



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 17, 2017 – 12:31 PM EDT

PDB ID : 5SX3  
Title : Crystal structure of the catalase-peroxidase KatG of *B. pseudomallei* at pH 4.5  
Authors : Loewen, P.C.  
Deposited on : unknown  
Resolution : 2.00 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 : rb-20029824  
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) : rb-20029824

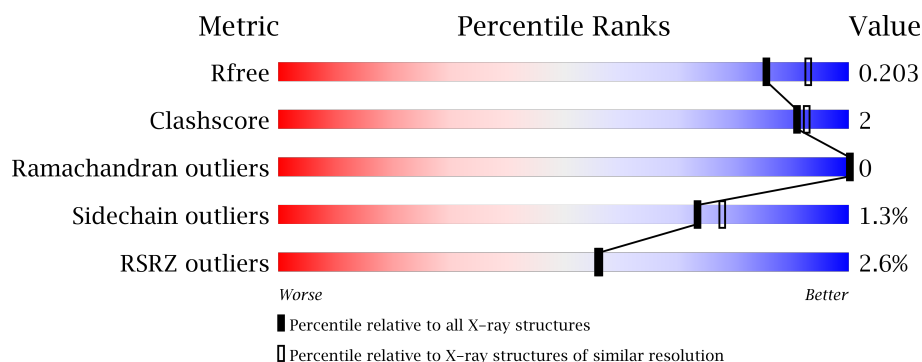
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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	728	<div> <div>3%</div> <div>91%</div> <div>6% ..</div> </div>
1	B	728	<div> <div>2%</div> <div>90%</div> <div>7% ..</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
3	NA	B	802	-	-	-	X
6	MPD	B	806	-	-	-	X

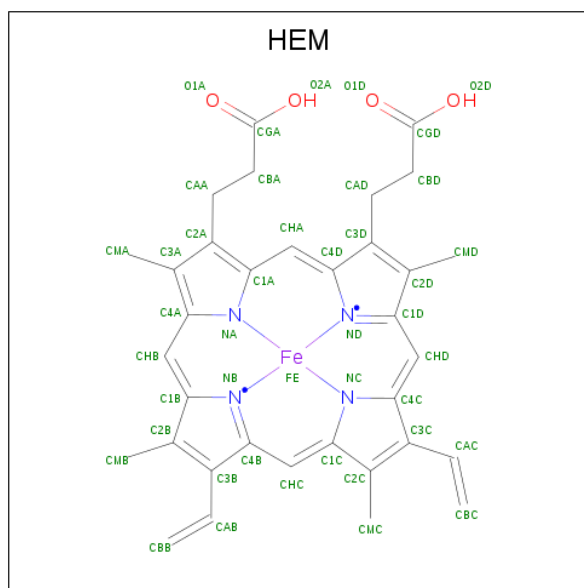


In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Catalase-peroxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	713	Total 5531	C 3495	N 981	O 1041	S 14	0	6	0
1	B	713	Total 5552	C 3508	N 988	O 1042	S 14	0	9	0

- 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

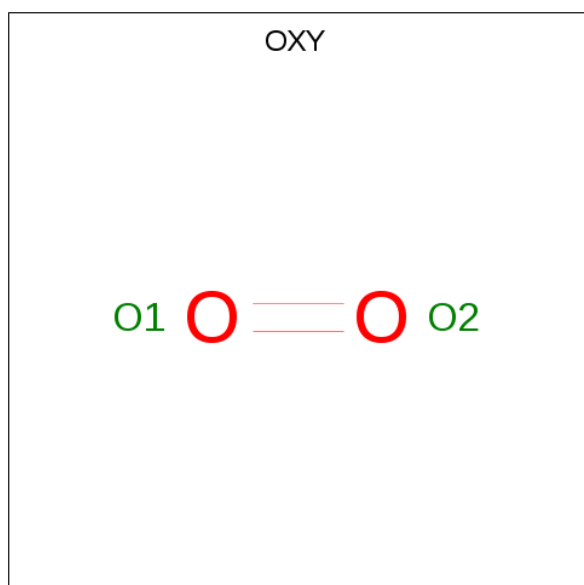
- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Na 1 1	0	0
3	A	1	Total Na 1 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

