



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2017 – 07:31 AM EDT

PDB ID : 3N2R  
Title : Structure of neuronal nitric oxide synthase heme domain in complex with 6-((3R,4R/3S,4S)-4-(3-Phenoxyphenoxy)pyrrolidin-3-yl)methyl)pyridin-2-amine  
Authors : Li, H.; Poulos, T.L.  
Deposited on : unknown  
Resolution : 1.90 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-20030345  
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-20030345

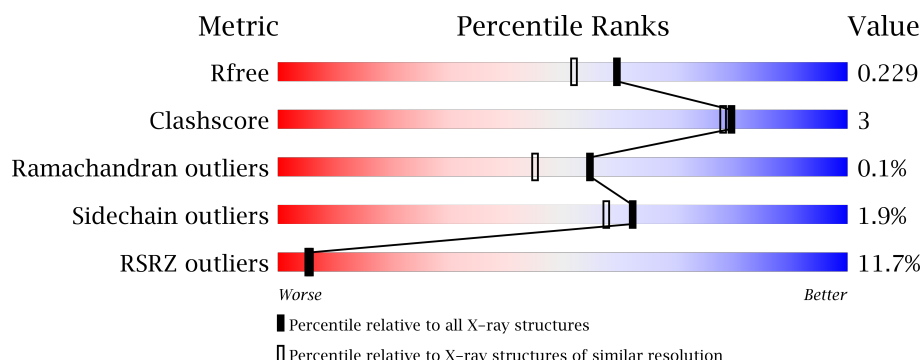
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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	<div> <div>17%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div>• •</div> </div> </div>
1	B	422	<div> <div>6%</div> <div> <div></div> <div>92%</div> <div>5%</div> <div>•</div> </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	ACT	A	860	-	-	-	X
5	XJH	A	800	-	-	-	X
5	XJH	B	800	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7233 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	1	0
			3316	2123	566	605	22			
1	B	411	Total	C	N	O	S	0	3	0
			3354	2146	574	612	22			

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



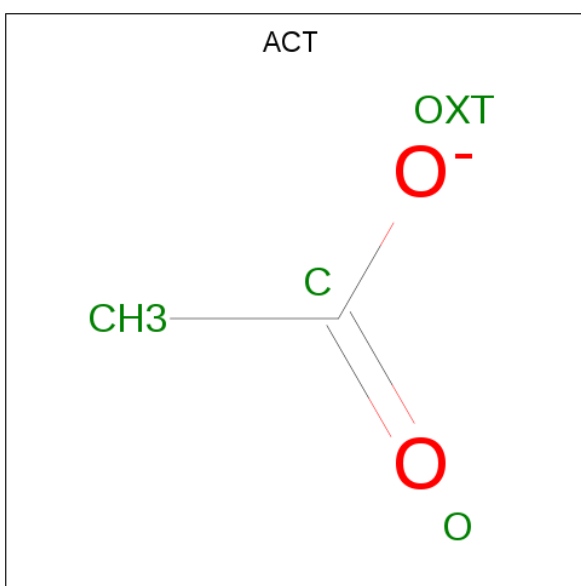
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



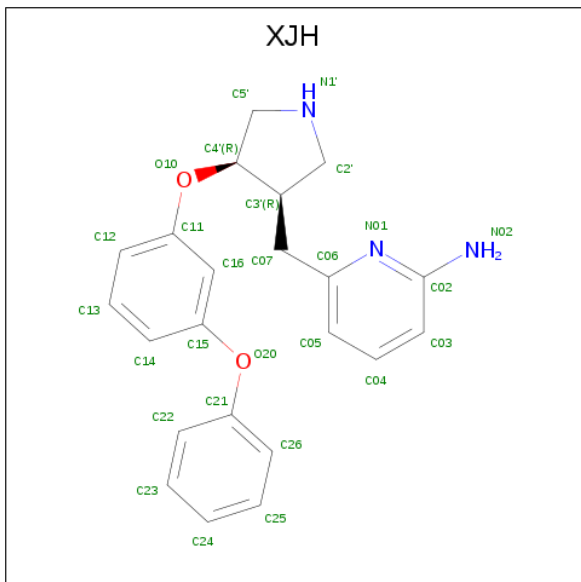
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



