



# Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 03:32 AM GMT

PDB ID : 4FVX  
Title : Structure of rat nNOS heme domain in complex with N(omega)-ethoxy-L-arginine  
Authors : Li, H.; Poulos, T.L.  
Deposited on : 2012-06-29  
Resolution : 2.00 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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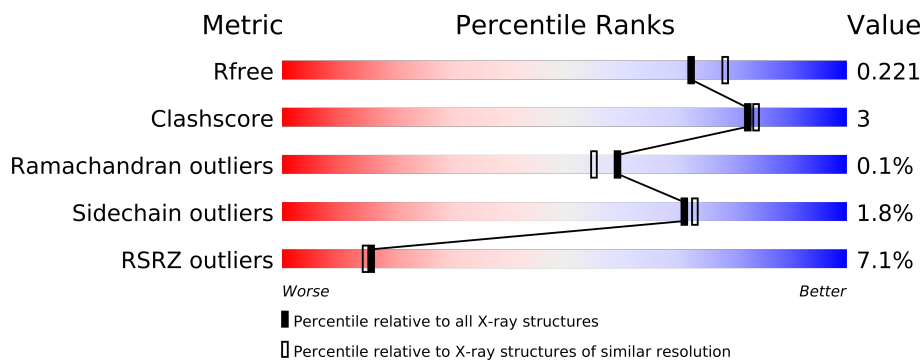
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

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))
$R_{free}$	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	422	
1	B	422	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
5	TFA	A	804	-	X
5	TFA	B	804	-	X

## 2 Entry composition i

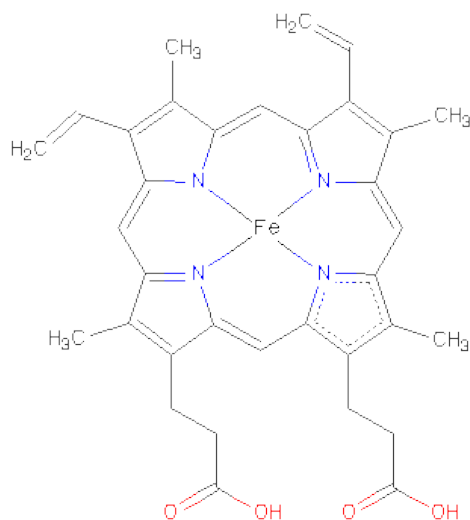
There are 7 unique types of molecules in this entry. The entry contains 7211 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

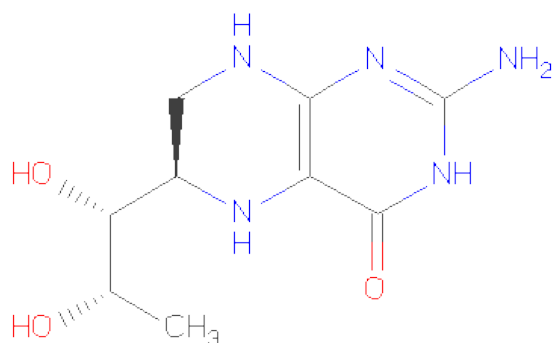
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	0	0
			3313	2121	566	605	21			
1	B	411	Total	C	N	O	S	0	0	0
			3345	2140	574	610	21			

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



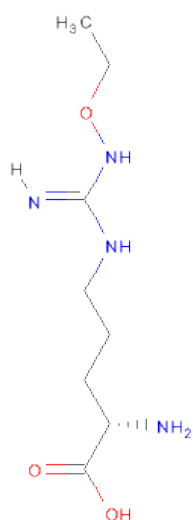
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula:  $C_9H_{15}N_5O_3$ ).



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 5 -(N-ETHOXYCARBAMIMIDOYL)-L-ORNITHINE (three-letter code: 2KJ) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>4</sub>O<sub>3</sub>).