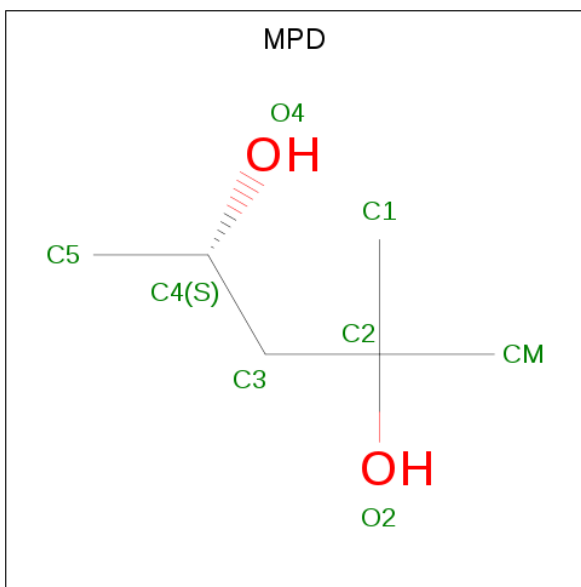
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Cl 1 1	0	0
4	A	1	Total Cl 1 1	0	0

- Molecule 5 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O 2 2	0	0
5	B	1	Total O 2 2	0	0

- Molecule 6 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			8	6	2		
6	A	1	Total	C	O	0	0
			8	6	2		
6	B	1	Total	C	O	0	0
			8	6	2		
6	B	1	Total	C	O	0	0
			8	6	2		

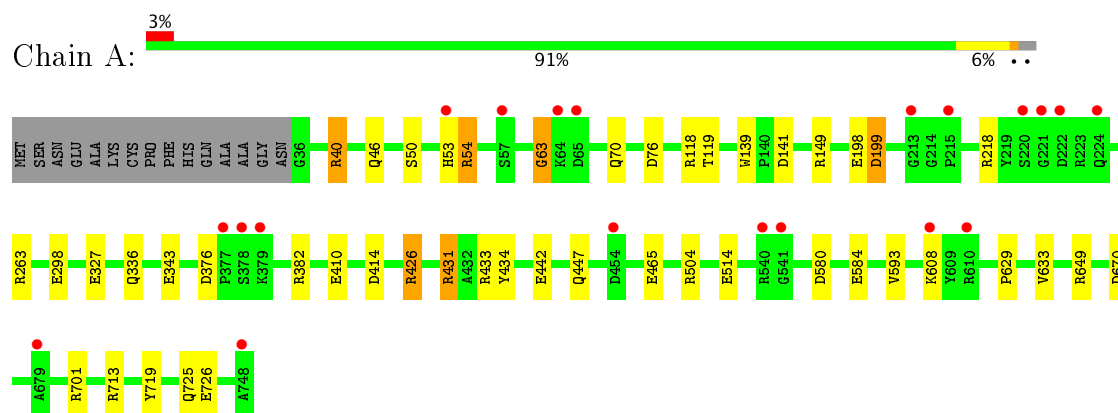
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	661	Total	O	0	0
			661	661		
7	B	702	Total	O	0	0
			702	702		

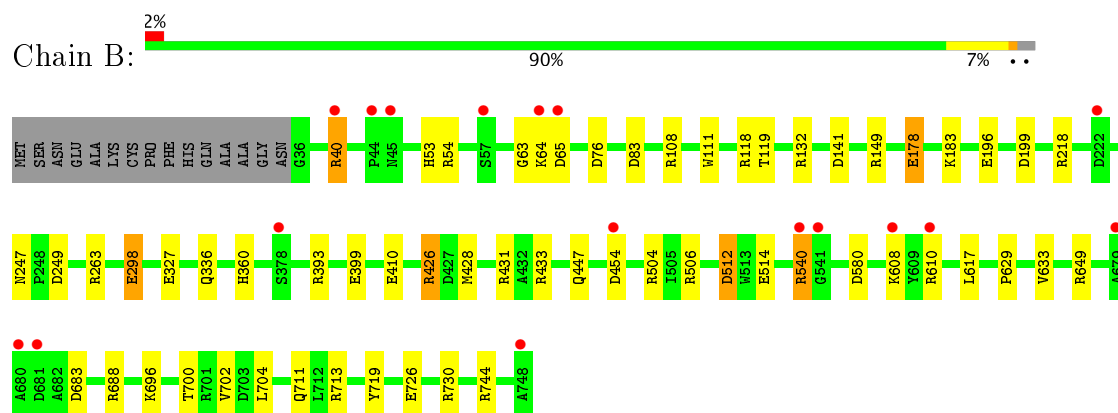
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: Catalase-peroxidase



