



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:59 AM EDT

PDB ID : 2QMB / pdb_00002qmb
Title : Structure determination of haemoglobin from Turkey(meleagris gallopavo) at 2.8 Angstrom resolution
Authors : Packianathan, C.; Sundaresan, S.; Ponnuswamy, M.N.
Deposited on : 2007-07-15
Resolution : 2.80 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

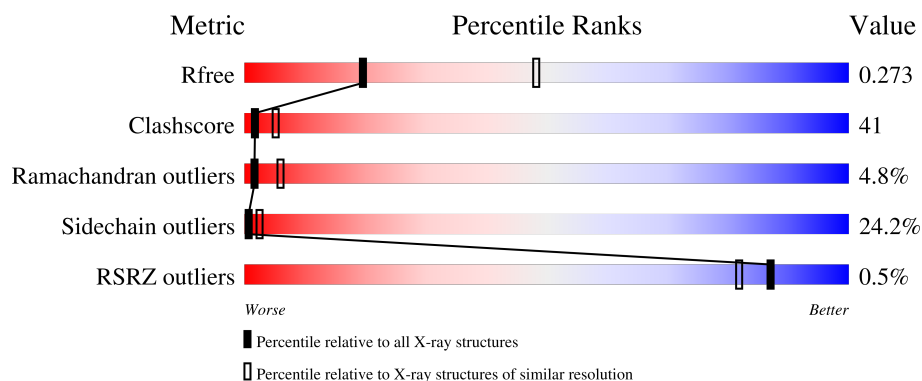
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	142	% 27% 40% 25% 7% .
1	C	142	% 23% 37% 28% 11% .
2	B	146	27% 46% 22% 5%
2	D	146	% 18% 42% 31% 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4657 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

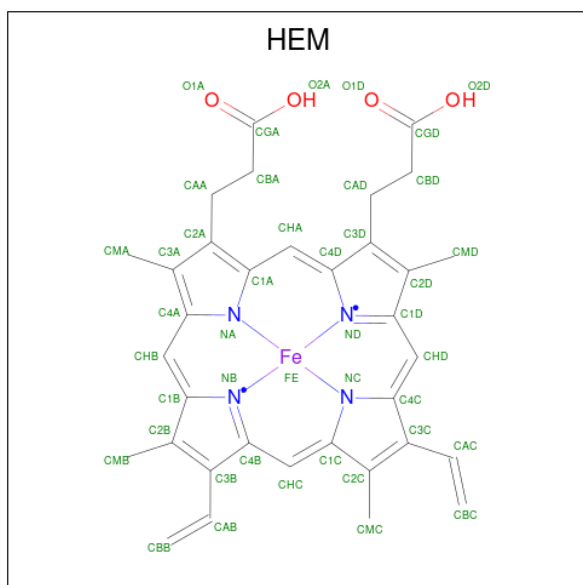
- Molecule 1 is a protein called Hemoglobin subunit alpha-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1082	698	188	193	3			
1	C	141	Total	C	N	O	S	0	1	0
			1089	703	190	193	3			

- Molecule 2 is a protein called Hemoglobin beta chain.

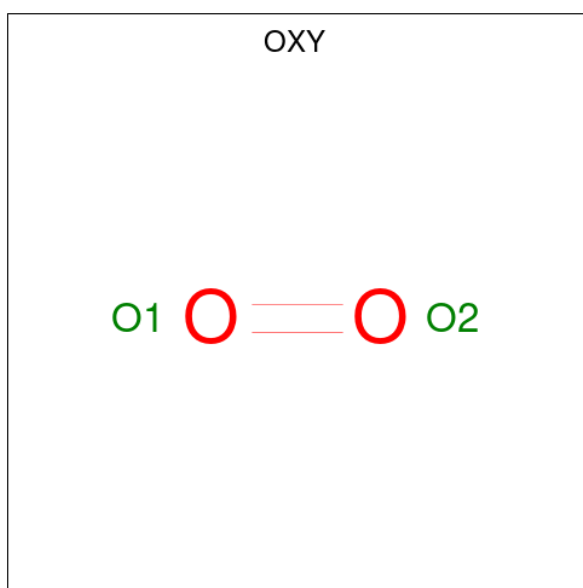
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1153	744	204	201	4			
2	D	146	Total	C	N	O	S	0	0	0
			1153	744	204	201	4			

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



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

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

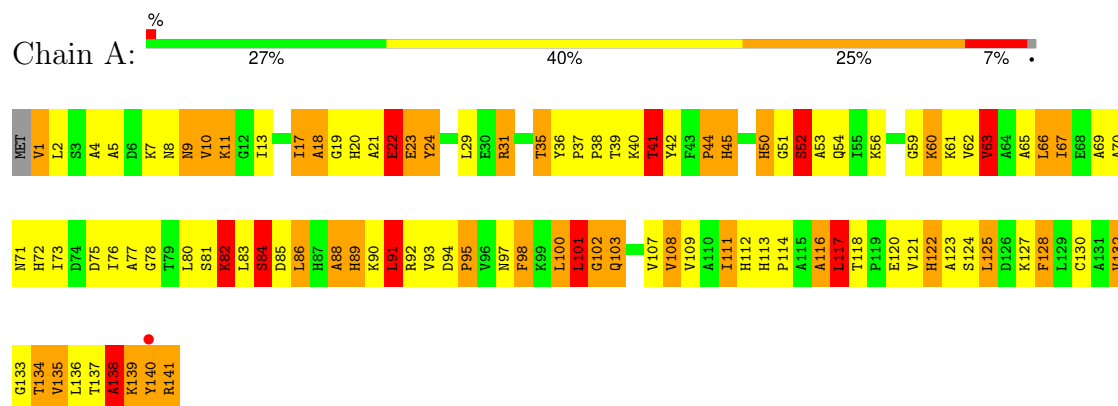


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O	0	0
			2	2		
4	B	1	Total	O	0	0
			2	2		
4	C	1	Total	O	0	0
			2	2		
4	D	1	Total	O	0	0
			2	2		

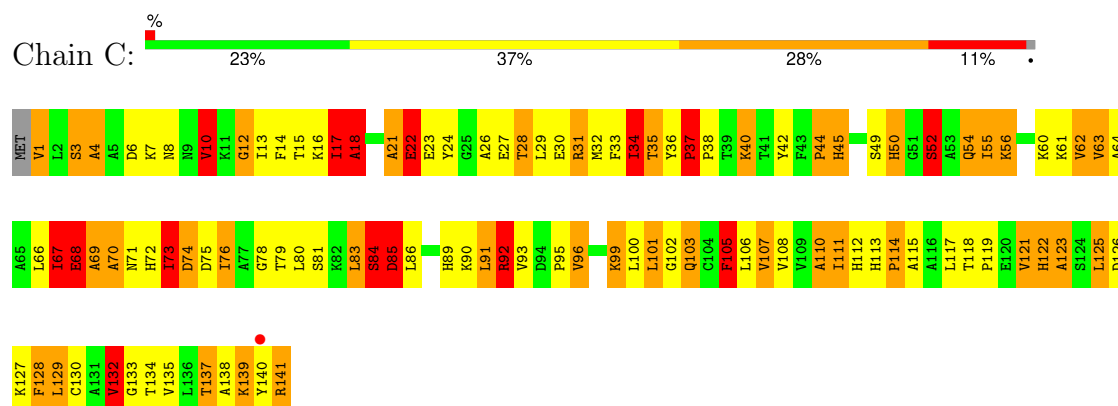
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

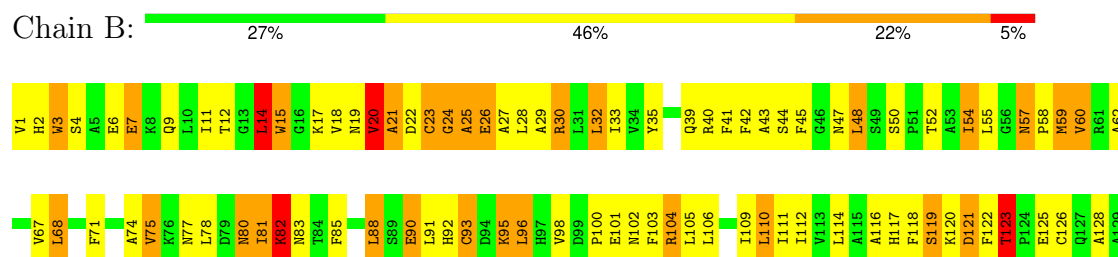
• Molecule 1: Hemoglobin subunit alpha-A



• Molecule 1: Hemoglobin subunit alpha-A

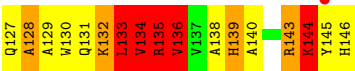
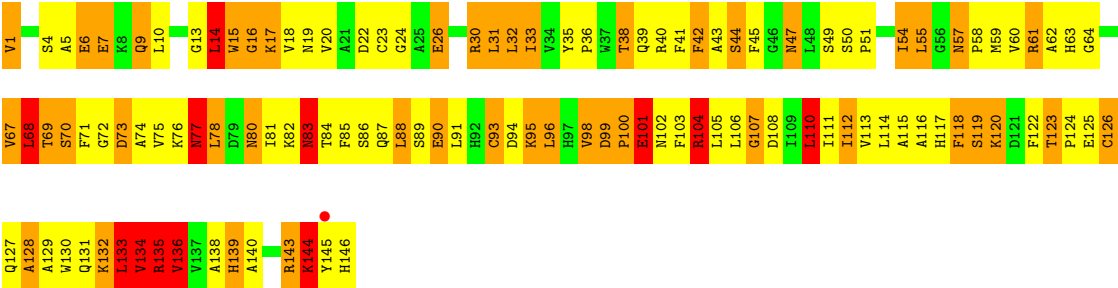
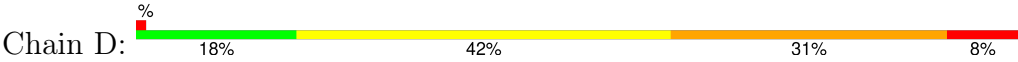


• Molecule 2: Hemoglobin beta chain





● Molecule 2: Hemoglobin beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.00Å 79.80Å 103.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.43 – 2.80 25.43 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.7 (25.43-2.80) 98.5 (25.43-2.80)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.24 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.172 , 0.284 0.167 , 0.273	Depositor DCC
R_{free} test set	1042 reflections (7.43%)	wwPDB-VP
Wilson B-factor (Å ²)	52.4	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 77.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4657	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality i

5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	2.26	48/1108 (4.3%)	2.08	45/1502 (3.0%)
1	C	2.24	35/1119 (3.1%)	2.10	44/1517 (2.9%)
2	B	2.40	55/1182 (4.7%)	2.10	36/1603 (2.2%)
2	D	2.03	30/1182 (2.5%)	1.96	40/1603 (2.5%)
All	All	2.24	168/4591 (3.7%)	2.06	165/6225 (2.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
2	D	0	3
All	All	0	4

