2
1	A	141	ARG	2.2
2	D	46	GLY	2.2
2	B	96	LEU	2.1
2	D	86	ALA	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

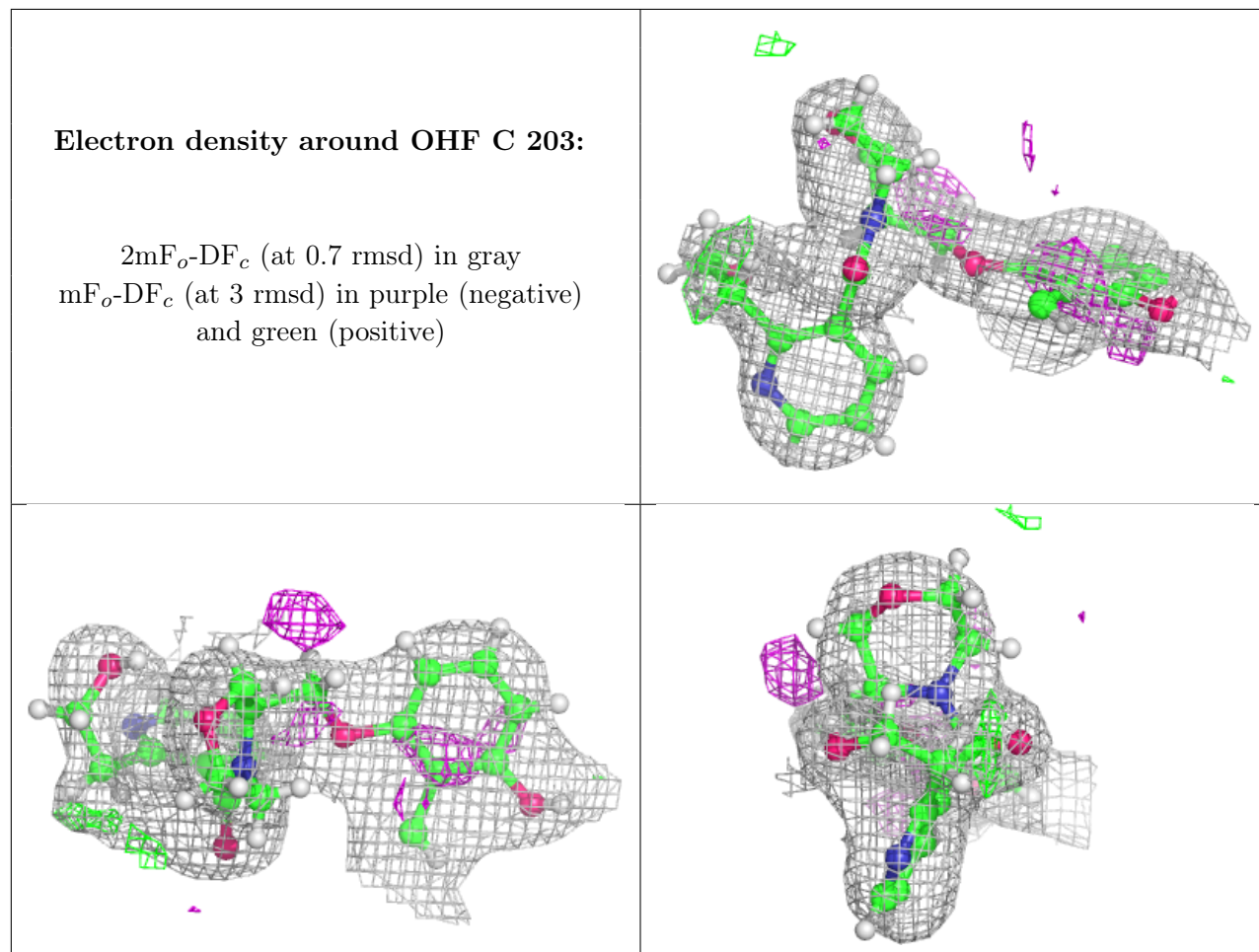
## 6.4 Ligands [i](#)

