



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 05:45 pm BST

PDB ID : 3RE8  
Title : Structural and Kinetic Analysis of the Beef liver Catalase interacting with Nitric Oxide  
Authors : Purwar, N.; Schmidt, M.  
Deposited on : 2011-04-03  
Resolution : 1.90 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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

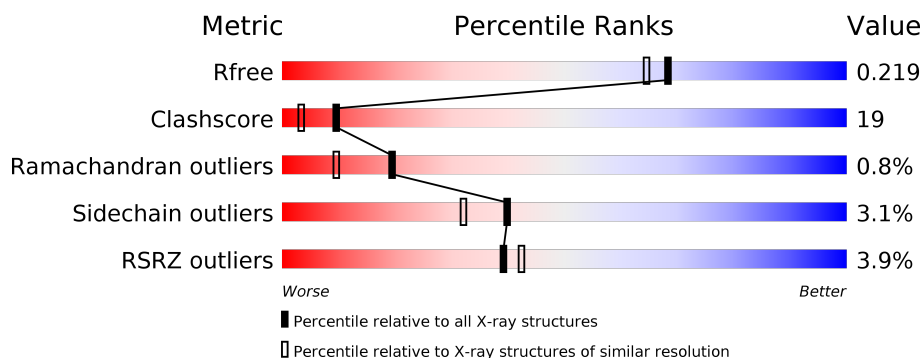
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	499	<div> <div>2%</div> <div> <div></div> <div>72%</div> <div>26%</div> <div></div> </div> </div>
1	B	499	<div> <div>5%</div> <div> <div></div> <div>63%</div> <div>34%</div> <div></div> </div> </div>
1	C	499	<div> <div>4%</div> <div> <div></div> <div>72%</div> <div>26%</div> <div></div> </div> </div>
1	D	499	<div> <div>4%</div> <div> <div></div> <div>69%</div> <div>31%</div> <div></div> </div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 17527 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 Catalase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total	C	N	O	S	0	1	0
			4018	2548	717	738	15			
1	B	499	Total	C	N	O	S	0	1	0
			4018	2548	717	738	15			
1	C	499	Total	C	N	O	S	0	1	0
			4018	2548	717	738	15			
1	D	499	Total	C	N	O	S	0	1	0
			4018	2548	717	738	15			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



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

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

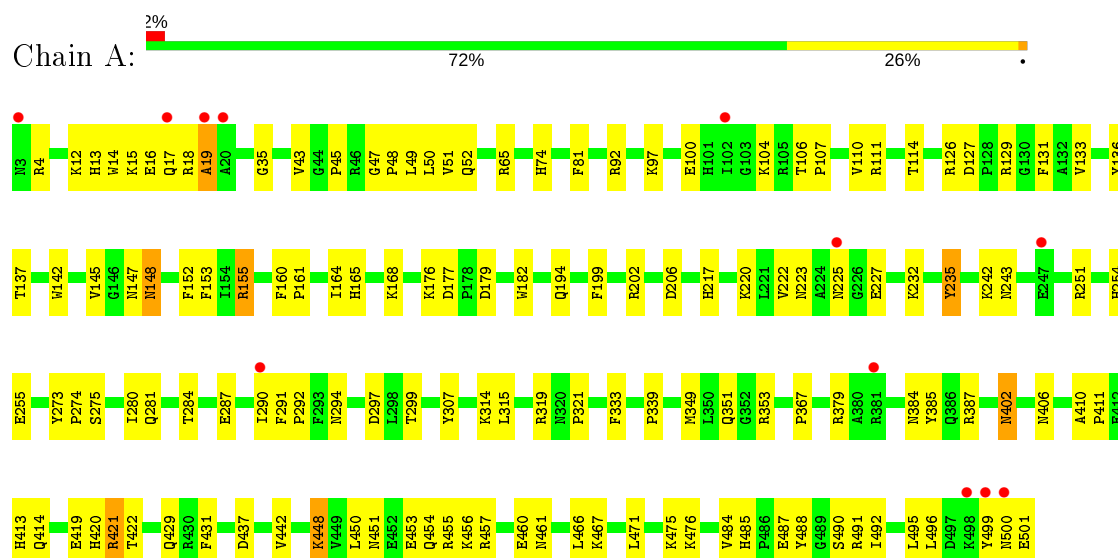
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	300	Total	O	0	0
			300	300		
3	B	319	Total	O	0	0
			319	319		
3	C	356	Total	O	0	0
			356	356		
3	D	308	Total	O	0	0
			308	308		

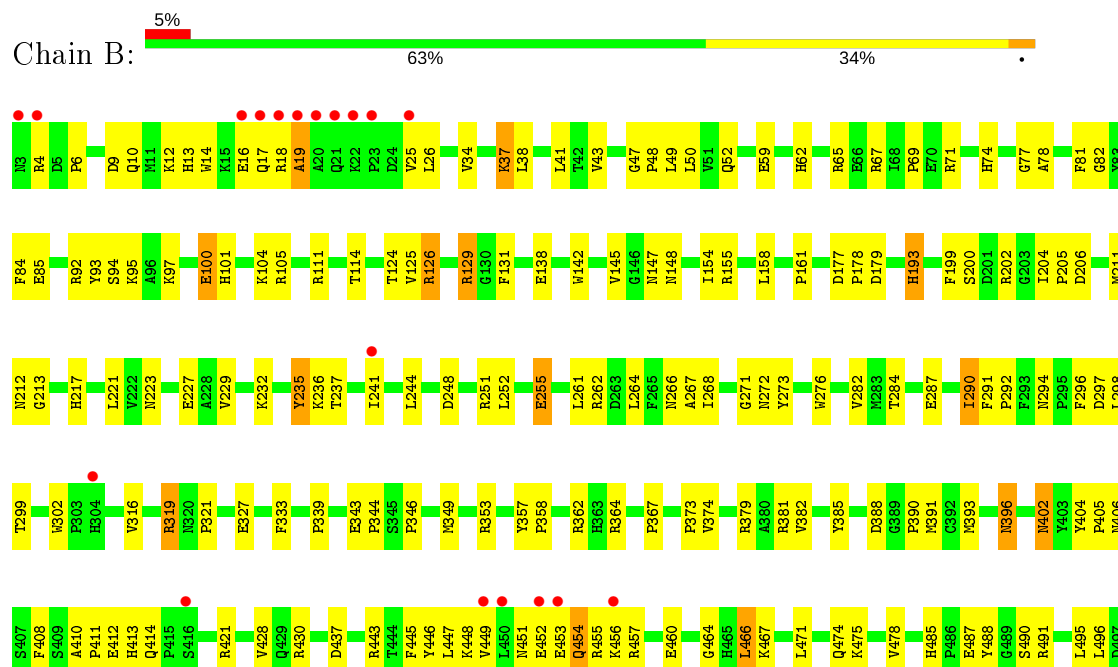
### 3 Residue-property plots

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: Catalase

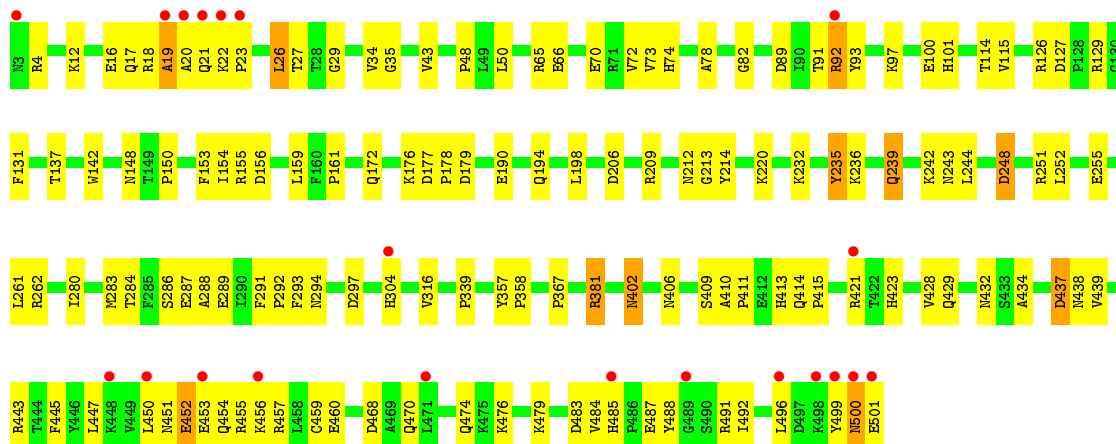


#### • Molecule 1: Catalase

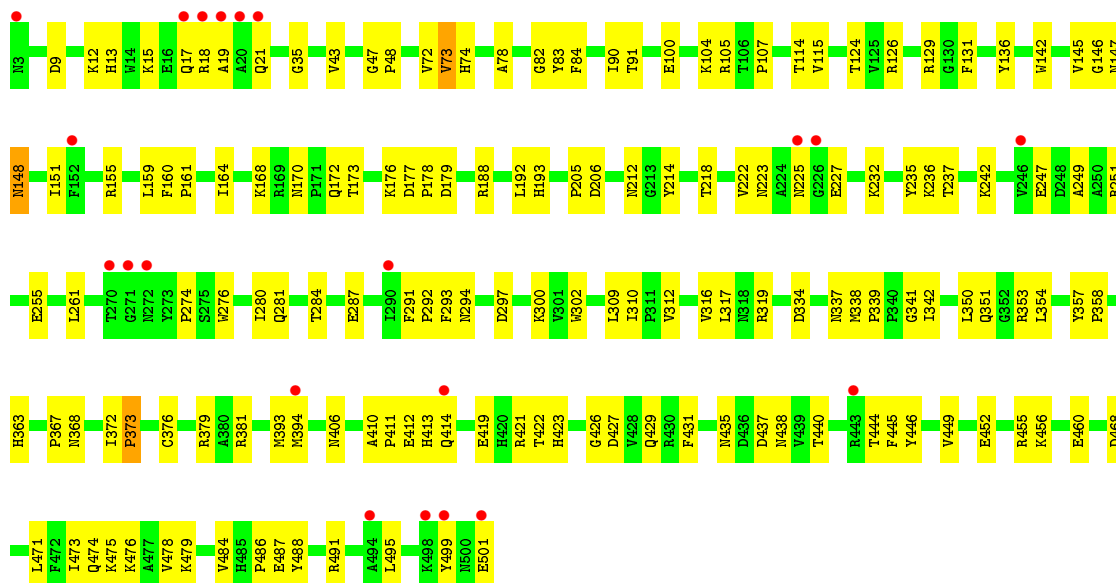




● Molecule 1: Catalase



● Molecule 1: Catalase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.22Å 140.92Å 229.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.40 – 1.90 38.44 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.3 (38.40-1.90) 97.5 (38.44-1.90)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.18 (at 1.89Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.221 , 0.259 0.220 , 0.219	Depositor DCC
$R_{free}$ test set	10401 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.2	Xtriage
Anisotropy	0.439	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 57.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.37$ , $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	17527	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

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

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.35	0/4143	0.61	0/5628
1	B	0.36	0/4143	0.61	0/5628
1	C	0.36	0/4143	0.63	0/5628
1	D	0.34	0/4143	0.59	0/5628
All	All	0.35	0/16572	0.61	0/22512

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4018	0	3844	138	0
1	B	4018	0	3844	216	0
1	C	4018	0	3844	154	0
1	D	4018	0	3844	147	0
2	A	43	0	30	2	0
2	B	43	0	30	2	0
2	C	43	0	30	0	0
2	D	43	0	30	1	0
3	A	300	0	0	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	319	0	0	40	1
3	C	356	0	0	40	1
3	D	308	0	0	41	0
All	All	17527	0	15496	618	1

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 19.

