



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 09:46 am GMT

PDB ID : 3QI8  
Title : Evolved variant of cytochrome P450 (BM3, CYP102A1)  
Authors : Rentmeister, A.; Brown, T.R.; Snow, C.D.; Carbone, M.N.; Arnold, F.H.  
Deposited on : 2011-01-26  
Resolution : 3.20 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

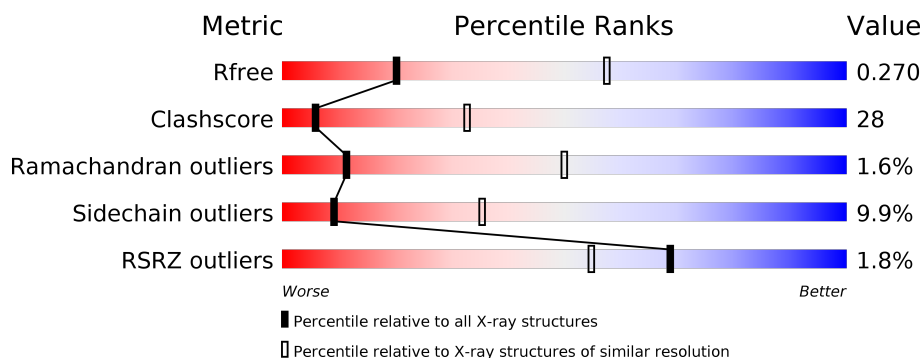
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	100719	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)

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. 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	472	<div> <div>3%</div> <div> <div></div> <div>47%</div> <div>38%</div> <div>5%</div> <div>10%</div> </div> </div>
1	B	472	<div> <div>47%</div> <div>42%</div> <div>6%</div> <div>•</div> </div>

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7080 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 Evolved Cytochrome P450 variant (22A3).

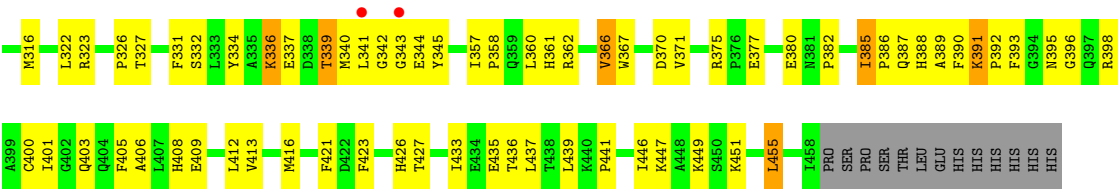
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	452	Total	C	N	O	S	0	0	0
			3626	2310	626	672	18			
1	A	424	Total	C	N	O	S	0	0	0
			3368	2153	576	621	18			

- 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		





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.35Å 83.77Å 143.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.38 – 3.20 45.38 – 3.10	Depositor EDS
% Data completeness (in resolution range)	95.5 (45.38-3.20) 95.3 (45.38-3.10)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.70 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.208 , 0.274 0.195 , 0.270	Depositor DCC
$R_{free}$ test set	839 reflections (5.20%)	DCC
Wilson B-factor (Å <sup>2</sup> )	66.2	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 65.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.038 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7080	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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	0.46	0/3440	0.71	4/4650 (0.1%)
1	B	0.48	0/3706	0.71	3/5007 (0.1%)
All	All	0.47	0/7146	0.71	7/9657 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	ARG	NE-CZ-NH1	-12.98	113.81	120.30
1	B	106	ARG	NE-CZ-NH2	-12.47	114.06	120.30
1	B	106	ARG	NE-CZ-NH1	11.73	126.16	120.30
1	A	106	ARG	NE-CZ-NH2	11.37	125.99	120.30
1	A	106	ARG	CD-NE-CZ	6.39	132.55	123.60
1	B	106	ARG	CD-NE-CZ	5.97	131.95	123.60
1	A	455	LEU	N-CA-C	-5.50	96.15	111.00

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	3368	0	3343	187	0
1	B	3626	0	3597	222	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	43	0	30	5	0
2	B	43	0	30	6	0
All	All	7080	0	7000	390	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 28.

All (390) 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:B:95:ASN:ND2	1:B:95:ASN:H	1.56	1.01
1:A:223:ARG:HH22	1:A:229:GLN:HA	1.25	0.98
1:B:95:ASN:HD22	1:B:95:ASN:N	1.58	0.95
1:B:428:ASN:HB2	1:A:312:LYS:HG2	1.49	0.94
1:A:122:ILE:HG22	1:A:148:LEU:HD12	1.49	0.94
1:B:151:ASP:OD1	1:B:164:SER:HB2	1.67	0.93
2:B:472:HEM:HHD	2:B:472:HEM:HBC2	1.52	0.90
2:B:472:HEM:HHC	2:B:472:HEM:HBB2	1.53	0.90
1:B:253:ASN:HA	1:B:256:TYR:HD2	1.39	0.88
1:B:122:ILE:HG22	1:B:148:LEU:HD12	1.56	0.88
1:B:190:ARG:HG2	1:B:198:TYR:CZ	2.10	0.86
1:A:33:ALA:HB2	1:A:40:PHE:CE1	2.12	0.85
1:B:442:LYS:CE	1:A:110:GLN:HG3	2.07	0.85
1:A:151:ASP:OD1	1:A:164:SER:HB2	1.77	0.84
1:A:253:ASN:HA	1:A:256:TYR:HD2	1.41	0.84
1:B:428:ASN:HD22	1:A:312:LYS:HE3	1.42	0.84
1:A:272:LEU:HD13	1:A:322:LEU:HG	1.61	0.83
1:A:97:LYS:HD3	1:A:101:ASN:ND2	1.93	0.82
1:B:33:ALA:HB2	1:B:40:PHE:CE1	2.14	0.82
1:B:272:LEU:HD13	1:B:322:LEU:HG	1.60	0.82
1:A:173:PHE:CD1	1:A:215:LEU:HD23	2.14	0.82
1:B:95:ASN:HD22	1:B:95:ASN:H	0.81	0.79
1:B:86:LEU:HD21	1:B:100:ARG:HB2	1.64	0.79
1:B:35:GLU:CA	1:A:65:SER:HB3	2.12	0.78
1:B:205:PHE:CE2	1:B:209:ILE:HD11	2.18	0.78
1:B:35:GLU:CB	1:A:65:SER:HB3	2.14	0.78
1:B:216:VAL:HG13	1:B:258:ILE:HG21	1.67	0.77
1:B:173:PHE:CD1	1:B:215:LEU:HD23	2.19	0.77
1:A:262:LEU:O	1:A:266:HIS:HD2	1.69	0.76
1:B:97:LYS:HD3	1:B:101:ASN:ND2	2.01	0.75
1:B:241:LYS:HD2	1:B:248:PRO:HG3	1.68	0.75

