



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 06:48 am GMT

PDB ID : 2C6H  
Title : CRYSTAL STRUCTURE OF YC-17-BOUND CYTOCHROME P450 PIKC  
(CYP107L1)  
Authors : Sherman, D.H.; Li, S.; Yermalitskaya, L.V.; Kim, Y.; Smith, J.A.; Waterman,  
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Deposited on : 2005-11-09  
Resolution : 2.35 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.

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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 : 1.7.2 (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

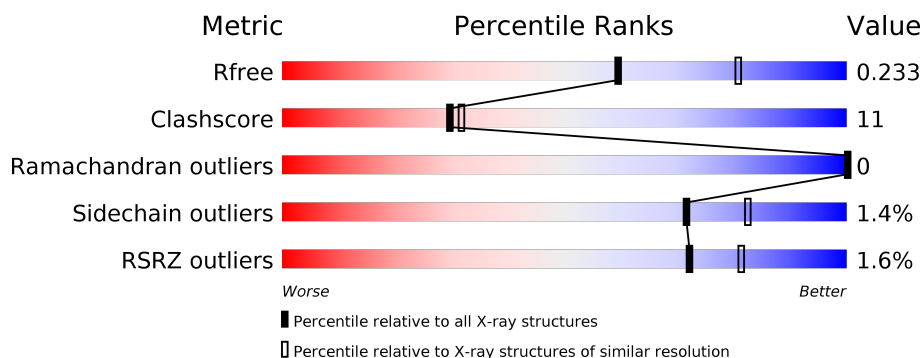
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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	1522 (2.38-2.34)
Clashscore	112137	1626 (2.38-2.34)
Ramachandran outliers	110173	1605 (2.38-2.34)
Sidechain outliers	110143	1606 (2.38-2.34)
RSRZ outliers	101464	1528 (2.38-2.34)

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	436	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%; text-align: center;">%</div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 19%, green 71%, grey 100%);"></div> <div style="position: absolute; bottom: -10px; left: 0; width: 100%; text-align: center;"> <span style="display: inline-block; width: 1%;"></span> 1%           <span style="display: inline-block; width: 1%;"></span> 1%           <span style="display: inline-block; width: 18%;"></span> 19%           <span style="display: inline-block; width: 71%;"></span> 71%           <span style="display: inline-block; width: 10%;"></span> 10%         </div> </div> </div>
1	B	436	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%; text-align: center;">2%</div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 2%, yellow 18%, green 72%, grey 100%);"></div> <div style="position: absolute; bottom: -10px; left: 0; width: 100%; text-align: center;"> <span style="display: inline-block; width: 2%;"></span> 2%           <span style="display: inline-block; width: 2%;"></span> 2%           <span style="display: inline-block; width: 18%;"></span> 18%           <span style="display: inline-block; width: 72%;"></span> 72%           <span style="display: inline-block; width: 9%;"></span> 9%         </div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SO4	A	1432	-	-	-	X
4	SO4	B	1433	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6492 atoms, of which 0 are hydrogens and 0 are deuteriums.

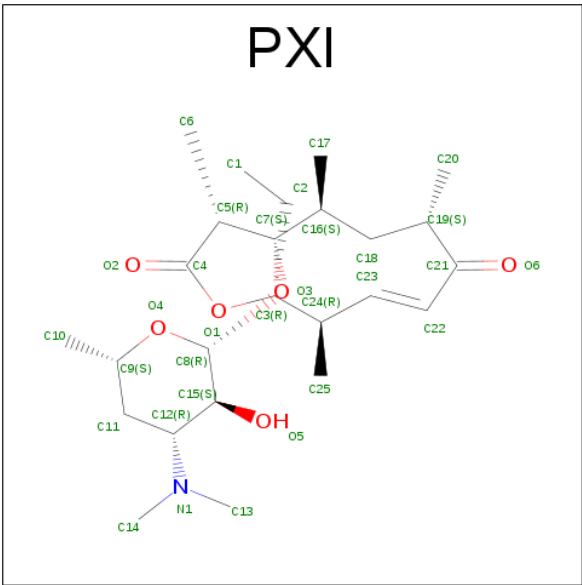
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CYTOCHROME P450 MONOOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	394	Total	C	N	O	S	0	0	1
			3043	1918	546	566	13			
1	B	395	Total	C	N	O	S	0	0	1
			3058	1929	547	569	13			