All (618) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:350:LEU:HG	3:D:773:HOH:O	1.42	1.20
1:D:444:THR:HB	3:D:1074:HOH:O	1.50	1.09
1:C:91:THR:HB	3:C:1015:HOH:O	1.55	1.06
1:B:374:VAL:HG23	3:B:517:HOH:O	1.59	0.99
3:A:869:HOH:O	1:C:409:SER:HB3	1.63	0.99
1:B:319:ARG:HB3	1:B:319:ARG:HH11	1.32	0.94
1:C:92:ARG:HD2	3:C:572:HOH:O	1.65	0.94
1:A:429:GLN:HB3	1:B:421:ARG:HD2	1.49	0.94
1:B:327:GLU:HA	1:B:374:VAL:HG21	1.48	0.94
1:A:314:LYS:HG3	3:A:939:HOH:O	1.70	0.92
1:B:466:LEU:HD22	1:B:474:GLN:HG2	1.50	0.91
1:C:452:GLU:HG3	3:C:769:HOH:O	1.71	0.90
1:C:155:ARG:HH22	1:C:438:ASN:HD21	1.17	0.89
1:A:111:ARG:CZ	3:A:505:HOH:O	2.20	0.89
1:B:126:ARG:CZ	3:B:737:HOH:O	2.21	0.88
1:A:111:ARG:NE	3:A:505:HOH:O	2.07	0.87
1:A:126:ARG:NH2	3:A:846:HOH:O	2.07	0.87
1:B:155:ARG:HG3	3:B:833:HOH:O	1.74	0.86
1:B:62:HIS:HE1	1:D:368:ASN:HD21	1.25	0.85
1:B:4:ARG:CZ	3:B:655:HOH:O	2.24	0.84
1:C:126:ARG:NE	3:C:639:HOH:O	2.11	0.84
1:A:176:LYS:HE2	3:A:667:HOH:O	1.77	0.84
1:C:487:GLU:O	1:C:491:ARG:HG3	1.77	0.84
1:A:155:ARG:NH2	3:A:649:HOH:O	2.11	0.84
1:A:307:TYR:HA	3:A:651:HOH:O	1.78	0.82
1:B:290:ILE:O	1:B:290:ILE:HD13	1.79	0.82
1:A:155:ARG:NE	3:A:649:HOH:O	2.12	0.82
1:C:206:ASP:HA	1:C:244:LEU:CD2	2.10	0.81
1:D:223:ASN:HD21	1:D:227:GLU:HB2	1.43	0.81
1:D:12:LYS:HG3	3:D:1056:HOH:O	1.81	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:37:LYS:O	1:B:37:LYS:HG3	1.80	0.81
1:B:406:ASN:HD21	1:B:410:ALA:HB3	1.44	0.81
1:B:25:VAL:HG13	1:D:414:GLN:HG3	1.63	0.80
1:C:155:ARG:NH2	1:C:438:ASN:HD21	1.79	0.80
1:C:89:ASP:OD1	1:C:91:THR:HG22	1.82	0.79
1:B:62:HIS:HD2	3:B:504:HOH:O	1.66	0.79
1:B:4:ARG:NE	3:B:655:HOH:O	2.15	0.79
1:A:126:ARG:CZ	3:A:899:HOH:O	2.32	0.78
1:A:155:ARG:HB3	1:A:155:ARG:HH11	1.49	0.77
1:C:161:PRO:HG2	3:C:644:HOH:O	1.85	0.77
1:D:338:MET:CE	1:D:342:ILE:HG22	2.15	0.77
1:B:319:ARG:HD3	3:B:612:HOH:O	1.84	0.77
1:C:126:ARG:CZ	3:C:639:HOH:O	2.30	0.77
1:B:491:ARG:O	1:B:495:LEU:HD23	1.83	0.77
1:A:111:ARG:NH2	3:A:505:HOH:O	2.19	0.76
1:D:376[A]:CYS:SG	3:D:659:HOH:O	2.44	0.76
1:A:155:ARG:CZ	3:A:649:HOH:O	2.34	0.75
1:B:126:ARG:HE	1:B:199:PHE:HA	1.51	0.75
1:B:138:GLU:HG2	3:B:974:HOH:O	1.86	0.75
1:C:21:GLN:HB3	3:C:662:HOH:O	1.85	0.75
1:D:452:GLU:HG3	3:D:1189:HOH:O	1.86	0.75
1:C:262:ARG:NH1	3:C:1073:HOH:O	2.19	0.75
1:B:452:GLU:HG3	3:B:796:HOH:O	1.86	0.75
1:A:251:ARG:HB3	1:A:251:ARG:HH11	1.51	0.75
1:C:451:ASN:HD21	1:C:453:GLU:HB2	1.51	0.75
1:D:406:ASN:HD21	1:D:410:ALA:HB3	1.51	0.74
1:D:354:LEU:HG	3:D:773:HOH:O	1.87	0.74
1:C:155:ARG:HH22	1:C:438:ASN:ND2	1.87	0.73
1:B:77:GLY:CA	1:B:111:ARG:HH12	2.02	0.73
1:B:487:GLU:O	1:B:491:ARG:HG3	1.89	0.73
1:B:37:LYS:H	1:D:413:HIS:CE1	2.07	0.72
1:C:284:THR:OG1	1:C:287:GLU:HG3	1.89	0.72
1:C:381:ARG:HD3	3:C:810:HOH:O	1.90	0.72
3:A:1188:HOH:O	1:D:176:LYS:HE2	1.88	0.72
1:C:78:ALA:HB2	1:C:261:LEU:HD22	1.70	0.71
1:B:202:ARG:HH21	1:B:241:ILE:HD13	1.53	0.71
1:A:126:ARG:HH12	1:A:461:ASN:HB3	1.55	0.71
1:B:319:ARG:CB	1:B:319:ARG:HH11	2.02	0.71
1:B:4:ARG:NH2	3:B:655:HOH:O	2.22	0.71
1:A:12:LYS:O	1:A:16:GLU:HG3	1.90	0.71
1:D:284:THR:OG1	1:D:287:GLU:HG3	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:LYS:HA	1:A:448:LYS:HE3	1.71	0.71
1:D:471:LEU:O	1:D:475:LYS:HG3	1.91	0.71
1:B:13:HIS:HD2	3:B:726:HOH:O	1.73	0.71
1:A:319:ARG:NH1	3:A:585:HOH:O	2.15	0.71
1:C:492:ILE:O	1:C:496:LEU:HD23	1.91	0.71
1:D:338:MET:HE2	1:D:342:ILE:HG22	1.73	0.70
1:D:170:ASN:ND2	1:D:172:GLN:H	1.88	0.70
1:D:13:HIS:O	1:D:17:GLN:HG3	1.90	0.70
1:C:206:ASP:HA	1:C:244:LEU:HD21	1.71	0.70
1:B:111:ARG:CZ	3:B:615:HOH:O	2.39	0.70
1:C:476:LYS:HB3	1:C:476:LYS:NZ	2.07	0.70
1:B:178:PRO:HG2	3:B:1149:HOH:O	1.89	0.70
1:D:456:LYS:O	1:D:460:GLU:HG3	1.90	0.70
1:B:77:GLY:HA3	1:B:111:ARG:HH12	1.57	0.70
1:A:485:HIS:HD2	1:A:487:GLU:H	1.40	0.69
1:C:150:PRO:HG3	1:C:214:TYR:CE1	2.27	0.69
1:C:438:ASN:N	3:C:678:HOH:O	2.26	0.69
1:B:12:LYS:O	1:B:16:GLU:HG2	1.93	0.69
1:C:91:THR:CB	3:C:1015:HOH:O	2.24	0.69
3:A:632:HOH:O	1:C:18:ARG:HD2	1.93	0.68
1:B:454:GLN:NE2	3:B:905:HOH:O	2.18	0.68
1:C:206:ASP:HA	1:C:244:LEU:HD22	1.75	0.68
1:B:261:LEU:CD1	3:B:1281:HOH:O	2.41	0.68
1:B:105:ARG:HD2	3:B:1245:HOH:O	1.92	0.68
1:C:414:GLN:CD	3:C:1030:HOH:O	2.31	0.68
1:D:491:ARG:NH1	3:D:896:HOH:O	2.27	0.68
1:A:17:GLN:HG2	3:A:975:HOH:O	1.92	0.68
1:B:100:GLU:HB3	1:B:104:LYS:HD2	1.77	0.67
1:C:291:PHE:CD1	1:C:292:PRO:HD2	2.30	0.67
1:C:381:ARG:HB2	1:C:381:ARG:HH11	1.60	0.67
1:A:491:ARG:O	1:A:495:LEU:HD23	1.95	0.67
1:A:225:ASN:HB2	1:A:227:GLU:OE2	1.95	0.66
1:B:248:ASP:O	1:B:252:LEU:HD13	1.95	0.66
1:B:138:GLU:H	1:B:138:GLU:CD	1.98	0.66
1:B:62:HIS:HE1	1:D:368:ASN:ND2	1.91	0.66
1:C:17:GLN:HG3	3:C:695:HOH:O	1.94	0.66
1:B:126:ARG:HH21	1:B:199:PHE:C	1.99	0.66
1:D:429:GLN:HB2	3:D:750:HOH:O	1.94	0.66
1:B:77:GLY:HA3	1:B:111:ARG:NH1	2.11	0.66
1:A:351:GLN:HG3	3:A:989:HOH:O	1.96	0.66
1:A:126:ARG:NH1	1:A:461:ASN:HB3	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:486:PRO:HA	3:D:948:HOH:O	1.94	0.65
1:C:432:ASN:ND2	1:C:434:ALA:H	1.95	0.65
1:B:447:LEU:HD12	1:B:448:LYS:N	2.11	0.65
1:A:421:ARG:HG2	3:A:878:HOH:O	1.97	0.65
1:B:161:PRO:HG2	3:B:543:HOH:O	1.96	0.65
1:A:422:THR:N	3:A:619:HOH:O	2.30	0.65
1:A:50:LEU:HD12	1:B:48:PRO:HB2	1.79	0.64
1:A:476:LYS:HE3	3:A:551:HOH:O	1.96	0.64
1:B:264:LEU:O	1:B:268:ILE:HD13	1.96	0.64
1:A:451:ASN:H	1:A:454:GLN:HE21	1.45	0.64
1:C:43:VAL:CG1	1:C:48:PRO:HD2	2.28	0.64
1:D:170:ASN:HD22	1:D:173:THR:H	1.45	0.64
1:D:456:LYS:HD2	1:D:460:GLU:OE1	1.98	0.64
1:C:474:GLN:NE2	1:C:496:LEU:HD12	2.12	0.63
1:B:267:ALA:HA	3:B:1117:HOH:O	1.99	0.63
1:D:124:THR:HA	3:D:1133:HOH:O	1.98	0.63
1:A:485:HIS:CD2	1:A:487:GLU:H	2.16	0.63
1:C:500:ASN:ND2	3:C:882:HOH:O	2.30	0.63
1:B:456:LYS:O	1:B:460:GLU:HG3	1.98	0.63
1:C:26:LEU:HG	1:C:34:VAL:HG21	1.81	0.63
1:B:205:PRO:HG3	1:B:211:MET:CE	2.28	0.63
1:C:261:LEU:CD2	3:C:1279:HOH:O	2.46	0.63
1:C:421:ARG:HG2	3:C:876:HOH:O	2.00	0.62
1:B:406:ASN:ND2	1:B:410:ALA:HB3	2.13	0.62
1:D:294:ASN:HB3	1:D:297:ASP:HB2	1.82	0.62
1:B:475:LYS:HD2	3:B:1120:HOH:O	1.99	0.62
1:C:209:ARG:O	1:C:239:GLN:HG2	1.99	0.62
1:B:10:GLN:HE21	1:C:172:GLN:NE2	1.98	0.62
1:B:202:ARG:HH21	1:B:241:ILE:CD1	2.11	0.62
1:B:41:LEU:HD11	1:C:428:VAL:CG1	2.30	0.61
1:B:498:LYS:HD3	1:B:498:LYS:O	2.00	0.61
1:B:129:ARG:HB2	1:B:211:MET:HE1	1.82	0.61
1:C:236:LYS:HE2	3:C:1106:HOH:O	1.98	0.61
1:A:421:ARG:CG	3:A:878:HOH:O	2.48	0.61
1:B:10:GLN:HE21	1:C:172:GLN:HE21	1.48	0.61
1:C:445:PHE:O	1:C:450:LEU:HD13	1.99	0.61
1:D:293:PHE:HZ	1:D:440:THR:HG21	1.65	0.61
1:B:205:PRO:HG3	1:B:211:MET:HE3	1.82	0.61
1:B:261:LEU:HD12	3:B:1281:HOH:O	2.00	0.61
1:B:111:ARG:NE	3:B:615:HOH:O	2.34	0.61
1:D:151:ILE:HD13	1:D:193:HIS:CD2	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:251:ARG:HD3	3:D:1228:HOH:O	2.01	0.60