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:LYS:O	1:A:102:ILE:HG13	1.87	0.75
1:A:140:GLU:HB3	1:A:143:GLU:OE1	1.86	0.74
1:A:33:ALA:HB2	1:A:40:PHE:HE1	1.52	0.74
1:B:189:GLN:HE21	1:A:243:PRO:HB3	1.51	0.74
1:B:140:GLU:HB3	1:B:143:GLU:OE1	1.88	0.74
1:B:262:LEU:O	1:B:266:HIS:HD2	1.69	0.74
1:B:442:LYS:HE2	1:A:110:GLN:HG3	1.68	0.74
1:B:189:GLN:NE2	1:A:243:PRO:HB3	2.01	0.73
1:A:148:LEU:HD21	1:A:413:VAL:HG21	1.70	0.73
1:B:33:ALA:HB2	1:B:40:PHE:HE1	1.54	0.72
1:A:206:GLN:HA	1:A:206:GLN:NE2	2.06	0.71
1:A:203:ARG:HH11	1:A:203:ARG:HG2	1.55	0.71
1:B:428:ASN:ND2	1:A:312:LYS:HE3	2.05	0.71
1:B:98:LYS:O	1:B:102:ILE:HG13	1.91	0.71
1:B:148:LEU:HD21	1:B:413:VAL:HG21	1.72	0.71
1:A:223:ARG:NH2	1:A:229:GLN:HA	2.03	0.70
1:B:206:GLN:NE2	1:B:206:GLN:HA	2.07	0.69
1:A:66:ARG:HB2	1:A:67:PHE:CD2	2.28	0.69
1:B:198:TYR:O	1:B:201:ASN:HB2	1.92	0.69
1:A:216:VAL:HG13	1:A:258:ILE:HG21	1.73	0.68
1:B:442:LYS:NZ	1:A:110:GLN:HG3	2.09	0.67
1:B:206:GLN:HE21	1:B:206:GLN:CA	2.08	0.67
1:B:434:GLU:OE1	1:B:442:LYS:HE3	1.94	0.66
1:B:66:ARG:HB2	1:B:67:PHE:CD2	2.30	0.66
1:A:206:GLN:HA	1:A:206:GLN:HE21	1.59	0.66
1:B:237:MET:HE2	1:B:257:GLN:HB3	1.77	0.66
1:B:215:LEU:O	1:B:219:ILE:HG13	1.95	0.66
1:A:215:LEU:O	1:A:219:ILE:HG13	1.95	0.66
1:B:58:VAL:HG21	1:B:360:LEU:HD22	1.78	0.66
1:A:366:VAL:HG11	1:A:389:ALA:HB2	1.78	0.66
1:A:206:GLN:CA	1:A:206:GLN:HE21	2.09	0.65
1:A:289:LYS:HD3	1:A:313:TYR:CZ	2.32	0.65
1:B:206:GLN:HE21	1:B:206:GLN:HA	1.60	0.65
1:B:203:ARG:HH11	1:B:203:ARG:HG2	1.62	0.64
1:B:171:HIS:HD2	1:B:173:PHE:H	1.43	0.64
1:A:203:ARG:HG2	1:A:203:ARG:NH1	2.12	0.63
1:B:1:THR:O	1:B:1:THR:HG23	1.98	0.63
1:A:341:LEU:HD12	1:A:342:GLY:N	2.13	0.63
1:A:323:ARG:HB2	1:A:390:PHE:HE1	1.64	0.63
1:B:370:ASP:CG	1:B:375:ARG:HH22	2.02	0.63
1:A:69:LYS:HE2	1:A:70:ASN:O	1.98	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:LYS:HA	1:B:190:ARG:HD2	1.81	0.63
1:B:106:ARG:HD3	1:B:236:HIS:CE1	2.34	0.62
1:A:323:ARG:HA	1:A:361:HIS:ND1	2.14	0.62
1:B:69:LYS:HE2	1:B:70:ASN:O	1.99	0.62
1:A:322:LEU:HD22	1:A:392:PRO:HB3	1.81	0.62
1:A:216:VAL:HG21	1:A:259:ILE:HG12	1.81	0.62
1:A:370:ASP:CG	1:A:375:ARG:HH22	2.03	0.62
1:B:289:LYS:HD3	1:B:313:TYR:CZ	2.35	0.62
1:A:58:VAL:HG21	1:A:360:LEU:HD22	1.81	0.62
1:B:35:GLU:HB2	1:A:65:SER:HB3	1.82	0.61
1:A:303:PRO:HA	1:A:307:GLN:OE1	1.99	0.61
1:B:96:TRP:CE3	1:B:97:LYS:HB2	2.35	0.61
1:A:253:ASN:O	1:A:257:GLN:HG2	2.01	0.61
1:A:236:HIS:C	1:A:238:LEU:H	2.03	0.61
1:B:161:ARG:HG2	1:B:161:ARG:HH11	1.65	0.61
1:A:213:ASN:OD1	1:A:259:ILE:HD11	2.01	0.61
1:B:30:MET:O	1:B:34:ASP:HB2	2.00	0.60
1:B:21:ASN:HB2	1:A:101:ASN:ND2	2.15	0.60
1:B:35:GLU:HA	1:A:65:SER:HB3	1.82	0.60
1:A:391:LYS:HE2	1:A:395:ASN:HB2	1.83	0.60
1:A:97:LYS:CD	1:A:101:ASN:ND2	2.65	0.60
1:B:253:ASN:HA	1:B:256:TYR:CD2	2.30	0.60
1:B:77:PHE:HE2	1:B:188:LEU:HD23	1.67	0.60
1:A:96:TRP:CE3	1:A:97:LYS:HB2	2.37	0.60
1:B:253:ASN:O	1:B:257:GLN:HG2	2.02	0.60
1:B:92:HIS:O	1:B:92:HIS:CD2	2.55	0.60
1:A:69:LYS:HG2	1:A:70:ASN:H	1.67	0.59
1:B:203:ARG:NH1	1:B:203:ARG:HG2	2.17	0.59
1:B:71:LEU:C	1:B:72:SER:O	2.41	0.59
1:A:171:HIS:HD2	1:A:173:PHE:H	1.49	0.59
