



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 11, 2017 – 11:07 AM EST

PDB ID : 5FYF
Title : Structure of CYP153A from *Marinobacter aquaeolei*
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Deposited on : 2016-03-07
Resolution : 2.04 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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (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

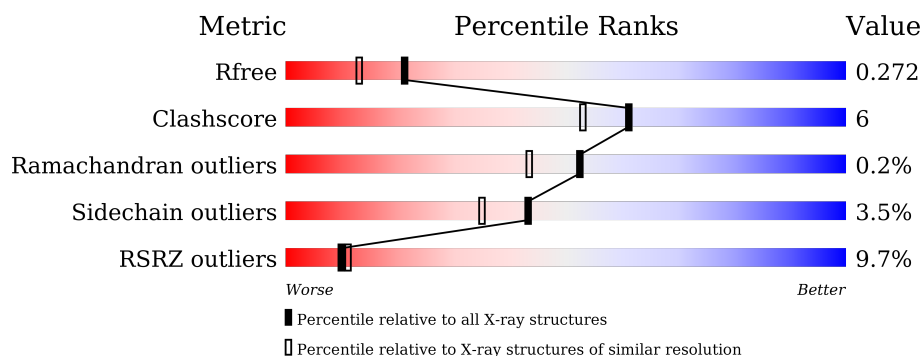
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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 ≥ 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	470	<div> <div>9%</div> <div>79%</div> <div>9%</div> <div>11%</div> </div>
1	B	470	<div> <div>9%</div> <div>75%</div> <div>10%</div> <div>13%</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	EDO	A	1476	-	-	-	X
3	EDO	A	1477	-	-	-	X

2 Entry composition [i](#)

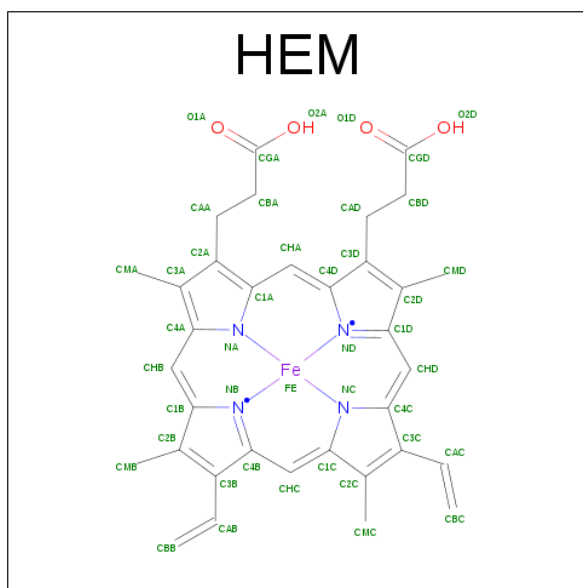
There are 4 unique types of molecules in this entry. The entry contains 6869 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	420	Total	C	N	O	S	0	0	0
			3281	2080	576	608	17			
1	B	411	Total	C	N	O	S	0	0	0
			3204	2037	559	592	16			

- 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 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	184	Total	O	0	0
			184	184		
4	B	102	Total	O	0	0
			102	102		