#### • Molecule 1: Catalase-peroxidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.05Å 114.85Å 174.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.05 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.7 (20.00-2.00) 98.8 (20.05-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.44 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, $R_{free}$	0.162 , 0.196 0.173 , 0.203	Depositor DCC
$R_{free}$ test set	6790 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.5	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12572	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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: NA, MPD, OXY, HEM, CL

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	1.17	15/5695 (0.3%)	1.06	25/7744 (0.3%)
1	B	1.17	15/5726 (0.3%)	1.08	28/7784 (0.4%)
All	All	1.17	30/11421 (0.3%)	1.07	53/15528 (0.3%)

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	725	GLN	CD-NE2	8.70	1.54	1.32
1	B	726	GLU	CD-OE1	8.08	1.34	1.25
1	B	327	GLU	CD-OE2	8.06	1.34	1.25
1	A	343	GLU	CD-OE1	7.98	1.34	1.25
1	B	410	GLU	CG-CD	7.89	1.63	1.51
1	A	327	GLU	CG-CD	7.48	1.63	1.51
1	B	298	GLU	CD-OE2	7.45	1.33	1.25
1	A	725	GLN	CG-CD	7.33	1.68	1.51
1	B	327	GLU	CG-CD	7.22	1.62	1.51
1	B	399	GLU	CD-OE1	7.20	1.33	1.25
1	B	726	GLU	CG-CD	6.75	1.62	1.51
1	B	63	GLY	N-CA	6.50	1.55	1.46
1	B	514	GLU	CD-OE2	-6.41	1.18	1.25
1	A	410	GLU	CD-OE2	6.19	1.32	1.25
1	B	512	ASP	CG-OD2	6.01	1.39	1.25
1	A	726	GLU	CG-CD	5.71	1.60	1.51
1	B	336	GLN	CG-CD	5.69	1.64	1.51
1	A	584	GLU	CG-CD	5.62	1.60	1.51
1	B	247	ASN	CB-CG	5.61	1.64	1.51
1	A	298	GLU	CD-OE2	5.53	1.31	1.25
1	A	725	GLN	CD-OE1	5.49	1.36	1.24
1	A	63	GLY	N-CA	5.38	1.54	1.46
1	B	426	ARG	CZ-NH2	5.35	1.40	1.33
1	A	139	TRP	CZ3-CH2	5.30	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	410	GLU	CG-CD	5.21	1.59	1.51
1	A	514	GLU	CD-OE1	-5.18	1.20	1.25
1	A	465	GLU	CD-OE1	5.16	1.31	1.25
1	B	196	GLU	CG-CD	5.13	1.59	1.51
1	B	178	GLU	CG-CD	5.04	1.59	1.51
1	A	70	GLN	CG-CD	5.01	1.62	1.51