1:C:12:LYS:O	1:C:16:GLU:HG3	2.01	0.60
1:C:155:ARG:HH12	1:C:438:ASN:ND2	1.99	0.60
1:D:473:ILE:HA	1:D:476:LYS:HE2	1.82	0.60
3:A:619:HOH:O	1:B:428:VAL:CG2	2.49	0.60
1:A:142:TRP:HB2	1:A:339:PRO:HD3	1.83	0.60
1:A:43:VAL:O	1:A:43:VAL:HG13	2.01	0.60
1:A:453:GLU:HG2	1:A:457:ARG:HH12	1.67	0.60
1:B:382:VAL:HG13	3:B:669:HOH:O	2.01	0.60
1:C:499:TYR:CZ	3:C:1036:HOH:O	2.50	0.60
1:A:43:VAL:CG1	1:A:48:PRO:HD2	2.31	0.60
1:B:49:LEU:HD23	1:B:50:LEU:N	2.16	0.59
1:D:310:ILE:HD11	3:D:1200:HOH:O	2.02	0.59
1:A:160:PHE:HB3	1:A:161:PRO:HD3	1.85	0.59
1:C:451:ASN:ND2	1:C:453:GLU:HB2	2.17	0.59
1:D:146:GLY:HA3	1:D:214:TYR:O	2.03	0.59
1:A:126:ARG:NH2	3:A:899:HOH:O	2.35	0.59
1:A:126:ARG:HH12	1:A:461:ASN:CB	2.14	0.59
1:A:206:ASP:CB	1:A:242:LYS:HD2	2.33	0.58
1:C:476:LYS:HB3	1:C:476:LYS:HZ3	1.68	0.58
1:D:393:MET:CA	3:D:753:HOH:O	2.51	0.58
1:D:223:ASN:ND2	1:D:227:GLU:HB2	2.15	0.58
1:C:451:ASN:H	1:C:454:GLN:NE2	2.00	0.58
1:C:73:VAL:HG12	1:C:74:HIS:CD2	2.39	0.58
1:A:65:ARG:HD3	1:C:367:PRO:HG3	1.86	0.57
1:B:294:ASN:HB3	1:B:297:ASP:HB2	1.86	0.57
1:D:435:ASN:OD1	3:D:1026:HOH:O	2.17	0.57
1:A:164:ILE:O	1:A:168:LYS:HG2	2.05	0.57
1:B:148:ASN:CB	1:B:211:MET:HE2	2.35	0.57
1:B:298:LEU:HA	3:B:926:HOH:O	2.04	0.57
1:D:212:ASN:OD1	1:D:236:LYS:HA	2.05	0.57
1:B:388:ASP:H	1:B:396:ASN:HD21	1.52	0.57
1:D:280:ILE:O	1:D:280:ILE:HG13	2.04	0.57
1:B:138:GLU:CD	1:B:138:GLU:N	2.58	0.57
1:C:156:ASP:HB3	1:C:159:LEU:HD23	1.87	0.57
1:B:100:GLU:HB3	1:B:104:LYS:CD	2.35	0.56
1:B:464:GLY:O	1:B:467:LYS:HE3	2.05	0.56
1:C:468:ASP:OD2	3:C:936:HOH:O	2.17	0.56
1:C:251:ARG:HG3	1:C:252:LEU:N	2.19	0.56
1:B:126:ARG:HH12	1:B:204:ILE:HG13	1.71	0.56
1:A:155:ARG:HH12	1:A:299:THR:CG2	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:LYS:HE2	3:A:939:HOH:O	2.04	0.56
1:B:379:ARG:NH2	3:B:907:HOH:O	2.35	0.56
3:A:619:HOH:O	1:B:428:VAL:HG23	2.04	0.56
1:D:170:ASN:HD22	1:D:172:GLN:H	1.52	0.56
1:D:90:ILE:HG21	1:D:312:VAL:HG22	1.87	0.56
1:B:391:MET:HE1	1:D:372:ILE:HD11	1.86	0.56
1:C:150:PRO:HG3	1:C:214:TYR:CD1	2.41	0.56
3:C:570:HOH:O	1:D:363:HIS:HD2	1.88	0.56
1:B:284:THR:OG1	1:B:287:GLU:HG3	2.06	0.56
1:C:26:LEU:HD12	1:C:27:THR:N	2.21	0.56
1:A:492:ILE:O	1:A:496:LEU:HD13	2.07	0.55
1:B:129:ARG:CB	1:B:211:MET:HE1	2.36	0.55
1:B:92:ARG:HD2	1:B:93:TYR:CZ	2.41	0.55
1:B:223:ASN:HD21	1:B:227:GLU:HB2	1.71	0.55
1:B:138:GLU:CG	3:B:974:HOH:O	2.51	0.55
1:B:9:ASP:OD2	3:B:929:HOH:O	2.18	0.55
1:C:92:ARG:HG3	1:C:92:ARG:HH11	1.70	0.55
1:B:296:PHE:CD2	1:B:346:PRO:HG2	2.42	0.55
1:D:168:LYS:HB3	3:D:895:HOH:O	2.05	0.55
1:D:232:LYS:HB2	1:D:281:GLN:CG	2.36	0.55
1:D:91:THR:HG21	3:D:649:HOH:O	2.06	0.55
1:A:499:TYR:C	1:A:501:GLU:H	2.09	0.55
1:C:50:LEU:HB3	3:C:508:HOH:O	2.05	0.55
1:B:447:LEU:HA	1:B:455:ARG:NH1	2.22	0.55
1:C:126:ARG:HD2	1:C:198:LEU:O	2.06	0.55
1:D:394:MET:N	3:D:753:HOH:O	2.21	0.55
1:B:37:LYS:H	1:D:413:HIS:HE1	1.53	0.54
1:D:393:MET:O	3:D:988:HOH:O	2.18	0.54
1:D:82:GLY:HA3	1:D:316:VAL:O	2.07	0.54
1:A:321:PRO:HG2	3:D:607:HOH:O	2.06	0.54
1:B:229:VAL:HG21	1:B:282:VAL:CG1	2.38	0.54
1:D:100:GLU:HB3	1:D:104:LYS:HD2	1.89	0.54
1:A:176:LYS:NZ	3:A:615:HOH:O	2.40	0.54
1:C:97:LYS:O	1:C:100:GLU:HB2	2.07	0.54
1:B:34:VAL:HG11	1:B:37:LYS:HB3	1.89	0.54
1:B:43:VAL:HG13	1:B:43:VAL:O	2.07	0.54
1:B:126:ARG:NH1	3:B:737:HOH:O	2.37	0.54
1:C:381:ARG:NH1	3:C:810:HOH:O	2.41	0.54
1:B:177:ASP:OD1	1:B:179:ASP:HB2	2.08	0.54
1:B:147:ASN:CG	2:B:1:HEM:HAC	2.29	0.54
1:D:393:MET:HA	3:D:753:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:393:MET:HB3	3:D:753:HOH:O	2.07	0.53
1:D:446:TYR:O	1:D:455:ARG:HD3	2.08	0.53
1:C:73:VAL:HG12	1:C:74:HIS:HD2	1.73	0.53
1:A:487:GLU:HA	1:A:490:SER:OG	2.09	0.53
1:B:125:VAL:HG22	3:B:643:HOH:O	2.08	0.53
1:B:126:ARG:NE	1:B:199:PHE:HA	2.22	0.53
1:C:92:ARG:CD	3:C:572:HOH:O	2.40	0.53
1:B:402:ASN:C	1:B:402:ASN:HD22	2.11	0.53
1:C:456:LYS:O	1:C:460:GLU:HG3	2.09	0.53
1:D:406:ASN:ND2	1:D:410:ALA:HB3	2.21	0.53
1:A:287:GLU:HA	1:A:290:ILE:HG12	1.91	0.53
1:A:485:HIS:CD2	1:A:487:GLU:HB3	2.44	0.53
1:B:147:ASN:ND2	2:B:1:HEM:HAC	2.24	0.53
1:A:13:HIS:HD2	3:A:594:HOH:O	1.91	0.53
1:A:223:ASN:HD21	1:A:227:GLU:HB2	1.74	0.53
1:B:154:ILE:HG13	1:B:349:MET:CE	2.39	0.53
1:B:428:VAL:O	1:B:428:VAL:HG23	2.09	0.52
1:D:487:GLU:O	1:D:491:ARG:HG3	2.08	0.52
1:C:92:ARG:HG3	1:C:92:ARG:NH1	2.24	0.52
1:C:19:ALA:O	1:C:20:ALA:HB3	2.08	0.52
1:B:4:ARG:HB2	1:B:4:ARG:NH1	2.25	0.52
3:A:869:HOH:O	1:C:409:SER:CB	2.39	0.52
1:C:43:VAL:O	1:C:43:VAL:HG13	2.08	0.52
1:D:338:MET:HE3	1:D:342:ILE:HG22	1.92	0.52
1:C:176:LYS:HE3	3:C:525:HOH:O	2.09	0.52
1:D:160:PHE:HB3	1:D:161:PRO:HD3	1.92	0.52
1:B:358:PRO:O	1:B:362:ARG:HG3	2.10	0.52
3:A:883:HOH:O	1:B:430:ARG:HG3	2.09	0.52
1:D:232:LYS:HB2	1:D:281:GLN:HG2	1.92	0.52
1:C:450:LEU:HA	1:C:454:GLN:NE2	2.25	0.52
1:C:402:ASN:HD22	1:C:402:ASN:C	2.13	0.52
1:D:74:HIS:CE1	1:D:115:VAL:HG22	2.44	0.52
1:A:155:ARG:HH11	1:A:155:ARG:CB	2.19	0.51
1:A:202:ARG:HH11	1:A:202:ARG:HG3	1.74	0.51
1:B:498:LYS:HD3	1:B:498:LYS:C	2.31	0.51
1:C:155:ARG:HH12	1:C:438:ASN:HD22	1.58	0.51
1:D:142:TRP:HB2	1:D:339:PRO:HD3	1.91	0.51
1:A:206:ASP:HB2	1:A:242:LYS:HD2	1.92	0.51
1:B:321:PRO:HG2	3:C:1280:HOH:O	2.08	0.51
1:C:92:ARG:NE	1:C:93:TYR:CE2	2.78	0.51
1:D:148:ASN:N	1:D:148:ASN:HD22	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:LYS:CG	3:A:939:HOH:O	2.41	0.51
1:D:43:VAL:CG1	1:D:48:PRO:HD2	2.40	0.51
1:A:495:LEU:CD2	3:A:978:HOH:O	2.58	0.51
1:B:138:GLU:CD	3:B:974:HOH:O	2.49	0.51
1:D:357:TYR:HB2	1:D:358:PRO:HD3	1.93	0.51
1:B:421:ARG:HG3	3:B:1071:HOH:O	2.10	0.51
1:A:387:ARG:O	1:C:66:GLU:HG2	2.10	0.51
1:D:280:ILE:HG23	1:D:312:VAL:HG21	1.91	0.51
1:C:443:ARG:HG2	1:C:484:VAL:O	2.11	0.51
1:B:466:LEU:CD2	1:B:474:GLN:HG2	2.31	0.51
1:B:490:SER:HA	3:B:1268:HOH:O	2.10	0.51
1:B:4:ARG:CB	1:B:4:ARG:HH11	2.23	0.51
1:D:12:LYS:CG	3:D:1056:HOH:O	2.51	0.51
1:D:249:ALA:HB3	3:D:1062:HOH:O	2.10	0.51
1:D:456:LYS:N	3:D:896:HOH:O	2.44	0.51
1:B:321:PRO:CG	3:C:1280:HOH:O	2.59	0.51
1:C:92:ARG:HG3	3:C:809:HOH:O	2.11	0.50
1:D:129:ARG:HG3	1:D:205:PRO:HG3	1.92	0.50
1:D:155:ARG:NH2	1:D:438:ASN:OD1	2.35	0.50
1:A:314:LYS:CE	3:A:939:HOH:O	2.58	0.50
1:B:129:ARG:HG2	1:B:211:MET:HE1	1.93	0.50
1:D:148:ASN:H	1:D:148:ASN:HD22	1.59	0.50
1:A:501:GLU:HA	1:A:501:GLU:OE1	2.10	0.50
1:A:74:HIS:HA	1:A:114:THR:O	2.11	0.50
1:A:177:ASP:OD1	1:A:179:ASP:HB2	2.11	0.50
1:A:148:ASN:H	1:A:148:ASN:HD22	1.59	0.50
1:B:251:ARG:O	1:B:255:GLU:HB2	2.11	0.50
1:A:35:GLY:HA2	1:C:414:GLN:O	2.10	0.50
1:A:43:VAL:O	1:A:47:GLY:HA3	2.12	0.50
1:B:453:GLU:OE2	1:B:457:ARG:NH1	2.45	0.50
1:B:475:LYS:NZ	1:B:475:LYS:HB3	2.26	0.50
1:A:155:ARG:NH1	1:A:297:ASP:OD1	2.44	0.50
1:B:466:LEU:HD13	1:B:496:LEU:HD11	1.94	0.50