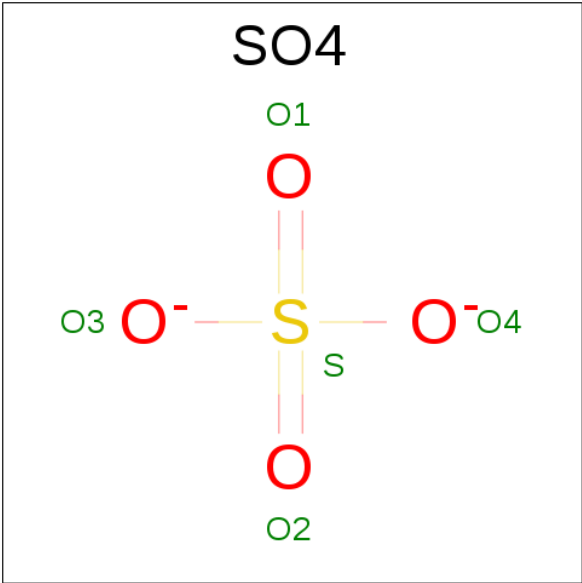
- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			32	25	1	6		
3	B	1	Total	C	N	O	0	0
			32	25	1	6		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

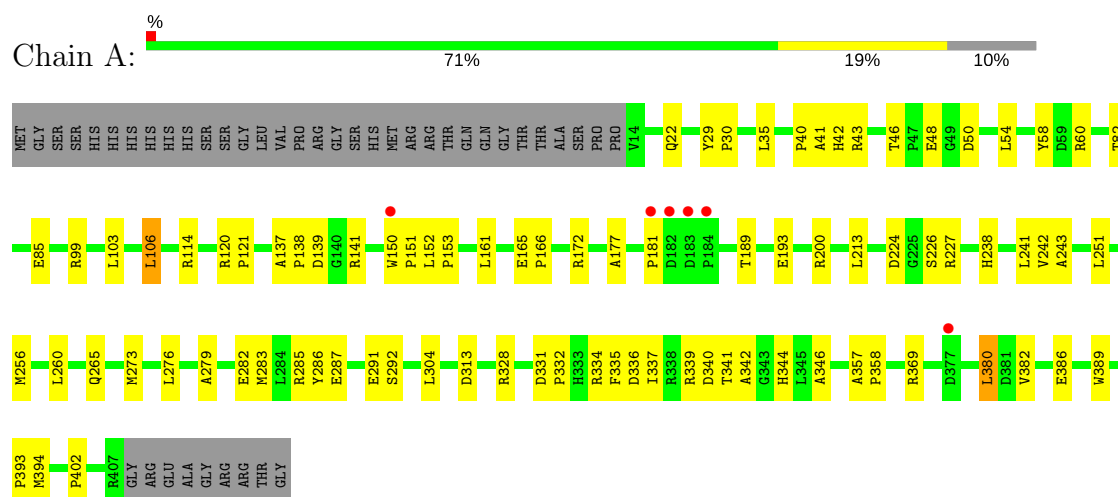
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	109	Total	O	0	0
			109	109		
5	B	107	Total	O	0	0
			107	107		

