



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:02 PM GMT

PDB ID : 4KCO  
Title : Structure of neuronal nitric oxide synthase heme domain in complex with N-(3-((ethyl(3-fluorophenethyl)amino)methyl)phenyl)thiophene-2-carboximidamide  
Authors : Li, H.; Poulos, T.L.  
Deposited on : 2013-04-24  
Resolution : 1.86 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

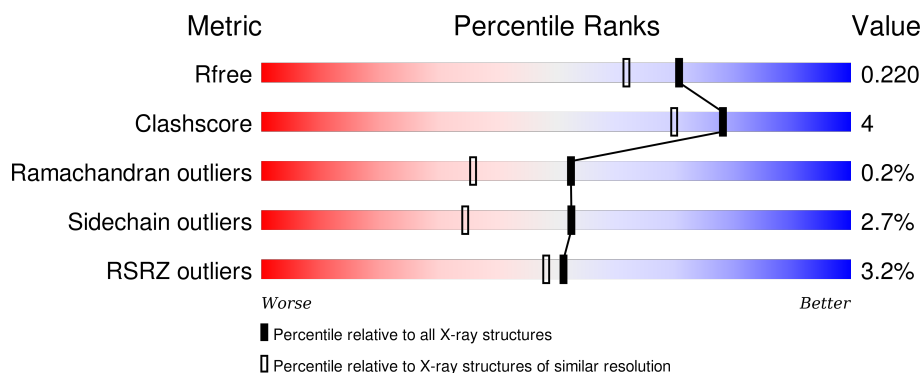
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 1.86 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	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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	422	 4% 88% 7% . .
1	B	422	 2% 86% 10% . .

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
6	ZN	A	805	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7241 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 Nitric oxide synthase, brain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	3	0
			3327	2130	567	609	21			
1	B	411	Total	C	N	O	S	0	3	0
			3357	2148	574	614	21			

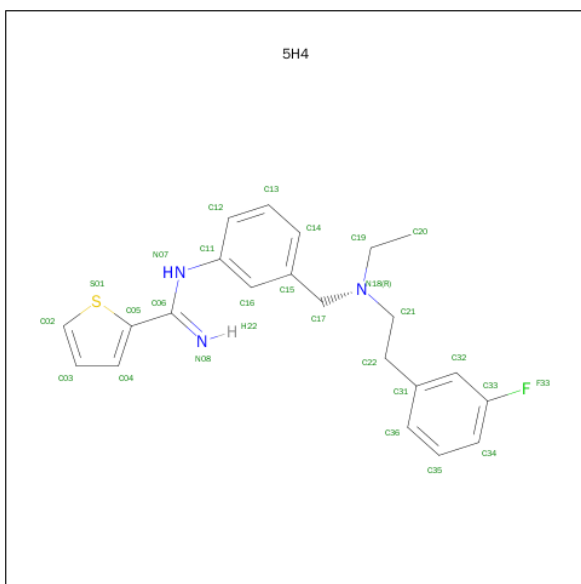
- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is N-[3-({ETHYL[2-(3-FLUOROPHENYL)ETHYL]AMINO}METHYL)PHENYL]THIOPHENE-2-CARBOXIMIDAMIDE (three-letter code: 5H4) (formula: C<sub>22</sub>H<sub>24</sub>FN<sub>3</sub>S).



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	F	N	S	0	0
			27	22	1	3	1		

- Molecule 5 is BROMIDE ION (three-letter code: BR) (formula: Br).

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

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Zn	0	0
			1	1		

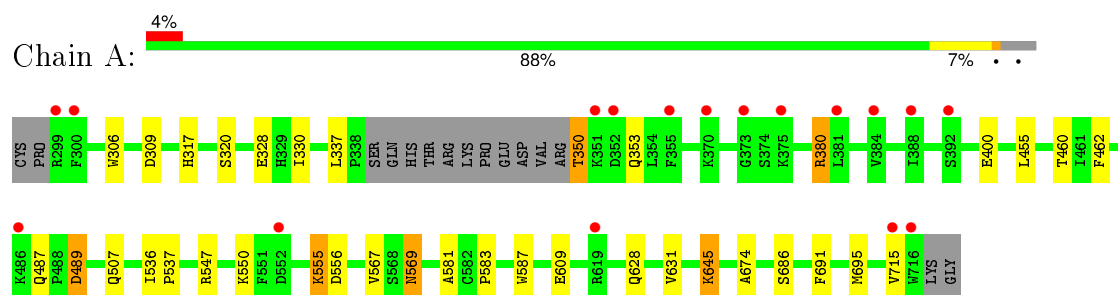
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	153	Total	O	0	0
			153	153		
7	B	227	Total	O	0	0
			227	227		

