



Full wwPDB X-ray Structure Validation Report ⓘ

May 7, 2026 – 11:42 AM EDT

PDB ID : 3K8B / pdb_00003k8b
Title : Crystal structure of Turkey (Meleagiris gallopova)hemoglobin at 2.3 Angstrom
Authors : Ramesh, P.; Sundaresan, S.S.; Ponnuswamy, M.N.
Deposited on : 2009-10-14
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

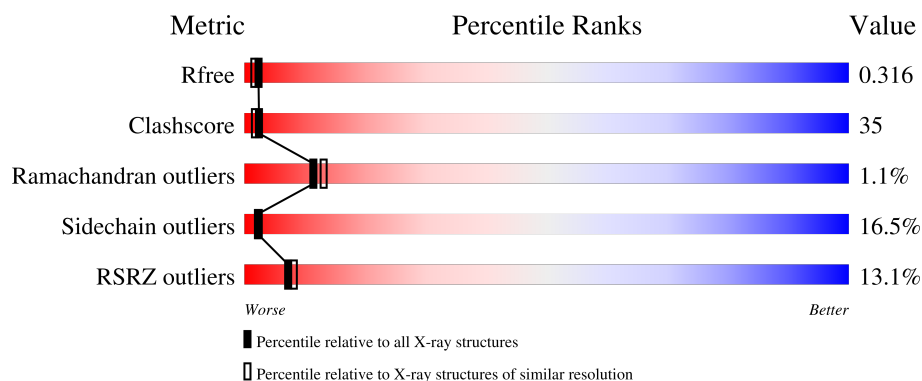
1 Overall quality at a glance

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	
1	C	141	
2	B	146	
2	D	146	

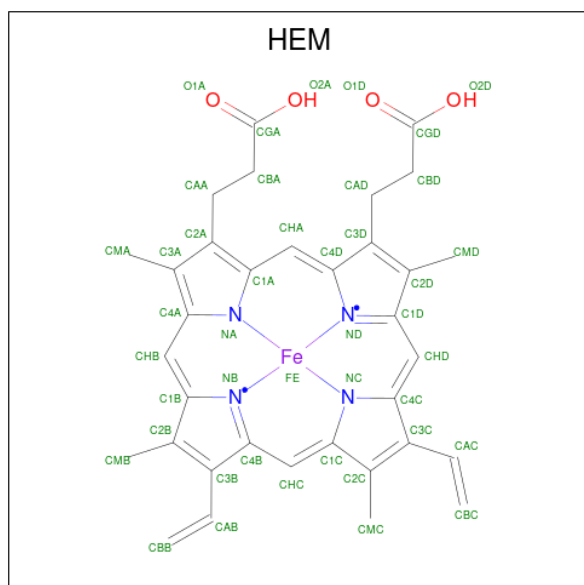
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 2 is a protein called Hemoglobin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total 1082	C 698	N 188	O 193	S 3	0	0	0
1	C	141	Total 1082	C 698	N 188	O 193	S 3	0	0	0

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total 1153	C 744	N 204	O 201	S 4	0	0	0
2	D	146	Total 1152	C 744	N 204	O 200	S 4	0	0	0

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $\text{C}_{34}\text{H}_{32}\text{FeN}_4\text{O}_4$).



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

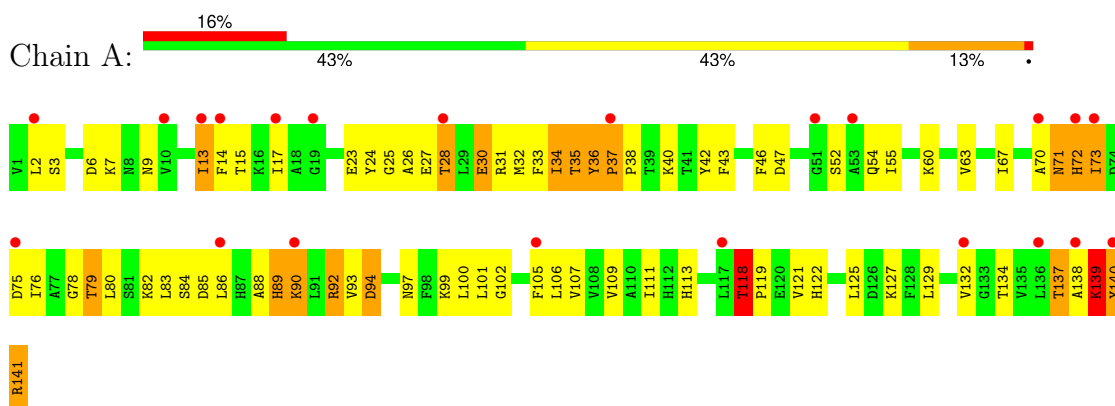
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	41	Total 41	O 41	0	0
4	B	33	Total 33	O 33	0	0
4	C	29	Total 29	O 29	0	0
4	D	45	Total 45	O 45	0	0

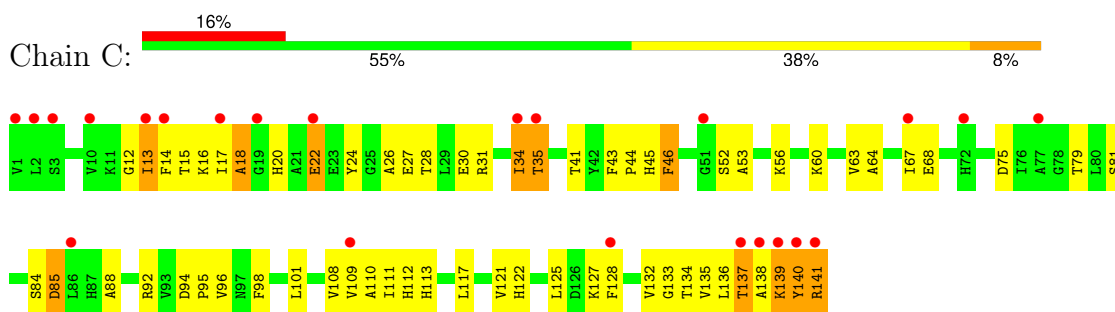
3 Residue-property plots [i](#)

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.

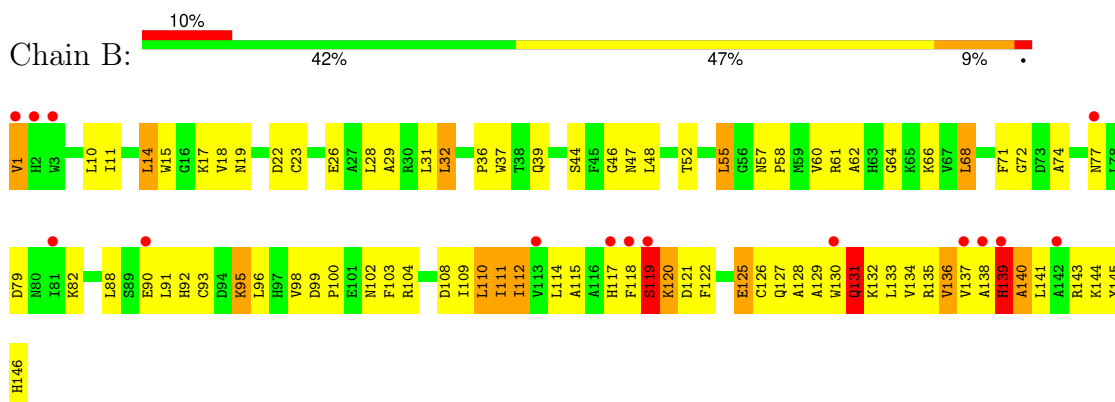
- Molecule 1: Hemoglobin subunit alpha-A



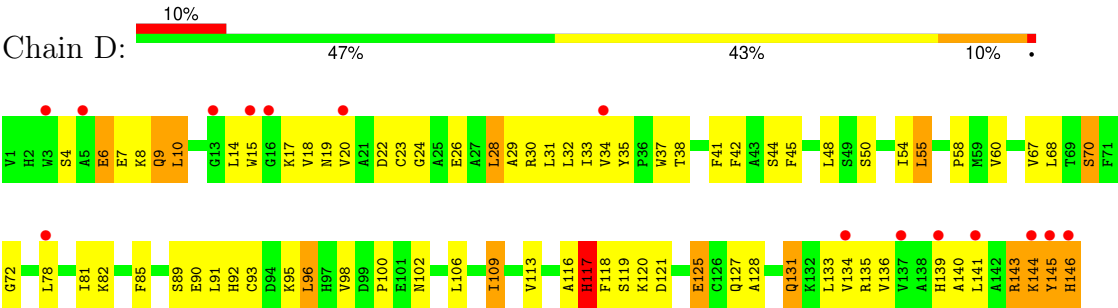
- Molecule 1: Hemoglobin subunit alpha-A



- Molecule 2: Hemoglobin beta chain



● Molecule 2: Hemoglobin beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.00Å 79.52Å 64.39Å 90.00° 96.05° 90.00°	Depositor
Resolution (Å)	25.56 – 2.30 25.56 – 2.30	Depositor EDS
% Data completeness (in resolution range)	89.6 (25.56-2.30) 89.5 (25.56-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.264 , 0.311 0.279 , 0.316	Depositor DCC
R_{free} test set	1156 reflections (4.53%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 59.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4789	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.82% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.93	3/1108 (0.3%)	1.38	18/1502 (1.2%)
1	C	0.75	0/1108	1.15	2/1502 (0.1%)
2	B	0.83	1/1182 (0.1%)	1.15	3/1603 (0.2%)
2	D	0.75	1/1181 (0.1%)	1.10	7/1603 (0.4%)
All	All	0.82	5/4579 (0.1%)	1.20	30/6210 (0.5%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	37	PRO	C-N	8.69	1.44	1.34
1	A	37	PRO	C-O	-8.54	1.15	1.24
1	A	137	THR	C-N	-7.18	1.23	1.33
2	B	112	ILE	CA-CB	6.37	1.61	1.54
2	D	32	LEU	CA-C	5.19	1.59	1.52