All (168) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	37	PRO	CA-C	13.23	1.64	1.52
2	B	117	HIS	C-O	-11.92	1.07	1.23
2	B	27	ALA	C-O	-9.78	1.12	1.24
1	C	64	ALA	CA-CB	9.38	1.68	1.53
2	B	138	ALA	CA-CB	-9.31	1.38	1.53
1	A	84	SER	CA-C	-9.13	1.41	1.52
2	D	98	VAL	CA-CB	8.77	1.63	1.53
2	B	62	ALA	CA-CB	-8.58	1.39	1.53
2	B	25	ALA	CA-CB	-8.28	1.40	1.53
1	C	60	LYS	CA-C	-8.24	1.42	1.52
2	D	134	VAL	CA-CB	8.08	1.65	1.54
2	B	112	ILE	CA-CB	-8.07	1.44	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	98	VAL	CA-C	7.95	1.62	1.52
2	B	93	CYS	CA-C	-7.93	1.42	1.52
2	B	95	LYS	N-CA	-7.88	1.36	1.46
2	B	128	ALA	CA-CB	-7.80	1.39	1.53
2	D	112	ILE	CA-CB	-7.74	1.44	1.54
2	B	29	ALA	CA-CB	-7.70	1.41	1.53
2	D	18	VAL	CA-CB	7.69	1.63	1.54
1	C	18	ALA	CA-CB	7.66	1.66	1.53
2	B	119	SER	C-O	-7.60	1.16	1.24
1	A	76	ILE	CA-CB	7.58	1.63	1.54
2	D	128	ALA	CA-CB	-7.51	1.41	1.53
2	B	22	ASP	C-O	-7.51	1.15	1.24
2	B	19	ASN	CA-C	7.48	1.62	1.52
2	D	105	LEU	C-O	7.43	1.32	1.24
1	A	21	ALA	C-O	-7.26	1.15	1.24
2	B	20	VAL	CA-CB	-7.12	1.44	1.54
1	A	116	ALA	CA-CB	-7.07	1.44	1.54
1	A	117	LEU	C-O	-7.02	1.15	1.24
2	D	55	LEU	CA-C	6.96	1.62	1.52
2	B	112	ILE	C-O	-6.94	1.16	1.24
2	B	98	VAL	CA-CB	-6.92	1.45	1.54
1	C	35	THR	CA-CB	-6.81	1.42	1.53
2	B	90	GLU	N-CA	-6.76	1.38	1.46
2	B	27	ALA	CA-CB	-6.75	1.42	1.53
1	A	72	HIS	CA-C	-6.73	1.43	1.53
1	C	108	VAL	CA-CB	-6.70	1.46	1.54
2	B	138	ALA	CA-C	-6.66	1.43	1.52
1	A	8	ASN	N-CA	6.64	1.54	1.46
1	C	45	HIS	N-CA	-6.54	1.37	1.46
1	A	10	VAL	CA-C	-6.54	1.45	1.52
1	C	111	ILE	CA-CB	-6.53	1.46	1.54
1	C	110	ALA	CA-C	-6.50	1.43	1.52
1	A	10	VAL	N-CA	-6.48	1.38	1.46
1	A	88	ALA	N-CA	-6.48	1.38	1.46
2	B	117	HIS	CA-C	-6.44	1.43	1.52
2	B	136	VAL	N-CA	-6.42	1.38	1.46
2	B	21	ALA	CA-CB	-6.38	1.43	1.53
1	A	35	THR	C-O	-6.37	1.16	1.24
1	C	32	MET	C-O	-6.35	1.16	1.24
1	C	31	ARG	N-CA	-6.30	1.37	1.46
2	B	74	ALA	CA-CB	-6.27	1.43	1.53
2	B	67	VAL	C-O	6.26	1.31	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	136	VAL	CA-CB	6.20	1.62	1.54
2	D	108	ASP	CA-C	-6.18	1.44	1.52
1	A	98	PHE	N-CA	-6.14	1.38	1.46
2	B	109	ILE	CG1-CD1	-6.11	1.27	1.51
2	D	44	SER	CA-C	6.07	1.60	1.52
2	D	136	VAL	CA-CB	-6.07	1.46	1.54
1	A	5	ALA	CA-C	6.05	1.61	1.52
1	C	27	GLU	N-CA	-6.04	1.39	1.46
2	B	141	LEU	CA-C	-6.03	1.44	1.52
2	B	114	LEU	N-CA	6.02	1.54	1.46
1	A	86	LEU	N-CA	-6.01	1.38	1.46
1	C	4	ALA	CA-C	6.01	1.60	1.52
2	B	130	TRP	CB-CG	-5.99	1.31	1.50
1	C	63	VAL	N-CA	5.98	1.54	1.46
1	A	95	PRO	C-O	-5.97	1.16	1.24
1	A	50	HIS	N-CA	5.97	1.53	1.46
1	C	101	LEU	N-CA	5.97	1.53	1.46
1	A	117	LEU	CA-CB	-5.97	1.43	1.53
2	D	70	SER	N-CA	-5.94	1.38	1.46
2	B	18	VAL	CB-CG1	-5.91	1.33	1.52
1	C	69	ALA	CA-CB	-5.90	1.45	1.53
2	D	73	ASP	C-O	-5.87	1.17	1.24
1	A	13	ILE	CA-CB	-5.86	1.46	1.54
2	B	40	ARG	C-O	-5.85	1.17	1.24
1	A	65	ALA	CA-CB	-5.85	1.44	1.53
1	A	132	VAL	CA-CB	5.83	1.61	1.54
2	B	135	ARG	CZ-NH1	5.82	1.41	1.32
2	B	14	LEU	C-O	-5.81	1.17	1.24
2	B	138	ALA	C-O	-5.81	1.16	1.24
1	A	112	HIS	C-O	-5.80	1.16	1.24
1	C	68	GLU	CA-C	-5.80	1.45	1.52
1	A	65	ALA	N-CA	-5.76	1.39	1.46
1	C	129	LEU	N-CA	-5.75	1.39	1.46
1	A	111	ILE	CA-CB	-5.73	1.47	1.54
1	C	103	GLN	C-O	-5.73	1.16	1.24
1	C	17	ILE	CA-CB	-5.68	1.46	1.54
2	B	12	THR	CB-CG2	-5.66	1.33	1.52
1	C	85	ASP	N-CA	-5.65	1.39	1.46
1	A	63	VAL	CA-CB	5.64	1.60	1.54
2	D	61	ARG	N-CA	5.63	1.53	1.46
2	D	57	ASN	CA-C	5.63	1.59	1.52
2	D	64	GLY	C-O	5.62	1.31	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	42	TYR	N-CA	5.61	1.53	1.46
1	A	1	VAL	CB-CG2	5.59	1.71	1.52
2	B	111	ILE	CA-C	-5.58	1.45	1.52
2	D	101	GLU	CG-CD	5.58	1.66	1.52
2	D	110	LEU	CA-C	-5.55	1.45	1.52
2	D	54	ILE	CA-CB	5.55	1.60	1.54
2	D	68	LEU	CA-C	5.55	1.60	1.52
1	A	29	LEU	N-CA	-5.55	1.39	1.46
1	C	37	PRO	C-O	5.55	1.30	1.24
2	D	127	GLN	N-CA	-5.55	1.39	1.46
1	C	54	GLN	CA-C	-5.53	1.45	1.52
1	A	95	PRO	N-CA	5.52	1.54	1.47
1	A	130	CYS	N-CA	-5.50	1.39	1.46
2	D	73	ASP	CA-C	-5.50	1.46	1.52
2	D	87	GLN	C-O	5.50	1.31	1.24
2	B	41	PHE	N-CA	-5.47	1.39	1.46
1	C	22	GLU	CB-CG	5.46	1.68	1.52
1	A	101	LEU	CG-CD2	-5.46	1.34	1.52
2	B	30	ARG	CA-CB	-5.46	1.44	1.53
2	B	28	LEU	N-CA	-5.45	1.39	1.46
2	B	15	TRP	N-CA	-5.44	1.39	1.46
2	B	24	GLY	C-O	-5.44	1.17	1.23
2	D	83	ASN	C-O	-5.44	1.17	1.24
1	A	17	ILE	CA-CB	-5.43	1.47	1.54
1	A	8	ASN	CA-C	-5.42	1.46	1.52
1	A	123	ALA	CA-CB	-5.40	1.44	1.53
2	B	23	CYS	CA-C	-5.39	1.45	1.52
2	D	7	GLU	CA-C	5.39	1.59	1.52
1	A	4	ALA	C-O	5.39	1.30	1.24
2	B	90	GLU	CA-C	-5.39	1.45	1.52
2	B	111	ILE	N-CA	-5.38	1.39	1.46
2	D	98	VAL	C-O	5.37	1.30	1.23
2	B	12	THR	CA-CB	-5.36	1.45	1.53
1	A	9	ASN	C-O	-5.35	1.18	1.24
2	B	103	PHE	CA-CB	-5.34	1.45	1.53
2	D	101	GLU	CA-C	5.33	1.60	1.52
1	A	5	ALA	C-O	5.32	1.31	1.24
2	B	41	PHE	CA-C	-5.32	1.45	1.52
1	C	62	VAL	CA-CB	5.30	1.60	1.54
1	A	102	GLY	C-O	5.29	1.30	1.23
1	C	99	LYS	CA-C	5.29	1.59	1.52
1	C	16	LYS	CD-CE	5.29	1.68	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	110	ALA	C-O	-5.29	1.17	1.24
1	C	26	ALA	CA-CB	-5.28	1.45	1.53
1	C	135	VAL	CA-C	5.26	1.59	1.52
1	A	24	TYR	CA-C	-5.24	1.45	1.52
2	D	68	LEU	N-CA	-5.21	1.39	1.46
1	A	69	ALA	CA-C	-5.19	1.45	1.52
2	B	39	GLN	CA-C	-5.18	1.45	1.52
1	C	132	VAL	C-O	-5.16	1.18	1.24
2	B	112	ILE	C-N	-5.15	1.27	1.33
1	A	41	THR	CA-C	-5.14	1.45	1.52
2	B	80	ASN	CA-C	-5.12	1.46	1.52
2	B	3	TRP	N-CA	5.12	1.52	1.46
1	C	117	LEU	CA-C	5.12	1.59	1.53
2	B	114	LEU	CG-CD2	-5.11	1.35	1.52
2	B	121	ASP	N-CA	-5.08	1.39	1.46
1	A	38	PRO	N-CA	-5.06	1.40	1.47
1	A	107	VAL	C-O	5.05	1.30	1.24
1	A	103	GLN	CA-C	-5.05	1.46	1.52
2	B	75	VAL	CA-CB	-5.05	1.47	1.54
1	C	10	VAL	CA-CB	-5.04	1.47	1.54
1	A	56	LYS	C-O	-5.04	1.17	1.24
1	A	53	ALA	CA-CB	5.04	1.61	1.54
2	D	73	ASP	N-CA	-5.04	1.40	1.46
1	A	11	LYS	C-O	5.04	1.30	1.24
1	C	123	ALA	C-O	5.02	1.29	1.24
2	D	139	HIS	CA-C	-5.02	1.45	1.52
1	A	82	LYS	C-O	5.02	1.30	1.24
2	B	133	LEU	CG-CD2	-5.01	1.36	1.52
1	A	125	LEU	CA-CB	-5.00	1.45	1.53
1	A	100	LEU	N-CA	-5.00	1.40	1.46

All (165) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	69	ALA	N-CA-C	-14.27	92.21	113.61
1	A	17	ILE	CB-CA-C	-13.03	89.92	111.29
2	D	99	ASP	CA-C-N	12.05	133.06	119.32
2	D	99	ASP	C-N-CA	12.05	133.06	119.32
1	C	70	ALA	N-CA-C	-11.94	98.43	113.23
1	A	112	HIS	N-CA-C	10.91	124.48	111.82
1	A	31	ARG	N-CA-C	-10.90	98.62	112.90
2	B	98	VAL	N-CA-C	10.36	123.35	109.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	131	GLN	N-CA-C	-10.29	99.88	111.82
2	B	12	THR	N-CA-C	9.85	122.02	111.28
1	A	133	GLY	N-CA-C	-9.07	101.84	112.73
2	B	123	THR	N-CA-C	9.05	122.42	109.84
2	D	107	GLY	N-CA-C	-9.02	101.83	112.83
2	D	133	LEU	N-CA-C	-8.86	101.19	111.03
1	A	53	ALA	N-CA-C	-8.84	102.22	113.72
2	B	25	ALA	N-CA-C	-8.77	101.72	111.28
2	B	123	THR	N-CA-CB	-8.59	97.06	110.03
2	B	57	ASN	N-CA-C	8.40	121.58	109.48
1	A	8	ASN	CB-CA-C	-8.22	97.97	110.88
2	B	3	TRP	N-CA-C	8.10	121.45	108.41
2	B	103	PHE	N-CA-C	-8.00	102.42	112.90
2	B	54	ILE	N-CA-C	7.99	118.09	110.42
1	C	67	ILE	N-CA-C	-7.99	102.99	112.98
2	B	121	ASP	N-CA-C	7.85	121.95	112.38
2	B	116	ALA	N-CA-C	-7.81	103.54	113.23
2	B	26	GLU	N-CA-C	7.78	119.39	111.07
1	C	67	ILE	CA-C-N	-7.74	108.87	122.26
1	C	67	ILE	C-N-CA	-7.74	108.87	122.26
2	B	111	ILE	N-CA-C	-7.74	103.38	111.58
2	D	126	CYS	N-CA-C	-7.70	102.81	112.90
1	A	121	VAL	N-CA-C	7.67	119.36	110.62
1	A	45	HIS	N-CA-C	7.58	122.17	113.15
1	C	37	PRO	N-CA-C	7.51	119.86	110.70
2	B	136	VAL	N-CA-C	-7.48	103.56	110.82
1	A	135	VAL	N-CA-C	7.43	118.16	110.36
1	A	44	PRO	N-CA-C	-7.43	97.17	112.47
1	A	111	ILE	CB-CA-C	-7.25	102.52	112.02
2	B	11	ILE	N-CA-C	-7.22	103.13	111.00
1	C	135	VAL	N-CA-C	7.18	117.90	110.36
1	C	68	GLU	N-CA-C	-7.12	104.63	113.38
1	C	107	VAL	CB-CA-C	-7.10	102.80	111.88
1	C	17	ILE	CB-CA-C	-7.07	99.69	111.29
2	B	60	VAL	CB-CA-C	-7.05	102.94	111.97
2	B	110	LEU	CB-CG-CD1	-6.99	89.73	110.70
2	B	123	THR	CA-C-N	-6.96	111.38	119.32
2	B	123	THR	C-N-CA	-6.96	111.38	119.32
2	D	143	ARG	N-CA-C	-6.90	103.37	111.03
1	A	8	ASN	N-CA-CB	6.80	119.87	110.01
1	C	44	PRO	N-CA-C	-6.76	105.41	113.86
2	B	140	ALA	N-CA-C	-6.76	104.00	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	115	ALA	N-CA-C	-6.75	103.73	112.23
2	D	108	ASP	N-CA-C	-6.69	103.80	112.23
1	A	140	TYR	N-CA-C	-6.68	104.04	112.93
1	C	52	SER	N-CA-C	6.67	119.91	110.23
1	C	101	LEU	N-CA-C	-6.67	104.01	111.28
1	C	60	LYS	N-CA-C	-6.60	104.17	111.36
2	D	57	ASN	CA-C-N	-6.60	112.83	119.56
2	D	57	ASN	C-N-CA	-6.60	112.83	119.56
1	A	22	GLU	N-CA-C	6.54	119.23	111.71
1	C	74	ASP	N-CA-C	6.52	118.04	111.07
2	D	80	ASN	N-CA-C	6.47	118.69	110.61
1	A	10	VAL	N-CA-C	-6.43	104.38	110.42
2	B	104	ARG	N-CA-C	-6.41	103.98	110.97
2	B	139	HIS	N-CA-C	-6.38	104.98	112.89
1	C	22	GLU	N-CA-C	6.33	118.99	111.33
2	D	100	PRO	CB-CA-C	-6.33	101.63	112.64
2	B	125	GLU	N-CA-C	-6.32	104.47	111.36
1	C	84	SER	CA-C-N	-6.31	112.02	120.54
1	C	84	SER	C-N-CA	-6.31	112.02	120.54
1	A	62	VAL	CB-CA-C	6.24	119.69	111.70
1	A	41	THR	N-CA-C	-6.20	104.81	112.38
1	A	67	ILE	CB-CA-C	-6.18	101.16	111.29
2	D	1	VAL	CA-C-N	-6.15	114.44	123.05
2	D	1	VAL	C-N-CA	-6.15	114.44	123.05
2	B	134	VAL	N-CA-C	-6.12	103.25	111.44
1	C	83	LEU	N-CA-C	6.10	119.92	112.23
1	C	103	GLN	CA-CB-CG	-6.09	101.92	114.10
2	B	60	VAL	N-CA-C	-6.03	104.64	110.42
2	B	137	VAL	CB-CA-C	-6.00	104.18	112.04
1	A	66	LEU	N-CA-CB	-5.97	101.41	110.07
2	B	20	VAL	N-CA-C	-5.97	103.63	111.09
1	A	84	SER	N-CA-C	-5.94	104.16	111.40
2	D	135	ARG	N-CA-C	-5.91	104.82	112.68
2	D	42	PHE	CA-C-N	-5.91	110.65	121.52
2	D	42	PHE	C-N-CA	-5.91	110.65	121.52
1	A	124	SER	N-CA-C	-5.89	104.86	111.28
2	B	145	TYR	N-CA-C	-5.88	98.27	110.80
1	C	125	LEU	CA-C-N	-5.88	112.45	120.44
1	C	125	LEU	C-N-CA	-5.88	112.45	120.44
1	C	106	LEU	N-CA-C	-5.86	104.81	111.14
2	D	140	ALA	N-CA-C	-5.84	106.20	113.38
2	B	6	GLU	N-CA-C	-5.84	104.82	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	29	LEU	CD1-CG-CD2	-5.82	98.00	110.80
1	A	103	GLN	CA-CB-CG	-5.80	102.50	114.10
1	A	89	HIS	CA-C-N	-5.75	111.10	120.71
1	A	89	HIS	C-N-CA	-5.75	111.10	120.71
2	B	81	ILE	N-CA-C	-5.72	104.76	111.00
1	C	62	VAL	N-CA-CB	5.72	116.86	110.62
2	D	67	VAL	N-CA-C	5.71	115.84	110.30
1	A	59	GLY	CA-C-N	-5.69	112.66	120.28
1	A	59	GLY	C-N-CA	-5.69	112.66	120.28
1	A	121	VAL	CB-CA-C	-5.68	104.59	112.04
1	C	12	GLY	N-CA-C	-5.62	105.84	112.64
1	C	55	ILE	N-CA-C	-5.60	104.90	111.00
1	A	35	THR	CA-C-N	-5.59	115.91	123.46
1	A	35	THR	C-N-CA	-5.59	115.91	123.46
2	B	41	PHE	CA-C-N	-5.59	114.84	123.17
2	B	41	PHE	C-N-CA	-5.59	114.84	123.17
2	D	23	CYS	N-CA-C	-5.58	104.82	111.69
2	D	132	LYS	N-CA-C	-5.58	105.20	112.23
1	C	128	PHE	CA-C-N	5.58	127.69	120.44
1	C	128	PHE	C-N-CA	5.58	127.69	120.44
1	C	32	MET	N-CA-C	-5.56	104.86	111.69
1	C	105	PHE	CA-C-N	-5.55	112.89	120.44
1	C	105	PHE	C-N-CA	-5.55	112.89	120.44
1	C	92	ARG	CB-CG-CD	5.55	124.06	111.30
1	A	13	ILE	N-CA-C	-5.54	104.02	111.44
2	D	96	LEU	N-CA-C	5.54	119.75	112.89
2	B	60	VAL	N-CA-CB	5.52	117.01	110.55
2	D	90	GLU	N-CA-C	-5.52	105.34	111.36
1	C	16	LYS	N-CA-C	-5.52	105.17	111.07
1	C	21	ALA	CA-C-N	5.50	127.91	120.38
1	C	21	ALA	C-N-CA	5.50	127.91	120.38
1	A	7	LYS	CA-C-N	-5.47	113.33	120.44
1	A	7	LYS	C-N-CA	-5.47	113.33	120.44
1	A	130	CYS	N-CA-C	-5.46	104.97	111.69
2	B	35	TYR	N-CA-CB	-5.43	102.29	111.30
2	D	124	PRO	CB-CA-C	-5.42	103.20	112.26
2	D	110	LEU	N-CA-C	-5.41	104.78	111.33
2	B	114	LEU	N-CA-CB	5.39	118.60	110.30
2	D	107	GLY	CA-C-N	-5.37	111.55	120.68
2	D	107	GLY	C-N-CA	-5.37	111.55	120.68
1	A	108	VAL	CA-C-N	-5.37	112.79	120.42
1	A	108	VAL	C-N-CA	-5.37	112.79	120.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	68	GLU	CA-C-N	-5.37	113.91	122.29
1	C	68	GLU	C-N-CA	-5.37	113.91	122.29
1	A	121	VAL	N-CA-CB	5.37	117.18	110.47
1	A	54	GLN	N-CA-C	-5.35	105.11	111.69
1	A	91	LEU	CB-CG-CD2	-5.35	94.66	110.70
1	C	40	LYS	N-CA-C	-5.34	106.03	112.54
1	C	34	ILE	CB-CA-C	-5.33	105.22	111.94
2	D	110	LEU	CB-CA-C	-5.29	101.68	110.68
1	C	121	VAL	CB-CA-C	-5.28	105.12	112.04
1	C	50	HIS	CA-C-N	-5.27	117.17	123.08
1	C	50	HIS	C-N-CA	-5.27	117.17	123.08
1	C	93	VAL	N-CA-C	5.26	116.47	109.37
2	D	69	THR	N-CA-C	-5.26	105.55	111.28
1	A	71	ASN	N-CA-C	5.20	118.73	112.38
2	D	127	GLN	N-CA-C	-5.20	105.68	112.23
2	D	77	ASN	N-CA-C	5.17	116.63	109.54
2	D	138	ALA	CA-C-N	-5.16	111.52	121.58
2	D	138	ALA	C-N-CA	-5.16	111.52	121.58
1	C	139	LYS	N-CA-C	-5.15	107.28	113.21
2	D	104	ARG	N-CA-C	-5.15	105.36	111.69
2	D	125	GLU	N-CA-C	-5.13	106.53	112.89
2	D	33	ILE	CB-CA-C	-5.11	104.45	111.65
2	B	71	PHE	N-CA-C	5.08	116.50	111.07
2	D	14	LEU	CA-C-N	-5.07	113.74	120.63
2	D	14	LEU	C-N-CA	-5.07	113.74	120.63
1	A	17	ILE	CB-CG1-CD1	-5.04	103.22	113.80
2	D	30	ARG	NE-CZ-NH1	-5.03	116.47	121.50
1	A	128	PHE	N-CA-C	-5.02	105.52	111.69
1	A	52	SER	CA-C-N	-5.00	114.31	122.26
1	A	52	SER	C-N-CA	-5.00	114.31	122.26
1	A	138	ALA	N-CA-C	5.00	121.45	110.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	114	PRO	Peptide
2	D	118	PHE	Peptide
2	D	144	LYS	Peptide
2	D	15	TRP	Peptide

