



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:48 PM GMT

PDB ID : 1VAG  
Title : Neuronal nitric oxide synthase oxygenase domain complexed with the inhibitor AR-R17477  
Authors : Fedorov, R.; Vasan, R.; Ghosh, D.K.; Schlichting, I.  
Deposited on : 2004-02-16  
Resolution : 2.00 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

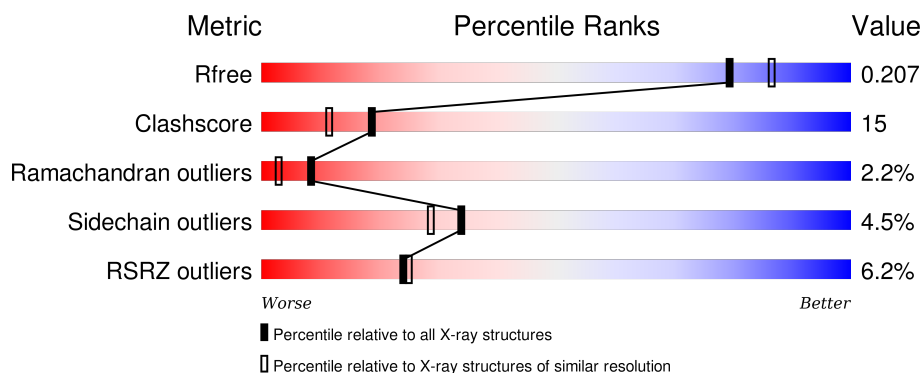
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 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))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (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. 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	420	<div> <div>6%</div> <div>71%</div> <div>25%</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
5	ARR	A	902	-	-	-	X

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3735 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	420	Total	C	N	O	S	0	0	0
			3418	2183	589	625	21			

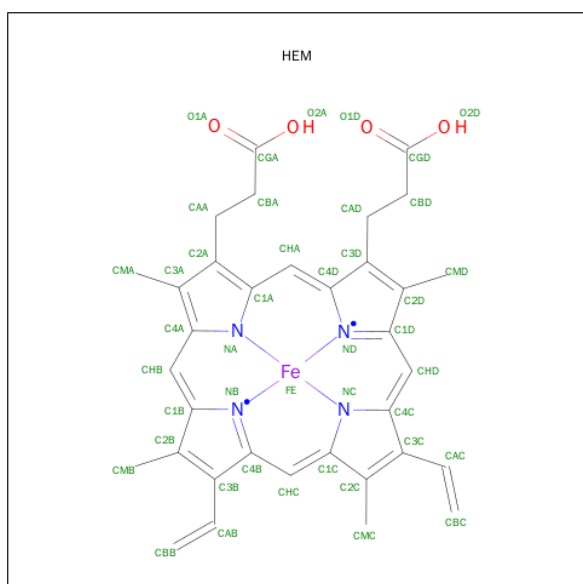
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	297	GLY	-	CLONING ARTIFACT	UNP P29476

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

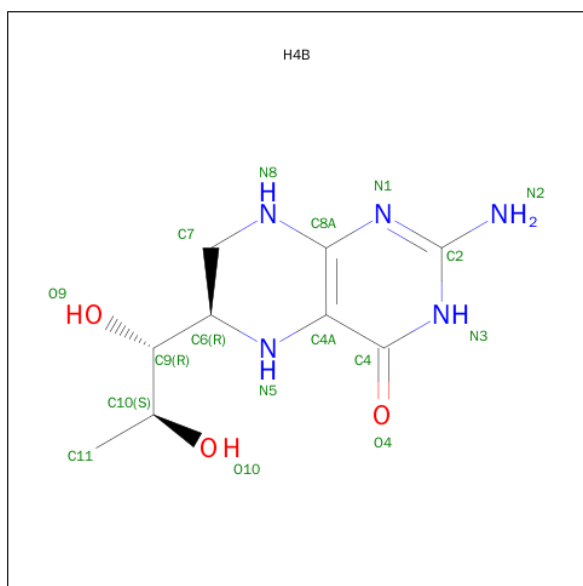
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