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	76	ILE	N-CA-C	-11.26	99.14	110.62
1	C	34	ILE	N-CA-C	9.91	119.93	111.90
1	A	92	ARG	CA-C-N	9.57	134.49	122.43
1	A	92	ARG	C-N-CA	9.57	134.49	122.43
2	D	33	ILE	CB-CA-C	-8.37	103.69	111.06
1	A	118	THR	N-CA-C	-8.06	98.16	110.32
1	A	92	ARG	O-C-N	-7.98	113.19	123.32
1	A	73	ILE	N-CA-C	-7.83	103.59	113.22
1	A	113	HIS	CA-C-N	7.16	126.41	118.97
1	A	113	HIS	C-N-CA	7.16	126.41	118.97
1	A	36	TYR	CA-C-N	6.89	127.48	120.38
1	A	36	TYR	C-N-CA	6.89	127.48	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	ARG	N-CA-C	6.85	119.58	111.02
2	B	110	LEU	N-CA-C	-6.77	103.59	110.97
1	A	37	PRO	CA-C-N	-6.74	112.75	119.56
1	A	37	PRO	C-N-CA	-6.74	112.75	119.56
2	D	93	CYS	N-CA-C	6.71	121.51	113.12
2	B	140	ALA	N-CA-C	-6.42	104.71	112.54
2	D	117	HIS	N-CA-C	6.39	118.04	111.14
2	D	10	LEU	N-CA-C	6.26	121.10	112.90
1	C	46	PHE	N-CA-C	6.23	119.80	109.46
1	A	132	VAL	CB-CA-C	-6.20	103.90	112.02
2	B	139	HIS	N-CA-C	-6.12	104.53	111.14
1	A	71	ASN	N-CA-C	5.38	117.00	111.03
2	D	34	VAL	CB-CA-C	-5.24	103.62	112.16
1	A	139	LYS	N-CA-C	-5.21	105.66	113.89
2	D	35	TYR	CA-C-N	5.17	125.24	119.87
2	D	35	TYR	C-N-CA	5.17	125.24	119.87
1	A	89	HIS	CB-CA-C	-5.16	102.74	110.90
1	A	90	LYS	N-CA-C	-5.06	105.22	111.40

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	1082	0	1102	113	0
1	C	1082	0	1102	94	0
2	B	1153	0	1163	90	0
2	D	1152	0	1163	77	0
3	A	43	0	30	2	0
3	B	43	0	30	3	0
3	C	43	0	30	0	0
3	D	43	0	30	8	0
4	A	41	0	0	11	0
4	B	33	0	0	6	0
4	C	29	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	45	0	0	4	0
All	All	4789	0	4650	328	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 35.