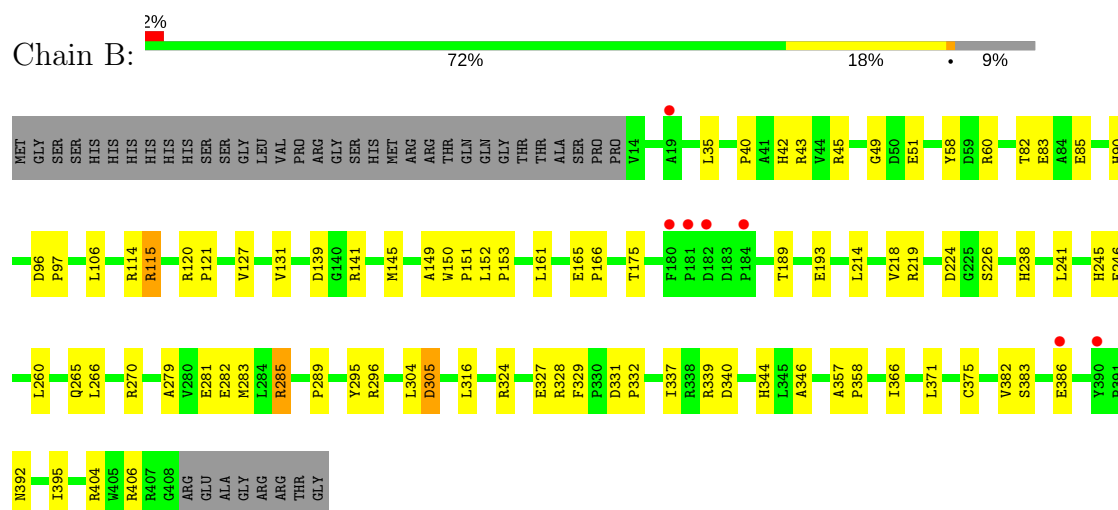
### 3 Residue-property plots

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 P450 MONOOXYGENASE



#### • Molecule 1: CYTOCHROME P450 MONOOXYGENASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.46Å 104.70Å 153.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.56 – 2.35 49.56 – 2.35	Depositor EDS
% Data completeness (in resolution range)	93.3 (49.56-2.35) 96.4 (49.56-2.35)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.10 (at 2.34Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.195 , 0.231 0.199 , 0.233	Depositor DCC
$R_{free}$ test set	3907 reflections (10.89%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.7	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 42.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6492	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.67% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, PXI, SO4

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	0.33	0/3113	0.57	0/4249
1	B	0.34	0/3129	0.58	0/4270
All	All	0.33	0/6242	0.57	0/8519

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

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	3043	0	3006	58	0
1	B	3058	0	3019	74	0
2	A	43	0	30	2	0
2	B	43	0	30	0	0
3	A	32	0	43	2	0
3	B	32	0	43	0	0
4	A	20	0	0	1	0
4	B	5	0	0	0	0
5	A	109	0	0	3	0
5	B	107	0	0	5	0
All	All	6492	0	6171	133	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 11.