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	393	ARG	NE-CZ-NH2	-10.83	114.89	120.30
1	B	433	ARG	NE-CZ-NH1	10.80	125.70	120.30
1	B	713	ARG	NE-CZ-NH1	9.81	125.20	120.30
1	A	649	ARG	NE-CZ-NH1	8.24	124.42	120.30
1	A	670	ASP	CB-CG-OD2	-7.82	111.26	118.30
1	B	149	ARG	NE-CZ-NH2	-7.64	116.48	120.30
1	B	433	ARG	NE-CZ-NH2	-7.57	116.52	120.30
1	A	433	ARG	NE-CZ-NH1	7.54	124.07	120.30
1	B	649	ARG	NE-CZ-NH1	7.44	124.02	120.30
1	B	263	ARG	NE-CZ-NH1	7.35	123.98	120.30
1	A	713	ARG	NE-CZ-NH1	7.18	123.89	120.30
1	B	506	ARG	NE-CZ-NH1	7.15	123.88	120.30
1	A	76	ASP	CB-CG-OD2	-7.13	111.88	118.30
1	A	40	ARG	NE-CZ-NH1	6.90	123.75	120.30
1	A	149	ARG	NE-CZ-NH2	-6.79	116.90	120.30
1	B	65	ASP	CB-CG-OD1	-6.76	112.22	118.30
1	A	218	ARG	NE-CZ-NH2	-6.75	116.92	120.30
1	A	149	ARG	NE-CZ-NH1	6.74	123.67	120.30
1	B	40	ARG	NE-CZ-NH1	6.72	123.66	120.30
1	A	414	ASP	CB-CG-OD1	-6.70	112.27	118.30
1	B	108	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	A	376	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	B	506	ARG	NE-CZ-NH2	-6.62	116.99	120.30
1	A	713	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	A	701	ARG	NE-CZ-NH1	6.23	123.42	120.30
1	B	218	ARG	NE-CZ-NH2	-6.22	117.19	120.30
1	A	649	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	B	580	ASP	CB-CG-OD1	-6.08	112.83	118.30
1	A	263	ARG	NE-CZ-NH1	6.03	123.31	120.30
1	A	426	ARG	NE-CZ-NH2	-5.75	117.43	120.30
1	A	199	ASP	CB-CG-OD1	-5.74	113.14	118.30
1	A	263	ARG	NE-CZ-NH2	-5.69	117.46	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	649	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	B	393	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	B	683	ASP	CB-CG-OD2	-5.57	113.29	118.30
1	A	54	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	A	580	ASP	CB-CG-OD1	-5.45	113.40	118.30
1	B	83	ASP	CB-CG-OD2	5.42	123.18	118.30
1	A	514	GLU	OE1-CD-OE2	-5.38	116.84	123.30
1	B	512	ASP	CB-CG-OD1	-5.38	113.46	118.30
1	B	744	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	A	434	TYR	CB-CG-CD1	5.33	124.20	121.00
1	B	132	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	B	704	LEU	CB-CG-CD2	5.21	119.86	111.00
1	A	504	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	B	713	ARG	NE-CZ-NH2	-5.17	117.72	120.30
1	B	688	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	B	249	ASP	CB-CG-OD2	5.14	122.93	118.30
1	B	428	MET	CA-CB-CG	-5.13	104.59	113.30
1	A	382	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	B	504	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	B	512	ASP	CB-CG-OD2	5.04	122.83	118.30
1	A	431	ARG	NE-CZ-NH2	5.02	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	5531	0	5344	12	0
1	B	5552	0	5374	24	0
2	A	43	0	30	0	0
2	B	43	0	30	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	16	0	28	4	0
6	B	16	0	28	4	0
7	A	661	0	0	4	0
7	B	702	0	0	15	0
All	All	12572	0	10834	43	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 2.

All (43) 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:A:119[B]:THR:HG21	7:A:1019:HOH:O	1.71	0.90
1:B:119[B]:THR:HG21	7:B:1134:HOH:O	1.73	0.89
1:B:730[B]:ARG:HD2	7:B:1502:HOH:O	1.87	0.75
1:B:512:ASP:OD1	7:B:901:HOH:O	2.07	0.72
1:B:76:ASP:OD1	7:B:902:HOH:O	2.09	0.70
1:B:178:GLU:OE1	7:B:903:HOH:O	2.10	0.69
1:B:730[B]:ARG:HG2	7:B:938:HOH:O	1.94	0.65
1:B:360:HIS:ND1	7:B:906:HOH:O	2.30	0.64
1:A:629:PRO:O	1:A:633[A]:VAL:HG23	1.98	0.64
1:B:629:PRO:O	1:B:633[A]:VAL:HG23	1.99	0.62
1:B:540:ARG:CZ	1:B:540:ARG:HA	2.29	0.62
6:A:806:MPD:C5	6:A:806:MPD:H11	2.31	0.60
1:B:540:ARG:NH1	1:B:540:ARG:HA	2.16	0.60
1:A:336:GLN:HG2	7:A:1396:HOH:O	2.01	0.60
1:B:696:LYS:HE2	7:B:981:HOH:O	2.02	0.59
1:A:119[B]:THR:HG23	1:A:593:VAL:HG11	1.86	0.58
6:B:805:MPD:O4	6:B:805:MPD:H12	2.03	0.58
1:B:730[B]:ARG:CG	7:B:938:HOH:O	2.50	0.56
6:A:805:MPD:HM1	6:A:805:MPD:O4	2.06	0.56
1:A:50:SER:HA	1:A:53:HIS:CD2	2.41	0.55
6:A:805:MPD:O4	6:A:805:MPD:CM	2.55	0.54
1:B:711[A]:GLN:NE2	7:B:913:HOH:O	2.41	0.53
1:A:63:GLY:O	7:A:902:HOH:O	2.19	0.53
1:A:633[B]:VAL:CG1	1:A:719:TYR:CZ	2.95	0.50
1:B:53:HIS:HE1	7:B:1000:HOH:O	1.94	0.50
6:B:806:MPD:H52	6:B:806:MPD:O2	2.12	0.50
1:A:442:GLU:OE2	7:A:901:HOH:O	2.18	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:805:MPD:O4	6:B:805:MPD:C1	2.63	0.47
1:B:119[B]:THR:HG23	7:B:1376:HOH:O	2.13	0.47
1:B:633[B]:VAL:CG1	1:B:719:TYR:CZ	2.98	0.47
6:B:806:MPD:H51	7:B:1196:HOH:O	2.15	0.46
6:A:806:MPD:H11	6:A:806:MPD:H53	1.97	0.45
1:B:53:HIS:CE1	7:B:1000:HOH:O	2.71	0.43
1:B:54:ARG:NE	1:B:199:ASP:OD2	2.50	0.43
1:A:431:ARG:HD2	1:A:447:GLN:OE1	2.19	0.43
1:B:454:ASP:N	1:B:454:ASP:OD1	2.52	0.42
1:A:54:ARG:NE	1:A:199:ASP:OD2	2.50	0.42
1:B:700:THR:HB	7:B:1418:HOH:O	2.20	0.41
1:B:431:ARG:HD2	1:B:447:GLN:OE1	2.20	0.41
1:A:426:ARG:HA	1:A:426:ARG:HD2	1.96	0.41
1:A:46:GLN:NE2	1:B:298:GLU:O	2.55	0.40
1:B:617:LEU:HD22	1:B:702:VAL:HG13	2.04	0.40
1:B:426:ARG:HA	1:B:426:ARG:HD2	1.92	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	717/728 (98%)	706 (98%)	11 (2%)	0	100	100
1	B	720/728 (99%)	708 (98%)	12 (2%)	0	100	100
All	All	1437/1456 (99%)	1414 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	556/561 (99%)	551 (99%)	5 (1%)	82	87
1	B	559/561 (100%)	550 (98%)	9 (2%)	68	72
All	All	1115/1122 (99%)	1101 (99%)	14 (1%)	73	78

