



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 14, 2016 – 12:01 PM EST

PDB ID : 5LI7  
Title : Crystal structure of Mycobacterium tuberculosis CYP126A1 in complex with  
1-(3-(1H-imidazol-1-yl)propyl)-3-((3s,5s,7s)-adamantan-1-yl)urea  
Authors : Levy, C.; Munro, A.W.; Leys, D.  
Deposited on : 2016-07-14  
Resolution : 1.58 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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028442  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : rb-20028442

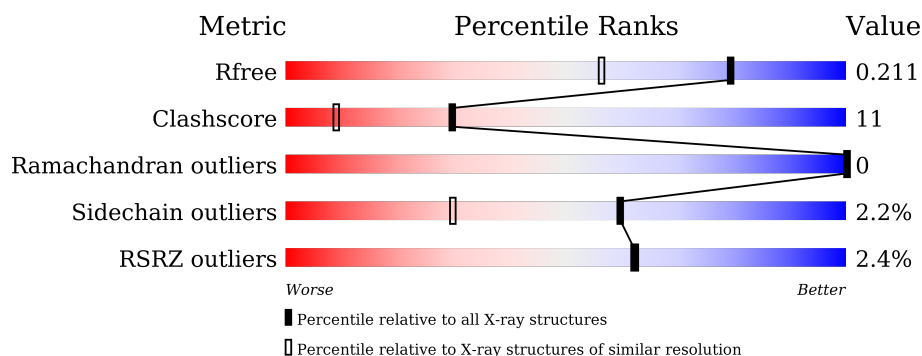
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.58 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))
$R_{free}$	91344	3815 (1.60-1.56)
Clashscore	102246	4131 (1.60-1.56)
Ramachandran outliers	100387	4021 (1.60-1.56)
Sidechain outliers	100360	4018 (1.60-1.56)
RSRZ outliers	91569	3823 (1.60-1.56)

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	414	 % 73% 14% • 10%
1	B	414	 4% 74% 14% • 10%

## 2 Entry composition [i](#)

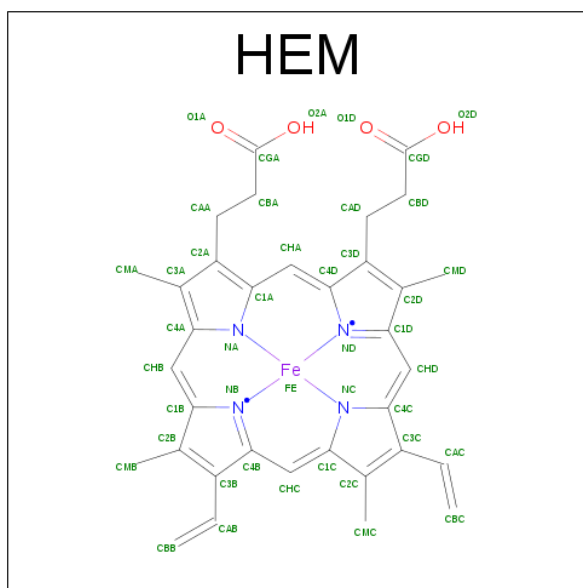
There are 4 unique types of molecules in this entry. The entry contains 7108 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Putative cytochrome P450 126.

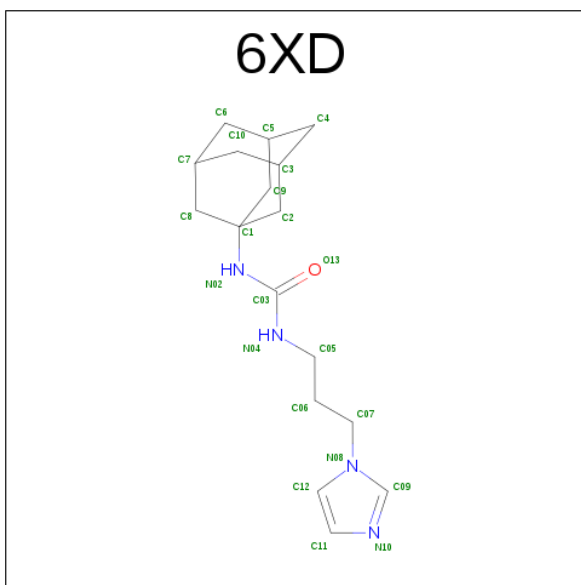
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	373	Total	C	N	O	S	0	8	0
			3006	1896	548	554	8			
1	B	372	Total	C	N	O	S	0	5	0
			2974	1879	540	547	8			