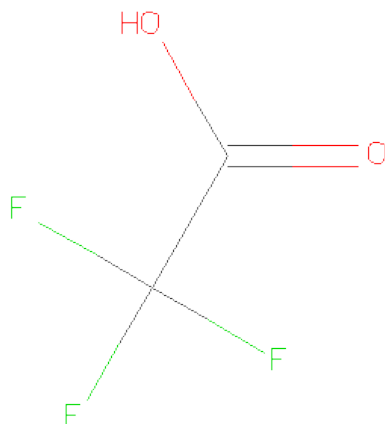
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			15	8	4	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			15	8	4	3		

- Molecule 5 is TRIFLUOROACETIC ACID (three-letter code: TFA) (formula: C<sub>2</sub>HF<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	F	O	0	0
			7	2	3	2		
5	B	1	Total	C	F	O	0	0
			7	2	3	2		

- 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		

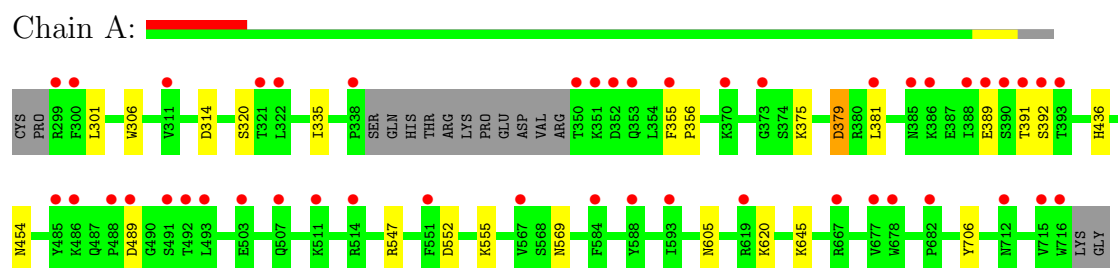
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	161	Total	O	0	0
			161	161		
7	B	227	Total	O	0	0
			227	227		

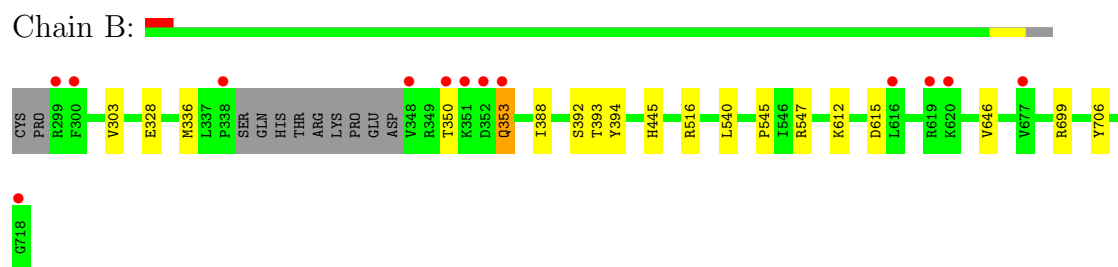
### 3 Residue-property plots

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 ( $RSRZ > 2$ ). 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, $\alpha$ , $\beta$ , $\gamma$	52.00Å 111.28Å 165.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.80 – 2.00 37.80 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (37.80-2.00) 99.5 (37.80-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.52 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.4.0069	Depositor
R, $R_{free}$	0.181 , 0.221 0.181 , 0.221	Depositor DCC
$R_{free}$ test set	3215 reflections (5.19%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.2	Xtriage
Anisotropy	0.742	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 50.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 65204 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7211	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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, TFA, H4B, 2KJ

