



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 08:46 am BST

PDB ID : 2PCB
Title : CRYSTAL STRUCTURE OF A COMPLEX BETWEEN ELECTRON
TRANSFER PARTNERS, CYTOCHROME C PEROXIDASE AND CY-
TOCHROME C
Authors : Pelletier, H.; Kraut, J.
Deposited on : 1993-04-14
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

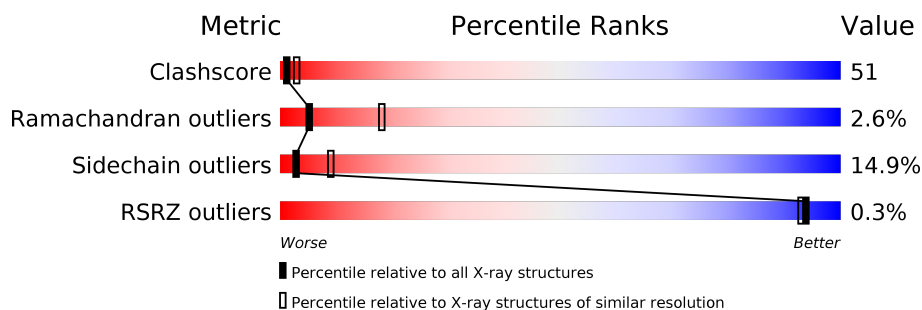
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

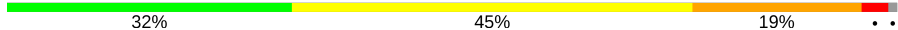
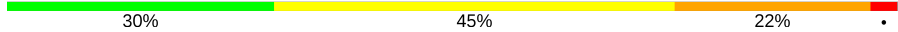

The reported resolution of this entry is 2.80 Å.

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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 on 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	296	 32% 45% 19% ..
1	C	296	 30% 45% 22% ..
2	B	104	 15% 50% 28% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6031 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 CYTOCHROME C PEROXIDASE (CCP).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	0	0
			2371	1514	395	456	6			
1	C	294	Total	C	N	O	S	0	0	0
			2371	1514	395	456	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	ILE	THR	CONFLICT	UNP P00431
A	152	GLY	ASP	CONFLICT	UNP P00431
C	53	ILE	THR	CONFLICT	UNP P00431
C	152	GLY	ASP	CONFLICT	UNP P00431

- Molecule 2 is a protein called CYTOCHROME C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	104	Total	C	N	O	S	0	0	0
			823	524	144	151	4			

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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		

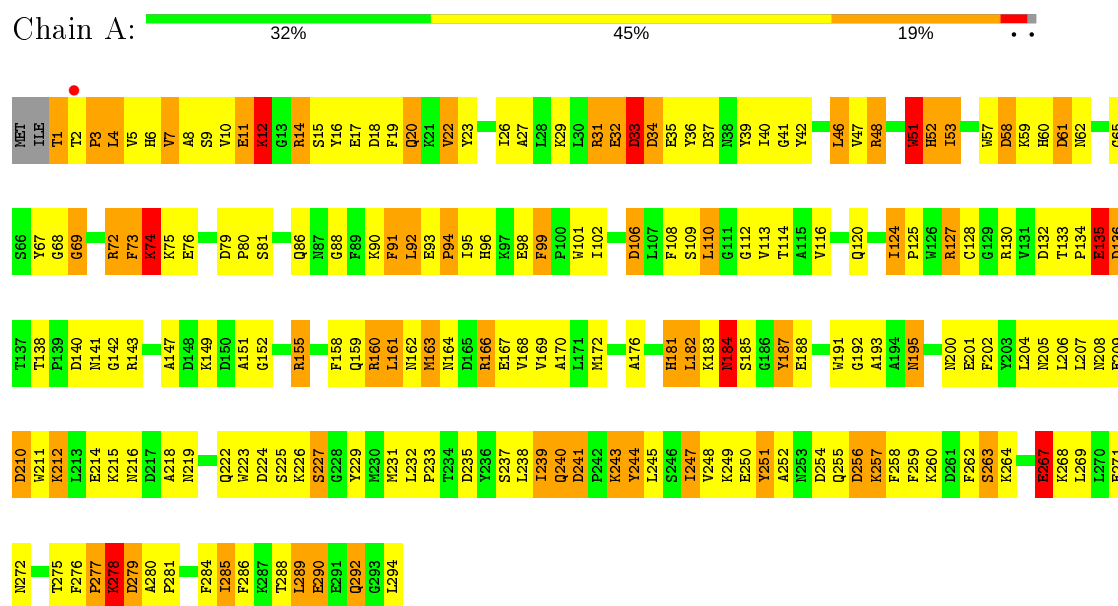
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	146	Total	O	0	0
			146	146		
4	B	41	Total	O	0	0
			41	41		
4	C	150	Total	O	0	0
			150	150		

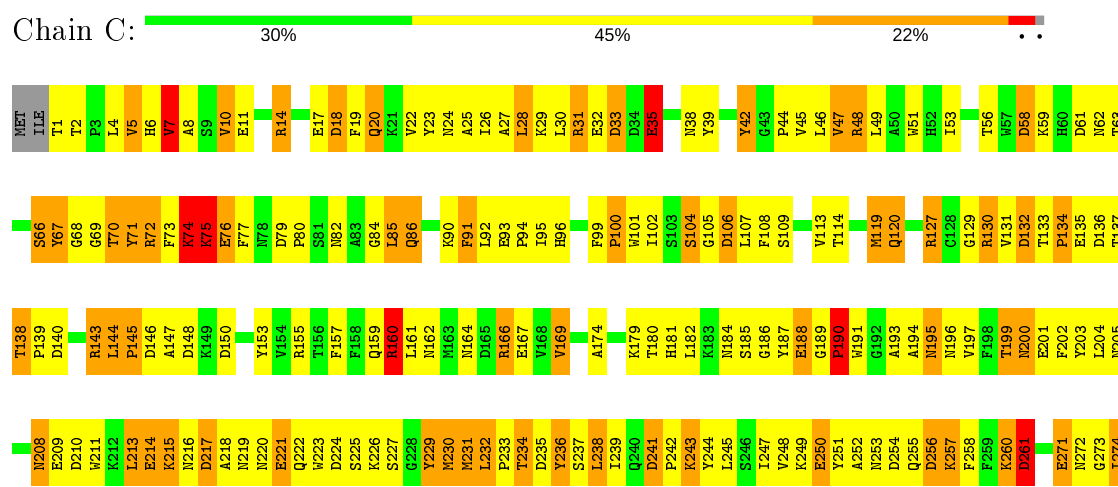
3 Residue-property plots

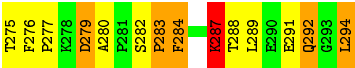
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: CYTOCHROME C PEROXIDASE (CCP)

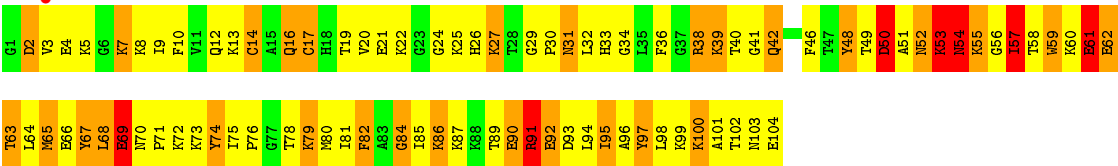
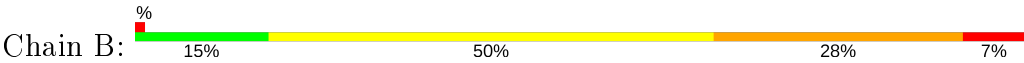


• Molecule 1: CYTOCHROME C PEROXIDASE (CCP)





● Molecule 2: CYTOCHROME C



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.30 Å 105.30 Å 186.20 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.80 11.51 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.00-2.80) 94.2 (11.51-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.82 Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.178 , (Not available) 0.173 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	39.7	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 126.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6031	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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	1.15	2/2438 (0.1%)	2.18	112/3302 (3.4%)
1	C	1.13	1/2438 (0.0%)	2.28	128/3302 (3.9%)
2	B	0.97	0/839	2.22	35/1118 (3.1%)
All	All	1.11	3/5715 (0.1%)	2.23	275/7722 (3.6%)

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	A	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	192	GLY	N-CA	6.73	1.56	1.46
1	C	104	SER	CB-OG	6.21	1.50	1.42
1	A	109	SER	CB-OG	5.96	1.50	1.42