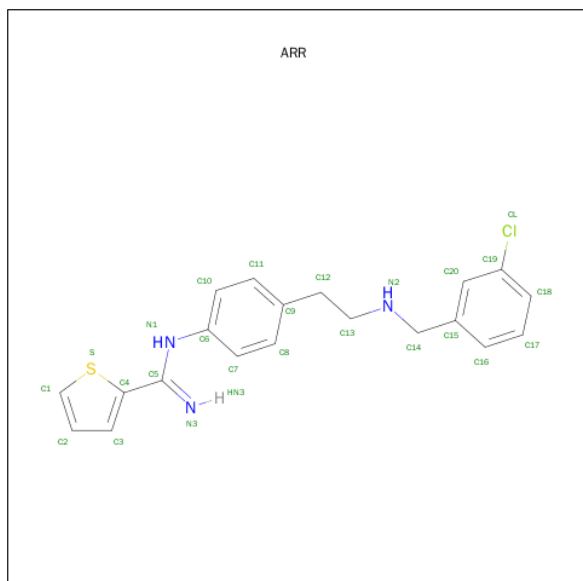
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
							0	0

- Molecule 4 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula:  $C_9H_{15}N_5O_3$ ).



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

- Molecule 5 is N-(4-{2-[(3-CHLOROBENZYL)AMINO]ETHYL}PHENYL)THIOPHENE-2-CARBOXIMIDAMIDE (three-letter code: ARR) (formula:  $C_{20}H_{20}ClN_3S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Cl	N	S	0	0
			25	20	1	3	1		

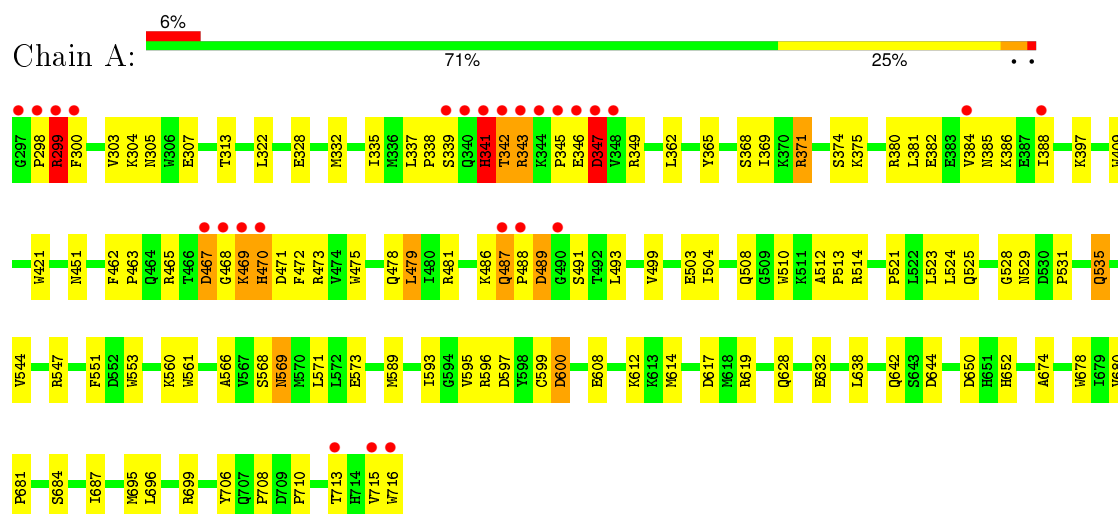
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	231	Total	O	0	0
			231	231		

### 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: Nitric-oxide synthase, brain



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	45.27Å 109.20Å 164.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.00 45.52 – 1.95	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.00) 94.1 (45.52-1.95)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.97 (at 1.95Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.193 , 0.229 0.193 , 0.207	Depositor DCC
$R_{free}$ test set	1343 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.4	Xtriage
Anisotropy	0.676	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 64.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 28743 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3735	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% 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 [i](#)

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

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

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	0.35	0/3515	0.59	1/4770 (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	A	589	MET	N-CA-C	-5.57	95.95	111.00

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	3418	0	3324	106	0
2	A	1	0	0	0	0
3	A	43	0	30	0	0
4	A	17	0	15	0	0
5	A	25	0	19	1	0
6	A	231	0	0	7	0
All	All	3735	0	3388	106	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 15.