All (328) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:93:CYS:SG	2:B:145:TYR:CE2	2.45	1.09
1:A:35:THR:HG21	2:B:127:GLN:HG2	1.32	1.08
2:B:1:VAL:N	2:D:146:HIS:CE1	2.29	1.01
1:C:34:ILE:HD12	4:D:188:HOH:O	1.61	1.00
1:A:141:ARG:HA	1:C:127:LYS:CE	1.92	1.00
2:B:1:VAL:N	2:D:146:HIS:NE2	2.09	1.00
1:C:34:ILE:CD1	4:D:188:HOH:O	2.12	0.98
2:B:139:HIS:NE2	2:D:146:HIS:HA	1.79	0.97
1:A:28:THR:HG21	1:A:105:PHE:CD2	2.01	0.96
2:B:37:TRP:HE3	1:C:140:TYR:HE1	1.05	0.95
2:B:132:LYS:O	2:B:136:VAL:HG13	1.68	0.94
1:A:13:ILE:HD13	1:A:109:VAL:HG11	1.51	0.93
2:B:139:HIS:CE1	2:D:146:HIS:HA	2.04	0.91
1:C:24:TYR:O	1:C:28:THR:HG23	1.71	0.91
2:D:143:ARG:HH11	2:D:143:ARG:HB2	1.33	0.91
3:D:150:HEM:HBA2	3:D:150:HEM:HHA	1.51	0.90
1:A:31:ARG:NH2	1:A:111:ILE:HD12	1.86	0.89
1:A:31:ARG:NH2	1:A:111:ILE:CD1	2.36	0.88
1:A:31:ARG:O	1:A:35:THR:HG23	1.72	0.88
1:A:70:ALA:HB1	4:A:226:HOH:O	1.74	0.88
1:A:13:ILE:CD1	1:A:109:VAL:HG11	2.05	0.87
2:B:1:VAL:H1	2:D:146:HIS:CE1	1.88	0.87
2:B:99:ASP:CG	1:C:96:VAL:HG21	2.00	0.87
1:A:137:THR:O	1:A:140:TYR:HD1	1.57	0.86
1:A:85:ASP:O	1:A:90:LYS:HG3	1.74	0.86
1:A:28:THR:HG21	1:A:105:PHE:HD2	1.36	0.86
2:B:37:TRP:HE3	1:C:140:TYR:CE1	1.95	0.84
1:A:127:LYS:HD3	1:C:141:ARG:HA	1.59	0.84
2:D:82:LYS:HA	2:D:140:ALA:HB1	1.57	0.84
1:A:31:ARG:HH22	1:A:111:ILE:HD11	1.45	0.82
2:B:93:CYS:SG	2:B:145:TYR:CD2	2.73	0.81
1:A:35:THR:CG2	2:B:127:GLN:HG2	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ALA:HB3	1:A:139:LYS:HB3	1.64	0.78
1:C:64:ALA:O	1:C:68:GLU:HB2	1.83	0.78
1:A:137:THR:O	1:A:140:TYR:CD1	2.37	0.78
1:A:141:ARG:HA	1:C:127:LYS:HE3	1.63	0.77
2:D:143:ARG:HB2	2:D:143:ARG:NH1	1.99	0.77
2:B:1:VAL:H2	2:D:146:HIS:CE1	2.02	0.77
1:C:17:ILE:HD13	1:C:24:TYR:HD1	1.49	0.76
1:C:139:LYS:O	1:C:140:TYR:HD2	1.68	0.76
1:A:37:PRO:CD	1:A:38:PRO:HD2	2.16	0.75
1:C:88:ALA:HB3	1:C:139:LYS:HB2	1.67	0.75
1:A:138:ALA:HB2	1:A:141:ARG:NH2	2.02	0.74
2:D:50:SER:O	2:D:54:ILE:HD12	1.86	0.74
1:A:31:ARG:HH22	1:A:111:ILE:CD1	1.95	0.74
3:B:150:HEM:HMC2	3:B:150:HEM:HBC2	1.70	0.73
2:B:37:TRP:CE3	1:C:140:TYR:HE1	1.98	0.73
1:A:26:ALA:O	1:A:30:GLU:HG2	1.89	0.73
1:A:37:PRO:HG2	1:A:38:PRO:HD3	1.69	0.72
1:A:141:ARG:HA	1:C:127:LYS:CD	2.20	0.72
1:C:31:ARG:HD3	2:D:127:GLN:OE1	1.89	0.72
2:B:111:ILE:HG13	2:B:131:GLN:HG2	1.72	0.71
2:B:130:TRP:CZ3	2:B:133:LEU:HD23	2.25	0.71
1:A:140:TYR:HB2	1:A:141:ARG:HG3	1.73	0.71
1:A:37:PRO:HD2	1:A:38:PRO:HD2	1.72	0.70
1:C:26:ALA:O	1:C:30:GLU:HG3	1.93	0.69
1:A:35:THR:HG21	2:B:127:GLN:CG	2.17	0.69
2:B:119:SER:O	2:B:121:ASP:N	2.25	0.69
2:B:132:LYS:O	2:B:136:VAL:CG1	2.40	0.69
1:A:140:TYR:CD2	2:D:37:TRP:HE3	2.10	0.69
2:B:135:ARG:HD3	4:B:151:HOH:O	1.91	0.69
1:A:140:TYR:CE2	2:D:37:TRP:HB3	2.29	0.68
2:B:32:LEU:HG	2:B:39:GLN:HG2	1.75	0.68
2:B:36:PRO:HD2	1:C:140:TYR:CD1	2.29	0.68
1:A:40:LYS:HB2	4:A:277:HOH:O	1.93	0.68
2:D:28:LEU:HD23	2:D:60:VAL:HG13	1.75	0.68
2:D:119:SER:O	2:D:121:ASP:N	2.27	0.68
1:A:38:PRO:HD3	4:A:204:HOH:O	1.94	0.67
1:A:127:LYS:HG2	1:C:141:ARG:HB3	1.76	0.67
1:C:30:GLU:O	1:C:34:ILE:HG22	1.95	0.67
1:A:47:ASP:HB3	4:A:143:HOH:O	1.93	0.67
2:B:62:ALA:O	2:B:66:LYS:HG3	1.94	0.67
2:D:29:ALA:HB1	2:D:55:LEU:HD13	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:138:ALA:O	1:C:140:TYR:N	2.29	0.66
1:A:37:PRO:N	1:A:38:PRO:HD2	2.11	0.65
1:C:17:ILE:HD13	1:C:24:TYR:CD1	2.30	0.65
1:C:117:LEU:HD12	1:C:121:VAL:HG12	1.77	0.65
1:A:141:ARG:HB3	1:C:127:LYS:HG2	1.77	0.65
1:A:13:ILE:HD11	1:A:109:VAL:HG21	1.78	0.65
1:A:140:TYR:HE2	2:D:37:TRP:HB3	1.62	0.65
2:B:130:TRP:CE2	4:B:196:HOH:O	2.49	0.64
2:B:130:TRP:C	2:B:132:LYS:N	2.50	0.64
1:C:138:ALA:C	1:C:140:TYR:H	2.05	0.64
2:B:31:LEU:O	2:B:31:LEU:HG	1.97	0.64
2:B:130:TRP:CE3	2:B:133:LEU:HD23	2.33	0.64
2:D:145:TYR:O	2:D:146:HIS:C	2.39	0.64
1:A:37:PRO:CD	1:A:38:PRO:CD	2.76	0.63
2:B:11:ILE:HG23	4:B:196:HOH:O	1.99	0.63
2:D:19:ASN:HB3	2:D:22:ASP:HB2	1.80	0.63
2:D:30:ARG:HB3	2:D:109:ILE:HD13	1.79	0.63
1:A:31:ARG:HH21	1:A:111:ILE:HD12	1.62	0.63
1:A:35:THR:HG22	2:B:128:ALA:HB2	1.81	0.63
1:A:137:THR:O	1:A:139:LYS:N	2.30	0.63
2:B:19:ASN:O	2:B:23:CYS:HB2	1.99	0.62
2:D:42:PHE:O	2:D:48:LEU:HD11	1.99	0.62
1:A:80:LEU:HD22	1:A:83:LEU:HD12	1.80	0.62
1:A:88:ALA:CB	1:A:139:LYS:HB3	2.28	0.62
2:B:37:TRP:HE1	2:B:102:ASN:HD21	1.47	0.62
1:A:88:ALA:HB3	1:A:139:LYS:CB	2.29	0.62
1:A:138:ALA:O	1:A:139:LYS:HD2	1.99	0.62
2:B:18:VAL:HG13	2:B:23:CYS:SG	2.39	0.62
2:D:131:GLN:HE22	2:D:135:ARG:NE	1.97	0.62
2:D:31:LEU:HD22	2:D:106:LEU:HD13	1.80	0.62
2:D:38:THR:HB	3:D:150:HEM:HBC1	1.81	0.62
1:A:137:THR:C	1:A:139:LYS:H	2.08	0.61
2:B:47:ASN:O	2:B:48:LEU:HD23	2.00	0.61
2:B:26:GLU:OE1	2:B:117:HIS:NE2	2.33	0.61
2:B:26:GLU:OE1	2:B:117:HIS:CE1	2.53	0.61
2:B:108:ASP:O	2:B:112:ILE:HD12	2.00	0.61
2:B:125:GLU:HG2	4:B:243:HOH:O	2.00	0.61
1:A:122:HIS:HD2	1:A:122:HIS:O	1.83	0.61
1:C:17:ILE:HG12	1:C:24:TYR:HE1	1.66	0.61
1:C:139:LYS:C	1:C:140:TYR:HD2	2.09	0.61
1:A:122:HIS:C	1:A:122:HIS:CD2	2.79	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:150:HEM:FE	4:A:287:HOH:O	1.52	0.60
1:C:17:ILE:HD11	1:C:109:VAL:HG12	1.84	0.60
1:A:138:ALA:CB	1:A:141:ARG:NH2	2.65	0.59
1:A:88:ALA:CB	1:A:139:LYS:CB	2.80	0.59
1:C:110:ALA:HB2	1:C:117:LEU:HD23	1.83	0.59
1:C:35:THR:OG1	2:D:127:GLN:HG2	2.01	0.59
1:C:139:LYS:C	1:C:140:TYR:CD2	2.80	0.59
2:D:15:TRP:CZ2	2:D:72:GLY:HA3	2.37	0.59
2:B:110:LEU:O	2:B:111:ILE:C	2.44	0.59
2:D:19:ASN:O	2:D:23:CYS:HB2	2.02	0.59
1:A:55:ILE:HD11	4:A:197:HOH:O	2.03	0.59
1:C:17:ILE:HG12	1:C:24:TYR:CE1	2.37	0.59
2:D:91:LEU:O	2:D:96:LEU:HB2	2.02	0.59
1:A:118:THR:HG22	1:A:121:VAL:H	1.68	0.58
2:D:24:GLY:HA2	2:D:68:LEU:HD12	1.85	0.58
1:C:14:PHE:O	1:C:17:ILE:O	2.21	0.58
1:A:93:VAL:HG12	1:A:94:ASP:O	2.04	0.58
1:C:43:PHE:HB3	1:C:46:PHE:HB2	1.85	0.58
2:D:100:PRO:HG3	2:D:145:TYR:HD2	1.67	0.58
3:B:150:HEM:HBC2	3:B:150:HEM:CMC	2.34	0.57
1:C:17:ILE:O	1:C:18:ALA:HB2	2.04	0.57
1:C:12:GLY:O	1:C:15:THR:HG22	2.04	0.57
1:C:138:ALA:HA	1:C:141:ARG:HE	1.69	0.57
1:A:72:HIS:HB2	1:A:79:THR:HG21	1.87	0.56
2:B:14:LEU:HD13	2:B:118:PHE:CZ	2.40	0.56
2:B:146:HIS:ND1	2:D:139:HIS:CE1	2.73	0.56
3:A:150:HEM:NA	4:A:287:HOH:O	2.32	0.56
2:B:28:LEU:HD22	2:B:64:GLY:N	2.20	0.56
2:B:103:PHE:HB2	2:B:138:ALA:HB1	1.87	0.56
2:D:143:ARG:HH11	2:D:143:ARG:CB	2.13	0.56
1:C:28:THR:HG22	1:C:108:VAL:HG21	1.87	0.56
1:A:67:ILE:O	1:A:71:ASN:ND2	2.37	0.56
1:A:37:PRO:HG2	4:A:204:HOH:O	2.04	0.56
1:C:13:ILE:HD13	1:C:13:ILE:H	1.71	0.56
2:B:122:PHE:CE2	2:B:127:GLN:HB2	2.41	0.55
1:C:84:SER:HB3	1:C:139:LYS:HD3	1.88	0.55
1:A:13:ILE:HD11	1:A:17:ILE:HD11	1.89	0.55
1:A:14:PHE:HA	1:A:17:ILE:HB	1.88	0.55
1:A:140:TYR:O	1:C:127:LYS:HE2	2.07	0.55
1:C:14:PHE:HD1	1:C:67:ILE:HG12	1.72	0.55
1:C:17:ILE:HD11	1:C:109:VAL:CG1	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:ARG:C	1:C:127:LYS:HD3	2.32	0.55
1:A:37:PRO:N	1:A:38:PRO:CD	2.69	0.54
1:C:140:TYR:HB2	1:C:141:ARG:HG3	1.90	0.54
2:D:26:GLU:OE2	2:D:30:ARG:NH2	2.40	0.54
2:B:10:LEU:HD13	2:B:126:CYS:HA	1.90	0.54
1:A:31:ARG:HA	1:A:34:ILE:HG22	1.90	0.54
2:D:113:VAL:O	2:D:116:ALA:HB3	2.07	0.54
2:D:117:HIS:CD2	4:D:152:HOH:O	2.60	0.54
1:C:98:PHE:HE1	1:C:136:LEU:HD12	1.73	0.54
2:B:140:ALA:O	2:B:143:ARG:HG2	2.08	0.53