All (275) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	91	ARG	NE-CZ-NH1	25.01	132.80	120.30
1	C	72	ARG	NE-CZ-NH2	-18.27	111.17	120.30
1	A	155	ARG	NE-CZ-NH1	-16.91	111.84	120.30
1	C	58	ASP	CB-CG-OD2	-15.56	104.29	118.30
1	C	160	ARG	NE-CZ-NH1	15.50	128.05	120.30
1	C	127	ARG	NE-CZ-NH1	-13.62	113.49	120.30
1	C	72	ARG	NE-CZ-NH1	12.88	126.74	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	143	ARG	NE-CZ-NH1	12.18	126.39	120.30
1	C	106	ASP	CB-CG-OD1	11.76	128.88	118.30
1	A	31	ARG	NE-CZ-NH2	-11.59	114.51	120.30
1	C	254	ASP	CB-CG-OD1	11.47	128.62	118.30
1	C	217	ASP	CB-CG-OD2	-11.23	108.19	118.30
1	A	132	ASP	CB-CG-OD1	10.82	128.04	118.30
1	C	217	ASP	CB-CG-OD1	10.67	127.91	118.30
1	C	14	ARG	NE-CZ-NH2	-10.33	115.13	120.30
1	C	136	ASP	CB-CG-OD1	-10.32	109.01	118.30
2	B	91	ARG	NE-CZ-NH2	-10.22	115.19	120.30
1	A	33	ASP	CB-CG-OD2	10.21	127.49	118.30
1	A	159	GLN	CA-CB-CG	9.99	135.37	113.40
1	A	18	ASP	CB-CG-OD2	-9.81	109.47	118.30
1	A	279	ASP	CB-CG-OD2	-9.67	109.60	118.30
1	C	166	ARG	CD-NE-CZ	-9.40	110.44	123.60
2	B	67	TYR	CB-CG-CD2	9.09	126.45	121.00
1	A	33	ASP	CB-CG-OD1	-8.94	110.26	118.30
1	C	144	LEU	CB-CA-C	8.88	127.07	110.20
2	B	91	ARG	CD-NE-CZ	8.80	135.93	123.60
1	C	160	ARG	NE-CZ-NH2	-8.52	116.04	120.30
1	A	74	LYS	N-CA-CB	8.52	125.94	110.60
1	A	18	ASP	CB-CG-OD1	8.49	125.94	118.30
1	A	14	ARG	NE-CZ-NH2	8.35	124.47	120.30
1	A	155	ARG	NH1-CZ-NH2	8.32	128.55	119.40
1	C	31	ARG	NE-CZ-NH2	-8.22	116.19	120.30
1	A	184	ASN	N-CA-CB	8.14	125.26	110.60
1	C	30	LEU	CA-CB-CG	8.05	133.81	115.30
1	A	160	ARG	CD-NE-CZ	7.99	134.78	123.60
1	A	251	TYR	CB-CG-CD2	-7.95	116.23	121.00
1	C	221	GLU	CA-CB-CG	7.92	130.82	113.40
1	A	75	LYS	CA-CB-CG	7.88	130.74	113.40
1	A	218	ALA	C-N-CA	7.84	141.30	121.70
1	C	71	TYR	CB-CG-CD2	7.77	125.66	121.00
1	C	31	ARG	CD-NE-CZ	-7.75	112.75	123.60
1	C	32	GLU	OE1-CD-OE2	-7.73	114.03	123.30
1	C	287	LYS	CA-CB-CG	7.71	130.36	113.40
1	C	35	GLU	CA-CB-CG	7.68	130.30	113.40
2	B	93	ASP	CA-CB-CG	7.68	130.30	113.40
1	A	163	MET	CA-CB-CG	7.65	126.31	113.30
1	C	209	GLU	C-N-CA	7.62	140.74	121.70
1	C	32	GLU	CA-CB-CG	7.50	129.90	113.40
2	B	92	GLU	CA-CB-CG	7.48	129.86	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	98	GLU	OE1-CD-OE2	-7.47	114.33	123.30
1	C	48	ARG	NE-CZ-NH1	7.43	124.01	120.30
1	A	39	TYR	CA-CB-CG	-7.42	99.29	113.40
1	A	36	TYR	CB-CG-CD1	7.41	125.45	121.00
1	A	160	ARG	NE-CZ-NH1	7.37	123.99	120.30
1	C	291	GLU	OE1-CD-OE2	7.36	132.13	123.30
1	A	32	GLU	CA-CB-CG	7.33	129.53	113.40
1	A	187	TYR	CB-CG-CD1	-7.29	116.63	121.00
1	A	241	ASP	CB-CG-OD2	7.28	124.86	118.30
1	C	127	ARG	NE-CZ-NH2	7.21	123.90	120.30
1	A	224	ASP	CB-CG-OD1	7.17	124.75	118.30
2	B	38	ARG	NE-CZ-NH1	7.16	123.88	120.30
1	A	138	THR	CA-CB-CG2	7.11	122.36	112.40
1	C	7	VAL	CB-CA-C	7.06	124.81	111.40
2	B	67	TYR	CB-CG-CD1	-7.04	116.78	121.00
1	C	32	GLU	CG-CD-OE1	7.01	132.32	118.30
1	C	132	ASP	CB-CG-OD2	-7.00	112.00	118.30
1	A	36	TYR	CB-CG-CD2	-7.00	116.80	121.00
2	B	59	TRP	CB-CA-C	6.99	124.38	110.40
1	C	71	TYR	CG-CD1-CE1	6.98	126.89	121.30
1	A	48	ARG	NE-CZ-NH2	-6.95	116.83	120.30
1	C	260	LYS	N-CA-CB	6.89	122.99	110.60
1	C	235	ASP	CB-CG-OD2	-6.88	112.10	118.30
2	B	62	GLU	CB-CA-C	6.87	124.14	110.40
2	B	62	GLU	CB-CG-CD	6.85	132.70	114.20
1	A	279	ASP	CB-CG-OD1	6.84	124.45	118.30
2	B	82	PHE	CB-CA-C	6.82	124.03	110.40
1	C	75	LYS	CA-CB-CG	6.81	128.39	113.40
1	C	28	LEU	CA-CB-CG	6.78	130.90	115.30
1	A	120	GLN	CA-CB-CG	6.77	128.30	113.40
1	C	42	TYR	CB-CG-CD1	-6.77	116.94	121.00
2	B	91	ARG	NH1-CZ-NH2	-6.72	112.00	119.40
1	C	188	GLU	OE1-CD-OE2	-6.70	115.26	123.30
2	B	24	GLY	N-CA-C	-6.69	96.37	113.10
1	C	287	LYS	O-C-N	6.67	133.37	122.70
1	C	148	ASP	CB-CG-OD1	6.67	124.30	118.30
2	B	54	ASN	CB-CA-C	6.66	123.71	110.40
1	A	113	VAL	CA-CB-CG1	-6.64	100.93	110.90
1	C	61	ASP	N-CA-CB	-6.64	98.65	110.60
1	C	260	LYS	O-C-N	6.61	133.27	122.70
1	C	166	ARG	NE-CZ-NH2	-6.59	117.00	120.30
2	B	51	ALA	CB-CA-C	6.57	119.96	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	160	ARG	CD-NE-CZ	6.57	132.80	123.60
1	A	143	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	61	ASP	CB-CA-C	6.48	123.37	110.40
1	C	58	ASP	CB-CG-OD1	6.47	124.12	118.30
2	B	68	LEU	CB-CA-C	6.43	122.42	110.20
1	C	261	ASP	CB-CG-OD1	-6.43	112.52	118.30
1	A	191	TRP	C-N-CA	-6.39	108.89	122.30
1	C	5	VAL	CB-CA-C	-6.38	99.28	111.40
1	A	161	LEU	CA-CB-CG	6.38	129.96	115.30
1	A	22	VAL	CB-CA-C	6.32	123.41	111.40
1	A	31	ARG	CA-CB-CG	6.32	127.30	113.40
1	C	196	ASN	N-CA-CB	6.31	121.95	110.60
1	C	130	ARG	NE-CZ-NH1	6.29	123.45	120.30
1	C	101	TRP	CA-CB-CG	6.27	125.61	113.70
1	A	210	ASP	CB-CG-OD1	-6.25	112.67	118.30
1	A	219	ASN	CB-CA-C	6.24	122.88	110.40
1	C	211	TRP	O-C-N	6.23	132.66	122.70
1	C	74	LYS	O-C-N	6.22	132.66	122.70
1	A	286	PHE	O-C-N	6.22	132.66	122.70
1	A	240	GLN	CA-CB-CG	6.21	127.05	113.40
1	C	31	ARG	NH1-CZ-NH2	6.16	126.18	119.40
1	C	208	ASN	CB-CA-C	6.15	122.70	110.40
1	A	152	GLY	O-C-N	6.14	132.52	122.70
1	A	73	PHE	CA-CB-CG	6.13	128.62	113.90
2	B	38	ARG	CD-NE-CZ	6.13	132.18	123.60
1	A	223	TRP	CA-C-O	-6.12	107.26	120.10
1	A	229	TYR	O-C-N	6.11	132.47	122.70
1	C	174	ALA	O-C-N	6.10	132.46	122.70
1	A	142	GLY	N-CA-C	6.09	128.34	113.10
1	A	48	ARG	O-C-N	-6.08	112.96	122.70
1	A	286	PHE	CA-C-N	-6.04	103.92	117.20
2	B	62	GLU	CG-CD-OE1	6.03	130.36	118.30
1	C	190	PRO	O-C-N	-6.02	113.06	122.70
1	A	106	ASP	CB-CA-C	6.02	122.44	110.40
1	A	223	TRP	CA-CB-CG	-5.98	102.34	113.70
2	B	104	GLU	CA-CB-CG	5.98	126.55	113.40
2	B	53	LYS	CB-CA-C	-5.93	98.54	110.40
1	C	253	ASN	N-CA-CB	-5.93	99.93	110.60
1	C	271	GLU	CA-CB-CG	5.92	126.44	113.40
1	A	74	LYS	CA-C-O	-5.92	107.68	120.10
1	A	278	LYS	C-N-CA	5.92	136.49	121.70
1	C	284	PHE	O-C-N	5.90	132.15	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	42	TYR	CB-CG-CD2	5.90	124.54	121.00
1	A	184	ASN	O-C-N	5.87	132.10	122.70
1	A	20	GLN	CB-CG-CD	5.85	126.80	111.60
1	A	224	ASP	OD1-CG-OD2	-5.84	112.20	123.30
1	C	271	GLU	CB-CG-CD	5.84	129.96	114.20
1	A	48	ARG	NE-CZ-NH1	5.83	123.21	120.30
1	A	136	ASP	CB-CG-OD1	5.83	123.54	118.30
1	A	17	GLU	CG-CD-OE1	5.82	129.94	118.30
1	C	91	PHE	O-C-N	5.80	131.99	122.70
1	A	135	GLU	CA-CB-CG	5.80	126.17	113.40
1	A	248	VAL	CA-CB-CG2	5.80	119.60	110.90
1	C	210	ASP	O-C-N	5.80	131.97	122.70
1	A	241	ASP	CA-CB-CG	5.79	126.14	113.40
1	A	211	TRP	CA-CB-CG	-5.77	102.73	113.70
2	B	53	LYS	CA-C-N	-5.75	104.54	117.20
1	C	150	ASP	CB-CG-OD1	5.75	123.47	118.30
1	A	17	GLU	CB-CG-CD	5.74	129.70	114.20
1	A	214	GLU	OE1-CD-OE2	-5.73	116.42	123.30
2	B	38	ARG	N-CA-CB	5.73	120.91	110.60
1	A	39	TYR	O-C-N	5.72	131.85	122.70
1	C	119	MET	CA-C-O	5.72	132.11	120.10
1	C	261	ASP	CB-CG-OD2	5.69	123.42	118.30
1	A	159	GLN	CB-CA-C	5.68	121.77	110.40
1	C	279	ASP	CA-CB-CG	-5.67	100.92	113.40
1	C	134	PRO	N-CD-CG	-5.66	94.72	103.20
1	A	46	LEU	CB-CA-C	5.65	120.94	110.20
1	C	91	PHE	N-CA-CB	5.65	120.77	110.60
1	A	286	PHE	CB-CG-CD1	-5.65	116.85	120.80
2	B	93	ASP	CB-CG-OD1	5.61	123.35	118.30
1	A	106	ASP	CA-CB-CG	5.61	125.74	113.40
1	C	18	ASP	CB-CG-OD1	-5.61	113.25	118.30
1	C	201	GLU	OE1-CD-OE2	5.60	130.02	123.30
1	A	285	ILE	N-CA-C	-5.60	95.88	111.00
1	C	106	ASP	N-CA-CB	5.60	120.68	110.60
1	C	38	ASN	O-C-N	5.59	131.64	122.70
1	C	61	ASP	CB-CG-OD1	5.59	123.33	118.30
1	A	279	ASP	CA-C-N	-5.58	104.91	117.20
1	A	69	GLY	C-N-CA	5.57	135.63	121.70
1	C	201	GLU	C-N-CA	5.57	135.63	121.70
1	A	244	TYR	CB-CG-CD1	5.57	124.34	121.00
1	C	67	TYR	CB-CG-CD1	-5.56	117.66	121.00
1	A	51	TRP	CB-CA-C	5.56	121.52	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	166	ARG	CB-CA-C	5.55	121.51	110.40
1	C	254	ASP	CB-CG-OD2	-5.55	113.31	118.30
1	A	209	GLU	CG-CD-OE2	5.54	129.38	118.30
1	A	76	GLU	OE1-CD-OE2	-5.53	116.66	123.30
1	A	3	PRO	CA-C-O	5.53	133.47	120.20
1	A	14	ARG	CA-C-O	5.52	131.69	120.10
1	A	37	ASP	C-N-CA	5.52	135.50	121.70
1	C	224	ASP	O-C-N	5.52	131.53	122.70
1	C	127	ARG	CD-NE-CZ	-5.51	115.89	123.60
1	C	127	ARG	CA-C-O	-5.50	108.55	120.10
1	A	208	ASN	CA-CB-CG	-5.50	101.30	113.40
1	C	113	VAL	CA-CB-CG2	-5.50	102.65	110.90
1	C	5	VAL	CG1-CB-CG2	5.48	119.66	110.90
1	A	40	ILE	O-C-N	5.47	132.50	123.20
1	C	271	GLU	OE1-CD-OE2	-5.46	116.75	123.30
2	B	74	TYR	CB-CG-CD1	5.46	124.27	121.00
1	A	170	ALA	CB-CA-C	5.43	118.25	110.10
1	C	31	ARG	NE-CZ-NH1	-5.42	117.59	120.30
1	C	109	SER	CB-CA-C	5.41	120.38	110.10
1	C	10	VAL	O-C-N	5.41	131.36	122.70
1	A	231	MET	CA-CB-CG	-5.40	104.12	113.30
2	B	53	LYS	CA-CB-CG	5.40	125.28	113.40
1	C	232	LEU	CB-CG-CD2	-5.40	101.82	111.00
1	A	39	TYR	CB-CG-CD2	-5.38	117.77	121.00
2	B	50	ASP	CB-CG-OD1	5.38	123.14	118.30
1	C	205	ASN	CB-CG-OD1	5.38	132.36	121.60
1	C	150	ASP	O-C-N	5.38	131.31	122.70
1	A	210	ASP	CA-CB-CG	-5.37	101.59	113.40
1	C	213	LEU	CB-CA-C	5.36	120.39	110.20
1	C	235	ASP	CB-CG-OD1	5.35	123.12	118.30
1	C	20	GLN	CB-CA-C	-5.35	99.70	110.40
1	C	273	GLY	N-CA-C	5.35	126.48	113.10
1	A	76	GLU	CA-CB-CG	5.35	125.17	113.40
1	C	215	LYS	CD-CE-NZ	-5.35	99.39	111.70
1	A	72	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	A	241	ASP	OD1-CG-OD2	-5.34	113.15	123.30
1	C	46	LEU	CB-CA-C	5.34	120.35	110.20
1	C	294	LEU	CB-CG-CD2	-5.34	101.93	111.00
1	A	58	ASP	CB-CG-OD2	5.33	123.09	118.30
2	B	90	GLU	OE1-CD-OE2	5.32	129.69	123.30
1	C	195	ASN	CA-CB-CG	-5.32	101.70	113.40
1	A	72	ARG	NE-CZ-NH2	-5.32	117.64	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	113	VAL	CG1-CB-CG2	5.31	119.40	110.90
1	C	25	ALA	N-CA-CB	-5.31	102.66	110.10
1	C	185	SER	N-CA-CB	-5.31	102.53	110.50
1	C	169	VAL	CA-C-N	5.31	128.87	117.20
1	C	214	GLU	CA-CB-CG	5.31	125.07	113.40
1	A	251	TYR	CB-CG-CD1	5.30	124.18	121.00
1	C	284	PHE	CB-CA-C	-5.29	99.81	110.40
1	A	92	LEU	CB-CG-CD1	-5.29	102.00	111.00
1	C	287	LYS	CB-CG-CD	5.29	125.36	111.60
1	C	145	PRO	O-C-N	5.29	131.16	122.70
1	C	291	GLU	CG-CD-OE1	-5.29	107.73	118.30
1	A	254	ASP	CB-CG-OD1	-5.28	113.55	118.30
1	A	290	GLU	CG-CD-OE2	-5.27	107.76	118.30
1	C	32	GLU	CB-CG-CD	5.27	128.44	114.20
1	A	223	TRP	O-C-N	5.27	131.13	122.70
1	C	241	ASP	CB-CG-OD1	-5.27	113.56	118.30
1	A	187	TYR	CB-CG-CD2	5.26	124.16	121.00
1	C	120	GLN	CB-CG-CD	5.26	125.28	111.60
1	C	74	LYS	CA-C-N	-5.25	105.66	117.20
1	A	224	ASP	CB-CG-OD2	5.20	122.98	118.30
1	C	143	ARG	NH1-CZ-NH2	-5.20	113.68	119.40
1	A	181	HIS	CA-CB-CG	-5.19	104.78	113.60
1	C	238	LEU	CB-CA-C	5.19	120.05	110.20
1	C	231	MET	O-C-N	-5.18	114.41	122.70
1	C	159	GLN	CB-CA-C	5.18	120.77	110.40
1	C	187	TYR	N-CA-CB	5.18	119.92	110.60
1	A	53	ILE	C-N-CA	5.17	134.63	121.70
1	A	184	ASN	CA-C-O	-5.17	109.24	120.10
1	A	256	ASP	CB-CG-OD2	5.17	122.95	118.30
1	C	184	ASN	O-C-N	5.15	130.94	122.70
2	B	69	GLU	CG-CD-OE1	5.14	128.58	118.30
1	C	234	THR	CA-CB-OG1	5.14	119.79	109.00
2	B	61	GLU	N-CA-CB	5.13	119.83	110.60
1	A	163	MET	CB-CG-SD	5.12	127.76	112.40
1	C	136	ASP	OD1-CG-OD2	5.12	133.03	123.30
1	C	199	THR	N-CA-CB	5.11	120.00	110.30
1	C	190	PRO	CA-C-O	5.11	132.45	120.20
1	A	12	LYS	N-CA-CB	5.08	119.75	110.60
2	B	62	GLU	OE1-CD-OE2	-5.08	117.20	123.30
1	C	236	TYR	CB-CA-C	5.08	120.56	110.40
2	B	95	ILE	CB-CA-C	5.08	121.75	111.60
1	A	193	ALA	O-C-N	-5.07	114.59	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	17	CYS	CA-CB-SG	-5.07	104.88	114.00
2	B	62	GLU	CA-CB-CG	5.05	124.52	113.40
1	C	283	PRO	O-C-N	5.05	130.78	122.70
2	B	57	ILE	CB-CA-C	5.04	121.69	111.60
1	A	98	GLU	CG-CD-OE1	5.04	128.37	118.30
1	C	209	GLU	OE1-CD-OE2	5.04	129.34	123.30
1	A	140	ASP	CB-CG-OD2	-5.03	113.77	118.30
1	C	132	ASP	CB-CG-OD1	5.03	122.83	118.30
1	A	52	HIS	CA-C-N	5.03	128.26	117.20
1	A	99	PHE	O-C-N	5.02	130.64	121.10
1	A	267	GLU	CB-CG-CD	5.02	127.76	114.20
1	C	100	PRO	CA-C-N	-5.02	106.16	117.20
1	A	27	ALA	O-C-N	5.02	130.73	122.70
1	C	250	GLU	CA-CB-CG	5.01	124.43	113.40
1	C	155	ARG	NE-CZ-NH1	5.01	122.80	120.30
1	A	61	ASP	N-CA-CB	-5.00	101.59	110.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	127	ARG	Sidechain
1	A	166	ARG	Sidechain

