



# Full wwPDB X-ray Structure Validation Report i

Feb 28, 2014 – 05:47 PM GMT

PDB ID : 3NLP  
Title : Structure of neuronal nitric oxide synthase D597N/M336V mutant heme domain in complex with 6-{{(3'S,4'S)-3'-[2''-(3'''-fluorophenethylamino)ethoxy]pyrrolidin-4'-yl}methyl}-4-methylpyridin-2-amine  
Authors : Li, H.; Delker, S.L.; Poulos, T.L.  
Deposited on : 2010-06-21  
Resolution : 2.02 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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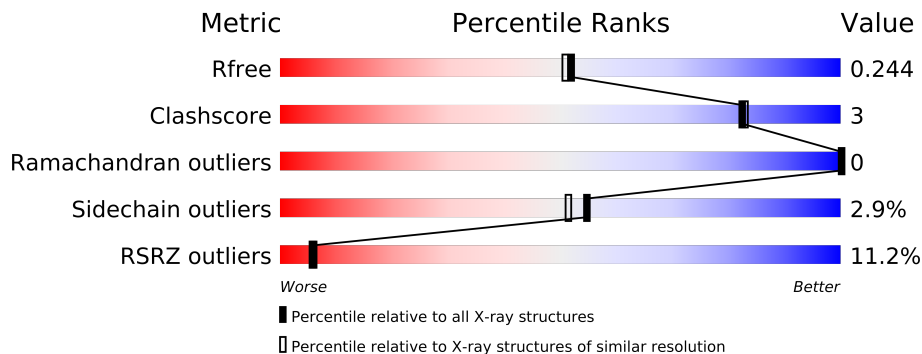
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.02 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	6003 (2.04-2.00)
Clashscore	79885	7467 (2.04-2.00)
Ramachandran outliers	78287	7370 (2.04-2.00)
Sidechain outliers	78261	7368 (2.04-2.00)
RSRZ outliers	66119	6006 (2.04-2.00)

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
3	GOL	A	719	-	X
3	GOL	A	880	-	X
6	ACT	A	860	-	X
6	ACT	B	860	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7135 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.

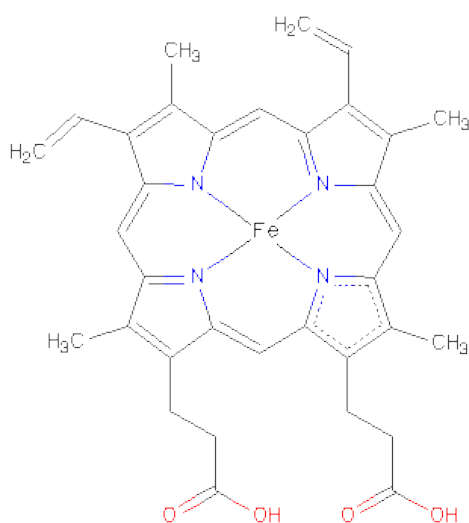
- Molecule 1 is a protein called Nitric oxide synthase, brain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	0	0
			3312	2121	567	604	20			
1	B	411	Total	C	N	O	S	0	0	0
			3344	2140	575	609	20			

There are 4 discrepancies between the modelled and reference sequences:

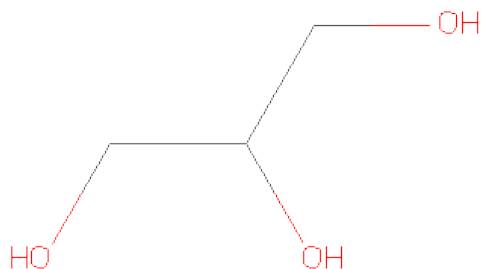
Chain	Residue	Modelled	Actual	Comment	Reference
A	336	VAL	MET	ENGINEERED MUTATION	UNP P29476
A	597	ASN	ASP	ENGINEERED MUTATION	UNP P29476
B	336	VAL	MET	ENGINEERED MUTATION	UNP P29476
B	597	ASN	ASP	ENGINEERED MUTATION	UNP P29476