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	81	0
1	C	1089	0	1109	102	5
2	B	1153	0	1163	72	6
2	D	1153	0	1163	130	1
3	A	43	0	30	9	0
3	B	43	0	30	11	0
3	C	43	0	30	3	0
3	D	43	0	30	15	0
4	A	2	0	0	0	0
4	B	2	0	0	1	0
4	C	2	0	0	1	0
4	D	2	0	0	1	0
All	All	4657	0	4657	379	6

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 41.

All (379) 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:D:93:CYS:SG	2:D:145:TYR:CZ	2.13	1.39
1:C:7:LYS:NZ	1:C:74:ASP:OD1	1.62	1.32
2:D:19:ASN:ND2	2:D:22:ASP:OD2	1.71	1.22
2:B:4:SER:HB3	2:B:7:GLU:HG3	1.22	1.18
1:C:138:ALA:HA	1:C:141:ARG:NH2	1.61	1.14
2:D:93:CYS:SG	2:D:145:TYR:OH	2.06	1.11
1:C:17:ILE:HG22	1:C:18:ALA:N	1.48	1.10
2:B:4:SER:HB3	2:B:7:GLU:CG	1.83	1.07
2:D:106:LEU:HD23	3:D:150:HEM:CBB	1.86	1.05
3:A:150:HEM:HBC2	3:A:150:HEM:HMC2	1.33	1.03
2:D:104:ARG:HH11	2:D:104:ARG:CG	1.72	1.01
3:B:150:HEM:HBB2	3:B:150:HEM:HHC	1.41	0.99
3:A:150:HEM:HBC2	3:A:150:HEM:CMC	1.89	0.99
2:D:14:LEU:HD13	2:D:118:PHE:CE1	1.99	0.98
1:C:89[B]:HIS:NE2	1:C:139:LYS:CB	2.29	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:ILE:CG2	1:C:18:ALA:N	2.22	0.95
1:A:17:ILE:HG22	1:A:18:ALA:N	1.79	0.95
1:C:17:ILE:HG22	1:C:18:ALA:H	1.20	0.93
1:A:44:PRO:HD2	1:A:45:HIS:H	1.34	0.93
2:B:26:GLU:OE2	2:B:30:ARG:NH1	2.02	0.93
1:A:89:HIS:HE1	1:A:139:LYS:HD3	1.34	0.92
2:D:73:ASP:O	2:D:77:ASN:ND2	2.04	0.90
2:D:41:PHE:CE1	2:D:98:VAL:HG22	2.06	0.90
2:D:91:LEU:O	2:D:96:LEU:HD12	1.71	0.90
2:D:106:LEU:HD23	3:D:150:HEM:HBB2	1.54	0.89
1:C:128:PHE:O	1:C:132:VAL:HG23	1.72	0.89
2:B:123:THR:HG22	2:B:126:CYS:H	1.38	0.89
1:C:70:ALA:HA	1:C:73:ILE:HG12	1.56	0.88
1:C:89[B]:HIS:NE2	1:C:139:LYS:HB2	1.89	0.87
2:D:104:ARG:HH11	2:D:104:ARG:HG2	1.39	0.87
1:C:138:ALA:HA	1:C:141:ARG:HH22	1.39	0.87
2:D:93:CYS:SG	2:D:145:TYR:CE2	2.67	0.86
3:D:150:HEM:HBC2	3:D:150:HEM:CMC	2.07	0.85
2:B:93:CYS:SG	2:B:145:TYR:CE2	2.71	0.84
1:A:41:THR:HG21	2:D:40:ARG:HH22	1.41	0.84
2:B:82:LYS:HG3	2:B:143:ARG:HH11	1.39	0.84
1:C:89[B]:HIS:NE2	1:C:139:LYS:HB3	1.93	0.82
1:A:41:THR:CG2	2:D:40:ARG:NH2	2.42	0.82
2:B:93:CYS:SG	2:B:145:TYR:CZ	2.73	0.81
1:C:72:HIS:O	1:C:75:ASP:N	2.12	0.81
2:D:104:ARG:HH11	2:D:104:ARG:HG3	1.45	0.80
2:B:146:HIS:HB2	2:D:139:HIS:CD2	2.16	0.80
1:C:10:VAL:O	1:C:13:ILE:HG22	1.82	0.80
1:A:44:PRO:CD	1:A:45:HIS:H	1.94	0.80
3:A:150:HEM:HMB1	3:A:150:HEM:HBB2	1.64	0.80
1:A:44:PRO:HD2	1:A:45:HIS:HD2	1.46	0.79
2:D:104:ARG:CG	2:D:104:ARG:NH1	2.43	0.78
2:B:57:ASN:ND2	2:B:59:MET:H	1.81	0.78
1:C:17:ILE:CG2	1:C:18:ALA:H	1.77	0.78
2:D:117:HIS:CD2	2:D:118:PHE:CE2	2.73	0.77
2:D:117:HIS:CD2	2:D:118:PHE:HE2	2.03	0.77
2:D:143:ARG:O	2:D:145:TYR:N	2.16	0.76
1:A:89:HIS:CE1	1:A:139:LYS:HD3	2.20	0.76
2:D:71:PHE:O	2:D:74:ALA:HB3	1.86	0.76
2:D:117:HIS:NE2	2:D:118:PHE:HE2	1.85	0.75
2:D:50:SER:HB2	2:D:51:PRO:HD2	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:47:ASN:C	2:B:48:LEU:HD23	2.11	0.75
3:A:150:HEM:HMC2	3:A:150:HEM:CBC	2.15	0.75
2:B:4:SER:CB	2:B:7:GLU:HG3	2.11	0.74
2:D:83:ASN:N	2:D:83:ASN:HD22	1.84	0.74
1:C:7:LYS:HG2	1:C:73:ILE:CG2	2.18	0.74
1:A:117:LEU:O	2:B:30:ARG:NH2	2.20	0.74
2:D:107:GLY:HA3	2:D:134:VAL:CG1	2.19	0.73
3:B:150:HEM:NC	3:B:150:HEM:FE	1.55	0.73
3:B:150:HEM:HBB2	3:B:150:HEM:CHC	2.13	0.73
1:C:36:TYR:C	1:C:38:PRO:HD2	2.13	0.72
3:D:150:HEM:HBC2	3:D:150:HEM:HMC2	1.70	0.72
1:A:84:SER:O	1:A:85:ASP:C	2.31	0.72
2:D:50:SER:O	2:D:54:ILE:HG13	1.90	0.71
2:D:104:ARG:HG2	2:D:104:ARG:NH1	2.04	0.71
1:A:137:THR:O	1:A:140:TYR:CD1	2.43	0.71
3:D:150:HEM:HBB2	3:D:150:HEM:HHC	1.71	0.71
2:B:48:LEU:HD23	2:B:48:LEU:N	2.03	0.71
1:A:51:GLY:O	1:A:52:SER:O	2.09	0.70
3:D:150:HEM:HMC2	3:D:150:HEM:CBC	2.19	0.70
1:A:17:ILE:CG2	1:A:18:ALA:N	2.43	0.70
1:A:85:ASP:HA	1:A:89:HIS:ND1	2.06	0.70
1:C:24:TYR:O	1:C:28:THR:HG23	1.92	0.70
1:C:31:ARG:NH2	2:D:122:PHE:O	2.23	0.70
1:A:83:LEU:HD21	3:A:150:HEM:HMA1	1.72	0.70
2:D:107:GLY:HA3	2:D:134:VAL:HG13	1.72	0.70
2:B:57:ASN:HD22	2:B:60:VAL:H	1.38	0.68
2:D:91:LEU:CD1	2:D:95:LYS:HE3	2.25	0.67
1:C:30:GLU:O	1:C:34:ILE:HG12	1.94	0.67
2:D:6:GLU:OE1	2:D:6:GLU:N	2.27	0.67
3:D:150:HEM:HBB2	3:D:150:HEM:CHC	2.23	0.67
1:C:118:THR:OG1	1:C:121:VAL:HG23	1.95	0.67
2:D:57:ASN:HD21	2:D:59:MET:HB2	1.60	0.67
1:A:77:ALA:O	1:A:81:SER:OG	2.12	0.66
2:D:9:GLN:HG3	2:D:10:LEU:N	2.10	0.66
1:C:122:HIS:C	1:C:122:HIS:HD1	2.03	0.66
2:D:91:LEU:HD12	2:D:95:LYS:HE3	1.76	0.66
2:D:24:GLY:N	2:D:68:LEU:HD12	2.10	0.66
1:C:112:HIS:O	1:C:113:HIS:CG	2.49	0.65
2:D:51:PRO:O	2:D:55:LEU:HB2	1.96	0.65
2:D:41:PHE:CE1	2:D:98:VAL:CG2	2.80	0.65
1:C:89[B]:HIS:CE1	1:C:139:LYS:HB2	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:112:HIS:O	1:C:113:HIS:ND1	2.29	0.65
2:D:14:LEU:CD1	2:D:118:PHE:CE1	2.78	0.65
2:D:101:GLU:OE2	2:D:104:ARG:HD3	1.96	0.65
2:D:35:TYR:O	2:D:38:THR:OG1	2.14	0.65
1:A:138:ALA:C	1:A:140:TYR:H	2.05	0.65
2:B:20:VAL:HG12	2:B:21:ALA:N	2.10	0.65
2:D:133:LEU:C	2:D:133:LEU:HD22	2.21	0.64
2:B:93:CYS:SG	2:B:145:TYR:OH	2.53	0.64
1:C:14:PHE:HA	1:C:17:ILE:HD12	1.78	0.64
1:C:67:ILE:HD12	1:C:67:ILE:O	1.97	0.64
1:A:44:PRO:HD2	1:A:45:HIS:CD2	2.30	0.64
1:A:44:PRO:CD	1:A:45:HIS:HD2	2.11	0.64
1:C:141:ARG:CA	1:C:141:ARG:HE	2.04	0.64
1:A:141:ARG:O	1:C:1:VAL:N	2.26	0.63
1:C:89[A]:HIS:HD2	1:C:90:LYS:NZ	1.97	0.63
2:B:23:CYS:HB2	2:B:68:LEU:CD1	2.28	0.63
2:D:93:CYS:SG	2:D:145:TYR:CE1	2.79	0.63
1:C:70:ALA:HA	1:C:73:ILE:CG1	2.26	0.62
1:A:41:THR:HG22	2:D:40:ARG:NH2	2.14	0.62
1:A:44:PRO:CD	1:A:45:HIS:N	2.62	0.62
2:B:47:ASN:O	2:B:48:LEU:HD23	2.00	0.62
1:C:44:PRO:HD2	1:C:45:HIS:ND1	2.13	0.62
2:D:31:LEU:HD21	2:D:38:THR:HG21	1.82	0.62
1:A:127:LYS:NZ	1:C:141:ARG:HA	2.14	0.62
2:B:143:ARG:O	2:B:145:TYR:N	2.30	0.61
1:C:72:HIS:C	1:C:74:ASP:N	2.55	0.61
2:D:15:TRP:O	2:D:17:LYS:N	2.34	0.61
2:B:144:LYS:O	2:B:145:TYR:CG	2.52	0.61
1:A:41:THR:HG21	2:D:40:ARG:NH2	2.06	0.61
1:A:111:ILE:HG23	2:B:119:SER:HA	1.83	0.61
1:A:82:LYS:NZ	1:A:82:LYS:HB3	2.15	0.60
2:B:144:LYS:O	2:B:145:TYR:CD2	2.55	0.60
1:C:3:SER:O	1:C:6:ASP:HB2	2.02	0.59
1:C:113:HIS:N	1:C:114:PRO:HD3	2.17	0.59
2:D:106:LEU:CD2	3:D:150:HEM:HBB2	2.32	0.59
2:B:146:HIS:CD2	2:D:135:ARG:HG3	2.38	0.59
2:D:57:ASN:ND2	2:D:59:MET:HB2	2.16	0.59
1:C:132:VAL:O	1:C:133:GLY:C	2.43	0.59
1:A:86:LEU:O	1:A:91:LEU:HD22	2.02	0.59
2:D:39:GLN:O	2:D:40:ARG:C	2.46	0.59
3:D:150:HEM:CBB	3:D:150:HEM:HHC	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:THR:CG2	2:D:40:ARG:HH22	2.03	0.59
1:A:122:HIS:HD2	2:B:30:ARG:HE	1.49	0.59
2:D:117:HIS:CG	2:D:117:HIS:O	2.55	0.58
1:A:22:GLU:HG3	1:A:60:LYS:HG2	1.84	0.58
2:B:57:ASN:ND2	2:B:59:MET:N	2.51	0.58
1:A:138:ALA:O	1:A:141:ARG:O	2.20	0.58
3:D:150:HEM:CMC	3:D:150:HEM:CBC	2.71	0.58
3:A:150:HEM:HBB2	3:A:150:HEM:CMB	2.32	0.58
1:A:51:GLY:O	1:A:52:SER:C	2.46	0.58
1:C:24:TYR:O	1:C:28:THR:CG2	2.51	0.58
2:D:82:LYS:NZ	2:D:143:ARG:HH12	2.01	0.58
1:C:14:PHE:CZ	1:C:128:PHE:HE2	2.22	0.58
1:C:122:HIS:C	1:C:122:HIS:ND1	2.61	0.58
1:A:94:ASP:HB3	1:A:97:ASN:ND2	2.19	0.57
2:D:70:SER:O	2:D:73:ASP:HB2	2.04	0.57
2:D:41:PHE:CZ	2:D:98:VAL:HG22	2.39	0.57
2:B:2:HIS:C	2:B:2:HIS:CD2	2.83	0.57
1:C:45:HIS:NE2	3:C:150:HEM:O2D	2.30	0.56
1:C:71:ASN:O	1:C:72:HIS:CD2	2.58	0.56
2:D:47:ASN:OD1	2:D:47:ASN:C	2.47	0.56
2:D:61:ARG:O	2:D:62:ALA:C	2.48	0.56
2:D:143:ARG:C	2:D:145:TYR:H	2.13	0.56
1:A:20:HIS:ND1	1:A:23:GLU:OE2	2.35	0.56
1:C:138:ALA:HA	1:C:141:ARG:CZ	2.31	0.56
2:B:93:CYS:HG	2:B:145:TYR:HE2	1.40	0.56
2:B:57:ASN:HD22	2:B:59:MET:N	2.04	0.56
2:B:20:VAL:HG22	2:B:68:LEU:HB3	1.88	0.56
2:B:59:MET:HE2	2:B:59:MET:HA	1.87	0.56
2:D:104:ARG:HG3	2:D:135:ARG:NH1	2.21	0.56
1:A:63:VAL:CG2	1:A:63:VAL:O	2.55	0.55
2:B:92:HIS:NE2	3:B:150:HEM:NC	2.55	0.55
2:B:142:ALA:O	2:B:145:TYR:HD2	1.89	0.55
1:A:135:VAL:O	1:A:138:ALA:HB2	2.07	0.55
2:B:50:SER:O	2:B:54:ILE:HG13	2.07	0.55
3:A:150:HEM:HMB1	3:A:150:HEM:CBB	2.36	0.54
1:C:84:SER:O	1:C:85:ASP:C	2.44	0.54
2:D:107:GLY:HA3	2:D:134:VAL:HG11	1.90	0.54
2:D:38:THR:HG22	3:D:150:HEM:HBC1	1.90	0.54
1:C:118:THR:OG1	1:C:121:VAL:CG2	2.56	0.54
2:D:32:LEU:HD11	2:D:42:PHE:CD1	2.42	0.54
2:B:14:LEU:HD21	2:B:118:PHE:CD2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:63:VAL:O	1:C:67:ILE:HG23	2.08	0.53
2:D:117:HIS:NE2	2:D:118:PHE:CE2	2.71	0.53
2:D:32:LEU:HD11	2:D:42:PHE:CE1	2.43	0.53
2:D:83:ASN:N	2:D:83:ASN:ND2	2.50	0.53
2:D:81:ILE:O	2:D:84:THR:N	2.42	0.53
1:A:75:ASP:OD2	1:A:78:GLY:HA3	2.09	0.53
3:B:150:HEM:CBC	3:B:150:HEM:CMC	2.80	0.53
2:B:82:LYS:HG3	2:B:143:ARG:NH1	2.18	0.53
