



Full wwPDB X-ray Structure Validation Report

Sep 19, 2014 – 03:15 AM EDT

PDB ID : 4UPM
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with N',N'-{[(2R)-3-aminopropane-1,2-diyl]bis(oxymethanediylbenzene-3,1-diyl)}dithiophene-2-carboximidamide
Authors : Li, H.; Poulos, T.L.
Deposited on : 2014-06-17
Resolution : 1.90 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

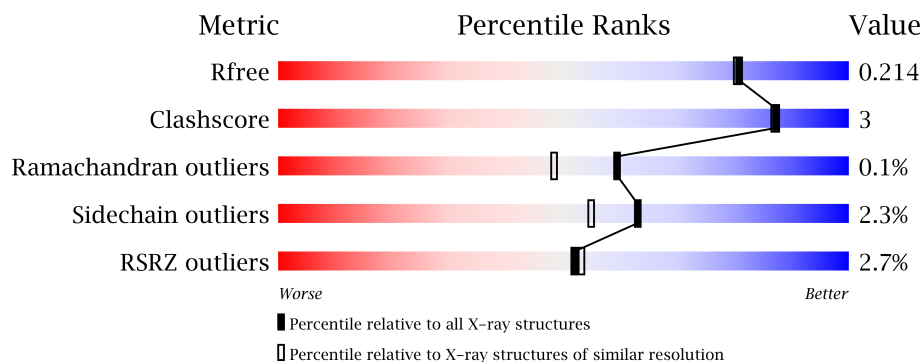
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable23489
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) : stable23489

1 Overall quality at a glance

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}	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (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 ≥ 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
4	I5U	A	800	-	X
5	ACT	A	860	-	X

2 Entry composition i

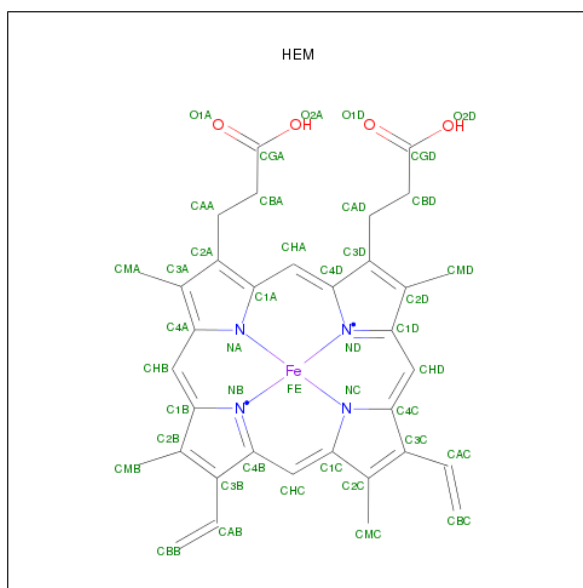
There are 7 unique types of molecules in this entry. The entry contains 7191 atoms, of which 0 are hydrogen and 0 are deuterium.

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 NEURONAL NITRIC OXIDE SYNTHASE.

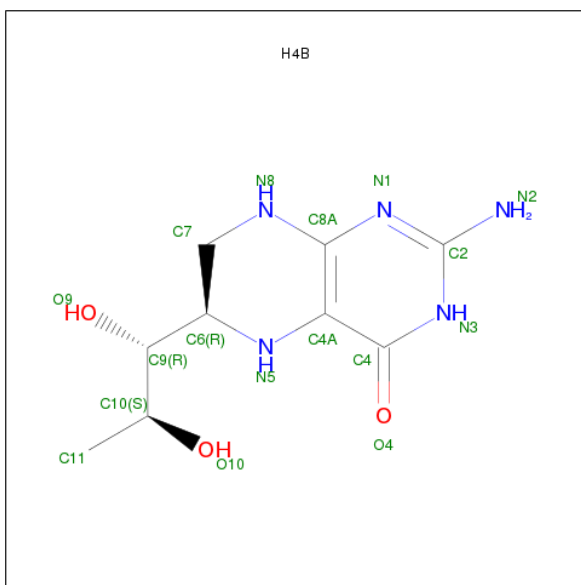
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	0	1
			3314	2121	567	605	21			
1	B	411	Total	C	N	O	S	0	0	0
			3345	2140	574	610	21			