1:A:54:GLN:HB2	4:A:142:HOH:O	2.07	0.53
1:A:141:ARG:HA	1:C:127:LYS:HE2	1.86	0.53
2:B:130:TRP:O	2:B:131:GLN:C	2.51	0.53
2:D:6:GLU:O	2:D:10:LEU:HD12	2.08	0.53
1:A:118:THR:O	1:A:119:PRO:C	2.51	0.53
1:C:138:ALA:HA	1:C:141:ARG:NE	2.24	0.53
1:A:14:PHE:CD1	1:A:67:ILE:HG22	2.43	0.53
2:D:26:GLU:O	2:D:26:GLU:HG3	2.07	0.53
1:A:13:ILE:CD1	1:A:109:VAL:CG1	2.84	0.53
1:A:107:VAL:HG13	2:B:115:ALA:HB2	1.90	0.53
1:A:31:ARG:NH2	1:A:111:ILE:HD11	2.12	0.53
2:D:67:VAL:HG11	2:D:106:LEU:HD21	1.91	0.53
1:A:141:ARG:HA	1:C:127:LYS:HD3	1.90	0.52
1:A:137:THR:C	1:A:139:LYS:N	2.66	0.52
2:D:41:PHE:HB3	3:D:150:HEM:HMD1	1.90	0.52
1:A:138:ALA:HB2	1:A:141:ARG:HH22	1.71	0.52
2:D:131:GLN:NE2	2:D:135:ARG:NE	2.57	0.52
1:C:63:VAL:HG12	1:C:67:ILE:HD12	1.92	0.52
1:A:72:HIS:N	1:A:72:HIS:CD2	2.77	0.51
1:C:43:PHE:HA	1:C:45:HIS:CE1	2.45	0.51
1:A:31:ARG:NH1	2:B:127:GLN:OE1	2.41	0.51
2:B:96:LEU:HB3	2:B:98:VAL:HG23	1.92	0.51
2:D:78:LEU:HA	2:D:81:ILE:HG13	1.92	0.51
2:D:4:SER:O	2:D:8:LYS:HG3	2.11	0.51
1:C:34:ILE:HD11	4:D:188:HOH:O	1.93	0.51
1:C:85:ASP:HA	1:C:139:LYS:HG2	1.93	0.51
1:C:128:PHE:O	1:C:132:VAL:HG23	2.11	0.51
2:B:37:TRP:HB3	1:C:140:TYR:OH	2.10	0.50
2:B:92:HIS:HE1	3:B:150:HEM:NA	2.09	0.50
2:B:82:LYS:HE2	2:B:143:ARG:CZ	2.42	0.50
1:A:3:SER:OG	1:A:6:ASP:OD1	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:PRO:HG2	1:A:38:PRO:CD	2.38	0.50
1:A:63:VAL:O	1:A:67:ILE:HG23	2.10	0.50
1:C:17:ILE:CD1	1:C:24:TYR:CD1	2.94	0.50
2:B:88:LEU:HD12	4:B:148:HOH:O	2.10	0.50
1:C:98:PHE:CE1	1:C:136:LEU:HD12	2.46	0.50
1:A:75:ASP:O	1:A:78:GLY:N	2.42	0.49
1:C:110:ALA:HB2	1:C:117:LEU:CD2	2.41	0.49
2:B:22:ASP:OD2	2:B:61:ARG:NH2	2.44	0.49
1:C:94:ASP:CG	1:C:96:VAL:HG22	2.37	0.49
2:D:45:PHE:N	2:D:45:PHE:CD2	2.80	0.49
1:A:55:ILE:HG13	4:A:142:HOH:O	2.12	0.49
2:B:130:TRP:CZ2	4:B:196:HOH:O	2.64	0.49
1:C:45:HIS:ND1	1:C:45:HIS:N	2.58	0.48
1:C:138:ALA:C	1:C:140:TYR:N	2.71	0.48
1:C:139:LYS:HD2	1:C:139:LYS:HA	1.43	0.48
2:D:125:GLU:CD	2:D:125:GLU:H	2.21	0.48
2:D:7:GLU:HA	2:D:10:LEU:HD12	1.95	0.48
1:C:34:ILE:HB	4:C:222:HOH:O	2.14	0.48
1:C:140:TYR:N	1:C:140:TYR:CD2	2.82	0.48
1:A:88:ALA:O	1:A:92:ARG:HD3	2.13	0.48
1:C:122:HIS:C	1:C:122:HIS:CD2	2.91	0.48
1:A:37:PRO:CG	1:A:38:PRO:CD	2.92	0.48
1:C:94:ASP:OD1	1:C:95:PRO:HD2	2.13	0.48
2:D:85:PHE:HE2	3:D:150:HEM:HMB2	1.79	0.48
1:A:122:HIS:O	1:A:122:HIS:CD2	2.64	0.48
2:B:130:TRP:C	2:B:132:LYS:H	2.22	0.48
1:A:37:PRO:O	1:A:40:LYS:HG3	2.13	0.48
1:A:42:TYR:OH	1:A:93:VAL:HA	2.14	0.48
2:D:92:HIS:O	2:D:98:VAL:HG23	2.14	0.48
2:D:82:LYS:HA	2:D:140:ALA:CB	2.38	0.47
1:C:133:GLY:O	1:C:137:THR:OG1	2.31	0.47
2:B:119:SER:C	2:B:121:ASP:H	2.22	0.47
1:C:35:THR:CG2	2:D:131:GLN:HG3	2.45	0.47
2:D:45:PHE:HD1	2:D:60:VAL:HG22	1.79	0.47
1:C:26:ALA:HB2	1:C:56:LYS:HA	1.96	0.47
1:C:27:GLU:O	1:C:31:ARG:HG3	2.14	0.47
1:C:17:ILE:CD1	1:C:24:TYR:HD1	2.24	0.47
2:D:92:HIS:CD2	3:D:150:HEM:NC	2.82	0.47
2:B:31:LEU:HA	2:B:109:ILE:CD1	2.45	0.47
2:B:15:TRP:CZ2	2:B:72:GLY:HA3	2.50	0.47
1:C:41:THR:O	1:C:44:PRO:HD3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:ASP:O	1:C:79:THR:HG22	2.15	0.47
1:A:14:PHE:HD1	1:A:67:ILE:HG22	1.77	0.46
2:D:100:PRO:HG3	2:D:145:TYR:CD2	2.50	0.46
1:A:43:PHE:O	1:A:46:PHE:HB2	2.15	0.46
1:A:86:LEU:HA	1:A:90:LYS:HG3	1.98	0.46
2:B:23:CYS:HB3	2:B:68:LEU:CD1	2.46	0.46
2:D:38:THR:HB	3:D:150:HEM:CBC	2.45	0.46
1:A:25:GLY:HA3	1:A:63:VAL:CG2	2.46	0.46
1:A:26:ALA:O	1:A:30:GLU:CG	2.62	0.46
1:A:102:GLY:HA2	1:A:129:LEU:HD22	1.97	0.46
1:A:141:ARG:CA	1:C:127:LYS:HD3	2.46	0.46
1:A:24:TYR:O	1:A:28:THR:HG23	2.16	0.46
2:B:39:GLN:HB3	2:B:48:LEU:HD12	1.97	0.46
1:A:3:SER:HG	1:A:6:ASP:CG	2.23	0.46
1:A:37:PRO:HD2	1:A:38:PRO:CD	2.41	0.46
1:A:55:ILE:CD1	4:A:197:HOH:O	2.62	0.46
2:D:17:LYS:HB3	2:D:118:PHE:HE1	1.80	0.46
1:A:84:SER:HB3	1:A:139:LYS:HD3	1.98	0.45
1:C:35:THR:HG23	2:D:131:GLN:HG3	1.97	0.45
1:C:92:ARG:HG3	1:C:92:ARG:HH11	1.80	0.45
2:D:6:GLU:HA	2:D:9:GLN:NE2	2.31	0.45
2:B:29:ALA:HB1	2:B:55:LEU:HD13	1.98	0.45
2:B:91:LEU:HD12	2:B:95:LYS:HD2	1.98	0.45
1:C:34:ILE:HG23	1:C:35:THR:N	2.32	0.45
2:D:133:LEU:O	2:D:136:VAL:HG22	2.15	0.45
1:C:111:ILE:HG12	2:D:119:SER:HA	1.98	0.45
2:B:1:VAL:H2	2:D:146:HIS:HE1	1.59	0.45
2:B:99:ASP:CB	1:C:96:VAL:HG21	2.47	0.45
1:A:141:ARG:CB	1:C:127:LYS:HG2	2.47	0.45
1:A:85:ASP:O	1:A:89:HIS:HB2	2.17	0.45
2:D:4:SER:HB3	2:D:7:GLU:HG3	1.99	0.45
2:B:112:ILE:O	2:B:115:ALA:HB3	2.17	0.45
1:C:138:ALA:O	1:C:141:ARG:N	2.50	0.45
1:A:107:VAL:HG13	2:B:115:ALA:CB	2.47	0.44
2:B:37:TRP:CE3	1:C:140:TYR:CE1	2.86	0.44
2:B:130:TRP:O	2:B:132:LYS:N	2.51	0.44
1:C:18:ALA:C	1:C:20:HIS:H	2.25	0.44
2:D:92:HIS:HE1	3:D:150:HEM:NA	2.12	0.44
2:B:125:GLU:CD	2:B:125:GLU:H	2.24	0.44
1:C:68:GLU:OE1	1:C:79:THR:OG1	2.35	0.44
2:D:18:VAL:HG22	2:D:118:PHE:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:GLU:HG2	1:A:31:ARG:HE	1.83	0.43
2:B:104:ARG:NH1	2:B:108:ASP:OD1	2.51	0.43
2:D:30:ARG:HB3	2:D:109:ILE:CD1	2.48	0.43
1:A:25:GLY:CA	1:A:63:VAL:HG21	2.48	0.43
2:B:23:CYS:HB3	2:B:68:LEU:HD11	2.00	0.43
1:A:35:THR:HB	2:B:128:ALA:HA	1.99	0.43
1:A:93:VAL:O	1:A:94:ASP:C	2.61	0.43
1:C:22:GLU:HB3	1:C:60:LYS:HG3	2.00	0.43
2:D:90:GLU:CG	2:D:144:LYS:HD3	2.49	0.43
2:B:99:ASP:OD2	1:C:96:VAL:HG11	2.19	0.43
1:C:52:SER:O	1:C:53:ALA:C	2.59	0.43
2:D:68:LEU:C	2:D:70:SER:N	2.76	0.43
2:B:11:ILE:HD11	2:B:129:ALA:O	2.18	0.43
1:A:7:LYS:HD3	1:A:73:ILE:CG2	2.49	0.43
2:D:45:PHE:N	2:D:45:PHE:HD2	2.16	0.43
1:C:110:ALA:O	2:D:116:ALA:HA	2.19	0.43
2:B:14:LEU:HD13	2:B:118:PHE:CE2	2.54	0.43
2:B:98:VAL:O	2:B:145:TYR:OH	2.22	0.42
2:D:37:TRP:HE1	2:D:102:ASN:HD21	1.67	0.42
2:B:57:ASN:HB3	2:B:60:VAL:HB	2.00	0.42
2:B:71:PHE:O	2:B:74:ALA:HB3	2.19	0.42
2:B:110:LEU:HG	2:B:114:LEU:HG	2.00	0.42
1:A:32:MET:CE	1:A:33:PHE:CE1	3.03	0.42
1:A:37:PRO:CG	1:A:38:PRO:HD3	2.44	0.42
1:A:140:TYR:CE2	2:D:37:TRP:HE3	2.36	0.42
2:B:28:LEU:HD22	2:B:64:GLY:H	1.84	0.42
2:B:119:SER:HB2	2:B:120:LYS:H	1.66	0.42
2:D:41:PHE:HB3	3:D:150:HEM:CMD	2.50	0.42
1:A:36:TYR:C	1:A:38:PRO:HD2	2.44	0.42
2:B:57:ASN:HA	2:B:58:PRO:HD3	1.91	0.42
2:D:28:LEU:O	2:D:29:ALA:C	2.61	0.42
1:A:9:ASN:O	1:A:13:ILE:CG2	2.67	0.42
2:B:146:HIS:CG	2:D:139:HIS:CE1	3.08	0.41
2:D:24:GLY:CA	2:D:68:LEU:HD12	2.50	0.41
2:B:99:ASP:HA	2:B:100:PRO:HD3	1.90	0.41
1:C:112:HIS:O	1:C:113:HIS:ND1	2.54	0.41
2:B:130:TRP:O	2:B:133:LEU:N	2.53	0.41
1:C:35:THR:OG1	2:D:128:ALA:HA	2.20	0.41
1:C:35:THR:HA	2:D:128:ALA:CB	2.51	0.41
1:A:97:ASN:O	1:A:100:LEU:HB2	2.21	0.41
1:A:138:ALA:HA	1:A:141:ARG:CZ	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:14:LEU:CD1	2:B:118:PHE:CE2	3.04	0.41
2:B:119:SER:C	2:B:121:ASP:N	2.80	0.40
1:C:81:SER:O	1:C:84:SER:HB2	2.20	0.40
1:C:111:ILE:O	2:D:119:SER:HB3	2.21	0.40
1:C:139:LYS:O	1:C:140:TYR:CD2	2.59	0.40
2:B:46:GLY:O	2:B:48:LEU:HG	2.22	0.40
2:D:118:PHE:HB3	2:D:121:ASP:HB2	2.04	0.40
1:A:25:GLY:HA3	1:A:63:VAL:HG21	2.04	0.40
1:A:134:THR:O	1:A:138:ALA:HB2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
1	C	139/141 (99%)	127 (91%)	10 (7%)	2 (1%)	9	9
2	B	144/146 (99%)	131 (91%)	10 (7%)	3 (2%)	5	4
2	D	144/146 (99%)	135 (94%)	8 (6%)	1 (1%)	18	23
All	All	566/574 (99%)	520 (92%)	40 (7%)	6 (1%)	11	13