All (106) 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:342:THR:HG23	1:A:706:TYR:HB2	1.57	0.87
1:A:298:PRO:HD2	1:A:299:ARG:HH11	1.44	0.81
1:A:343:ARG:HA	1:A:343:ARG:CZ	2.11	0.80
1:A:469:LYS:O	1:A:470:HIS:HB2	1.81	0.79
1:A:470:HIS:HB3	1:A:528:GLY:HA3	1.64	0.79
1:A:298:PRO:HD2	1:A:299:ARG:NH1	2.01	0.75
1:A:299:ARG:HG2	1:A:300:PHE:CD2	2.22	0.74
1:A:371:ARG:HB3	1:A:371:ARG:HH11	1.54	0.72
1:A:504:ILE:O	1:A:508:GLN:HG2	1.90	0.71
1:A:371:ARG:HB3	1:A:371:ARG:NH1	2.07	0.70
1:A:307:GLU:HG3	6:A:192:HOH:O	1.94	0.68
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.77	0.66
1:A:298:PRO:CD	1:A:299:ARG:HH11	2.09	0.66
1:A:488:PRO:HG2	1:A:489:ASP:OD1	1.96	0.66
1:A:322:LEU:HB2	1:A:699:ARG:HB2	1.78	0.64
1:A:699:ARG:HH11	1:A:699:ARG:HG2	1.63	0.64
1:A:332:MET:HE3	1:A:335:ILE:HG13	1.82	0.61
1:A:715:VAL:O	1:A:716:TRP:HB3	1.99	0.61
1:A:304:LYS:HG2	1:A:305:ASN:N	2.16	0.61
1:A:684:SER:HB3	1:A:687:ILE:CD1	2.32	0.60
1:A:486:LYS:HE3	1:A:499:VAL:HG11	1.84	0.60
1:A:471:ASP:HB2	6:A:36:HOH:O	2.00	0.60
1:A:298:PRO:O	1:A:299:ARG:HB3	2.01	0.59
1:A:479:LEU:HD13	1:A:568:SER:HB3	1.86	0.57
1:A:569:ASN:H	1:A:569:ASN:HD22	1.52	0.57
1:A:470:HIS:HB3	1:A:528:GLY:CA	2.33	0.57
1:A:684:SER:HB3	1:A:687:ILE:HD11	1.87	0.56
1:A:524:LEU:O	1:A:531:PRO:HA	2.05	0.56
1:A:343:ARG:HG3	1:A:571:LEU:HD13	1.87	0.56
1:A:486:LYS:HG3	1:A:499:VAL:HG11	1.88	0.56
1:A:535:GLN:HG2	6:A:100:HOH:O	2.06	0.55
1:A:386:LYS:HD3	6:A:128:HOH:O	2.06	0.55
1:A:596:ARG:O	1:A:600:ASP:HB2	2.07	0.55
1:A:473:ARG:NH2	1:A:710:PRO:HD3	2.23	0.54
1:A:684:SER:O	1:A:687:ILE:HG12	2.07	0.54
1:A:525:GLN:HG3	1:A:529:ASN:O	2.07	0.54
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.44	0.53
1:A:638:LEU:O	1:A:642:GLN:HG3	2.09	0.53
1:A:345:PRO:HB3	1:A:708:PRO:HG2	1.89	0.53
1:A:470:HIS:CB	1:A:528:GLY:HA3	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:PRO:HB2	1:A:472:PHE:CE1	2.43	0.53
1:A:337:LEU:C	1:A:339:SER:H	2.11	0.53
1:A:362:LEU:HD12	1:A:381:LEU:HD23	1.90	0.52
1:A:328:GLU:H	1:A:328:GLU:CD	2.13	0.52
1:A:684:SER:HB3	1:A:687:ILE:HG12	1.91	0.51
1:A:499:VAL:O	1:A:503:GLU:HG2	2.09	0.51
1:A:544:VAL:HG13	1:A:644:ASP:OD1	2.10	0.51
1:A:699:ARG:NH1	1:A:699:ARG:HG2	2.24	0.51
1:A:593:ILE:HA	1:A:597:ASP:HB2	1.93	0.51
1:A:343:ARG:HA	1:A:343:ARG:NH1	2.25	0.50
1:A:650:ASP:OD2	1:A:652:HIS:HB2	2.11	0.50
1:A:369:ILE:HG13	1:A:371:ARG:HG3	1.92	0.50
1:A:569:ASN:N	1:A:569:ASN:HD22	2.07	0.49