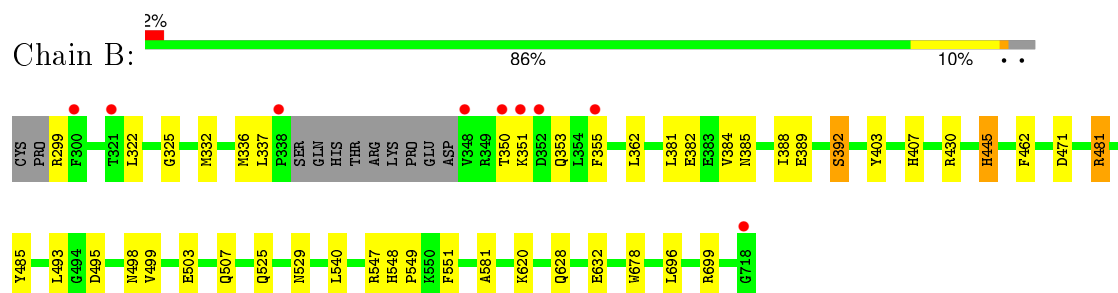
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

- Molecule 1: Nitric oxide synthase, brain



- Molecule 1: Nitric oxide synthase, brain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.05Å 110.93Å 165.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.69 – 1.86 49.64 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.69-1.86) 99.0 (49.64-1.85)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.187 , 0.220 0.186 , 0.220	Depositor DCC
$R_{free}$ test set	3986 reflections (5.20%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.4	Xtriage
Anisotropy	0.740	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 46.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 81036 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7241	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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, ZN, 5H4, H4B, BR

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	0.61	0/3429	0.72	0/4652
1	B	0.74	0/3459	0.80	5/4689 (0.1%)
All	All	0.68	0/6888	0.76	5/9341 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	471	ASP	CB-CG-OD2	5.62	123.35	118.30
1	B	430	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	B	471	ASP	CB-CG-OD1	-5.32	113.52	118.30
1	B	495	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	B	495	ASP	CB-CG-OD1	5.13	122.92	118.30

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	3327	0	3238	21	0
1	B	3357	0	3275	26	0
2	A	43	0	30	1	0
2	B	43	0	30	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	27	0	23	1	0
4	B	27	0	24	5	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	1	0	0	0	0
7	A	153	0	0	1	0
7	B	227	0	0	3	0
All	All	7241	0	6650	49	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 4.