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	118	ARG
1	A	141	ASP
1	A	198	GLU
1	A	608	LYS
1	B	40	ARG
1	B	64	LYS
1	B	111	TRP
1	B	118	ARG
1	B	141	ASP
1	B	183	LYS
1	B	540	ARG
1	B	608	LYS
1	B	610	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	247	ASN
1	B	227	ASN
1	B	650	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](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

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	801	1,7	28,50,50	1.18	3 (10%)	17,82,82	2.16	8 (47%)
5	OXY	A	804	-	1,1,1	0.17	0	0,0,0	0.00	-
6	MPD	A	805	-	7,7,7	0.51	0	9,10,10	1.36	1 (11%)
6	MPD	A	806	-	7,7,7	0.88	0	9,10,10	1.26	0
2	HEM	B	801	1,7	28,50,50	1.78	6 (21%)	17,82,82	2.54	7 (41%)
5	OXY	B	804	-	1,1,1	0.05	0	0,0,0	0.00	-
6	MPD	B	805	-	7,7,7	0.41	0	9,10,10	1.70	3 (33%)
6	MPD	B	806	-	7,7,7	1.52	2 (28%)	9,10,10	0.85	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	801	1,7	-	0/6/54/54	0/0/8/8
5	OXY	A	804	-	-	0/0/0/0	0/0/0/0
6	MPD	A	805	-	-	0/5/5/5	0/0/0/0
6	MPD	A	806	-	-	0/5/5/5	0/0/0/0
2	HEM	B	801	1,7	-	0/6/54/54	0/0/8/8
5	OXY	B	804	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MPD	B	805	-	-	0/5/5/5	0/0/0/0
6	MPD	B	806	-	-	0/5/5/5	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	HEM	C3C-C2C	-3.66	1.35	1.40
2	A	801	HEM	C1B-NB	-3.23	1.33	1.36
2	B	801	HEM	C3B-C2B	-3.16	1.36	1.40
2	B	801	HEM	C1C-NC	-2.94	1.33	1.36
2	B	801	HEM	C1B-NB	-2.61	1.33	1.36
2	A	801	HEM	CMC-C2C	-2.14	1.47	1.51
6	B	806	MPD	C3-C2	2.42	1.60	1.53
2	B	801	HEM	C3C-CAC	2.52	1.52	1.47
2	A	801	HEM	C4C-NC	2.87	1.40	1.36
6	B	806	MPD	O2-C2	2.95	1.52	1.44
2	B	801	HEM	C4C-NC	4.81	1.42	1.36