- 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		

- Molecule 3 is 1-(1-adamantyl)-3-(3-imidazol-1-ylpropyl)urea (three-letter code: 6XD) (formula:  $C_{17}H_{26}N_4O$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 22	C 17	N 4	O 1	0	0
3	B	1	Total 22	C 17	N 4	O 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	545	Total O 545 545	0	0
4	B	453	Total O 453 453	0	0

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 ( $RSRZ > 2$ ). 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.

- Chain A:
- 
- 73% 14% 10%
- MET THR THR ALA ALA GLY L7 D16 H17 F18 R31 R32 Y37 R40 P46 E49 W52 A58 E59 R65 D66 Y70 R79 Q86 G92 Q93 M98 D99 P101 R102 H103 T104 V110 S111 V122 R127 R131 D135 Q156
- T167 D168 R169 F173 V176 GLU PRO GLY PHE ASP PHE ARG GLY SER ARG ARG ALA THR MET PRO ARG LEU ASN VAL GLU ASP ALA GLY SER R201 R202 Y203 Y204 M221 A228 T228 ASP ASP PRO ASP ALA PRO ALA L238 Y244 H248 L249 L250 A253 E256 W257
- G264 D274 Q275 R280 R295 L296 T297 S298 P299 S300 R304 R305 R309 A310 V311 Q316 E319 Q322 E328 V337 F338 D339 R340 D345 I346 K349 P350 H353 G359 Y362 G365 R374 P382 H401 R405 R412 GLY

- Chain B:
- 
- 4% 74% 14% 10%
- | Amino Acid | Frequency (%) |
|------------|---------------|
| L172       | 4%            |
| F173       | 4%            |
| E174       | 4%            |
| A175       | 4%            |
| V176       | 4%            |
| GLU        | 74%           |
| PRO        | 74%           |
| GLY        | 74%           |
| PHE        | 74%           |
| ASP        | 74%           |
| PHE        | 74%           |
| ARG        | 74%           |
| GLY        | 74%           |
| SER        | 74%           |
| ARG        | 74%           |
| ARG        | 74%           |
| ALA        | 74%           |
| ALA        | 74%           |
| THR        | 74%           |
| MET        | 74%           |
| PRO        | 74%           |
| ARG        | 74%           |
| LEU        | 74%           |
| ASN        | 74%           |
| VAL        | 74%           |
| GLU        | 74%           |
| ASP        | 74%           |
| ALA        | 74%           |
| GLY        | 74%           |
| SER        | 74%           |
| ARG        | 74%           |
| L202       | 74%           |
| Y203       | 74%           |
| A215       | 74%           |
| E216       | 74%           |
| A228       | 74%           |
| THR        | 74%           |
| ILE        | 74%           |
| ASP        | 74%           |
| ASP        | 74%           |
| PRO        | 74%           |
| ASP        | 74%           |
| ALA        | 74%           |
| PRO        | 74%           |
| ALA        | 74%           |
| L238       | 74%           |
| S239       | 74%           |
| D240       | 74%           |
| A241       | 74%           |
| E242       | 74%           |
| H248       | 74%           |
| F251       | 74%           |
| S252       | 74%           |
| A253       | 74%           |
| Q254       | 74%           |
| A255       | 74%           |
| E256       | 74%           |
| T257       | 74%           |
| L266       | 74%           |
| D274       | 74%           |
| Q275       | 74%           |
| L276       | 74%           |
| Q277       | 74%           |
| L286       | 74%           |
| E292       | 74%           |
| R295       | 74%           |
| R304       | 74%           |
| R305       | 74%           |
| E319       | 74%           |
| Q322       | 74%           |
| R340       | 74%           |
| I346       | 74%           |
| T347       | 74%           |
| R348       | 74%           |
| Q358       | 74%           |
| L364       | 74%           |
| R374       | 74%           |
| V375       | 74%           |
| L376       | 74%           |
| R383       | 74%           |
| E394       | 74%           |
| R401       | 74%           |
| R405       | 74%           |
| R412       | 74%           |
| GLY        | 74%           |
| GLY        | 74%           |
| ALA        | 74%           |
| GLY        | 74%           |
| ALA        | 74%           |
| ALA        | 74%           |
| GLY        | 74%           |
| L7         | 74%           |
| S8         | 74%           |
| G9         | 74%           |
| L12        | 74%           |
| T13        | 74%           |
| D14        | 74%           |
| A28        | 74%           |
| R31        | 74%           |
| R32        | 74%           |
| E33        | 74%           |
| Y37        | 74%           |
| R38        | 74%           |
| H39        | 74%           |
| E43        | 74%           |
| E49        | 74%           |
| G50        | 74%           |
| F51        | 74%           |
| W52        | 74%           |
| L61        | 74%           |
| E62        | 74%           |
| R78        | 74%           |
| R79        | 74%           |
| G82        | 74%           |
| Q86        | 74%           |
| Q93        | 74%           |
| R102       | 74%           |
| H103       | 74%           |
| R107       | 74%           |
| L114       | 74%           |
| D125       | 74%           |
| M155       | 74%           |
| Q156       | 74%           |
| T167       | 74%           |
| D168       | 74%           |
| R169       | 74%           |
| H170       | 74%           |
| H171       | 74%           |

