



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:18 PM GMT

PDB ID : 3WSP  
Title : Crystal Structure of P450BM3 with N-perfluorononanoyl-L-tryptophan  
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Deposited on : 2014-03-20  
Resolution : 1.80 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

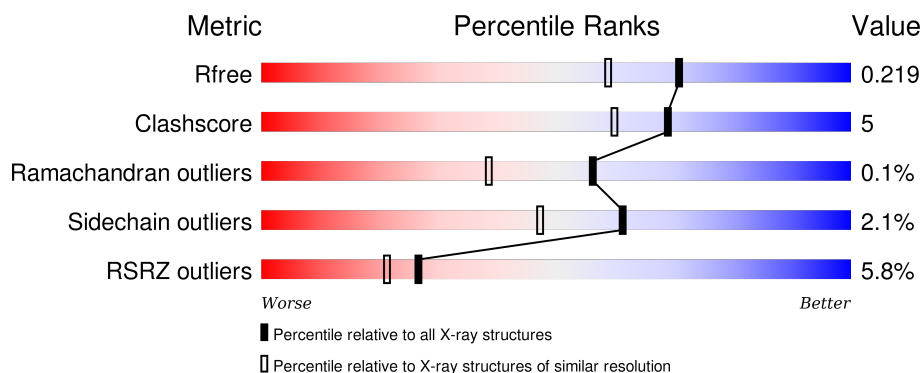
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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))
$R_{free}$	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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. 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	456	<div> <div>7%</div> <div>90%</div> <div>8% ..</div> </div>
1	B	456	<div> <div>5%</div> <div>92%</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
4	DMS	A	503	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8174 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 Bifunctional P-450/NADPH-P450 reductase.

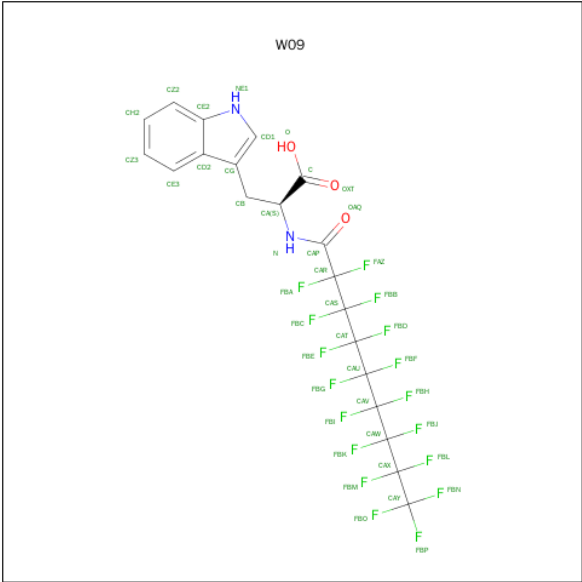
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	0	19	0
			3780	2419	638	705	18			
1	B	453	Total	C	N	O	S	0	1	0
			3660	2339	621	682	18			

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



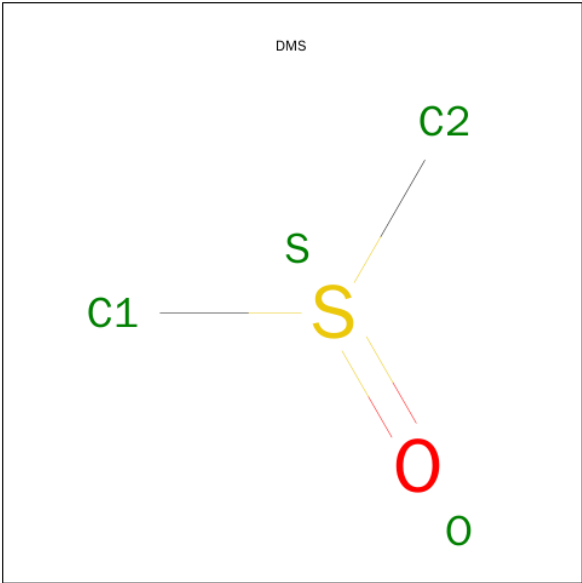
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is N-(2,2,3,3,4,4,5,5,6,6,7,7,8,8,9,9,9-HEPTADEC AFLUORONANOYL)-L-TRYPTOPHAN (three-letter code: W09) (formula:  $C_{20}H_{11}F_{17}N_2O_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			42	20	17	2	3		
3	B	1	Total	C	F	N	O	0	0
			42	20	17	2	3		

