



# wwPDB X-ray Structure Validation Summary Report

Mar 1, 2014 – 12:35 AM GMT

PDB ID : 2V0M  
Title : CRYSTAL STRUCTURE OF HUMAN P450 3A4 IN COMPLEX WITH KE-  
TOCONAZOLE  
Authors : Sjogren, T.; Ekroos, M.  
Deposited on : 2007-05-15  
Resolution : 2.80 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

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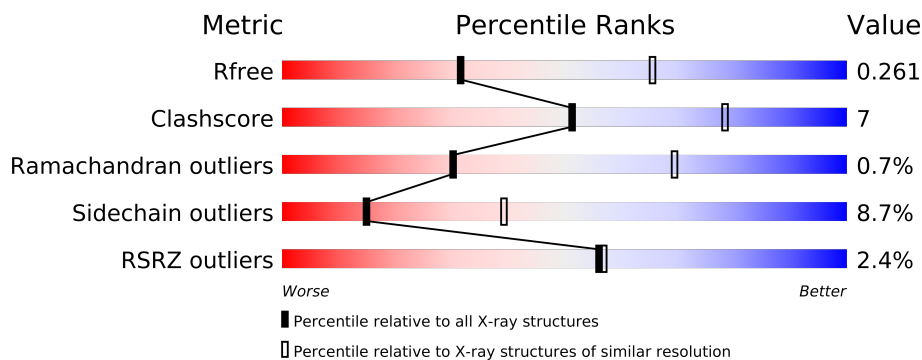
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	485	
1	B	485	
1	C	485	
1	D	485	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15068 atoms, of which 0 are hydrogen and 0 are deuterium.

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 3A4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	455	Total	C	N	O	S	0	0	0
			3651	2379	596	652	24			
1	B	451	Total	C	N	O	S	0	0	0
			3623	2361	592	646	24			
1	C	465	Total	C	N	O	S	0	0	0
			3734	2425	613	672	24			
1	D	453	Total	C	N	O	S	0	0	0
			3642	2374	594	650	24			

There are 28 discrepancies between the modelled and reference sequences:

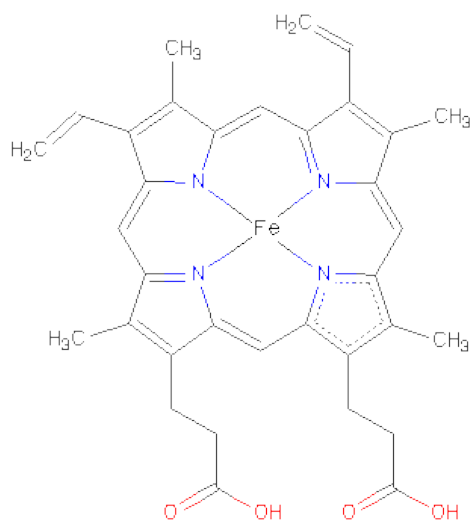
Chain	Residue	Modelled	Actual	Comment	Reference
A	23	MET	-	EXPRESSION TAG	UNP P08684
A	24	ALA	-	EXPRESSION TAG	UNP P08684
A	504	HIS	-	EXPRESSION TAG	UNP P08684
A	505	HIS	-	EXPRESSION TAG	UNP P08684
A	506	HIS	-	EXPRESSION TAG	UNP P08684
A	507	HIS	-	EXPRESSION TAG	UNP P08684
A	392	VAL	TRP	CONFLICT	UNP P08684
B	23	MET	-	EXPRESSION TAG	UNP P08684
B	24	ALA	-	EXPRESSION TAG	UNP P08684
B	504	HIS	-	EXPRESSION TAG	UNP P08684
B	505	HIS	-	EXPRESSION TAG	UNP P08684
B	506	HIS	-	EXPRESSION TAG	UNP P08684
B	507	HIS	-	EXPRESSION TAG	UNP P08684
B	392	VAL	TRP	CONFLICT	UNP P08684
C	23	MET	-	EXPRESSION TAG	UNP P08684
C	24	ALA	-	EXPRESSION TAG	UNP P08684
C	504	HIS	-	EXPRESSION TAG	UNP P08684
C	505	HIS	-	EXPRESSION TAG	UNP P08684
C	506	HIS	-	EXPRESSION TAG	UNP P08684
C	507	HIS	-	EXPRESSION TAG	UNP P08684
C	392	VAL	TRP	CONFLICT	UNP P08684