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



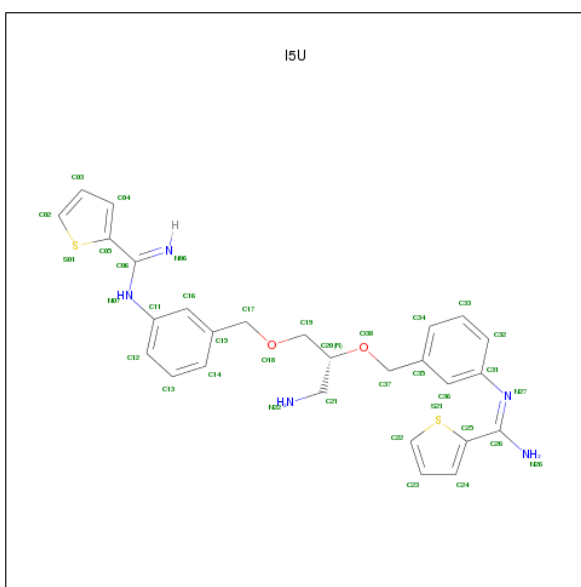
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



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

- Molecule 4 is N',N'-[[(2R)-3-AMINOPROPANE-1,2-DIYL]BIS(OXYMETHANEDIYLBENZENE-3,1-DIYL)]DITHIOPHENE-2-CARBOXIMIDAMIDE (three-letter code: I5U) (formula: C₂₇H₂₉N₅O₂S₂).



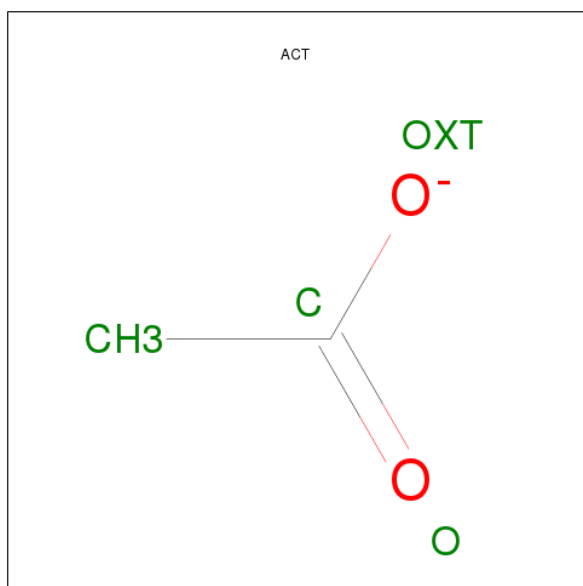
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			36	27	5	2	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			36	27	5	2	2		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

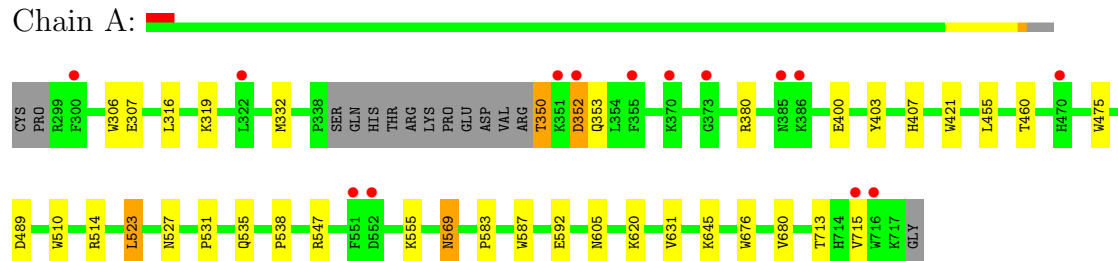
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	145	Total	O	0	0
			145	145		
7	B	186	Total	O	0	0
			186	186		

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.