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

- Molecule 5 is 6-[[[(3R,4R)-4-(3-phenoxyphenoxy)pyrrolidin-3-yl]methyl]pyridin-2-amine (three-letter code: XJH) (formula: C<sub>22</sub>H<sub>23</sub>N<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			27	22	3	2		
5	B	1	Total	C	N	O	0	0
			27	22	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		

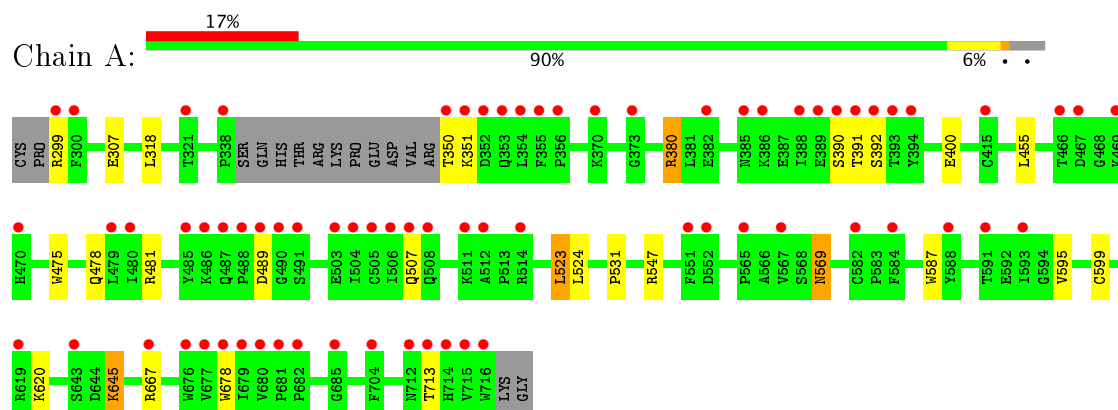
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	161	Total	O	0	0
			161	161		
7	B	219	Total	O	0	0
			219	219		

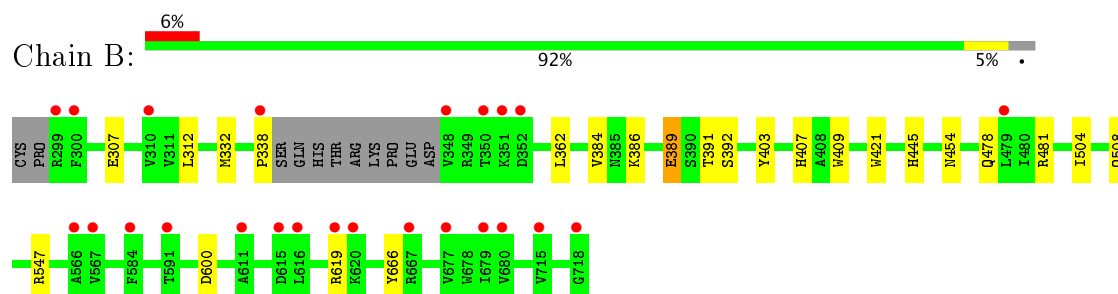
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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: Nitric oxide synthase



- Molecule 1: Nitric oxide synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.28Å 111.56Å 164.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.36 – 1.90 38.66 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (47.36-1.90) 98.8 (38.66-1.90)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.39 (at 1.91Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.182 , 0.215 0.196 , 0.229	Depositor DCC
$R_{free}$ test set	3757 reflections (5.23%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.5	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 41.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7233	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, ZN, ACT, H4B, XJH