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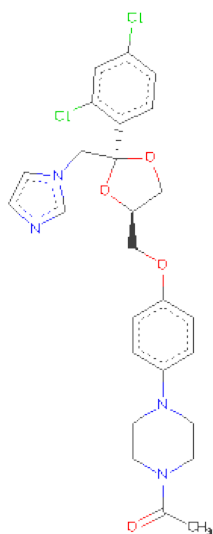
Chain	Residue	Modelled	Actual	Comment	Reference
D	23	MET	-	EXPRESSION TAG	UNP P08684
D	24	ALA	-	EXPRESSION TAG	UNP P08684
D	504	HIS	-	EXPRESSION TAG	UNP P08684
D	505	HIS	-	EXPRESSION TAG	UNP P08684
D	506	HIS	-	EXPRESSION TAG	UNP P08684
D	507	HIS	-	EXPRESSION TAG	UNP P08684
D	392	VAL	TRP	CONFLICT	UNP P08684

- 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 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is 1-ACETYL-4-(4-{[(2S,4R)-2-(2,4-DICHLOROPHENYL)-2-(1H-IMIDAZOL-1-YLMETHYL)-1,3-DIOXOLAN-4-YL]METHOXY}PHENYL)PIPERAZINE (three-letter code: KLN) (formula:  $C_{26}H_{28}Cl_2N_4O_4$ ).



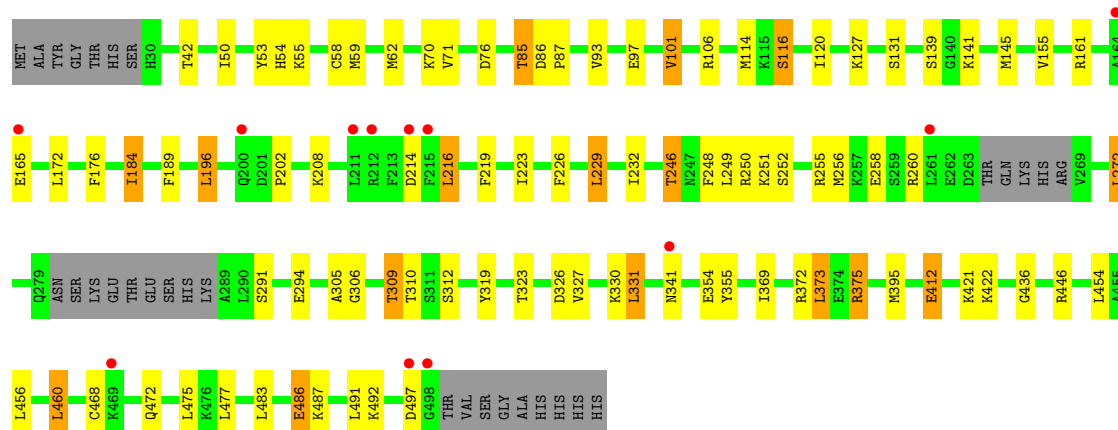
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			36	26	2	4	4		
3	A	1	Total	C	Cl	N	O	0	0
			36	26	2	4	4		
3	B	1	Total	C	Cl	N	O	0	0
			36	26	2	4	4		
3	B	1	Total	C	N	O		0	0
			22	16	2	4			
3	C	1	Total	C	Cl	N	O	0	0
			36	26	2	4	4		
3	C	1	Total	C	N	O		0	0
			22	16	2	4			
3	D	1	Total	C	Cl	N	O	0	0
			36	26	2	4	4		
3	D	1	Total	C	N	O		0	0
			22	16	2	4			

### 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 errors 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 ( $\text{RSRZ} > 2$ ). 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.