1:B:112:MET:SD	1:B:405:PHE:HA	2.43	0.59
1:B:69:LYS:HG2	1:B:70:ASN:H	1.67	0.59
1:B:275:PHE:CZ	1:B:441:PRO:HD3	2.38	0.59
1:A:380:GLU:O	1:A:382:PRO:HD3	2.02	0.59
1:B:116:HIS:HD2	1:B:408:HIS:NE2	2.01	0.59
1:A:220:ILE:HG22	1:A:224:LYS:HE2	1.84	0.58
1:B:205:PHE:CE2	1:B:209:ILE:CD1	2.86	0.58
1:B:96:TRP:CZ3	1:B:97:LYS:HB2	2.39	0.58
1:B:303:PRO:HA	1:B:307:GLN:OE1	2.04	0.58
1:A:275:PHE:CZ	1:A:441:PRO:HD3	2.39	0.58
1:B:387:GLN:O	1:B:388:HIS:HB2	2.02	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:337:GLU:O	1:A:339:THR:HG22	2.04	0.58
1:A:236:HIS:C	1:A:238:LEU:N	2.56	0.58
1:A:235:THR:O	1:A:239:HIS:HB2	2.04	0.57
1:B:205:PHE:HE2	1:B:209:ILE:HD11	1.69	0.57
1:A:116:HIS:HD2	1:A:408:HIS:NE2	2.03	0.57
1:A:435:GLU:HG2	1:A:439:LEU:HD23	1.86	0.57
1:B:391:LYS:HE2	1:B:395:ASN:HB2	1.86	0.57
1:A:237:MET:CE	1:A:257:GLN:HB3	2.35	0.57
1:B:423:PHE:HB3	1:B:446:ILE:HD12	1.87	0.57
1:A:387:GLN:O	1:A:388:HIS:HB2	2.05	0.56
1:B:13:GLU:O	1:B:13:GLU:OE2	2.23	0.56
1:B:66:ARG:O	1:B:336:LYS:HB2	2.06	0.56
1:B:209:ILE:O	1:B:209:ILE:HG22	2.05	0.56
1:B:19:LEU:C	1:B:20:LEU:HD23	2.25	0.56
1:B:83:GLY:HA2	1:B:84:ASP:C	2.26	0.56
1:A:184:VAL:O	1:A:188:LEU:HG	2.05	0.56
1:B:70:ASN:OD1	1:B:334:TYR:HB3	2.05	0.56
1:B:220:ILE:HG22	1:B:224:LYS:HE2	1.87	0.56
1:B:323:ARG:HA	1:B:361:HIS:ND1	2.21	0.56
1:B:366:VAL:HG11	1:B:389:ALA:HB2	1.86	0.56
1:B:95:ASN:ND2	1:B:95:ASN:N	2.31	0.56
1:A:70:ASN:HB3	1:A:332:SER:HB3	1.86	0.56
1:B:25:PRO:HD2	1:B:435:GLU:OE1	2.07	0.55
1:B:459:PRO:O	1:B:460:SER:HB2	2.06	0.55
1:B:337:GLU:O	1:B:339:THR:HG22	2.07	0.55
1:A:367:TRP:CH2	1:A:385:ILE:HG23	2.42	0.55
1:B:77:PHE:CE2	1:B:188:LEU:HD23	2.41	0.55
1:B:128:GLN:O	1:B:132:ARG:HG3	2.07	0.55
1:B:171:HIS:CD2	1:B:173:PHE:H	2.23	0.55
1:B:142:PRO:HG3	1:B:274:THR:HG21	1.87	0.55
1:A:358:PRO:O	1:A:362:ARG:HG3	2.07	0.55
1:A:253:ASN:HA	1:A:256:TYR:CD2	2.32	0.55
1:A:70:ASN:OD1	1:A:334:TYR:HB3	2.06	0.55
1:B:85:GLY:HA2	1:B:257:GLN:HE22	1.72	0.55
1:A:211:VAL:O	1:A:214:ASP:HB2	2.07	0.55
1:A:106:ARG:HD2	1:A:236:HIS:CE1	2.42	0.55
1:A:370:ASP:CG	1:A:375:ARG:NH2	2.60	0.54
1:A:96:TRP:CZ3	1:A:97:LYS:HB2	2.42	0.54
1:A:66:ARG:HB2	1:A:67:PHE:CE2	2.43	0.54
1:B:370:ASP:CG	1:B:375:ARG:NH2	2.60	0.54
1:A:112:MET:SD	1:A:405:PHE:HA	2.46	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:199:ASP:C	1:B:201:ASN:H	2.11	0.54
1:B:236:HIS:C	1:B:238:LEU:H	2.11	0.54
1:B:435:GLU:HG2	1:B:439:LEU:HD23	1.89	0.54
1:A:126:LEU:HB2	1:A:165:PHE:CZ	2.43	0.54
1:A:237:MET:HE2	1:A:257:GLN:HB3	1.88	0.54
1:A:423:PHE:HB3	1:A:446:ILE:HD12	1.90	0.54
1:B:184:VAL:O	1:B:188:LEU:HG	2.08	0.54
1:B:236:HIS:C	1:B:238:LEU:N	2.60	0.54
1:B:70:ASN:HB3	1:B:332:SER:HB3	1.89	0.54
1:B:74:ALA:O	1:B:78:VAL:HG23	2.07	0.54
1:A:19:LEU:C	1:A:20:LEU:HD23	2.27	0.54
1:A:323:ARG:HB2	1:A:390:PHE:CE1	2.41	0.54
1:A:66:ARG:O	1:A:336:LYS:HB2	2.08	0.53
1:B:75:ARG:HD3	1:B:88:THR:HG23	1.90	0.53
1:A:223:ARG:NH2	1:A:229:GLN:HG3	2.23	0.53
1:A:200:GLU:N	1:A:203:ARG:HB3	2.24	0.53
1:A:30:MET:O	1:A:34:ASP:HB2	2.08	0.53
1:A:68:ASP:HB3	1:A:334:TYR:CE1	2.42	0.53
1:B:14:LEU:HD13	1:B:18:PRO:HG3	1.89	0.53
1:B:237:MET:CE	1:B:257:GLN:HB3	2.38	0.53