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	0/3412	0.62	0/4629
1	B	0.70	0/3456	0.65	1/4685 (0.0%)
All	All	0.65	0/6868	0.63	1/9314 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	600	ASP	CB-CG-OD2	5.07	122.86	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	3316	0	3226	16	0
1	B	3354	0	3274	12	0
2	A	43	0	30	4	0
2	B	43	0	30	3	0
3	A	17	0	15	1	0
3	B	17	0	15	0	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	27	0	23	6	0
5	B	27	0	23	6	0
6	A	1	0	0	0	0
7	A	161	0	0	2	0
7	B	219	0	0	2	0
All	All	7233	0	6642	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 3.

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)
5:A:800:XJH:H12	5:A:800:XJH:H5'A	1.49	0.94
2:A:750:HEM:HMC2	2:A:750:HEM:HBC2	1.73	0.71
5:A:800:XJH:H12	5:A:800:XJH:C5'	2.20	0.69
1:A:307:GLU:HG3	7:B:1172:HOH:O	1.97	0.64
7:A:1106:HOH:O	1:B:307:GLU:HG3	2.00	0.61
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.82	0.61
5:A:800:XJH:C12	5:A:800:XJH:H5'A	2.28	0.60
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.86	0.58
5:B:800:XJH:C5'	5:B:800:XJH:C12	2.80	0.56
5:B:800:XJH:H5'	5:B:800:XJH:H12	1.87	0.56
1:A:380:ARG:HD3	1:A:400:GLU:OE1	2.05	0.55
1:A:667:ARG:HD3	7:A:1118:HOH:O	2.06	0.55
1:B:338:PRO:HG3	7:B:1368:HOH:O	2.06	0.55
1:B:403:TYR:CE1	1:B:407:HIS:CE1	2.98	0.52
2:A:750:HEM:HHC	2:A:750:HEM:HBB2	1.91	0.52
5:A:800:XJH:C12	5:A:800:XJH:C5'	2.88	0.51
2:A:750:HEM:O2D	5:A:800:XJH:H16	2.10	0.51
1:A:299:ARG:HE	1:A:318:LEU:HD13	1.77	0.50
5:B:800:XJH:C5'	5:B:800:XJH:H12	2.42	0.49
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.94	0.49
2:A:750:HEM:HBA2	5:A:800:XJH:H07A	1.95	0.49
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.95	0.47
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.96	0.47
2:B:750:HEM:HBB2	2:B:750:HEM:HHC	1.97	0.47
5:B:800:XJH:H5'	5:B:800:XJH:C12	2.45	0.46
1:A:391:THR:O	1:A:392:SER:OG	2.28	0.46
1:B:362:LEU:HD11	1:B:384:VAL:HG21	2.00	0.44
1:B:619:ARG:HB2	1:B:619:ARG:HE	1.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:595:VAL:O	1:A:599:CYS:HB2	2.18	0.43
2:B:750:HEM:O2A	5:B:800:XJH:H4'	2.18	0.43
1:A:569:ASN:HD22	1:A:569:ASN:H	1.66	0.43
1:B:391:THR:O	1:B:392:SER:HB2	2.18	0.43
1:A:524:LEU:O	1:A:531:PRO:HA	2.19	0.43
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.54	0.43
1:A:455:LEU:HD12	1:A:587:TRP:CB	2.49	0.42
1:A:645:LYS:HB2	1:A:645:LYS:HE3	1.84	0.42
2:B:750:HEM:HBA2	5:B:800:XJH:H07A	2.02	0.41
1:B:386:LYS:O	1:B:389:GLU:HG3	2.20	0.41
1:B:445:HIS:C	1:B:445:HIS:CD2	2.94	0.41
1:A:351:LYS:HE2	1:A:392:SER:HB3	2.03	0.41
1:A:678:TRP:HA	3:A:760:H4B:N1	2.36	0.40
1:B:504:ILE:O	1:B:508:GLN:HG2	2.20	0.40
1:B:312:LEU:HB3	1:B:666:TYR:CD2	2.57	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	404/422 (96%)	393 (97%)	10 (2%)	1 (0%)	51	41
1	B	410/422 (97%)	405 (99%)	5 (1%)	0	100	100
All	All	814/844 (96%)	798 (98%)	15 (2%)	1 (0%)	55	45