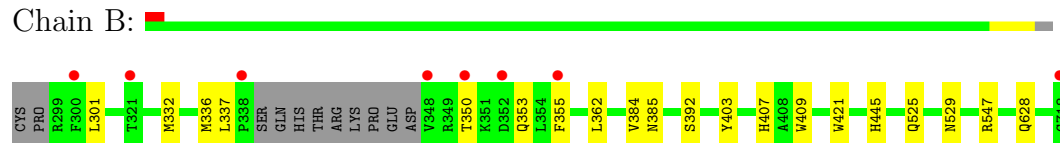
• Molecule 1: NEURONAL NITRIC OXIDE SYNTHASE

Chain A:



• Molecule 1: NEURONAL NITRIC OXIDE SYNTHASE

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.06Å 111.36Å 165.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	92.35 – 1.90 49.66 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.0 (92.35-1.90) 99.1 (49.66-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.177 , 0.210 0.183 , 0.214	Depositor DCC
R_{free} test set	3746 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.670	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 75599 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7191	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, ZN, I5U, H4B, ACT

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	0.64	2/3407 (0.1%)	0.67	0/4623
1	B	0.68	0/3438	0.68	0/4661
All	All	0.66	2/6845 (0.0%)	0.67	0/9284

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	421	TRP	CD2-CE2	5.08	1.47	1.41
1	A	510	TRP	CD2-CE2	5.02	1.47	1.41

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	3314	0	3221	20	0
1	B	3345	0	3259	9	0
2	A	43	0	30	3	0
2	B	43	0	30	4	0
3	A	17	0	15	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	17	0	15	0	0
4	A	36	0	0	2	0
4	B	36	0	0	1	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	1	0	0	0	0
7	A	145	0	0	1	0
7	B	186	0	0	1	0
All	All	7191	0	6576	34	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 (34) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:750:HEM:HMC2	2:B:750:HEM:HBC2	1.64	0.80
2:A:750:HEM:HMC2	2:A:750:HEM:HBC2	1.71	0.71
1:A:350:THR:N	1:A:353:GLN:HE21	1.91	0.69
2:B:750:HEM:HBB2	2:B:750:HEM:HHC	1.74	0.69
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.79	0.63
1:A:350:THR:N	1:A:353:GLN:NE2	2.50	0.58
1:A:535:GLN:HE21	1:A:538:PRO:HD3	1.67	0.58
2:A:750:HEM:HHC	2:A:750:HEM:HBB2	1.86	0.56
1:A:306:TRP:CE2	1:B:336:MET:HE3	2.45	0.52
1:A:316:LEU:HD12	1:A:319:LYS:HD2	1.94	0.50
2:B:750:HEM:CMC	2:B:750:HEM:HBC2	2.40	0.50
1:A:307:GLU:HG3	7:B:2155:HOH:O	2.12	0.49
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.96	0.48
1:A:631:VAL:HG11	1:B:628:GLN:HG2	1.95	0.48
1:B:355:PHE:CE1	1:B:385:ASN:HB2	2.49	0.47
2:B:750:HEM:C4B	4:B:800:I5U:S21	3.08	0.47
2:A:750:HEM:CMC	2:A:750:HEM:HBC2	2.42	0.46
1:A:332:MET:HE2	1:B:301:LEU:HD22	1.98	0.45
1:A:380:ARG:HD3	1:A:400:GLU:OE2	2.18	0.44
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.53	0.43
1:A:592:GLU:OE1	4:A:800:I5U:N27	2.52	0.43
1:A:460:THR:O	1:A:583:PRO:HD2	2.18	0.43
1:B:362:LEU:HD11	1:B:384:VAL:HG21	2.00	0.43
1:B:403:TYR:CE2	1:B:407:HIS:CE1	3.07	0.43
1:A:403:TYR:CE2	1:A:407:HIS:CE1	3.07	0.42
1:A:569:ASN:HD22	1:A:569:ASN:H	1.66	0.42
1:B:525:GLN:HG3	1:B:529:ASN:O	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:445:HIS:CD2	1:B:445:HIS:C	2.94	0.41
1:A:605:ASN:ND2	7:A:2111:HOH:O	2.47	0.41
1:A:527:ASN:HD22	1:A:527:ASN:HA	1.75	0.41
1:A:676:TRP:CE2	1:A:680:VAL:HG21	2.55	0.41
4:A:800:I5U:C25	4:A:800:I5U:C32	2.96	0.41
1:A:352:ASP:N	1:A:352:ASP:OD1	2.52	0.40
1:A:475:TRP:HB2	1:A:523:LEU:HB3	2.03	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%)	396 (98%)	7 (2%)	1 (0%)	56	44
1	B	407/422 (96%)	402 (99%)	5 (1%)	0	100	100
All	All	811/844 (96%)	798 (98%)	12 (2%)	1 (0%)	59	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	489	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	363/377 (96%)	352 (97%)	11 (3%)	53	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	366/377 (97%)	360 (98%)	6 (2%)	75	70
All	All	729/754 (97%)	712 (98%)	17 (2%)	63	55