- Molecule 4 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C<sub>2</sub>H<sub>6</sub>OS).



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

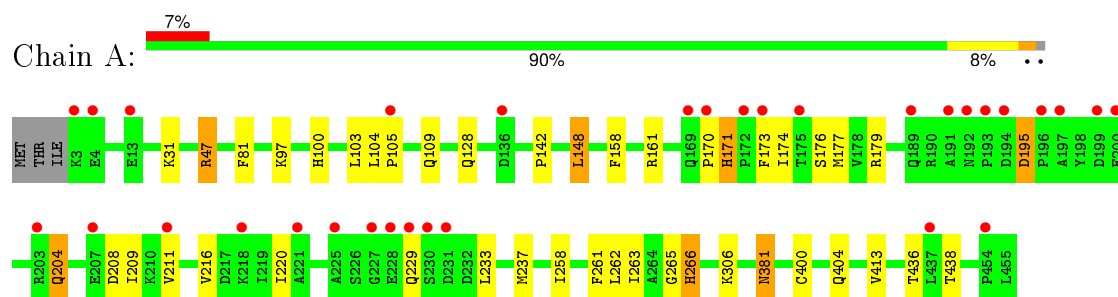
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	287	Total 287	O 287	0	0
5	B	269	Total 269	O 269	0	0

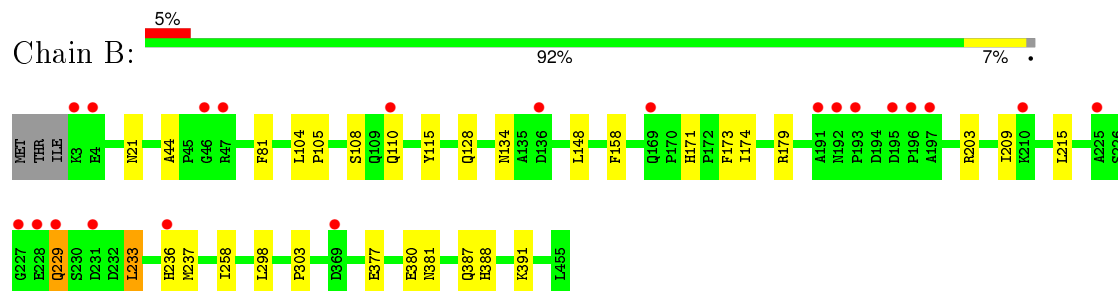
### 3 Residue-property plots

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: Bifunctional P-450/NADPH-P450 reductase



- Molecule 1: Bifunctional P-450/NADPH-P450 reductase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.88 Å 145.39 Å 63.03 Å 90.00° 97.06° 90.00°	Depositor
Resolution (Å)	19.96 – 1.80 19.96 – 1.80	Depositor EDS
% Data completeness (in resolution range)	94.3 (19.96-1.80) 94.3 (19.96-1.80)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.27 (at 1.80 Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.174 , 0.212 0.183 , 0.219	Depositor DCC
$R_{free}$ test set	4600 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	18.3	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 45.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 91739 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8174	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.28% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, DMS, W09

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	0.67	0/3890	0.55	0/5259
1	B	0.66	0/3748	0.54	0/5066
All	All	0.66	0/7638	0.55	0/10325

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3780	0	3775	46	0
1	B	3660	0	3633	18	0
2	A	43	0	30	9	0
2	B	43	0	30	2	0
3	A	42	0	10	1	0
3	B	42	0	10	1	0
4	A	4	0	6	0	0
4	B	4	0	6	0	0
5	A	287	0	0	7	0
5	B	269	0	0	2	0
All	All	8174	0	7500	69	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 5.