All (49) 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)
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.61	0.83
1:B:481:ARG:HD3	1:B:498:ASN:ND2	2.00	0.77
1:B:325:GLY:O	1:B:332:MET:HG3	1.91	0.71
1:B:481:ARG:HD3	1:B:498:ASN:HD21	1.56	0.70
1:A:609:GLU:HG3	7:A:928:HOH:O	1.96	0.64
1:A:350:THR:N	1:A:353:GLN:HE21	1.98	0.62
1:B:678:TRP:HH2	4:B:803:5H4:H6	1.66	0.60
1:A:350:THR:N	1:A:353:GLN:NE2	2.49	0.59
1:B:551:PHE:HE2	1:B:632:GLU:HG3	1.67	0.58
1:A:380:ARG:HD3	1:A:400:GLU:OE1	2.05	0.56
1:B:362:LEU:HD12	1:B:381:LEU:HD23	1.88	0.56
1:A:555:LYS:HG3	1:A:556:ASP:N	2.21	0.55
1:B:362:LEU:HD11	1:B:384:VAL:HG21	1.92	0.52
1:A:306:TRP:CD2	1:B:336:MET:HE3	2.46	0.51
1:A:569:ASN:H	1:A:569:ASN:HD22	1.59	0.49
2:A:801:HEM:HHC	2:A:801:HEM:HBB2	1.94	0.49
1:B:355:PHE:CE1	1:B:385:ASN:HB2	2.50	0.47
1:A:317:HIS:O	1:A:320:SER:HB3	2.16	0.46
1:A:631:VAL:HG11	1:B:628:GLN:HG2	1.97	0.46
1:A:330:ILE:HD11	1:B:696:LEU:HB3	1.98	0.45
1:B:299:ARG:HB3	1:B:299:ARG:NH1	2.31	0.45
1:A:328:GLU:H	1:A:328:GLU:CD	2.20	0.45
1:B:388:ILE:O	1:B:392:SER:HA	2.16	0.45
1:A:462:PHE:HB2	1:A:581:ALA:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:481:ARG:CD	1:B:498:ASN:HD21	2.28	0.45
1:A:487:GLN:HB3	1:A:489:ASP:HB3	1.98	0.44
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.06	0.44
1:A:686:SER:HA	1:A:691:PHE:CG	2.52	0.44
1:A:567:VAL:HG21	4:A:803:5H4:C14	2.48	0.44
1:B:350:THR:HG22	1:B:351:LYS:N	2.33	0.44
4:B:803:5H4:H14	4:B:803:5H4:H16	1.80	0.44
1:B:299:ARG:HB3	1:B:299:ARG:HH11	1.83	0.43
1:A:645:LYS:HB2	1:A:645:LYS:HE3	1.78	0.43
1:A:674:ALA:HB3	1:A:695:MET:HB3	2.00	0.43
1:A:628:GLN:NE2	1:B:632:GLU:OE2	2.51	0.43
1:B:445:HIS:C	1:B:445:HIS:CD2	2.93	0.42
1:B:322:LEU:HD13	1:B:699:ARG:HH21	1.84	0.42
1:A:455:LEU:HD12	1:A:587:TRP:HB3	2.02	0.42
1:B:507:GLN:NE2	7:B:965:HOH:O	2.51	0.42
1:B:485:TYR:HB2	1:B:493:LEU:HB3	2.00	0.42
4:B:803:5H4:H11	4:B:803:5H4:H5	1.72	0.42
4:B:803:5H4:H12	7:B:1035:HOH:O	2.20	0.42
1:B:499:VAL:O	1:B:503:GLU:HG3	2.20	0.42
1:B:525:GLN:HG3	1:B:529:ASN:O	2.19	0.42
1:A:536:ILE:O	1:A:537:PRO:C	2.57	0.42
4:B:803:5H4:C20	7:B:1035:HOH:O	2.67	0.41
1:B:548:HIS:CG	1:B:549:PRO:HD2	2.56	0.40
1:B:462:PHE:HB2	1:B:581:ALA:HB3	2.02	0.40
1:A:460:THR:O	1:A:583:PRO:HD2	2.22	0.40

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	406/422 (96%)	393 (97%)	11 (3%)	2 (0%)	34 17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	410/422 (97%)	403 (98%)	7 (2%)	0	100	100
All	All	816/844 (97%)	796 (98%)	18 (2%)	2 (0%)	52	36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	489	ASP
1	A	309	ASP

### 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	366/377 (97%)	356 (97%)	10 (3%)	52	34
1	B	369/377 (98%)	359 (97%)	10 (3%)	52	34
All	All	735/754 (98%)	715 (97%)	20 (3%)	52	34

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	337	LEU
1	A	350	THR
1	A	380	ARG
1	A	507	GLN
1	A	547	ARG
1	A	550	LYS
1	A	555	LYS
1	A	569	ASN
1	A	645	LYS
1	A	715	VAL
1	B	337	LEU
1	B	353	GLN
1	B	382	GLU
1	B	389	GLU

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Mol	Chain	Res	Type
1	B	392	SER
1	B	445	HIS
1	B	481	ARG
1	B	540	LEU
1	B	547	ARG
1	B	620	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	454	ASN
1	A	527	ASN
1	A	569	ASN
1	A	628	GLN
1	A	697	ASN
1	B	364	GLN
1	B	454	ASN
1	B	601	ASN
1	B	605	ASN
1	B	628	GLN
1	B	697	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](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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	30,50,50	2.10	7 (23%)	24,82,82	2.39	8 (33%)
3	H4B	A	802	-	13,18,18	1.37	1 (7%)	11,26,26	2.54	6 (54%)
4	5H4	A	803	-	28,29,29	1.38	3 (10%)	31,38,38	2.06	5 (16%)
2	HEM	B	801	1	30,50,50	2.06	7 (23%)	24,82,82	2.81	11 (45%)
3	H4B	B	802	-	13,18,18	1.75	2 (15%)	11,26,26	2.80	6 (54%)
4	5H4	B	803	-	28,29,29	1.58	7 (25%)	31,38,38	1.79	8 (25%)