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



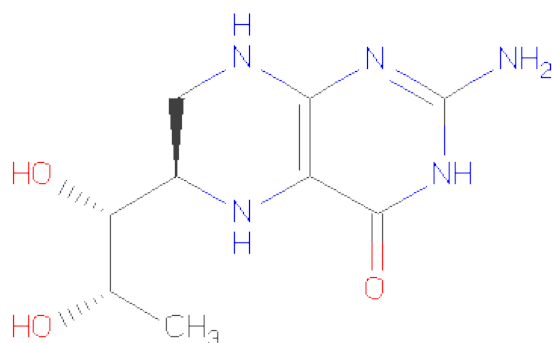
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



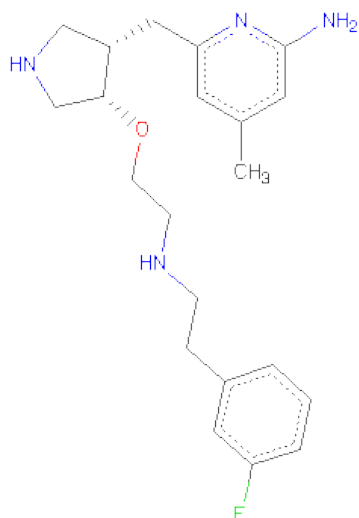
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		

- 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	0	0
			17	9	5	3		
4	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 5 is 6-[[[(3S,4S)-4-(2-{[2-(3-FLUOROPHENYL)ETHYL]AMINO}ETHOXY)PYRROLIDIN-3-YL]METHYL]-4-METHYLPYRIDIN-2-AMINE (three-letter code: JSS) (formula: C<sub>21</sub>H<sub>29</sub>FN<sub>4</sub>O).



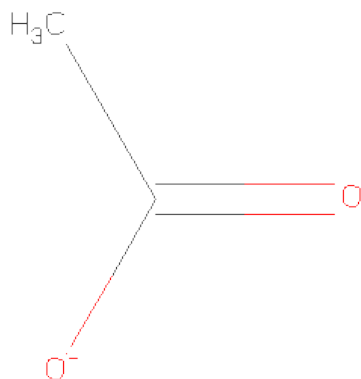
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	F	N	O	0	0
			27	21	1	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	F	N	O	0	0
			27	21	1	4	1		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



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

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 8 is water.

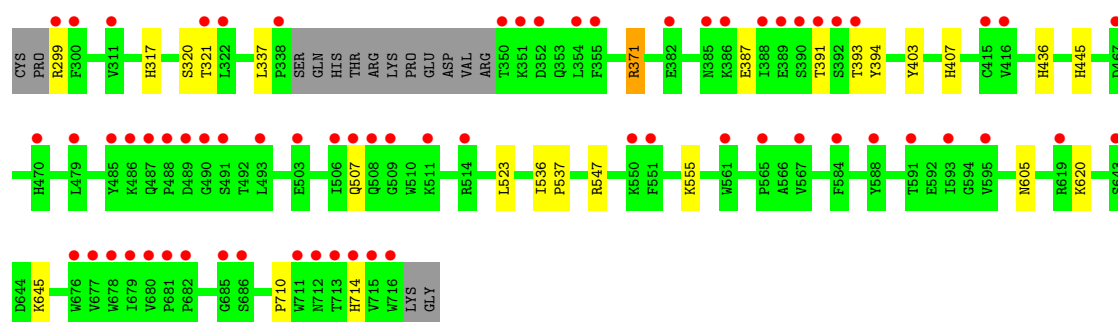
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	123	Total	O	0	0
			123	123		
8	B	161	Total	O	0	0
			161	161		

### 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.

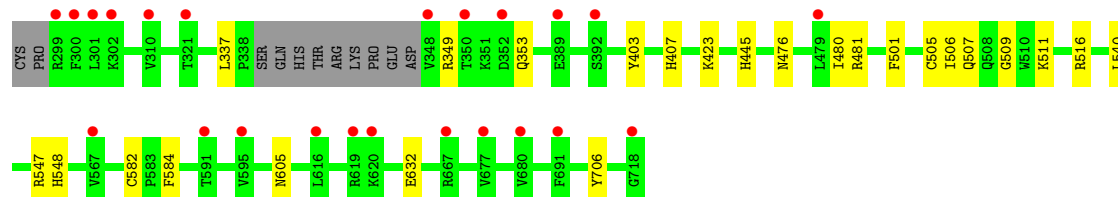
- Molecule 1: Nitric oxide synthase, brain