All (133) 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:45:ARG:HE	1:B:49:GLY:HA2	1.20	1.04
1:B:406:ARG:HB3	1:B:406:ARG:NH1	1.90	0.86
1:B:406:ARG:HB3	1:B:406:ARG:HH11	1.42	0.83
1:B:43:ARG:HH12	1:B:51:GLU:HB3	1.43	0.83
1:B:114:ARG:HG3	5:B:2033:HOH:O	1.82	0.78
1:B:58:TYR:CD2	1:B:328:ARG:HG3	2.20	0.76
1:A:152:LEU:HB3	1:A:153:PRO:HD3	1.67	0.75
1:A:58:TYR:CD2	1:A:328:ARG:HG3	2.20	0.75
1:B:45:ARG:NE	1:B:49:GLY:HA2	2.00	0.73
1:A:22:GLN:HE22	1:A:389:TRP:H	1.38	0.70
1:B:265:GLN:NE2	1:B:337:ILE:H	1.91	0.69
1:B:152:LEU:HB3	1:B:153:PRO:HD3	1.74	0.69
1:A:273:MET:HE2	1:A:369:ARG:CZ	2.25	0.67
1:B:139:ASP:OD2	1:B:141:ARG:HB2	1.94	0.67
1:A:189:THR:O	1:A:193:GLU:HG3	1.94	0.66
1:B:344:HIS:HD2	1:B:346:ALA:H	1.44	0.65
1:A:82:THR:OG1	1:A:85:GLU:HG3	1.95	0.65
1:A:139:ASP:OD2	1:A:141:ARG:HB2	1.97	0.65
1:A:344:HIS:HD2	1:A:346:ALA:H	1.43	0.65
1:A:58:TYR:CG	1:A:328:ARG:HG3	2.31	0.65
1:B:82:THR:OG1	1:B:85:GLU:HG3	1.98	0.64
1:A:60:ARG:HD2	1:A:304:LEU:HD22	1.80	0.63
1:B:90:HIS:HB2	5:B:2063:HOH:O	1.99	0.63
1:B:175:THR:HG23	5:B:2107:HOH:O	1.98	0.61
1:B:83:GLU:CD	1:B:83:GLU:H	2.03	0.61
1:B:224:ASP:OD1	1:B:226:SER:HB3	2.01	0.60
1:A:150:TRP:HB3	1:A:151:PRO:HD3	1.83	0.60
1:B:282:GLU:OE1	1:B:285:ARG:HD2	2.03	0.59
1:B:141:ARG:HH22	1:B:404:ARG:NH1	2.00	0.59
1:B:150:TRP:HB3	1:B:151:PRO:HD3	1.85	0.57
1:A:150:TRP:CZ2	1:A:172:ARG:HB2	2.39	0.57
1:A:242:VAL:HG11	3:A:1408:PXI:H173	1.85	0.57
1:A:114:ARG:HG3	1:A:114:ARG:HH11	1.70	0.57
1:A:46:THR:OG1	1:A:50:ASP:HB2	2.05	0.56
1:B:392:ASN:HB3	1:B:395:ILE:HG22	1.87	0.56
1:B:60:ARG:NH2	1:B:305:ASP:OD1	2.39	0.55
1:A:382:VAL:HG22	1:A:386:GLU:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:LEU:HB3	1:A:42:HIS:CD2	2.42	0.54
1:B:43:ARG:HH11	1:B:43:ARG:HG2	1.73	0.54
1:A:224:ASP:OD1	1:A:226:SER:HB3	2.07	0.54
1:A:177:ALA:O	1:A:181:PRO:HB3	2.08	0.53
1:B:43:ARG:NH1	1:B:51:GLU:HB3	2.19	0.53
1:B:120:ARG:HB3	1:B:121:PRO:HD3	1.91	0.53
1:A:120:ARG:HB3	1:A:121:PRO:HD3	1.92	0.52
1:B:265:GLN:HE21	1:B:337:ILE:H	1.58	0.52
1:B:329:PHE:O	1:B:332:PRO:HG3	2.10	0.52
1:B:406:ARG:CB	1:B:406:ARG:NH1	2.70	0.52
1:B:279:ALA:O	1:B:283:MET:HG3	2.09	0.52
1:B:127:VAL:HG21	1:B:366:ILE:HG22	1.93	0.51
1:A:29:TYR:HB2	1:A:30:PRO:HD3	1.91	0.51
1:A:339:ARG:HG2	1:A:340:ASP:N	2.26	0.51
1:A:48:GLU:CD	1:A:48:GLU:H	2.14	0.51
1:B:382:VAL:HG22	1:B:383:SER:N	2.26	0.50
1:B:45:ARG:HE	1:B:49:GLY:CA	2.07	0.50
1:A:161:LEU:HD12	1:A:241:LEU:CD2	2.42	0.50
1:B:357:ALA:HB3	1:B:358:PRO:HD3	1.94	0.50
1:B:295:TYR:CD1	1:B:316:LEU:HD21	2.46	0.49
1:B:295:TYR:CE1	1:B:316:LEU:HD21	2.47	0.49
1:B:214:LEU:O	1:B:218:VAL:HG23	2.13	0.49
1:B:161:LEU:CD1	1:B:241:LEU:HG	2.43	0.49
1:B:371:LEU:O	1:B:375:CYS:HB2	2.13	0.49
1:A:276:LEU:HD13	1:A:276:LEU:C	2.33	0.48
1:B:43:ARG:HG2	1:B:43:ARG:NH1	2.27	0.48
1:A:282:GLU:HG3	1:A:335:PHE:CE1	2.48	0.48
1:B:35:LEU:HB3	1:B:42:HIS:CD2	2.49	0.48
1:A:165:GLU:HB3	1:A:166:PRO:HD3	1.95	0.48
1:B:339:ARG:HG2	1:B:340:ASP:N	2.29	0.48
1:A:331:ASP:N	1:A:332:PRO:HD3	2.29	0.47
1:A:161:LEU:HD23	1:A:213:LEU:HB3	1.95	0.47
1:B:331:ASP:N	1:B:332:PRO:HD3	2.28	0.47
1:A:265:GLN:NE2	1:A:337:ILE:H	2.13	0.46