1:A:223:ARG:HH22	1:A:229:GLN:HG3	1.75	0.53
1:B:428:ASN:HB2	1:A:312:LYS:CG	2.31	0.53
1:A:216:VAL:HG21	1:A:259:ILE:CG1	2.39	0.52
1:B:205:PHE:HE2	1:B:209:ILE:CD1	2.21	0.52
1:A:412:LEU:O	1:A:416:MET:HG3	2.10	0.52
1:A:19:LEU:O	1:A:20:LEU:HD23	2.10	0.52
1:B:380:GLU:O	1:B:382:PRO:HD3	2.09	0.52
1:B:78:VAL:HG21	1:B:437:LEU:HD11	1.90	0.52
1:A:203:ARG:HH11	1:A:203:ARG:CG	2.19	0.52
1:B:203:ARG:CG	1:B:203:ARG:HH11	2.23	0.52
1:B:237:MET:O	1:B:254:ILE:HD13	2.10	0.52
1:B:30:MET:CE	1:B:358:PRO:HB2	2.40	0.51
1:B:160:TYR:CD2	1:B:219:ILE:HG12	2.45	0.51
1:B:23:ASP:C	1:B:25:PRO:HD3	2.31	0.51
1:B:71:LEU:O	1:B:72:SER:O	2.27	0.51
1:B:322:LEU:HD22	1:B:392:PRO:HB3	1.92	0.51
1:A:161:ARG:HG2	1:A:161:ARG:HH11	1.74	0.51
1:A:236:HIS:O	1:A:238:LEU:N	2.43	0.51
1:B:287:LEU:HD23	1:B:287:LEU:C	2.31	0.51
1:A:14:LEU:HD13	1:A:18:PRO:HG3	1.92	0.51
1:A:323:ARG:HA	1:A:361:HIS:HD1	1.74	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:ARG:HB2	1:B:67:PHE:CE2	2.46	0.51
1:A:169:GLN:O	1:A:170:PRO:C	2.48	0.51
1:A:326:PRO:HD2	1:A:358:PRO:HG3	1.93	0.51
1:B:262:LEU:O	1:B:266:HIS:CD2	2.59	0.51
1:A:23:ASP:C	1:A:25:PRO:HD3	2.31	0.50
1:B:11:PHE:CZ	1:B:19:LEU:HD21	2.46	0.50
1:B:307:GLN:O	1:B:310:GLN:HG2	2.11	0.50
1:A:106:ARG:O	1:A:107:LEU:HD23	2.11	0.50
1:B:195:ASP:OD1	1:B:196:PRO:HD2	2.12	0.50
1:B:97:LYS:CD	1:B:101:ASN:ND2	2.72	0.50
1:A:171:HIS:CD2	1:A:173:PHE:H	2.29	0.50
1:B:106:ARG:O	1:B:107:LEU:HD23	2.12	0.50
1:B:183:GLU:HG2	1:B:205:PHE:HD1	1.76	0.50
1:A:237:MET:O	1:A:254:ILE:HD13	2.11	0.50
1:B:308:VAL:HG21	1:B:412:LEU:HD13	1.95	0.49
1:A:262:LEU:O	1:A:266:HIS:CD2	2.58	0.49
1:B:150:LEU:HD22	1:B:174:ILE:HD11	1.95	0.49
1:B:71:LEU:O	1:B:72:SER:C	2.50	0.49
1:B:26:VAL:O	1:B:30:MET:HG3	2.13	0.49
1:B:126:LEU:HB2	1:B:165:PHE:CZ	2.47	0.49
1:A:141:VAL:HG12	1:A:274:THR:HG23	1.95	0.48
1:B:35:GLU:HB2	1:A:65:SER:CB	2.41	0.48
1:B:206:GLN:NE2	1:B:206:GLN:CA	2.71	0.48
1:A:10:THR:O	1:A:11:PHE:HD2	1.95	0.48
1:A:150:LEU:HD22	1:A:174:ILE:HD11	1.94	0.48
1:A:183:GLU:HG2	1:A:205:PHE:HD1	1.78	0.48
1:B:19:LEU:O	1:B:20:LEU:HD23	2.13	0.48
1:B:336:LYS:C	1:B:337:GLU:HG2	2.33	0.48
1:B:49:THR:CG2	1:B:51:TYR:CE1	2.97	0.48
1:A:391:LYS:HE3	1:A:391:LYS:HB3	1.51	0.48
1:B:82:ALA:O	1:B:256:TYR:HB3	2.14	0.48
1:A:242:ASP:HB3	1:A:247:GLU:O	2.13	0.48
1:A:331:PHE:HD2	1:A:357:ILE:HD11	1.78	0.48
1:A:265:GLY:HA2	2:A:472:HEM:CAC	2.44	0.48
1:B:191:ALA:HB3	1:A:244:GLU:O	2.13	0.48
1:A:308:VAL:HG21	1:A:412:LEU:HD13	1.95	0.48
1:B:77:PHE:O	1:B:80:ASP:HB2	2.14	0.48
1:B:35:GLU:HB2	1:A:65:SER:CA	2.44	0.47
1:A:127:VAL:HG11	1:A:455:LEU:HD22	1.96	0.47
1:A:153:ILE:HG23	1:A:154:GLY:N	2.29	0.47
1:A:341:LEU:HD12	1:A:342:GLY:H	1.79	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:GLY:O	1:B:233:LEU:HB3	2.14	0.47
1:B:83:GLY:CA	1:B:84:ASP:C	2.82	0.47
1:A:104:LEU:N	1:A:105:PRO:HD2	2.30	0.47
1:A:345:TYR:CD2	1:A:345:TYR:N	2.82	0.47
1:B:323:ARG:HB2	1:B:390:PHE:HE1	1.78	0.47
1:A:61:ALA:HA	1:A:67:PHE:CD2	2.49	0.47
1:B:173:PHE:CD2	1:B:173:PHE:C	2.87	0.47
1:A:298:LEU:HD22	1:A:303:PRO:HB3	1.96	0.47
1:A:26:VAL:O	1:A:30:MET:HG3	2.14	0.47