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	364/377 (97%)	354 (97%)	10 (3%)	50	42
1	B	369/377 (98%)	365 (99%)	4 (1%)	78	77
All	All	733/754 (97%)	719 (98%)	14 (2%)	62	57

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

Mol	Chain	Res	Type
1	A	350	THR
1	A	380	ARG
1	A	390	SER
1	A	507	GLN
1	A	523	LEU
1	A	547	ARG
1	A	569	ASN
1	A	620	LYS
1	A	645	LYS
1	A	713	THR
1	B	332	MET
1	B	389	GLU
1	B	454	ASN
1	B	547	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	385	ASN
1	A	454	ASN
1	A	527	ASN
1	A	569	ASN
1	A	605	ASN
1	A	697	ASN
1	B	364	GLN
1	B	385	ASN

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Mol	Chain	Res	Type
1	B	425	GLN
1	B	454	ASN
1	B	507	GLN
1	B	601	ASN
1	B	605	ASN
1	B	697	ASN

### 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 ⓘ

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	750	1	28,50,50	2.21	9 (32%)	17,82,82	1.92	4 (23%)
3	H4B	A	760	-	14,18,18	1.06	2 (14%)	12,26,26	2.65	5 (41%)
5	XJH	A	800	-	27,30,30	0.97	0	33,40,40	1.77	7 (21%)
4	ACT	A	860	-	1,3,3	1.72	0	0,3,3	0.00	-
2	HEM	B	750	1	28,50,50	2.42	11 (39%)	17,82,82	1.97	4 (23%)
3	H4B	B	760	-	14,18,18	1.04	1 (7%)	12,26,26	2.53	4 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	XJH	B	800	-	27,30,30	0.91	0	33,40,40	1.64	8 (24%)
4	ACT	B	860	-	1,3,3	1.54	0	0,3,3	0.00	-

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	750	1	-	0/6/54/54	0/0/8/8
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2
5	XJH	A	800	-	-	0/12/22/22	0/4/4/4
4	ACT	A	860	-	-	0/0/0/0	0/0/0/0
2	HEM	B	750	1	-	0/6/54/54	0/0/8/8
3	H4B	B	760	-	-	0/8/17/17	0/2/2/2
5	XJH	B	800	-	-	0/12/22/22	0/4/4/4
4	ACT	B	860	-	-	0/0/0/0	0/0/0/0

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	750	HEM	C3C-C2C	-5.63	1.32	1.40
2	A	750	HEM	C3B-C2B	-4.99	1.33	1.40
2	B	750	HEM	C3B-C2B	-4.54	1.34	1.40
2	A	750	HEM	C3C-C2C	-3.79	1.35	1.40
3	B	760	H4B	C4-C4A	-2.52	1.38	1.41
2	B	750	HEM	C4D-ND	2.07	1.39	1.36
2	A	750	HEM	CMB-C2B	2.10	1.56	1.51
2	A	750	HEM	CMD-C2D	2.10	1.55	1.51
2	B	750	HEM	CMC-C2C	2.16	1.56	1.51
3	A	760	H4B	C4-N3	2.21	1.37	1.33
2	A	750	HEM	C1B-NB	2.22	1.39	1.36
2	B	750	HEM	CAA-C2A	2.30	1.55	1.52
2	B	750	HEM	C1B-NB	2.50	1.39	1.36
2	B	750	HEM	CAD-C3D	2.51	1.57	1.52
3	A	760	H4B	C2-N2	2.53	1.39	1.34
2	A	750	HEM	C4D-ND	2.55	1.39	1.36
2	B	750	HEM	CMD-C2D	3.10	1.57	1.51
2	B	750	HEM	C3B-CAB	3.48	1.54	1.47
2	A	750	HEM	C3B-CAB	3.58	1.55	1.47
2	A	750	HEM	C3C-CAC	3.59	1.54	1.47
2	B	750	HEM	C3C-CAC	4.13	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	750	HEM	C3D-C2D	4.33	1.50	1.37
2	A	750	HEM	C3D-C2D	4.60	1.51	1.37