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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	OHF	C	203	27/28	0.90	0.14	31,71,104,115	0
3	HEM	A	201	43/43	0.91	0.17	44,70,98,113	0
5	OHF	A	203	27/28	0.92	0.18	29,86,125,126	0
3	HEM	D	201	43/43	0.93	0.19	58,85,126,145	0
3	HEM	B	201	43/43	0.95	0.16	41,66,102,121	0
4	FOR	D	202	2/2	0.96	0.13	106,106,106,114	0
4	FOR	A	202	2/2	0.97	0.16	129,129,129,129	0
3	HEM	C	201	43/43	0.97	0.10	26,40,69,83	0
4	FOR	C	202	2/2	0.98	0.11	68,68,68,83	0
4	FOR	B	202	2/2	0.98	0.11	142,142,142,144	0

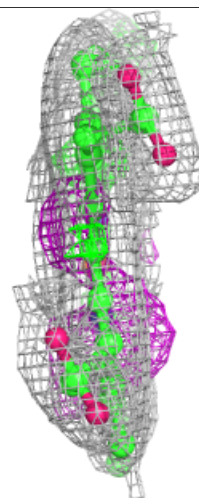
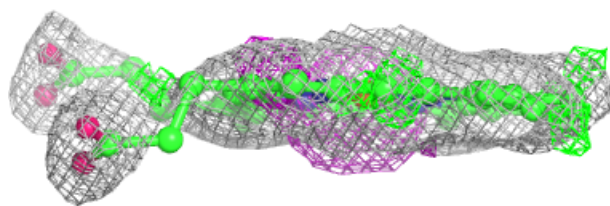
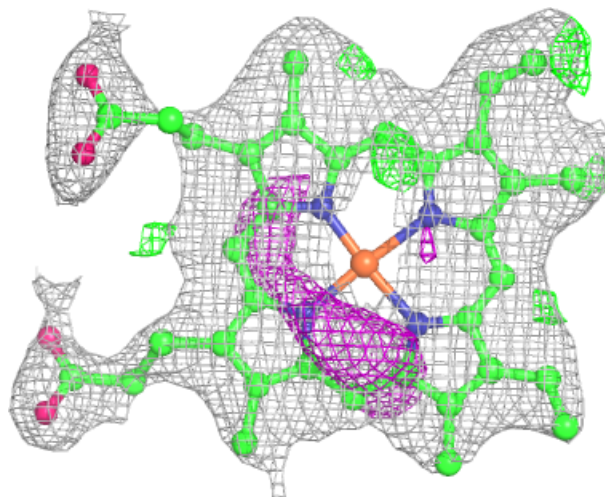
The following is a graphical depiction of the model fit to experimental electron density of all