- Molecule 1: CYTOCHROME P450



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.59 Å 71.11 Å 215.18 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	107.59 – 2.04 107.59 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.9 (107.59-2.04) 99.9 (107.59-2.04)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 2.03 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.198 , 0.237 0.261 , 0.272	Depositor DCC
R_{free} test set	2918 reflections (5.18%)	DCC
Wilson B-factor (Å ²)	39.4	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.66 , 55.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6869	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.93	3/3356 (0.1%)	1.13	17/4550 (0.4%)
1	B	0.79	0/3279	0.98	17/4451 (0.4%)
All	All	0.86	3/6635 (0.0%)	1.05	34/9001 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	353	ARG	C-N	10.24	1.57	1.34
1	A	363	ARG	CD-NE	-6.00	1.36	1.46
1	A	104	SER	CA-CB	5.07	1.60	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	363	ARG	NE-CZ-NH2	-24.14	108.23	120.30
1	A	363	ARG	NE-CZ-NH1	22.19	131.40	120.30
1	A	317	ARG	NE-CZ-NH1	14.46	127.53	120.30
1	A	317	ARG	NE-CZ-NH2	-14.20	113.20	120.30
1	B	317	ARG	NE-CZ-NH1	13.18	126.89	120.30
1	B	317	ARG	NE-CZ-NH2	-12.65	113.97	120.30
1	A	353	ARG	CA-C-N	-9.77	95.71	117.20
1	A	353	ARG	O-C-N	8.73	136.67	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	270	ARG	NE-CZ-NH1	8.26	124.43	120.30
1	A	363	ARG	CD-NE-CZ	8.06	134.88	123.60
1	B	215	LEU	C-N-CA	-7.21	103.67	121.70
1	A	270	ARG	NE-CZ-NH1	7.00	123.80	120.30
1	A	215	LEU	C-N-CA	-6.84	104.59	121.70
1	B	285	LEU	CA-CB-CG	6.48	130.20	115.30
1	B	262	ARG	NE-CZ-NH1	6.30	123.45	120.30
1	A	216	ASP	CB-CG-OD2	6.30	123.97	118.30
1	A	126	ASP	CB-CG-OD1	6.02	123.72	118.30
1	B	69	LEU	CA-CB-CG	5.81	128.66	115.30
1	A	93	ARG	NE-CZ-NH1	5.61	123.10	120.30
1	A	363	ARG	CG-CD-NE	-5.54	100.16	111.80
1	B	86	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	A	394	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	B	270	ARG	NE-CZ-NH2	-5.37	117.61	120.30
1	B	392	ASP	CB-CG-OD1	5.36	123.13	118.30
1	A	317	ARG	CB-CG-CD	-5.21	98.06	111.60
1	A	394	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	B	135	ILE	CG1-CB-CG2	5.14	122.70	111.40
1	B	295	ILE	CB-CA-C	-5.12	101.35	111.60
1	B	262	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	B	215	LEU	O-C-N	-5.06	114.60	122.70
1	B	442	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	A	442	ARG	NE-CZ-NH1	5.02	122.81	120.30
1	B	86	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	B	363	ARG	NE-CZ-NH1	5.01	122.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	353	ARG	Mainchain

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	3281	0	3129	33	0
1	B	3204	0	3035	38	0
2	A	43	0	30	2	0
2	B	43	0	30	1	0
3	A	8	0	12	1	0
3	B	4	0	6	0	0
4	A	184	0	0	2	0
4	B	102	0	0	3	0
All	All	6869	0	6242	71	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 6.