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	-	0/10/54/54	0/0/8/8
3	H4B	A	802	-	-	0/8/17/17	0/2/2/2
4	5H4	A	803	-	-	0/15/19/19	0/3/3/3
2	HEM	B	801	1	-	0/10/54/54	0/0/8/8
3	H4B	B	802	-	-	0/8/17/17	0/2/2/2
4	5H4	B	803	-	-	0/15/19/19	0/3/3/3

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	HEM	C2D-C3D	-6.44	1.35	1.54
2	A	801	HEM	C2D-C3D	-6.06	1.36	1.54
2	A	801	HEM	C2C-C1C	-5.79	1.41	1.52
2	B	801	HEM	C2C-C1C	-5.06	1.43	1.52
2	A	801	HEM	C3B-C4B	-3.47	1.48	1.51
2	A	801	HEM	C3D-C4D	-3.33	1.47	1.51
2	B	801	HEM	C2B-C1B	-3.25	1.41	1.51
2	B	801	HEM	C3D-C4D	-2.85	1.47	1.51
4	A	803	5H4	C11-N07	-2.70	1.36	1.41
2	B	801	HEM	C3B-C4B	-2.34	1.49	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	803	5H4	C06-N07	-2.31	1.34	1.39
2	A	801	HEM	C2B-C1B	-2.17	1.44	1.51
4	B	803	5H4	C11-N07	-2.00	1.37	1.41
4	B	803	5H4	C34-C33	2.11	1.41	1.37
2	B	801	HEM	FE-NC	2.18	2.04	1.95
2	A	801	HEM	C1C-NC	2.41	1.39	1.36
4	B	803	5H4	C16-C11	2.50	1.43	1.39
3	B	802	H4B	O4-C4	2.62	1.31	1.24
4	B	803	5H4	C13-C14	2.71	1.44	1.38
2	B	801	HEM	C1C-NC	2.85	1.39	1.36
2	A	801	HEM	FE-NC	3.01	2.07	1.95
4	A	803	5H4	C13-C14	3.04	1.45	1.38
3	A	802	H4B	C2-N2	3.18	1.40	1.34
4	B	803	5H4	C05-C06	3.71	1.50	1.45
4	B	803	5H4	C05-S01	4.02	1.77	1.72
4	A	803	5H4	C05-C06	4.18	1.51	1.45
3	B	802	H4B	C7-N8	4.22	1.51	1.46