1:C:52:SER:O	1:C:56:LYS:HG3	2.09	0.53
2:D:117:HIS:CD2	2:D:118:PHE:CD2	2.96	0.53
1:C:137:THR:O	1:C:140:TYR:HB2	2.10	0.52
2:D:14:LEU:HD13	2:D:118:PHE:CZ	2.43	0.52
2:D:50:SER:HB2	2:D:51:PRO:CD	2.36	0.52
2:D:57:ASN:HD22	2:D:60:VAL:H	1.56	0.52
3:D:150:HEM:HBC2	3:D:150:HEM:HMC3	1.88	0.52
1:C:123:ALA:O	1:C:127:LYS:HG3	2.10	0.52
2:D:85:PHE:O	2:D:89:SER:HB2	2.10	0.52
1:A:92:ARG:HG3	1:A:92:ARG:HH11	1.75	0.52
3:B:150:HEM:NC	4:B:151:OXY:O1	2.42	0.52
2:D:82:LYS:HZ1	2:D:143:ARG:HH12	1.58	0.52
1:A:41:THR:CG2	2:D:40:ARG:HH21	2.22	0.52
1:A:41:THR:CG2	1:A:41:THR:O	2.55	0.52
1:A:31:ARG:NH2	2:B:122:PHE:O	2.42	0.52
1:C:138:ALA:C	1:C:140:TYR:H	2.18	0.52
1:A:41:THR:HG22	2:D:40:ARG:HH21	1.75	0.51
2:B:43:ALA:C	2:B:45:PHE:H	2.18	0.51
1:C:110:ALA:HB1	2:D:116:ALA:HB2	1.92	0.51
1:A:1:VAL:HG22	1:A:2:LEU:H	1.76	0.51
1:A:17:ILE:O	1:A:19:GLY:N	2.43	0.51
1:C:68:GLU:O	1:C:79:THR:HG21	2.09	0.51
2:D:86:SER:O	2:D:89:SER:HB3	2.10	0.51
2:D:15:TRP:O	2:D:16:GLY:C	2.53	0.51
2:D:15:TRP:C	2:D:17:LYS:N	2.68	0.51
2:D:26:GLU:CD	2:D:30:ARG:HE	2.19	0.51
1:C:80:LEU:O	1:C:81:SER:C	2.54	0.50
2:D:81:ILE:O	2:D:82:LYS:C	2.55	0.50
2:B:14:LEU:O	2:B:15:TRP:C	2.52	0.50
1:A:35:THR:O	1:A:37:PRO:HD3	2.11	0.50
2:D:75:VAL:O	2:D:76:LYS:C	2.53	0.50
1:C:119:PRO:HB3	2:D:33:ILE:CD1	2.42	0.50
3:B:150:HEM:CBC	3:B:150:HEM:HMC1	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:72:HIS:O	1:C:74:ASP:N	2.45	0.50
2:D:67:VAL:O	2:D:70:SER:HB3	2.11	0.50
2:B:146:HIS:CB	2:D:139:HIS:CD2	2.93	0.50
3:B:150:HEM:NC	3:B:150:HEM:ND	2.60	0.49
3:D:150:HEM:CBB	3:D:150:HEM:CHC	2.90	0.49
2:B:142:ALA:O	2:B:143:ARG:C	2.55	0.49
1:A:36:TYR:O	1:A:39:THR:OG1	2.28	0.49
1:C:80:LEU:HD22	1:C:83:LEU:HD12	1.93	0.49
2:B:32:LEU:HD11	2:B:42:PHE:CD2	2.48	0.49
2:D:57:ASN:ND2	2:D:59:MET:H	2.11	0.49
2:D:24:GLY:CA	2:D:68:LEU:HD12	2.43	0.49
1:C:105:PHE:C	1:C:105:PHE:CD2	2.91	0.49
2:D:51:PRO:HA	2:D:54:ILE:HD12	1.95	0.49
2:D:77:ASN:O	2:D:78:LEU:C	2.55	0.49
1:C:72:HIS:O	1:C:73:ILE:C	2.56	0.48
2:D:101:GLU:OE2	2:D:104:ARG:CD	2.61	0.48
1:C:30:GLU:O	1:C:34:ILE:CG1	2.59	0.48
2:D:88:LEU:HD21	3:D:150:HEM:HMA1	1.96	0.48
1:C:78:GLY:C	1:C:80:LEU:H	2.21	0.48
2:D:38:THR:HG22	3:D:150:HEM:CBC	2.44	0.48
2:B:43:ALA:C	2:B:45:PHE:N	2.65	0.48
1:A:82:LYS:HB3	1:A:82:LYS:HZ3	1.77	0.48
1:C:49:SER:O	1:C:50:HIS:C	2.56	0.47
2:D:15:TRP:C	2:D:17:LYS:H	2.22	0.47
1:A:141:ARG:HA	1:C:127:LYS:HD3	1.96	0.47
2:D:71:PHE:O	2:D:75:VAL:HG23	2.14	0.47
2:D:123:THR:O	2:D:126:CYS:HB3	2.14	0.47
2:D:130:TRP:CZ3	2:D:133:LEU:HD12	2.49	0.47
1:A:116:ALA:C	1:A:118:THR:H	2.23	0.47
1:A:92:ARG:HG3	1:A:92:ARG:NH1	2.28	0.47
1:A:101:LEU:O	1:A:102:GLY:C	2.57	0.47
1:C:86:LEU:HG	1:C:91:LEU:CD2	2.45	0.47
2:D:118:PHE:O	2:D:119:SER:C	2.56	0.47
2:B:57:ASN:HA	2:B:58:PRO:HD3	1.80	0.47
2:B:132:LYS:O	2:B:136:VAL:HG23	2.15	0.47
2:B:133:LEU:C	2:B:133:LEU:CD2	2.87	0.46
1:C:89[A]:HIS:HD2	1:C:90:LYS:HZ2	1.62	0.46
1:A:20:HIS:HB2	1:A:24:TYR:CE2	2.51	0.46
1:A:113:HIS:N	1:A:114:PRO:CD	2.79	0.46
1:A:127:LYS:HZ1	1:C:141:ARG:HA	1.78	0.46
2:D:9:GLN:CG	2:D:10:LEU:N	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:ALA:O	1:A:73:ILE:HB	2.14	0.46
1:C:89[A]:HIS:HD2	1:C:90:LYS:HZ3	1.63	0.46
1:C:119:PRO:HB3	2:D:33:ILE:HD12	1.98	0.46
1:A:17:ILE:O	1:A:18:ALA:C	2.59	0.46
1:A:91:LEU:HB3	1:A:93:VAL:HG23	1.96	0.46
2:D:82:LYS:NZ	2:D:143:ARG:NH1	2.64	0.46
2:D:99:ASP:O	2:D:102:ASN:ND2	2.47	0.46
2:B:133:LEU:O	2:B:137:VAL:HG23	2.15	0.46
2:B:135:ARG:HB3	2:D:146:HIS:CD2	2.51	0.46
1:A:85:ASP:O	1:A:89:HIS:HB2	2.16	0.46
1:C:72:HIS:HB2	1:C:79:THR:OG1	2.15	0.46
2:B:24:GLY:O	2:B:25:ALA:C	2.54	0.45
2:B:96:LEU:HA	2:B:96:LEU:HD12	1.56	0.45
2:D:57:ASN:O	2:D:58:PRO:C	2.57	0.45
1:C:36:TYR:O	1:C:37:PRO:C	2.59	0.45
2:D:128:ALA:O	2:D:129:ALA:C	2.60	0.45
1:A:61:LYS:HD3	3:A:150:HEM:HBA1	1.98	0.45
1:C:35:THR:O	1:C:35:THR:HG22	2.17	0.45
1:C:125:LEU:HA	1:C:125:LEU:HD23	1.63	0.45
3:B:150:HEM:NC	3:B:150:HEM:NB	2.63	0.45
1:A:1:VAL:HA	1:C:141:ARG:OXT	2.17	0.45
1:C:138:ALA:CA	1:C:141:ARG:HH22	2.20	0.45
1:C:141:ARG:N	1:C:141:ARG:NE	2.64	0.45
2:D:81:ILE:HD13	2:D:136:VAL:HG11	1.98	0.45
2:D:88:LEU:HD12	2:D:88:LEU:HA	1.37	0.44
1:C:89[B]:HIS:CE1	1:C:139:LYS:CB	2.93	0.44
2:B:57:ASN:HD22	2:B:59:MET:H	1.56	0.44
2:B:59:MET:HA	2:B:59:MET:CE	2.48	0.44
1:A:83:LEU:HD21	3:A:150:HEM:CMA	2.43	0.44
2:B:33:ILE:HG21	2:B:33:ILE:HD13	1.57	0.44
1:C:101:LEU:O	1:C:102:GLY:C	2.59	0.44
1:C:7:LYS:HG2	1:C:73:ILE:HG23	1.96	0.44
1:C:119:PRO:HG2	2:D:55:LEU:HD11	1.99	0.44
1:A:138:ALA:C	1:A:140:TYR:N	2.74	0.44
2:D:1:VAL:O	2:D:1:VAL:HG13	2.17	0.44
2:D:99:ASP:HA	2:D:100:PRO:HD3	1.68	0.44
2:D:112:ILE:O	2:D:112:ILE:HG22	2.17	0.44
2:B:100:PRO:O	2:B:101:GLU:C	2.60	0.44
1:C:6:ASP:O	1:C:7:LYS:C	2.59	0.43
1:C:33:PHE:HB3	1:C:40:LYS:HG3	2.00	0.43
1:A:141:ARG:NH1	1:C:130:CYS:SG	2.92	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:57:ASN:ND2	2:B:60:VAL:H	2.10	0.43
2:B:146:HIS:HB2	2:D:139:HIS:HD2	1.79	0.43
1:C:119:PRO:CB	2:D:33:ILE:HD13	2.48	0.43
1:A:94:ASP:OD1	1:A:95:PRO:HD2	2.19	0.43
2:B:141:LEU:HD23	2:B:141:LEU:HA	1.64	0.43
1:C:107:VAL:HG12	1:C:111:ILE:HD12	2.00	0.43
1:A:89:HIS:HB2	1:A:90:LYS:HD2	2.00	0.43
1:C:92:ARG:HA	1:C:140:TYR:OH	2.18	0.43
1:A:141:ARG:C	1:C:1:VAL:H2	2.22	0.43
2:D:10:LEU:HA	2:D:10:LEU:HD23	1.79	0.43
1:A:116:ALA:C	1:A:118:THR:N	2.76	0.43
1:A:88:ALA:O	1:A:92:ARG:HA	2.19	0.43
2:B:133:LEU:C	2:B:133:LEU:HD22	2.43	0.43
2:D:78:LEU:C	2:D:80:ASN:H	2.27	0.43
1:A:127:LYS:HZ3	1:C:141:ARG:HA	1.83	0.42
1:A:108:VAL:O	1:A:109:VAL:C	2.59	0.42
2:B:3:TRP:CZ3	2:B:132:LYS:HD3	2.54	0.42
2:B:100:PRO:C	2:B:102:ASN:N	2.77	0.42
2:D:43:ALA:C	2:D:45:PHE:H	2.28	0.42
1:A:128:PHE:O	1:A:132:VAL:HG23	2.20	0.42
1:C:62:VAL:HG22	4:C:151:OXY:O2	2.19	0.42
2:D:19:ASN:ND2	2:D:22:ASP:CG	2.68	0.42
2:D:63:HIS:NE2	4:D:151:OXY:O2	2.51	0.42
1:A:35:THR:C	1:A:37:PRO:HD3	2.44	0.42
1:A:98:PHE:HE1	1:A:136:LEU:CD2	2.31	0.42
2:D:15:TRP:CZ2	2:D:72:GLY:CA	3.02	0.42
2:D:103:PHE:N	2:D:103:PHE:CD1	2.84	0.42
2:D:107:GLY:CA	2:D:134:VAL:HG11	2.49	0.42
1:C:37:PRO:N	1:C:38:PRO:CD	2.83	0.42
1:A:2:LEU:HA	1:A:2:LEU:HD12	1.45	0.41
1:C:12:GLY:O	1:C:15:THR:HB	2.19	0.41
1:C:22:GLU:H	1:C:22:GLU:HG2	1.28	0.41
1:A:50:HIS:ND1	1:A:51:GLY:N	2.67	0.41
2:D:133:LEU:HA	2:D:133:LEU:HD23	1.71	0.41
2:B:57:ASN:HD21	2:B:59:MET:HB2	1.86	0.41
2:D:19:ASN:CG	2:D:22:ASP:OD2	2.55	0.41
1:A:138:ALA:O	1:A:141:ARG:N	2.53	0.41
1:A:9:ASN:O	1:A:10:VAL:C	2.57	0.41
1:A:40:LYS:C	1:A:42:TYR:H	2.28	0.41
1:C:78:GLY:C	1:C:80:LEU:N	2.76	0.41
1:C:95:PRO:O	1:C:96:VAL:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:118:THR:O	1:C:119:PRO:C	2.62	0.41
2:D:68:LEU:HA	2:D:68:LEU:HD23	1.76	0.41
2:B:81:ILE:O	2:B:82:LYS:C	2.62	0.41
1:C:66:LEU:C	1:C:68:GLU:H	2.27	0.41
1:C:141:ARG:CA	1:C:141:ARG:NE	2.76	0.41
2:D:99:ASP:CG	2:D:100:PRO:HD2	2.46	0.41
2:B:135:ARG:HA	2:B:135:ARG:HD3	1.57	0.41
2:B:20:VAL:CG1	2:B:21:ALA:N	2.72	0.41
2:B:68:LEU:HD23	2:B:68:LEU:HA	1.87	0.41
2:B:133:LEU:CD2	2:B:133:LEU:O	2.69	0.41
1:C:61:LYS:HD3	3:C:150:HEM:HBA1	2.03	0.41
1:C:70:ALA:CA	1:C:73:ILE:HG12	2.39	0.41
2:B:91:LEU:HG	2:B:96:LEU:HD22	2.02	0.41
2:B:133:LEU:O	2:B:133:LEU:HD22	2.20	0.41
2:B:146:HIS:HB2	2:D:139:HIS:NE2	2.35	0.41
1:C:36:TYR:C	1:C:38:PRO:CD	2.90	0.41
2:D:35:TYR:O	2:D:36:PRO:C	2.64	0.41
2:B:118:PHE:O	2:B:119:SER:C	2.56	0.40
1:C:37:PRO:N	1:C:38:PRO:HD2	2.36	0.40
1:C:63:VAL:O	1:C:63:VAL:HG12	2.18	0.40
2:D:104:ARG:HG3	2:D:104:ARG:NH1	2.20	0.40
1:A:41:THR:O	1:A:41:THR:HG23	2.21	0.40
1:A:134:THR:HG22	1:A:135:VAL:N	2.35	0.40
2:B:106:LEU:HD23	3:B:150:HEM:CBB	2.51	0.40
3:B:150:HEM:HHA	3:B:150:HEM:HAA1	1.84	0.40
1:C:67:ILE:O	1:C:67:ILE:CD1	2.67	0.40
1:C:69:ALA:HA	1:C:79:THR:HG21	2.02	0.40
2:D:7:GLU:OE1	2:D:132:LYS:NZ	2.46	0.40
2:D:50:SER:CB	2:D:51:PRO:CD	2.98	0.40
1:A:85:ASP:HA	1:A:89:HIS:CE1	2.55	0.40
3:C:150:HEM:HHA	3:C:150:HEM:HAA2	1.67	0.40
2:D:5:ALA:HB3	2:D:6:GLU:OE1	2.21	0.40
2:B:85:PHE:HD1	2:B:88:LEU:HD23	1.87	0.40
1:C:73:ILE:HA	1:C:76:ILE:HD11	2.02	0.40
2:B:23:CYS:HB2	2:B:68:LEU:HD12	2.04	0.40
2:D:110:LEU:HA	2:D:110:LEU:HD23	1.72	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2:HIS:CE1	1:C:72:HIS:CE1[2_555]	1.36	0.84
2:B:2:HIS:CE1	1:C:72:HIS:NE2[2_555]	1.88	0.32
2:B:2:HIS:NE2	1:C:72:HIS:CE1[2_555]	2.03	0.17
2:B:2:HIS:NE2	1:C:72:HIS:NE2[2_555]	2.12	0.08
2:B:2:HIS:CE1	1:C:72:HIS:ND1[2_555]	2.18	0.02
2:B:90:GLU:OE2	2:D:19:ASN:OD1[3_555]	2.19	0.01