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	2371	0	2251	176	0
1	C	2371	0	2252	199	1
2	B	823	0	849	195	0
3	A	43	0	30	5	0
3	B	43	0	30	19	0
3	C	43	0	30	1	0
4	A	146	0	0	27	2
4	B	41	0	0	15	1
4	C	150	0	0	26	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6031	0	5442	572	3

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 51.

All (572) 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:14:CYS:SG	3:B:105:HEM:HAB	1.79	1.22
2:B:14:CYS:SG	3:B:105:HEM:CAB	2.33	1.17
1:C:147:ALA:O	1:C:233:PRO:HD2	1.51	1.06
2:B:50:ASP:HA	2:B:53:LYS:HE2	1.42	1.02
1:C:164:ASN:ND2	1:C:167:GLU:HG3	1.74	1.02
1:C:84:GLY:H	1:C:86:GLN:NE2	1.57	1.01
2:B:41:GLY:HA2	2:B:48:TYR:CE1	1.96	1.00
1:A:195:ASN:H	1:A:195:ASN:HD22	1.09	1.00
2:B:79:LYS:HG3	3:B:105:HEM:O2D	1.63	0.98
1:C:74:LYS:NZ	1:C:74:LYS:HB2	1.77	0.97
1:A:292:GLN:HB2	1:A:294:LEU:CD1	1.96	0.96
1:C:84:GLY:H	1:C:86:GLN:HE22	1.04	0.94
1:C:26:ILE:HG22	1:C:114:THR:HG21	1.48	0.92
1:C:28:LEU:HD13	1:C:289:LEU:HD13	1.50	0.91
2:B:19:THR:HG23	2:B:27:LYS:HD3	1.53	0.91
1:C:4:LEU:HG	4:C:657:HOH:O	1.70	0.91
1:A:185:SER:HB3	3:A:295:HEM:HBA1	1.52	0.91
2:B:34:GLY:O	2:B:38:ARG:HD3	1.70	0.90
1:C:74:LYS:HZ1	1:C:74:LYS:HB2	1.33	0.90
1:C:272:ASN:HA	4:C:692:HOH:O	1.72	0.90
1:C:63:THR:HA	4:C:623:HOH:O	1.72	0.90
2:B:65:MET:HE1	2:B:92:GLU:HG2	1.55	0.89
2:B:65:MET:HE1	2:B:92:GLU:CG	2.03	0.89
2:B:9:ILE:CD1	2:B:90:GLU:HG3	2.04	0.88
1:C:244:TYR:O	1:C:248:VAL:HG23	1.72	0.88
2:B:53:LYS:HB2	2:B:54:ASN:ND2	1.89	0.87
1:C:69:GLY:O	1:C:72:ARG:HG2	1.75	0.87
1:C:28:LEU:HD13	1:C:289:LEU:CD1	2.04	0.86
2:B:54:ASN:HD22	2:B:54:ASN:N	1.69	0.86
1:C:69:GLY:HA2	4:C:630:HOH:O	1.75	0.86
1:A:176:ALA:O	4:A:303:HOH:O	1.92	0.86
1:A:35:GLU:HB2	4:A:356:HOH:O	1.72	0.86
2:B:3:VAL:HG12	2:B:97:TYR:HA	1.56	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:VAL:HG13	1:A:128:CYS:SG	2.16	0.85
2:B:57:ILE:HD13	2:B:63:THR:HG21	1.58	0.85
2:B:41:GLY:HA2	2:B:48:TYR:CD1	2.12	0.84
1:A:33:ASP:OD1	1:A:33:ASP:N	2.07	0.83
1:A:216:ASN:HD22	1:A:222:GLN:NE2	1.75	0.83
1:C:20:GLN:HE22	1:C:287:LYS:H	1.22	0.83
2:B:25:LYS:HE3	2:B:27:LYS:HE2	1.61	0.83
1:C:31:ARG:HD2	4:C:608:HOH:O	1.80	0.82
1:C:215:LYS:HE3	1:C:221:GLU:OE1	1.80	0.81
1:A:292:GLN:HB2	1:A:294:LEU:HD13	1.61	0.81
1:A:1:THR:HG23	1:A:2:THR:H	1.44	0.81
1:C:20:GLN:NE2	1:C:287:LYS:H	1.79	0.81
1:C:75:LYS:HB2	4:C:619:HOH:O	1.81	0.80
1:C:161:LEU:O	1:C:162:ASN:HB3	1.82	0.80
2:B:70:ASN:OD1	2:B:72:LYS:HG3	1.81	0.80
2:B:26:HIS:CD2	2:B:31:ASN:H	2.01	0.79
2:B:41:GLY:HA2	2:B:48:TYR:CZ	2.17	0.79
2:B:9:ILE:HD11	2:B:90:GLU:HG3	1.65	0.79
2:B:39:LYS:O	2:B:42:GLN:HB2	1.83	0.78
1:C:26:ILE:CG2	1:C:114:THR:HG21	2.13	0.78
2:B:90:GLU:HB2	4:B:475:HOH:O	1.82	0.78
2:B:82:PHE:O	4:B:325:HOH:O	2.02	0.77
1:C:169:VAL:HG22	1:C:238:LEU:HD22	1.65	0.76
1:A:271:GLU:HG2	1:A:276:PHE:HE2	1.49	0.76
1:A:256:ASP:HB2	4:A:446:HOH:O	1.84	0.75
1:A:216:ASN:HD22	1:A:222:GLN:HE21	1.33	0.75
1:A:147:ALA:O	1:A:233:PRO:HD2	1.86	0.75
2:B:66:GLU:OE1	2:B:74:TYR:HE2	1.70	0.74
1:A:22:VAL:HG11	1:A:102:ILE:HD13	1.69	0.74
2:B:59:TRP:CE3	2:B:59:TRP:HA	2.22	0.74
1:C:216:ASN:HD22	1:C:222:GLN:NE2	1.85	0.74
2:B:2:ASP:HB2	2:B:5:LYS:H	1.52	0.73
1:A:32:GLU:HG3	4:A:359:HOH:O	1.88	0.72
1:A:68:GLY:HA3	1:A:133:THR:OG1	1.88	0.72
2:B:50:ASP:CA	2:B:53:LYS:HE2	2.19	0.72
1:C:223:TRP:O	1:C:230:MET:HA	1.89	0.72
2:B:3:VAL:HG12	2:B:97:TYR:CA	2.18	0.72
2:B:65:MET:CE	2:B:92:GLU:HG2	2.19	0.72
1:A:130:ARG:HG3	1:A:130:ARG:HH11	1.52	0.72
1:A:22:VAL:HG11	1:A:102:ILE:CD1	2.20	0.72
2:B:59:TRP:CZ3	2:B:64:LEU:HD23	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:ILE:HG22	1:C:71:TYR:HB2	1.71	0.71
2:B:49:THR:O	2:B:53:LYS:NZ	2.23	0.71
2:B:54:ASN:ND2	2:B:54:ASN:N	2.37	0.71
1:A:1:THR:HG23	1:A:2:THR:N	2.04	0.71
2:B:64:LEU:HB2	2:B:95:ILE:CD1	2.20	0.70
2:B:39:LYS:HA	2:B:57:ILE:O	1.91	0.70
1:A:99:PHE:O	1:A:102:ILE:HG22	1.91	0.70
1:C:225:SER:O	4:C:441:HOH:O	2.10	0.70
1:C:96:HIS:CD2	1:C:107:LEU:HD22	2.26	0.70
1:A:53:ILE:HD13	1:A:108:PHE:HB2	1.73	0.70
2:B:57:ILE:CD1	2:B:63:THR:HG21	2.22	0.70
1:A:195:ASN:ND2	1:A:195:ASN:H	1.86	0.69
1:A:240:GLN:HG2	4:A:396:HOH:O	1.91	0.69
2:B:82:PHE:CE2	2:B:84:GLY:HA2	2.28	0.69
1:C:200:ASN:ND2	1:C:255:GLN:OE1	2.26	0.69
2:B:17:CYS:SG	3:B:105:HEM:CAC	2.81	0.69
1:C:66:SER:HB2	1:C:130:ARG:HD3	1.73	0.69
1:C:67:TYR:HD2	1:C:274:ILE:HG23	1.57	0.69
1:C:7:VAL:HA	1:C:275:THR:O	1.93	0.69
1:A:47:VAL:HG22	1:A:116:VAL:HG23	1.75	0.69
1:C:146:ASP:O	1:C:234:THR:HG21	1.93	0.69
1:A:14:ARG:HG2	1:A:101:TRP:CZ3	2.27	0.69
1:A:125:PRO:HB2	1:A:267:GLU:OE1	1.92	0.68
2:B:26:HIS:CD2	2:B:31:ASN:N	2.62	0.68
1:C:93:GLU:N	1:C:94:PRO:HD2	2.08	0.68
2:B:32:LEU:O	2:B:102:THR:CG2	2.42	0.68
2:B:66:GLU:HG2	2:B:74:TYR:CD2	2.28	0.68
1:A:195:ASN:HD22	1:A:195:ASN:N	1.89	0.68
1:C:84:GLY:N	1:C:86:GLN:HE22	1.87	0.68
2:B:64:LEU:HB2	2:B:95:ILE:HD13	1.76	0.68
2:B:82:PHE:HA	4:B:357:HOH:O	1.94	0.68
1:C:71:TYR:HA	1:C:76:GLU:CG	2.24	0.68
1:C:8:ALA:HB1	1:C:129:GLY:HA3	1.76	0.67
1:A:216:ASN:ND2	1:A:222:GLN:HE21	1.91	0.67
1:A:271:GLU:HB3	4:A:447:HOH:O	1.93	0.67
1:C:84:GLY:N	1:C:86:GLN:NE2	2.39	0.67
1:A:128:CYS:SG	4:A:492:HOH:O	2.52	0.67
1:A:47:VAL:HG22	1:A:116:VAL:CG2	2.24	0.67
3:B:105:HEM:HHD	3:B:105:HEM:HBC2	1.77	0.67
2:B:16:GLN:OE1	2:B:16:GLN:N	2.28	0.67
2:B:36:PHE:HA	2:B:59:TRP:O	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:GLU:O	1:A:14:ARG:HB2	1.96	0.66
2:B:53:LYS:HB2	2:B:54:ASN:HD22	1.61	0.66
1:C:143:ARG:CG	4:C:672:HOH:O	2.42	0.66
1:A:62:ASN:HB2	4:A:382:HOH:O	1.96	0.66
1:C:58:ASP:HB2	1:C:143:ARG:NH1	2.10	0.66
2:B:26:HIS:HD2	2:B:31:ASN:N	1.93	0.66
1:C:29:LYS:HG2	1:C:91:PHE:CZ	2.31	0.66
2:B:39:LYS:C	2:B:42:GLN:NE2	2.50	0.65
2:B:9:ILE:HD13	2:B:90:GLU:CG	2.26	0.65
1:C:119:MET:O	1:C:120:GLN:HB2	1.95	0.65
1:A:155:ARG:NH2	1:A:243:LYS:HE3	2.11	0.65
2:B:9:ILE:CD1	2:B:90:GLU:CG	2.74	0.65
1:C:292:GLN:HB3	1:C:294:LEU:HD12	1.79	0.65
2:B:3:VAL:HA	2:B:97:TYR:HB2	1.79	0.64
1:A:59:LYS:HD2	1:A:162:ASN:HD21	1.62	0.64
1:A:53:ILE:HD13	1:A:108:PHE:CB	2.28	0.64
2:B:39:LYS:HB3	2:B:42:GLN:NE2	2.12	0.64
1:A:106:ASP:OD1	1:A:130:ARG:NH1	2.31	0.64
1:C:75:LYS:HE3	1:C:140:ASP:HA	1.80	0.64
1:A:278:LYS:HG2	1:A:279:ASP:N	2.11	0.64