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.25Å 69.91Å 226.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.31 – 1.58 57.32 – 1.58	Depositor EDS
% Data completeness (in resolution range)	100.0 (57.31-1.58) 99.8 (57.32-1.58)	Depositor EDS
$R_{merge}$	0.02	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.41 (at 1.58Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.170 , 0.203 0.178 , 0.211	Depositor DCC
$R_{free}$ test set	6486 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	17.2	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 49.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7108	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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, 6XD

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	1.31	10/3080 (0.3%)	1.23	31/4183 (0.7%)
1	B	1.19	6/3048 (0.2%)	1.05	10/4141 (0.2%)
All	All	1.25	16/6128 (0.3%)	1.14	41/8324 (0.5%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	49	GLU	CB-CG	-10.15	1.32	1.52
1	A	98	MET	CB-CG	-7.50	1.27	1.51
1	A	127	ARG	CB-CG	-7.17	1.33	1.52
1	B	49	GLU	CB-CG	-7.10	1.38	1.52
1	B	292	GLU	CD-OE2	7.04	1.33	1.25
1	A	49	GLU	CG-CD	6.97	1.62	1.51
1	B	33	GLU	CB-CG	5.98	1.63	1.52
1	A	37	TYR	CG-CD2	-5.63	1.31	1.39
1	B	254	GLY	C-O	5.51	1.32	1.23
1	A	110	VAL	CB-CG1	5.50	1.64	1.52
1	A	316	GLN	CD-OE1	5.47	1.35	1.24
1	A	92	GLY	C-O	5.42	1.32	1.23
1	B	62	GLU	CG-CD	5.38	1.60	1.51
1	B	252	SER	CB-OG	5.24	1.49	1.42
1	A	311	VAL	CB-CG1	5.22	1.63	1.52
1	A	328	GLU	CD-OE2	5.00	1.31	1.25