Chain A: 



- Molecule 1: Nitric oxide synthase, brain

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.76Å 111.00Å 164.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.60 – 2.02 37.85 – 2.02	Depositor EDS
% Data completeness (in resolution range)	98.6 (38.60-2.02) 98.6 (37.85-2.02)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.85 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.187 , 0.228 0.210 , 0.244	Depositor DCC
$R_{free}$ test set	3078 reflections (4.96%)	DCC
Wilson B-factor (Å <sup>2</sup> )	40.6	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 38.4	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 62080 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7135	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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: GOL, ZN, H4B, JSS, ACT, HEM

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	0.73	0/3405	0.71	0/4621
1	B	0.81	1/3437 (0.0%)	0.77	0/4661
All	All	0.77	1/6842 (0.0%)	0.74	0/9282

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	582	CYS	CB-SG	6.27	1.93	1.82

There are no bond angle outliers.

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	3312	0	0	10	0
1	B	3344	0	0	9	0
2	A	43	0	0	2	0
2	B	43	0	0	2	0
3	A	12	0	8	0	0
4	A	17	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	17	0	0	0	0
5	A	27	0	0	0	0
5	B	27	0	0	0	0
6	A	4	0	0	0	0
6	B	4	0	0	0	0
7	A	1	0	0	0	0
8	A	123	0	0	3	0
8	B	161	0	0	1	0
All	All	7135	0	8	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)
2:A:750:HEM:O2A	8:A:1072:HOH:O	2.16	0.62
1:A:436:HIS:ND1	8:A:1083:HOH:O	2.31	0.61
1:A:371:ARG:CG	1:A:371:ARG:NH2	2.65	0.58
1:B:584:PHE:CD1	2:B:750:HEM:CAC	2.89	0.55
1:B:403:TYR:CE1	1:B:407:HIS:CE1	2.98	0.52
1:B:605:ASN:ND2	8:B:1132:HOH:O	2.43	0.51
1:A:536:ILE:O	1:A:537:PRO:C	2.50	0.49
1:B:505:CYS:O	1:B:506:ILE:C	2.51	0.48
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.02	0.48
1:A:605:ASN:ND2	8:A:1037:HOH:O	2.48	0.47
1:A:387:GLU:O	1:A:391:THR:OG1	2.33	0.46
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.51	0.44
1:A:299:ARG:O	1:A:317:HIS:CE1	2.71	0.43
1:B:501:PHE:CE2	1:B:505:CYS:SG	3.12	0.43
1:B:706:TYR:OH	2:B:750:HEM:O1D	2.37	0.42
2:A:750:HEM:CBC	2:A:750:HEM:CMC	2.97	0.42
1:A:393:THR:OG1	1:A:394:TYR:N	2.53	0.42
1:A:710:PRO:O	1:A:714:HIS:N	2.52	0.42
1:B:445:HIS:C	1:B:445:HIS:CD2	2.94	0.41
1:B:509:GLY:O	1:B:511:LYS:NZ	2.53	0.41
1:A:445:HIS:C	1:A:445:HIS:CD2	2.94	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%)	391 (97%)	12 (3%)	0	100	100
1	B	407/422 (96%)	397 (98%)	10 (2%)	0	100	100
All	All	810/844 (96%)	788 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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%)	353 (97%)	10 (3%)	56	53
1	B	366/377 (97%)	355 (97%)	11 (3%)	53	50
All	All	729/754 (97%)	708 (97%)	21 (3%)	55	51

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	320	SER
1	A	321	THR
1	A	337	LEU
1	A	371	ARG
1	A	507	GLN
1	A	523	LEU
1	A	547	ARG
1	A	555	LYS
1	A	620	LYS
1	A	645	LYS
1	B	337	LEU