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	HEM	CAA-CBA-CGA	-4.84	104.38	112.66
2	A	801	HEM	CAA-CBA-CGA	-4.29	105.33	112.66
2	B	801	HEM	CMA-C3A-C4A	-3.42	123.20	128.46
2	A	801	HEM	C4A-C3A-C2A	-3.26	104.73	107.00
6	B	805	MPD	CM-C2-C1	-3.01	103.72	110.42
2	A	801	HEM	C4C-C3C-C2C	-2.28	105.31	106.90
2	B	801	HEM	CAA-C2A-C3A	-2.21	122.70	129.00
6	B	805	MPD	O2-C2-CM	2.05	115.10	108.00
2	A	801	HEM	C1D-C2D-C3D	2.06	108.43	107.00
6	A	805	MPD	CM-C2-C3	2.15	120.75	110.08
6	B	805	MPD	C1-C2-C3	2.23	121.16	110.08
2	A	801	HEM	CMC-C2C-C3C	2.42	129.39	124.89
2	A	801	HEM	CBA-CAA-C2A	2.57	117.40	112.48
2	B	801	HEM	C4A-C3A-C2A	3.10	109.15	107.00
2	B	801	HEM	CBD-CAD-C3D	3.15	118.47	112.47
2	A	801	HEM	CBD-CAD-C3D	3.18	118.53	112.47
2	A	801	HEM	CMB-C2B-C3B	3.48	131.35	124.89
2	B	801	HEM	C1D-C2D-C3D	3.80	109.64	107.00
2	B	801	HEM	CAD-CBD-CGD	4.38	120.14	112.66

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
6	A	805	MPD	2	0
6	A	806	MPD	2	0
6	B	805	MPD	2	0
6	B	806	MPD	2	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	713/728 (97%)	-0.33	20 (2%) 53 53	21, 31, 56, 98	0
1	B	713/728 (97%)	-0.42	17 (2%) 59 59	21, 28, 51, 98	0
All	All	1426/1456 (97%)	-0.37	37 (2%) 56 56	21, 29, 54, 98	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	748	ALA	6.8
1	B	748	ALA	6.2
1	B	680	ALA	5.6
1	B	610	ARG	5.1
1	A	215	PRO	4.8
1	B	679	ALA	4.5
1	A	610	ARG	4.4
1	B	65	ASP	3.9
1	A	221	GLY	3.8
1	A	540	ARG	3.8
1	B	64	LYS	3.7
1	A	222	ASP	3.7
1	A	65	ASP	3.6
1	B	608	LYS	3.5
1	B	45	ASN	3.5
1	B	44	PRO	3.5
1	B	540	ARG	3.3
1	A	64	LYS	3.2
1	B	40	ARG	3.2
1	A	541	GLY	3.2
1	A	378	SER	3.0
1	A	213	GLY	3.0
1	A	608	LYS	2.8
1	A	220	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	454	ASP	2.5
1	A	377	PRO	2.5
1	B	681	ASP	2.4
1	B	57	SER	2.3
1	A	53	HIS	2.3
1	A	57	SER	2.2
1	B	222	ASP	2.2
1	B	454	ASP	2.2
1	B	541	GLY	2.1
1	A	224	GLN	2.1
1	A	679	ALA	2.1
1	B	378	SER	2.0
1	A	379	LYS	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
6	MPD	B	806	8/8	0.90	0.21	11.56	51,52,55,57	0
3	NA	B	802	1/1	0.99	0.08	2.18	26,26,26,26	0
6	MPD	B	805	8/8	0.94	0.11	1.52	49,54,58,58	0
6	MPD	A	805	8/8	0.94	0.12	0.88	69,73,73,74	0
2	HEM	A	801	43/43	0.98	0.07	-0.71	25,29,32,33	0
2	HEM	B	801	43/43	0.98	0.07	-1.22	21,22,24,28	0
4	CL	A	803	1/1	0.99	0.05	-1.53	46,46,46,46	0
4	CL	B	803	1/1	0.98	0.03	-1.72	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NA	A	802	1/1	0.98	0.05	-2.35	28,28,28,28	0
5	OXY	B	804	2/2	0.95	0.19	-	36,36,36,36	0
5	OXY	A	804	2/2	0.93	0.34	-	53,53,53,53	0
6	MPD	A	806	8/8	0.90	0.13	-	50,53,63,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.