All (69) 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:171:HIS:HB3	1:A:174:ILE:HG22	1.45	0.99
1:B:171:HIS:HB3	1:B:174:ILE:HD13	1.65	0.78
1:A:161:ARG:H	1:B:134:ASN:HD21	1.35	0.74
1:A:97:LYS:HB2	5:A:830:HOH:O	1.90	0.72
1:A:170:PRO:O	1:A:174:ILE:HG21	1.90	0.71
1:A:171:HIS:HB3	1:A:174:ILE:CG2	2.21	0.69
1:A:176:SER:OG	1:A:211[B]:VAL:HG11	1.92	0.69
1:A:158:PHE:CE1	1:A:258:ILE:HG12	2.28	0.69
1:A:174:ILE:HD11	5:A:793:HOH:O	1.93	0.68
1:A:220:ILE:HD11	1:A:258:ILE:HD12	1.76	0.66
1:A:306:LYS:HE3	5:A:636:HOH:O	1.97	0.64
1:A:436[B]:THR:C	1:A:438[B]:THR:H	2.03	0.62
1:A:177:MET:SD	1:A:263[A]:ILE:HG13	2.40	0.61
1:A:261:PHE:O	1:A:265[A]:GLY:N	2.35	0.60
1:A:195:ASP:OD1	1:A:195:ASP:C	2.40	0.59
2:A:501:HEM:HMB2	2:A:501:HEM:HBB2	1.86	0.58
1:A:104:LEU:N	1:A:105:PRO:HD2	2.18	0.58
1:A:216:VAL:O	1:A:220:ILE:HG12	2.03	0.57
1:B:388:HIS:HA	1:B:391:LYS:HE2	1.87	0.57
2:A:501:HEM:HBC2	2:A:501:HEM:HMC2	1.87	0.56
2:A:501:HEM:HBC2	2:A:501:HEM:CMC	2.37	0.55
1:A:265[A]:GLY:HA2	2:A:501:HEM:C2C	2.43	0.54
1:A:47:ARG:HD3	3:A:502:W09:CZ2	2.37	0.54
1:A:148:LEU:HD21	1:A:413:VAL:HG21	1.90	0.54
1:A:170:PRO:O	1:A:171:HIS:HB2	2.07	0.53
2:A:501:HEM:CMB	2:A:501:HEM:HBB2	2.40	0.52
1:A:170:PRO:O	1:A:171:HIS:CB	2.56	0.52
1:B:174:ILE:N	1:B:174:ILE:HD12	2.25	0.52
1:B:173:PHE:HB2	1:B:215:LEU:HD22	1.91	0.52
1:A:436[B]:THR:C	1:A:438[B]:THR:N	2.64	0.51
1:A:262:LEU:O	1:A:266[A]:HIS:HD2	1.93	0.51
1:A:100:HIS:CE1	1:A:104:LEU:HD11	2.46	0.51
2:B:501:HEM:HBC2	2:B:501:HEM:CMC	2.42	0.49
1:B:44:ALA:HB3	3:B:502:W09:H8	1.95	0.49
1:A:261:PHE:O	1:A:265[A]:GLY:HA3	2.12	0.48
1:A:170:PRO:O	1:A:174:ILE:CG2	2.58	0.48