1:C:445:PHE:CZ	1:C:450:LEU:HD11	2.46	0.50
1:B:10:GLN:NE2	1:C:172:GLN:HE21	2.10	0.50
1:C:243:ASN:ND2	3:C:697:HOH:O	2.45	0.50
1:C:452:GLU:OE1	1:C:452:GLU:HA	2.12	0.50
1:A:18:ARG:O	1:A:19:ALA:C	2.49	0.49
1:B:404:TYR:HE1	1:B:412:GLU:OE2	1.95	0.49
1:A:155:ARG:NH1	1:A:299:THR:OG1	2.40	0.49
1:A:456:LYS:O	1:A:460:GLU:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:HIS:HD2	1:B:299:THR:O	1.95	0.49
1:C:445:PHE:CE2	1:C:450:LEU:HD11	2.47	0.49
1:B:101:HIS:CE1	1:B:104:LYS:HB2	2.48	0.49
1:C:154:ILE:HD12	1:C:159:LEU:HB2	1.94	0.49
1:C:439:VAL:O	1:C:443:ARG:HG3	2.12	0.49
1:D:136:TYR:O	1:D:379:ARG:HG3	2.12	0.49
1:A:126:ARG:NH1	1:A:199:PHE:HA	2.26	0.49
1:B:262:ARG:HB3	3:B:1241:HOH:O	2.11	0.49
1:C:499:TYR:C	1:C:501:GLU:H	2.15	0.49
1:A:453:GLU:CG	1:A:457:ARG:HH12	2.25	0.49
1:B:148:ASN:HD22	1:B:211:MET:HE2	1.76	0.49
1:A:429:GLN:HB3	1:B:421:ARG:CD	2.31	0.49
1:D:18:ARG:HG3	1:D:21:GLN:HB2	1.94	0.49
1:C:206:ASP:OD2	1:C:242:LYS:NZ	2.45	0.49
1:C:286:SER:O	1:C:289:GLU:HB3	2.12	0.49
1:C:447:LEU:HD11	1:C:485:HIS:CD2	2.47	0.49
1:D:350:LEU:C	3:D:773:HOH:O	2.51	0.49
1:C:423:HIS:HA	1:D:427:ASP:HA	1.95	0.49
1:B:443:ARG:O	1:B:447:LEU:HG	2.13	0.48
1:A:421:ARG:C	1:A:421:ARG:HD2	2.33	0.48
1:B:125:VAL:HG22	1:B:126:ARG:N	2.28	0.48
1:C:248:ASP:CG	1:C:251:ARG:HH12	2.17	0.48
1:D:84:PHE:O	1:D:105:ARG:HA	2.13	0.48
1:B:237:THR:HA	1:B:276:TRP:CD1	2.48	0.48
1:B:373:PRO:CG	3:D:753:HOH:O	2.61	0.48
1:B:385:TYR:CE2	1:B:404:TYR:HB2	2.48	0.48
1:C:22:LYS:HD3	1:C:23:PRO:HD2	1.95	0.48
1:D:74:HIS:HA	1:D:114:THR:O	2.14	0.48
1:B:499:TYR:C	1:B:501:GLU:H	2.16	0.48
1:C:451:ASN:H	1:C:454:GLN:HE21	1.62	0.48
1:C:452:GLU:CG	3:C:769:HOH:O	2.44	0.48
1:A:129:ARG:H	1:A:148:ASN:ND2	2.11	0.48
1:C:82:GLY:HA3	1:C:316:VAL:O	2.13	0.48
1:D:145:VAL:HB	1:D:353:ARG:NH2	2.29	0.48
1:A:429:GLN:CB	1:B:421:ARG:HD2	2.32	0.48
1:A:104:LYS:HG3	3:A:542:HOH:O	2.13	0.48
1:B:71:ARG:HD2	1:B:111:ARG:HH21	1.77	0.48
1:A:419:GLU:CD	1:A:419:GLU:H	2.17	0.47
1:B:126:ARG:NH1	1:B:204:ILE:HG13	2.29	0.47
1:B:487:GLU:HG2	1:B:491:ARG:HD2	1.96	0.47
1:C:153:PHE:CZ	1:C:194:GLN:HG3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:351:GLN:HG3	3:D:744:HOH:O	2.14	0.47
1:D:410:ALA:HB1	1:D:411:PRO:HD2	1.95	0.47
1:D:444:THR:CB	3:D:1074:HOH:O	2.32	0.47
1:C:293:PHE:HE2	1:C:437:ASP:OD2	1.97	0.47
1:A:15:LYS:NZ	3:A:869:HOH:O	2.46	0.47
1:B:357:TYR:HB2	1:B:358:PRO:HD3	1.96	0.47
1:B:381:ARG:HH11	1:B:381:ARG:HG2	1.79	0.47
1:A:148:ASN:HD22	1:A:148:ASN:N	2.12	0.47
1:B:111:ARG:NH2	3:B:615:HOH:O	2.44	0.47
1:D:232:LYS:O	1:D:280:ILE:HA	2.14	0.47
1:B:62:HIS:CE1	1:D:368:ASN:HD21	2.17	0.47
1:C:414:GLN:NE2	3:C:1030:HOH:O	2.48	0.47
1:D:456:LYS:HG2	1:D:491:ARG:HH22	1.78	0.47
1:A:152:PHE:CD1	2:A:1:HEM:HMC3	2.49	0.47
1:C:101:HIS:CE1	3:C:770:HOH:O	2.67	0.47
1:A:220:LYS:HZ2	1:A:420:HIS:HB3	1.79	0.47
1:C:190:GLU:HA	1:C:438:ASN:ND2	2.29	0.47
1:D:274:PRO:HD2	1:D:317:LEU:O	2.14	0.47
1:C:429:GLN:OE1	1:D:421:ARG:HD2	2.15	0.47
1:D:145:VAL:HB	1:D:353:ARG:HH22	1.79	0.47
1:D:460:GLU:HA	1:D:495:LEU:HD13	1.95	0.47
1:A:92:ARG:HB3	3:A:597:HOH:O	2.15	0.47
1:B:271:GLY:HA2	1:B:273:TYR:CZ	2.50	0.47
1:B:4:ARG:HB2	1:B:4:ARG:HH11	1.79	0.47
1:C:432:ASN:HD21	1:C:434:ALA:CB	2.28	0.47
1:B:410:ALA:HB1	1:B:411:PRO:HD2	1.96	0.47
1:B:78:ALA:HB2	1:B:261:LEU:HD12	1.96	0.47
1:C:381:ARG:CB	1:C:381:ARG:HH11	2.26	0.47
1:D:72:VAL:HG13	1:D:73:VAL:HG22	1.96	0.47
1:A:97:LYS:NZ	3:A:1135:HOH:O	2.47	0.47
1:C:206:ASP:CA	1:C:244:LEU:HD22	2.45	0.47
1:A:242:LYS:HD3	1:A:243:ASN:N	2.31	0.46
1:B:232:LYS:HE2	1:B:302:TRP:CE2	2.50	0.46
1:B:410:ALA:HB1	1:B:411:PRO:CD	2.45	0.46
1:D:159:LEU:HD21	1:D:188:ARG:CZ	2.45	0.46
1:A:406:ASN:HD21	1:A:410:ALA:HB3	1.80	0.46
1:B:447:LEU:CD1	1:B:448:LYS:HE2	2.45	0.46
1:B:82:GLY:HA3	1:B:316:VAL:O	2.15	0.46
1:A:14:TRP:CH2	1:A:18:ARG:HD2	2.51	0.46
1:A:153:PHE:CE1	1:A:194:GLN:HG3	2.50	0.46
1:A:385:TYR:HE1	1:C:26:LEU:HD22	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:LEU:HD21	1:B:37:LYS:HD3	1.98	0.46
1:C:251:ARG:O	1:C:255:GLU:HG3	2.16	0.46
1:A:50:LEU:CD1	1:B:48:PRO:HB2	2.44	0.46
1:C:177:ASP:OD1	1:C:179:ASP:HB2	2.16	0.46
1:D:393:MET:CB	3:D:753:HOH:O	2.64	0.46
1:D:446:TYR:CZ	1:D:455:ARG:HD2	2.51	0.46
1:D:43:VAL:HG13	1:D:48:PRO:HD2	1.98	0.46
1:D:9:ASP:CG	3:D:609:HOH:O	2.54	0.46
1:A:275:SER:HA	1:A:315:LEU:O	2.15	0.46
1:B:445:PHE:HA	1:B:449:VAL:CG2	2.46	0.46
1:C:220:LYS:NZ	3:C:1236:HOH:O	2.48	0.46
1:A:451:ASN:H	1:A:454:GLN:NE2	2.12	0.46
1:A:51:VAL:HG21	1:B:49:LEU:HB3	1.97	0.46
1:B:193:HIS:HE1	3:B:650:HOH:O	1.98	0.46
1:B:229:VAL:HG23	1:B:284:THR:HA	1.97	0.46
1:B:471:LEU:HD21	1:B:500:ASN:ND2	2.31	0.46
1:C:437:ASP:N	3:C:678:HOH:O	2.48	0.46
1:D:126:ARG:NE	3:D:613:HOH:O	2.24	0.46
1:A:453:GLU:HG2	1:A:457:ARG:NH1	2.32	0.46
1:B:126:ARG:NH2	1:B:200:SER:O	2.49	0.46
1:D:274:PRO:HG2	1:D:317:LEU:HB2	1.97	0.45
1:A:235:TYR:N	1:A:235:TYR:CD1	2.84	0.45
1:A:485:HIS:HD2	1:A:487:GLU:N	2.09	0.45
1:B:14:TRP:O	1:B:17:GLN:HG2	2.17	0.45
1:C:26:LEU:HG	1:C:34:VAL:CG2	2.46	0.45
1:C:479:LYS:O	1:C:479:LYS:HD2	2.16	0.45
1:B:349:MET:O	1:B:353:ARG:HG3	2.16	0.45
1:C:248:ASP:HA	1:C:251:ARG:NH1	2.31	0.45
1:C:232:LYS:O	1:C:280:ILE:HA	2.15	0.45
1:D:479:LYS:O	1:D:479:LYS:HD3	2.16	0.45
1:D:222:VAL:HG22	1:D:341:GLY:HA2	1.99	0.45
1:B:25:VAL:CG1	1:D:414:GLN:HG3	2.40	0.45
1:D:479:LYS:C	1:D:479:LYS:HD3	2.37	0.45
1:B:217:HIS:CD2	1:B:353:ARG:HH11	2.35	0.45
1:A:232:LYS:HB2	1:A:281:GLN:HB2	1.97	0.45
1:A:217:HIS:CD2	1:A:353:ARG:HH11	2.34	0.45
1:B:37:LYS:HE2	1:B:59:GLU:OE1	2.16	0.45
1:B:408:PHE:HA	1:D:15:LYS:HD2	1.98	0.45
1:B:49:LEU:HD23	1:B:50:LEU:H	1.82	0.45
1:A:48:PRO:HB2	1:B:50:LEU:HD12	1.98	0.45
1:D:319:ARG:NH1	3:D:1137:HOH:O	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:VAL:CG2	3:B:643:HOH:O	2.64	0.45
1:B:81:PHE:HB2	1:B:319:ARG:NH1	2.31	0.45
1:C:452:GLU:N	1:C:455:ARG:NH2	2.64	0.45
1:D:107:PRO:HG2	1:D:136:TYR:HB2	1.99	0.45
1:A:147:ASN:CG	2:A:1:HEM:HAC	2.37	0.45
1:A:51:VAL:HG22	1:B:49:LEU:O	2.17	0.45
1:B:69:PRO:HG2	1:B:364:ARG:HA	1.98	0.45
1:B:446:TYR:CZ	1:B:455:ARG:HD2	2.52	0.45
1:B:213:GLY:HA3	1:B:235:TYR:CE2	2.52	0.45
1:B:84:PHE:O	1:B:105:ARG:HA	2.17	0.45
1:C:72:VAL:HG13	1:C:73:VAL:HG23	1.99	0.45
1:A:254:HIS:CE1	1:A:255:GLU:HG3	2.52	0.45
1:B:454:GLN:HE21	1:B:454:GLN:HB3	1.52	0.45
1:D:445:PHE:HA	1:D:449:VAL:CG2	2.47	0.45
1:D:445:PHE:CE1	1:D:449:VAL:HG11	2.51	0.45
1:B:12:LYS:HG3	3:C:1090:HOH:O	2.17	0.44
1:B:94:SER:HB2	1:B:221:LEU:HB3	1.99	0.44
1:B:268:ILE:HD12	1:B:268:ILE:N	2.32	0.44
1:B:6:PRO:HG2	1:B:266:ASN:OD1	2.17	0.44
1:C:450:LEU:HD12	1:C:450:LEU:N	2.32	0.44
1:D:309:LEU:C	1:D:310:ILE:HD12	2.38	0.44
1:B:52:GLN:HB2	3:D:503:HOH:O	2.16	0.44
1:D:193:HIS:HB2	3:D:511:HOH:O	2.16	0.44
1:D:43:VAL:O	1:D:47:GLY:HA3	2.17	0.44