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	120	LYS
2	D	120	LYS
1	C	18	ALA
1	C	139	LYS
2	B	131	GLN
2	B	119	SER

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	114/114 (100%)	92 (81%)	22 (19%)	1	1
1	C	114/114 (100%)	102 (90%)	12 (10%)	6	8
2	B	122/122 (100%)	100 (82%)	22 (18%)	2	2
2	D	122/122 (100%)	100 (82%)	22 (18%)	2	2
All	All	472/472 (100%)	394 (84%)	78 (16%)	2	2

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	13	ILE
1	A	15	THR
1	A	23	GLU
1	A	28	THR
1	A	30	GLU
1	A	34	ILE
1	A	35	THR
1	A	52	SER
1	A	60	LYS
1	A	72	HIS
1	A	79	THR
1	A	82	LYS
1	A	94	ASP
1	A	99	LYS
1	A	101	LEU
1	A	106	LEU
1	A	118	THR
1	A	125	LEU
1	A	139	LYS
1	A	140	TYR
1	A	141	ARG
2	B	1	VAL
2	B	14	LEU

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Mol	Chain	Res	Type
2	B	17	LYS
2	B	32	LEU
2	B	44	SER
2	B	52	THR
2	B	55	LEU
2	B	68	LEU
2	B	77	ASN
2	B	79	ASP
2	B	90	GLU
2	B	95	LYS
2	B	111	ILE
2	B	119	SER
2	B	125	GLU
2	B	131	GLN
2	B	134	VAL
2	B	136	VAL
2	B	137	VAL
2	B	139	HIS
2	B	141	LEU
2	B	144	LYS
1	C	13	ILE
1	C	16	LYS
1	C	22	GLU
1	C	35	THR
1	C	85	ASP
1	C	101	LEU
1	C	125	LEU
1	C	134	THR
1	C	135	VAL
1	C	137	THR
1	C	140	TYR
1	C	141	ARG
2	D	6	GLU
2	D	9	GLN
2	D	14	LEU
2	D	20	VAL
2	D	28	LEU
2	D	44	SER
2	D	55	LEU
2	D	58	PRO
2	D	70	SER
2	D	89	SER

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Mol	Chain	Res	Type
2	D	95	LYS
2	D	96	LEU
2	D	109	ILE
2	D	117	HIS
2	D	125	GLU
2	D	131	GLN
2	D	134	VAL
2	D	141	LEU
2	D	143	ARG
2	D	144	LYS
2	D	145	TYR
2	D	146	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	HIS
1	A	58	HIS
1	A	97	ASN
2	B	63	HIS
2	B	102	ASN
1	C	8	ASN
1	C	50	HIS
1	C	97	ASN
1	C	122	HIS
2	D	9	GLN
2	D	77	ASN
2	D	83	ASN
2	D	87	GLN
2	D	102	ASN
2	D	131	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

4 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	B	150	2	50,50,50	1.97	7 (14%)	67,82,82	1.26	4 (5%)
3	HEM	A	150	1	50,50,50	2.11	10 (20%)	67,82,82	1.29	7 (10%)
3	HEM	D	150	4,2	50,50,50	2.07	8 (16%)	67,82,82	1.41	11 (16%)
3	HEM	C	150	1	50,50,50	1.95	8 (16%)	67,82,82	1.33	6 (8%)

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	150	2	-	4/14/54/54	-
3	HEM	A	150	1	-	8/14/54/54	-
3	HEM	D	150	4,2	-	5/14/54/54	-
3	HEM	C	150	1	-	2/14/54/54	-

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	150	HEM	C3D-C2D	8.03	1.54	1.36
3	D	150	HEM	C3D-C2D	7.88	1.53	1.36
3	B	150	HEM	C3D-C2D	7.86	1.53	1.36
3	C	150	HEM	C3D-C2D	7.33	1.52	1.36
3	A	150	HEM	FE-NA	7.14	2.18	1.95
3	C	150	HEM	FE-NB	7.11	2.16	1.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	150	HEM	FE-NA	6.72	2.17	1.95
3	B	150	HEM	FE-NA	6.22	2.15	1.95
3	D	150	HEM	FE-ND	5.97	2.13	1.94
3	A	150	HEM	FE-ND	5.70	2.12	1.94
3	B	150	HEM	FE-ND	4.03	2.07	1.94
3	C	150	HEM	FE-NA	3.83	2.07	1.95
3	B	150	HEM	FE-NB	3.44	2.05	1.94
3	C	150	HEM	CAB-C3B	3.36	1.56	1.47
3	C	150	HEM	FE-NC	3.27	2.06	1.95
3	A	150	HEM	CAB-C3B	3.22	1.56	1.47
3	B	150	HEM	CAC-C3C	3.19	1.55	1.47
3	D	150	HEM	CAC-C3C	3.07	1.55	1.47
3	D	150	HEM	FE-NC	2.94	2.04	1.95
3	A	150	HEM	FE-NB	2.90	2.03	1.94
3	B	150	HEM	CAB-C3B	2.87	1.55	1.47
3	C	150	HEM	CAC-C3C	2.79	1.54	1.47
3	A	150	HEM	CAC-C3C	2.79	1.54	1.47
3	D	150	HEM	CAB-C3B	2.69	1.54	1.47
3	B	150	HEM	FE-NC	2.59	2.03	1.95
3	D	150	HEM	CAA-C2A	2.30	1.57	1.51
3	A	150	HEM	CMB-C2B	2.28	1.55	1.50
3	A	150	HEM	CMD-C2D	2.18	1.55	1.50
3	D	150	HEM	CMA-C3A	2.13	1.55	1.50
3	A	150	HEM	CAA-C2A	2.12	1.56	1.51
3	A	150	HEM	CMA-C3A	2.10	1.55	1.50
3	C	150	HEM	CMD-C2D	2.06	1.55	1.50
3	C	150	HEM	CMB-C2B	2.05	1.55	1.50

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	150	HEM	C4D-ND-C1D	5.77	112.04	105.21
3	D	150	HEM	C4D-ND-C1D	5.23	111.40	105.21
3	B	150	HEM	C4D-ND-C1D	5.19	111.36	105.21
3	C	150	HEM	C4D-ND-C1D	4.92	111.03	105.21
3	C	150	HEM	CBD-CAD-C3D	-4.48	100.15	112.53
3	C	150	HEM	CMD-C2D-C1D	3.33	130.24	125.03
3	D	150	HEM	C1B-NB-C4B	2.83	108.56	105.21
3	D	150	HEM	C3B-C2B-C1B	2.64	108.39	106.41
3	C	150	HEM	O1D-CGD-CBD	-2.60	114.84	123.09
3	D	150	HEM	CHD-C1D-ND	2.56	127.18	124.42
3	D	150	HEM	C3B-C4B-NB	-2.54	107.64	109.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	150	HEM	CHA-C4D-ND	2.46	127.41	124.37
3	D	150	HEM	C2B-C1B-NB	-2.44	107.04	109.84
3	A	150	HEM	CMD-C2D-C1D	2.42	128.81	125.03
3	D	150	HEM	CAA-C2A-C1A	2.41	129.64	124.94
3	D	150	HEM	CBD-CAD-C3D	-2.40	105.91	112.53
3	B	150	HEM	CBD-CAD-C3D	-2.35	106.04	112.53
3	A	150	HEM	CAD-C3D-C4D	2.32	128.74	124.70
3	A	150	HEM	C3B-C2B-C1B	2.31	108.15	106.41
3	C	150	HEM	CHA-C4D-ND	2.20	127.09	124.37
3	B	150	HEM	C1B-NB-C4B	2.18	107.79	105.21
3	D	150	HEM	C4A-C3A-C2A	2.18	109.31	106.82
3	A	150	HEM	CHC-C1C-NC	2.18	126.82	124.45
3	C	150	HEM	CHC-C1C-NC	2.12	126.76	124.45
3	D	150	HEM	CHA-C4D-ND	2.10	126.96	124.37
3	A	150	HEM	C1B-NB-C4B	2.09	107.69	105.21
3	D	150	HEM	O1D-CGD-CBD	-2.06	116.56	123.09
3	A	150	HEM	C4C-NC-C1C	2.05	109.17	105.82

There are no chirality outliers.