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	340	ARG	NE-CZ-NH1	13.86	127.23	120.30
1	A	127	ARG	NE-CZ-NH2	-10.31	115.14	120.30
1	A	340	ARG	NE-CZ-NH2	-8.54	116.03	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	127	ARG	CG-CD-NE	-8.52	93.90	111.80
1	A	66	ASP	CB-CG-OD2	-8.17	110.94	118.30
1	B	107	ARG	NE-CZ-NH1	8.08	124.34	120.30
1	B	383	ARG	NE-CZ-NH2	-7.93	116.33	120.30
1	B	102[A]	ARG	NE-CZ-NH1	-7.90	116.35	120.30
1	B	102[B]	ARG	NE-CZ-NH1	-7.90	116.35	120.30
1	B	240	ASP	CB-CG-OD2	-7.32	111.71	118.30
1	A	374	ARG	NE-CZ-NH2	-7.21	116.70	120.30
1	A	40	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	A	405	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	A	305	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	A	374	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	B	31	ARG	NE-CZ-NH1	6.17	123.38	120.30
1	A	339	ASP	CB-CG-OD1	6.10	123.79	118.30
1	B	305	ARG	NE-CZ-NH1	6.05	123.33	120.30
1	A	127	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	A	18	PHE	CB-CG-CD1	-6.00	116.60	120.80
1	A	339	ASP	CB-CG-OD2	-5.91	112.98	118.30
1	A	18	PHE	CB-CG-CD2	5.88	124.92	120.80
1	A	295	ARG	NE-CZ-NH2	-5.88	117.36	120.30
1	A	250	LEU	CB-CG-CD1	5.75	120.78	111.00
1	A	16	ASP	CB-CG-OD2	-5.75	113.13	118.30
1	A	59	GLU	OE1-CD-OE2	-5.69	116.47	123.30
1	B	78	ARG	NE-CZ-NH1	5.67	123.14	120.30
1	A	309	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	A	40	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	A	345	ASP	CB-CG-OD2	-5.64	113.22	118.30
1	A	305	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	B	14	ASP	CB-CG-OD1	5.54	123.29	118.30
1	A	99	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	280	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	A	280	ARG	CG-CD-NE	-5.30	100.67	111.80
1	A	374	ARG	CG-CD-NE	-5.27	100.74	111.80
1	A	65	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	A	135	ASP	CB-CG-OD1	5.18	122.97	118.30
1	B	32	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	A	345	ASP	CB-CG-OD1	5.05	122.85	118.30
1	A	31	ARG	NE-CZ-NH1	5.03	122.81	120.30