1:B:68:ASP:HB3	1:B:334:TYR:CE1	2.49	0.47
1:A:366:VAL:HG12	1:A:386:PRO:HG2	1.97	0.47
1:A:3:LYS:HB3	1:A:344:GLU:HB3	1.97	0.47
1:B:104:LEU:N	1:B:105:PRO:HD2	2.29	0.47
1:B:92:HIS:O	1:B:92:HIS:HD2	1.96	0.47
1:B:406:ALA:HB2	2:B:472:HEM:CBB	2.43	0.47
1:A:322:LEU:HD22	1:A:392:PRO:CB	2.44	0.47
1:A:375:ARG:HG3	1:A:377:GLU:OE1	2.15	0.47
1:B:171:HIS:HD2	1:B:173:PHE:N	2.12	0.47
1:B:331:PHE:HD2	1:B:357:ILE:HD11	1.80	0.47
1:A:61:ALA:HA	1:A:67:PHE:CE2	2.50	0.46
1:B:14:LEU:HB3	1:B:18:PRO:HD3	1.96	0.46
1:A:160:TYR:CD2	1:A:219:ILE:HG12	2.51	0.46
1:A:157:GLY:O	1:A:233:LEU:HB3	2.15	0.46
1:B:69:LYS:HE3	2:B:472:HEM:O2D	2.16	0.46
1:A:242:ASP:HB3	1:A:247:GLU:C	2.36	0.46
1:A:436:THR:O	1:A:437:LEU:HB2	2.15	0.46
1:B:61:ALA:HA	1:B:67:PHE:CD2	2.51	0.46
1:A:406:ALA:HB2	2:A:472:HEM:CMC	2.46	0.46
1:B:250:ASP:OD1	1:B:253:ASN:HB3	2.16	0.46
1:B:345:TYR:HA	1:B:346:PRO:HD3	1.73	0.46
1:B:358:PRO:O	1:B:362:ARG:HG3	2.15	0.46
1:B:236:HIS:O	1:B:238:LEU:N	2.49	0.45
1:B:153:ILE:HG23	1:B:154:GLY:N	2.31	0.45
1:B:211:VAL:O	1:B:214:ASP:HB2	2.16	0.45
1:B:345:TYR:N	1:B:345:TYR:CD2	2.84	0.45
1:B:312:LYS:O	1:B:316:MET:HG3	2.17	0.45
1:B:35:GLU:HB2	1:A:65:SER:HA	1.99	0.45
2:B:472:HEM:HHC	2:B:472:HEM:CBB	2.37	0.45
2:B:472:HEM:HHD	2:B:472:HEM:CBC	2.35	0.45
1:A:421:PHE:O	1:A:451:LYS:HE2	2.17	0.45
1:B:72:SER:HA	1:B:354:MET:CE	2.46	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:PHE:HB2	2:A:472:HEM:O1A	2.17	0.45
1:A:30:MET:CE	1:A:358:PRO:HB2	2.47	0.45
1:A:312:LYS:O	1:A:316:MET:HG3	2.16	0.45
1:B:412:LEU:O	1:B:416:MET:HG3	2.17	0.45
1:A:49:THR:CG2	1:A:51:TYR:CE1	3.00	0.45
1:A:97:LYS:HD3	1:A:101:ASN:HD22	1.78	0.45
1:B:20:LEU:C	1:B:22:THR:H	2.21	0.45
1:B:61:ALA:HA	1:B:67:PHE:CE2	2.52	0.45
1:A:215:LEU:HD12	1:A:215:LEU:O	2.17	0.44
1:A:307:GLN:O	1:A:310:GLN:HG2	2.17	0.44
1:A:393:PHE:CD1	1:A:403:GLN:HB2	2.53	0.44
1:B:141:VAL:HG12	1:B:274:THR:HG23	1.98	0.44
1:B:89:SER:CB	1:B:93:GLU:OE1	2.65	0.44
1:B:3:LYS:HB3	1:B:344:GLU:HB3	2.00	0.44
1:A:254:ILE:O	1:A:258:ILE:HG13	2.18	0.44
1:B:112:MET:CE	1:B:115:TYR:CD2	3.00	0.44
1:B:161:ARG:NH1	1:B:161:ARG:HG2	2.31	0.44
1:B:323:ARG:HA	1:B:361:HIS:HD1	1.82	0.44
1:B:77:PHE:C	1:B:79:ARG:H	2.21	0.44
1:A:242:ASP:HA	1:A:243:PRO:HD3	1.77	0.44
1:B:192:ASN:O	1:B:198:TYR:HE2	2.01	0.44
1:B:298:LEU:HD22	1:B:303:PRO:HB3	1.98	0.44
1:A:271:GLY:HA3	1:A:327:THR:HG21	1.99	0.44
1:B:112:MET:CE	1:B:115:TYR:HD2	2.31	0.44
1:A:60:GLU:O	1:A:63:ASP:HB3	2.17	0.44
1:B:116:HIS:HE1	1:B:303:PRO:O	2.00	0.44
1:A:27:GLN:NE2	1:A:433:ILE:HB	2.33	0.43
1:B:127:VAL:HG11	1:B:455:LEU:HD22	2.00	0.43
1:A:406:ALA:HB2	2:A:472:HEM:HMC3	1.99	0.43
1:B:107:LEU:HD23	1:B:107:LEU:HA	1.74	0.43
1:A:128:GLN:O	1:A:132:ARG:HG3	2.18	0.43
1:A:398:ARG:HB3	2:A:472:HEM:O1D	2.19	0.43
1:B:391:LYS:HE3	1:B:391:LYS:HB3	1.57	0.43
1:A:25:PRO:HD2	1:A:435:GLU:OE1	2.18	0.43
1:B:300:ASP:HB2	1:B:302:VAL:O	2.19	0.43
1:B:32:ILE:O	1:B:35:GLU:HG3	2.19	0.43
1:A:222:ASP:O	1:A:226:SER:HB2	2.19	0.43
1:B:428:ASN:HB2	1:A:312:LYS:HE3	2.01	0.43
1:B:279:PHE:O	1:B:283:ASN:ND2	2.50	0.43
1:B:436:THR:O	1:B:437:LEU:HB2	2.19	0.43
1:B:420:HIS:CE1	1:B:455:LEU:HB2	2.53	0.43