1:B:145:VAL:HG22	1:B:333:PHE:HB3	1.99	0.44
1:C:89:ASP:OD1	1:C:91:THR:CG2	2.60	0.44
1:A:414:GLN:O	1:C:35:GLY:HA2	2.18	0.44
1:A:450:LEU:HA	1:A:454:GLN:NE2	2.33	0.44
1:D:338:MET:HE2	1:D:342:ILE:C	2.37	0.44
1:D:78:ALA:HB2	1:D:261:LEU:HG	2.00	0.44
1:B:74:HIS:HA	1:B:114:THR:O	2.17	0.44
1:B:206:ASP:HA	1:B:244:LEU:HG	1.99	0.44
1:C:437:ASP:C	3:C:678:HOH:O	2.56	0.44
1:B:223:ASN:ND2	1:B:227:GLU:HB2	2.32	0.44
1:B:154:ILE:HG13	1:B:349:MET:HE2	2.00	0.44
1:D:468:ASP:OD2	3:D:763:HOH:O	2.20	0.44
1:B:343:GLU:HB3	1:B:344:PRO:HD2	1.99	0.44
1:B:373:PRO:CD	3:D:753:HOH:O	2.66	0.44
1:C:410:ALA:HB1	1:C:411:PRO:CD	2.48	0.44
1:C:451:ASN:O	1:C:454:GLN:N	2.51	0.44
1:A:222:VAL:HG21	1:A:420:HIS:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:ASN:HD22	1:B:211:MET:CE	2.31	0.44
1:D:475:LYS:HE3	3:D:1277:HOH:O	2.17	0.44
1:A:165:HIS:HB3	1:B:402:ASN:ND2	2.32	0.43
1:C:126:ARG:HH11	1:C:126:ARG:HG2	1.83	0.43
1:D:206:ASP:OD2	1:D:242:LYS:HE2	2.18	0.43
1:B:124:THR:HG21	1:B:252:LEU:HD23	2.00	0.43
1:B:148:ASN:ND2	1:B:211:MET:HE2	2.34	0.43
1:A:51:VAL:CG2	1:B:49:LEU:HB3	2.48	0.43
1:C:213:GLY:HA3	1:C:235:TYR:CE2	2.54	0.43
1:D:293:PHE:CG	1:D:300:LYS:HD3	2.54	0.43
1:D:474:GLN:O	1:D:478:VAL:HG23	2.19	0.43
1:A:251:ARG:NH1	1:A:251:ARG:HB3	2.27	0.43
1:B:41:LEU:HD12	1:B:50:LEU:HB2	2.00	0.43
1:C:432:ASN:HD21	1:C:434:ALA:HB3	1.83	0.43
1:D:310:ILE:N	1:D:310:ILE:HD12	2.33	0.43
1:C:126:ARG:O	1:C:127:ASP:HB2	2.17	0.43
1:C:220:LYS:HE2	3:C:884:HOH:O	2.19	0.43
1:D:17:GLN:NE2	3:D:852:HOH:O	2.51	0.43
1:D:381:ARG:HG2	1:D:381:ARG:HH11	1.84	0.43
1:A:284:THR:OG1	1:A:287:GLU:HG3	2.18	0.43
1:A:410:ALA:HB1	1:A:411:PRO:HD2	2.00	0.43
1:A:442:VAL:HG12	1:A:484:VAL:HG11	2.00	0.43
1:B:12:LYS:CE	3:B:1023:HOH:O	2.66	0.43
1:D:456:LYS:HE2	3:D:919:HOH:O	2.18	0.43
1:D:73:VAL:HG11	1:D:164:ILE:HD12	2.00	0.43
1:A:126:ARG:O	1:A:127:ASP:HB2	2.18	0.43
1:B:100:GLU:HG3	1:B:101:HIS:HD2	1.83	0.43
1:C:470:GLN:HE21	1:C:470:GLN:HB2	1.58	0.43
1:A:467:LYS:HD3	1:A:499:TYR:CD1	2.54	0.43
1:A:384:ASN:HA	1:C:26:LEU:HD13	2.00	0.43
1:C:357:TYR:HB2	1:C:358:PRO:HD3	2.00	0.43
1:D:334:ASP:O	1:D:337:ASN:HB2	2.18	0.43
1:A:182:TRP:CD2	1:A:466:LEU:HD13	2.53	0.42
1:B:65:ARG:HD3	1:D:367:PRO:HG3	2.01	0.42
1:C:406:ASN:HD21	1:C:410:ALA:HB3	1.84	0.42
1:D:291:PHE:HA	1:D:292:PRO:HD3	1.91	0.42
1:B:100:GLU:HG3	1:B:101:HIS:CD2	2.54	0.42
1:B:404:TYR:CD1	1:B:405:PRO:HA	2.53	0.42
1:D:148:ASN:HA	1:D:212:ASN:O	2.18	0.42
1:B:97:LYS:O	1:B:100:GLU:HB2	2.20	0.42
1:B:319:ARG:CB	1:B:319:ARG:NH1	2.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:LEU:HD11	1:C:428:VAL:HG13	2.01	0.42
1:B:447:LEU:HD23	1:B:485:HIS:CD2	2.54	0.42
1:C:443:ARG:NE	1:C:484:VAL:O	2.52	0.42
1:D:251:ARG:O	1:D:255:GLU:HG3	2.18	0.42
1:D:177:ASP:OD1	1:D:179:ASP:HB2	2.20	0.42
1:B:262:ARG:HG2	1:B:266:ASN:ND2	2.35	0.42
1:B:454:GLN:CD	3:B:905:HOH:O	2.54	0.42
1:D:176:LYS:NZ	3:D:725:HOH:O	2.53	0.42
1:D:410:ALA:HB1	1:D:411:PRO:CD	2.49	0.42
1:A:110:VAL:HG22	1:A:133:VAL:HG22	2.02	0.42
1:A:145:VAL:HG22	1:A:333:PHE:HB3	2.01	0.42
1:A:410:ALA:HB1	1:A:411:PRO:CD	2.50	0.42
1:C:402:ASN:ND2	1:C:402:ASN:C	2.73	0.42
1:B:129:ARG:CG	1:B:211:MET:HE1	2.49	0.42
1:B:43:VAL:CG1	1:B:48:PRO:HD2	2.49	0.42
1:C:22:LYS:HD3	1:C:23:PRO:CD	2.49	0.42
1:A:429:GLN:HG3	1:A:431:PHE:CE2	2.54	0.42
1:B:229:VAL:HG21	1:B:282:VAL:HG13	2.02	0.42
3:B:637:HOH:O	1:C:70:GLU:HG2	2.19	0.42
1:D:237:THR:HA	1:D:276:TRP:CD1	2.55	0.42
1:D:445:PHE:O	1:D:449:VAL:HB	2.20	0.42
1:B:271:GLY:HA2	1:B:273:TYR:CE1	2.55	0.42
1:C:142:TRP:HB2	1:C:339:PRO:HD3	2.02	0.42
1:A:45:PRO:HD3	1:D:431:PHE:CE2	2.55	0.42
1:A:273:TYR:HA	1:A:274:PRO:HD3	1.80	0.42
1:A:402:ASN:HD22	1:A:402:ASN:C	2.23	0.42
1:A:448:LYS:HA	1:A:448:LYS:CE	2.45	0.42
1:B:367:PRO:HD2	1:B:390:PRO:HG2	2.01	0.42
1:A:136:TYR:O	1:A:379:ARG:HG3	2.19	0.41
1:A:451:ASN:O	1:A:455:ARG:HG3	2.20	0.41
1:A:499:TYR:C	1:A:501:GLU:N	2.74	0.41
1:B:291:PHE:CD1	1:B:292:PRO:HD2	2.55	0.41
1:B:85:GLU:OE2	1:B:105:ARG:NE	2.45	0.41
1:C:209:ARG:O	1:C:239:GLN:CG	2.65	0.41
1:D:499:TYR:C	1:D:501:GLU:H	2.23	0.41
1:A:18:ARG:HH11	1:A:18:ARG:HG2	1.85	0.41
1:B:385:TYR:CD2	1:B:404:TYR:HB2	2.55	0.41
1:D:473:ILE:HA	1:D:476:LYS:CE	2.50	0.41
1:B:374:VAL:CG2	3:B:517:HOH:O	2.40	0.41
1:C:452:GLU:H	1:C:455:ARG:NH2	2.18	0.41
1:B:126:ARG:HH21	1:B:199:PHE:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:212:ASN:OD1	1:B:236:LYS:HA	2.20	0.41
1:C:499:TYR:CE2	3:C:1036:HOH:O	2.71	0.41
1:C:500:ASN:O	1:C:501:GLU:C	2.59	0.41
1:C:74:HIS:HA	1:C:114:THR:O	2.20	0.41
1:D:147:ASN:ND2	2:D:1:HEM:HAC	2.35	0.41
1:A:81:PHE:HE1	1:A:321:PRO:HB3	1.85	0.41
1:C:294:ASN:HB3	1:C:297:ASP:HB2	2.03	0.41
1:B:414:GLN:O	1:D:35:GLY:HA2	2.20	0.41
1:B:38:LEU:HG	1:D:413:HIS:CE1	2.56	0.41
1:A:155:ARG:HH12	1:A:299:THR:CB	2.33	0.41
1:A:232:LYS:O	1:A:280:ILE:HA	2.20	0.41
1:A:367:PRO:HG3	1:C:65:ARG:HD3	2.02	0.41
1:B:18:ARG:O	1:B:19:ALA:C	2.58	0.41
1:C:148:ASN:HA	1:C:212:ASN:O	2.21	0.41
1:D:218:THR:HG23	1:D:302:TRP:CZ2	2.56	0.41
1:B:158:LEU:HD11	1:B:430:ARG:HH21	1.84	0.41
1:B:467:LYS:HD3	1:B:499:TYR:CD1	2.56	0.41
1:D:476:LYS:HE3	1:D:476:LYS:HB2	1.83	0.41
1:B:43:VAL:O	1:B:47:GLY:HA3	2.21	0.41
1:B:451:ASN:OD1	1:B:454:GLN:HG2	2.20	0.41
1:C:177:ASP:HA	1:C:178:PRO:HD2	1.94	0.41
1:C:155:ARG:CZ	1:C:438:ASN:HD21	2.31	0.41
1:A:471:LEU:O	1:A:475:LYS:HG3	2.21	0.41
1:B:456:LYS:HD3	1:B:456:LYS:O	2.21	0.41
1:A:106:THR:HA	1:A:107:PRO:HD3	1.94	0.41
1:B:142:TRP:HB2	1:B:339:PRO:HD3	2.02	0.41
1:D:192:LEU:HD13	1:D:484:VAL:CG2	2.51	0.41
1:D:419:GLU:H	1:D:419:GLU:CD	2.23	0.41
1:D:83:TYR:CD1	1:D:83:TYR:C	2.95	0.41
1:B:95:LYS:NZ	3:B:778:HOH:O	2.52	0.40
1:A:223:ASN:ND2	1:A:227:GLU:HB2	2.36	0.40
1:B:34:VAL:HG11	1:B:37:LYS:CB	2.51	0.40
1:B:474:GLN:O	1:B:478:VAL:HG23	2.20	0.40
1:C:74:HIS:CE1	1:C:115:VAL:HG22	2.56	0.40
1:C:414:GLN:HA	1:C:414:GLN:OE1	2.20	0.40
1:C:453:GLU:O	1:C:457:ARG:NH1	2.55	0.40
1:D:223:ASN:OD1	1:D:225:ASN:HB2	2.21	0.40
1:D:426:GLY:HA3	3:D:768:HOH:O	2.21	0.40
1:A:291:PHE:HA	1:A:292:PRO:HD3	1.90	0.40
1:A:52:GLN:HB2	3:C:550:HOH:O	2.20	0.40
1:B:71:ARG:CZ	1:B:111:ARG:HE	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:29:GLY:HA3	3:C:515:HOH:O	2.22	0.40
1:C:414:GLN:HA	1:C:415:PRO:HD2	1.92	0.40
1:D:319:ARG:HH11	1:D:319:ARG:HG2	1.86	0.40
1:D:422:THR:HG22	1:D:423:HIS:N	2.36	0.40
1:A:294:ASN:HB3	1:A:297:ASP:HB2	2.03	0.40
1:B:452:GLU:OE2	1:B:491:ARG:NH1	2.52	0.40
1:C:437:ASP:CA	3:C:678:HOH:O	2.69	0.40
1:C:459:CYS:HB3	1:C:492:ILE:HD13	2.02	0.40
1:D:129:ARG:H	1:D:148:ASN:ND2	2.20	0.40
1:D:177:ASP:HA	1:D:178:PRO:HD2	1.92	0.40
1:A:251:ARG:CB	1:A:251:ARG:HH11	2.28	0.40
1:A:349:MET:O	1:A:353:ARG:HG3	2.21	0.40
1:C:283:MET:SD	1:C:288:ALA:HA	2.61	0.40
1:D:337:ASN:HD22	1:D:337:ASN:HA	1.68	0.40