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	3006	0	2957	78	0
1	B	2974	0	2929	66	0
2	A	43	0	30	2	0
2	B	43	0	30	2	0
3	A	22	0	0	3	0
3	B	22	0	0	1	0
4	A	545	0	0	37	3
4	B	453	0	0	20	0
All	All	7108	0	5946	135	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (135) 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:274:ASP:HB3	4:B:932:HOH:O	1.32	1.21
1:A:316:GLN:HG3	4:A:895:HOH:O	1.43	1.14
1:A:274:ASP:HB3	4:A:982:HOH:O	1.47	1.11
1:A:65:ARG:NE	4:A:603:HOH:O	1.80	1.09
1:A:350:PRO:O	4:A:601:HOH:O	1.71	1.07
1:A:79:ARG:HH21	1:B:93:GLN:NE2	1.53	1.06
1:B:82:GLY:O	4:B:601:HOH:O	1.75	1.03
1:A:353:HIS:O	4:A:602:HOH:O	1.79	1.01
1:A:401:HIS:HD2	4:A:646:HOH:O	1.44	0.99
1:B:7:LEU:N	4:B:604:HOH:O	1.97	0.98
1:A:337:VAL:HG23	4:A:904:HOH:O	1.63	0.95
1:A:58:ALA:HB1	4:A:1028:HOH:O	1.67	0.93
1:A:264:GLY:O	4:A:604:HOH:O	1.87	0.92
1:A:340:ARG:NH2	4:A:606:HOH:O	2.02	0.91
1:B:12:LEU:H	1:B:39:HIS:HE1	1.23	0.85
1:A:248[B]:HIS:HD2	3:A:502:6XD:C7	1.88	0.85
1:A:79:ARG:NH2	1:B:93:GLN:NE2	2.24	0.85
1:A:79:ARG:HH21	1:B:93:GLN:HE22	1.20	0.84
1:B:50:GLY:O	4:B:602:HOH:O	1.94	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:VAL:HG13	4:A:927:HOH:O	1.78	0.83
1:A:221:MET:CE	4:A:974:HOH:O	2.27	0.83
1:A:401:HIS:CD2	4:A:646:HOH:O	2.22	0.81
1:A:70:TYR:OH	4:A:605:HOH:O	1.98	0.81
1:A:221:MET:HB3	4:A:974:HOH:O	1.80	0.81
1:B:238:LEU:N	4:B:607:HOH:O	2.13	0.79
1:B:103:HIS:HE1	2:B:501:HEM:O1D	1.67	0.77
1:A:274:ASP:OD1	4:A:607:HOH:O	2.03	0.76
1:A:244:TYR:OH	1:A:248[A]:HIS:HE1	1.69	0.76
1:A:65:ARG:HA	4:A:980:HOH:O	1.84	0.75
1:B:155:MET:HE1	1:B:255:ALA:HB2	1.67	0.75
1:B:238:LEU:N	4:B:609:HOH:O	2.21	0.74
1:A:244:TYR:CZ	1:A:248[A]:HIS:HE1	2.05	0.74
1:A:244:TYR:CZ	1:A:248[A]:HIS:CE1	2.76	0.73
1:B:86:GLN:HG2	4:B:621:HOH:O	1.88	0.73
1:B:277:GLN:NE2	4:B:603:HOH:O	1.97	0.72
1:A:201:ARG:NH2	4:A:610:HOH:O	2.23	0.72
1:B:7:LEU:CA	4:B:604:HOH:O	2.38	0.71
1:B:253:ALA:HA	1:B:257[B]:THR:HG22	1.72	0.71
1:B:202:LEU:N	4:B:610:HOH:O	2.25	0.70
1:A:79:ARG:NH1	4:A:609:HOH:O	2.21	0.70
1:A:79:ARG:NH2	1:B:242:GLU:OE2	2.25	0.69
1:B:295:ARG:O	4:B:605:HOH:O	2.11	0.68
1:A:221:MET:HE2	4:A:974:HOH:O	1.92	0.68
1:B:9:GLY:O	4:B:606:HOH:O	2.11	0.68
1:A:79:ARG:NH2	1:B:93:GLN:HE22	1.90	0.67
1:A:362:TYR:OH	4:A:608:HOH:O	2.03	0.65
1:B:202:LEU:N	4:B:612:HOH:O	2.30	0.65
1:A:248[B]:HIS:CD2	3:A:502:6XD:C7	2.77	0.64
1:A:103:HIS:HE1	2:A:501:HEM:O1D	1.81	0.64
1:A:31:ARG:HH21	1:A:32:ARG:NH2	1.95	0.64
1:A:359:GLY:HA3	4:A:980:HOH:O	1.98	0.64
1:B:86:GLN:CG	4:B:621:HOH:O	2.45	0.63
1:B:43:GLU:HG2	4:B:619:HOH:O	1.99	0.62
1:B:319:GLU:H	1:B:322:GLN:NE2	1.98	0.62
1:B:7:LEU:C	4:B:604:HOH:O	2.37	0.62
1:A:275:GLN:NE2	1:A:346:ILE:H	1.99	0.61
1:B:102[A]:ARG:HH11	1:B:102[A]:ARG:HG3	1.64	0.61
1:B:156:GLN:NE2	1:B:169:ARG:HH11	1.99	0.60
1:B:52:TRP:HE1	1:B:322:GLN:NE2	1.99	0.60
1:B:156:GLN:HE22	1:B:169:ARG:HH11	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ALA:HA	1:A:257[B]:THR:HG22	1.82	0.59
1:A:131:ARG:NH2	4:A:617:HOH:O	2.36	0.58
1:A:31:ARG:HH21	1:A:32:ARG:HH22	1.49	0.58
1:B:275:GLN:NE2	1:B:346:ILE:H	2.01	0.58
1:A:31:ARG:HE	1:A:32:ARG:NH1	2.01	0.58
1:A:79:ARG:HH21	1:B:93:GLN:HE21	1.46	0.58
1:A:103:HIS:HD2	4:A:654:HOH:O	1.86	0.58
