



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:32 PM GMT

PDB ID : 4IMS  
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with 6,6'-((5-(3-aminopropyl)-1,3-phenylene)bis(ethane-2,1-diyl))bis(4-methylpyridin-2-amine)  
Authors : Li, H.; Poulos, T.L.  
Deposited on : 2013-01-03  
Resolution : 2.15 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



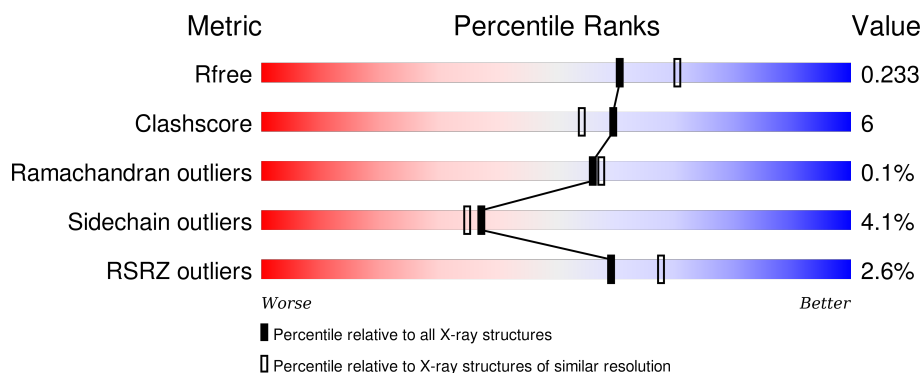
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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>3%</div> <div>80%</div> <div>14%</div> <div>• •</div> </div>
1	B	422	<div> <div>2%</div> <div>86%</div> <div>11%</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
3	12S	A	802	-	-	-	X
3	12S	B	802	-	-	-	X
4	ACT	A	803	-	-	-	X
4	ACT	B	803	-	-	-	X



## 2 Entry composition [i](#)

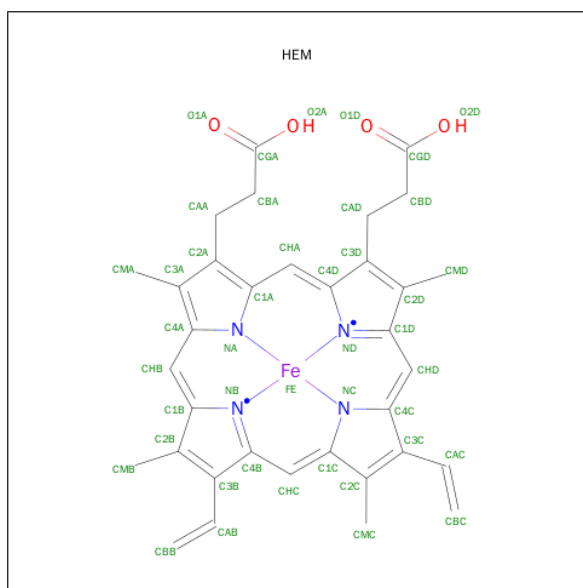
There are 7 unique types of molecules in this entry. The entry contains 7085 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	608	22			
1	B	411	Total	C	N	O	S	0	1	0
			3351	2144	574	612	21			

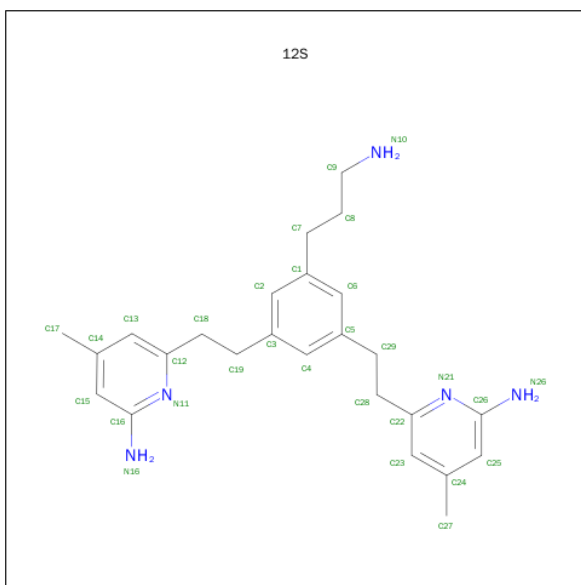
- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