1:A:279:ALA:O	1:A:283:MET:HG3	2.15	0.46
1:B:285:ARG:NH2	1:B:332:PRO:O	2.33	0.46
1:B:270:ARG:HG2	1:B:270:ARG:HH11	1.81	0.46
1:B:344:HIS:CD2	1:B:346:ALA:HB3	2.51	0.46
1:B:175:THR:HG22	1:B:246:GLU:OE1	2.16	0.45
1:B:127:VAL:O	1:B:131:VAL:HG23	2.16	0.45
1:B:189:THR:O	1:B:193:GLU:HG3	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:ARG:HD2	1:B:304:LEU:HD22	1.97	0.45
1:B:265:GLN:NE2	1:B:337:ILE:HG12	2.31	0.45
1:A:357:ALA:HB3	1:A:358:PRO:HD3	1.98	0.45
1:B:115:ARG:HB2	1:B:115:ARG:HH11	1.81	0.45
1:B:296:ARG:HG3	1:B:296:ARG:HH11	1.82	0.45
1:B:358:PRO:HD2	5:B:2098:HOH:O	2.16	0.44
1:A:344:HIS:HD2	1:A:346:ALA:N	2.13	0.44
1:B:281:GLU:OE1	1:B:344:HIS:HE1	2.00	0.44
1:A:99:ARG:HB2	4:A:1431:SO4:O1	2.16	0.44
1:B:382:VAL:HG22	1:B:386:GLU:HB2	1.98	0.44
1:A:265:GLN:NE2	1:A:337:ILE:HG12	2.33	0.44
1:B:165:GLU:HB3	1:B:166:PRO:HD3	1.98	0.44
1:A:334:ARG:HH11	1:A:336:ASP:HB2	1.83	0.44
1:A:334:ARG:HH11	1:A:334:ARG:HG2	1.82	0.44
1:B:260:LEU:HD23	1:B:266:LEU:HD22	1.99	0.44
1:A:227:ARG:HB3	5:A:2055:HOH:O	2.18	0.43
1:A:334:ARG:NH1	1:A:336:ASP:HB2	2.32	0.43
1:A:292:SER:HB2	1:A:394:MET:HA	2.01	0.43
1:B:175:THR:HG21	1:B:245:HIS:HD2	1.82	0.43
1:A:286:TYR:CD2	1:A:287:GLU:HG2	2.53	0.43
1:B:289:PRO:O	1:B:395:ILE:HD12	2.19	0.43
1:A:291:GLU:HB3	1:A:393:PRO:O	2.19	0.43
1:B:344:HIS:CD2	1:B:346:ALA:H	2.31	0.43
1:A:103:LEU:O	1:A:106:LEU:HB2	2.18	0.43
1:A:273:MET:HE3	1:A:276:LEU:HB2	2.01	0.43
1:B:395:ILE:O	1:B:395:ILE:HG23	2.18	0.42
1:A:273:MET:HE2	1:A:369:ARG:NH2	2.33	0.42
1:A:43:ARG:NH2	1:A:313:ASP:OD2	2.52	0.42
1:B:324:ARG:HA	1:B:332:PRO:HB3	2.02	0.42
2:A:1407:HEM:CMA	2:A:1407:HEM:HBA2	2.50	0.42
1:B:40:PRO:HB2	1:B:60:ARG:HG2	2.00	0.42
1:A:282:GLU:OE1	1:A:282:GLU:HA	2.20	0.42
1:A:41:ALA:HA	1:A:54:LEU:O	2.20	0.42
1:B:219:ARG:HG2	5:B:2057:HOH:O	2.20	0.42
1:A:40:PRO:HB2	1:A:60:ARG:HG2	2.02	0.42
1:B:150:TRP:CD1	1:B:245:HIS:HE1	2.39	0.41
1:B:282:GLU:HA	1:B:282:GLU:OE1	2.20	0.41
1:B:150:TRP:N	1:B:151:PRO:CD	2.83	0.41
1:A:137:ALA:HA	1:A:138:PRO:HD3	1.91	0.41
1:B:382:VAL:HG23	1:B:386:GLU:OE1	2.21	0.41
1:A:256:MET:O	1:A:260:LEU:HG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:LEU:HD23	1:A:402:PRO:O	2.21	0.41
1:B:161:LEU:HD12	1:B:241:LEU:CD2	2.50	0.41
1:B:145:MET:HA	1:B:149:ALA:HB3	2.01	0.41
1:A:200:ARG:NE	5:A:2042:HOH:O	2.38	0.41
1:A:344:HIS:CD2	1:A:346:ALA:H	2.32	0.41
1:B:265:GLN:HE21	1:B:337:ILE:HG23	1.84	0.41
1:A:251:LEU:HD22	2:A:1407:HEM:HBB1	2.02	0.40
1:A:358:PRO:HD2	5:A:2095:HOH:O	2.21	0.40
1:B:58:TYR:CG	1:B:328:ARG:HG3	2.56	0.40
1:A:243:ALA:HA	3:A:1408:PXI:O2	2.20	0.40
1:A:341:THR:O	1:A:342:ALA:C	2.60	0.40
1:B:344:HIS:HD2	1:B:346:ALA:N	2.14	0.40
1:B:327:GLU:H	1:B:327:GLU:CD	2.25	0.40
1:B:96:ASP:HB3	1:B:97:PRO:HD2	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	392/436 (90%)	379 (97%)	13 (3%)	0	100	100
1	B	393/436 (90%)	384 (98%)	9 (2%)	0	100	100
All	All	785/872 (90%)	763 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	317/355 (89%)	313 (99%)	4 (1%)	73	84
1	B	319/355 (90%)	314 (98%)	5 (2%)	68	79
All	All	636/710 (90%)	627 (99%)	9 (1%)	71	82