1:A:31:ARG:CZ	1:A:289:LEU:HD23	2.28	0.64
1:C:279:ASP:N	1:C:279:ASP:OD1	2.29	0.64
2:B:31:ASN:OD1	2:B:32:LEU:N	2.31	0.64
2:B:9:ILE:HG22	2:B:94:LEU:HD22	1.79	0.63
2:B:14:CYS:HB3	3:B:105:HEM:C3B	2.33	0.63
1:C:76:GLU:HB3	1:C:138:THR:CG2	2.29	0.63
2:B:3:VAL:HG12	2:B:97:TYR:N	2.13	0.63
1:C:104:SER:HB3	1:C:108:PHE:CE2	2.33	0.63
1:C:26:ILE:HA	1:C:95:ILE:HD11	1.81	0.62
2:B:66:GLU:OE1	2:B:74:TYR:CE2	2.52	0.62
1:A:281:PRO:HD3	4:A:338:HOH:O	1.98	0.62
1:C:134:PRO:HD2	1:C:137:THR:CG2	2.29	0.62
1:C:67:TYR:CD2	1:C:274:ILE:HG23	2.35	0.62
1:A:200:ASN:HA	4:A:423:HOH:O	1.98	0.62
2:B:38:ARG:O	2:B:59:TRP:N	2.33	0.62
1:A:163:MET:HE2	1:A:167:GLU:HB3	1.80	0.62
1:A:155:ARG:HA	1:A:244:TYR:OH	1.99	0.62
2:B:66:GLU:HG2	2:B:74:TYR:HD2	1.64	0.62
2:B:17:CYS:SG	3:B:105:HEM:CBC	2.88	0.61
2:B:30:PRO:HG3	2:B:46:PHE:CD2	2.34	0.61
1:C:282:SER:HB3	1:C:283:PRO:HD2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:23:TYR:HD1	1:C:24:ASN:HD22	1.48	0.61
1:A:72:ARG:NH2	1:A:73:PHE:CZ	2.68	0.61
2:B:59:TRP:HA	2:B:59:TRP:HE3	1.65	0.61
1:A:172:MET:SD	3:A:295:HEM:CBB	2.89	0.61
1:A:294:LEU:O	4:A:361:HOH:O	2.16	0.61
2:B:14:CYS:CB	3:B:105:HEM:CAB	2.79	0.61
1:C:10:VAL:HG12	1:C:11:GLU:O	1.99	0.61
1:C:26:ILE:HA	1:C:95:ILE:CD1	2.30	0.61
1:A:281:PRO:CD	4:A:338:HOH:O	2.49	0.61
1:C:135:GLU:O	1:C:135:GLU:HG3	1.99	0.60
1:C:248:VAL:O	1:C:252:ALA:HB2	2.02	0.60
2:B:80:MET:HB2	3:B:105:HEM:C1D	2.37	0.60
1:A:96:HIS:HE1	1:A:102:ILE:O	1.83	0.60
1:C:7:VAL:HG22	4:C:728:HOH:O	2.01	0.60
1:A:271:GLU:HG2	1:A:276:PHE:CE2	2.33	0.60
1:C:195:ASN:OD1	1:C:195:ASN:N	2.29	0.60
1:C:213:LEU:HD13	1:C:223:TRP:CE2	2.37	0.60
1:A:225:SER:OG	1:A:227:SER:HB2	2.03	0.59
1:C:261:ASP:OD1	1:C:261:ASP:N	2.35	0.59
1:A:4:LEU:HD12	1:A:6:HIS:CE1	2.38	0.59
2:B:40:THR:HG21	2:B:55:LYS:HB3	1.85	0.59
1:A:255:GLN:NE2	1:A:259:PHE:CZ	2.68	0.59
2:B:64:LEU:O	2:B:66:GLU:N	2.36	0.59
2:B:70:ASN:HB3	2:B:73:LYS:HB3	1.84	0.59
1:C:143:ARG:O	1:C:157:PHE:CE1	2.55	0.59
2:B:49:THR:C	2:B:53:LYS:NZ	2.56	0.59
1:A:166:ARG:HH21	1:A:257:LYS:HE3	1.67	0.58
1:C:134:PRO:HD2	1:C:137:THR:HG21	1.85	0.58
1:A:169:VAL:HG12	1:A:251:TYR:CE2	2.38	0.58
1:C:99:PHE:N	1:C:100:PRO:HD3	2.17	0.58
1:C:99:PHE:O	1:C:102:ILE:HG22	2.02	0.58
1:A:216:ASN:ND2	1:A:222:GLN:NE2	2.47	0.58
2:B:25:LYS:HE3	2:B:27:LYS:CE	2.33	0.58
2:B:55:LYS:HD3	2:B:55:LYS:O	2.03	0.58
1:A:93:GLU:HB3	1:A:94:PRO:HD3	1.84	0.58
2:B:79:LYS:HZ2	3:B:105:HEM:CGD	2.16	0.58
2:B:2:ASP:N	2:B:2:ASP:OD1	2.36	0.58
1:C:250:GLU:OE2	1:C:257:LYS:HE3	2.04	0.58
1:C:70:THR:HB	1:C:138:THR:HG23	1.86	0.58
1:A:124:ILE:HD13	1:A:263:SER:HA	1.85	0.58
2:B:14:CYS:HB3	3:B:105:HEM:CAB	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:MET:HE3	1:C:231:MET:CA	2.33	0.58
1:C:143:ARG:O	1:C:157:PHE:HE1	1.86	0.57
2:B:14:CYS:SG	3:B:105:HEM:CBB	2.91	0.57
2:B:53:LYS:C	2:B:54:ASN:HD22	2.07	0.57
2:B:82:PHE:HE2	2:B:84:GLY:HA2	1.68	0.57
2:B:3:VAL:CG1	2:B:97:TYR:HA	2.31	0.57
1:C:282:SER:HB3	1:C:283:PRO:CD	2.34	0.57
2:B:7:LYS:CD	4:B:415:HOH:O	2.52	0.57
2:B:9:ILE:HD13	2:B:90:GLU:HG2	1.86	0.57
1:C:22:VAL:O	1:C:23:TYR:C	2.42	0.57
1:C:130:ARG:HG3	1:C:130:ARG:HH11	1.69	0.57
2:B:55:LYS:O	2:B:57:ILE:HG23	2.04	0.57
1:C:130:ARG:NH1	1:C:130:ARG:HG3	2.20	0.57
1:C:26:ILE:HG13	1:C:95:ILE:HD13	1.87	0.57
1:C:28:LEU:HD13	1:C:289:LEU:HD11	1.87	0.57
3:B:105:HEM:HBB2	3:B:105:HEM:HHC	1.86	0.56
2:B:14:CYS:HB3	3:B:105:HEM:C4B	2.40	0.56
2:B:9:ILE:CG2	2:B:94:LEU:HD22	2.34	0.56
2:B:61:GLU:OE2	2:B:99:LYS:HE3	2.05	0.56
1:C:20:GLN:HE22	1:C:287:LYS:N	1.96	0.56
2:B:48:TYR:HA	2:B:79:LYS:HZ1	1.69	0.56
1:A:80:PRO:HD3	1:A:141:ASN:ND2	2.20	0.56
1:A:128:CYS:HB2	4:A:492:HOH:O	2.04	0.56
2:B:16:GLN:H	2:B:16:GLN:CD	2.09	0.56
2:B:14:CYS:HB3	3:B:105:HEM:CHC	2.36	0.56
1:C:216:ASN:HD22	1:C:222:GLN:HE21	1.54	0.56
1:C:24:ASN:O	1:C:28:LEU:HD22	2.05	0.56
2:B:64:LEU:CB	2:B:95:ILE:HD11	2.35	0.56
1:A:163:MET:CE	1:A:167:GLU:HB3	2.36	0.55
2:B:20:VAL:O	2:B:33:HIS:HB2	2.06	0.55
1:C:236:TYR:CE2	1:C:239:ILE:HD11	2.40	0.55
2:B:74:TYR:O	2:B:75:ILE:HG12	2.07	0.55
1:C:93:GLU:N	1:C:94:PRO:CD	2.70	0.55
2:B:42:GLN:HB3	4:B:468:HOH:O	2.06	0.55
1:C:204:LEU:O	1:C:208:ASN:HB2	2.07	0.55
1:A:16:TYR:CG	1:A:16:TYR:O	2.60	0.55
1:A:169:VAL:HG12	1:A:251:TYR:HE2	1.68	0.55
1:A:292:GLN:C	1:A:294:LEU:HD12	2.27	0.55
2:B:8:LYS:HG3	4:B:415:HOH:O	2.07	0.55
1:A:134:PRO:O	1:A:136:ASP:N	2.40	0.55
1:A:212:LYS:HE2	4:A:445:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:164:ASN:HD21	1:C:167:GLU:HG3	1.68	0.55
2:B:94:LEU:O	2:B:98:LEU:HG	2.07	0.54
1:A:158:PHE:HB3	1:A:163:MET:HB2	1.88	0.54
2:B:59:TRP:CE3	2:B:64:LEU:HD23	2.42	0.54
1:C:48:ARG:O	1:C:49:LEU:C	2.46	0.54
1:A:128:CYS:CB	4:A:492:HOH:O	2.56	0.54
1:C:72:ARG:NH2	1:C:133:THR:O	2.41	0.54
2:B:82:PHE:CE2	2:B:84:GLY:CA	2.91	0.54
1:A:277:PRO:HG2	4:A:487:HOH:O	2.07	0.54
1:C:271:GLU:O	1:C:274:ILE:HG13	2.08	0.54
1:C:292:GLN:CB	1:C:294:LEU:HD12	2.38	0.54
1:A:1:THR:CG2	1:A:2:THR:N	2.70	0.54
1:C:92:LEU:C	1:C:94:PRO:HD2	2.28	0.54
1:A:172:MET:SD	3:A:295:HEM:HBB2	2.47	0.54
1:C:82:ASN:O	1:C:85:LEU:HB2	2.07	0.54
1:A:15:SER:O	1:A:19:PHE:HD2	1.91	0.54
1:A:201:GLU:O	1:A:202:PHE:C	2.46	0.54
2:B:32:LEU:O	2:B:102:THR:HG22	2.08	0.54
2:B:81:ILE:HG12	4:B:456:HOH:O	2.08	0.54
1:C:166:ARG:HB2	1:C:247:ILE:HD13	1.90	0.54
1:A:147:ALA:HB1	1:A:232:LEU:HD13	1.90	0.54
1:A:59:LYS:HD2	1:A:162:ASN:ND2	2.23	0.54
2:B:65:MET:N	2:B:95:ILE:CD1	2.71	0.54
1:A:241:ASP:O	1:A:245:LEU:HB2	2.08	0.53
1:C:48:ARG:HD3	1:C:85:LEU:HD21	1.88	0.53
3:B:105:HEM:HHC	3:B:105:HEM:CBB	2.38	0.53
2:B:59:TRP:CE3	2:B:64:LEU:CD2	2.91	0.53
1:C:26:ILE:HG22	1:C:114:THR:CG2	2.31	0.53
1:C:230:MET:HE2	1:C:230:MET:O	2.08	0.53
2:B:62:GLU:HB2	4:B:352:HOH:O	2.09	0.53
1:C:203:TYR:HD1	1:C:248:VAL:HG13	1.74	0.53
2:B:30:PRO:HG3	2:B:46:PHE:CG	2.44	0.53
1:A:34:ASP:HA	4:A:411:HOH:O	2.08	0.52
2:B:21:GLU:CD	2:B:21:GLU:H	2.12	0.52
1:C:105:GLY:O	1:C:130:ARG:HD2	2.09	0.52
2:B:65:MET:N	2:B:95:ILE:HD11	2.24	0.52
1:C:133:THR:HB	1:C:134:PRO:CD	2.38	0.52
1:A:73:PHE:CE2	1:A:135:GLU:HA	2.45	0.52
1:A:182:LEU:N	1:A:187:TYR:O	2.43	0.52
1:C:33:ASP:N	1:C:33:ASP:OD1	2.43	0.52
1:A:130:ARG:HG3	1:A:130:ARG:NH1	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:80:MET:HB2	3:B:105:HEM:C4D	2.44	0.52