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

Mol	Chain	Res	Type
1	A	350	THR
1	A	352	ASP
1	A	514	ARG
1	A	523	LEU
1	A	547	ARG
1	A	555	LYS
1	A	569	ASN
1	A	620	LYS
1	A	645	LYS
1	A	713	THR
1	A	715	VAL
1	B	332	MET
1	B	337	LEU
1	B	350	THR
1	B	353	GLN
1	B	392	SER
1	B	547	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	454	ASN
1	A	527	ASN
1	A	535	GLN
1	A	569	ASN
1	A	601	ASN
1	A	697	ASN
1	B	364	GLN
1	B	454	ASN
1	B	601	ASN
1	B	605	ASN
1	B	642	GLN
1	B	697	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	HEM	A	750	1	42,50,50	2.66	20 (47%)	27,82,82	2.04	9 (33%)
3	H4B	A	760	-	18,18,18	1.23	2 (11%)	24,26,26	1.78	5 (20%)
4	I5U	A	800	-	39,39,39	1.32	4 (10%)	51,51,51	1.47	5 (9%)
5	ACT	A	860	-	1,3,3	1.72	0	0,3,3	0.00	-
2	HEM	B	750	1	42,50,50	2.52	16 (38%)	27,82,82	2.56	10 (37%)
3	H4B	B	760	-	18,18,18	1.32	3 (16%)	24,26,26	1.69	4 (16%)
4	I5U	B	800	-	39,39,39	1.21	4 (10%)	51,51,51	1.74	9 (17%)
5	ACT	B	860	-	1,3,3	1.03	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	-	0/14/114/114	0/0/8/8

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2
4	I5U	A	800	-	-	1/21/29/29	0/4/4/4
5	ACT	A	860	-	-	0/0/0/0	0/0/0/0
2	HEM	B	750	1	-	0/14/114/114	0/0/8/8
3	H4B	B	760	-	-	0/8/17/17	0/2/2/2
4	I5U	B	800	-	-	1/21/29/29	0/4/4/4
5	ACT	B	860	-	-	0/0/0/0	0/0/0/0