1:A:265[A]:GLY:HA2	2:A:501:HEM:C3C	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:LEU:HD21	1:A:237:MET:HG2	1.95	0.47
1:A:261:PHE:O	1:A:265[A]:GLY:CA	2.62	0.47
1:B:81:PHE:HB3	1:B:209:ILE:HG12	1.96	0.47
1:A:97:LYS:NZ	5:A:839:HOH:O	2.48	0.46
1:B:377:GLU:OE2	1:B:380:GLU:OE2	2.34	0.45
1:B:115:TYR:OH	1:B:233:LEU:HD13	2.16	0.45
1:B:104:LEU:HB3	1:B:105:PRO:HD3	1.99	0.45
1:B:236:HIS:HB3	5:B:868:HOH:O	2.16	0.45
1:A:81:PHE:HB3	1:A:209:ILE:HG12	1.99	0.45
1:A:171:HIS:O	1:A:174:ILE:HG23	2.17	0.45
1:B:108:SER:OG	1:B:110:GLN:HG2	2.17	0.44
1:A:128[A]:GLN:NE2	5:A:633:HOH:O	2.49	0.44
1:A:233:LEU:O	1:A:237:MET:HG3	2.17	0.44
1:A:128[A]:GLN:NE2	5:A:654:HOH:O	2.44	0.44
1:A:265[A]:GLY:HA2	2:A:501:HEM:HMC2	1.99	0.44
1:A:262:LEU:O	1:A:266[A]:HIS:CD2	2.71	0.43
1:A:208:ASP:HA	1:A:211[B]:VAL:HG12	2.02	0.42
1:B:158:PHE:CE1	1:B:258:ILE:HG12	2.54	0.42
1:A:173:PHE:C	1:A:173:PHE:CD1	2.93	0.42
1:A:31[B]:LYS:HG3	5:A:711:HOH:O	2.18	0.42
1:A:404:GLN:NE2	1:A:404:GLN:H	2.17	0.42
1:A:177:MET:SD	1:A:263[A]:ILE:CG1	3.06	0.42
1:A:381:ASN:C	1:A:381:ASN:HD22	2.22	0.42
1:A:400:CYS:HA	2:A:501:HEM:CHA	2.50	0.41
1:B:233:LEU:O	1:B:237:MET:HG3	2.19	0.41
1:B:174:ILE:CD1	1:B:174:ILE:N	2.82	0.41
1:B:128:GLN:NE2	5:B:652:HOH:O	2.40	0.41
2:B:501:HEM:HBC2	2:B:501:HEM:HMC2	2.02	0.41
1:B:298:LEU:HD22	1:B:303:PRO:HB3	2.03	0.41
1:A:265[A]:GLY:HA2	2:A:501:HEM:CMC	2.51	0.40
1:A:179:ARG:CZ	1:A:204:GLN:HE22	2.34	0.40
1:B:229:GLN:O	1:B:229:GLN:CG	2.70	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	470/456 (103%)	453 (96%)	16 (3%)	1 (0%)	52	35
1	B	452/456 (99%)	441 (98%)	11 (2%)	0	100	100
All	All	922/912 (101%)	894 (97%)	27 (3%)	1 (0%)	56	38