1:C:257:LYS:O	1:C:261:ASP:OD1	2.27	0.52
1:A:16:TYR:HD1	1:A:284:PHE:CD1	2.28	0.52
1:C:73:PHE:O	1:C:77:PHE:N	2.41	0.52
1:A:202:PHE:HZ	1:A:235:ASP:HB3	1.74	0.52
1:C:166:ARG:CA	1:C:247:ILE:HD13	2.40	0.52
1:A:280:ALA:HA	4:A:338:HOH:O	2.10	0.52
2:B:41:GLY:HA2	2:B:48:TYR:CG	2.45	0.52
2:B:25:LYS:CE	2:B:27:LYS:HE2	2.34	0.51
2:B:70:ASN:OD1	2:B:72:LYS:CG	2.54	0.51
1:C:73:PHE:O	1:C:77:PHE:HB2	2.11	0.51
2:B:69:GLU:HA	2:B:85:ILE:O	2.11	0.51
1:A:3:PRO:HB3	1:A:61:ASP:O	2.09	0.51
1:C:71:TYR:CE2	1:C:77:PHE:CE1	2.98	0.51
2:B:56:GLY:O	2:B:57:ILE:HG22	2.10	0.51
1:C:133:THR:HB	1:C:137:THR:HG21	1.92	0.51
1:C:182:LEU:HD11	1:C:218:ALA:HB2	1.93	0.51
2:B:41:GLY:HA2	2:B:48:TYR:CE2	2.46	0.51
1:C:58:ASP:HB2	1:C:143:ARG:HH12	1.74	0.51
1:C:145:PRO:HA	1:C:153:TYR:OH	2.10	0.51
1:C:179:LYS:HE3	1:C:180:THR:O	2.10	0.51
1:C:238:LEU:HD23	1:C:244:TYR:CD2	2.45	0.51
1:A:125:PRO:HG3	1:A:285:ILE:HD11	1.93	0.51
1:C:4:LEU:CG	4:C:657:HOH:O	2.45	0.51
2:B:50:ASP:O	2:B:54:ASN:HB2	2.11	0.51
2:B:7:LYS:HD3	4:B:415:HOH:O	2.09	0.51
1:C:230:MET:HE3	1:C:231:MET:C	2.31	0.51
1:C:39:TYR:HD2	4:C:429:HOH:O	1.93	0.51
1:A:275:THR:O	1:A:277:PRO:HD3	2.12	0.50
2:B:94:LEU:HD12	2:B:94:LEU:O	2.11	0.50
1:C:204:LEU:O	1:C:208:ASN:N	2.38	0.50
1:C:249:LYS:O	1:C:252:ALA:HB3	2.12	0.50
1:A:46:LEU:O	1:A:47:VAL:C	2.50	0.50
2:B:78:THR:OG1	2:B:79:LYS:N	2.45	0.50
2:B:32:LEU:O	2:B:102:THR:HB	2.11	0.50
2:B:12:GLN:NE2	4:B:413:HOH:O	2.33	0.50
2:B:68:LEU:C	2:B:91:ARG:HD2	2.31	0.50
1:C:139:PRO:HB3	1:C:143:ARG:HH21	1.76	0.50
1:A:26:ILE:HB	1:A:114:THR:HG21	1.93	0.49
1:A:26:ILE:CG2	1:A:114:THR:HG21	2.42	0.49
2:B:40:THR:HB	2:B:52:ASN:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:256:ASP:HB3	4:C:680:HOH:O	2.13	0.49
1:C:26:ILE:CG1	1:C:95:ILE:HD13	2.42	0.49
1:A:257:LYS:O	1:A:258:PHE:C	2.50	0.49
1:C:120:GLN:HB2	1:C:197:VAL:HG23	1.95	0.49
2:B:26:HIS:HB3	4:B:354:HOH:O	2.13	0.49
2:B:66:GLU:CD	2:B:74:TYR:CE2	2.86	0.49
2:B:48:TYR:HA	2:B:79:LYS:NZ	2.28	0.49
1:C:105:GLY:HA2	4:C:630:HOH:O	2.13	0.49
1:A:15:SER:O	1:A:19:PHE:CD2	2.65	0.49
1:A:51:TRP:O	1:A:52:HIS:C	2.46	0.49
2:B:87:LYS:HB3	2:B:87:LYS:HE2	1.66	0.49
1:C:144:LEU:CD1	4:C:612:HOH:O	2.60	0.49
1:A:164:ASN:O	1:A:168:VAL:HG13	2.12	0.49
1:A:47:VAL:CG2	1:A:116:VAL:CG2	2.91	0.49
1:A:79:ASP:OD2	4:A:432:HOH:O	2.20	0.49
1:C:119:MET:O	1:C:120:GLN:CB	2.60	0.49
1:C:179:LYS:HB3	1:C:190:PRO:HB3	1.94	0.49
1:A:184:ASN:ND2	3:A:295:HEM:O2A	2.46	0.49
1:A:58:ASP:OD1	1:A:60:HIS:ND1	2.46	0.49
2:B:16:GLN:CD	2:B:16:GLN:N	2.65	0.49
2:B:33:HIS:HA	2:B:102:THR:O	2.13	0.48
1:C:166:ARG:HA	1:C:247:ILE:HD13	1.94	0.48
2:B:64:LEU:CB	2:B:95:ILE:CD1	2.89	0.48
1:C:272:ASN:CA	4:C:692:HOH:O	2.45	0.48
1:A:212:LYS:HD3	4:A:445:HOH:O	2.12	0.48
2:B:57:ILE:CD1	2:B:58:THR:O	2.61	0.48
1:C:93:GLU:HB3	1:C:94:PRO:HD3	1.95	0.48
2:B:3:VAL:O	2:B:7:LYS:HB2	2.13	0.48
1:C:23:TYR:OH	1:C:288:THR:HG22	2.13	0.48
1:A:271:GLU:O	1:A:272:ASN:C	2.52	0.48
2:B:60:LYS:HB3	2:B:63:THR:OG1	2.14	0.48
1:A:166:ARG:NH2	1:A:250:GLU:OE2	2.46	0.48
1:C:143:ARG:HG3	4:C:672:HOH:O	2.13	0.48
1:A:181:HIS:C	1:A:187:TYR:O	2.53	0.48
2:B:14:CYS:C	2:B:16:GLN:N	2.64	0.48
1:C:214:GLU:O	1:C:221:GLU:HA	2.13	0.48
1:C:27:ALA:HB1	1:C:289:LEU:HG	1.96	0.48
2:B:7:LYS:HD2	4:B:415:HOH:O	2.10	0.47
1:C:44:PRO:HD2	4:C:712:HOH:O	2.13	0.47
1:A:73:PHE:CE1	1:A:135:GLU:HB2	2.50	0.47
1:C:42:TYR:CG	1:C:91:PHE:CD2	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:49:THR:O	2:B:52:ASN:N	2.38	0.47
1:C:186:GLY:O	1:C:220:ASN:ND2	2.41	0.47
1:A:155:ARG:NH2	1:A:241:ASP:OD1	2.42	0.47
2:B:98:LEU:O	2:B:99:LYS:C	2.53	0.47
1:A:68:GLY:CA	1:A:133:THR:OG1	2.62	0.47
1:A:202:PHE:CZ	1:A:235:ASP:HB3	2.49	0.47
1:C:213:LEU:HD13	1:C:223:TRP:NE1	2.29	0.47
1:C:48:ARG:NH1	1:C:85:LEU:HG	2.29	0.47
1:A:182:LEU:HB2	1:A:188:GLU:HB2	1.95	0.47
1:A:29:LYS:HE3	4:A:437:HOH:O	2.15	0.47
2:B:69:GLU:HB2	2:B:91:ARG:NH2	2.29	0.47
2:B:80:MET:HB2	3:B:105:HEM:ND	2.29	0.47
2:B:26:HIS:CB	4:B:354:HOH:O	2.62	0.47
1:C:134:PRO:HD2	1:C:137:THR:HG23	1.96	0.47
1:C:42:TYR:O	1:C:45:VAL:HG12	2.15	0.47
2:B:3:VAL:HG11	2:B:100:LYS:CD	2.44	0.47
2:B:70:ASN:HD22	2:B:73:LYS:NZ	2.12	0.47
1:A:290:GLU:O	1:A:290:GLU:HG3	2.14	0.47
1:C:133:THR:HB	1:C:134:PRO:HD3	1.95	0.47
1:A:20:GLN:O	1:A:23:TYR:HB3	2.15	0.47
1:A:34:ASP:N	1:A:34:ASP:OD1	2.48	0.46
1:A:69:GLY:O	1:A:72:ARG:HD3	2.15	0.46
2:B:22:LYS:HA	2:B:31:ASN:HD21	1.80	0.46
2:B:3:VAL:O	2:B:7:LYS:N	2.47	0.46
1:C:144:LEU:HD11	4:C:612:HOH:O	2.13	0.46
1:C:182:LEU:HB2	1:C:188:GLU:HG2	1.97	0.46
1:C:79:ASP:HA	1:C:80:PRO:HD3	1.82	0.46
1:A:155:ARG:HH22	1:A:241:ASP:CG	2.19	0.46
1:A:243:LYS:HB2	1:A:243:LYS:HE3	1.51	0.46
2:B:48:TYR:CA	2:B:79:LYS:HZ1	2.28	0.46
1:C:236:TYR:O	1:C:239:ILE:HG13	2.15	0.46
1:C:6:HIS:HB3	1:C:67:TYR:CE2	2.51	0.46
1:A:166:ARG:NH2	1:A:257:LYS:HE3	2.28	0.46
1:A:1:THR:O	1:A:3:PRO:HD3	2.15	0.46
2:B:36:PHE:HE1	2:B:98:LEU:HB3	1.80	0.46
2:B:62:GLU:O	2:B:63:THR:C	2.52	0.46
1:A:167:GLU:CD	1:A:268:LYS:HZ2	2.19	0.46
2:B:13:LYS:NZ	4:B:383:HOH:O	2.49	0.46
1:C:276:PHE:HA	1:C:277:PRO:HD2	1.64	0.46
2:B:26:HIS:CD2	2:B:30:PRO:HA	2.50	0.46
2:B:54:ASN:C	2:B:56:GLY:N	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:LEU:CB	4:C:657:HOH:O	2.63	0.46
2:B:39:LYS:C	2:B:42:GLN:HE21	2.18	0.46
1:A:59:LYS:CD	1:A:162:ASN:ND2	2.79	0.46
2:B:3:VAL:HG11	2:B:100:LYS:HG3	1.97	0.46
2:B:40:THR:HG23	2:B:57:ILE:H	1.79	0.46
1:A:10:VAL:HA	4:A:492:HOH:O	2.16	0.46
1:A:112:GLY:O	1:A:116:VAL:HG23	2.16	0.46
1:A:34:ASP:OD2	2:B:90:GLU:OE1	2.33	0.46
2:B:31:ASN:OD1	2:B:31:ASN:C	2.54	0.46
2:B:57:ILE:C	2:B:57:ILE:HD12	2.36	0.46
1:C:241:ASP:HA	1:C:242:PRO:HD3	1.74	0.46
1:A:46:LEU:C	1:A:48:ARG:N	2.69	0.46
1:A:4:LEU:O	1:A:62:ASN:ND2	2.48	0.46
1:A:7:VAL:HG23	1:A:8:ALA:O	2.15	0.46
1:C:200:ASN:HD22	1:C:200:ASN:H	1.63	0.46
1:C:215:LYS:HD3	1:C:219:ASN:O	2.15	0.46
1:A:232:LEU:HB2	1:A:235:ASP:OD2	2.15	0.45
2:B:56:GLY:O	2:B:57:ILE:CG2	2.64	0.45
1:C:138:THR:HA	1:C:139:PRO:HD3	1.83	0.45
1:C:19:PHE:CD2	1:C:284:PHE:HE2	2.33	0.45
1:C:71:TYR:HA	1:C:76:GLU:HG2	1.94	0.45
1:A:243:LYS:O	1:A:247:ILE:HG13	2.16	0.45
2:B:27:LYS:N	2:B:27:LYS:HD2	2.32	0.45
1:C:71:TYR:CE2	1:C:77:PHE:HE1	2.35	0.45