1:A:203:TYR:HD1	1:A:244:TYR:CZ	2.22	0.57
1:A:253:ALA:O	1:A:257[B]:THR:HG22	2.05	0.57
1:B:253:ALA:O	1:B:257[B]:THR:HG22	2.03	0.57
1:B:155:MET:CE	1:B:255:ALA:HB2	2.35	0.56
1:A:274:ASP:N	1:A:274:ASP:OD1	2.39	0.56
1:B:102[A]:ARG:NH1	1:B:102[A]:ARG:HG3	2.21	0.56
1:A:31:ARG:HE	1:A:32:ARG:HH12	1.53	0.56
1:A:221:MET:HE3	4:A:974:HOH:O	1.96	0.56
1:B:12:LEU:H	1:B:39:HIS:CE1	2.14	0.56
1:A:65:ARG:CZ	4:A:603:HOH:O	2.38	0.55
1:A:52:TRP:HE1	1:A:322:GLN:NE2	2.04	0.55
1:B:125:ASP:OD2	4:B:608:HOH:O	2.18	0.54
1:B:394:GLU:OE1	1:B:405:ARG:NH1	2.40	0.54
1:B:275:GLN:HE21	1:B:346:ILE:HG12	1.72	0.54
1:A:93:GLN:HE22	1:B:79:ARG:HE	1.55	0.54
1:A:111[A]:SER:HB2	4:A:753:HOH:O	2.08	0.53
1:B:376:LEU:HD13	1:B:376:LEU:C	2.30	0.52
1:A:221:MET:CB	4:A:974:HOH:O	2.48	0.51
1:B:253:ALA:HB2	3:B:502:6XD:C11	2.40	0.51
1:A:365:GLY:HA3	2:A:501:HEM:C3C	2.46	0.51
1:A:275:GLN:HE22	1:A:345:ASP:HA	1.77	0.50
1:B:155:MET:HG2	1:B:173:PHE:CE1	2.46	0.50
1:A:311:VAL:CG2	4:A:605:HOH:O	2.59	0.50
1:A:79:ARG:NH2	1:B:93:GLN:HE21	2.05	0.50
1:A:319:GLU:H	1:A:322:GLN:NE2	2.10	0.50
1:A:79:ARG:HH22	1:B:242:GLU:CD	2.14	0.50
1:B:61:LEU:HD11	1:B:358:GLN:HG2	1.93	0.50
1:A:79:ARG:HH11	1:A:79:ARG:HG3	1.78	0.49
1:A:311:VAL:HG22	4:A:605:HOH:O	2.12	0.49
1:A:65:ARG:NH2	4:A:603:HOH:O	2.46	0.49
1:A:256[B]:GLU:HG2	1:A:401:HIS:CD2	2.47	0.49
1:A:316:GLN:NE2	4:A:623:HOH:O	2.46	0.48
1:B:256[B]:GLU:HG2	1:B:401:HIS:CD2	2.49	0.48
1:B:215:ALA:HB2	4:B:819:HOH:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:THR:HB	4:A:931:HOH:O	2.13	0.47
1:B:31:ARG:HH21	1:B:32:ARG:NH2	2.11	0.47
1:A:309:ARG:NH2	4:A:624:HOH:O	2.48	0.47
1:B:107:ARG:HG3	1:B:364[A]:LEU:HD11	1.97	0.46
1:A:46:PRO:HB3	1:A:86[B]:GLN:CG	2.45	0.46
1:A:349:LYS:HE3	4:A:653:HOH:O	2.15	0.46
1:B:253:ALA:O	1:B:257[B]:THR:CG2	2.64	0.46
1:B:7:LEU:HD13	1:B:37:TYR:CE2	2.50	0.46
1:B:253:ALA:CA	1:B:257[B]:THR:HG22	2.43	0.45
1:B:348:ARG:HB3	4:B:623:HOH:O	2.16	0.45
1:A:156:GLN:NE2	1:A:169:ARG:HH11	2.15	0.45
1:B:286:LEU:HD13	1:B:374:ARG:HG3	1.99	0.44
1:B:31:ARG:HE	1:B:32:ARG:HH12	1.65	0.44
1:B:102[A]:ARG:HH11	1:B:102[A]:ARG:CG	2.24	0.44
1:B:340:ARG:NH2	4:B:620:HOH:O	2.50	0.44
1:A:221:MET:CG	4:A:974:HOH:O	2.66	0.43
1:A:253:ALA:O	1:A:257[B]:THR:CG2	2.66	0.43
1:B:266:LEU:HA	1:B:266:LEU:HD12	1.81	0.43
1:B:202:LEU:HD21	1:B:248[A]:HIS:CE1	2.53	0.43
1:B:31:ARG:HE	1:B:32:ARG:NH1	2.17	0.43
1:A:300:SER:C	4:A:612:HOH:O	2.57	0.43
1:A:275:GLN:HE22	1:A:346:ILE:H	1.64	0.42
1:B:31:ARG:HH21	1:B:32:ARG:HH22	1.68	0.42
1:B:61:LEU:HD11	1:B:358:GLN:CG	2.49	0.42
1:A:253:ALA:HB2	3:A:502:6XD:C11	2.50	0.42
1:B:103:HIS:CE1	2:B:501:HEM:O1D	2.58	0.42
1:A:79:ARG:NH1	1:A:79:ARG:CG	2.82	0.42
1:A:100:ASP:OD1	1:A:104:THR:OG1	2.34	0.41
1:B:114:LEU:HA	1:B:114:LEU:HD23	1.90	0.41
1:A:297:THR:O	1:A:298:SER:C	2.59	0.41
1:A:79:ARG:HH11	1:A:79:ARG:CG	2.33	0.41
1:B:28:ALA:O	1:B:32:ARG:HG2	2.21	0.40
1:A:203:TYR:CD1	1:A:244:TYR:CE2	3.09	0.40
1:A:244:TYR:OH	1:A:248[A]:HIS:CE1	2.60	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:749:HOH:O	4:A:844:HOH:O[4_555]	2.05	0.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:689:HOH:O	4:A:805:HOH:O[4_555]	2.13	0.07
4:A:1065:HOH:O	4:A:1103:HOH:O[4_545]	2.15	0.05