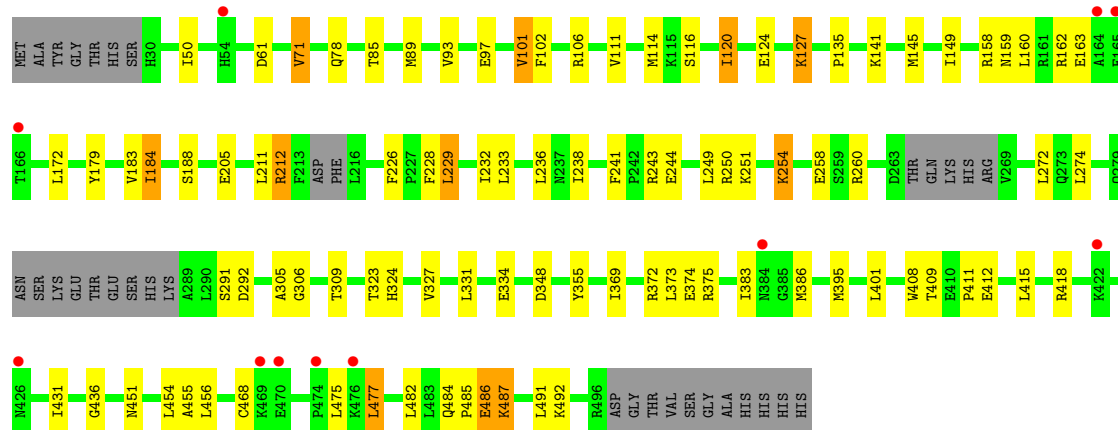
#### • Molecule 1: CYTOCHROME P450 3A4

Chain A: 



#### • Molecule 1: CYTOCHROME P450 3A4

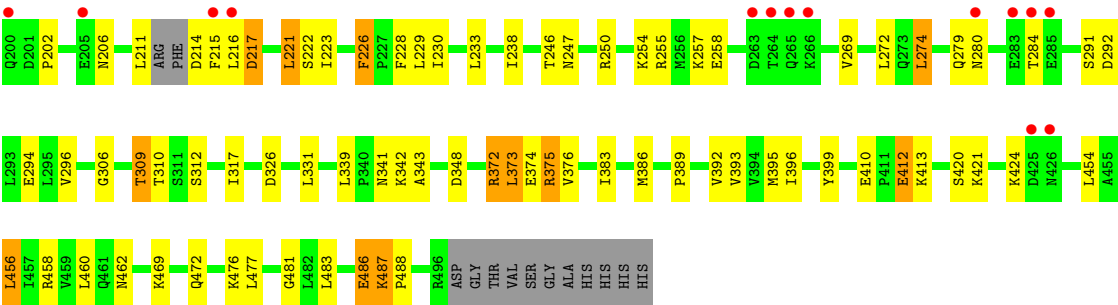
Chain B: 



#### • Molecule 1: CYTOCHROME P450 3A4

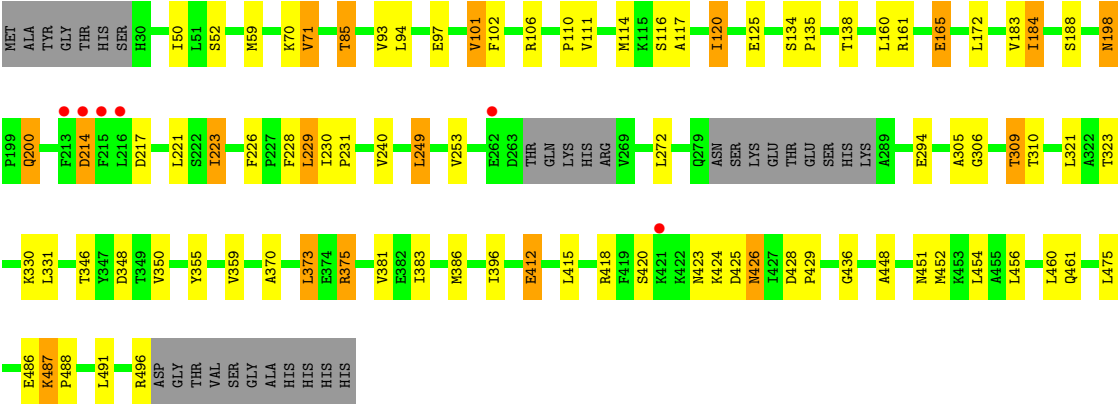
Chain C: 