1:C:191:TRP:HD1	1:C:231:MET:CE	2.29	0.45
1:A:2:THR:HG23	1:A:2:THR:O	2.17	0.45
1:A:42:TYR:CD2	1:A:91:PHE:CD2	3.04	0.45
2:B:31:ASN:ND2	4:B:349:HOH:O	2.23	0.45
1:A:204:LEU:O	1:A:205:ASN:C	2.55	0.45
2:B:38:ARG:O	2:B:58:THR:HA	2.16	0.45
2:B:65:MET:HE1	2:B:92:GLU:HG3	1.96	0.45
1:C:216:ASN:OD1	1:C:218:ALA:HB3	2.17	0.45
1:C:289:LEU:HD23	1:C:289:LEU:HA	1.69	0.45
1:C:68:GLY:O	1:C:72:ARG:NH1	2.50	0.45
2:B:89:THR:O	2:B:92:GLU:HB2	2.17	0.45
1:A:288:THR:O	1:A:292:GLN:HG3	2.17	0.45
1:A:47:VAL:CG2	1:A:116:VAL:HG22	2.47	0.45
2:B:64:LEU:O	2:B:65:MET:C	2.55	0.45
1:A:11:GLU:OE2	1:A:106:ASP:OD2	2.35	0.45
2:B:75:ILE:HA	2:B:76:PRO:HD2	1.74	0.45
1:C:127:ARG:CD	1:C:271:GLU:OE2	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:GLU:HA	2:B:4:GLU:OE1	2.17	0.45
1:C:24:ASN:O	1:C:28:LEU:CD2	2.65	0.45
1:A:53:ILE:CD1	1:A:108:PHE:HB2	2.44	0.44
1:A:110:LEU:HD23	1:A:110:LEU:O	2.16	0.44
2:B:33:HIS:CD2	2:B:103:ASN:HA	2.52	0.44
2:B:79:LYS:NZ	3:B:105:HEM:CGD	2.80	0.44
2:B:39:LYS:HB3	2:B:42:GLN:HE22	1.80	0.44
1:C:143:ARG:HG2	4:C:672:HOH:O	2.13	0.44
1:C:127:ARG:HG3	1:C:271:GLU:OE2	2.16	0.44
1:A:207:LEU:HD12	1:A:252:ALA:CB	2.46	0.44
1:C:6:HIS:HB3	1:C:67:TYR:CD2	2.53	0.44
1:A:58:ASP:CG	1:A:160:ARG:HD2	2.38	0.44
1:C:280:ALA:HA	4:C:622:HOH:O	2.16	0.44
2:B:54:ASN:O	2:B:55:LYS:C	2.54	0.44
1:C:216:ASN:ND2	1:C:222:GLN:NE2	2.61	0.44
1:A:151:ALA:CA	1:A:237:SER:HB3	2.47	0.44
3:A:295:HEM:HBC2	3:A:295:HEM:HMC1	2.00	0.44
2:B:48:TYR:HB3	2:B:53:LYS:HZ1	1.82	0.44
1:C:232:LEU:O	1:C:233:PRO:C	2.55	0.44
2:B:57:ILE:HD12	2:B:58:THR:O	2.18	0.44
2:B:66:GLU:CG	2:B:74:TYR:CD2	3.00	0.44
1:C:14:ARG:HB3	1:C:18:ASP:HB2	1.99	0.44
1:A:210:ASP:HB3	4:A:439:HOH:O	2.16	0.44
1:A:147:ALA:O	1:A:233:PRO:HB2	2.18	0.44
2:B:85:ILE:C	2:B:86:LYS:HD3	2.38	0.44
1:A:4:LEU:HD12	1:A:6:HIS:HE1	1.83	0.44
2:B:66:GLU:CD	2:B:74:TYR:HE2	2.19	0.44
1:C:130:ARG:NH2	4:C:664:HOH:O	2.51	0.44
1:A:237:SER:O	1:A:238:LEU:C	2.55	0.44
1:C:193:ALA:HB2	1:C:229:TYR:OH	2.18	0.44
1:A:206:LEU:HG	1:A:239:ILE:CG2	2.48	0.43
1:A:53:ILE:O	1:A:65:GLY:O	2.36	0.43
2:B:50:ASP:HA	2:B:53:LYS:CE	2.30	0.43
1:C:24:ASN:N	1:C:24:ASN:HD22	2.15	0.43
1:A:127:ARG:O	1:A:130:ARG:NH1	2.47	0.43
1:A:155:ARG:HH11	1:A:155:ARG:HD2	1.37	0.43
2:B:22:LYS:HB2	2:B:33:HIS:ND1	2.34	0.43
1:C:56:THR:HA	1:C:143:ARG:HB2	2.00	0.43
1:A:15:SER:OG	1:A:16:TYR:N	2.51	0.43
1:A:3:PRO:HG3	1:A:61:ASP:HA	2.00	0.43
1:A:57:TRP:HB3	1:A:161:LEU:HD22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:ALA:HB3	1:C:276:PHE:CD1	2.53	0.43
2:B:56:GLY:C	2:B:57:ILE:CG2	2.87	0.43
1:C:143:ARG:HB3	1:C:160:ARG:NH2	2.34	0.43
1:A:67:TYR:HA	1:A:130:ARG:HB3	2.01	0.43
1:C:243:LYS:HG3	4:C:639:HOH:O	2.18	0.43
1:C:19:PHE:CD2	1:C:284:PHE:CE2	3.07	0.43
1:A:48:ARG:NH1	4:A:364:HOH:O	2.49	0.43
1:C:74:LYS:HB3	1:C:75:LYS:H	1.25	0.43
1:A:130:ARG:CG	1:A:130:ARG:NH1	2.80	0.43
1:A:2:THR:HA	1:A:3:PRO:HD3	1.80	0.43
1:A:280:ALA:HA	1:A:281:PRO:HD3	1.53	0.42
1:A:74:LYS:HE3	1:A:74:LYS:HB2	1.82	0.42
1:C:62:ASN:O	1:C:62:ASN:CG	2.57	0.42
2:B:10:PHE:HA	2:B:14:CYS:SG	2.60	0.42
2:B:63:THR:HG22	2:B:74:TYR:OH	2.20	0.42
1:A:79:ASP:HA	1:A:141:ASN:ND2	2.34	0.42
1:C:42:TYR:CD2	1:C:91:PHE:CD2	3.08	0.42
1:A:11:GLU:O	1:A:12:LYS:C	2.57	0.42
2:B:10:PHE:C	2:B:10:PHE:CD1	2.92	0.42
1:C:144:LEU:HA	1:C:145:PRO:HD3	1.81	0.42
1:C:166:ARG:O	1:C:167:GLU:C	2.56	0.42
1:A:204:LEU:HD21	1:A:252:ALA:O	2.19	0.42
2:B:74:TYR:O	2:B:75:ILE:CG1	2.67	0.42
2:B:62:GLU:HA	2:B:65:MET:HB2	2.02	0.42
2:B:74:TYR:C	2:B:75:ILE:CG1	2.88	0.42
1:C:31:ARG:NE	4:C:740:HOH:O	2.48	0.42
1:A:241:ASP:O	1:A:245:LEU:CB	2.68	0.42
2:B:68:LEU:HB2	2:B:91:ARG:CG	2.50	0.42
1:A:271:GLU:C	4:A:447:HOH:O	2.58	0.42
2:B:59:TRP:CE3	2:B:64:LEU:HD21	2.55	0.42
1:C:106:ASP:OD1	1:C:130:ARG:NH1	2.49	0.42
1:C:238:LEU:HA	1:C:238:LEU:HD23	1.81	0.42
1:C:53:ILE:HG22	1:C:71:TYR:CB	2.44	0.42
2:B:65:MET:H	2:B:95:ILE:CD1	2.32	0.41
1:C:241:ASP:HB3	1:C:244:TYR:HB2	2.00	0.41
1:C:4:LEU:CA	4:C:657:HOH:O	2.68	0.41
1:C:127:ARG:HD2	1:C:127:ARG:HH11	1.53	0.41
1:C:131:VAL:O	1:C:132:ASP:C	2.58	0.41
1:C:42:TYR:CD2	1:C:91:PHE:HD2	2.39	0.41
1:C:230:MET:CE	1:C:230:MET:O	2.67	0.41
1:A:41:GLY:HA3	4:A:398:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:25:LYS:HE3	2:B:27:LYS:HB3	2.01	0.41
1:C:164:ASN:HD22	1:C:167:GLU:HG3	1.71	0.41
1:C:251:TYR:HB3	1:C:258:PHE:HB2	2.03	0.41
1:C:71:TYR:O	1:C:77:PHE:HD1	2.03	0.41
1:A:14:ARG:HG2	1:A:101:TRP:CE3	2.56	0.41
1:A:147:ALA:CB	1:A:232:LEU:HD13	2.50	0.41
1:A:278:LYS:C	1:A:280:ALA:H	2.24	0.41
1:A:79:ASP:HA	1:A:80:PRO:HD3	1.82	0.41
2:B:53:LYS:NZ	2:B:53:LYS:H	2.18	0.41
2:B:68:LEU:CB	2:B:91:ARG:HD2	2.50	0.41
2:B:67:TYR:O	2:B:71:PRO:HD3	2.19	0.41
2:B:49:THR:C	2:B:53:LYS:HZ3	2.21	0.41
2:B:46:PHE:HE2	2:B:79:LYS:HZ3	1.68	0.41
1:A:151:ALA:N	1:A:237:SER:HB3	2.36	0.41
1:A:262:PHE:O	1:A:263:SER:C	2.58	0.41
1:A:72:ARG:NH2	1:A:73:PHE:HZ	2.14	0.41
2:B:53:LYS:HG3	2:B:53:LYS:HZ2	1.41	0.41
1:C:68:GLY:O	1:C:132:ASP:HA	2.21	0.41
1:C:189:GLY:HA2	1:C:190:PRO:HD3	1.87	0.41
1:C:199:THR:HB	1:C:200:ASN:H	1.68	0.41
2:B:19:THR:CG2	2:B:25:LYS:O	2.69	0.41
2:B:29:GLY:HA2	2:B:30:PRO:HD3	1.84	0.41
2:B:72:LYS:HB3	2:B:72:LYS:HE3	1.89	0.41
1:C:179:LYS:HA	1:C:191:TRP:CZ3	2.56	0.41
1:A:245:LEU:HD12	1:A:245:LEU:O	2.21	0.41
2:B:49:THR:C	2:B:53:LYS:HZ1	2.23	0.41
2:B:62:GLU:O	2:B:65:MET:N	2.54	0.41
1:C:194:ALA:HB1	1:C:197:VAL:HG12	2.02	0.41
1:C:202:PHE:HB3	4:C:683:HOH:O	2.20	0.41
1:C:127:ARG:HG2	1:C:283:PRO:HB3	2.02	0.41
1:A:12:LYS:NZ	1:A:12:LYS:HB2	2.36	0.41
2:B:14:CYS:C	2:B:16:GLN:H	2.23	0.41
2:B:27:LYS:N	2:B:27:LYS:CD	2.84	0.41
1:A:32:GLU:HB3	1:A:33:ASP:OD1	2.21	0.40
1:A:73:PHE:CD2	1:A:135:GLU:HA	2.56	0.40
2:B:2:ASP:HB2	2:B:5:LYS:N	2.29	0.40
1:C:191:TRP:HD1	1:C:231:MET:HE2	1.86	0.40
2:B:40:THR:O	2:B:53:LYS:HA	2.21	0.40
1:C:214:GLU:O	1:C:222:GLN:N	2.49	0.40
1:A:92:LEU:O	1:A:95:ILE:HB	2.21	0.40
1:A:249:LYS:NZ	4:A:462:HOH:O	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:VAL:HG22	1:A:99:PHE:CG	2.56	0.40
1:A:11:GLU:H	1:A:11:GLU:HG2	1.50	0.40
1:A:88:GLY:O	1:A:92:LEU:HG	2.21	0.40
1:C:1:THR:HG23	1:C:2:THR:H	1.87	0.40
1:C:47:VAL:HG22	3:C:295:HEM:HMD3	2.04	0.40
1:A:264:LYS:NZ	1:C:35:GLU:OE1	2.55	0.40