1:A:300:PHE:HB3	1:A:313:THR:CG2	2.41	0.49
1:A:699:ARG:HG2	6:A:187:HOH:O	2.12	0.49
1:A:341:HIS:C	1:A:343:ARG:H	2.16	0.49
1:A:569:ASN:H	1:A:569:ASN:ND2	2.09	0.49
1:A:617:ASP:OD1	1:A:619:ARG:NE	2.45	0.49
1:A:674:ALA:HB3	1:A:695:MET:HB3	1.94	0.49
1:A:479:LEU:HD22	1:A:566:ALA:HB1	1.94	0.49
1:A:384:VAL:HG23	1:A:385:ASN:N	2.29	0.47
1:A:382:GLU:O	1:A:386:LYS:HG3	2.15	0.47
1:A:409:TRP:CZ3	1:A:421:TRP:HA	2.50	0.47
1:A:299:ARG:HD3	1:A:300:PHE:H	1.79	0.47
1:A:684:SER:HB3	1:A:687:ILE:CG1	2.45	0.47
1:A:349:ARG:HH22	1:A:573:GLU:CD	2.18	0.46
1:A:343:ARG:CG	1:A:571:LEU:HD13	2.45	0.46
1:A:468:GLY:O	1:A:469:LYS:C	2.54	0.46
1:A:560:LYS:HG2	1:A:561:TRP:N	2.30	0.46
1:A:342:THR:O	1:A:342:THR:HG22	2.16	0.46
1:A:678:TRP:HH2	5:A:902:ARR:H141	1.79	0.46
1:A:715:VAL:O	1:A:716:TRP:CB	2.63	0.46
1:A:468:GLY:O	1:A:470:HIS:N	2.49	0.45
1:A:510:TRP:CE2	1:A:521:PRO:HD3	2.51	0.45
1:A:487:GLN:HE22	1:A:493:LEU:HB2	1.82	0.44
1:A:608:GLU:O	1:A:612:LYS:HG3	2.17	0.44
1:A:551:PHE:HB3	1:A:553:TRP:CE2	2.52	0.44
1:A:298:PRO:CG	1:A:299:ARG:HH11	2.31	0.44
1:A:341:HIS:CD2	1:A:343:ARG:HH21	2.35	0.44
1:A:551:PHE:HB3	1:A:553:TRP:NE1	2.32	0.44
1:A:299:ARG:HG2	1:A:300:PHE:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:680:VAL:HA	1:A:681:PRO:HD3	1.84	0.43
1:A:300:PHE:HB3	1:A:313:THR:HG23	2.00	0.43
1:A:487:GLN:HB2	1:A:491:SER:HB2	2.00	0.43
1:A:303:VAL:CG1	1:A:696:LEU:HG	2.49	0.43
1:A:384:VAL:O	1:A:388:ILE:HG13	2.18	0.43
1:A:342:THR:HG21	6:A:106:HOH:O	2.18	0.42
1:A:347:ASP:N	1:A:347:ASP:OD1	2.52	0.42
1:A:349:ARG:NH2	1:A:573:GLU:CD	2.73	0.42
1:A:487:GLN:HE22	1:A:493:LEU:CB	2.33	0.42
1:A:521:PRO:HB3	1:A:535:GLN:OE1	2.20	0.42
1:A:298:PRO:HG2	1:A:299:ARG:HD2	2.02	0.41
1:A:475:TRP:HB2	1:A:523:LEU:HB3	2.02	0.41
1:A:371:ARG:HH12	1:A:374:SER:CB	2.33	0.41
1:A:371:ARG:HH12	1:A:374:SER:HB2	1.85	0.41
1:A:462:PHE:HB3	1:A:463:PRO:CD	2.50	0.41
1:A:512:ALA:HA	1:A:513:PRO:HD3	1.90	0.41
1:A:365:TYR:O	1:A:368:SER:HB2	2.20	0.41
1:A:595:VAL:O	1:A:599:CYS:HB2	2.20	0.41
1:A:614:MET:CE	1:A:632:GLU:HG3	2.51	0.41
1:A:469:LYS:O	1:A:470:HIS:CB	2.60	0.40
1:A:472:PHE:N	1:A:472:PHE:CD1	2.88	0.40
1:A:338:PRO:HD2	6:A:83:HOH:O	2.20	0.40
1:A:380:ARG:HD3	1:A:397:LYS:HE3	2.02	0.40
1:A:551:PHE:CD2	1:A:551:PHE:N	2.88	0.40
1:A:465:ARG:HD3	1:A:471:ASP:OD2	2.22	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	418/420 (100%)	387 (93%)	22 (5%)	9 (2%)	<b>8</b> <b>3</b>