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	0.60	0/3406	0.67	2/4621 (0.0%)
1	B	0.66	0/3438	0.67	0/4661
All	All	0.63	0/6844	0.67	2/9282 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	379	ASP	CB-CG-OD2	6.66	124.30	118.30
1	A	381	LEU	CA-CB-CG	5.32	127.54	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3313	0	0	10	0
1	B	3345	0	0	13	0
2	A	43	0	0	1	0
2	B	43	0	0	1	0
3	A	17	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	17	0	0	0	0
4	A	15	0	0	0	0
4	B	15	0	0	0	0
5	A	7	0	0	0	0
5	B	7	0	0	0	0
6	A	1	0	0	0	0
7	A	161	0	0	2	0
7	B	227	0	0	5	0
All	All	7211	0	0	21	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (21) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:706:TYR:OH	2:B:801:HEM:O1D	1.92	0.87
1:A:706:TYR:OH	2:A:801:HEM:O1D	2.13	0.67
1:A:436:HIS:ND1	7:A:980:HOH:O	2.30	0.65
1:A:355:PHE:N	1:A:356:PRO:CD	2.65	0.59
1:B:328:GLU:OE1	1:B:328:GLU:N	2.37	0.57
1:B:646:VAL:CG1	7:B:1033:HOH:O	2.53	0.55
1:B:303:VAL:CG1	7:B:1049:HOH:O	2.57	0.53
1:B:388:ILE:O	1:B:392:SER:N	2.45	0.49
1:B:445:HIS:C	1:B:445:HIS:CD2	2.87	0.48
1:A:391:THR:O	1:A:392:SER:OG	2.33	0.47
1:A:335:ILE:CD1	7:B:1049:HOH:O	2.62	0.47
1:A:375:LYS:NZ	1:A:379:ASP:OD1	2.49	0.45
1:A:306:TRP:CD2	1:B:336:MET:CE	2.99	0.45
1:A:605:ASN:ND2	7:A:931:HOH:O	2.50	0.44
1:B:516:ARG:CD	7:B:1111:HOH:O	2.66	0.44
1:B:612:LYS:O	1:B:615:ASP:N	2.51	0.43
1:B:350:THR:N	1:B:353:GLN:OE1	2.52	0.43
1:B:699:ARG:NE	7:B:1026:HOH:O	2.52	0.43
1:B:393:THR:OG1	1:B:394:TYR:N	2.52	0.41
1:A:306:TRP:CG	1:B:336:MET:CE	3.04	0.41
1:A:301:LEU:O	1:A:314:ASP:N	2.54	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	403/422 (96%)	390 (97%)	12 (3%)	1 (0%)	56	51
1	B	407/422 (96%)	399 (98%)	8 (2%)	0	100	100
All	All	810/844 (96%)	789 (97%)	20 (2%)	1 (0%)	59	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	489	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	363/377 (96%)	354 (98%)	9 (2%)	60	59
1	B	366/377 (97%)	362 (99%)	4 (1%)	84	86
All	All	729/754 (97%)	716 (98%)	13 (2%)	71	73

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	320	SER
1	A	389	GLU
1	A	454	ASN
1	A	547	ARG
1	A	552	ASP
1	A	555	LYS
1	A	569	ASN
1	A	620	LYS

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Mol	Chain	Res	Type
1	A	645	LYS
1	B	353	GLN
1	B	540	LEU
1	B	545	PRO
1	B	547	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

Of 9 ligands modelled in this entry, 1 is 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	49,50,50	2.56	15 (30%)	46,82,82	2.52	14 (30%)
3	H4B	A	802	-	18,18,18	0.84	1 (5%)	24,26,26	1.86	8 (33%)
4	2KJ	A	803	-	14,14,14	1.30	1 (7%)	16,16,16	1.98	2 (12%)
5	TFA	A	804	-	6,6,6	0.74	0	9,9,9	0.72	0
2	HEM	B	801	1	49,50,50	2.82	18 (36%)	46,82,82	2.27	11 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	H4B	B	802	-	18,18,18	1.26	2 (11%)	24,26,26	1.65	5 (20%)
4	2KJ	B	803	-	14,14,14	1.35	1 (7%)	16,16,16	1.88	5 (31%)
5	TFA	B	804	-	6,6,6	0.72	0	9,9,9	0.95	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	-	0/14/114/114	0/0/8/8
3	H4B	A	802	-	-	0/8/17/17	0/0/2/2
4	2KJ	A	803	-	-	0/13/15/15	0/0/0/0
5	TFA	A	804	-	-	0/6/6/6	0/0/0/0
2	HEM	B	801	1	-	0/14/114/114	0/0/8/8
3	H4B	B	802	-	-	0/8/17/17	0/0/2/2
4	2KJ	B	803	-	-	0/13/15/15	0/0/0/0
5	TFA	B	804	-	-	0/6/6/6	0/0/0/0