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		

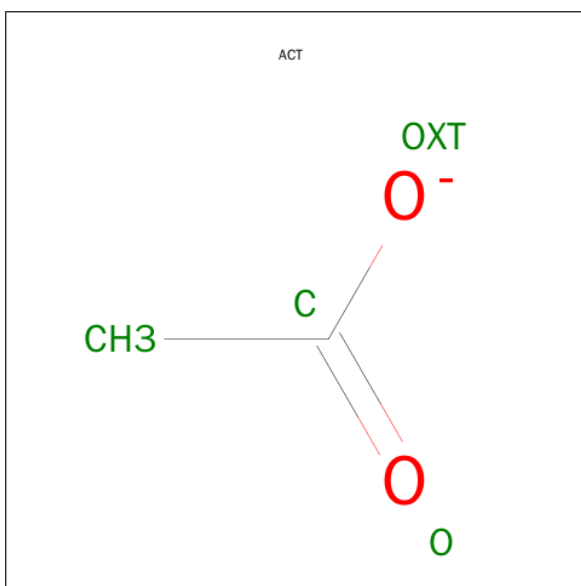
- Molecule 3 is 6,6'-{[5-(3-AMINOPROPYL)BENZENE-1,3-DIYL]DIETHANE-2,1-DIYL}BI S(4-METHYLPYRIDIN-2-AMINE) (three-letter code: 12S) (formula:  $C_{25}H_{33}N_5$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 30 25 5	0	0
3	B	1	Total C N 30 25 5	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula:  $\text{C}_2\text{H}_3\text{O}_2$ ).



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



- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	2	Total 2	Cl 2	0	0
6	A	2	Total 2	Cl 2	0	0

- Molecule 7 is water.

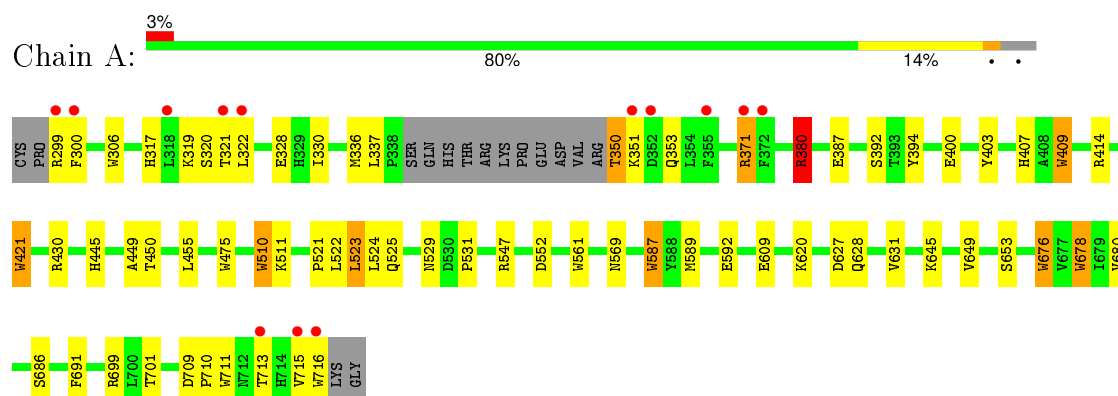
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	110	Total 110	O 110	0	0
7	B	136	Total 136	O 136	0	0