All (1) 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)
3:B:943:HOH:O	3:C:823:HOH:O[3_555]	1.87	0.33

## 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	498/499 (100%)	475 (95%)	19 (4%)	4 (1%)	19	9
1	B	498/499 (100%)	470 (94%)	24 (5%)	4 (1%)	19	9
1	C	498/499 (100%)	469 (94%)	25 (5%)	4 (1%)	19	9
1	D	498/499 (100%)	468 (94%)	27 (5%)	3 (1%)	25	15
All	All	1992/1996 (100%)	1882 (94%)	95 (5%)	15 (1%)	19	9



All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ALA
1	A	437	ASP
1	C	437	ASP
1	B	437	ASP
1	C	19	ALA
1	D	19	ALA
1	D	437	ASP
1	A	500	ASN
1	B	500	ASN
1	C	452	GLU
1	C	500	ASN
1	A	100	GLU
1	B	19	ALA
1	B	100	GLU
1	D	373	PRO

### 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	432/431 (100%)	420 (97%)	12 (3%)	43	36
1	B	432/431 (100%)	414 (96%)	18 (4%)	30	20
1	C	432/431 (100%)	417 (96%)	15 (4%)	36	27
1	D	432/431 (100%)	424 (98%)	8 (2%)	57	53
All	All	1728/1724 (100%)	1675 (97%)	53 (3%)	40	32

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
1	A	49	LEU
1	A	131	PHE
1	A	137	THR
1	A	148	ASN

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Mol	Chain	Res	Type
1	A	155	ARG
1	A	235	TYR
1	A	402	ASN
1	A	413	HIS
1	A	421	ARG
1	A	448	LYS
1	A	488	TYR
1	B	37	LYS
1	B	67	ARG
1	B	126	ARG
1	B	129	ARG
1	B	131	PHE
1	B	193	HIS
1	B	235	TYR
1	B	255	GLU
1	B	272	ASN
1	B	290	ILE
1	B	319	ARG
1	B	393	MET
1	B	396	ASN
1	B	402	ASN
1	B	413	HIS
1	B	454	GLN
1	B	466	LEU
1	B	488	TYR
1	C	4	ARG
1	C	26	LEU
1	C	92	ARG
1	C	129	ARG
1	C	131	PHE
1	C	137	THR
1	C	235	TYR
1	C	239	GLN
1	C	248	ASP
1	C	304	HIS
1	C	381	ARG
1	C	402	ASN
1	C	413	HIS
1	C	483	ASP
1	C	488	TYR
1	D	73	VAL
1	D	131	PHE

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Mol	Chain	Res	Type
1	D	148	ASN
1	D	235	TYR
1	D	247	GLU
1	D	373	PRO
1	D	412	GLU
1	D	488	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	HIS
1	A	17	GLN
1	A	148	ASN
1	A	320	ASN
1	A	337	ASN
1	A	402	ASN
1	A	420	HIS
1	A	454	GLN
1	A	465	HIS
1	A	485	HIS
1	A	500	ASN
1	B	13	HIS
1	B	17	GLN
1	B	62	HIS
1	B	193	HIS
1	B	210	HIS
1	B	254	HIS
1	B	272	ASN
1	B	337	ASN
1	B	396	ASN
1	B	402	ASN
1	B	454	GLN
1	B	461	ASN
1	B	500	ASN
1	C	3	ASN
1	C	21	GLN
1	C	88	HIS
1	C	172	GLN
1	C	210	HIS
1	C	225	ASN
1	C	243	ASN
1	C	272	ASN

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Mol	Chain	Res	Type
1	C	337	ASN
1	C	402	ASN
1	C	432	ASN
1	C	438	ASN
1	C	454	GLN
1	C	461	ASN
1	C	470	GLN
1	C	474	GLN
1	C	480	ASN
1	C	500	ASN
1	D	17	GLN
1	D	148	ASN
1	D	170	ASN
1	D	193	HIS
1	D	337	ASN
1	D	363	HIS
1	D	368	ASN
1	D	413	HIS
1	D	420	HIS
1	D	429	GLN
1	D	470	GLN
1	D	500	ASN

### 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](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	HEM	B	1	1	27,50,50	1.61	6 (22%)	17,82,82	0.91	1 (5%)
2	HEM	A	1	1	27,50,50	1.68	8 (29%)	17,82,82	1.24	2 (11%)
2	HEM	D	1	1	27,50,50	1.72	8 (29%)	17,82,82	1.04	1 (5%)
2	HEM	C	1	1	27,50,50	1.61	6 (22%)	17,82,82	1.32	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	B	1	1	-	0/6/54/54	-
2	HEM	A	1	1	-	0/6/54/54	-
2	HEM	D	1	1	-	0/6/54/54	-
2	HEM	C	1	1	-	0/6/54/54	-

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	HEM	C3B-CAB	-3.96	1.39	1.47
2	D	1	HEM	C3C-CAC	-3.36	1.40	1.47
2	B	1	HEM	C3B-CAB	-3.34	1.41	1.47
2	C	1	HEM	C3C-CAC	-3.32	1.41	1.47
2	A	1	HEM	C3C-CAC	-3.28	1.41	1.47
2	A	1	HEM	C3B-CAB	-3.17	1.41	1.47
2	B	1	HEM	C3C-CAC	-3.11	1.41	1.47
2	C	1	HEM	C3B-CAB	-3.01	1.41	1.47
2	B	1	HEM	C4B-NB	2.99	1.42	1.36
2	A	1	HEM	C3C-C2C	-2.92	1.36	1.40
2	D	1	HEM	CBC-CAC	2.65	1.46	1.29
2	A	1	HEM	C3B-C2B	-2.58	1.36	1.40
2	D	1	HEM	C3C-C2C	-2.56	1.36	1.40
2	D	1	HEM	CBB-CAB	2.52	1.46	1.29
2	C	1	HEM	CBC-CAC	2.50	1.45	1.29
2	C	1	HEM	CBB-CAB	2.46	1.45	1.29
2	B	1	HEM	CBB-CAB	2.43	1.45	1.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	HEM	C3C-C2C	-2.41	1.37	1.40
2	B	1	HEM	CBC-CAC	2.40	1.45	1.29
2	A	1	HEM	CBC-CAC	2.39	1.45	1.29
2	D	1	HEM	C1D-ND	2.37	1.41	1.36
2	A	1	HEM	CBB-CAB	2.34	1.44	1.29
2	A	1	HEM	C1D-ND	2.28	1.40	1.36
2	C	1	HEM	CAA-C2A	2.23	1.55	1.52
2	D	1	HEM	C3B-C2B	-2.22	1.37	1.40
2	B	1	HEM	C1C-C2C	2.19	1.47	1.42
2	A	1	HEM	C1C-C2C	2.12	1.47	1.42
2	D	1	HEM	C1C-C2C	2.07	1.47	1.42

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	HEM	C4C-C3C-C2C	-2.89	104.88	106.90
2	A	1	HEM	C1D-C2D-C3D	-2.68	105.13	107.00
2	B	1	HEM	CMB-C2B-C3B	2.07	128.54	124.68
2	C	1	HEM	CMB-C2B-C3B	2.06	128.54	124.68
2	D	1	HEM	C4A-C3A-C2A	2.06	108.43	107.00

There are no chirality outliers.

There are no torsion outliers.

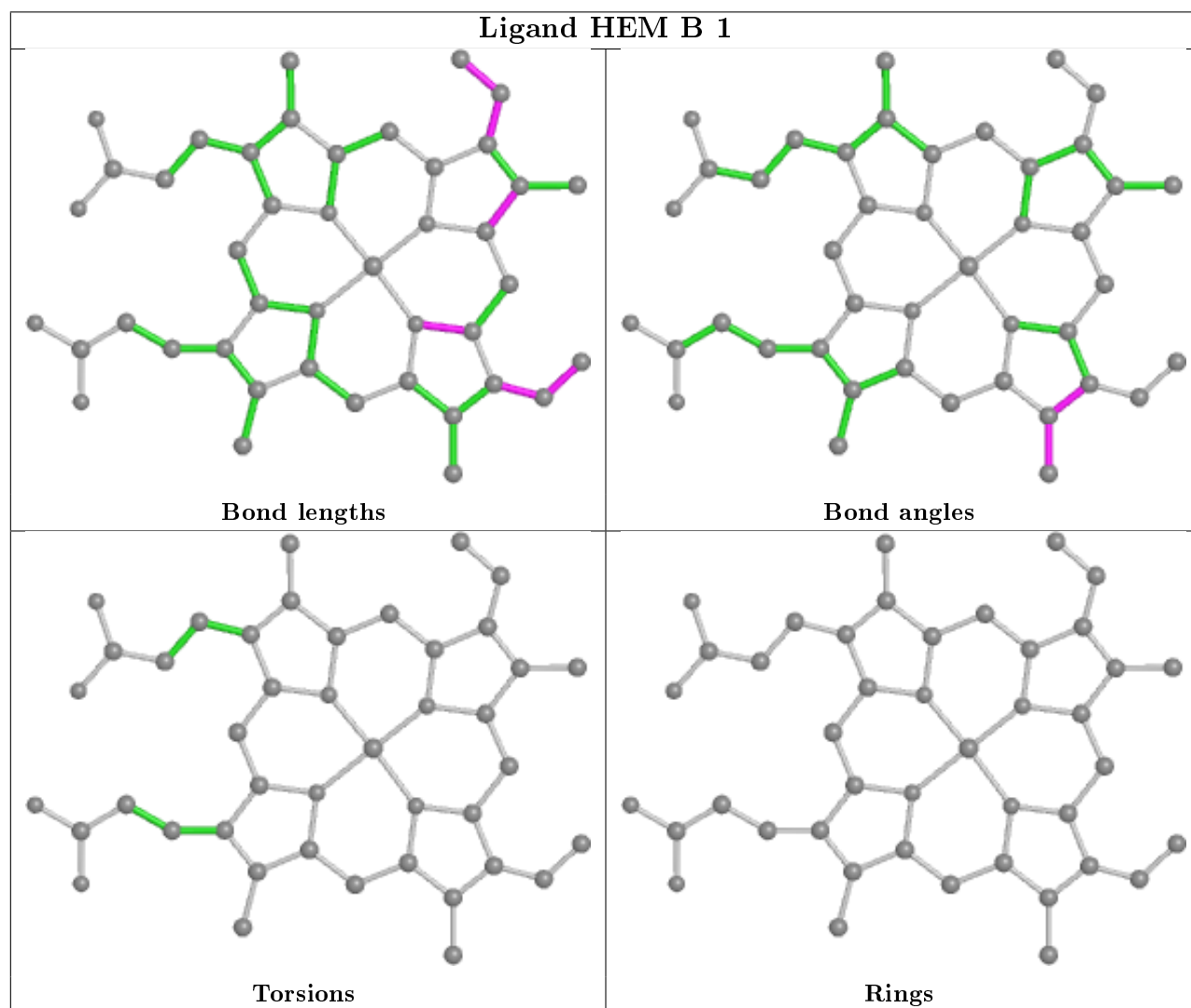
There are no ring outliers.