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

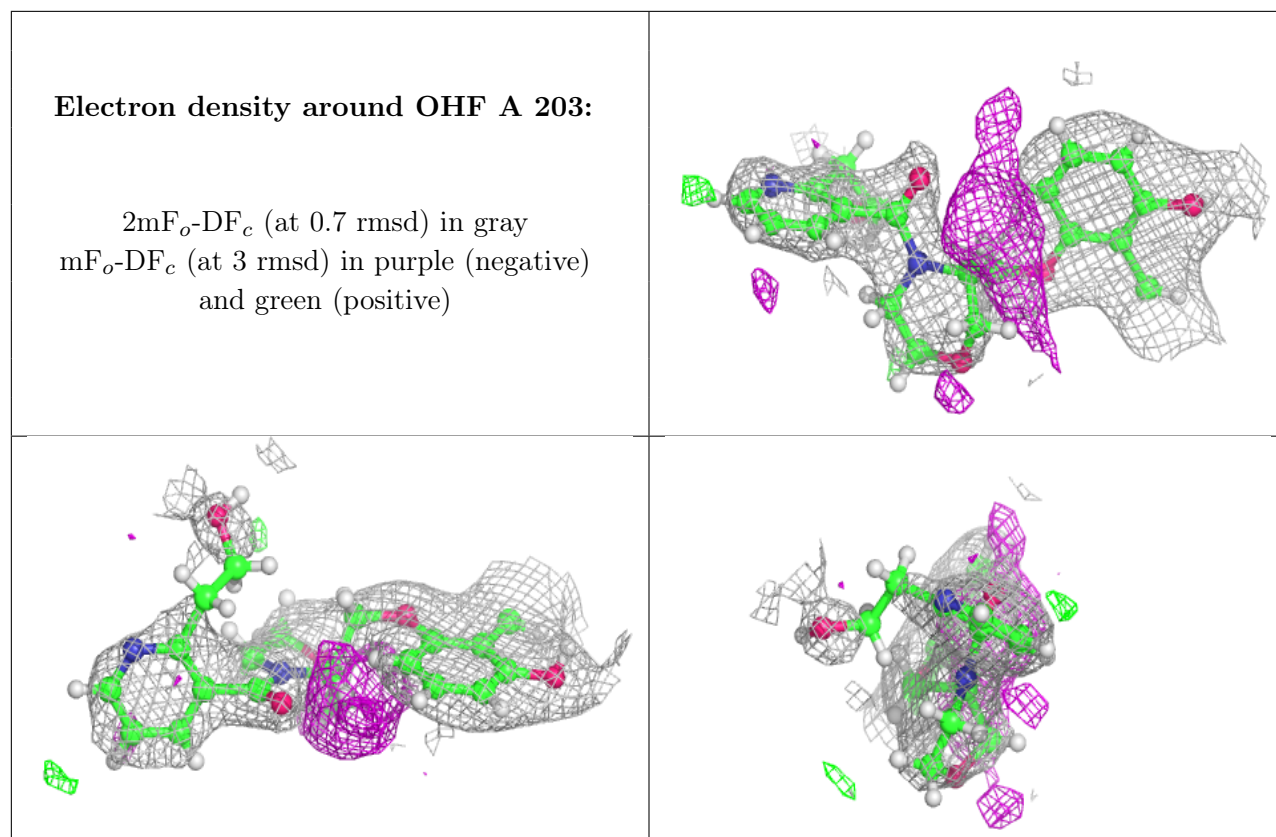


**Electron density around HEM A 201:**

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

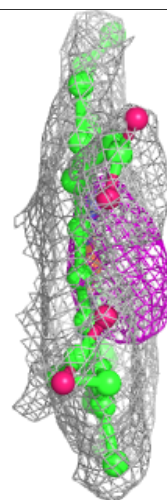
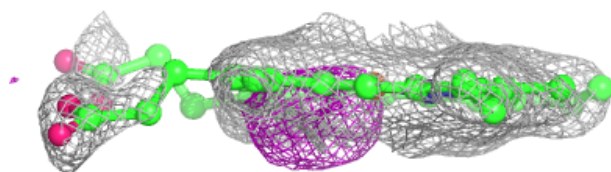
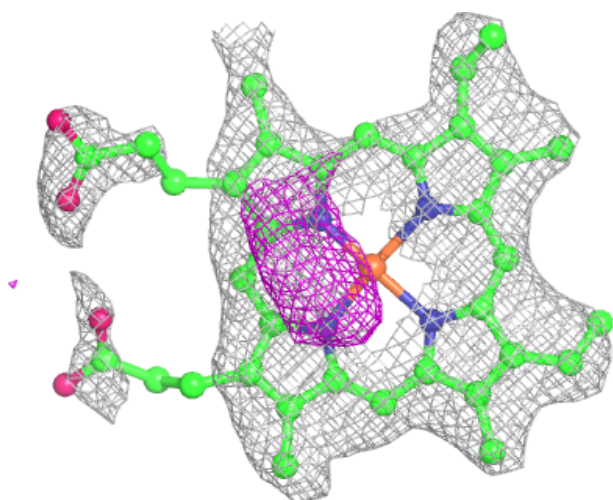






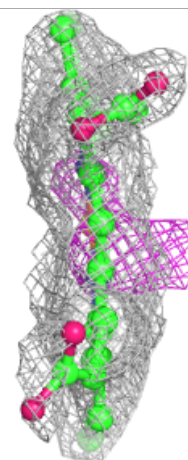
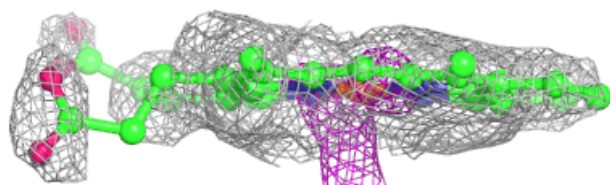
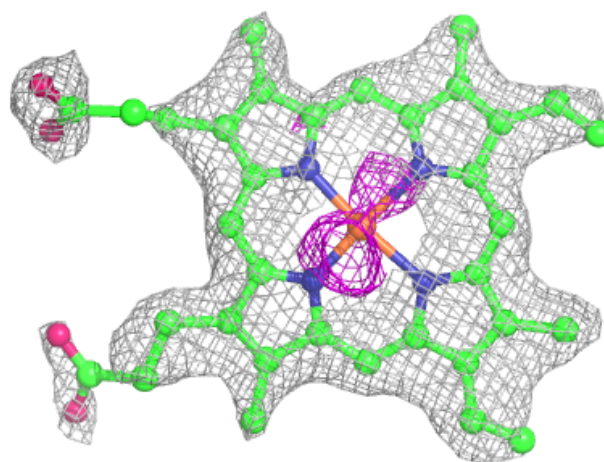
**Electron density around HEM D 201:**