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	750	HEM	CBA-CAA-C2A	-4.17	104.52	112.48
3	A	760	H4B	N3-C2-N1	-4.15	118.72	125.45
2	A	750	HEM	CBA-CAA-C2A	-4.08	104.69	112.48
2	A	750	HEM	CBD-CAD-C3D	-3.85	105.13	112.47
2	B	750	HEM	C1D-C2D-C3D	-3.69	104.43	107.00
3	B	760	H4B	N3-C2-N1	-3.38	119.97	125.45
5	A	800	XJH	C05-C06-N01	-2.97	118.58	122.40
2	B	750	HEM	CMA-C3A-C4A	-2.95	123.94	128.46
2	B	750	HEM	CBD-CAD-C3D	-2.44	107.82	112.47
5	B	800	XJH	C05-C06-N01	-2.04	119.78	122.40
5	B	800	XJH	C03-C02-N02	-2.00	117.66	121.26
5	A	800	XJH	C13-C12-C11	2.03	122.28	118.95
5	B	800	XJH	C13-C12-C11	2.13	122.45	118.95
2	A	750	HEM	C4C-C3C-C2C	2.18	108.42	106.90
3	B	760	H4B	C2-N1-C8A	2.26	119.61	114.51
5	A	800	XJH	C2'-C3'-C4'	2.47	106.54	103.40
3	A	760	H4B	N2-C2-N3	2.66	121.49	117.24
2	A	750	HEM	CMC-C2C-C3C	2.80	130.09	124.89
5	B	800	XJH	N02-C02-N01	2.91	121.54	116.64
5	A	800	XJH	N02-C02-N01	2.98	121.65	116.64
5	A	800	XJH	C5'-N1'-C2'	3.30	113.09	105.40
5	B	800	XJH	C02-N01-C06	3.37	120.55	118.17
5	B	800	XJH	C2'-C3'-C4'	3.38	107.70	103.40
5	A	800	XJH	C07-C06-N01	3.54	122.71	117.12
3	A	760	H4B	C2-N1-C8A	3.64	122.71	114.51
5	B	800	XJH	C5'-N1'-C2'	3.71	114.04	105.40
5	B	800	XJH	C07-C06-N01	3.90	123.28	117.12
3	A	760	H4B	C4-N3-C2	4.02	121.84	116.06
3	A	760	H4B	C4-C4A-C8A	4.30	118.46	114.56
3	B	760	H4B	C4-C4A-C8A	4.58	118.71	114.56
5	A	800	XJH	C02-N01-C06	4.71	121.50	118.17
3	B	760	H4B	C4-N3-C2	4.91	123.12	116.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	750	HEM	4	0
3	A	760	H4B	1	0
5	A	800	XJH	6	0
2	B	750	HEM	3	0
5	B	800	XJH	6	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	407/422 (96%)	0.90	72 (17%) 2 2	24, 47, 85, 107	0
1	B	411/422 (97%)	0.30	24 (5%) 24 27	23, 37, 59, 79	0
All	All	818/844 (96%)	0.60	96 (11%) 5 5	23, 41, 79, 107	0