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	171	HIS

### 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	414/400 (104%)	404 (98%)	10 (2%)	57	41
1	B	398/400 (100%)	390 (98%)	8 (2%)	63	49
All	All	812/800 (102%)	794 (98%)	18 (2%)	61	45

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	ARG
1	A	109	GLN
1	A	142	PRO
1	A	148	LEU
1	A	195	ASP
1	A	204	GLN
1	A	229	GLN
1	A	266[A]	HIS
1	A	266[B]	HIS
1	A	381	ASN
1	B	21	ASN

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Mol	Chain	Res	Type
1	B	148	LEU
1	B	179	ARG
1	B	203	ARG
1	B	229	GLN
1	B	233	LEU
1	B	381	ASN
1	B	387	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	110	GLN
1	A	186	ASN
1	A	189	GLN
1	A	283	ASN
1	A	288	GLN
1	A	381	ASN
1	A	404	GLN
1	B	21	ASN
1	B	128	GLN
1	B	134	ASN
1	B	186	ASN
1	B	387	GLN

### 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

6 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	1,4	30,50,50	2.15	8 (26%)	24,82,82	2.25	8 (33%)
3	W09	A	502	-	38,43,43	1.93	8 (21%)	59,74,74	0.90	2 (3%)
4	DMS	A	503	2	3,3,3	0.48	0	3,3,3	0.75	0
2	HEM	B	501	1,4	30,50,50	2.18	7 (23%)	24,82,82	2.33	9 (37%)
3	W09	B	502	-	38,43,43	2.15	7 (18%)	59,74,74	0.89	2 (3%)
4	DMS	B	503	2	3,3,3	0.44	0	3,3,3	0.24	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	501	1,4	-	0/10/54/54	0/0/8/8
3	W09	A	502	-	-	0/76/81/81	0/2/2/2
4	DMS	A	503	2	-	0/0/0/0	0/0/0/0
2	HEM	B	501	1,4	-	0/10/54/54	0/0/8/8
3	W09	B	502	-	-	0/76/81/81	0/2/2/2
4	DMS	B	503	2	-	0/0/0/0	0/0/0/0

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	W09	FBJ-CAW	-8.08	0.97	1.35
2	A	501	HEM	C2D-C3D	-6.90	1.33	1.54
3	A	502	W09	FBJ-CAW	-6.63	1.03	1.35
2	B	501	HEM	C2D-C3D	-6.37	1.35	1.54
2	A	501	HEM	C2C-C1C	-6.03	1.41	1.52
2	B	501	HEM	C2C-C1C	-5.91	1.41	1.52
2	B	501	HEM	C3B-C4B	-5.49	1.47	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	W09	CZ2-CE2	-4.37	1.33	1.41
3	A	502	W09	CZ2-CE2	-4.05	1.34	1.41
2	A	501	HEM	C3B-C4B	-4.03	1.48	1.51
3	A	502	W09	CE3-CD2	-3.81	1.34	1.42
3	A	502	W09	FBK-CAW	-3.75	1.17	1.35
3	B	502	W09	CE3-CD2	-3.73	1.34	1.42
3	B	502	W09	FBA-CAR	-3.64	1.23	1.35
3	A	502	W09	CD2-CE2	-3.10	1.34	1.42
3	B	502	W09	CD2-CE2	-2.99	1.34	1.42
3	B	502	W09	CD1-CG	-2.85	1.33	1.38
3	A	502	W09	CD1-CG	-2.81	1.33	1.38
2	A	501	HEM	C3D-C4D	-2.81	1.48	1.51
2	B	501	HEM	C3D-C4D	-2.78	1.48	1.51
3	A	502	W09	CB-CA	-2.57	1.49	1.53
2	B	501	HEM	C2B-C1B	-2.40	1.44	1.51
2	A	501	HEM	C2B-C1B	-2.19	1.44	1.51
2	A	501	HEM	C3B-CAB	-2.06	1.47	1.51
2	A	501	HEM	FE-NB	2.01	2.08	1.97
2	B	501	HEM	FE-NB	2.02	2.08	1.97
3	A	502	W09	FBB-CAS	2.36	1.46	1.35
2	B	501	HEM	FE-NC	2.40	2.05	1.95
2	A	501	HEM	FE-NC	2.86	2.07	1.95
3	B	502	W09	FAZ-CAR	4.34	1.50	1.35