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	CHC-C4B	5.44	1.46	1.39
4	A	800	I5U	C05-C06	5.10	1.51	1.45
2	A	750	HEM	C3C-C4C	5.07	1.49	1.45
2	B	750	HEM	CHC-C4B	5.03	1.45	1.39
2	A	750	HEM	C4A-NA	4.86	1.44	1.36
2	B	750	HEM	C1A-NA	4.78	1.44	1.36
4	B	800	I5U	C05-C06	4.63	1.50	1.45
2	B	750	HEM	C4A-NA	4.58	1.44	1.36
2	B	750	HEM	CMC-C2C	4.56	1.53	1.45
2	B	750	HEM	CMD-C2D	4.54	1.52	1.45
2	A	750	HEM	C1C-NC	4.44	1.44	1.33
2	B	750	HEM	C1C-NC	4.39	1.44	1.33
2	A	750	HEM	C4C-NC	4.33	1.44	1.33
2	B	750	HEM	C4C-NC	4.29	1.44	1.33
2	A	750	HEM	FE-NB	4.26	2.10	1.95
2	B	750	HEM	CMB-C2B	4.15	1.52	1.45
2	A	750	HEM	CMD-C2D	4.07	1.52	1.45
3	A	760	H4B	C2-N2	4.05	1.38	1.32
2	A	750	HEM	C1B-C2B	3.97	1.48	1.45
2	A	750	HEM	C1A-NA	3.79	1.42	1.36
2	B	750	HEM	C1B-C2B	3.67	1.48	1.45
2	A	750	HEM	CMB-C2B	3.66	1.51	1.45
2	A	750	HEM	C3C-C2C	3.56	1.48	1.45
2	A	750	HEM	FE-ND	3.38	2.09	1.95
2	B	750	HEM	FE-NB	3.36	2.07	1.95
4	B	800	I5U	C31-N27	-3.30	1.36	1.42
2	A	750	HEM	C3B-C2B	-3.25	1.42	1.45
2	A	750	HEM	C2A-C3A	3.22	1.47	1.37
4	A	800	I5U	C31-N27	-3.19	1.37	1.42
3	B	760	H4B	C7-C6	3.16	1.55	1.52
2	B	750	HEM	C3C-C4C	3.10	1.47	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C4A-C3A	3.03	1.48	1.43
2	B	750	HEM	FE-ND	3.02	2.07	1.95
3	B	760	H4B	C2-N2	2.96	1.36	1.32
2	B	750	HEM	C2A-C3A	2.91	1.46	1.37
2	A	750	HEM	CMC-C2C	2.76	1.50	1.45
2	B	750	HEM	C3C-CAC	2.53	1.48	1.40
2	A	750	HEM	C3C-CAC	2.45	1.48	1.40
3	B	760	H4B	C2-N1	2.40	1.36	1.33
4	A	800	I5U	C25-C26	2.40	1.48	1.45
2	A	750	HEM	C1A-C2A	2.38	1.47	1.43
2	B	750	HEM	C4A-C3A	2.36	1.47	1.43
2	B	750	HEM	C1A-C2A	2.30	1.47	1.43
2	A	750	HEM	C1C-C2C	2.28	1.49	1.43
4	B	800	I5U	C25-C26	2.18	1.48	1.45
4	A	800	I5U	C11-N07	-2.17	1.37	1.41
2	A	750	HEM	C3B-CAB	2.05	1.47	1.40
4	B	800	I5U	C11-N07	-2.03	1.37	1.41
3	A	760	H4B	C2-N1	2.03	1.36	1.33