• Molecule 1: CYTOCHROME P450 3A4

Chain D:



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	228.94Å 66.36Å 146.42Å 90.00° 102.80° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 29.76 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.1 (30.00-2.80) 97.1 (29.76-2.80)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.64 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.218 , 0.271 0.210 , 0.261	Depositor DCC
$R_{free}$ test set	2654 reflections (5.40%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.1	Xtriage
Anisotropy	0.147	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 3.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 51807 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	15068	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% of the height of the origin peak. No significant pseudotranslation is detected.*

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



## 5 Model quality

### 5.1 Standard geometry

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

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	0.41	0/3739	0.56	0/5059
1	B	0.40	0/3709	0.56	0/5017
1	C	0.41	0/3823	0.57	0/5172
1	D	0.42	0/3730	0.57	0/5047
All	All	0.41	0/15001	0.56	0/20295

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3651	0	3727	46	0
1	B	3623	0	3708	50	0
1	C	3734	0	3812	63	0
1	D	3642	0	3722	51	0
2	A	43	0	30	6	0
2	B	43	0	30	3	0
2	C	43	0	30	5	0
2	D	43	0	30	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	72	0	56	5	0
3	B	58	0	48	3	0
3	C	58	0	48	9	0
3	D	58	0	48	1	0
All	All	15068	0	15289	221	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

The worst 5 of 221 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:1499:KLN:C7	3:C:1499:KLN:C6	1.83	1.54
3:C:1499:KLN:O2	3:C:1499:KLN:C1	1.76	1.33
3:C:1499:KLN:C1	3:C:1499:KLN:O1	1.93	1.16
3:A:1501:KLN:CL2	3:A:1501:KLN:H6	1.92	1.05
1:B:305:ALA:O	1:B:309:THR:HG22	1.67	0.95

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	449/485 (93%)	421 (94%)	25 (6%)	3 (1%)	30	69
1	B	443/485 (91%)	419 (95%)	22 (5%)	2 (0%)	38	76
1	C	461/485 (95%)	431 (94%)	24 (5%)	6 (1%)	18	51
1	D	447/485 (92%)	432 (97%)	14 (3%)	1 (0%)	56	88
All	All	1800/1940 (93%)	1703 (95%)	85 (5%)	12 (1%)	30	69

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	497	ASP

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Mol	Chain	Res	Type
1	C	341	ASN
1	A	487	LYS
1	B	212	ARG
1	C	279	GLN

### 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	413/441 (94%)	376 (91%)	37 (9%)	14	37
1	B	411/441 (93%)	376 (92%)	35 (8%)	15	41
1	C	424/441 (96%)	388 (92%)	36 (8%)	15	41
1	D	413/441 (94%)	377 (91%)	36 (9%)	15	39
All	All	1661/1764 (94%)	1517 (91%)	144 (9%)	15	39

5 of 144 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	369	ILE
1	C	160	LEU
1	D	373	LEU
1	B	412	GLU
1	C	78	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	30	HIS
1	C	279	GLN
1	D	198	ASN
1	B	451	ASN
1	B	472	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

12 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	1499	1,3	49,50,50	2.38	16 (32%)	46,82,82	2.10	10 (21%)
3	KLN	A	1500	2	40,40,40	0.93	1 (2%)	57,57,57	1.51	10 (17%)
3	KLN	A	1501	-	40,40,40	0.71	0	57,57,57	1.69	9 (15%)
2	HEM	B	1497	1,3	49,50,50	2.27	15 (30%)	46,82,82	2.09	9 (19%)
3	KLN	B	1498	2	40,40,40	0.85	1 (2%)	57,57,57	1.51	9 (15%)
3	KLN	B	1499	-	22,24,40	0.58	0	29,32,57	1.74	7 (24%)
2	HEM	C	1497	1,3	49,50,50	2.51	14 (28%)	46,82,82	2.14	10 (21%)
3	KLN	C	1498	2	40,40,40	0.81	1 (2%)	57,57,57	1.41	8 (14%)
3	KLN	C	1499	-	22,22,40	2.07	4 (18%)	29,29,57	5.34	8 (27%)
2	HEM	D	1497	1,3	49,50,50	2.29	15 (30%)	46,82,82	1.95	8 (17%)
3	KLN	D	1498	2	40,40,40	0.72	0	57,57,57	1.30	6 (10%)
3	KLN	D	1499	-	22,24,40	0.83	1 (4%)	29,32,57	1.62	5 (17%)