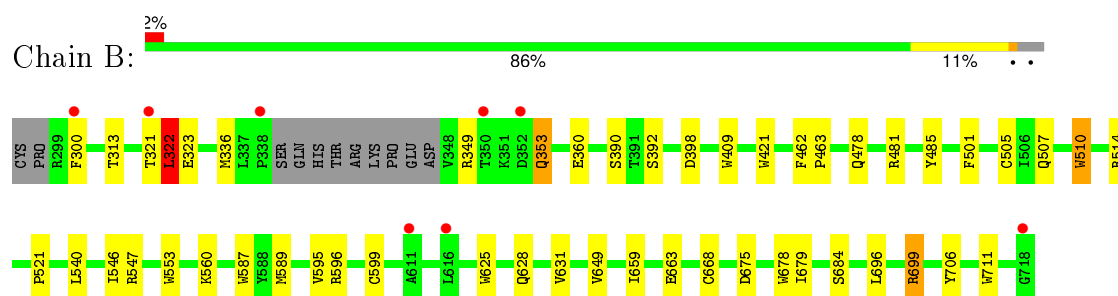
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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



- 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, $\alpha$ , $\beta$ , $\gamma$	51.84Å 110.42Å 164.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15 49.44 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.00-2.15) 99.2 (49.44-2.15)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.63 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.183 , 0.235 0.180 , 0.233	Depositor DCC
$R_{free}$ test set	2590 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.3	Xtriage
Anisotropy	0.828	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 43.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 52052 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7085	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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: ACT, HEM, ZN, 12S, CL

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	0.74	11/3429 (0.3%)	0.74	2/4652 (0.0%)
1	B	0.75	4/3447 (0.1%)	0.75	0/4673
All	All	0.74	15/6876 (0.2%)	0.75	2/9325 (0.0%)

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	421	TRP	CD2-CE2	6.03	1.48	1.41
1	B	510	TRP	CD2-CE2	5.92	1.48	1.41
1	B	625	TRP	CD2-CE2	5.69	1.48	1.41
1	B	553	TRP	CD2-CE2	5.57	1.48	1.41
1	A	678	TRP	CD2-CE2	5.55	1.48	1.41
1	A	716	TRP	CD2-CE2	5.53	1.48	1.41
1	A	676	TRP	CD2-CE2	5.47	1.48	1.41
1	A	587	TRP	CD2-CE2	5.41	1.47	1.41
1	A	561	TRP	CD2-CE2	5.36	1.47	1.41
1	A	409	TRP	CD2-CE2	5.33	1.47	1.41
1	A	306	TRP	CD2-CE2	5.29	1.47	1.41
1	A	711	TRP	CD2-CE2	5.26	1.47	1.41
1	B	711	TRP	CD2-CE2	5.17	1.47	1.41
1	A	475	TRP	CD2-CE2	5.07	1.47	1.41
1	A	510	TRP	CD2-CE2	5.07	1.47	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	430	ARG	NE-CZ-NH2	-5.53	117.53	120.30
1	A	380	ARG	NE-CZ-NH1	5.12	122.86	120.30

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	38	0
1	B	3351	0	3265	35	0
2	A	43	0	30	6	0
2	B	43	0	30	7	0
3	A	30	0	33	3	0
3	B	30	0	33	12	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
7	A	110	0	0	5	0
7	B	136	0	0	2	0
All	All	7085	0	6635	77	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 6.