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:LEU:C	1:A:22:THR:H	2.22	0.43
1:B:138:HIS:C	1:B:138:HIS:CD2	2.92	0.43
1:B:426:HIS:CG	1:B:447:LYS:HG3	2.54	0.43
1:A:142:PRO:HG3	1:A:274:THR:HG21	2.01	0.42
1:A:110:GLN:OE1	1:A:113:LYS:HE3	2.19	0.42
1:A:385:ILE:HG13	1:A:385:ILE:H	1.58	0.42
1:A:426:HIS:CG	1:A:447:LYS:HG3	2.54	0.42
1:B:199:ASP:C	1:B:201:ASN:N	2.72	0.42
1:B:1:THR:CG2	1:B:1:THR:O	2.65	0.42
1:B:30:MET:HB3	1:B:359:GLN:HG2	2.02	0.42
1:B:39:ILE:HA	1:B:51:TYR:O	2.20	0.42
1:B:21:ASN:HB2	1:A:101:ASN:HD22	1.82	0.42
1:A:283:ASN:N	1:A:283:ASN:HD22	2.17	0.42
1:A:97:LYS:CD	1:A:101:ASN:HD21	2.32	0.42
1:B:435:GLU:HG2	1:B:439:LEU:CD2	2.49	0.42
1:B:457:GLY:O	1:B:458:ILE:HG13	2.20	0.42
1:A:173:PHE:CD2	1:A:173:PHE:C	2.93	0.42
1:B:141:VAL:O	1:B:142:PRO:C	2.56	0.42
1:B:79:ARG:C	1:B:81:PHE:H	2.23	0.42
1:A:421:PHE:HB2	1:A:423:PHE:CZ	2.55	0.42
1:B:47:ARG:HG3	1:B:47:ARG:O	2.18	0.42
1:A:149:THR:HA	1:A:409:GLU:OE2	2.19	0.41
1:B:75:ARG:HD3	1:B:88:THR:CG2	2.49	0.41
1:B:195:ASP:HA	1:B:196:PRO:HD3	1.92	0.41
1:B:375:ARG:HG3	1:B:377:GLU:OE1	2.20	0.41
1:B:69:LYS:HG2	1:B:70:ASN:N	2.35	0.41
1:B:86:LEU:HD23	1:B:86:LEU:HA	1.72	0.41
1:A:336:LYS:C	1:A:337:GLU:HG2	2.41	0.41
1:A:262:LEU:HA	1:A:262:LEU:HD23	1.86	0.41
1:A:426:HIS:CD2	1:A:446:ILE:HA	2.56	0.41
1:B:458:ILE:HA	1:B:459:PRO:HD3	1.75	0.41
1:B:5:MET:HA	1:B:6:PRO:HD3	1.81	0.41
1:B:427:THR:HB	1:A:309:LYS:O	2.20	0.41
1:B:11:PHE:HZ	1:B:19:LEU:HD21	1.84	0.41
1:B:27:GLN:NE2	1:B:433:ILE:HB	2.35	0.41
1:B:366:VAL:HG12	1:B:386:PRO:HG2	2.02	0.41
1:B:72:SER:HA	1:B:354:MET:HE1	2.03	0.41
1:B:79:ARG:C	1:B:81:PHE:N	2.74	0.41
1:B:169:GLN:O	1:B:170:PRO:C	2.58	0.41
1:B:393:PHE:HB3	1:B:400:CYS:HB3	2.02	0.41
1:A:247:GLU:HA	1:A:248:PRO:HD2	1.90	0.41