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	1499	1,3	-	0/14/114/114	0/0/8/8
3	KLN	A	1500	2	-	0/24/45/45	0/5/5/5
3	KLN	A	1501	-	-	1/24/45/45	0/5/5/5
2	HEM	B	1497	1,3	-	0/14/114/114	0/0/8/8
3	KLN	B	1498	2	-	0/24/45/45	0/5/5/5
3	KLN	B	1499	-	-	0/13/30/45	0/3/3/5
2	HEM	C	1497	1,3	-	0/14/114/114	0/0/8/8
3	KLN	C	1498	2	-	0/24/45/45	0/5/5/5
3	KLN	C	1499	-	-	0/15/25/45	0/2/2/5
2	HEM	D	1497	1,3	-	0/14/114/114	0/0/8/8
3	KLN	D	1498	2	-	0/24/45/45	0/5/5/5
3	KLN	D	1499	-	-	0/13/30/45	0/3/3/5

The worst 5 of 68 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1499	KLN	C7-C6	7.82	1.83	1.51
2	C	1497	HEM	C2D-C1D	6.90	1.46	1.44
2	C	1497	HEM	C3D-C2D	5.78	1.53	1.43
2	C	1497	HEM	C3C-C2C	-5.76	1.33	1.43
2	A	1499	HEM	C3D-C2D	5.58	1.53	1.43

The worst 5 of 99 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1499	KLN	O1-C6-C7	-25.84	109.89	119.54
3	C	1499	KLN	O2-C7-C6	-9.75	99.63	113.28
2	A	1499	HEM	C3B-C4B-NB	-8.71	107.77	114.00
2	C	1497	HEM	C3B-C4B-NB	-8.44	107.96	114.00
2	D	1497	HEM	C3B-C4B-NB	-8.39	108.00	114.00

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1501	KLN	C4-C5-C8-C9

There are no ring outliers.

## 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

### 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	455/485 (93%)	-0.04	12 (2%) 53 54	12, 34, 59, 65	0
1	B	451/485 (92%)	0.01	11 (2%) 56 57	11, 34, 58, 66	0
1	C	465/485 (95%)	-0.15	15 (3%) 45 46	11, 27, 49, 76	0
1	D	453/485 (93%)	-0.31	6 (1%) 74 75	9, 23, 47, 58	0
All	All	1824/1940 (94%)	-0.12	44 (2%) 56 57	9, 29, 57, 76	0

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	498	GLY	6.3
1	A	215	PHE	4.7
1	C	216	LEU	4.3
1	C	284	THR	4.2
1	A	212	ARG	4.1

### 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. 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	KLN	C	1499	22/36	0.23	1.21	55,58,60,60	0
3	KLN	D	1499	22/36	0.25	0.82	54,59,62,63	0
3	KLN	C	1498	36/36	0.19	0.03	24,31,35,36	0
3	KLN	B	1498	36/36	0.20	-0.03	26,32,35,37	0
2	HEM	C	1497	43/43	0.17	-0.07	10,11,12,12	0
2	HEM	D	1497	43/43	0.17	-0.11	7,9,11,12	0
3	KLN	A	1501	36/36	0.22	-0.16	63,73,78,78	0
2	HEM	A	1499	43/43	0.16	-0.17	13,15,18,20	0
3	KLN	A	1500	36/36	0.19	-0.25	31,33,37,38	0
3	KLN	B	1499	22/36	0.19	-0.32	36,40,45,45	0
2	HEM	B	1497	43/43	0.16	-0.35	9,11,12,14	0
3	KLN	D	1498	36/36	0.17	-0.48	19,25,27,28	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.