All (19) torsion outliers are listed below:

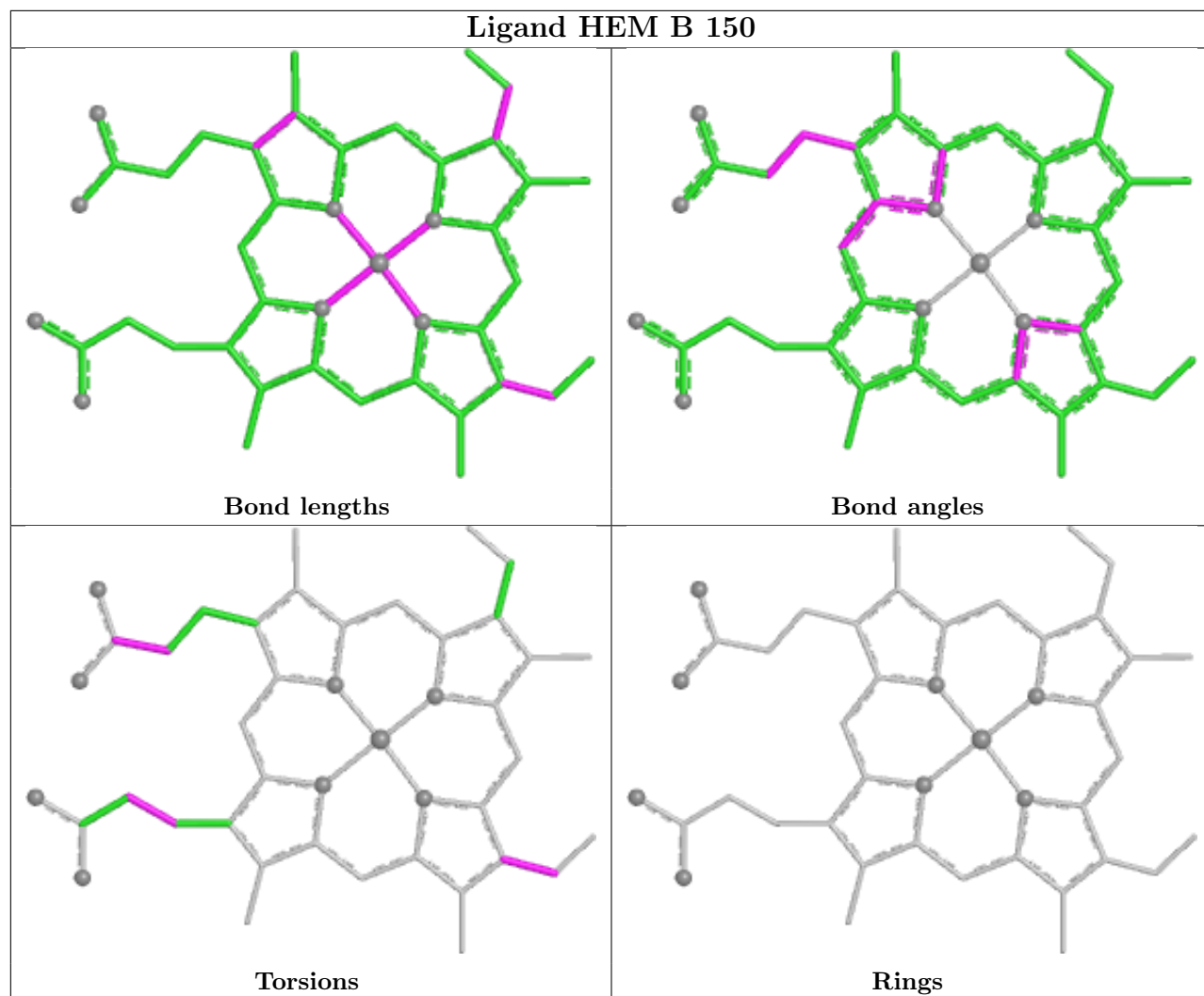
Mol	Chain	Res	Type	Atoms
3	B	150	HEM	C2B-C3B-CAB-CBB
3	A	150	HEM	C4D-C3D-CAD-CBD
3	D	150	HEM	C1A-C2A-CAA-CBA
3	A	150	HEM	C3D-CAD-CBD-CGD
3	D	150	HEM	C3A-C2A-CAA-CBA
3	A	150	HEM	C2D-C3D-CAD-CBD
3	D	150	HEM	C2B-C3B-CAB-CBB
3	B	150	HEM	C4B-C3B-CAB-CBB
3	C	150	HEM	C2C-C3C-CAC-CBC
3	D	150	HEM	C4B-C3B-CAB-CBB
3	D	150	HEM	C2A-CAA-CBA-CGA
3	B	150	HEM	C2A-CAA-CBA-CGA
3	A	150	HEM	CAD-CBD-CGD-O1D
3	A	150	HEM	CAD-CBD-CGD-O2D
3	A	150	HEM	C4C-C3C-CAC-CBC
3	C	150	HEM	C4C-C3C-CAC-CBC
3	B	150	HEM	CAD-CBD-CGD-O1D
3	A	150	HEM	CAA-CBA-CGA-O2A
3	A	150	HEM	C2C-C3C-CAC-CBC

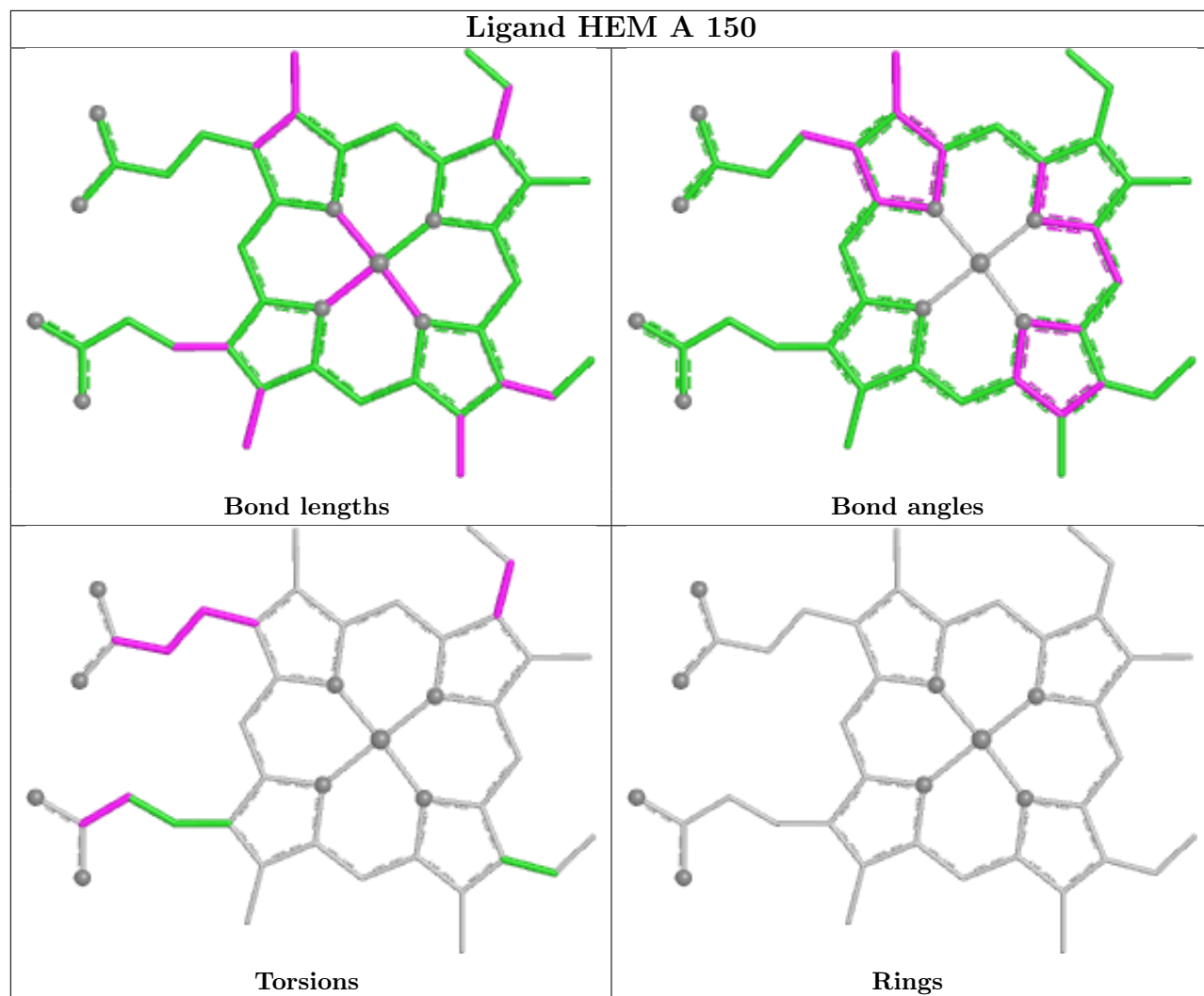
There are no ring outliers.

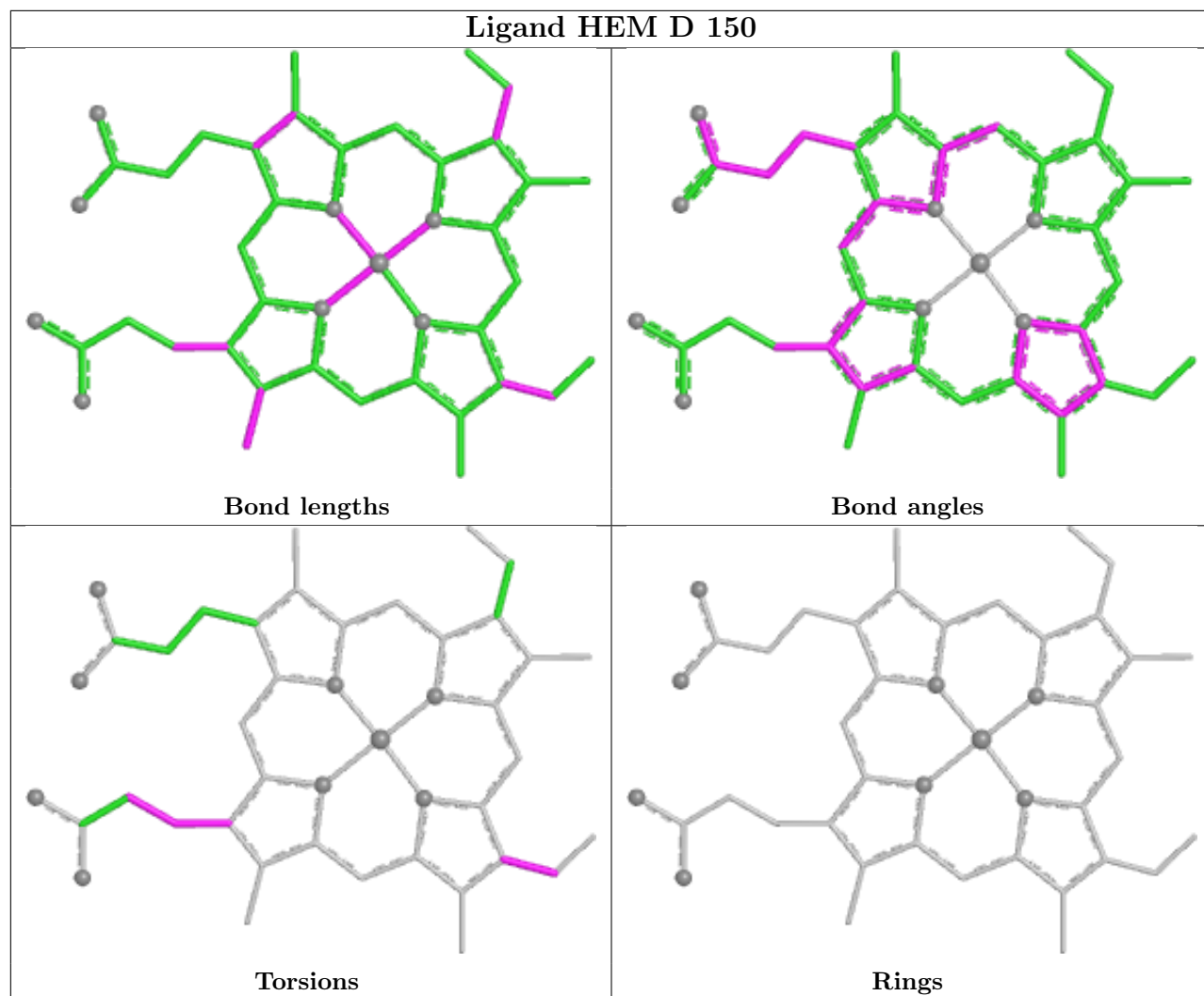
3 monomers are involved in 13 short contacts:

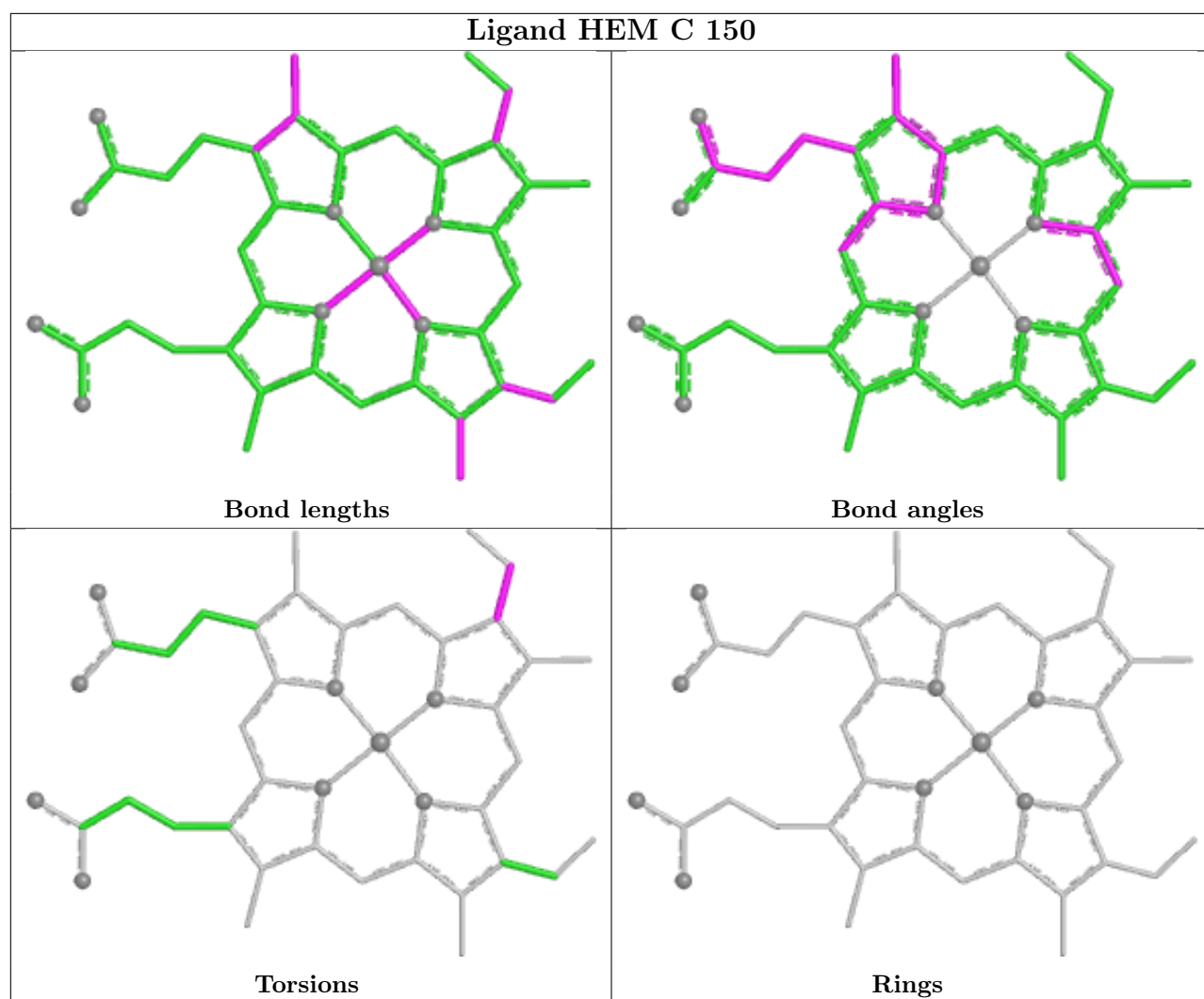
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	150	HEM	3	0
3	A	150	HEM	2	0
3	D	150	HEM	8	0

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%)	1.22	22 (15%) 5 6	21, 47, 67, 74	0
1	C	141/141 (100%)	1.14	23 (16%) 4 5	22, 48, 71, 76	0
2	B	146/146 (100%)	0.96	15 (10%) 12 13	12, 43, 58, 62	0
2	D	146/146 (100%)	1.04	15 (10%) 12 13	14, 45, 64, 66	0
All	All	574/574 (100%)	1.09	75 (13%) 7 8	12, 45, 67, 76	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	146	HIS	4.3
1	C	17	ILE	4.0
1	A	14	PHE	3.9
1	C	67	ILE	3.8
2	B	1	VAL	3.8
1	C	140	TYR	3.6
1	C	34	ILE	3.5
2	B	139	HIS	3.5
2	B	117	HIS	3.4
1	A	73	ILE	3.4
1	C	1	VAL	3.4
2	D	145	TYR	3.4
1	C	13	ILE	3.3
1	A	117	LEU	3.3
1	A	72	HIS	3.3
1	C	139	LYS	3.2
2	B	81	ILE	3.2
1	A	28	THR	3.2
1	C	10	VAL	3.1
1	A	132	VAL	3.1
1	C	72	HIS	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	3	SER	3.0
2	D	13	GLY	3.0
1	A	75	ASP	2.9
1	A	138	ALA	2.9
1	A	13	ILE	2.8
1	A	90	LYS	2.8
1	A	105	PHE	2.8
1	C	77	ALA	2.7
2	D	3	TRP	2.6
2	B	137	VAL	2.6
1	C	86	LEU	2.6
1	C	14	PHE	2.5
1	C	35	THR	2.5
1	C	109	VAL	2.4
1	A	140	TYR	2.4
2	D	139	HIS	2.4
1	A	17	ILE	2.4
1	A	136	LEU	2.4
2	B	90	GLU	2.4
1	C	137	THR	2.4
1	A	37	PRO	2.4
2	D	5	ALA	2.4
2	D	16	GLY	2.4
2	D	137	VAL	2.4
2	B	77	ASN	2.3
1	A	2	LEU	2.3
1	A	70	ALA	2.3
2	B	138	ALA	2.3
1	A	10	VAL	2.3
2	B	118	PHE	2.2
2	B	2	HIS	2.2
2	D	15	TRP	2.2
1	C	51	GLY	2.2
2	B	119	SER	2.2
1	C	2	LEU	2.2
1	A	19	GLY	2.2
2	B	142	ALA	2.2
1	A	51	GLY	2.2
2	B	113	VAL	2.1
1	C	138	ALA	2.1
2	D	134	VAL	2.1
1	C	128	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	53	ALA	2.1
1	A	86	LEU	2.1
2	D	34	VAL	2.1
2	B	3	TRP	2.1
1	C	141	ARG	2.1
1	C	19	GLY	2.1
2	D	144	LYS	2.0
2	D	20	VAL	2.0
2	B	130	TRP	2.0
1	C	22	GLU	2.0
2	D	78	LEU	2.0
2	D	141	LEU	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](#)