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:MET:HE2	1:B:115:TYR:CD2	2.56	0.41
1:B:74:ALA:HB2	1:B:188:LEU:HD11	2.03	0.41
1:A:171:HIS:HD2	1:A:173:PHE:N	2.16	0.41
1:A:393:PHE:HB3	1:A:400:CYS:HB3	2.03	0.41
1:A:393:PHE:HD1	1:A:400:CYS:HB3	1.85	0.41
1:A:97:LYS:HE3	1:A:97:LYS:HB2	1.87	0.41
1:A:161:ARG:HG2	1:A:161:ARG:NH1	2.35	0.41
1:A:113:LYS:HA	1:A:305:TYR:CD2	2.56	0.41
1:B:134:ASN:ND2	1:B:137:GLU:OE2	2.54	0.41
1:B:393:PHE:HD1	1:B:400:CYS:HB3	1.85	0.41
1:A:205:PHE:C	1:A:205:PHE:CD2	2.94	0.41
1:B:18:PRO:O	1:A:97:LYS:HD2	2.20	0.41
1:B:44:ALA:O	1:B:45:PRO:C	2.59	0.41
1:B:77:PHE:C	1:B:79:ARG:N	2.75	0.41
1:A:129:LYS:HE2	1:A:144:ASP:OD2	2.20	0.40
1:A:283:ASN:N	1:A:283:ASN:ND2	2.70	0.40
1:A:68:ASP:HB3	1:A:334:TYR:CZ	2.56	0.40
1:A:367:TRP:HB2	1:A:371:VAL:HG12	2.03	0.40
1:A:396:GLY:C	1:A:398:ARG:H	2.23	0.40
1:B:78:VAL:CG2	1:B:184:VAL:HG11	2.51	0.40
1:B:97:LYS:HB2	1:B:97:LYS:HE3	1.86	0.40
1:A:17:LEU:N	1:A:18:PRO:CD	2.84	0.40
1:B:149:THR:HA	1:B:409:GLU:OE2	2.21	0.40
1:B:113:LYS:HA	1:B:305:TYR:CD2	2.56	0.40
1:A:32:ILE:O	1:A:35:GLU:HG3	2.21	0.40
1:B:35:GLU:C	1:A:65:SER:HB3	2.41	0.40
1:B:396:GLY:C	1:B:398:ARG:H	2.25	0.40
1:B:426:HIS:CD2	1:B:446:ILE:HA	2.56	0.40
1:A:341:LEU:C	1:A:343:GLY:H	2.25	0.40
1:B:74:ALA:CA	1:B:188:LEU:HD11	2.52	0.40
1:B:338:ASP:OD1	1:B:348:GLU:HA	2.22	0.40