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	299	ARG
1	A	341	HIS
1	A	346	GLU
1	A	347	ASP
1	A	470	HIS
1	A	343	ARG
1	A	467	ASP
1	A	469	LYS
1	A	342	THR

### 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	375/375 (100%)	358 (96%)	17 (4%)	34	29

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	299	ARG
1	A	341	HIS
1	A	347	ASP
1	A	371	ARG
1	A	375	LYS
1	A	451	ASN
1	A	467	ASP
1	A	479	LEU
1	A	487	GLN
1	A	489	ASP
1	A	514	ARG
1	A	535	GLN
1	A	547	ARG
1	A	569	ASN
1	A	600	ASP
1	A	628	GLN

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Mol	Chain	Res	Type
1	A	713	THR

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	341	HIS
1	A	364	GLN
1	A	451	ASN
1	A	470	HIS
1	A	478	GLN
1	A	487	GLN
1	A	498	ASN
1	A	507	GLN
1	A	569	ASN
1	A	628	GLN
1	A	634	ASN
1	A	664	ASN
1	A	707	GLN
1	A	712	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 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	$\# Z  > 2$
3	HEM	A	900	1	30,50,50	2.61	11 (36%)	24,82,82	2.22	7 (29%)
4	H4B	A	901	-	13,18,18	2.36	4 (30%)	11,26,26	4.14	6 (54%)
5	ARR	A	902	-	26,27,27	4.56	13 (50%)	27,35,35	0.89	2 (7%)

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
3	HEM	A	900	1	-	0/10/54/54	0/0/8/8
4	H4B	A	901	-	-	0/8/17/17	0/2/2/2
5	ARR	A	902	-	-	0/11/15/15	0/3/3/3