All (3) 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)
4:A:444:HOH:O	4:A:444:HOH:O[8_665]	1.51	0.69
4:A:376:HOH:O	4:C:607:HOH:O[6_455]	1.61	0.59
1:C:279:ASP:CA	4:B:466:HOH:O[8_655]	2.09	0.11

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	292/296 (99%)	264 (90%)	23 (8%)	5 (2%)	9	29
1	C	292/296 (99%)	258 (88%)	29 (10%)	5 (2%)	9	29
2	B	102/104 (98%)	75 (74%)	19 (19%)	8 (8%)	1	2
All	All	686/696 (99%)	597 (87%)	71 (10%)	18 (3%)	5	18

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	GLU
1	A	277	PRO
2	B	61	GLU
2	B	65	MET

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Mol	Chain	Res	Type
2	B	100	LYS
2	B	101	ALA
1	C	85	LEU
2	B	96	ALA
2	B	97	TYR
1	C	229	TYR
1	A	12	LYS
2	B	48	TYR
1	C	59	LYS
1	C	74	LYS
1	A	34	ASP
1	C	190	PRO
1	A	33	ASP
2	B	84	GLY

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	252/254 (99%)	215 (85%)	37 (15%)	3	9
1	C	252/254 (99%)	220 (87%)	32 (13%)	4	14
2	B	86/86 (100%)	67 (78%)	19 (22%)	1	3
All	All	590/594 (99%)	502 (85%)	88 (15%)	3	9

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	THR
1	A	4	LEU
1	A	5	VAL
1	A	7	VAL
1	A	9	SER
1	A	11	GLU
1	A	12	LYS
1	A	51	TRP

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Mol	Chain	Res	Type
1	A	74	LYS
1	A	81	SER
1	A	86	GLN
1	A	90	LYS
1	A	91	PHE
1	A	94	PRO
1	A	110	LEU
1	A	124	ILE
1	A	135	GLU
1	A	149	LYS
1	A	182	LEU
1	A	183	LYS
1	A	184	ASN
1	A	195	ASN
1	A	212	LYS
1	A	215	LYS
1	A	226	LYS
1	A	227	SER
1	A	239	ILE
1	A	243	LYS
1	A	247	ILE
1	A	257	LYS
1	A	260	LYS
1	A	263	SER
1	A	267	GLU
1	A	269	LEU
1	A	278	LYS
1	A	289	LEU
1	A	292	GLN
2	B	2	ASP
2	B	7	LYS
2	B	14	CYS
2	B	16	GLN
2	B	27	LYS
2	B	31	ASN
2	B	39	LYS
2	B	42	GLN
2	B	50	ASP
2	B	52	ASN
2	B	53	LYS
2	B	54	ASN
2	B	55	LYS

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Mol	Chain	Res	Type
2	B	57	ILE
2	B	63	THR
2	B	69	GLU
2	B	79	LYS
2	B	86	LYS
2	B	91	ARG
1	C	5	VAL
1	C	7	VAL
1	C	17	GLU
1	C	33	ASP
1	C	35	GLU
1	C	47	VAL
1	C	51	TRP
1	C	66	SER
1	C	70	THR
1	C	74	LYS
1	C	75	LYS
1	C	76	GLU
1	C	86	GLN
1	C	90	LYS
1	C	138	THR
1	C	160	ARG
1	C	181	HIS
1	C	200	ASN
1	C	217	ASP
1	C	226	LYS
1	C	227	SER
1	C	230	MET
1	C	237	SER
1	C	243	LYS
1	C	245	LEU
1	C	256	ASP
1	C	257	LYS
1	C	260	LYS
1	C	261	ASP
1	C	274	ILE
1	C	287	LYS
1	C	292	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	HIS
1	A	96	HIS
1	A	117	GLN
1	A	141	ASN
1	A	162	ASN
1	A	195	ASN
1	A	222	GLN
2	B	26	HIS
2	B	42	GLN
2	B	54	ASN
2	B	103	ASN
1	C	20	GLN
1	C	24	ASN
1	C	86	GLN
1	C	162	ASN
1	C	200	ASN
1	C	208	ASN
1	C	222	GLN
1	C	292	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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	C	295	1,4	27,50,50	2.08	7 (25%)	17,82,82	2.81	11 (64%)
3	HEM	B	105	2	27,50,50	1.84	6 (22%)	17,82,82	2.31	7 (41%)
3	HEM	A	295	1	27,50,50	1.79	5 (18%)	17,82,82	1.64	6 (35%)

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	C	295	1,4	-	0/6/54/54	-
3	HEM	B	105	2	-	0/6/54/54	-
3	HEM	A	295	1	-	0/6/54/54	-

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	295	HEM	C3B-C2B	-5.01	1.33	1.40
3	B	105	HEM	C3C-C2C	-4.46	1.34	1.40
3	A	295	HEM	C3C-C2C	-4.20	1.34	1.40
3	B	105	HEM	C3B-C2B	-4.16	1.34	1.40
3	C	295	HEM	C3C-C2C	-3.76	1.35	1.40
3	A	295	HEM	C3B-C2B	-3.73	1.35	1.40
3	C	295	HEM	CAA-C2A	3.60	1.57	1.52
3	C	295	HEM	CAD-C3D	3.52	1.58	1.52
3	C	295	HEM	C3B-CAB	3.49	1.55	1.47
3	A	295	HEM	C3B-CAB	3.46	1.55	1.47
3	B	105	HEM	C3B-CAB	3.21	1.54	1.47
3	B	105	HEM	C3C-CAC	2.82	1.53	1.47
3	B	105	HEM	CAA-C2A	2.72	1.56	1.52
3	C	295	HEM	C3C-CAC	2.47	1.52	1.47
3	B	105	HEM	CMD-C2D	2.38	1.56	1.51
3	A	295	HEM	CAD-C3D	2.32	1.56	1.52
3	A	295	HEM	C3C-CAC	2.18	1.52	1.47
3	C	295	HEM	C1B-C2B	2.07	1.47	1.42

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	295	HEM	CAD-CBD-CGD	6.57	123.70	112.67
3	C	295	HEM	CAA-CBA-CGA	4.82	120.76	112.67
3	B	105	HEM	CMA-C3A-C4A	-4.48	121.57	128.46
3	B	105	HEM	CBD-CAD-C3D	4.06	119.96	112.48
3	C	295	HEM	CMA-C3A-C4A	-3.79	122.64	128.46
3	B	105	HEM	CMD-C2D-C1D	-3.55	123.01	128.46
3	C	295	HEM	CBA-CAA-C2A	3.45	118.85	112.49
3	B	105	HEM	CMA-C3A-C2A	3.34	131.25	124.94
3	C	295	HEM	CMD-C2D-C1D	-3.07	123.75	128.46
3	B	105	HEM	CMD-C2D-C3D	2.95	130.50	124.94
3	B	105	HEM	CAA-CBA-CGA	2.87	117.49	112.67
3	C	295	HEM	CBD-CAD-C3D	-2.76	107.40	112.48
3	A	295	HEM	C1D-C2D-C3D	-2.61	105.18	107.00
3	A	295	HEM	CMC-C2C-C3C	2.54	129.44	124.68
3	A	295	HEM	CMD-C2D-C3D	2.39	129.44	124.94
3	C	295	HEM	CMB-C2B-C3B	2.29	128.96	124.68
3	A	295	HEM	CAD-CBD-CGD	2.23	116.42	112.67
3	C	295	HEM	CMC-C2C-C3C	2.16	128.72	124.68
3	C	295	HEM	CMD-C2D-C3D	2.13	128.96	124.94
3	C	295	HEM	C4A-C3A-C2A	2.09	108.45	107.00
3	C	295	HEM	CMA-C3A-C2A	2.09	128.88	124.94
3	A	295	HEM	CAA-CBA-CGA	-2.06	109.21	112.67
3	A	295	HEM	CMD-C2D-C1D	-2.03	125.34	128.46
3	B	105	HEM	CBA-CAA-C2A	2.02	116.22	112.49

There are no chirality outliers.

There are no torsion outliers.

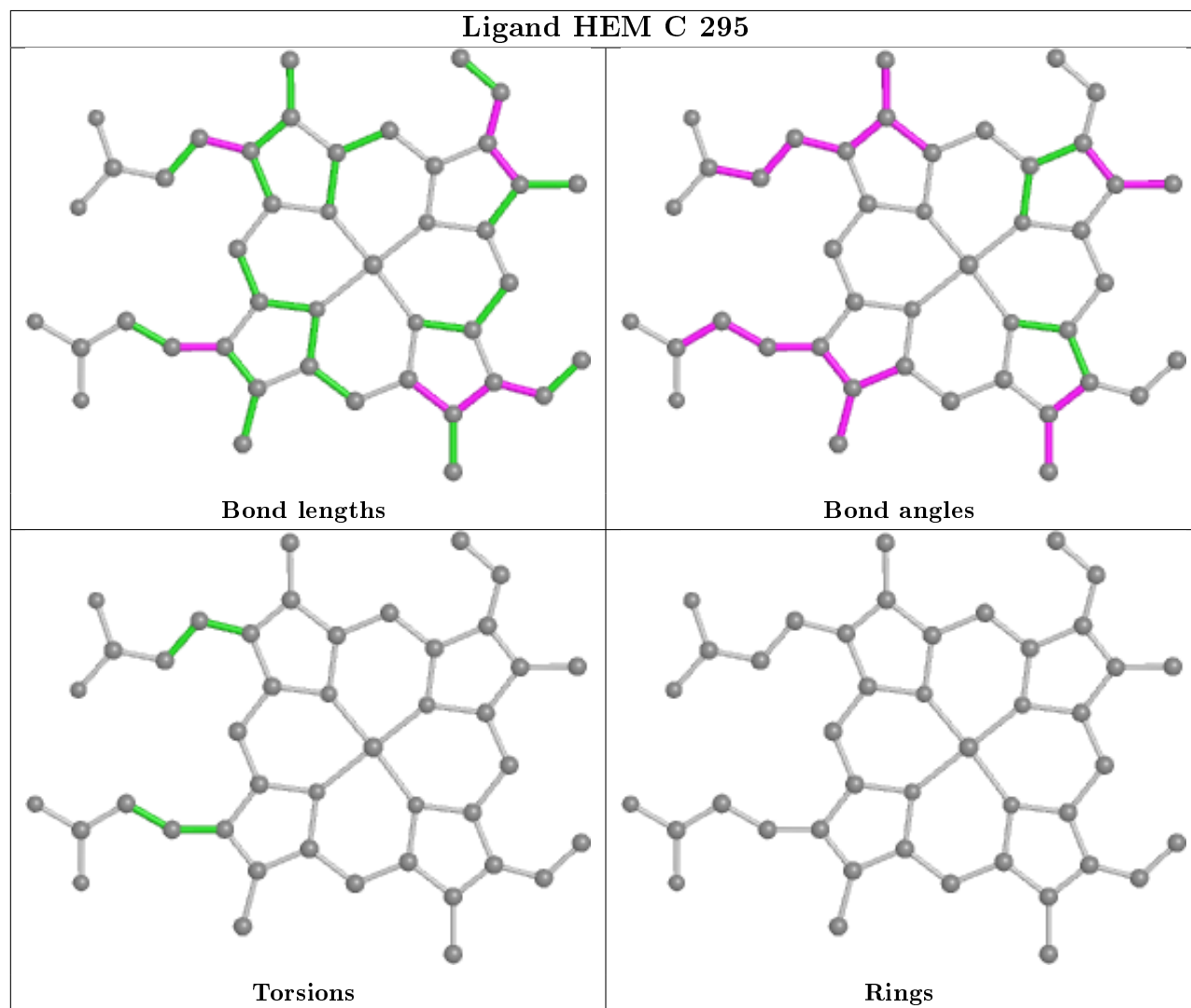
There are no ring outliers.

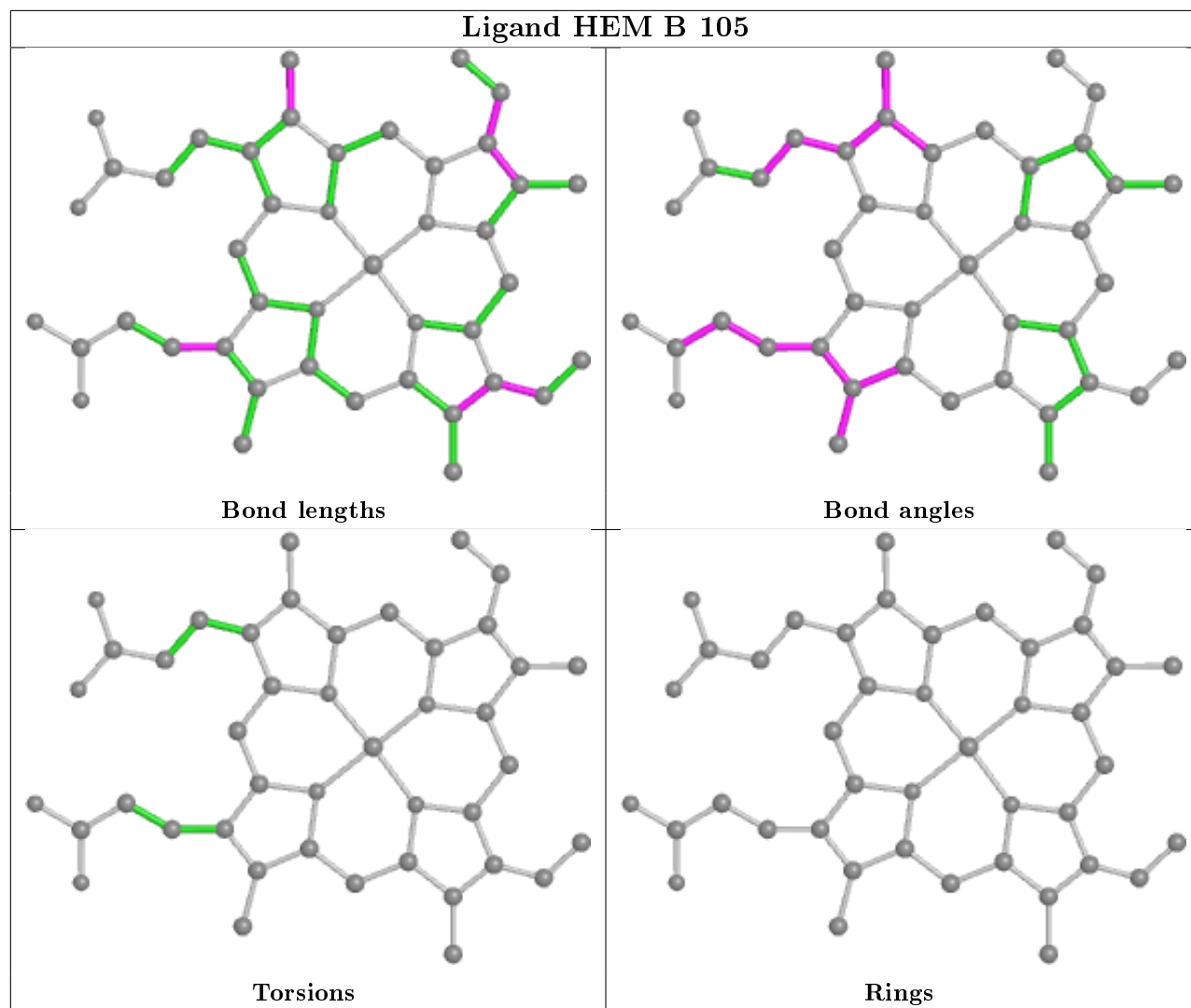
3 monomers are involved in 25 short contacts:

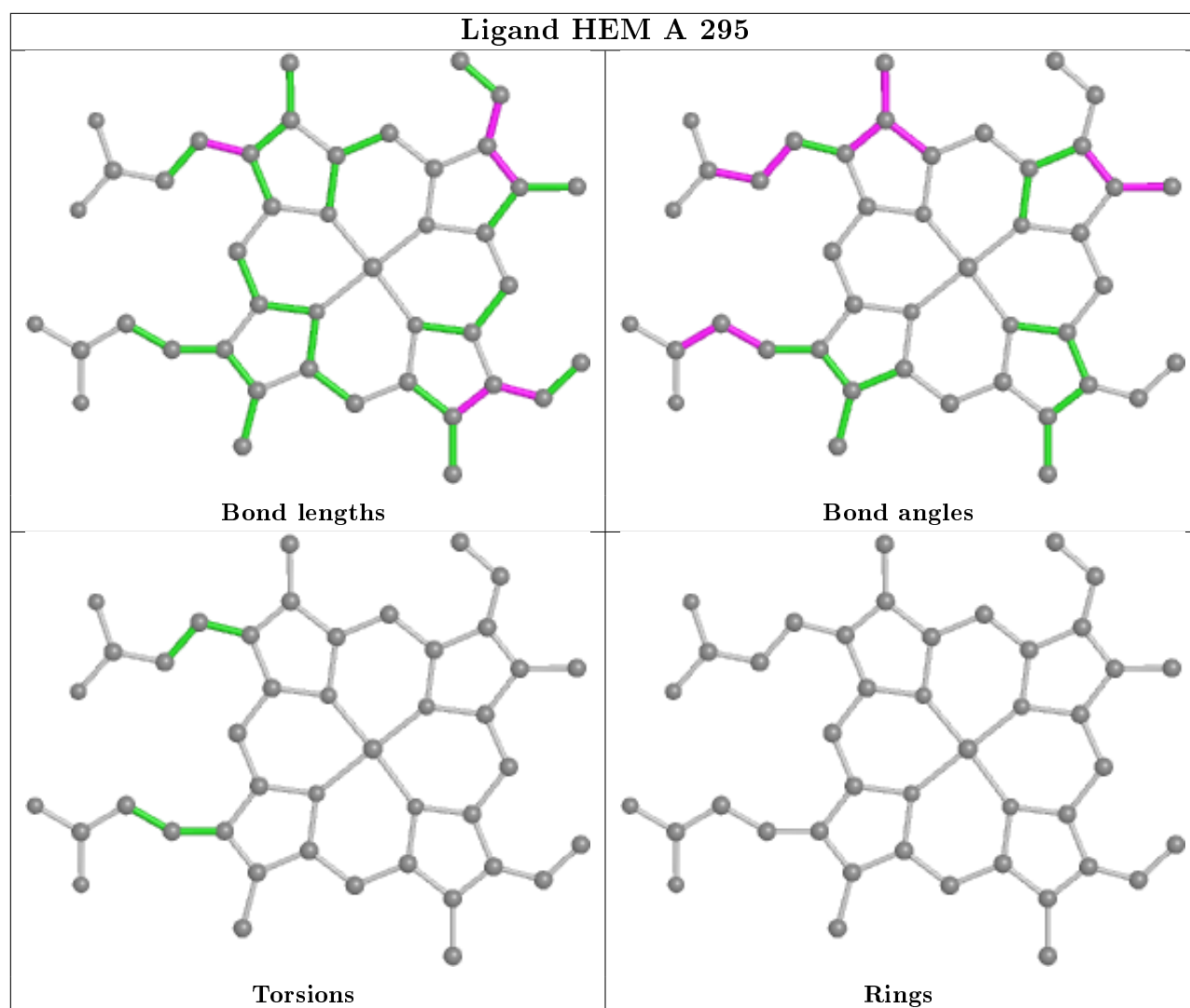
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	295	HEM	1	0
3	B	105	HEM	19	0
3	A	295	HEM	5	0

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	294/296 (99%)	-1.24	1 (0%) 94 93	10, 25, 47, 92	0
1	C	294/296 (99%)	-1.25	0 100 100	12, 26, 44, 62	0
2	B	104/104 (100%)	-0.28	1 (0%) 82 77	29, 68, 92, 107	0
All	All	692/696 (99%)	-1.10	2 (0%) 94 93	10, 27, 75, 107	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	THR	2.7
2	B	3	VAL	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 carbohydrates 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(Å ²)	Q<0.9
3	HEM	B	105	43/43	0.97	0.12	41,47,58,65	0

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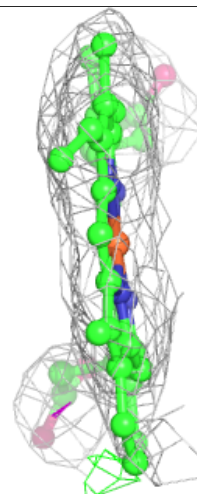
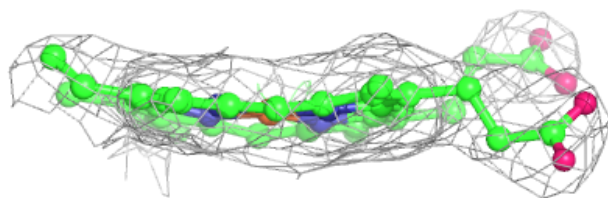
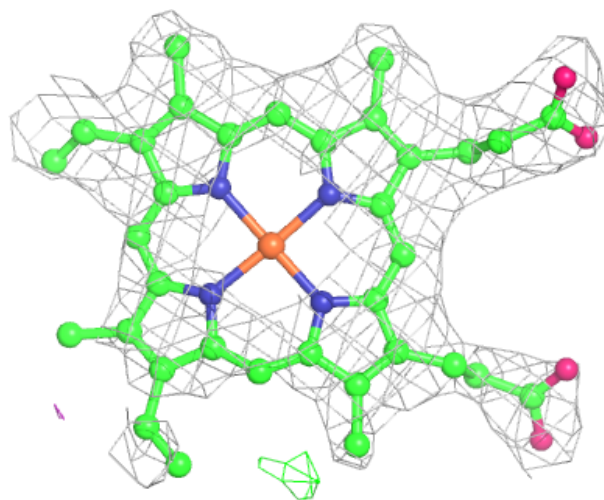
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	HEM	C	295	43/43	0.98	0.08	15,23,26,28	0
3	HEM	A	295	43/43	0.98	0.09	13,26,35,38	0

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.

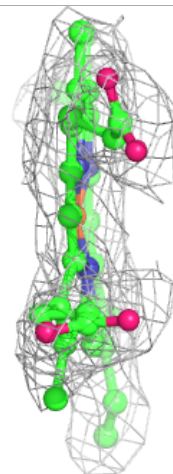
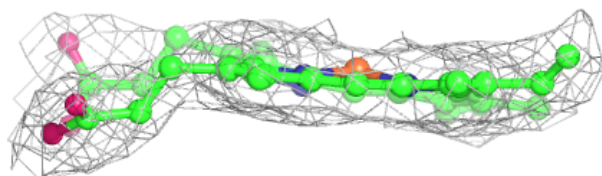
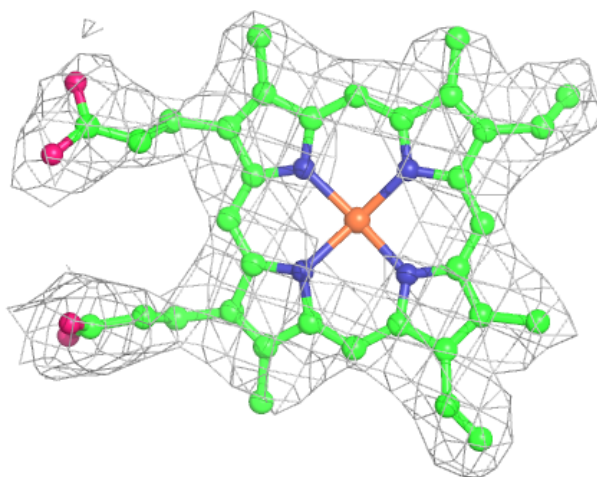
Electron density around HEM B 105:

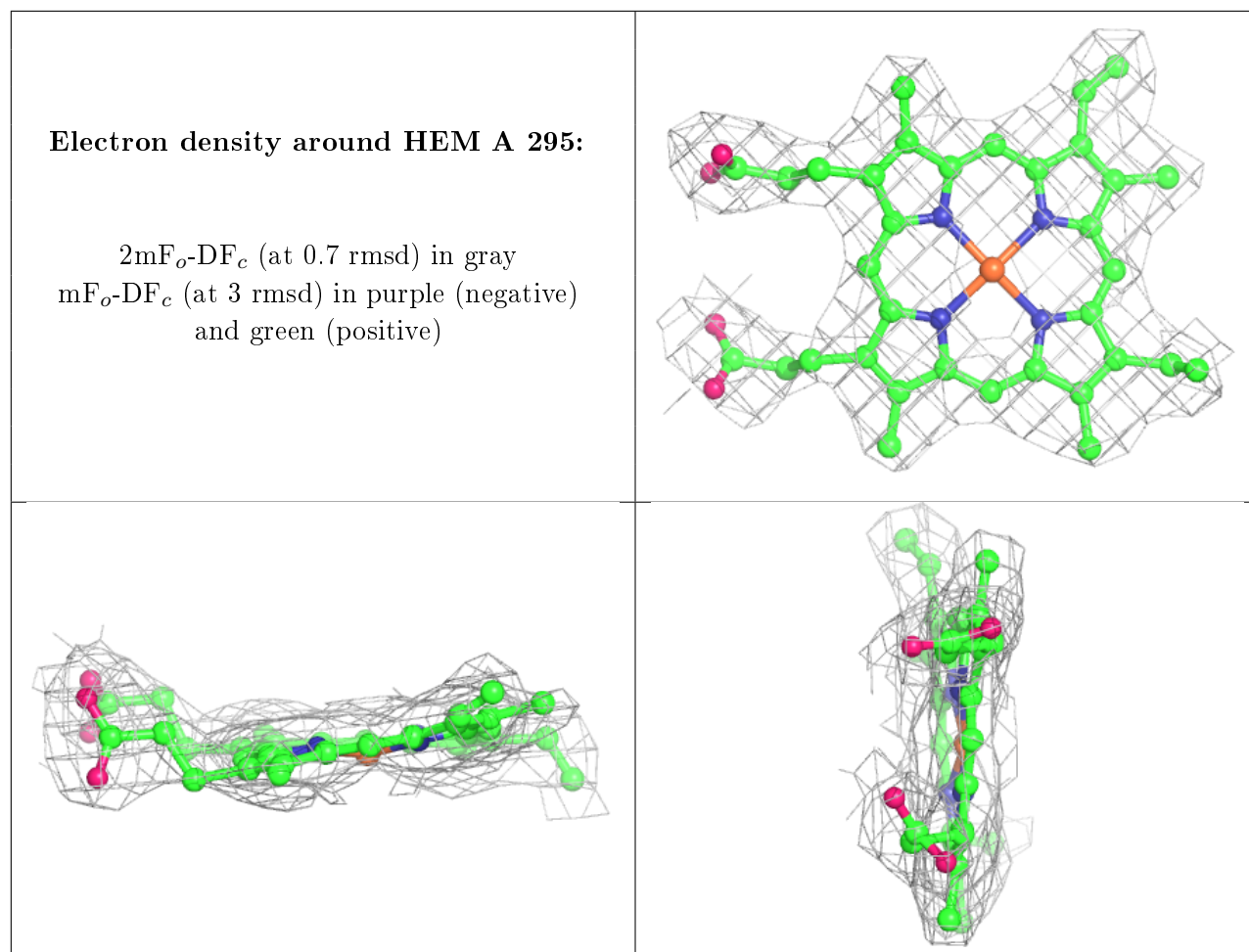
2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM C 295:

$2mF_o-DF_c$ (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.