All (77) 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:B:668:CYS:HB3	7:B:902:HOH:O	1.69	0.92
1:B:678:TRP:CZ3	3:B:802:12S:H10	2.13	0.84
2:A:801:HEM:HMC2	2:A:801:HEM:HBC2	1.60	0.83
2:A:801:HEM:HBA2	3:A:802:12S:H12	1.61	0.82
2:B:801:HEM:HBA2	3:B:802:12S:H12	1.64	0.80
1:A:371:ARG:HH21	1:A:371:ARG:HG2	1.46	0.78
1:B:659:ILE:O	1:B:663:GLU:HG3	1.87	0.75
1:A:587:TRP:H	2:A:801:HEM:HAB	1.54	0.72
1:B:481:ARG:NH2	3:B:802:12S:H16	2.06	0.71
1:A:351:LYS:HE2	1:A:392:SER:HB3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:ARG:HG2	1:A:371:ARG:NH2	2.04	0.66
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.77	0.65
1:A:380:ARG:HD3	1:A:400:GLU:OE1	1.96	0.65
1:B:481:ARG:HH21	3:B:802:12S:H20	1.46	0.63
1:A:701:THR:HG23	7:A:1009:HOH:O	1.97	0.63
1:B:481:ARG:HH22	3:B:802:12S:H16	1.62	0.62
1:B:706:TYR:OH	2:B:801:HEM:O2D	2.13	0.61
1:A:609:GLU:HG3	7:A:917:HOH:O	1.99	0.61
1:A:330:ILE:HD11	1:B:696:LEU:HD22	1.85	0.59
1:B:322:LEU:HD12	1:B:699:ARG:HB3	1.84	0.58
1:A:414:ARG:HD3	1:A:678:TRP:CD2	2.39	0.58
1:B:596:ARG:HE	3:B:802:12S:H18	1.70	0.55
1:A:322:LEU:HB2	1:A:699:ARG:HE	1.72	0.54
1:A:631:VAL:HG11	1:B:628:GLN:HG3	1.90	0.53
1:A:403:TYR:CE1	1:A:407:HIS:CE1	2.96	0.53
1:B:485:TYR:CE1	1:B:514:ARG:HA	2.44	0.53
1:B:678:TRP:CH2	3:B:802:12S:C29	2.93	0.51
2:A:801:HEM:CMC	2:A:801:HEM:HBC2	2.34	0.51
1:B:678:TRP:CH2	3:B:802:12S:H10	2.46	0.50
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.93	0.50
1:A:336:MET:HG2	7:A:922:HOH:O	2.11	0.50
1:B:398:ASP:HB2	7:B:917:HOH:O	2.11	0.50
2:B:801:HEM:O2A	3:B:802:12S:H9	2.10	0.50
1:A:628:GLN:HG2	1:B:631:VAL:HG11	1.93	0.50
1:A:592:GLU:OE1	3:A:802:12S:N11	2.45	0.49
1:B:300:PHE:HB3	1:B:313:THR:CG2	2.43	0.49
1:B:596:ARG:NE	3:B:802:12S:H18	2.28	0.49
1:A:510:TRP:CE2	1:A:521:PRO:HD3	2.48	0.48
1:A:450:THR:HA	1:A:455:LEU:HD22	1.95	0.48
1:A:380:ARG:CD	1:A:400:GLU:OE1	2.61	0.48
1:A:371:ARG:CG	1:A:371:ARG:HH21	2.21	0.48
1:B:510:TRP:CE2	1:B:521:PRO:HD3	2.49	0.48
1:B:587:TRP:H	2:B:801:HEM:HAB	1.80	0.46
1:A:387:GLU:OE1	1:A:394:TYR:HA	2.15	0.46
1:B:595:VAL:O	1:B:599:CYS:HB2	2.16	0.46
2:B:801:HEM:CBB	2:B:801:HEM:HHC	2.46	0.46
1:B:485:TYR:CZ	1:B:514:ARG:HA	2.50	0.46
1:A:686:SER:HA	1:A:691:PHE:CG	2.51	0.45
1:A:350:THR:N	1:A:353:GLN:HE21	2.15	0.45
1:B:596:ARG:HH12	2:B:801:HEM:CGA	2.29	0.45
1:A:709:ASP:HA	1:A:710:PRO:HD3	1.87	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:HIS:O	1:A:320:SER:HB3	2.17	0.45
1:A:589:MET:HA	1:A:649:VAL:O	2.16	0.45
1:B:678:TRP:CH2	3:B:802:12S:H11	2.52	0.45
1:A:676:TRP:CE2	1:A:680:VAL:HG21	2.53	0.44
1:B:462:PHE:HB3	1:B:463:PRO:CD	2.47	0.44
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.52	0.44
1:B:675:ASP:O	1:B:679:ILE:HG12	2.17	0.44
1:A:587:TRP:N	2:A:801:HEM:HAB	2.29	0.44
1:B:353:GLN:HG2	1:B:353:GLN:H	1.63	0.43
2:A:801:HEM:HBA2	3:A:802:12S:C4	2.41	0.43
1:A:449:ALA:O	1:A:455:LEU:HA	2.18	0.43
1:B:596:ARG:HE	3:B:802:12S:C9	2.32	0.43
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	2.00	0.43
1:A:627:ASP:OD2	1:B:684:SER:OG	2.31	0.43
1:B:478:GLN:HB2	1:B:481:ARG:HG3	2.01	0.42
1:A:299:ARG:N	1:A:317:HIS:HE2	2.17	0.42
1:B:349:ARG:HG2	1:B:353:GLN:HG3	2.02	0.42
1:A:445:HIS:C	1:A:445:HIS:CD2	2.93	0.42
1:B:501:PHE:CE2	1:B:505:CYS:SG	3.12	0.42
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.54	0.42
1:B:589:MET:HA	1:B:649:VAL:O	2.20	0.42
1:A:522:LEU:HB3	1:A:524:LEU:HD21	2.02	0.41
1:B:546:ILE:HG12	1:B:560:LYS:HA	2.02	0.41
1:A:350:THR:HG22	7:A:926:HOH:O	2.20	0.41
1:A:525:GLN:HG3	1:A:529:ASN:O	2.21	0.41
1:A:336:MET:CG	7:A:922:HOH:O	2.67	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%)	387 (95%)	19 (5%)	0	100	100
1	B	408/422 (97%)	403 (99%)	4 (1%)	1 (0%)	52	51
All	All	814/844 (96%)	790 (97%)	23 (3%)	1 (0%)	56	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	322	LEU