## 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	375/414 (91%)	363 (97%)	12 (3%)	0	100	100
1	B	371/414 (90%)	359 (97%)	12 (3%)	0	100	100
All	All	746/828 (90%)	722 (97%)	24 (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	320/342 (94%)	312 (98%)	8 (2%)	55	24
1	B	316/342 (92%)	309 (98%)	7 (2%)	60	30
All	All	636/684 (93%)	621 (98%)	15 (2%)	60	26

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	ARG

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Mol	Chain	Res	Type
1	A	102[A]	ARG
1	A	102[B]	ARG
1	A	127	ARG
1	A	131	ARG
1	A	167	THR
1	A	280	ARG
1	A	304	ARG
1	B	32	ARG
1	B	114	LEU
1	B	167	THR
1	B	216	GLU
1	B	286	LEU
1	B	304	ARG
1	B	405	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	93	GLN
1	A	103	HIS
1	A	156	GLN
1	A	227	ASN
1	A	272	ASN
1	A	275	GLN
1	A	322	GLN
1	A	358	GLN
1	A	401	HIS
1	B	39	HIS
1	B	93	GLN
1	B	103	HIS
1	B	156	GLN
1	B	227	ASN
1	B	272	ASN
1	B	275	GLN
1	B	322	GLN
1	B	401	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

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	A	501	1,3	24,50,50	2.06	6 (25%)	16,82,82	1.49	3 (18%)
3	6XD	A	502	2	24,25,25	1.52	6 (25%)	34,36,36	2.15	11 (32%)
2	HEM	B	501	1,3	24,50,50	2.32	7 (29%)	16,82,82	1.80	5 (31%)
3	6XD	B	502	2	24,25,25	1.54	6 (25%)	34,36,36	2.80	11 (32%)

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	501	1,3	-	0/6/54/54	0/0/8/8
3	6XD	A	502	2	-	0/12/39/39	0/1/4/4
2	HEM	B	501	1,3	-	0/6/54/54	0/0/8/8
3	6XD	B	502	2	-	0/12/39/39	0/1/4/4

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEM	C3B-C2B	-5.95	1.32	1.40
2	B	501	HEM	C3C-C2C	-5.69	1.33	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C3B-C2B	-4.82	1.34	1.40
2	A	501	HEM	C3C-C2C	-4.80	1.34	1.40
3	A	502	6XD	O13-C03	-2.94	1.17	1.23
2	A	501	HEM	C1A-CHA	-2.79	1.32	1.40
3	B	502	6XD	C6-C5	-2.58	1.46	1.52
3	A	502	6XD	C8-C1	-2.49	1.48	1.53
3	B	502	6XD	C8-C1	-2.37	1.49	1.53
3	A	502	6XD	C1-N02	-2.31	1.44	1.47
3	B	502	6XD	C9-C1	-2.04	1.49	1.53
3	B	502	6XD	C11-N10	2.04	1.47	1.37
3	A	502	6XD	C03-N02	2.12	1.40	1.35
2	B	501	HEM	C3C-CAC	2.14	1.52	1.47
2	B	501	HEM	C3D-C2D	2.14	1.44	1.37
2	B	501	HEM	C3B-CAB	2.34	1.52	1.47
3	A	502	6XD	C07-N08	2.34	1.55	1.49
3	B	502	6XD	C03-N02	2.47	1.40	1.35
2	B	501	HEM	C1C-NC	2.74	1.40	1.36
3	A	502	6XD	C03-N04	2.81	1.41	1.35
2	A	501	HEM	C4D-ND	2.91	1.40	1.36
2	A	501	HEM	CAA-C2A	2.94	1.57	1.52
2	A	501	HEM	C1C-NC	2.95	1.40	1.36
2	B	501	HEM	C4C-NC	3.21	1.41	1.36
3	B	502	6XD	C03-N04	3.74	1.44	1.35