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	HEM	C2D-C1D	8.30	1.46	1.44
2	A	801	HEM	C2B-C1B	7.18	1.46	1.44
2	B	801	HEM	C3D-C4D	6.63	1.46	1.44
2	A	801	HEM	C3B-C2B	-6.00	1.33	1.43
2	B	801	HEM	C3C-C2C	-5.63	1.33	1.43
2	B	801	HEM	C3B-C2B	-5.19	1.34	1.43
2	B	801	HEM	C3D-C2D	4.90	1.52	1.43
2	A	801	HEM	C3C-CAC	4.81	1.55	1.40
2	A	801	HEM	C3B-CAB	4.78	1.55	1.40
2	A	801	HEM	FE-ND	4.72	2.15	1.97
2	B	801	HEM	C3C-CAC	4.72	1.55	1.40
2	B	801	HEM	C4A-C3A	4.70	1.46	1.40
2	A	801	HEM	C3D-C2D	4.62	1.51	1.43
4	B	803	2KJ	CZ-NH2	-4.35	1.27	1.33
2	B	801	HEM	C2B-C1B	4.31	1.45	1.44
4	A	803	2KJ	CZ-NH2	-4.29	1.27	1.33
2	A	801	HEM	C3D-C4D	-4.23	1.43	1.44
2	A	801	HEM	FE-NA	4.20	2.10	1.92
2	A	801	HEM	C4A-C3A	4.20	1.45	1.40
2	B	801	HEM	C3B-CAB	4.14	1.53	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C3C-C2C	-3.89	1.37	1.43
2	B	801	HEM	FE-ND	3.55	2.10	1.97
2	B	801	HEM	C3B-C4B	3.41	1.48	1.44
2	B	801	HEM	CMB-C2B	3.33	1.57	1.47
2	B	801	HEM	CMD-C2D	3.16	1.57	1.47
2	B	801	HEM	FE-NA	3.15	2.05	1.92
2	A	801	HEM	FE-NB	2.96	2.08	1.97
3	B	802	H4B	C7-C6	2.90	1.55	1.52
2	A	801	HEM	CMC-C2C	2.83	1.56	1.47
2	A	801	HEM	CMB-C2B	2.79	1.56	1.47
2	B	801	HEM	FE-NB	2.72	2.07	1.97
2	B	801	HEM	CMC-C2C	2.65	1.55	1.47
2	B	801	HEM	CHA-C4D	2.60	1.39	1.35
2	A	801	HEM	CMD-C2D	2.57	1.55	1.47
3	A	802	H4B	C2-N2	2.44	1.36	1.32
2	B	801	HEM	FE-NC	2.37	2.06	1.97
3	B	802	H4B	C2-N1	2.31	1.36	1.33
2	A	801	HEM	C2D-C1D	2.18	1.45	1.44