3 monomers are involved in 5 short contacts:

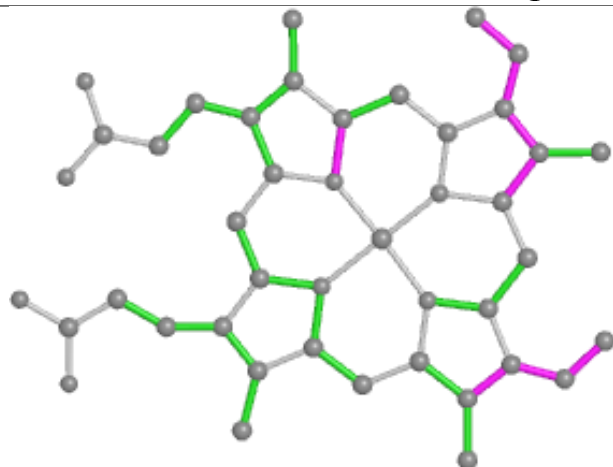
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	HEM	2	0
2	A	1	HEM	2	0
2	D	1	HEM	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

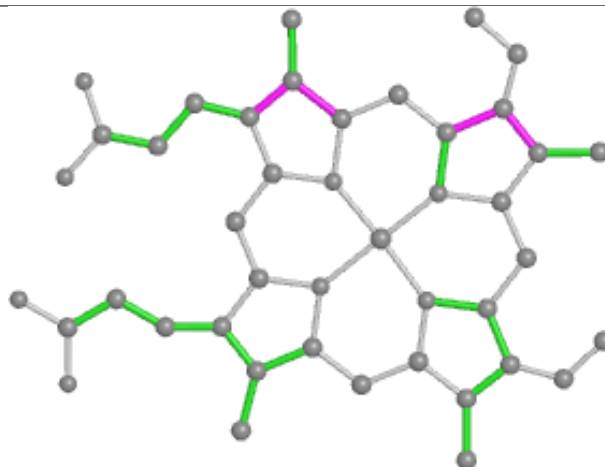
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