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	6XD	C4-C3-C10	-6.74	97.97	109.68
3	B	502	6XD	C1-C9-C5	-5.59	103.51	110.01
3	B	502	6XD	C5-C6-C7	-5.23	100.50	109.80
2	B	501	HEM	C3C-CAC-CBC	-4.18	118.00	126.40
3	B	502	6XD	C10-C3-C2	-3.49	101.87	109.10
3	A	502	6XD	C1-C9-C5	-3.41	106.03	110.01
3	A	502	6XD	C10-C3-C2	-3.41	102.04	109.10
2	A	501	HEM	CMA-C3A-C4A	-3.34	122.62	128.31
2	B	501	HEM	CMA-C3A-C4A	-3.27	122.75	128.31
3	B	502	6XD	C4-C5-C9	-3.15	102.58	109.10
3	A	502	6XD	C4-C3-C10	-3.10	104.30	109.68
3	B	502	6XD	C8-C1-N02	-2.92	102.85	110.02
3	A	502	6XD	C4-C5-C9	-2.65	103.62	109.10
2	B	501	HEM	CMD-C2D-C1D	-2.61	123.87	128.31
2	A	501	HEM	CMD-C2D-C1D	-2.42	124.20	128.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	6XD	C10-C7-C6	-2.34	105.61	109.68
2	A	501	HEM	C3B-C4B-NB	-2.27	106.28	109.21
3	A	502	6XD	C5-C6-C7	-2.12	106.02	109.80
3	B	502	6XD	C10-C7-C8	2.14	113.54	109.10
3	A	502	6XD	N04-C03-N02	2.14	116.08	114.81
3	A	502	6XD	C3-C4-C5	2.24	113.78	109.80
2	B	501	HEM	CMB-C2B-C3B	2.34	129.67	125.09
2	B	501	HEM	CAA-CBA-CGA	2.42	117.49	112.78
3	A	502	6XD	C10-C7-C8	3.07	115.47	109.10
3	B	502	6XD	C3-C10-C7	3.59	116.18	109.80
3	B	502	6XD	C3-C4-C5	3.83	116.61	109.80
3	A	502	6XD	C6-C5-C9	4.07	117.53	109.10
3	B	502	6XD	C2-C1-C9	4.86	114.77	108.89
3	B	502	6XD	C6-C5-C9	6.38	122.31	109.10
3	A	502	6XD	C2-C1-C9	6.56	116.82	108.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	2	0
3	A	502	6XD	3	0
2	B	501	HEM	2	0
3	B	502	6XD	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 ⓘ

### 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	373/414 (90%)	0.00	3 (0%) 87 88	7, 16, 32, 48	0
1	B	372/414 (89%)	-0.14	15 (4%) 42 41	13, 20, 36, 65	0
All	All	745/828 (89%)	-0.07	18 (2%) 62 62	7, 18, 34, 65	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	171	TRP	8.4
1	B	173	PHE	4.0
1	A	173	PHE	3.4
1	A	203	TYR	3.0
1	B	170	HIS	2.9
1	B	174	GLU	2.8
1	A	392	PRO	2.6
1	B	203	TYR	2.6
1	B	167	THR	2.6
1	B	172	LEU	2.6
1	B	251	PHE	2.6
1	B	37	TYR	2.4
1	B	255	ALA	2.4
1	B	216	GLU	2.2
1	B	175	ALA	2.2
1	B	202	LEU	2.2
1	B	8	SER	2.1
1	B	215	ALA	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 [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	501	43/43	0.99	0.09	-0.17	5,7,10,13	0
2	HEM	B	501	43/43	0.99	0.06	-0.28	10,13,15,17	0
3	6XD	A	502	22/22	0.95	0.10	-0.30	11,20,23,27	0
3	6XD	B	502	22/22	0.94	0.08	-0.38	17,26,30,34	0

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

There are no such residues in this entry.