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	750	HEM	CBA-CAA-C2A	-7.08	100.85	112.63
2	B	750	HEM	C3A-C4A-NA	6.51	113.85	109.50
4	B	800	I5U	N26-C26-N27	-6.13	117.96	125.41
4	A	800	I5U	N26-C26-N27	-5.58	118.62	125.41
2	A	750	HEM	CBA-CAA-C2A	-5.36	103.71	112.63
2	B	750	HEM	C4A-NA-C1A	-4.74	102.03	107.93
3	B	760	H4B	C4-C4A-C8A	4.52	118.65	114.56
4	B	800	I5U	O38-C20-C21	4.27	115.92	107.21
3	A	760	H4B	C4-C4A-C8A	4.25	118.41	114.56
4	A	800	I5U	C23-C22-S21	-4.02	108.85	113.18
2	A	750	HEM	C3A-C4A-NA	3.91	112.11	109.50
2	B	750	HEM	C4A-C3A-C2A	-3.79	104.36	107.00
3	A	760	H4B	N2-C2-N3	3.76	121.85	117.82
2	A	750	HEM	C4A-NA-C1A	-3.37	103.74	107.93
4	B	800	I5U	C22-S21-C25	-3.19	90.50	91.91
3	B	760	H4B	N2-C2-N3	3.17	121.22	117.82
3	A	760	H4B	C4A-C8A-N8	3.05	122.03	118.43
4	B	800	I5U	C02-S01-C05	3.05	93.25	91.91
2	A	750	HEM	CMC-C2C-C3C	2.96	131.26	124.26
3	A	760	H4B	C4-N3-C2	2.67	121.71	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	750	HEM	CMB-C2B-C3B	2.67	132.34	126.21
2	B	750	HEM	CMC-C2C-C3C	2.64	130.51	124.26
3	B	760	H4B	N8-C8A-N1	2.63	119.68	115.82
2	B	750	HEM	CAD-C3D-C4D	2.63	129.30	125.60
2	A	750	HEM	CAD-CBD-CGD	-2.61	108.61	113.53
3	B	760	H4B	C4-C4A-N5	2.55	122.72	119.07
3	A	760	H4B	C4-C4A-N5	2.53	122.69	119.07
2	A	750	HEM	C4A-C3A-C2A	-2.48	105.27	107.00
4	B	800	I5U	C03-C02-S01	-2.39	110.61	113.18
2	A	750	HEM	C2A-C1A-NA	2.31	112.94	109.73
2	B	750	HEM	O2D-CGD-CBD	2.31	122.17	114.19
4	A	800	I5U	C22-S21-C25	2.31	92.92	91.91
2	A	750	HEM	O1D-CGD-CBD	-2.27	115.38	123.06
4	A	800	I5U	C12-C11-N07	2.24	127.94	120.41
4	B	800	I5U	C12-C11-N07	2.19	127.76	120.41
2	B	750	HEM	C2A-C1A-NA	2.15	112.72	109.73
4	A	800	I5U	O38-C20-C21	2.15	111.60	107.21
4	B	800	I5U	C24-C25-S21	2.10	113.52	111.02
2	B	750	HEM	O1D-CGD-CBD	-2.09	115.99	123.06
2	A	750	HEM	CAD-C3D-C4D	2.08	128.53	125.60
4	B	800	I5U	C37-C35-C36	-2.03	115.28	120.29
4	B	800	I5U	C12-C11-C16	-2.00	117.30	119.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	800	I5U	N26-C26-N27-C31
4	B	800	I5U	N26-C26-N27-C31

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, 95th 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 ²)	Q<0.9
1	A	408/422 (96%)	0.27	14 (3%) 43 44	26, 50, 90, 120	0
1	B	411/422 (97%)	0.07	8 (1%) 64 65	25, 39, 66, 86	0
All	All	819/844 (97%)	0.17	22 (2%) 52 53	25, 44, 84, 120	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	PHE	5.9
1	B	348	VAL	5.7
1	A	355	PHE	4.6
1	A	352	ASP	4.1
1	A	300	PHE	3.4
1	A	552	ASP	3.1
1	B	338	PRO	3.0
1	B	350	THR	3.0
1	A	716	TRP	2.9
1	A	373	GLY	2.8
1	A	386	LYS	2.8
1	B	321	THR	2.8
1	A	715	VAL	2.7
1	A	551	PHE	2.7
1	A	351	LYS	2.7
1	A	322	LEU	2.5
1	B	352	ASP	2.5
1	B	718	GLY	2.5
1	A	470	HIS	2.4
1	B	355	PHE	2.3
1	A	385	ASN	2.1
1	A	370	LYS	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	ACT	A	860	4/4	0.20	4.40	54,56,58,59	0
4	I5U	A	800	36/36	0.17	2.35	24,68,107,116	0
2	HEM	B	750	43/43	0.13	1.85	25,28,34,41	0
4	I5U	B	800	36/36	0.15	1.61	23,55,98,110	0
2	HEM	A	750	43/43	0.12	0.64	26,29,36,40	0
5	ACT	B	860	4/4	0.12	0.51	43,46,47,48	0
6	ZN	A	1717	1/1	0.10	0.18	34,34,34,34	0
3	H4B	B	760	17/17	0.11	-0.36	28,30,33,35	0
3	H4B	A	760	17/17	0.09	-1.78	29,31,34,35	0

6.5 Other polymers ⓘ

There are no such residues in this entry.