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	LEU
1	A	238	HIS
1	A	285	ARG
1	A	380	LEU
1	B	106	LEU
1	B	115	ARG
1	B	238	HIS
1	B	285	ARG
1	B	305	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	188	GLN
1	A	208	GLN
1	A	265	GLN
1	A	344	HIS
1	B	186	GLN
1	B	188	GLN
1	B	238	HIS
1	B	245	HIS
1	B	265	GLN
1	B	344	HIS

### 5.3.3 RNA ⓘ

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](#)

9 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	1407	1	28,50,50	1.59	6 (21%)	17,82,82	1.00	0
3	PXI	A	1408	-	32,33,33	1.75	5 (15%)	39,47,47	2.24	11 (28%)
4	SO4	A	1430	-	4,4,4	0.39	0	6,6,6	0.11	0
4	SO4	A	1431	-	4,4,4	0.34	0	6,6,6	0.09	0
4	SO4	A	1432	-	4,4,4	0.42	0	6,6,6	0.11	0
4	SO4	A	1434	-	4,4,4	0.38	0	6,6,6	0.13	0
2	HEM	B	1408	1	28,50,50	1.69	4 (14%)	17,82,82	1.10	1 (5%)
3	PXI	B	1409	-	32,33,33	1.73	6 (18%)	39,47,47	2.18	11 (28%)
4	SO4	B	1433	-	4,4,4	0.35	0	6,6,6	0.12	0

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	1407	1	-	0/6/54/54	0/0/8/8
3	PXI	A	1408	-	-	0/43/59/59	0/1/2/2
4	SO4	A	1430	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1431	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1432	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	A	1434	-	-	0/0/0/0	0/0/0/0
2	HEM	B	1408	1	-	0/6/54/54	0/0/8/8
3	PXI	B	1409	-	-	0/43/59/59	0/1/2/2
4	SO4	B	1433	-	-	0/0/0/0	0/0/0/0

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1408	HEM	C3C-CAC	-4.55	1.38	1.47
2	A	1407	HEM	C3C-CAC	-4.39	1.39	1.47
2	B	1408	HEM	C3B-CAB	-3.92	1.40	1.47
2	B	1408	HEM	C3C-C2C	-3.43	1.35	1.40
2	A	1407	HEM	C3B-CAB	-3.43	1.41	1.47
2	A	1407	HEM	C3C-C2C	-2.56	1.37	1.40
2	B	1408	HEM	C3B-C2B	-2.48	1.37	1.40
3	B	1409	PXI	C5-C7	2.02	1.59	1.55
3	B	1409	PXI	C11-C9	2.05	1.55	1.51
3	A	1408	PXI	O3-C7	2.08	1.48	1.43
2	A	1407	HEM	CBC-CAC	2.13	1.43	1.28
3	B	1409	PXI	O3-C7	2.19	1.49	1.43
3	A	1408	PXI	O4-C9	2.24	1.48	1.44
2	A	1407	HEM	C1C-NC	2.26	1.39	1.36
2	A	1407	HEM	CBB-CAB	2.33	1.45	1.28
3	B	1409	PXI	C15-C12	2.72	1.59	1.53
3	A	1408	PXI	C15-C12	3.24	1.60	1.53
3	B	1409	PXI	C24-C3	3.51	1.62	1.53
3	A	1408	PXI	C24-C3	3.88	1.63	1.53
3	A	1408	PXI	C16-C7	5.82	1.63	1.53
3	B	1409	PXI	C16-C7	5.87	1.64	1.53