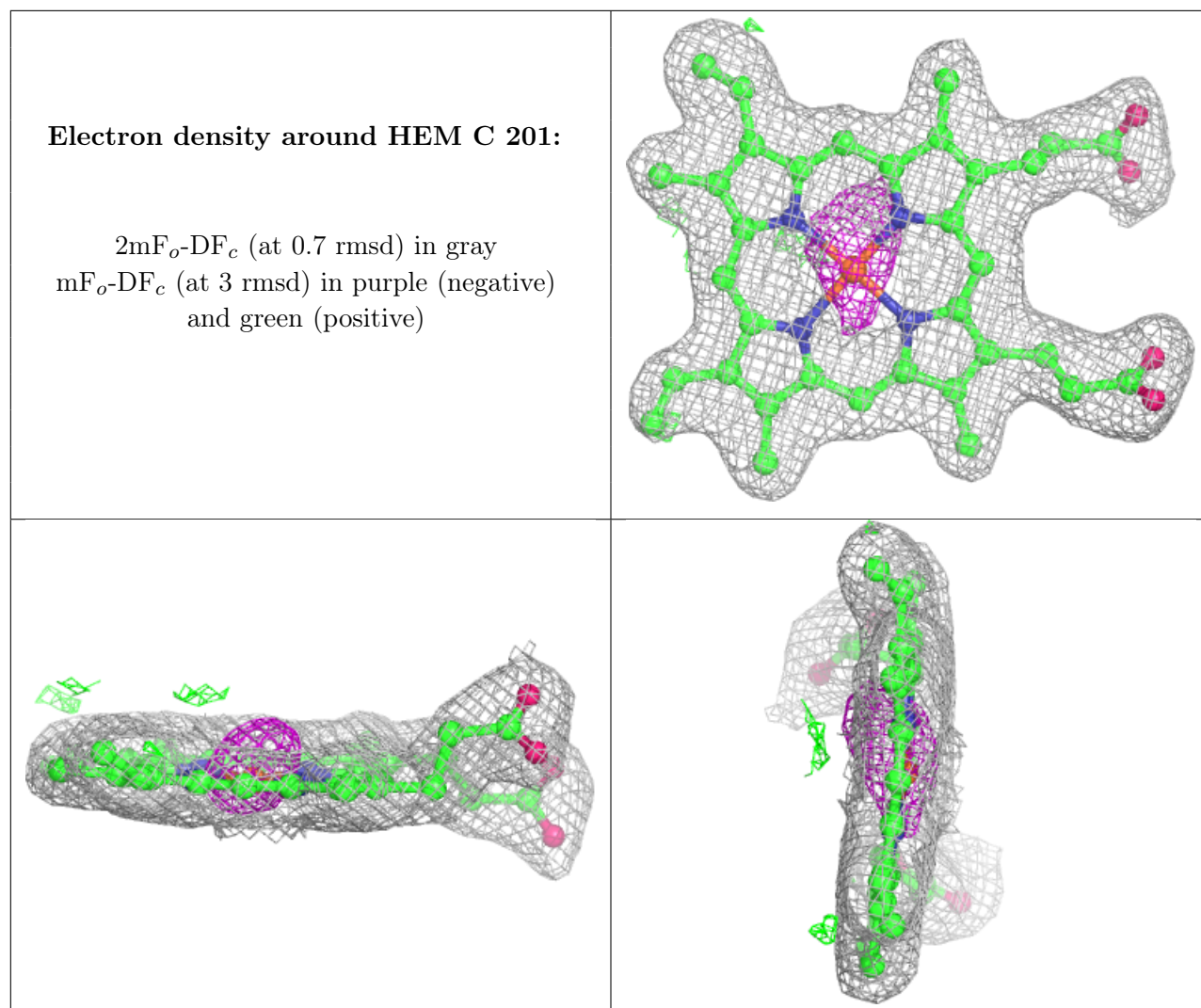
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**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)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.