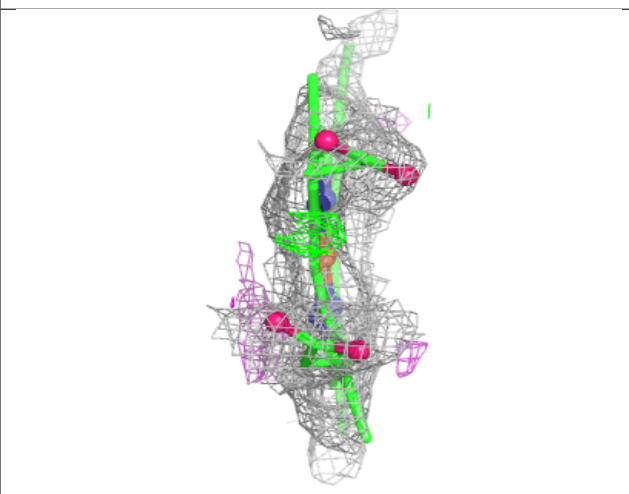
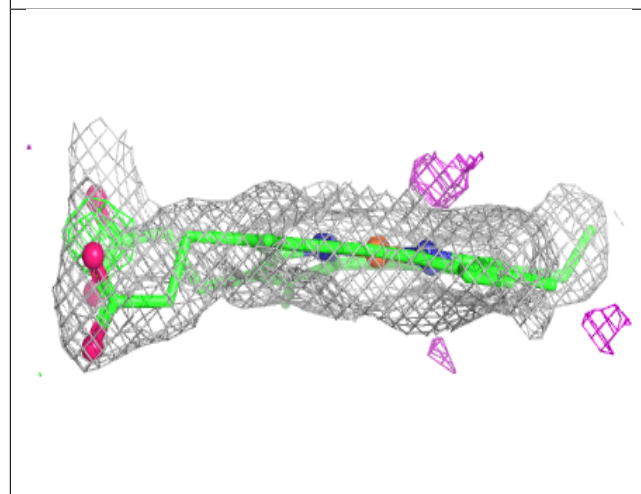
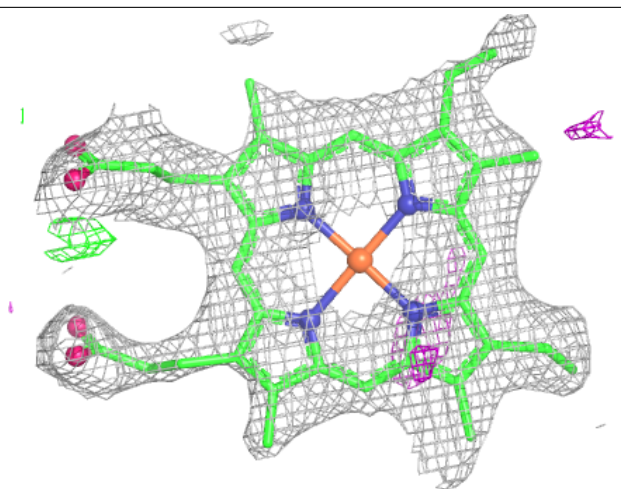
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	HEM	B	150	43/43	0.93	0.12	46,49,52,55	0
3	HEM	D	150	43/43	0.93	0.11	40,45,47,49	0
3	HEM	C	150	43/43	0.94	0.11	34,40,46,50	0
3	HEM	A	150	43/43	0.94	0.11	40,47,49,49	0

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

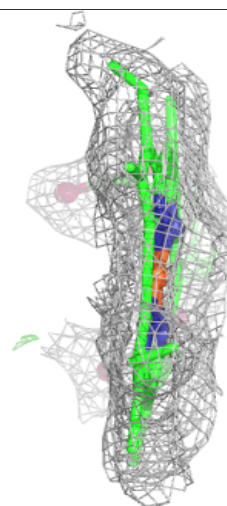
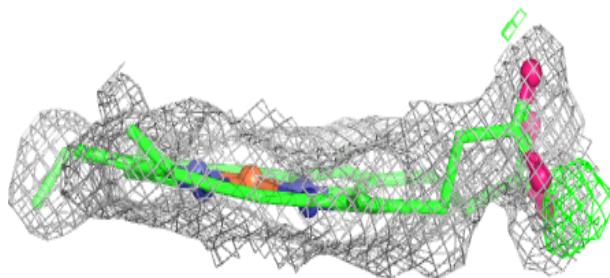
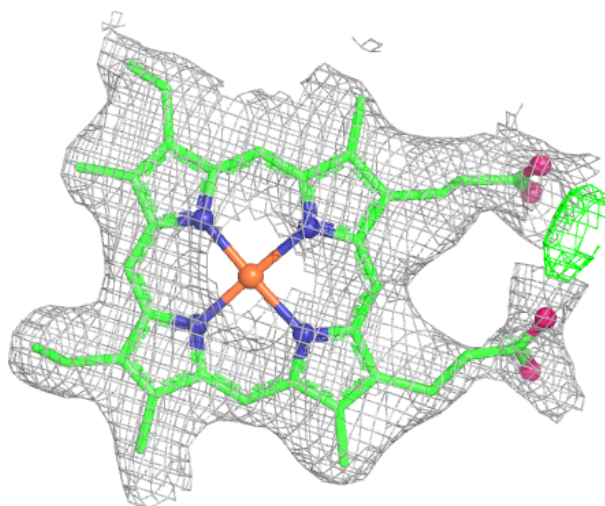
Electron density around HEM B 150:

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



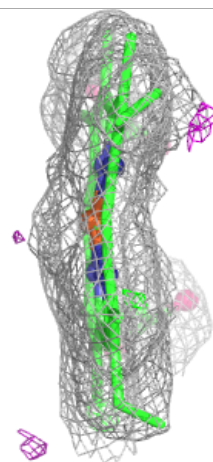
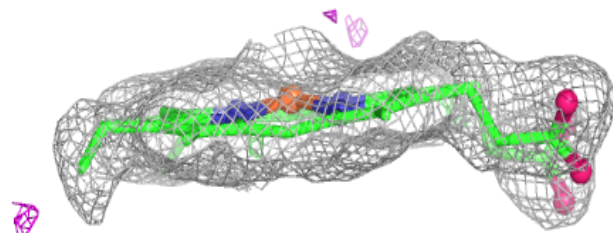
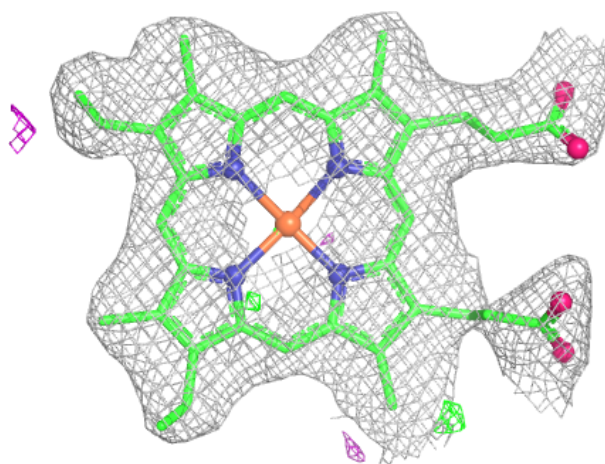
Electron density around HEM D 150:

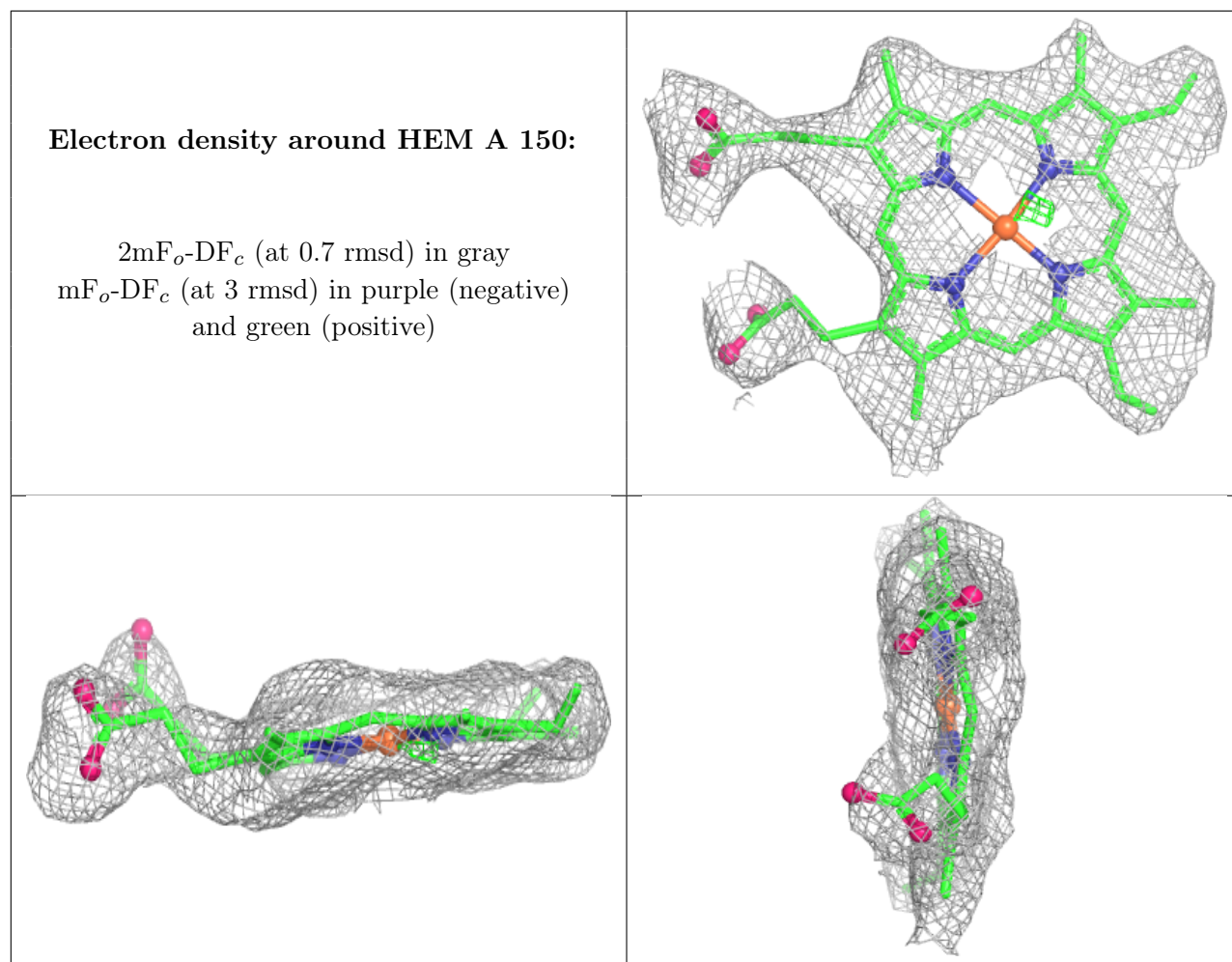
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM C 150:

$2mF_o-DF_c$ (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.