All (71) 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:386:TYR:HA	1:B:413:MET:CE	2.09	0.82
1:A:163:VAL:HG23	1:A:281:LEU:HD21	1.64	0.78
1:B:386:TYR:HA	1:B:413:MET:HE2	1.66	0.78
1:A:101:GLN:HE21	1:A:103:ASN:H	1.35	0.72
1:B:193:ASP:OD1	4:B:2034:HOH:O	2.07	0.71
1:B:270:ARG:HD2	1:B:275:GLU:OE1	1.90	0.71
1:B:136:LEU:HD12	1:B:383:VAL:HG21	1.74	0.70
1:A:363:ARG:HD2	3:A:1476:EDO:O1	1.93	0.69
1:B:118:ILE:HD13	1:B:413:MET:HE1	1.76	0.68
1:B:204:LYS:HG2	1:B:317:ARG:HD2	1.76	0.68
1:A:204:LYS:HG2	1:A:317:ARG:HD2	1.75	0.68
1:A:402:PHE:CE2	1:A:404:ILE:HD11	2.29	0.67
1:B:210:MET:HE2	1:B:427:LEU:HD11	1.78	0.65
1:B:353:ARG:HB2	1:B:412:HIS:HB3	1.79	0.65
1:B:91:ARG:NH1	1:B:95:GLU:OE1	2.29	0.64
1:A:317:ARG:HD3	4:A:2114:HOH:O	1.98	0.64
1:B:118:ILE:CD1	1:B:413:MET:HE1	2.27	0.64
1:B:264:TRP:NE1	1:B:295:ILE:HG12	2.13	0.63
1:A:471:THR:HG23	4:A:2184:HOH:O	1.98	0.63
1:B:97:PRO:HB3	4:B:2010:HOH:O	2.00	0.61
1:B:386:TYR:HA	1:B:413:MET:HE3	1.81	0.61
1:B:210:MET:HG2	1:B:431:GLN:NE2	2.15	0.61
1:B:118:ILE:HD13	1:B:413:MET:CE	2.32	0.59
1:A:353:ARG:O	1:A:356:THR:OG1	2.21	0.58
1:A:347:MET:HG3	1:A:404:ILE:HD12	1.86	0.56
1:B:210:MET:CE	1:B:427:LEU:HD11	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:LEU:HD22	1:B:308:LEU:HD22	1.87	0.55
1:B:353:ARG:HB2	1:B:412:HIS:CB	2.37	0.55
1:A:204:LYS:CG	1:A:317:ARG:HD2	2.36	0.55
1:B:123:LYS:NZ	1:B:417:TYR:HB3	2.21	0.54
1:B:204:LYS:CG	1:B:317:ARG:HD2	2.37	0.54
1:A:473:ASN:O	1:A:474:SER:OG	2.19	0.54
1:B:389:GLY:HA3	1:B:413:MET:CE	2.39	0.53
1:B:135:ILE:O	1:B:362:ARG:HD3	2.10	0.52
1:A:333:GLU:HB3	1:A:404:ILE:HG12	1.91	0.51
1:B:389:GLY:HA3	1:B:413:MET:HE1	1.91	0.51
1:A:315:THR:HB	2:A:1475:HEM:C3B	2.44	0.51
1:A:266:ASP:O	1:A:270:ARG:CG	2.59	0.50
1:A:340:LYS:CG	1:A:342:GLU:OE2	2.60	0.50
1:A:232:MET:CE	1:A:256:MET:CE	2.90	0.50
1:A:118:ILE:HG23	1:A:384:MET:HB3	1.94	0.49
1:A:63:ASP:O	1:A:66:THR:HG22	2.13	0.49
1:B:251:ASP:O	1:B:255:ASP:HB2	2.13	0.49
1:B:118:ILE:HG23	1:B:384:MET:HB3	1.95	0.48
1:B:363:ARG:HB2	1:B:382:VAL:HG13	1.95	0.48
1:A:228:TRP:CE3	1:A:256:MET:HG3	2.48	0.48
1:A:270:ARG:NE	1:A:275:GLU:OE2	2.46	0.48
1:A:267:LYS:HA	1:A:270:ARG:HG3	1.95	0.48
1:A:266:ASP:O	1:A:270:ARG:HG3	2.14	0.48
1:B:228:TRP:CE3	1:B:256:MET:HG3	2.50	0.47
1:B:123:LYS:HZ2	1:B:417:TYR:HB3	1.78	0.47
1:A:281:LEU:O	1:A:281:LEU:HD22	2.14	0.46
1:A:256:MET:HE2	1:A:256:MET:HB2	1.66	0.46
1:B:315:THR:HB	2:B:1475:HEM:C3B	2.51	0.46
1:A:232:MET:CE	1:A:256:MET:HE1	2.46	0.46
1:B:179:ILE:HD11	1:B:210:MET:HE2	1.97	0.46
1:A:446:ILE:HG13	1:A:470:LEU:CD2	2.46	0.45
1:B:118:ILE:HG21	1:B:413:MET:HE3	1.98	0.45
1:A:446:ILE:HG13	1:A:470:LEU:HD23	1.98	0.45
1:B:393:GLU:HA	1:B:396:PHE:O	2.16	0.45
1:A:393:GLU:HA	1:A:396:PHE:O	2.16	0.45
1:A:266:ASP:O	1:A:270:ARG:HG2	2.17	0.45
1:A:163:VAL:HG23	1:A:281:LEU:CD2	2.41	0.44
1:B:223:HIS:HB3	4:B:2014:HOH:O	2.17	0.44
1:B:63:ASP:HB3	1:B:66:THR:HG23	2.00	0.43
1:B:135:ILE:HD12	1:B:238:ALA:HB1	2.01	0.43
1:A:281:LEU:HD22	1:A:285:LEU:HG	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:LEU:HG	1:B:285:LEU:HD22	2.01	0.42
1:A:427:LEU:HD23	2:A:1475:HEM:HBC2	2.02	0.41
1:A:402:PHE:CE2	1:A:404:ILE:CD1	3.03	0.41
1:B:106:PHE:CB	1:B:136:LEU:HD23	2.50	0.41