There are no symmetry-related clashes.

## 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	418/472 (89%)	365 (87%)	47 (11%)	6 (1%)	13	53
1	B	446/472 (94%)	390 (87%)	48 (11%)	8 (2%)	10	47
All	All	864/944 (92%)	755 (87%)	95 (11%)	14 (2%)	11	50

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	72	SER
1	B	237	MET
1	B	251	ASP
1	A	237	MET
1	A	251	ASP
1	B	86	LEU
1	B	136	ASP
1	A	136	ASP
1	A	248	PRO
1	B	85	GLY
1	A	45	PRO
1	B	45	PRO
1	B	170	PRO
1	A	170	PRO

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	360/415 (87%)	325 (90%)	35 (10%)	9	36
1	B	390/415 (94%)	351 (90%)	39 (10%)	9	35
All	All	750/830 (90%)	676 (90%)	74 (10%)	9	35

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1	THR
1	B	10	THR
1	B	13	GLU
1	B	23	ASP
1	B	27	GLN
1	B	30	MET
1	B	35	GLU
1	B	49	THR
1	B	50	ARG
1	B	70	ASN
1	B	73	GLN
1	B	88	THR
1	B	95	ASN
1	B	97	LYS
1	B	106	ARG
1	B	124	VAL
1	B	126	LEU
1	B	135	SER
1	B	138	HIS
1	B	164	SER
1	B	176	SER
1	B	187	LYS
1	B	199	ASP
1	B	200	GLU
1	B	203	ARG
1	B	206	GLN
1	B	235	THR
1	B	237	MET
1	B	241	LYS
1	B	253	ASN
1	B	309	LYS
1	B	336	LYS
1	B	339	THR
1	B	340	MET
1	B	366	VAL
1	B	391	LYS
1	B	401	ILE
1	B	427	THR
1	B	449	LYS
1	A	2	ILE
1	A	23	ASP
1	A	27	GLN
1	A	30	MET

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	35	GLU
1	A	49	THR
1	A	50	ARG
1	A	69	LYS
1	A	70	ASN
1	A	97	LYS
1	A	106	ARG
1	A	124	VAL
1	A	126	LEU
1	A	135	SER
1	A	138	HIS
1	A	164	SER
1	A	176	SER
1	A	187	LYS
1	A	203	ARG
1	A	206	GLN
1	A	226	SER
1	A	229	GLN
1	A	235	THR
1	A	237	MET
1	A	302	VAL
1	A	309	LYS
1	A	336	LYS
1	A	339	THR
1	A	340	MET
1	A	366	VAL
1	A	385	ILE
1	A	391	LYS
1	A	401	ILE
1	A	427	THR
1	A	449	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	27	GLN
1	B	92	HIS
1	B	95	ASN
1	B	101	ASN
1	B	116	HIS
1	B	138	HIS
1	B	171	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	189	GLN
1	B	206	GLN
1	B	266	HIS
1	B	283	ASN
1	B	403	GLN
1	B	426	HIS
1	B	428	ASN
1	A	27	GLN
1	A	101	ASN
1	A	116	HIS
1	A	138	HIS
1	A	171	HIS
1	A	206	GLN
1	A	266	HIS
1	A	283	ASN
1	A	403	GLN
1	A	426	HIS

### 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](#)

2 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	A	472	1	28,50,50	2.27	7 (25%)	17,82,82	2.48	6 (35%)
2	HEM	B	472	1	28,50,50	2.33	8 (28%)	17,82,82	2.15	5 (29%)

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	A	472	1	-	0/6/54/54	0/0/8/8
2	HEM	B	472	1	-	0/6/54/54	0/0/8/8

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	472	HEM	C3C-C2C	-5.91	1.32	1.40
2	A	472	HEM	C3C-C2C	-5.89	1.32	1.40
2	B	472	HEM	C3B-C2B	-5.28	1.33	1.40
2	A	472	HEM	C3B-C2B	-4.02	1.35	1.40
2	A	472	HEM	C1D-ND	2.13	1.40	1.36
2	B	472	HEM	CMB-C2B	2.23	1.56	1.51
2	B	472	HEM	CMC-C2C	2.46	1.56	1.51
2	B	472	HEM	C3B-CAB	2.74	1.53	1.47
2	A	472	HEM	C3B-CAB	2.87	1.53	1.47
2	A	472	HEM	C3C-CAC	2.93	1.53	1.47
2	B	472	HEM	C4D-ND	3.01	1.40	1.36
2	B	472	HEM	C3C-CAC	3.47	1.54	1.47
2	A	472	HEM	C4D-ND	3.66	1.41	1.36
2	B	472	HEM	C3D-C2D	5.11	1.52	1.37
2	A	472	HEM	C3D-C2D	5.45	1.53	1.37

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	472	HEM	CAA-CBA-CGA	-4.81	104.44	112.66
2	B	472	HEM	CBA-CAA-C2A	-4.39	104.08	112.48
2	B	472	HEM	CAD-CBD-CGD	-4.35	105.23	112.66
2	A	472	HEM	CAA-C2A-C3A	-3.85	118.02	129.00
2	A	472	HEM	CBD-CAD-C3D	-2.82	107.09	112.47
2	B	472	HEM	C3B-C4B-NB	-2.14	106.44	109.21
2	A	472	HEM	CAD-CBD-CGD	-2.13	109.01	112.66
2	B	472	HEM	CBD-CAD-C3D	2.07	116.41	112.47

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	472	HEM	C4C-C3C-C2C	3.42	109.29	106.90
2	A	472	HEM	C4A-C3A-C2A	3.77	109.62	107.00
2	A	472	HEM	CBA-CAA-C2A	4.27	120.65	112.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	472	HEM	5	0
2	B	472	HEM	6	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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, 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	424/472 (89%)	-0.07	14 (3%)	47 31	44, 80, 146, 180	0
1	B	452/472 (95%)	-0.17	2 (0%)	92 89	40, 74, 126, 153	0
All	All	876/944 (92%)	-0.12	16 (1%)	69 55	40, 77, 136, 180	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	341	LEU	3.6
1	A	1	THR	3.5
1	A	256	TYR	3.3
1	A	14	LEU	3.1
1	A	201	ASN	2.8
1	A	36	LEU	2.7
1	A	247	GLU	2.7
1	B	249	LEU	2.6
1	A	3	LYS	2.5
1	A	243	PRO	2.5
1	A	4	GLU	2.3
1	B	84	ASP	2.2
1	A	2	ILE	2.1
1	A	343	GLY	2.1
1	A	185	MET	2.0
1	A	71	LEU	2.0

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

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



### 6.3 Carbohydrates [i](#)

There are no 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	HEM	A	472	43/43	0.97	0.21	0.13	39,59,86,95	0
2	HEM	B	472	43/43	0.97	0.20	-0.36	20,59,70,75	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.