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Mol	Chain	Res	Type
1	B	349	ARG
1	B	353	GLN
1	B	423	LYS
1	B	476	ASN
1	B	480	ILE
1	B	481	ARG
1	B	507	GLN
1	B	516	ARG
1	B	540	LEU
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 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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	GOL	A	719	-	5,5,5	0.42	0	5,5,5	0.83	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	HEM	A	750	1	49,50,50	2.43	19 (38%)	46,82,82	2.28	10 (21%)
4	H4B	A	760	-	18,18,18	1.38	3 (16%)	24,26,26	1.82	5 (20%)
5	JSS	A	800	-	29,29,29	0.67	1 (3%)	38,38,38	1.56	6 (15%)
6	ACT	A	860	-	1,3,3	1.02	0	0,3,3	0.00	-
3	GOL	A	880	-	5,5,5	0.44	0	5,5,5	0.39	0
2	HEM	B	750	1	49,50,50	2.44	18 (36%)	46,82,82	1.84	8 (17%)
4	H4B	B	760	-	18,18,18	0.97	1 (5%)	24,26,26	1.54	3 (12%)
5	JSS	B	800	-	29,29,29	0.82	1 (3%)	38,38,38	1.57	8 (21%)
6	ACT	B	860	-	1,3,3	1.18	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
3	GOL	A	719	-	-	0/4/4/4	0/0/0/0
2	HEM	A	750	1	-	0/14/114/114	0/0/8/8
4	H4B	A	760	-	-	0/8/17/17	0/0/2/2
5	JSS	A	800	-	-	0/13/23/23	0/3/3/3
6	ACT	A	860	-	-	0/0/0/0	0/0/0/0
3	GOL	A	880	-	-	0/4/4/4	0/0/0/0
2	HEM	B	750	1	-	0/14/114/114	0/0/8/8
4	H4B	B	760	-	-	0/8/17/17	0/0/2/2
5	JSS	B	800	-	-	0/13/23/23	0/3/3/3
6	ACT	B	860	-	-	0/0/0/0	0/0/0/0

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C3B-C2B	-5.99	1.33	1.43
2	B	750	HEM	C3C-C2C	-5.57	1.34	1.43
2	B	750	HEM	C3B-C2B	-5.45	1.34	1.43
2	A	750	HEM	C3C-C2C	-4.98	1.35	1.43
2	A	750	HEM	C3B-CAB	4.84	1.55	1.40
2	A	750	HEM	C2D-C1D	4.84	1.45	1.44
2	B	750	HEM	C3D-C4D	4.80	1.45	1.44
2	B	750	HEM	C3B-CAB	4.74	1.55	1.40
2	B	750	HEM	C3C-CAC	4.70	1.55	1.40
2	B	750	HEM	C3D-C2D	4.67	1.51	1.43
2	A	750	HEM	C3D-C2D	4.67	1.51	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	FE-NA	4.55	2.12	1.92
2	B	750	HEM	C2D-C1D	4.18	1.45	1.44
2	A	750	HEM	C3C-CAC	4.16	1.53	1.40
2	A	750	HEM	C4A-C3A	4.10	1.45	1.40
4	A	760	H4B	C2-N2	4.06	1.38	1.32
2	A	750	HEM	FE-ND	3.95	2.12	1.97
2	B	750	HEM	C2B-C1B	3.51	1.45	1.44
2	B	750	HEM	FE-NA	3.39	2.07	1.92
2	B	750	HEM	C3B-C4B	3.23	1.48	1.44
2	B	750	HEM	C4A-C3A	3.13	1.44	1.40
2	B	750	HEM	FE-NC	3.03	2.09	1.97
2	A	750	HEM	C2B-C1B	3.02	1.45	1.44
2	B	750	HEM	CMC-C2C	2.98	1.56	1.47
2	A	750	HEM	FE-NC	2.96	2.08	1.97
2	B	750	HEM	CMB-C2B	2.83	1.56	1.47
2	B	750	HEM	CMD-C2D	2.74	1.55	1.47
2	B	750	HEM	CHB-C1B	2.69	1.39	1.35
2	A	750	HEM	CHA-C4D	2.69	1.39	1.35
2	A	750	HEM	CMC-C2C	2.69	1.55	1.47
4	B	760	H4B	C7-C6	2.54	1.55	1.52
2	A	750	HEM	CMD-C2D	2.48	1.55	1.47
2	A	750	HEM	CMB-C2B	2.45	1.55	1.47
2	B	750	HEM	FE-ND	2.36	2.06	1.97
5	B	800	JSS	C14-C13	2.33	1.41	1.36
4	A	760	H4B	C2-N1	2.33	1.36	1.33
4	A	760	H4B	O4-C4	2.30	1.29	1.24
2	A	750	HEM	C3D-C4D	-2.29	1.44	1.44
2	B	750	HEM	CHA-C4D	2.27	1.39	1.35
2	A	750	HEM	CMA-C3A	2.23	1.56	1.51
2	A	750	HEM	FE-NB	2.17	2.05	1.97
5	A	800	JSS	C14-C13	2.05	1.41	1.36
2	A	750	HEM	C3B-C4B	2.04	1.46	1.44