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	139/142 (98%)	118 (85%)	17 (12%)	4 (3%)	3	13
1	C	140/142 (99%)	114 (81%)	17 (12%)	9 (6%)	1	3
2	B	144/146 (99%)	130 (90%)	10 (7%)	4 (3%)	4	14
2	D	144/146 (99%)	108 (75%)	26 (18%)	10 (7%)	1	2
All	All	567/576 (98%)	470 (83%)	70 (12%)	27 (5%)	2	6

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ALA
1	A	52	SER
1	A	138	ALA
2	B	144	LYS
1	C	17	ILE
1	C	18	ALA
1	C	21	ALA
2	D	16	GLY
2	D	44	SER
2	D	119	SER
2	D	144	LYS
1	C	4	ALA

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Mol	Chain	Res	Type
1	C	115	ALA
1	C	132	VAL
2	D	14	LEU
1	A	139	LYS
1	C	73	ILE
2	D	20	VAL
2	D	31	LEU
2	D	120	LYS
2	B	145	TYR
2	B	80	ASN
2	B	82	LYS
1	C	3	SER
2	D	13	GLY
2	D	136	VAL
1	C	10	VAL

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	114/115 (99%)	93 (82%)	21 (18%)	1	6
1	C	115/115 (100%)	84 (73%)	31 (27%)	0	1
2	B	122/122 (100%)	92 (75%)	30 (25%)	1	2
2	D	122/122 (100%)	90 (74%)	32 (26%)	0	2
All	All	473/474 (100%)	359 (76%)	114 (24%)	1	2

All (114) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LYS
1	A	22	GLU
1	A	23	GLU
1	A	41	THR
1	A	60	LYS
1	A	63	VAL

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Mol	Chain	Res	Type
1	A	66	LEU
1	A	67	ILE
1	A	80	LEU
1	A	82	LYS
1	A	84	SER
1	A	91	LEU
1	A	100	LEU
1	A	101	LEU
1	A	103	GLN
1	A	117	LEU
1	A	120	GLU
1	A	122	HIS
1	A	125	LEU
1	A	134	THR
1	A	141	ARG
2	B	1	VAL
2	B	7	GLU
2	B	9	GLN
2	B	14	LEU
2	B	17	LYS
2	B	20	VAL
2	B	32	LEU
2	B	44	SER
2	B	48	LEU
2	B	52	THR
2	B	55	LEU
2	B	59	MET
2	B	68	LEU
2	B	75	VAL
2	B	77	ASN
2	B	78	LEU
2	B	82	LYS
2	B	83	ASN
2	B	88	LEU
2	B	95	LYS
2	B	96	LEU
2	B	104	ARG
2	B	105	LEU
2	B	110	LEU
2	B	120	LYS
2	B	121	ASP
2	B	123	THR

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Mol	Chain	Res	Type
2	B	131	GLN
2	B	133	LEU
2	B	135	ARG
1	C	1	VAL
1	C	8	ASN
1	C	22	GLU
1	C	23	GLU
1	C	28	THR
1	C	29	LEU
1	C	34	ILE
1	C	37	PRO
1	C	52	SER
1	C	54	GLN
1	C	55	ILE
1	C	56	LYS
1	C	67	ILE
1	C	68	GLU
1	C	73	ILE
1	C	76	ILE
1	C	84	SER
1	C	85	ASP
1	C	91	LEU
1	C	92	ARG
1	C	96	VAL
1	C	99	LYS
1	C	100	LEU
1	C	103	GLN
1	C	105	PHE
1	C	122	HIS
1	C	126	ASP
1	C	129	LEU
1	C	134	THR
1	C	137	THR
1	C	141	ARG
2	D	4	SER
2	D	6	GLU
2	D	9	GLN
2	D	14	LEU
2	D	17	LYS
2	D	26	GLU
2	D	32	LEU
2	D	38	THR

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Mol	Chain	Res	Type
2	D	47	ASN
2	D	49	SER
2	D	68	LEU
2	D	69	THR
2	D	77	ASN
2	D	78	LEU
2	D	83	ASN
2	D	88	LEU
2	D	90	GLU
2	D	93	CYS
2	D	94	ASP
2	D	95	LYS
2	D	101	GLU
2	D	104	ARG
2	D	110	LEU
2	D	111	ILE
2	D	113	VAL
2	D	114	LEU
2	D	120	LYS
2	D	123	THR
2	D	133	LEU
2	D	134	VAL
2	D	135	ARG
2	D	144	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	45	HIS
1	A	71	ASN
2	B	2	HIS
2	B	9	GLN
2	B	57	ASN
2	B	83	ASN
2	B	131	GLN
2	B	146	HIS
1	C	8	ASN
1	C	20	HIS
1	C	71	ASN
1	C	72	HIS
2	D	57	ASN

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Mol	Chain	Res	Type
2	D	83	ASN
2	D	92	HIS
2	D	117	HIS
2	D	146	HIS

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	OXY	A	151	3	1,1,1	0.16	0	-		
4	OXY	D	151	3	1,1,1	0.02	0	-		
3	HEM	A	150	1,4	50,50,50	2.54	19 (38%)	67,82,82	3.03	32 (47%)
4	OXY	C	151	3	1,1,1	0.17	0	-		
3	HEM	B	150	4,2	50,50,50	3.20	24 (48%)	67,82,82	4.38	34 (50%)
4	OXY	B	151	3	1,1,1	0.13	0	-		
3	HEM	D	150	4,2	50,50,50	2.39	14 (28%)	67,82,82	2.08	25 (37%)
3	HEM	C	150	1,4	50,50,50	2.09	16 (32%)	67,82,82	2.63	36 (53%)

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	A	150	1,4	-	5/14/54/54	-
3	HEM	B	150	4,2	-	9/14/54/54	-
3	HEM	D	150	4,2	-	6/14/54/54	-
3	HEM	C	150	1,4	-	10/14/54/54	-