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	414/470 (88%)	401 (97%)	11 (3%)	2 (0%)	34	22
1	B	405/470 (86%)	395 (98%)	10 (2%)	0	100	100
All	All	819/940 (87%)	796 (97%)	21 (3%)	2 (0%)	52	43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	141	GLU
1	A	146	GLU

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	337/413 (82%)	327 (97%)	10 (3%)	48	41
1	B	326/413 (79%)	313 (96%)	13 (4%)	38	29
All	All	663/826 (80%)	640 (96%)	23 (4%)	43	35

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	MET
1	A	66	THR
1	A	84	GLN
1	A	104	SER
1	A	164	GLN
1	A	221	GLU
1	A	231	ARG
1	A	270	ARG
1	A	281	LEU
1	A	404	ILE
1	B	67	LEU
1	B	69	LEU
1	B	84	GLN
1	B	91	ARG
1	B	126	ASP
1	B	127	LEU
1	B	135	ILE
1	B	221	GLU
1	B	231	ARG
1	B	285	LEU
1	B	295	ILE
1	B	382	VAL
1	B	444	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	GLN
1	A	101	GLN
1	A	133	GLN
1	A	164	GLN

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Mol	Chain	Res	Type
1	A	411	ASN
1	B	84	GLN
1	B	133	GLN
1	B	288	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 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	1475	1	24,50,50	1.49	5 (20%)	16,82,82	1.46	3 (18%)
3	EDO	A	1476	-	3,3,3	0.72	0	2,2,2	0.30	0
3	EDO	A	1477	-	3,3,3	0.51	0	2,2,2	0.40	0
2	HEM	B	1475	1	24,50,50	1.17	2 (8%)	16,82,82	1.21	1 (6%)
3	EDO	B	1476	-	3,3,3	0.35	0	2,2,2	0.37	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	1475	1	-	0/6/54/54	0/0/8/8
3	EDO	A	1476	-	-	0/1/1/1	0/0/0/0
3	EDO	A	1477	-	-	0/1/1/1	0/0/0/0
2	HEM	B	1475	1	-	0/6/54/54	0/0/8/8
3	EDO	B	1476	-	-	0/1/1/1	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1475	HEM	C3B-C2B	-3.38	1.36	1.40
2	A	1475	HEM	C1B-NB	-3.22	1.32	1.36
2	B	1475	HEM	C4D-ND	-3.02	1.32	1.36
2	B	1475	HEM	C3B-C2B	-2.93	1.36	1.40
2	A	1475	HEM	C4D-ND	-2.86	1.32	1.36
2	A	1475	HEM	C3D-C2D	-2.21	1.31	1.37
2	A	1475	HEM	C3C-C2C	2.75	1.43	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1475	HEM	CMA-C3A-C4A	-2.98	123.25	128.31
2	A	1475	HEM	CBA-CAA-C2A	-2.09	108.81	112.49
2	A	1475	HEM	CMC-C2C-C3C	2.36	129.71	125.09
2	B	1475	HEM	CMC-C2C-C3C	3.11	131.18	125.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1475	HEM	2	0
3	A	1476	EDO	1	0