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	750	HEM	C3B-C4B-NB	-9.74	107.03	114.00
2	B	750	HEM	C3B-C4B-NB	-8.02	108.26	114.00
2	A	750	HEM	C4D-ND-C1D	6.28	111.59	105.16
5	A	800	JSS	C2'-C3'-C4'	5.31	107.62	103.48
5	B	800	JSS	C2'-C3'-C4'	4.73	107.17	103.48
4	A	760	H4B	C4-C4A-C8A	4.63	118.85	114.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	750	HEM	C4D-ND-C1D	4.14	109.40	105.16
4	B	760	H4B	C4-C4A-C8A	4.10	118.36	114.56
2	A	750	HEM	C2D-C1D-ND	-4.00	108.21	112.93
5	A	800	JSS	C6A-N1A-C2A	3.79	120.89	118.23
2	A	750	HEM	C4C-NC-C1C	3.70	109.38	105.53
2	A	750	HEM	C1B-NB-C4B	3.32	108.56	105.16
4	A	760	H4B	N2-C2-N3	3.21	121.39	117.86
5	B	800	JSS	C6A-N1A-C2A	3.19	120.47	118.23
5	A	800	JSS	C14-C13-C12	-3.10	119.05	123.32
5	B	800	JSS	C14-C13-C12	-3.06	119.11	123.32
2	A	750	HEM	CBD-CAD-C3D	-3.05	107.73	114.37
5	B	800	JSS	C3A-C2A-N1A	-2.97	119.68	122.99
4	A	760	H4B	C4-C4A-N5	2.96	123.40	119.10
2	B	750	HEM	C4A-CHB-C1B	-2.83	123.75	127.47
2	A	750	HEM	CHD-C4C-NC	2.82	127.19	124.73
4	A	760	H4B	C2-N1-C8A	2.78	121.56	117.61
5	A	800	JSS	C3A-C2A-N1A	-2.62	120.07	122.99
4	B	760	H4B	C9-C6-N5	2.61	114.56	109.69
5	A	800	JSS	C5'-N1'-C2'	2.55	112.35	105.92
2	B	750	HEM	CBD-CAD-C3D	-2.47	108.98	114.37
2	B	750	HEM	CAD-C3D-C4D	2.47	128.97	124.53
5	B	800	JSS	C5'-N1'-C2'	2.47	112.15	105.92
5	B	800	JSS	C16-C11-C12	2.43	122.20	118.53
2	B	750	HEM	CBA-CAA-C2A	-2.43	108.41	112.69
2	A	750	HEM	CAD-CBD-CGD	-2.26	106.42	113.48
5	B	800	JSS	C3-N2-C2	2.26	121.48	113.30
2	B	750	HEM	CMA-C3A-C4A	-2.22	125.20	128.62
4	A	760	H4B	C6-C7-N8	-2.21	108.81	111.66
4	B	760	H4B	C4A-N5-C6	-2.15	115.32	121.16
2	A	750	HEM	CHA-C4D-ND	2.14	127.24	124.31
2	A	750	HEM	C3A-C4A-NA	-2.05	107.86	109.41
2	B	750	HEM	C3A-C4A-NA	-2.03	107.88	109.41
5	A	800	JSS	C8A-C4A-C3A	-2.02	117.67	120.93
5	B	800	JSS	C3-C4-C11	-2.01	108.36	112.81