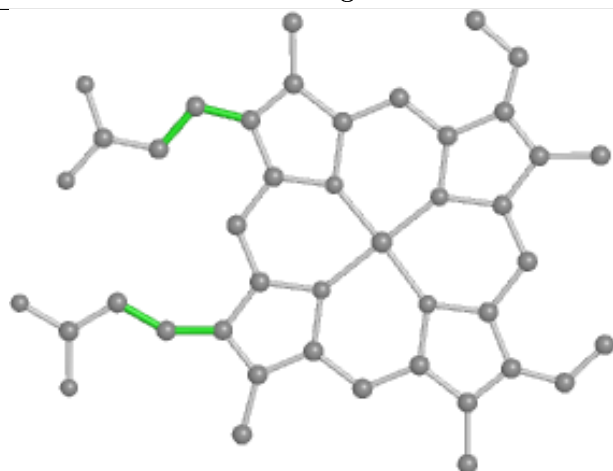
## Ligand HEM A 1



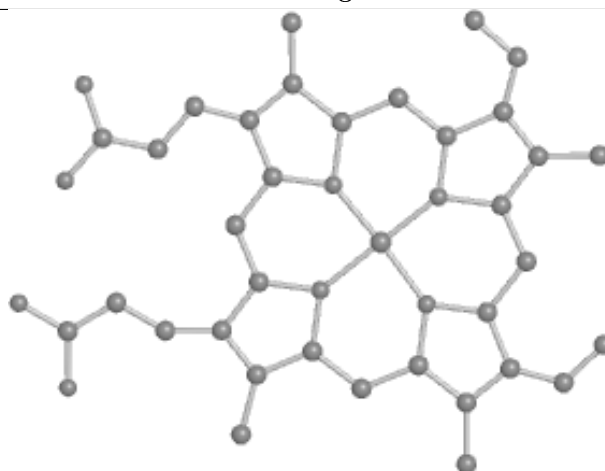
Bond lengths



Bond angles



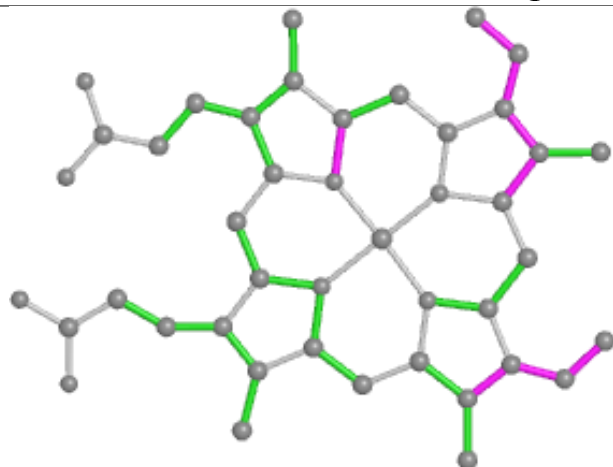
Torsions



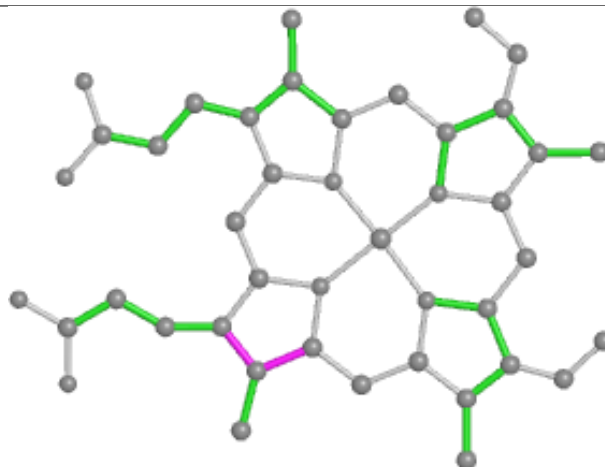
Rings



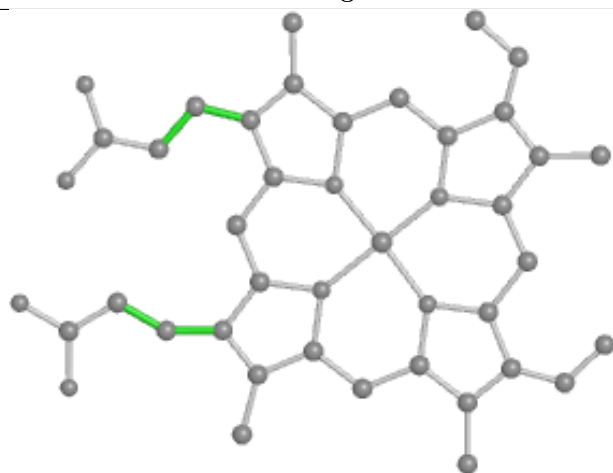
## Ligand HEM D 1



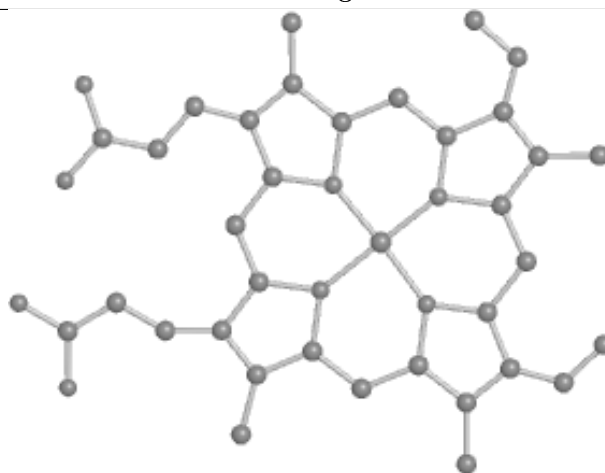
Bond lengths



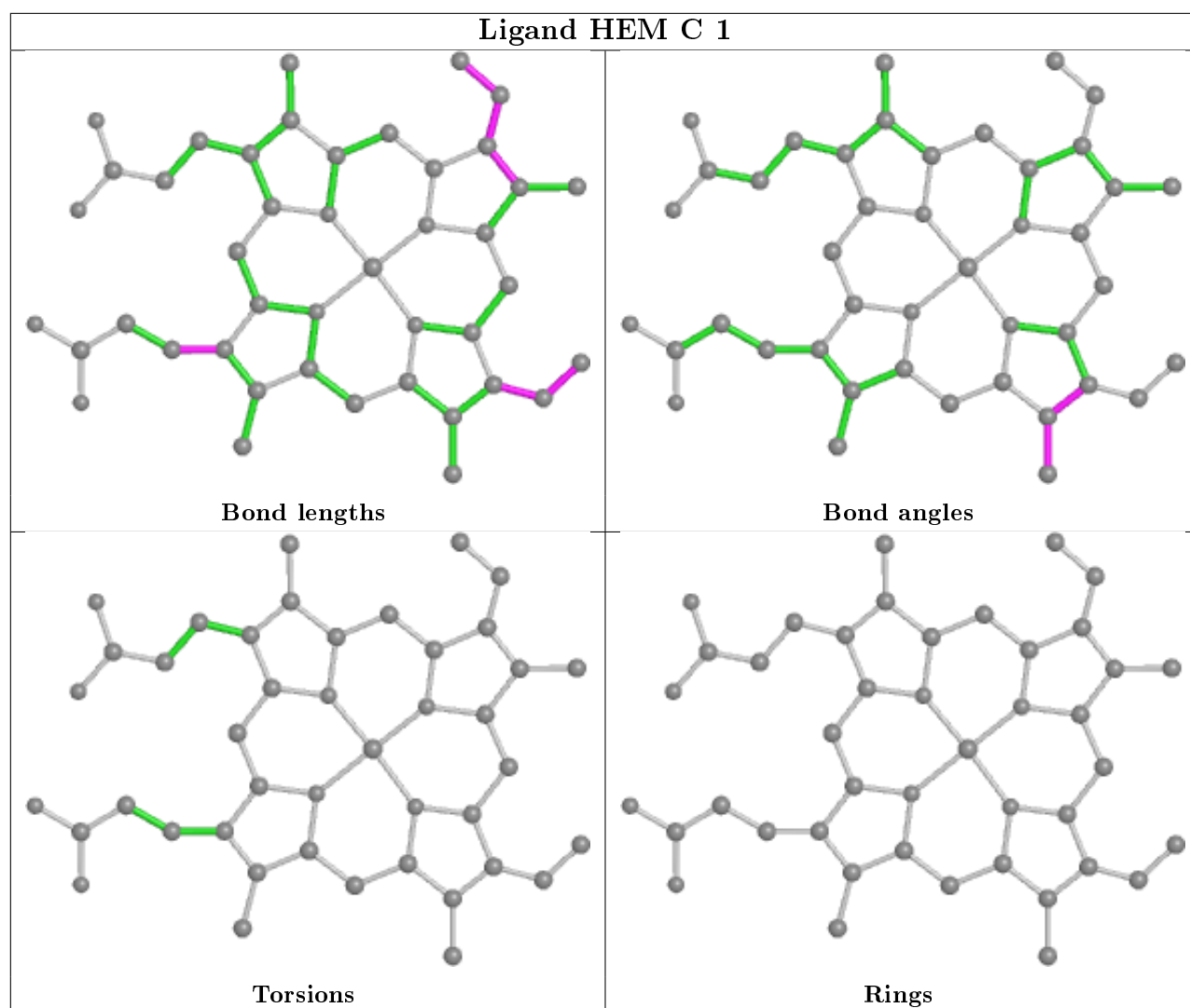
Bond angles



Torsions



Rings



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	499/499 (100%)	0.14	12 (2%) 59 62	12, 24, 39, 61	0
1	B	499/499 (100%)	0.22	23 (4%) 32 35	12, 25, 42, 60	0
1	C	499/499 (100%)	0.20	21 (4%) 36 39	12, 23, 43, 78	0
1	D	499/499 (100%)	0.35	21 (4%) 36 39	11, 28, 43, 73	0
All	All	1996/1996 (100%)	0.23	77 (3%) 39 42	11, 25, 42, 78	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	20	ALA	6.2
1	C	20	ALA	5.8
1	B	449	VAL	5.0
1	D	19	ALA	4.7
1	B	19	ALA	4.7
1	B	20	ALA	4.5
1	C	3	ASN	4.5
1	C	501	GLU	4.4
1	A	3	ASN	4.3
1	C	499	TYR	4.3
1	D	499	TYR	4.2
1	C	19	ALA	4.2
1	D	394	MET	4.1
1	D	20	ALA	3.9
1	D	290	ILE	3.8
1	B	501	GLU	3.6
1	B	3	ASN	3.6
1	D	17	GLN	3.5
1	C	22	LYS	3.5
1	C	421	ARG	3.4
1	B	22	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	C	453	GLU	3.4
1	D	3	ASN	3.2
1	B	499	TYR	3.2
1	D	501	GLU	3.1
1	D	494	ALA	3.1
1	C	496	LEU	3.0
1	C	498	LYS	2.9
1	B	17	GLN	2.9
1	C	471	LEU	2.8
1	C	21	GLN	2.8
1	D	18	ARG	2.8
1	A	225	ASN	2.7
1	A	19	ALA	2.7
1	A	17	GLN	2.7
1	A	498	LYS	2.6
1	D	498	LYS	2.6
1	A	500	ASN	2.6
1	B	304	HIS	2.6
1	D	152	PHE	2.6
1	C	448	LYS	2.6
1	A	499	TYR	2.5
1	B	23	PRO	2.5
1	A	247	GLU	2.5
1	C	500	ASN	2.5
1	D	21	GLN	2.5
1	D	225	ASN	2.5
1	B	21	GLN	2.5
1	B	4	ARG	2.4
1	C	23	PRO	2.4
1	B	498	LYS	2.4
1	D	271	GLY	2.3
1	A	102	ILE	2.3
1	B	18	ARG	2.3
1	C	456	LYS	2.3
1	C	304	HIS	2.3
1	B	500	ASN	2.3
1	D	272	ASN	2.2
1	C	489	GLY	2.2
1	B	416	SER	2.2
1	B	453	GLU	2.2
1	C	450	LEU	2.2
1	D	226	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	92	ARG	2.2
1	B	452	GLU	2.2
1	A	290	ILE	2.2
1	A	381	ARG	2.1
1	B	456	LYS	2.1
1	B	16	GLU	2.1
1	C	485	HIS	2.1
1	B	450	LEU	2.1
1	D	246	VAL	2.1
1	D	270	THR	2.1
1	D	414	GLN	2.0
1	B	25	VAL	2.0
1	B	241	ILE	2.0
1	D	443	ARG	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

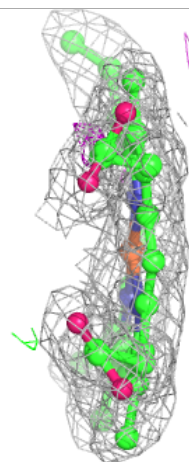
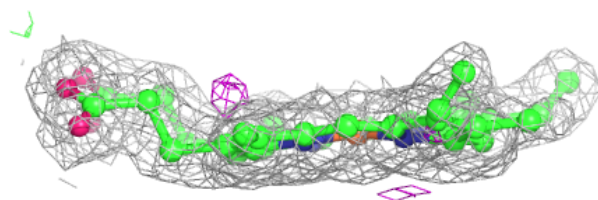
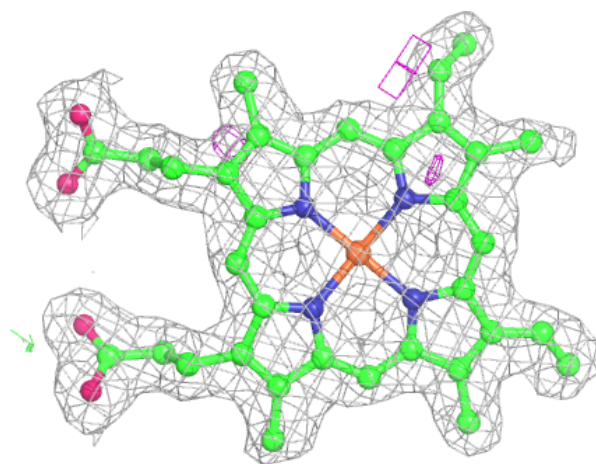
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	HEM	B	1	43/43	0.98	0.12	13,19,23,26	0
2	HEM	A	1	43/43	0.98	0.14	15,19,23,25	0
2	HEM	D	1	43/43	0.98	0.13	13,21,25,26	0
2	HEM	C	1	43/43	0.98	0.14	12,18,23,24	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.

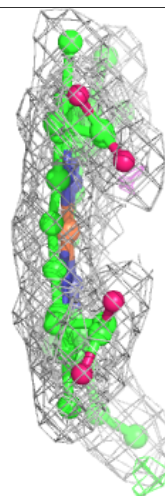
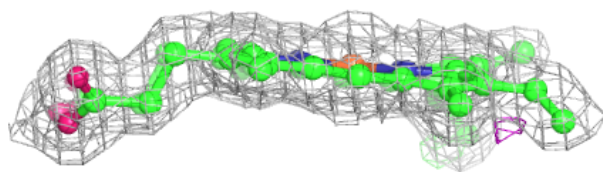
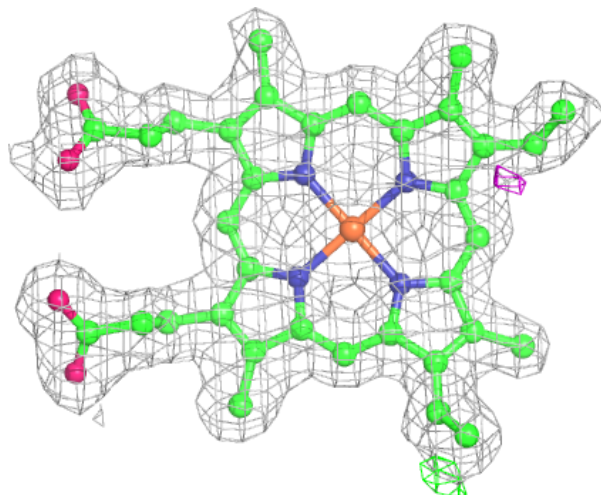
**Electron density around HEM B 1:**

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



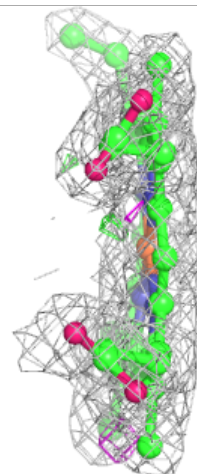
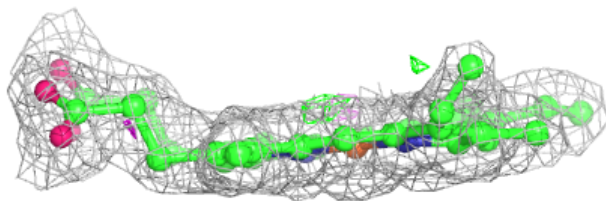
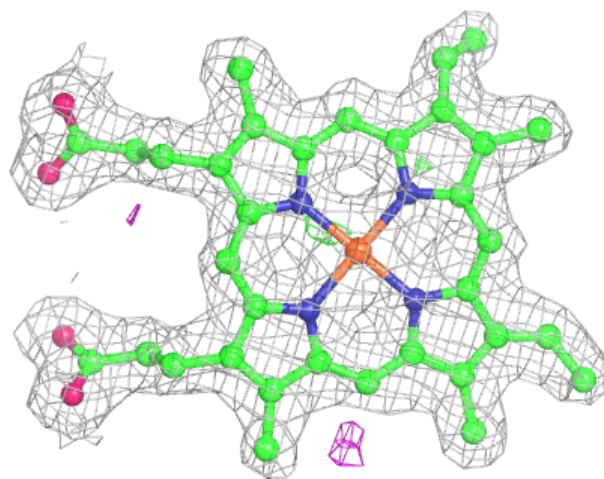
**Electron density around HEM A 1:**

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

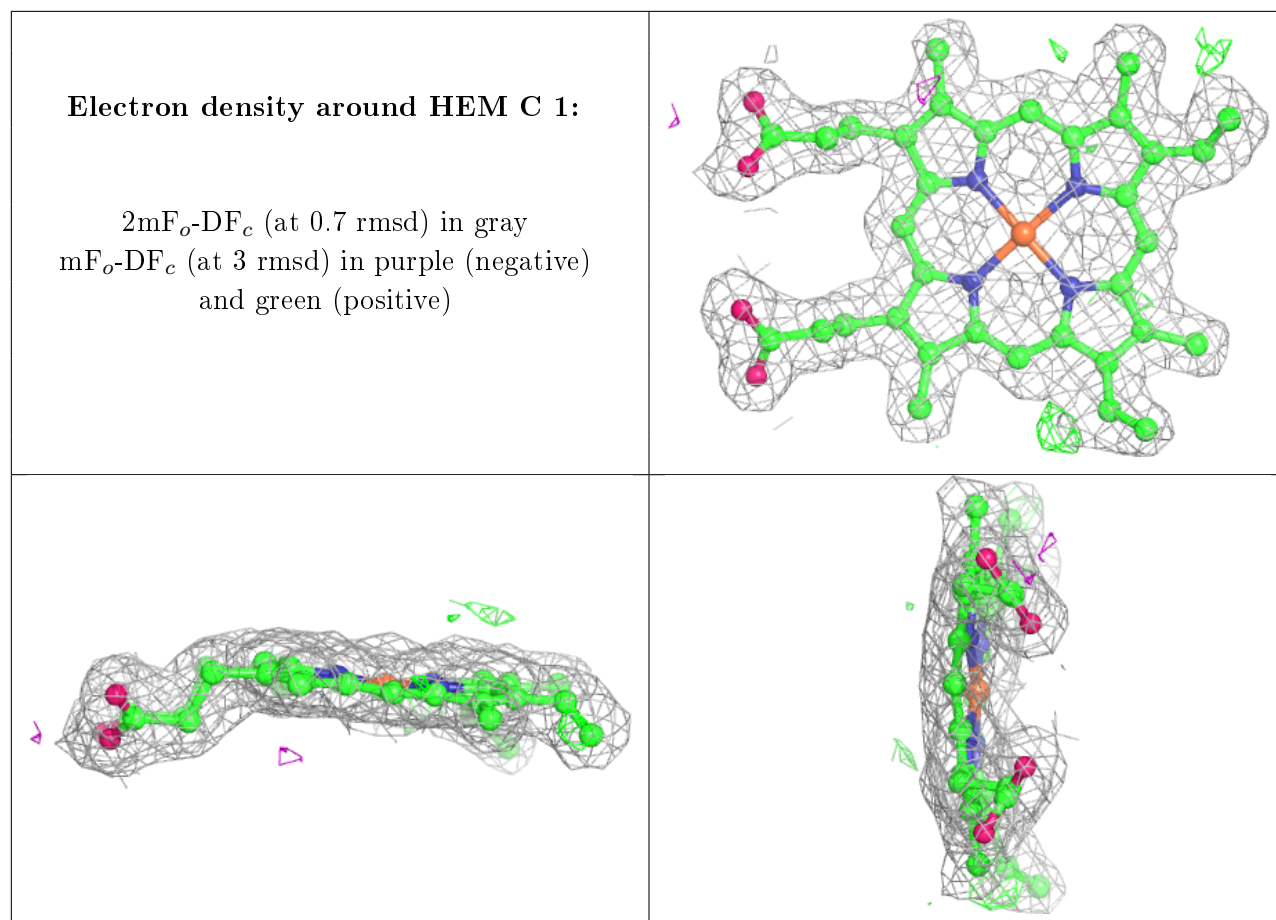


**Electron density around HEM D 1:**

$2mF_o-DF_c$  (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.