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	PHE	8.9
1	B	348	VAL	8.0
1	A	715	VAL	7.9
1	A	716	TRP	7.2
1	A	350	THR	6.5
1	A	355	PHE	6.1
1	A	388	ILE	6.1
1	A	488	PRO	5.5
1	A	351	LYS	5.4
1	A	486	LYS	5.3
1	B	619	ARG	4.9
1	A	352	ASP	4.8
1	B	350	THR	4.8
1	A	714	HIS	4.3
1	A	300	PHE	4.2
1	A	507	GLN	4.2
1	A	386	LYS	3.9
1	A	392	SER	3.9
1	A	490	GLY	3.9
1	A	713	THR	3.9
1	A	385	ASN	3.8
1	A	391	THR	3.7
1	B	718	GLY	3.7
1	A	567	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	393	THR	3.6
1	B	338	PRO	3.5
1	A	487	GLN	3.4
1	A	469	LYS	3.4
1	B	620	LYS	3.4
1	A	503	GLU	3.4
1	A	504	ILE	3.4
1	A	643	SER	3.3
1	B	667	ARG	3.3
1	A	511	LYS	3.2
1	A	491	SER	3.2
1	A	338	PRO	3.2
1	A	667	ARG	3.2
1	A	679	ILE	3.2
1	A	389	GLU	3.1
1	B	680	VAL	3.1
1	A	415	CYS	3.1
1	A	390	SER	3.0
1	A	470	HIS	3.0
1	A	480	ILE	3.0
1	A	506	ILE	3.0
1	B	352	ASP	3.0
1	A	512	ALA	3.0
1	B	299	ARG	3.0
1	A	299	ARG	2.9
1	A	551	PHE	2.9
1	B	567	VAL	2.9
1	A	382	GLU	2.9
1	A	619	ARG	2.9
1	B	616	LEU	2.9
1	A	373	GLY	2.8
1	A	680	VAL	2.8
1	A	514	ARG	2.8
1	A	353	GLN	2.8
1	A	354	LEU	2.7
1	A	508	GLN	2.7
1	A	479	LEU	2.7
1	A	677	VAL	2.6
1	B	715	VAL	2.6
1	B	351	LYS	2.6
1	A	712	ASN	2.6
1	A	682	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	321	THR	2.6
1	A	704	PHE	2.6
1	A	678	TRP	2.6
1	A	593	ILE	2.5
1	B	566	ALA	2.5
1	A	584	PHE	2.5
1	B	479	LEU	2.5
1	A	489	ASP	2.4
1	A	552	ASP	2.4
1	B	679	ILE	2.4
1	A	467	ASP	2.4
1	A	591	THR	2.4
1	A	485	TYR	2.4
1	A	505	CYS	2.4
1	A	370	LYS	2.3
1	A	356	PRO	2.3
1	B	310	VAL	2.3
1	B	615	ASP	2.3
1	A	582	CYS	2.3
1	B	591	THR	2.2
1	A	685	GLY	2.2
1	A	676	TRP	2.1
1	A	588	TYR	2.1
1	B	584	PHE	2.1
1	B	677	VAL	2.1
1	B	611	ALA	2.1
1	A	565	PRO	2.0
1	A	681	PRO	2.0
1	A	466	THR	2.0
1	A	394	TYR	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
5	XJH	A	800	27/27	0.80	0.33	3.21	28,58,83,83	0
4	ACT	A	860	4/4	0.95	0.15	2.66	57,57,57,58	0
5	XJH	B	800	27/27	0.81	0.27	2.64	29,58,83,83	0
3	H4B	B	760	17/17	0.96	0.18	1.04	25,28,31,33	0
2	HEM	A	750	43/43	0.97	0.20	0.98	24,28,35,38	0
2	HEM	B	750	43/43	0.98	0.17	0.84	20,25,35,38	0
3	H4B	A	760	17/17	0.96	0.17	0.56	26,29,34,34	0
6	ZN	A	900	1/1	1.00	0.08	-0.17	33,33,33,33	0
4	ACT	B	860	4/4	0.97	0.08	-0.95	41,41,43,45	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.