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%)	0.88	67 (16%) 2 2	33, 60, 109, 140	0
1	B	411/422 (97%)	0.41	23 (5%) 24 23	29, 48, 77, 97	0
All	All	818/844 (96%)	0.65	90 (11%) 6 6	29, 54, 98, 140	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	PHE	7.5
1	B	348	VAL	6.6
1	A	300	PHE	6.4
1	A	352	ASP	5.6
1	A	715	VAL	5.5
1	A	355	PHE	5.3
1	A	486	LYS	5.2
1	A	716	TRP	5.0
1	A	488	PRO	4.9
1	A	507	GLN	4.5
1	B	619	ARG	4.4
1	B	350	THR	4.4
1	A	351	LYS	4.3
1	A	551	PHE	4.1
1	B	310	VAL	4.0
1	B	352	ASP	3.9
1	A	713	THR	3.7
1	A	392	SER	3.5
1	A	567	VAL	3.5
1	B	301	LEU	3.5
1	A	489	ASP	3.4
1	A	299	ARG	3.4
1	A	619	ARG	3.3
1	A	712	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	503	GLU	3.3
1	A	350	THR	3.2
1	A	354	LEU	3.2
1	A	487	GLN	3.2
1	B	680	VAL	3.2
1	A	391	THR	3.2
1	A	680	VAL	3.1
1	A	382	GLU	3.1
1	A	322	LEU	3.1
1	A	491	SER	3.1
1	A	678	TRP	3.1
1	A	390	SER	3.1
1	A	389	GLU	3.1
1	B	616	LEU	3.0
1	A	677	VAL	3.0
1	A	593	ILE	3.0
1	A	321	THR	3.0
1	A	415	CYS	3.0
1	A	508	GLN	2.9
1	A	711	TRP	2.8
1	B	718	GLY	2.8
1	A	511	LYS	2.8
1	A	311	VAL	2.8
1	A	490	GLY	2.8
1	A	479	LEU	2.7
1	A	676	TRP	2.7
1	A	588	TYR	2.7
1	A	416	VAL	2.7
1	A	385	ASN	2.7
1	A	506	ILE	2.7
1	A	514	ARG	2.7
1	A	714	HIS	2.7
1	B	302	LYS	2.7
1	B	620	LYS	2.7
1	A	682	PRO	2.7
1	A	591	THR	2.7
1	A	550	LYS	2.6
1	B	691	PHE	2.5
1	A	685	GLY	2.5
1	B	321	THR	2.5
1	B	479	LEU	2.5
1	B	389	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	388	ILE	2.5
1	A	584	PHE	2.5
1	A	470	HIS	2.4
1	B	299	ARG	2.4
1	B	567	VAL	2.4
1	A	467	ASP	2.4
1	A	679	ILE	2.4
1	B	595	VAL	2.4
1	B	591	THR	2.4
1	A	509	GLY	2.4
1	A	393	THR	2.3
1	B	677	VAL	2.3
1	B	667	ARG	2.3
1	A	338	PRO	2.3
1	A	386	LYS	2.3
1	A	493	LEU	2.3
1	A	485	TYR	2.2
1	B	392	SER	2.2
1	A	643	SER	2.2
1	A	686	SER	2.2
1	A	561	TRP	2.1
1	A	681	PRO	2.1
1	A	595	VAL	2.1
1	A	565	PRO	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( $\text{\AA}^2$ )	Q<0.9
3	GOL	A	719	6/6	0.77	12.21	43,45,46,47	6
3	GOL	A	880	6/6	0.88	11.00	76,77,81,85	6
6	ACT	A	860	4/4	0.23	3.88	80,82,83,84	0
6	ACT	B	860	4/4	0.16	2.55	61,62,63,64	0
5	JSS	A	800	27/27	0.30	1.58	38,53,83,85	0
5	JSS	B	800	27/27	0.21	1.01	38,50,83,86	0
2	HEM	A	750	43/43	0.23	0.72	35,39,54,57	0
2	HEM	B	750	43/43	0.18	0.63	33,39,51,59	0
4	H4B	A	760	17/17	0.21	0.60	36,39,45,46	0
4	H4B	B	760	17/17	0.19	0.46	33,40,44,47	0
7	ZN	A	900	1/1	0.09	-1.00	44,44,44,44	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.