All (73) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	150	HEM	FE-NC	-12.14	1.55	1.95
3	D	150	HEM	C3D-C2D	8.93	1.56	1.36
3	D	150	HEM	FE-NA	7.98	2.21	1.95
3	A	150	HEM	FE-NB	-7.56	1.71	1.94
3	A	150	HEM	C3D-C2D	6.89	1.51	1.36
3	B	150	HEM	C3D-C2D	6.26	1.50	1.36
3	C	150	HEM	C3D-C2D	6.17	1.50	1.36
3	B	150	HEM	FE-NA	6.07	2.15	1.95
3	B	150	HEM	C3C-C2C	-5.64	1.25	1.37
3	A	150	HEM	CMB-C2B	4.94	1.60	1.50
3	B	150	HEM	CMC-C2C	4.51	1.60	1.50
3	A	150	HEM	FE-ND	4.50	2.08	1.94
3	B	150	HEM	C1A-NA	-4.49	1.31	1.39
3	C	150	HEM	CAB-C3B	4.29	1.58	1.47
3	B	150	HEM	C4D-ND	-4.27	1.32	1.40
3	B	150	HEM	FE-NB	4.25	2.08	1.94
3	B	150	HEM	C1C-NC	4.19	1.47	1.39
3	D	150	HEM	CAB-C3B	4.10	1.58	1.47
3	D	150	HEM	FE-ND	4.05	2.07	1.94
3	A	150	HEM	C3B-C2B	-4.01	1.29	1.37
3	B	150	HEM	C4D-C3D	3.95	1.51	1.45
3	A	150	HEM	C4D-ND	-3.82	1.33	1.40
3	B	150	HEM	C1B-NB	-3.80	1.33	1.40
3	C	150	HEM	FE-NB	3.67	2.06	1.94
3	A	150	HEM	CMD-C2D	3.51	1.58	1.50
3	B	150	HEM	C3B-C2B	-3.50	1.30	1.37
3	B	150	HEM	C4A-NA	-3.49	1.33	1.39
3	A	150	HEM	C1A-NA	-3.44	1.33	1.39
3	A	150	HEM	CAB-C3B	3.44	1.56	1.47
3	A	150	HEM	CHA-C1A	-3.44	1.31	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	150	HEM	FE-NC	-3.38	1.84	1.95
3	B	150	HEM	CAC-C3C	3.37	1.56	1.47
3	D	150	HEM	CAC-C3C	3.33	1.56	1.47
3	A	150	HEM	C2A-C3A	-3.31	1.30	1.38
3	C	150	HEM	C3C-C2C	-3.31	1.30	1.37
3	C	150	HEM	FE-NC	3.22	2.05	1.95
3	B	150	HEM	CHB-C1B	-3.16	1.32	1.38
3	C	150	HEM	CHB-C1B	3.11	1.44	1.38
3	D	150	HEM	CMA-C3A	3.09	1.57	1.50
3	B	150	HEM	FE-ND	3.08	2.04	1.94
3	D	150	HEM	C3C-C2C	-3.05	1.31	1.37
3	A	150	HEM	C1D-ND	-2.99	1.33	1.38
3	C	150	HEM	C2A-C3A	-2.95	1.31	1.38
3	D	150	HEM	O1D-CGD	2.94	1.31	1.22
3	B	150	HEM	O1A-CGA	2.94	1.31	1.22
3	C	150	HEM	C4C-NC	-2.91	1.34	1.39
3	C	150	HEM	C1D-ND	-2.83	1.33	1.38
3	C	150	HEM	CMC-C2C	2.78	1.56	1.50
3	D	150	HEM	C4C-NC	-2.77	1.34	1.39
3	C	150	HEM	C1B-C2B	2.59	1.49	1.44
3	B	150	HEM	CHA-C1A	-2.47	1.33	1.39
3	B	150	HEM	CMD-C2D	2.46	1.55	1.50
3	D	150	HEM	CMD-C2D	2.45	1.55	1.50
3	C	150	HEM	CHD-C1D	-2.45	1.33	1.39
3	C	150	HEM	O2D-CGD	-2.42	1.22	1.30
3	A	150	HEM	FE-NA	2.41	2.03	1.95
3	C	150	HEM	O1A-CGA	2.41	1.30	1.22
3	B	150	HEM	CHD-C1D	-2.40	1.33	1.39
3	B	150	HEM	CAB-C3B	2.38	1.53	1.47
3	A	150	HEM	CHB-C4A	-2.38	1.34	1.39
3	A	150	HEM	CHA-C4D	-2.32	1.33	1.38
3	A	150	HEM	CMC-C2C	2.32	1.55	1.50
3	D	150	HEM	FE-NB	2.30	2.02	1.94
3	D	150	HEM	CMB-C2B	2.23	1.55	1.50
3	A	150	HEM	O1A-CGA	2.21	1.29	1.22
3	A	150	HEM	C1B-C2B	2.16	1.48	1.44
3	C	150	HEM	CAC-C3C	2.16	1.53	1.47
3	D	150	HEM	C1D-ND	-2.14	1.34	1.38
3	C	150	HEM	C1A-C2A	-2.11	1.40	1.44
3	D	150	HEM	FE-NC	2.03	2.01	1.95
3	B	150	HEM	CHC-C1C	2.03	1.42	1.38
3	B	150	HEM	O2D-CGD	-2.02	1.24	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	150	HEM	C4C-NC	2.01	1.43	1.39

All (127) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	150	HEM	CHD-C4C-NC	17.71	143.74	124.45
3	B	150	HEM	CMC-C2C-C1C	10.36	142.97	124.73
3	B	150	HEM	CAA-CBA-CGA	-9.68	87.99	113.67
3	B	150	HEM	C4C-C3C-C2C	9.62	115.16	106.81
3	A	150	HEM	CAA-CBA-CGA	-8.56	90.96	113.67
3	B	150	HEM	CHC-C1C-NC	8.38	133.58	124.45
3	B	150	HEM	CHD-C4C-C3C	-8.38	111.08	125.21
3	B	150	HEM	CMC-C2C-C3C	-8.03	109.00	128.43
3	B	150	HEM	C1C-CHC-C4B	-7.40	110.30	126.02
3	B	150	HEM	C4C-CHD-C1D	-7.30	110.51	126.02
3	C	150	HEM	CHC-C1C-NC	-6.85	116.99	124.45
3	A	150	HEM	C4C-C3C-C2C	6.67	112.60	106.81
3	A	150	HEM	C4D-ND-C1D	6.63	113.05	105.21
3	A	150	HEM	CMB-C2B-C1B	6.55	135.27	125.03
3	A	150	HEM	C3C-C2C-C1C	-6.38	101.01	107.05
3	B	150	HEM	C1A-CHA-C4D	6.26	140.98	126.25
3	C	150	HEM	CAA-CBA-CGA	-6.25	97.09	113.67
3	B	150	HEM	CHA-C4D-ND	-6.21	116.69	124.37
3	A	150	HEM	CHC-C4B-NB	5.79	130.66	124.42
3	D	150	HEM	C4D-ND-C1D	5.78	112.06	105.21
3	A	150	HEM	C1B-NB-C4B	-5.78	98.36	105.21
3	D	150	HEM	CAD-C3D-C2D	5.09	137.40	127.87
3	B	150	HEM	CAD-C3D-C4D	5.00	133.41	124.70
3	C	150	HEM	CMC-C2C-C1C	4.91	133.38	124.73
3	A	150	HEM	C3B-C4B-NB	4.84	112.95	109.47
3	C	150	HEM	CHA-C1A-NA	4.69	132.36	123.86
3	B	150	HEM	CAA-C2A-C3A	4.68	137.57	127.07
3	C	150	HEM	CAA-C2A-C1A	-4.62	115.92	124.94
3	B	150	HEM	C2D-C1D-ND	4.56	115.18	109.90
3	C	150	HEM	CAD-C3D-C4D	4.55	132.62	124.70
3	A	150	HEM	C1C-CHC-C4B	-4.52	116.41	126.02
3	C	150	HEM	CAA-C2A-C3A	4.50	137.16	127.07
3	B	150	HEM	CAA-C2A-C1A	-4.44	116.26	124.94
3	A	150	HEM	CHC-C4B-C3B	-4.35	116.39	125.07
3	C	150	HEM	C4A-C3A-C2A	4.34	111.78	106.82
3	A	150	HEM	CMC-C2C-C1C	4.29	132.28	124.73
3	C	150	HEM	C3B-C2B-C1B	4.28	109.62	106.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	150	HEM	C4B-C3B-C2B	4.14	111.09	107.28
3	B	150	HEM	C1D-C2D-C3D	-4.06	102.71	106.98
3	B	150	HEM	CAC-C3C-C2C	-4.05	115.27	128.43
3	A	150	HEM	C3B-C2B-C1B	-3.96	103.44	106.41
3	D	150	HEM	C4C-CHD-C1D	3.94	134.39	126.02
3	C	150	HEM	C4C-CHD-C1D	3.80	134.09	126.02
3	C	150	HEM	C3A-C4A-NA	-3.75	104.13	110.14
3	B	150	HEM	CHC-C4B-NB	3.72	128.43	124.42
3	A	150	HEM	C2B-C1B-NB	3.68	114.07	109.84
3	C	150	HEM	C2B-C1B-NB	-3.59	105.72	109.84
3	D	150	HEM	CMA-C3A-C2A	3.59	133.23	125.62
3	B	150	HEM	CMA-C3A-C2A	3.41	132.85	125.62
3	C	150	HEM	CHA-C4D-ND	-3.40	120.16	124.37
3	D	150	HEM	C3B-C4B-NB	-3.39	107.04	109.47
3	A	150	HEM	CAD-C3D-C4D	3.34	130.51	124.70
3	B	150	HEM	CBD-CAD-C3D	-3.26	103.52	112.53
3	C	150	HEM	C4D-ND-C1D	3.26	109.06	105.21
3	A	150	HEM	CHC-C1C-NC	-3.19	120.98	124.45
3	C	150	HEM	CHC-C1C-C2C	3.19	132.12	125.49
3	A	150	HEM	CHD-C4C-NC	3.18	127.91	124.45
3	B	150	HEM	CHA-C4D-C3D	3.17	131.07	125.23
3	A	150	HEM	C4A-NA-C1A	-3.17	100.66	105.82
3	D	150	HEM	CAD-CBD-CGD	-3.01	105.69	113.67
3	D	150	HEM	CMD-C2D-C1D	-3.00	120.34	125.03
3	C	150	HEM	CMB-C2B-C3B	-3.00	121.16	128.43
3	D	150	HEM	C4D-C3D-C2D	-2.99	102.54	106.89
3	A	150	HEM	C3A-C4A-NA	2.98	114.92	110.14
3	A	150	HEM	CMD-C2D-C1D	2.98	129.69	125.03
3	D	150	HEM	CHD-C1D-ND	2.97	127.62	124.42
3	A	150	HEM	CMB-C2B-C3B	-2.96	121.27	128.43
3	A	150	HEM	C2C-C1C-NC	2.92	115.03	109.64
3	D	150	HEM	CHD-C4C-C3C	2.91	130.11	125.21
3	C	150	HEM	CHC-C4B-NB	2.89	127.54	124.42
3	B	150	HEM	O2A-CGA-O1A	2.84	130.63	123.33
3	D	150	HEM	CAC-C3C-C4C	2.80	131.50	124.82
3	A	150	HEM	C4A-C3A-C2A	-2.79	103.62	106.82
3	C	150	HEM	CMC-C2C-C3C	-2.78	121.69	128.43
3	C	150	HEM	C4C-C3C-C2C	2.75	109.20	106.81
3	A	150	HEM	CBC-CAC-C3C	-2.74	113.81	127.53
3	D	150	HEM	CMA-C3A-C4A	-2.73	121.27	125.42
3	A	150	HEM	CMA-C3A-C4A	2.71	129.55	125.42
3	D	150	HEM	CBB-CAB-C3B	-2.71	114.00	127.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	150	HEM	CMD-C2D-C1D	2.69	129.23	125.03
3	D	150	HEM	C1B-NB-C4B	2.68	108.38	105.21
3	D	150	HEM	CAD-C3D-C4D	-2.67	120.04	124.70
3	C	150	HEM	C3B-C4B-NB	2.67	111.39	109.47
3	D	150	HEM	CMD-C2D-C3D	2.66	133.34	126.15
3	B	150	HEM	CAD-C3D-C2D	-2.61	122.98	127.87
3	A	150	HEM	O2A-CGA-O1A	2.61	130.04	123.33
3	C	150	HEM	CHA-C1A-C2A	-2.59	119.63	125.30
3	C	150	HEM	CMA-C3A-C4A	-2.58	121.49	125.42
3	C	150	HEM	CMB-C2B-C1B	2.57	129.04	125.03
3	D	150	HEM	CAC-C3C-C2C	-2.56	120.11	128.43
3	B	150	HEM	C4A-NA-C1A	2.54	109.97	105.82
3	C	150	HEM	CHB-C1B-NB	2.53	127.50	124.37
3	A	150	HEM	C2A-C1A-NA	2.51	112.93	110.15
3	A	150	HEM	C1D-C2D-C3D	-2.49	104.36	106.98
3	A	150	HEM	CHA-C4D-ND	2.48	127.44	124.37
3	B	150	HEM	CHC-C1C-C2C	-2.48	120.33	125.49
3	D	150	HEM	CHC-C4B-NB	2.42	127.03	124.42
3	D	150	HEM	O1A-CGA-CBA	-2.39	115.51	123.09
3	C	150	HEM	CAD-C3D-C2D	-2.37	123.42	127.87
3	D	150	HEM	CMC-C2C-C1C	2.37	128.91	124.73
3	C	150	HEM	C4A-CHB-C1B	-2.36	120.69	126.25
3	B	150	HEM	C4D-C3D-C2D	-2.32	103.52	106.89
3	B	150	HEM	CHB-C1B-NB	2.31	127.23	124.37
3	B	150	HEM	CBC-CAC-C3C	2.30	139.04	127.53
3	B	150	HEM	CMA-C3A-C4A	-2.30	121.91	125.42
3	C	150	HEM	C3C-C2C-C1C	-2.30	104.87	107.05
3	D	150	HEM	CHB-C1B-NB	2.30	127.21	124.37
3	B	150	HEM	O2A-CGA-CBA	-2.28	106.79	114.00
3	C	150	HEM	C1D-C2D-C3D	-2.27	104.59	106.98
3	A	150	HEM	CBA-CAA-C2A	2.26	118.77	112.53
3	C	150	HEM	C4A-NA-C1A	2.23	109.46	105.82
3	B	150	HEM	CMB-C2B-C1B	2.23	128.52	125.03
3	C	150	HEM	CHA-C4D-C3D	2.21	129.31	125.23
3	D	150	HEM	CMC-C2C-C3C	-2.20	123.10	128.43
3	D	150	HEM	C1C-CHC-C4B	-2.20	121.35	126.02
3	B	150	HEM	CHD-C1D-ND	-2.18	122.08	124.42
3	D	150	HEM	CAA-CBA-CGA	-2.17	107.91	113.67
3	C	150	HEM	CBA-CAA-C2A	2.16	118.52	112.53
3	D	150	HEM	CHA-C4D-ND	2.13	127.00	124.37
3	B	150	HEM	CAD-CBD-CGD	-2.12	108.04	113.67
3	A	150	HEM	C4D-C3D-C2D	-2.10	103.83	106.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	150	HEM	C2A-C1A-NA	-2.09	107.83	110.15
3	A	150	HEM	CHB-C4A-C3A	-2.08	121.39	127.43
3	C	150	HEM	CHC-C4B-C3B	-2.06	120.95	125.07
3	C	150	HEM	O2D-CGD-CBD	2.05	120.48	114.00
3	C	150	HEM	C4D-C3D-C2D	-2.03	103.93	106.89
3	B	150	HEM	C2C-C1C-NC	-2.00	105.93	109.64

There are no chirality outliers.