### 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%)	348 (95%)	18 (5%)	31	26
1	B	367/377 (97%)	355 (97%)	12 (3%)	45	44
All	All	733/754 (97%)	703 (96%)	30 (4%)	37	35

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	300	PHE
1	A	319	LYS
1	A	321	THR
1	A	328	GLU
1	A	337	LEU
1	A	350	THR
1	A	371	ARG
1	A	380	ARG
1	A	511	LYS
1	A	523	LEU
1	A	547	ARG
1	A	552	ASP
1	A	569	ASN
1	A	620	LYS
1	A	645	LYS

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Mol	Chain	Res	Type
1	A	653	SER
1	A	713	THR
1	A	715	VAL
1	B	321	THR
1	B	322	LEU
1	B	323	GLU
1	B	336	MET
1	B	353	GLN
1	B	360	GLU
1	B	390	SER
1	B	392	SER
1	B	507	GLN
1	B	540	LEU
1	B	547	ARG
1	B	699	ARG

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	353	GLN
1	A	454	ASN
1	A	569	ASN
1	A	605	ASN
1	A	697	ASN
1	B	385	ASN
1	B	454	ASN
1	B	527	ASN
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 13 ligands modelled in this entry, 7 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	2.76	15 (50%)	24,82,82	2.82	10 (41%)
3	12S	A	802	-	32,32,32	0.77	1 (3%)	43,43,43	1.97	8 (18%)
4	ACT	A	803	-	1,3,3	2.18	1 (100%)	0,3,3	0.00	-
2	HEM	B	801	1	30,50,50	2.62	11 (36%)	24,82,82	2.95	10 (41%)
3	12S	B	802	-	32,32,32	0.93	1 (3%)	43,43,43	2.50	17 (39%)
4	ACT	B	803	-	1,3,3	1.30	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	801	1	-	0/10/54/54	0/0/8/8
3	12S	A	802	-	-	0/14/14/14	0/3/3/3
4	ACT	A	803	-	-	0/0/0/0	0/0/0/0
2	HEM	B	801	1	-	0/10/54/54	0/0/8/8
3	12S	B	802	-	-	0/14/14/14	0/3/3/3
4	ACT	B	803	-	-	0/0/0/0	0/0/0/0