2	B	1475	HEM	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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, 95th 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 ²)	Q<0.9
1	A	420/470 (89%)	0.86	40 (9%) 10 11	25, 40, 68, 84	0
1	B	411/470 (87%)	0.69	41 (9%) 9 10	30, 51, 78, 97	0
All	All	831/940 (88%)	0.78	81 (9%) 10 11	25, 45, 75, 97	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	143	LEU	8.3
1	A	53	MET	8.1
1	A	142	GLY	6.6
1	A	378	LYS	5.7
1	B	145	VAL	5.7
1	A	253	ALA	5.1
1	A	54	PRO	5.0
1	B	96	ALA	4.9
1	B	417	TYR	4.9
1	B	110	TRP	4.9
1	A	145	VAL	4.7
1	B	372	GLY	4.4
1	B	233	ALA	4.4
1	B	373	GLY	4.3
1	B	126	ASP	4.2
1	A	55	GLU	4.0
1	A	379	GLY	4.0
1	A	380	ASP	3.9
1	A	247	ASN	3.9
1	A	250	PHE	3.7
1	B	272	ALA	3.5
1	A	268	GLU	3.5
1	B	109	PHE	3.5
1	A	264	TRP	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	100	TYR	3.3
1	B	89	PHE	3.3
1	B	127	LEU	3.3
1	A	377	LYS	3.2
1	A	376	ILE	3.2
1	A	269	ALA	3.2
1	B	365	ALA	3.0
1	B	124	SER	3.0
1	A	263	LEU	3.0
1	B	92	LEU	3.0
1	A	257	ALA	2.9
1	A	216	ASP	2.9
1	B	371	LEU	2.9
1	B	72	ILE	2.9
1	B	382	VAL	2.9
1	B	120	PHE	2.9
1	B	291	THR	2.9
1	A	260	PHE	2.8
1	B	193	ASP	2.7
1	A	273	ALA	2.7
1	B	64	VAL	2.7
1	A	277	PRO	2.7
1	A	232	MET	2.7
1	A	282	ILE	2.6
1	A	275	GLU	2.6
1	B	69	LEU	2.6
1	A	286	GLN	2.6
1	B	99	HIS	2.5
1	B	56	PHE	2.5
1	B	125	HIS	2.5
1	A	474	SER	2.4
1	B	271	ARG	2.4
1	A	67	LEU	2.3
1	B	367	GLN	2.3
1	B	62	PRO	2.3
1	B	71	ASP	2.3
1	B	154	PRO	2.3
1	A	302	ILE	2.3
1	A	278	GLY	2.3
1	B	473	ASN	2.2
1	A	215	LEU	2.2
1	A	279	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	291	THR	2.2
1	B	293	ASP	2.2
1	A	297	ARG	2.2
1	B	98	VAL	2.2
1	B	294	LEU	2.1
1	A	66	THR	2.1
1	A	110	TRP	2.1
1	B	66	THR	2.1
1	A	298	PRO	2.1
1	B	151	MET	2.1
1	A	369	VAL	2.1
1	B	339	ALA	2.1
1	B	274	GLY	2.1
1	B	384	MET	2.0
1	A	254	ALA	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, 95th 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 ²)	Q<0.9
3	EDO	A	1476	4/4	0.88	0.53	14.48	34,39,40,41	0
3	EDO	A	1477	4/4	0.95	0.22	3.05	29,36,37,37	0
3	EDO	B	1476	4/4	0.90	0.17	0.55	38,46,46,47	0
2	HEM	B	1475	43/43	0.94	0.14	-0.57	32,40,46,49	0
2	HEM	A	1475	43/43	0.94	0.15	-0.57	21,26,30,37	0

6.5 Other polymers

There are no such residues in this entry.