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	902	ARR	C4-S	-20.43	1.47	1.72
3	A	900	HEM	C3C-CAC	-6.13	1.39	1.51
3	A	900	HEM	C2D-C3D	-5.91	1.36	1.54
3	A	900	HEM	C3B-CAB	-5.20	1.41	1.51
3	A	900	HEM	C3D-C4D	-4.96	1.45	1.51
5	A	902	ARR	C4-C5	-4.77	1.39	1.45
5	A	902	ARR	C1-S	-4.72	1.47	1.70
3	A	900	HEM	C3B-C4B	-4.10	1.48	1.51
3	A	900	HEM	C2C-C1C	-2.59	1.47	1.52
3	A	900	HEM	C2B-C1B	-2.43	1.43	1.51
3	A	900	HEM	C2D-C1D	-2.14	1.44	1.51
5	A	902	ARR	C2-C3	-2.13	1.32	1.39
5	A	902	ARR	C8-C9	2.04	1.43	1.38
5	A	902	ARR	C17-C18	2.09	1.43	1.38
5	A	902	ARR	C7-C8	2.11	1.42	1.38
5	A	902	ARR	C16-C15	2.27	1.43	1.38
5	A	902	ARR	C7-C6	2.43	1.43	1.39
4	A	901	H4B	C8A-N1	2.47	1.39	1.34
5	A	902	ARR	C18-C19	2.61	1.43	1.38
5	A	902	ARR	C20-C19	2.78	1.43	1.38

*Continued on next page...*

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	902	ARR	C20-C15	2.83	1.44	1.39
3	A	900	HEM	FE-NC	3.05	2.07	1.95
3	A	900	HEM	C1C-NC	3.11	1.39	1.36
3	A	900	HEM	C4C-NC	3.45	1.40	1.36
4	A	901	H4B	C6-N5	3.66	1.53	1.45
4	A	901	H4B	C4A-N5	3.69	1.46	1.38
5	A	902	ARR	C10-C6	3.79	1.45	1.39
4	A	901	H4B	C4-N3	5.57	1.43	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	901	H4B	N3-C2-N1	-4.98	117.37	125.53
5	A	902	ARR	C3-C2-C1	-2.06	108.41	113.92
3	A	900	HEM	CAA-C2A-C3A	-2.01	123.27	129.00
3	A	900	HEM	CMD-C2D-C3D	2.75	126.50	114.35
5	A	902	ARR	C4-C5-N1	2.75	122.93	115.07
3	A	900	HEM	CAD-C3D-C2D	3.08	122.08	113.22
4	A	901	H4B	N2-C2-N1	3.11	122.34	117.20
3	A	900	HEM	C2D-C3D-C4D	3.53	107.49	101.50
4	A	901	H4B	C4A-C8A-N8	3.54	122.60	118.43
4	A	901	H4B	C2-N1-C8A	3.66	122.77	114.54
3	A	900	HEM	CMC-C2C-C3C	4.47	127.68	116.53
3	A	900	HEM	CAD-C3D-C4D	5.09	130.44	112.47
3	A	900	HEM	CMB-C2B-C3B	5.36	129.90	116.53
4	A	901	H4B	C4-N3-C2	6.67	125.20	115.94
4	A	901	H4B	C4-C4A-C8A	8.85	122.58	114.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	902	ARR	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, 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	420/420 (100%)	0.09	26 (6%)	24 25	12, 28, 70, 115	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	343	ARG	11.3
1	A	342	THR	8.5
1	A	341	HIS	7.2
1	A	340	GLN	6.6
1	A	347	ASP	5.0
1	A	469	LYS	4.9
1	A	344	LYS	4.5
1	A	716	TRP	3.9
1	A	468	GLY	3.8
1	A	715	VAL	3.7
1	A	345	PRO	3.6
1	A	299	ARG	3.6
1	A	346	GLU	3.5
1	A	488	PRO	3.5
1	A	300	PHE	3.3
1	A	298	PRO	3.1
1	A	467	ASP	2.8
1	A	470	HIS	2.7
1	A	348	VAL	2.6
1	A	490	GLY	2.6
1	A	297	GLY	2.5
1	A	384	VAL	2.3
1	A	487	GLN	2.3
1	A	388	ILE	2.2
1	A	339	SER	2.1
1	A	713	THR	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( $\text{\AA}^2$ )	Q<0.9
5	ARR	A	902	25/25	0.84	0.19	6.92	11,28,58,59	0
3	HEM	A	900	43/43	0.98	0.11	0.99	8,17,28,35	0
4	H4B	A	901	17/17	0.96	0.11	0.10	10,17,23,23	0
2	ZN	A	950	1/1	0.99	0.04	-	21,21,21,21	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.