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C3B-C4B	-4.16	1.48	1.51
2	B	801	HEM	C3B-C4B	-3.59	1.48	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C3D-C4D	-3.52	1.47	1.51
2	A	801	HEM	C2D-C3D	-2.68	1.46	1.54
2	A	801	HEM	C3B-CAB	-2.31	1.47	1.51
2	B	801	HEM	C2D-C3D	-2.28	1.47	1.54
2	A	801	HEM	C2C-C1C	-2.19	1.48	1.52
3	A	802	12S	C22-N21	2.05	1.38	1.34
3	B	802	12S	C22-N21	2.13	1.38	1.34
4	A	803	ACT	CH3-C	2.18	1.51	1.48
2	B	801	HEM	C1A-CHA	2.21	1.45	1.39
2	A	801	HEM	FE-ND	2.30	2.09	1.97
2	A	801	HEM	CHD-C1D	2.48	1.45	1.38
2	B	801	HEM	FE-NB	2.48	2.10	1.97
2	A	801	HEM	FE-NB	2.65	2.11	1.97
2	A	801	HEM	CHC-C4B	2.70	1.46	1.38
2	A	801	HEM	C4A-CHB	2.75	1.47	1.39
2	B	801	HEM	CHC-C4B	2.93	1.47	1.38
2	B	801	HEM	FE-ND	2.96	2.13	1.97
2	A	801	HEM	C2A-C3A	3.04	1.46	1.37
2	B	801	HEM	C2A-C3A	3.22	1.47	1.37
2	B	801	HEM	CHC-C1C	4.14	1.46	1.36
2	A	801	HEM	CHD-C4C	4.28	1.46	1.36
2	A	801	HEM	CHC-C1C	4.42	1.46	1.36
2	B	801	HEM	CHD-C4C	4.65	1.47	1.36
2	A	801	HEM	C4C-NC	6.46	1.44	1.36
2	B	801	HEM	C4C-NC	6.64	1.44	1.36
2	B	801	HEM	C1C-NC	6.85	1.44	1.36
2	A	801	HEM	C1C-NC	6.90	1.44	1.36