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1408	PXI	O3-C7-C5	-6.69	98.98	111.12
3	B	1409	PXI	O3-C7-C5	-6.11	100.02	111.12
3	A	1408	PXI	C10-C9-C11	-3.27	108.14	113.39
3	B	1409	PXI	C10-C9-C11	-3.02	108.56	113.39
3	A	1408	PXI	C13-N1-C12	-2.80	104.92	113.08
3	A	1408	PXI	C25-C24-C23	-2.73	103.16	110.07
3	B	1409	PXI	C25-C24-C23	-2.69	103.25	110.07
3	B	1409	PXI	C13-N1-C12	-2.59	105.53	113.08
2	B	1408	HEM	CAA-C2A-C3A	-2.59	121.62	129.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1408	PXI	C6-C5-C7	-2.48	107.27	112.86
3	B	1409	PXI	C6-C5-C7	-2.37	107.52	112.86
3	B	1409	PXI	O3-C8-O4	2.15	115.91	110.70
3	B	1409	PXI	C17-C16-C7	2.17	114.84	111.24
3	A	1408	PXI	O3-C8-O4	2.42	116.57	110.70
3	B	1409	PXI	C7-C5-C4	2.51	115.21	110.07
3	A	1408	PXI	C17-C16-C7	2.58	115.52	111.24
3	A	1408	PXI	C7-C5-C4	2.74	115.70	110.07
3	B	1409	PXI	C8-O3-C7	2.84	124.92	118.00
3	A	1408	PXI	C8-O3-C7	3.16	125.68	118.00
3	A	1408	PXI	O1-C3-C2	3.48	112.73	106.89
3	B	1409	PXI	O1-C3-C2	4.35	114.20	106.89
3	A	1408	PXI	C3-O1-C4	7.61	129.23	117.92
3	B	1409	PXI	C3-O1-C4	7.70	129.36	117.92

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	A	1407	HEM	2	0
3	A	1408	PXI	2	0
4	A	1431	SO4	1	0

## 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, 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	394/436 (90%)	0.02	6 (1%) 74 83	13, 28, 48, 59	0
1	B	395/436 (90%)	0.03	7 (1%) 69 78	14, 29, 54, 69	0
All	All	789/872 (90%)	0.03	13 (1%) 72 81	13, 28, 51, 69	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	180	PHE	3.1
1	B	390	TYR	3.1
1	A	183	ASP	2.7
1	B	184	PRO	2.6
1	A	377	ASP	2.6
1	B	181	PRO	2.3
1	A	182	ASP	2.2
1	B	182	ASP	2.1
1	A	184	PRO	2.1
1	B	19	ALA	2.1
1	A	150	TRP	2.1
1	A	181	PRO	2.1
1	B	386	GLU	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(Å <sup>2</sup> )	Q<0.9
4	SO4	A	1432	5/5	0.84	0.23	8.00	81,82,83,83	0
4	SO4	B	1433	5/5	0.91	0.22	5.12	68,69,70,71	0
4	SO4	A	1434	5/5	0.89	0.21	1.63	80,80,81,82	0
3	PXI	A	1408	32/32	0.92	0.18	1.05	25,30,36,38	0
3	PXI	B	1409	32/32	0.94	0.15	0.84	26,31,36,37	0
2	HEM	B	1408	43/43	0.97	0.12	-0.26	12,19,22,23	0
2	HEM	A	1407	43/43	0.97	0.12	-0.67	9,15,19,21	0
4	SO4	A	1431	5/5	0.92	0.20	-	71,71,72,72	0
4	SO4	A	1430	5/5	0.88	0.20	-	71,72,73,73	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.