All (30) torsion outliers are listed below:

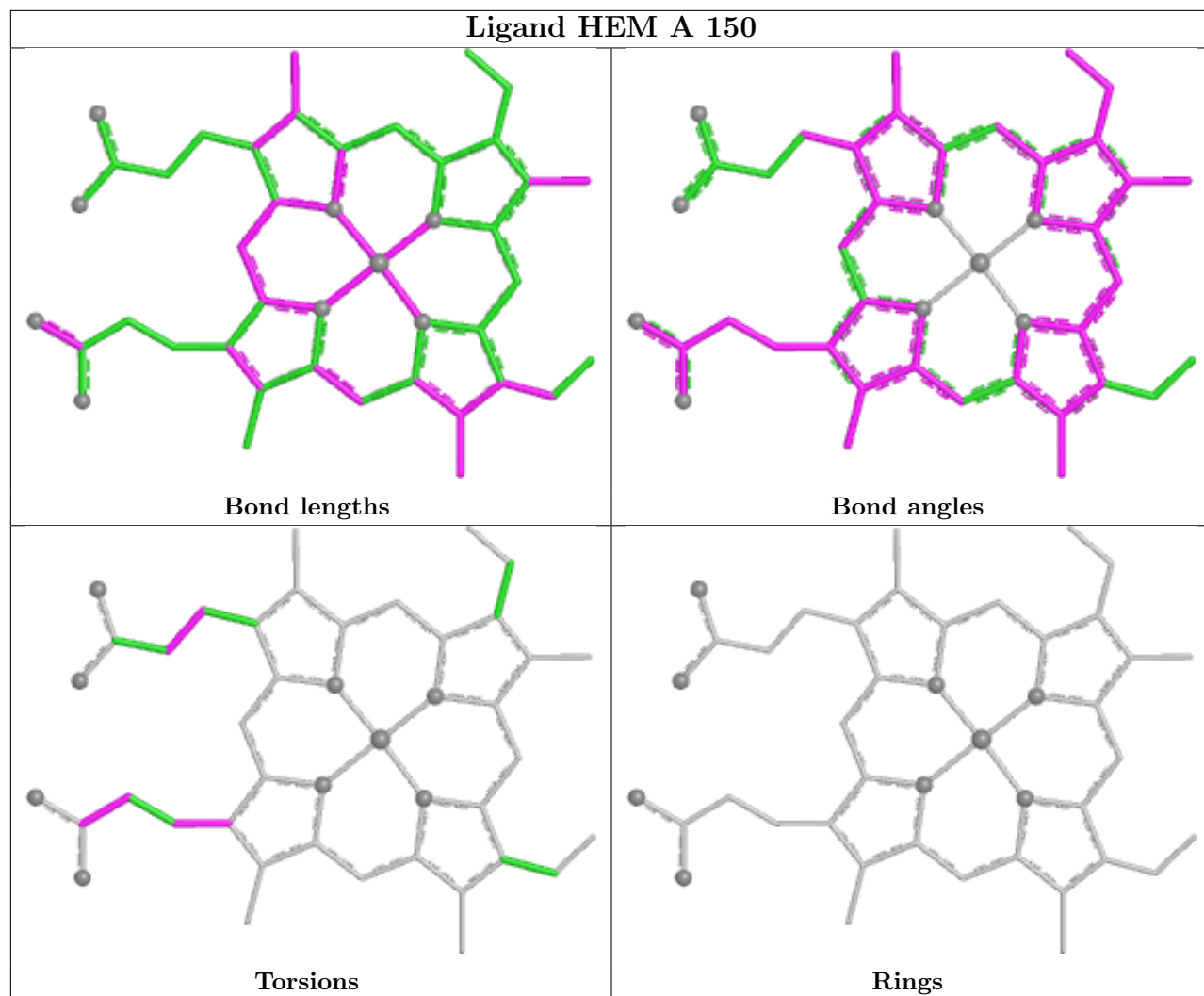
Mol	Chain	Res	Type	Atoms
3	A	150	HEM	C1A-C2A-CAA-CBA
3	A	150	HEM	C3A-C2A-CAA-CBA
3	B	150	HEM	C2C-C3C-CAC-CBC
3	C	150	HEM	C1A-C2A-CAA-CBA
3	C	150	HEM	C3A-C2A-CAA-CBA
3	D	150	HEM	C2D-C3D-CAD-CBD
3	D	150	HEM	C4D-C3D-CAD-CBD
3	A	150	HEM	C3D-CAD-CBD-CGD
3	B	150	HEM	C3A-C2A-CAA-CBA
3	C	150	HEM	C4D-C3D-CAD-CBD
3	C	150	HEM	C2D-C3D-CAD-CBD
3	B	150	HEM	C1A-C2A-CAA-CBA
3	D	150	HEM	C3D-CAD-CBD-CGD
3	C	150	HEM	C2C-C3C-CAC-CBC
3	B	150	HEM	C4B-C3B-CAB-CBB
3	B	150	HEM	C4C-C3C-CAC-CBC
3	C	150	HEM	CAA-CBA-CGA-O2A
3	B	150	HEM	CAD-CBD-CGD-O1D
3	A	150	HEM	CAA-CBA-CGA-O2A
3	B	150	HEM	CAD-CBD-CGD-O2D
3	B	150	HEM	CAA-CBA-CGA-O2A
3	C	150	HEM	CAA-CBA-CGA-O1A
3	D	150	HEM	CAD-CBD-CGD-O1D
3	A	150	HEM	CAA-CBA-CGA-O1A
3	B	150	HEM	CAA-CBA-CGA-O1A
3	C	150	HEM	C4B-C3B-CAB-CBB
3	C	150	HEM	C4C-C3C-CAC-CBC
3	D	150	HEM	CAD-CBD-CGD-O2D
3	D	150	HEM	CAA-CBA-CGA-O2A
3	C	150	HEM	C2B-C3B-CAB-CBB

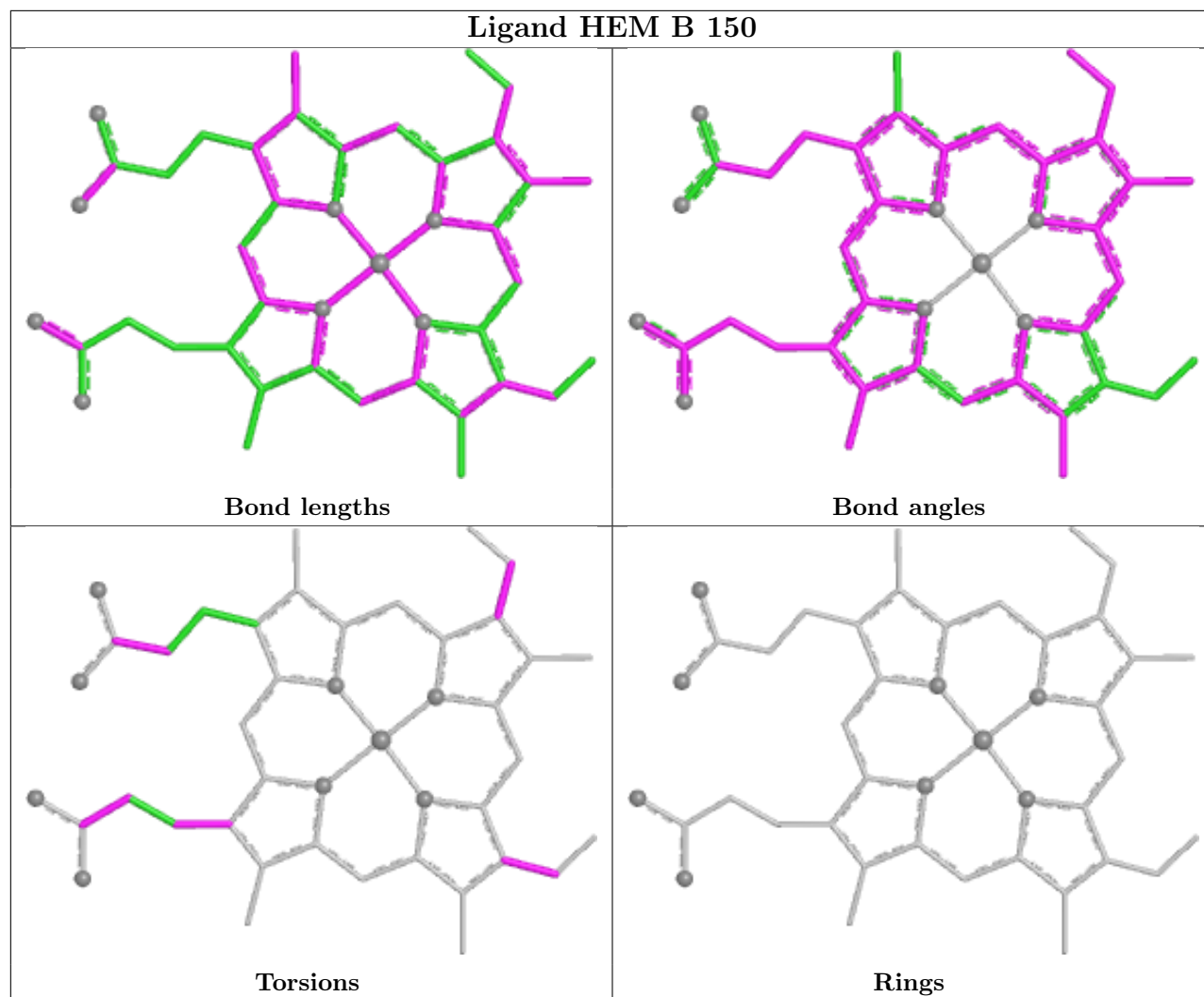
There are no ring outliers.

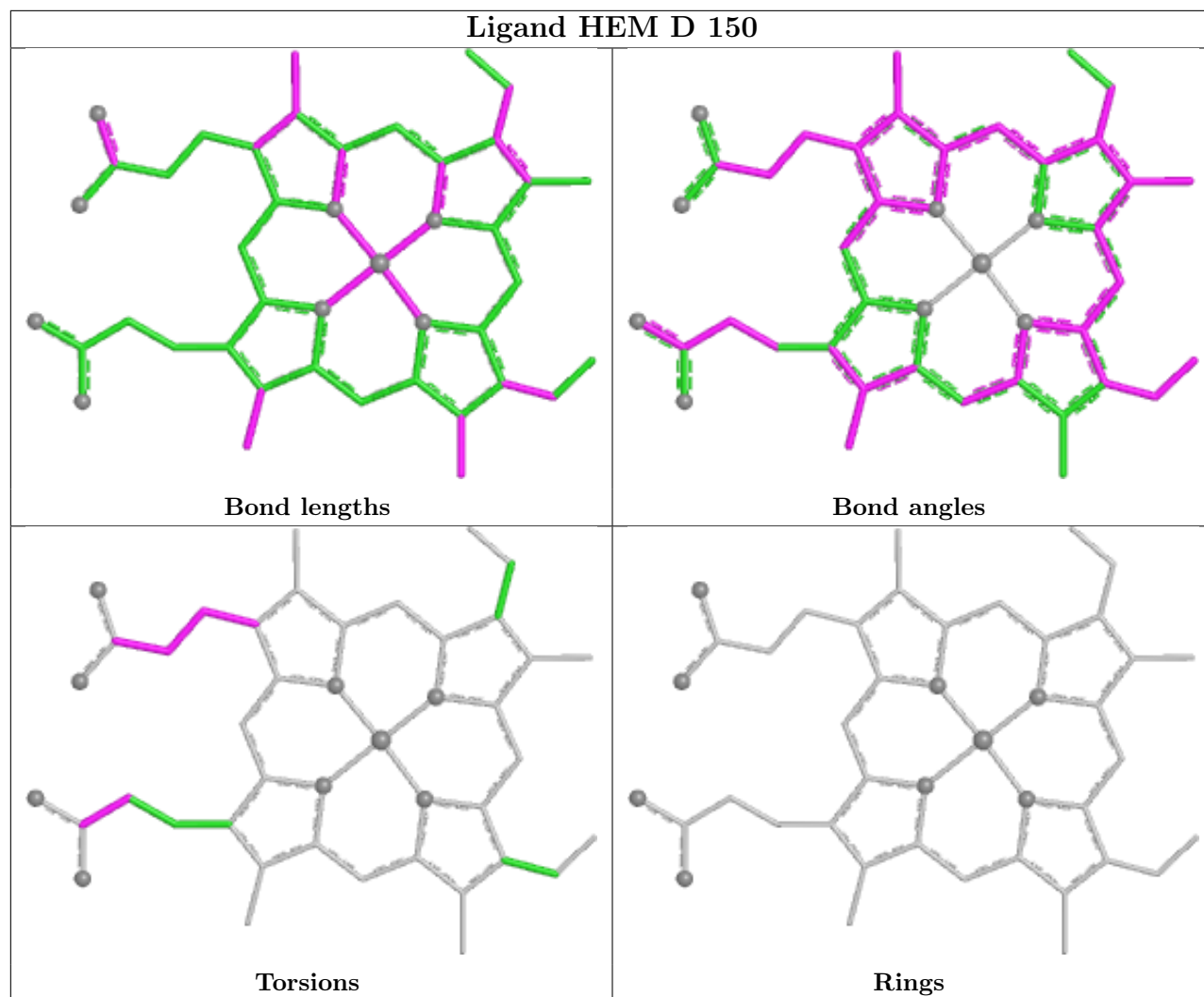
7 monomers are involved in 40 short contacts:

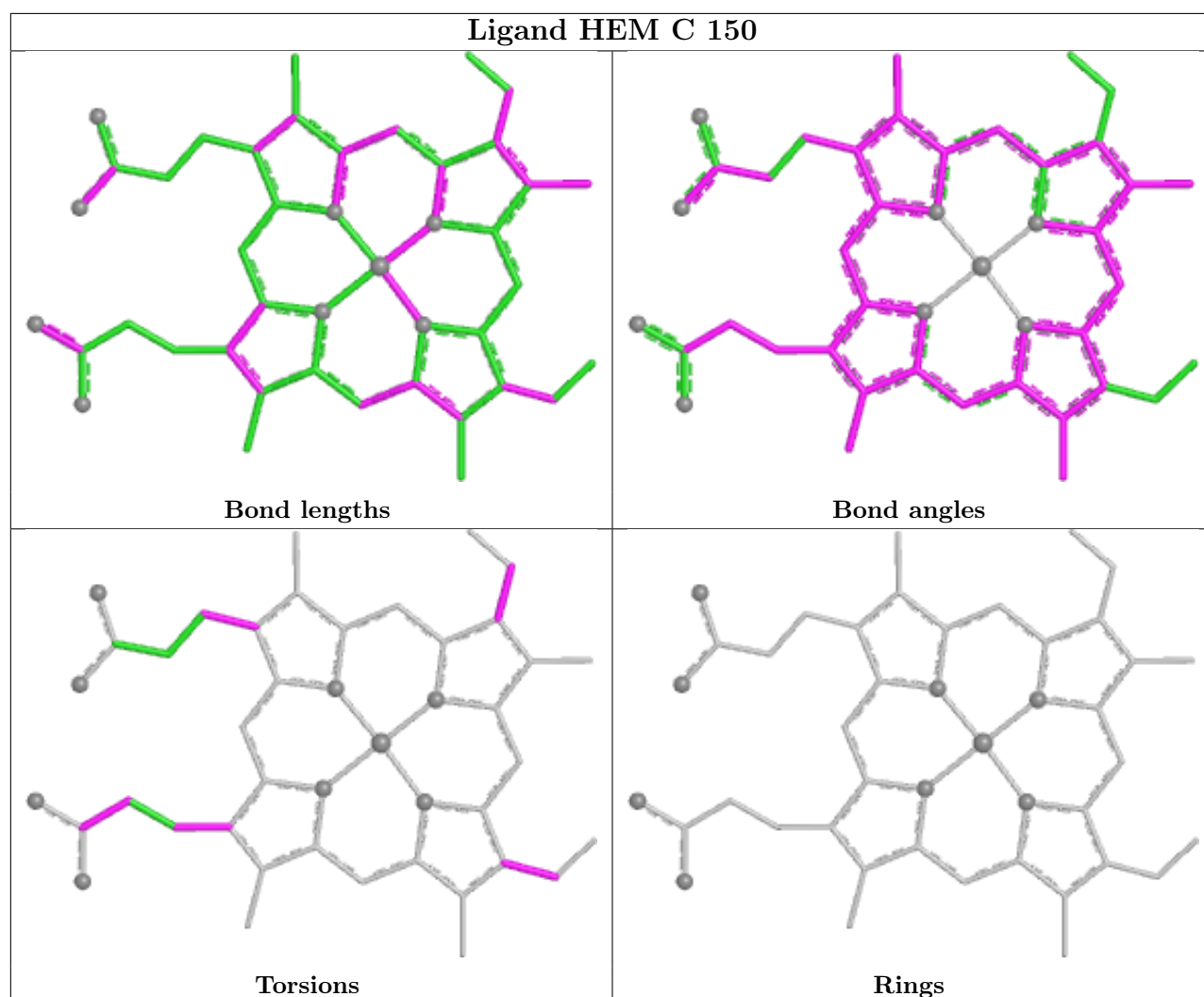
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	151	OXY	1	0
3	A	150	HEM	9	0
4	C	151	OXY	1	0
3	B	150	HEM	11	0
4	B	151	OXY	1	0
3	D	150	HEM	15	0
3	C	150	HEM	3	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	141/142 (99%)	-0.73	1 (0%) 84 77	15, 34, 62, 122	0
1	C	141/142 (99%)	-0.56	1 (0%) 84 77	19, 42, 73, 104	1 (0%)
2	B	146/146 (100%)	-0.80	0 100 100	12, 33, 58, 94	0
2	D	146/146 (100%)	-0.55	1 (0%) 84 77	27, 49, 68, 103	0
All	All	574/576 (99%)	-0.66	3 (0%) 87 82	12, 39, 69, 122	1 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	TYR	4.6
1	C	140	TYR	4.3
2	D	145	TYR	2.2

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](#)

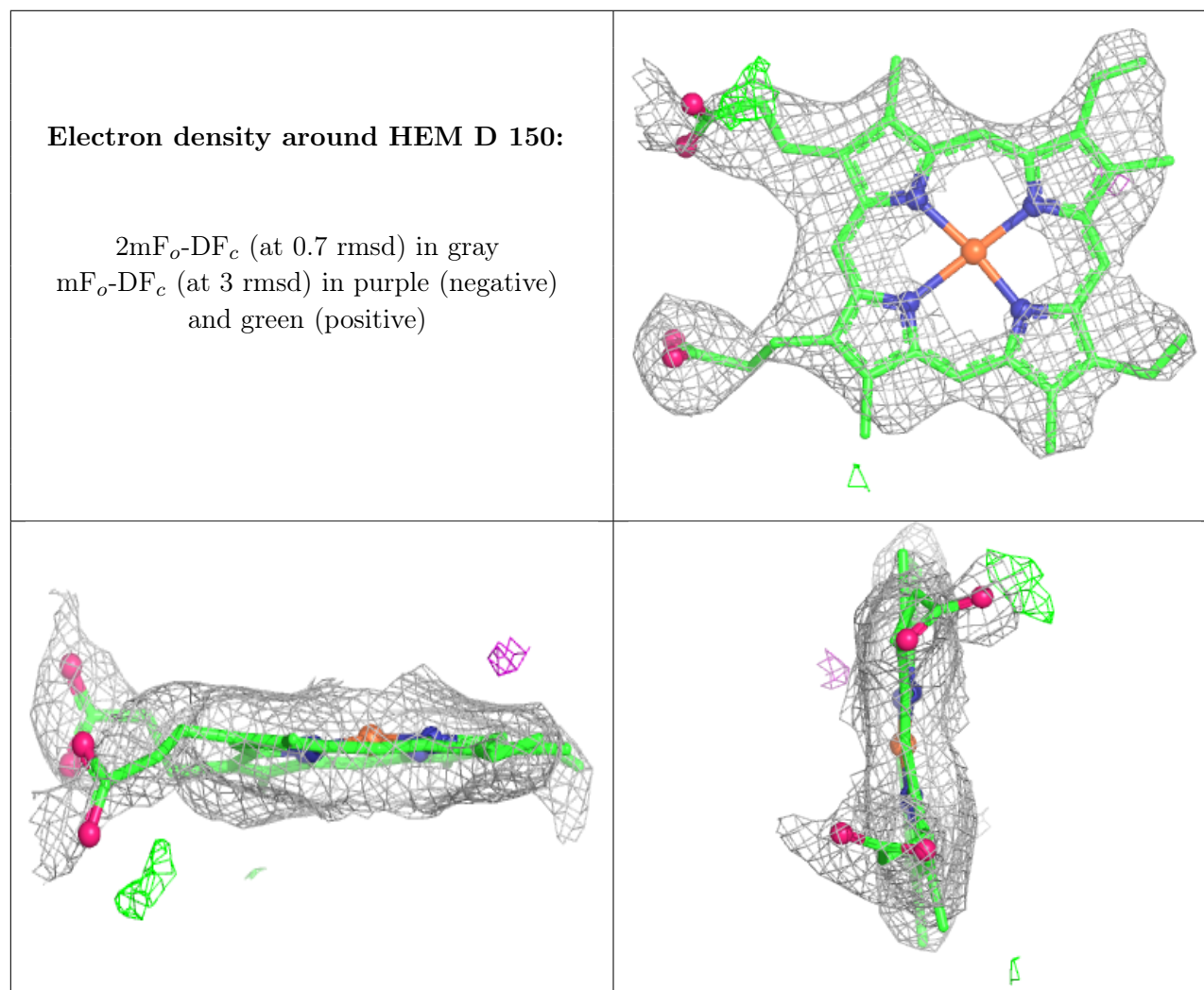
There are no oligosaccharides in this entry.

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.

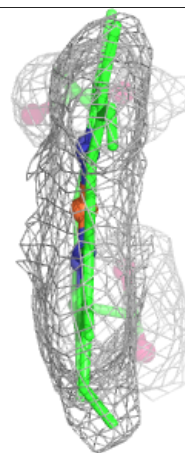
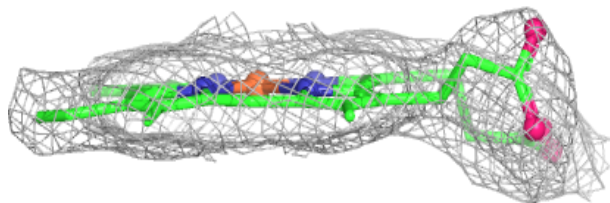
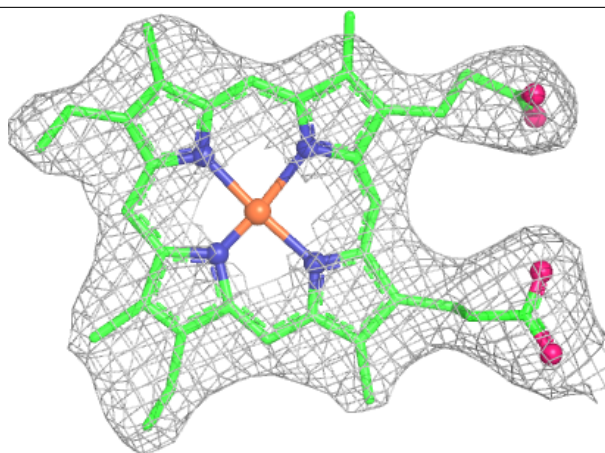
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	HEM	D	150	43/43	0.92	0.09	35,58,73,84	0
4	OXY	A	151	2/2	0.94	0.10	44,44,44,46	0
4	OXY	D	151	2/2	0.96	0.08	46,46,46,67	0
4	OXY	B	151	2/2	0.97	0.07	34,34,34,48	0
3	HEM	B	150	43/43	0.98	0.06	16,28,44,50	0
3	HEM	C	150	43/43	0.98	0.05	19,30,54,65	0
4	OXY	C	151	2/2	0.98	0.05	60,60,60,64	0
3	HEM	A	150	43/43	0.98	0.06	17,33,57,67	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.



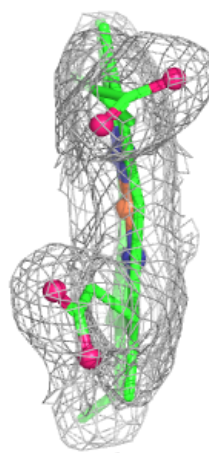
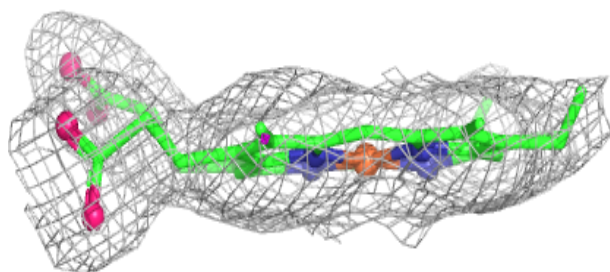
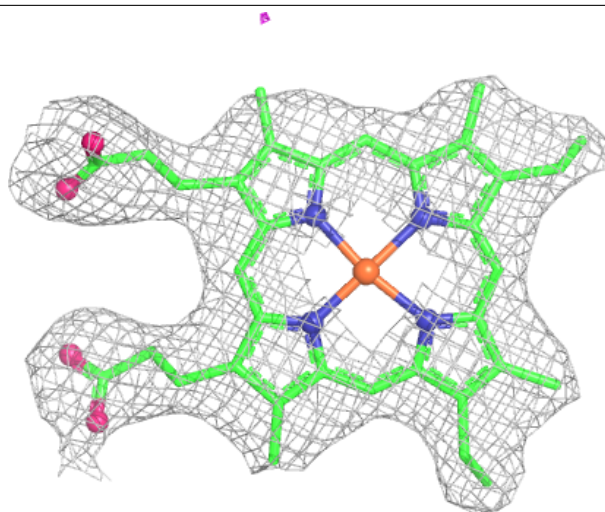
Electron density around HEM B 150:

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



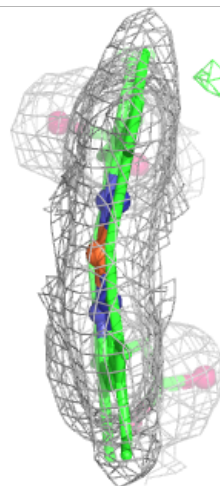
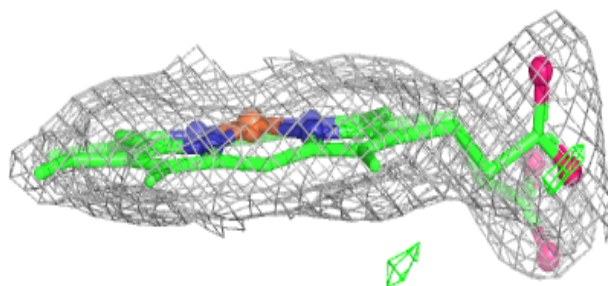
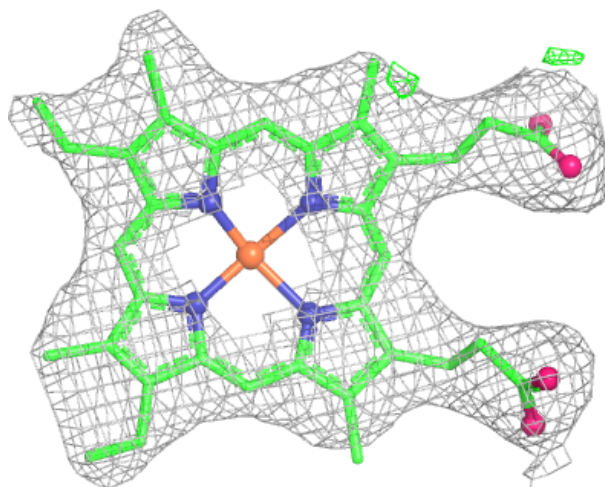
Electron density around HEM C 150:

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



Electron density around HEM A 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 ⓘ

There are no such residues in this entry.