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	HEM	CBA-CAA-C2A	-5.24	103.14	112.53
3	B	802	12S	C13-C12-N11	-4.48	117.90	122.96
3	B	802	12S	C19-C3-C2	-4.03	113.80	120.56
3	B	802	12S	C23-C22-N21	-3.98	118.46	122.96
3	A	802	12S	C13-C12-N11	-3.70	118.78	122.96
2	A	801	HEM	C3C-CAC-CBC	-3.58	118.97	124.46
3	A	802	12S	C23-C22-N21	-3.52	118.99	122.96
2	A	801	HEM	CAA-CBA-CGA	-3.50	106.33	112.75
2	B	801	HEM	CAA-CBA-CGA	-3.44	106.44	112.75
2	A	801	HEM	C3B-CAB-CBB	-3.39	119.26	124.46
3	A	802	12S	C28-C22-C23	-3.29	116.51	121.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	HEM	C3B-CAB-CBB	-2.84	120.09	124.46
3	B	802	12S	C29-C5-C6	-2.83	115.82	120.56
2	B	801	HEM	C3C-CAC-CBC	-2.39	120.79	124.46
2	A	801	HEM	CAD-CBD-CGD	-2.29	103.69	113.02
3	B	802	12S	C28-C22-C23	-2.24	117.99	121.13
3	B	802	12S	C8-C7-C1	-2.05	105.89	113.71
3	B	802	12S	C17-C14-C15	-2.00	117.91	120.95
3	B	802	12S	C13-C14-C15	2.26	120.97	118.08
3	B	802	12S	C25-C24-C23	2.32	121.04	118.08
3	B	802	12S	C29-C28-C22	2.36	117.07	112.53
3	B	802	12S	C29-C5-C4	2.39	124.56	120.56
3	A	802	12S	C18-C12-C13	2.42	124.52	121.13
2	B	801	HEM	C2C-C1C-NC	2.50	114.42	110.21
3	B	802	12S	N26-C26-N21	2.69	121.40	116.50
2	A	801	HEM	C2C-C1C-NC	2.81	114.94	110.21
2	A	801	HEM	CMD-C2D-C3D	3.05	127.84	114.35
3	B	802	12S	C18-C12-N11	3.09	120.26	115.69
2	B	801	HEM	CMD-C2D-C3D	3.36	129.21	114.35
2	A	801	HEM	CAD-C3D-C4D	4.09	126.88	112.47
3	A	802	12S	C19-C18-C12	4.12	120.46	112.53
3	A	802	12S	C26-N21-C22	4.18	121.20	118.23
3	B	802	12S	C19-C3-C4	4.24	127.67	120.56
2	B	801	HEM	CAD-C3D-C4D	4.65	128.85	112.47
2	B	801	HEM	CMC-C2C-C3C	5.20	129.51	116.53
3	B	802	12S	C28-C22-N21	5.31	123.53	115.69
3	A	802	12S	C16-N11-C12	5.53	122.16	118.23
2	B	801	HEM	CAD-C3D-C2D	5.55	129.18	113.22
2	A	801	HEM	CAD-C3D-C2D	5.57	129.24	113.22
2	A	801	HEM	CMC-C2C-C3C	5.58	130.46	116.53
3	A	802	12S	C28-C22-N21	5.97	124.50	115.69
3	B	802	12S	C26-N21-C22	6.10	122.57	118.23
2	A	801	HEM	CMB-C2B-C3B	6.12	131.82	116.53
2	B	801	HEM	CMB-C2B-C3B	6.59	132.99	116.53
3	B	802	12S	C16-N11-C12	7.09	123.27	118.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 24 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEM	6	0
3	A	802	12S	3	0
2	B	801	HEM	7	0
3	B	802	12S	12	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%)	0.08	13 (3%) 51 61	31, 49, 82, 107	0
1	B	411/422 (97%)	-0.04	8 (1%) 70 78	30, 43, 69, 98	0
All	All	818/844 (96%)	0.02	21 (2%) 59 68	30, 46, 78, 107	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	300	PHE	6.0
1	B	338	PRO	5.4
1	A	355	PHE	3.9
1	A	299	ARG	3.7
1	B	718	GLY	3.1
1	B	616	LEU	3.0
1	B	321	THR	2.9
1	A	352	ASP	2.8
1	A	322	LEU	2.8
1	B	350	THR	2.8
1	A	715	VAL	2.6
1	B	300	PHE	2.6
1	A	716	TRP	2.6
1	A	321	THR	2.5
1	A	351	LYS	2.5
1	B	352	ASP	2.4
1	A	371	ARG	2.3
1	A	713	THR	2.2
1	B	611	ALA	2.2
1	A	372	PHE	2.1
1	A	318	LEU	2.1



## 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
4	ACT	A	803	4/4	0.95	0.23	7.89	59,64,65,67	0
3	12S	A	802	30/30	0.92	0.19	2.55	35,68,98,101	0
4	ACT	B	803	4/4	0.96	0.17	2.31	53,58,59,66	0
3	12S	B	802	30/30	0.92	0.16	2.25	35,56,82,87	0
2	HEM	B	801	43/43	0.98	0.13	0.69	32,37,59,66	0
2	HEM	A	801	43/43	0.98	0.13	0.68	32,36,62,83	0
6	CL	B	806	1/1	0.98	0.11	0.12	56,56,56,56	0
5	ZN	A	804	1/1	0.98	0.10	-0.15	45,45,45,45	0
6	CL	A	807	1/1	0.97	0.07	-1.31	58,58,58,58	0
5	ZN	A	805	1/1	0.98	0.09	-1.66	40,40,40,40	1
6	CL	B	805	1/1	0.98	0.08	-	53,53,53,53	0
6	CL	A	806	1/1	0.97	0.08	-	49,49,49,49	0
5	ZN	B	804	1/1	0.99	0.07	-	43,43,43,43	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.