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	HEM	C3B-C4B-NB	-9.41	107.26	114.00
2	A	801	HEM	C3B-C4B-NB	-8.24	108.10	114.00
4	A	803	2KJ	C2-OH-NH1	6.85	123.44	109.91
2	B	801	HEM	CBA-CAA-C2A	-6.55	101.15	112.69
2	A	801	HEM	C4D-ND-C1D	6.53	111.84	105.16
2	A	801	HEM	CBA-CAA-C2A	-6.47	101.29	112.69
2	A	801	HEM	CBD-CAD-C3D	-5.86	101.59	114.37
4	B	803	2KJ	C2-OH-NH1	5.11	120.00	109.91
2	B	801	HEM	CBD-CAD-C3D	-4.65	104.23	114.37
3	A	802	H4B	C4-C4A-C8A	4.43	118.66	114.56
3	B	802	H4B	C4-C4A-C8A	4.10	118.36	114.56
2	A	801	HEM	C2D-C1D-ND	-4.04	108.16	112.93
2	A	801	HEM	C3A-C4A-NA	-3.80	106.55	109.41
3	A	802	H4B	N2-C2-N3	3.70	121.93	117.86
2	B	801	HEM	C4D-ND-C1D	3.63	108.87	105.16
2	B	801	HEM	C4A-CHB-C1B	-3.29	123.15	127.47
3	A	802	H4B	C2-N1-C8A	3.17	122.12	117.61
2	A	801	HEM	CMA-C3A-C4A	-2.93	124.11	128.62
2	B	801	HEM	C3A-C4A-NA	-2.79	107.31	109.41
2	B	801	HEM	C1A-C2A-C3A	2.71	109.73	106.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	803	2KJ	CD-NE-CZ	-2.69	119.29	124.03
3	B	802	H4B	C4A-C4-N3	2.69	120.95	114.06
4	B	803	2KJ	CD-NE-CZ	-2.64	119.39	124.03
4	B	803	2KJ	OH-NH1-CZ	2.52	123.21	114.55
2	A	801	HEM	C4C-NC-C1C	2.51	108.14	105.53
3	B	802	H4B	N2-C2-N3	2.49	120.60	117.86
2	B	801	HEM	CMA-C3A-C4A	-2.45	124.85	128.62
3	B	802	H4B	C2-N1-C8A	2.41	121.04	117.61
2	B	801	HEM	C2A-C1A-NA	-2.38	106.42	109.73
2	A	801	HEM	C4A-C3A-C2A	2.37	108.65	107.00
3	B	802	H4B	N8-C8A-N1	2.30	119.19	115.82
3	A	802	H4B	C4A-C8A-N8	2.25	122.32	119.23
4	B	803	2KJ	OA1-C-OA2	-2.25	118.99	124.07
3	A	802	H4B	C4A-C4-N3	2.25	119.82	114.06
4	B	803	2KJ	OH-C2-C1	2.20	110.94	107.40
2	A	801	HEM	CHD-C1D-ND	2.17	126.39	124.58
2	A	801	HEM	CHD-C4C-NC	2.14	126.59	124.73
3	A	802	H4B	N8-C8A-N1	2.13	118.94	115.82
2	A	801	HEM	CHA-C4D-ND	2.11	127.20	124.31
2	B	801	HEM	C1B-NB-C4B	2.08	107.29	105.16
2	A	801	HEM	C1A-CHA-C4D	-2.08	124.74	127.47
3	A	802	H4B	C4-C4A-N5	2.08	122.12	119.10
3	A	802	H4B	N2-C2-N1	-2.07	117.51	120.31
2	A	801	HEM	C4A-CHB-C1B	-2.05	124.77	127.47
2	B	801	HEM	CHA-C1A-NA	2.00	127.92	124.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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%)	0.48	46 (11%) 6 5	26, 50, 91, 116	0
1	B	411/422 (97%)	0.03	13 (3%) 45 45	25, 39, 66, 85	0
All	All	818/844 (96%)	0.25	59 (7%) 16 14	25, 44, 85, 116	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	PHE	7.1
1	A	716	TRP	6.7
1	A	352	ASP	5.4
1	B	348	VAL	5.3
1	A	355	PHE	4.6
1	A	488	PRO	4.5
1	B	718	GLY	4.4
1	A	300	PHE	4.1
1	B	352	ASP	4.0
1	A	351	LYS	3.9
1	B	350	THR	3.8
1	B	619	ARG	3.7
1	A	322	LEU	3.5
1	A	507	GLN	3.5
1	A	715	VAL	3.4
1	A	486	LYS	3.4
1	A	491	SER	3.4
1	A	299	ARG	3.2
1	B	338	PRO	3.1
1	A	311	VAL	3.1
1	A	392	SER	3.0
1	A	567	VAL	3.0
1	A	514	ARG	3.0
1	A	389	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	321	THR	2.8
1	A	619	ARG	2.8
1	A	338	PRO	2.7
1	B	353	GLN	2.6
1	A	388	ILE	2.6
1	A	390	SER	2.6
1	A	393	THR	2.5
1	B	616	LEU	2.5
1	A	350	THR	2.5
1	A	678	TRP	2.5
1	A	682	PRO	2.4
1	A	503	GLU	2.4
1	A	489	ASP	2.4
1	A	485	TYR	2.4
1	A	386	LYS	2.4
1	A	493	LEU	2.4
1	A	492	THR	2.3
1	A	370	LYS	2.3
1	B	351	LYS	2.3
1	A	551	PHE	2.3
1	A	593	ILE	2.3
1	A	584	PHE	2.2
1	A	353	GLN	2.2
1	A	391	THR	2.2
1	B	677	VAL	2.2
1	A	385	ASN	2.2
1	B	620	LYS	2.2
1	A	712	ASN	2.1
1	A	511	LYS	2.1
1	B	299	ARG	2.1
1	A	677	VAL	2.0
1	A	381	LEU	2.0
1	A	667	ARG	2.0
1	A	588	TYR	2.0
1	A	373	GLY	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 ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	TFA	B	804	7/7	0.24	8.64	49,51,54,55	7
5	TFA	A	804	7/7	0.19	2.41	60,60,61,61	7
4	2KJ	A	803	15/15	0.26	1.49	32,35,44,46	0
3	H4B	A	802	17/17	0.18	0.58	26,30,35,36	0
4	2KJ	B	803	15/15	0.17	0.54	30,34,44,47	0
2	HEM	A	801	43/43	0.19	0.45	26,31,39,46	0
2	HEM	B	801	43/43	0.14	0.36	23,28,36,44	0
3	H4B	B	802	17/17	0.13	0.06	24,28,32,34	0
6	ZN	A	805	1/1	0.07	-0.79	37,37,37,37	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.