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	803	5H4	C03-C02-S01	-7.97	104.40	113.23
2	B	801	HEM	C1D-CHD-C4C	-4.48	118.33	125.82
4	B	803	5H4	C03-C02-S01	-4.20	108.58	113.23
2	A	801	HEM	C1D-CHD-C4C	-4.19	118.81	125.82
2	B	801	HEM	C3C-CAC-CBC	-4.18	118.05	124.46
2	B	801	HEM	CBA-CAA-C2A	-3.91	105.51	112.53
3	B	802	H4B	N3-C2-N1	-3.28	120.16	125.53
2	A	801	HEM	CBA-CAA-C2A	-3.26	106.69	112.53
3	A	802	H4B	N3-C2-N1	-3.04	120.56	125.53
4	B	803	5H4	C17-C15-C14	-3.03	115.06	120.78
4	B	803	5H4	C14-C13-C12	-2.97	116.00	120.24
2	B	801	HEM	C3B-CAB-CBB	-2.88	120.04	124.46
2	B	801	HEM	C3B-C4B-NB	-2.81	106.26	111.63
4	A	803	5H4	C11-N07-C06	-2.77	121.52	128.32
4	B	803	5H4	C34-C33-C32	-2.54	120.07	123.35
3	B	802	H4B	C7-C6-N5	-2.34	105.60	110.45
2	B	801	HEM	CMA-C3A-C4A	-2.05	124.97	128.36
4	B	803	5H4	C11-C16-C15	-2.05	117.61	120.81
2	A	801	HEM	C3B-C4B-NB	-2.01	107.78	111.63
4	A	803	5H4	C14-C13-C12	-2.01	117.37	120.24
3	B	802	H4B	N2-C2-N1	2.10	120.67	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	H4B	C4A-C8A-N8	2.10	120.90	118.43
4	B	803	5H4	C14-C15-C16	2.17	121.76	118.55
3	B	802	H4B	C2-N1-C8A	2.68	120.57	114.54
2	B	801	HEM	CMD-C2D-C3D	2.92	127.27	114.35
3	A	802	H4B	C2-N1-C8A	3.07	121.44	114.54
2	A	801	HEM	CMB-C2B-C3B	3.07	124.20	116.53
2	A	801	HEM	CMD-C2D-C3D	3.26	128.77	114.35
3	A	802	H4B	C4-N3-C2	3.34	120.58	115.94
3	A	802	H4B	N2-C2-N1	3.43	122.89	117.20
4	A	803	5H4	C13-C12-C11	3.57	124.25	119.72
4	B	803	5H4	C15-C17-N18	3.68	120.28	113.16
4	B	803	5H4	C13-C12-C11	3.77	124.50	119.72
4	A	803	5H4	C14-C15-C16	3.82	124.20	118.55
3	B	802	H4B	C4-N3-C2	4.15	121.70	115.94
2	A	801	HEM	CAD-C3D-C4D	4.25	127.45	112.47
2	B	801	HEM	CAD-C3D-C4D	4.62	128.76	112.47
2	B	801	HEM	CAD-C3D-C2D	4.68	126.66	113.22
2	B	801	HEM	CMC-C2C-C3C	4.69	128.24	116.53
2	A	801	HEM	CMC-C2C-C3C	4.81	128.54	116.53
3	A	802	H4B	C4-C4A-C8A	4.85	118.95	114.56
2	B	801	HEM	CMB-C2B-C3B	4.95	128.88	116.53
2	A	801	HEM	CAD-C3D-C2D	5.25	128.30	113.22
3	B	802	H4B	C4-C4A-C8A	6.19	120.17	114.56

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	801	HEM	1	0
4	A	803	5H4	1	0
2	B	801	HEM	1	0
4	B	803	5H4	5	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, 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	407/422 (96%)	0.24	17 (4%) 40 37	23, 46, 83, 111	0
1	B	411/422 (97%)	-0.03	9 (2%) 65 63	22, 35, 62, 90	0
All	All	818/844 (96%)	0.11	26 (3%) 51 48	22, 40, 79, 111	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	338	PRO	4.6
1	A	355	PHE	4.6
1	B	300	PHE	3.8
1	A	715	VAL	3.5
1	B	348	VAL	3.5
1	A	381	LEU	3.2
1	A	373	GLY	3.1
1	A	375	LYS	3.0
1	A	299	ARG	2.8
1	A	716	TRP	2.8
1	A	370	LYS	2.7
1	B	350	THR	2.6
1	B	352	ASP	2.6
1	A	300	PHE	2.6
1	A	552	ASP	2.5
1	A	486	LYS	2.5
1	A	351	LYS	2.5
1	A	352	ASP	2.4
1	A	388	ILE	2.3
1	B	355	PHE	2.2
1	B	718	GLY	2.2
1	A	384	VAL	2.2
1	A	392	SER	2.1
1	B	321	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	619	ARG	2.0
1	B	351	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	ZN	A	805	1/1	1.00	0.13	3.55	33,33,33,33	0
4	5H4	B	803	27/27	0.95	0.14	1.82	25,30,80,81	0
5	BR	A	804	1/1	0.99	0.11	1.64	40,40,40,40	0
4	5H4	A	803	27/27	0.94	0.15	1.55	24,30,86,87	0
2	HEM	B	801	43/43	0.98	0.12	1.38	22,24,29,30	0
3	H4B	B	802	17/17	0.96	0.12	0.75	25,27,29,29	0
2	HEM	A	801	43/43	0.98	0.11	0.54	25,27,31,32	0
5	BR	B	804	1/1	0.97	0.10	-0.32	47,47,47,47	0
3	H4B	A	802	17/17	0.97	0.09	-1.85	23,26,28,28	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.