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	HEM	C3B-CAB-CBB	-2.66	120.37	124.46
2	B	501	HEM	C3C-CAC-CBC	-2.28	120.97	124.46
2	A	501	HEM	C3B-C4B-NB	-2.24	107.34	111.63
3	A	502	W09	CAY-CAX-CAW	-2.16	108.30	117.13
2	B	501	HEM	CBD-CAD-C3D	-2.07	107.53	113.55
3	B	502	W09	CAY-CAX-CAW	-2.06	108.73	117.13
2	A	501	HEM	CHC-C4B-NB	2.23	129.90	124.52
2	B	501	HEM	CMD-C2D-C3D	2.31	124.59	114.35
3	A	502	W09	OAQ-CAP-CAR	2.39	120.83	118.49
2	A	501	HEM	CMD-C2D-C3D	2.40	124.95	114.35
3	B	502	W09	OAQ-CAP-CAR	2.42	120.85	118.49
2	B	501	HEM	C2D-C3D-C4D	2.72	106.11	101.50
2	A	501	HEM	C2D-C3D-C4D	2.76	106.18	101.50
2	A	501	HEM	CAD-C3D-C2D	4.12	125.07	113.22
2	B	501	HEM	CMC-C2C-C3C	4.14	126.86	116.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	HEM	CMB-C2B-C3B	4.24	127.12	116.53
2	B	501	HEM	CAD-C3D-C4D	4.31	127.68	112.47
2	B	501	HEM	CAD-C3D-C2D	4.51	126.19	113.22
2	A	501	HEM	CAD-C3D-C4D	4.57	128.59	112.47
2	B	501	HEM	CMB-C2B-C3B	4.59	128.00	116.53
2	A	501	HEM	CMC-C2C-C3C	4.74	128.38	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	9	0
3	A	502	W09	1	0
2	B	501	HEM	2	0
3	B	502	W09	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	453/456 (99%)	0.11	32 (7%) 19 15	10, 18, 48, 76	0
1	B	453/456 (99%)	0.01	21 (4%) 36 30	11, 19, 51, 82	0
All	All	906/912 (99%)	0.06	53 (5%) 26 21	10, 19, 50, 82	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	193	PRO	6.1
1	A	225	ALA	6.0
1	B	196	PRO	5.3
1	B	3	LYS	5.3
1	B	191	ALA	5.2
1	B	231	ASP	5.2
1	B	229	GLN	4.6
1	A	229	GLN	4.5
1	A	4	GLU	4.3
1	A	228	GLU	4.2
1	A	3	LYS	4.2
1	B	192	ASN	4.2
1	A	191	ALA	4.1
1	A	169	GLN	4.0
1	B	136	ASP	4.0
1	A	172	PRO	4.0
1	B	169	GLN	3.9
1	B	193	PRO	3.8
1	A	231	ASP	3.7
1	B	225	ALA	3.7
1	B	197	ALA	3.6
1	B	4	GLU	3.5
1	A	221	ALA	3.5
1	A	192	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	195	ASP	3.2
1	A	230	SER	3.2
1	A	196	PRO	3.1
1	A	454	PRO	3.1
1	A	136	ASP	3.1
1	A	227	GLY	3.0
1	A	194	ASP	3.0
1	A	437[A]	LEU	2.9
1	A	173	PHE	2.8
1	A	105	PRO	2.8
1	B	46	GLY	2.7
1	A	203	ARG	2.6
1	B	210	LYS	2.6
1	A	189	GLN	2.6
1	A	170	PRO	2.6
1	B	227	GLY	2.5
1	A	199	ASP	2.5
1	A	207	GLU	2.5
1	A	200	GLU	2.5
1	B	110	GLN	2.5
1	B	47	ARG	2.4
1	B	228	GLU	2.4
1	B	236	HIS	2.3
1	A	211[A]	VAL	2.3
1	A	197	ALA	2.1
1	A	13	GLU	2.1
1	A	175	THR	2.0
1	A	218	LYS	2.0
1	B	369	ASP	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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	DMS	A	503	4/4	0.96	0.19	2.96	27,29,30,30	0
3	W09	B	502	42/42	0.90	0.13	0.44	27,42,49,50	0
3	W09	A	502	42/42	0.90	0.12	0.24	25,42,52,55	0
2	HEM	B	501	43/43	0.98	0.08	-0.55	9,11,14,21	0
2	HEM	A	501	43/43	0.98	0.08	-0.61	11,12,16,22	0
4	DMS	B	503	4/4	0.97	0.14	-	23,24,25,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.