



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:59 PM GMT

PDB ID : 4K5G
Title : Structure of neuronal nitric oxide synthase heme domain in complex with ((2S, 3S)-1,3-bis((6-(2,5-dimethyl-1H-pyrrol-1-yl)-4-methylpyridin-2-yl)methoxy)-2-aminobutane
Authors : Li, H.; Poulos, T.L.
Deposited on : 2013-04-14
Resolution : 1.85 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

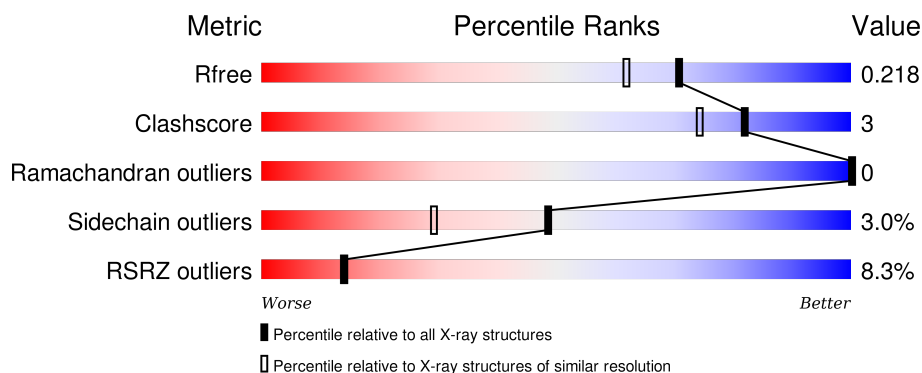
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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. 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	
1	B	422	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	Q13	A	803	-	-	-	X
4	Q13	B	803	-	-	-	X
5	ACT	A	804	-	-	-	X
5	ACT	B	804	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7238 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.

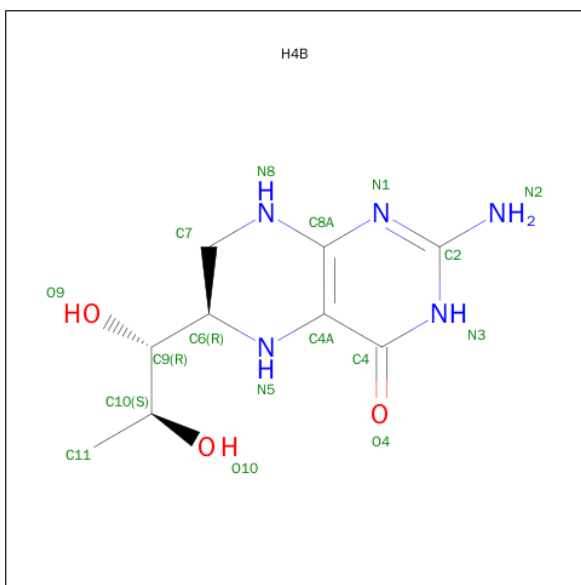
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	2	0
			3323	2128	566	608	21			
1	B	411	Total	C	N	O	S	0	3	0
			3357	2148	574	614	21			

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



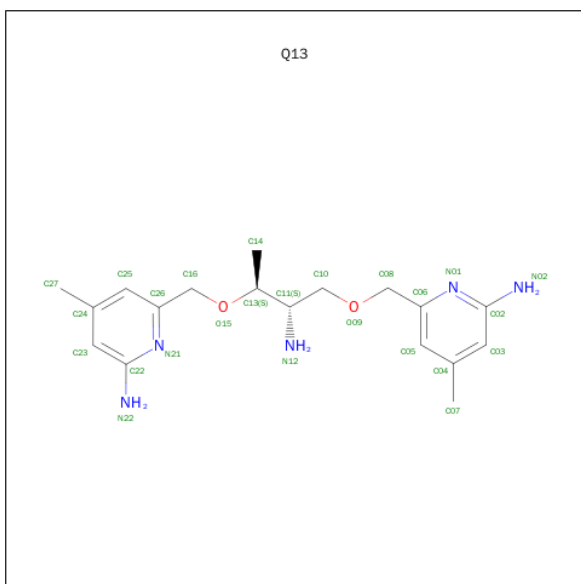
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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

- Molecule 4 is 6,6'-{[(2S,3S)-2-AMINO-1,3-BIS(OXYMETHANEDIYL)BUTANE]}BIS(4-METHYLPYRIDIN-2-AMINE) (three-letter code: Q13) (formula: C₁₈H₂₇N₅O₂).



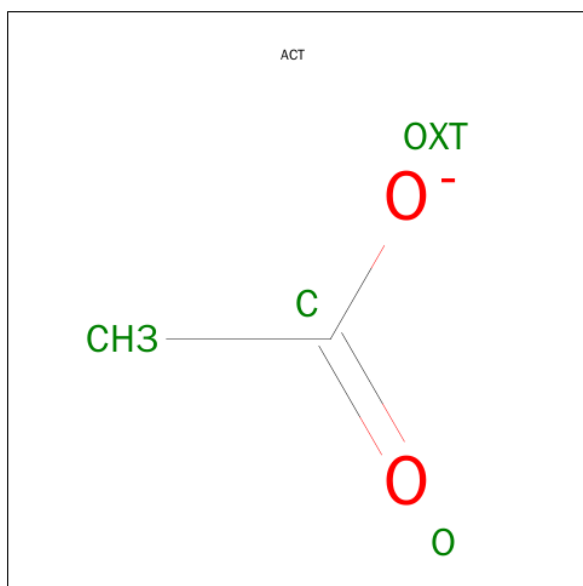
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			25	18	5	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			25	18	5	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		

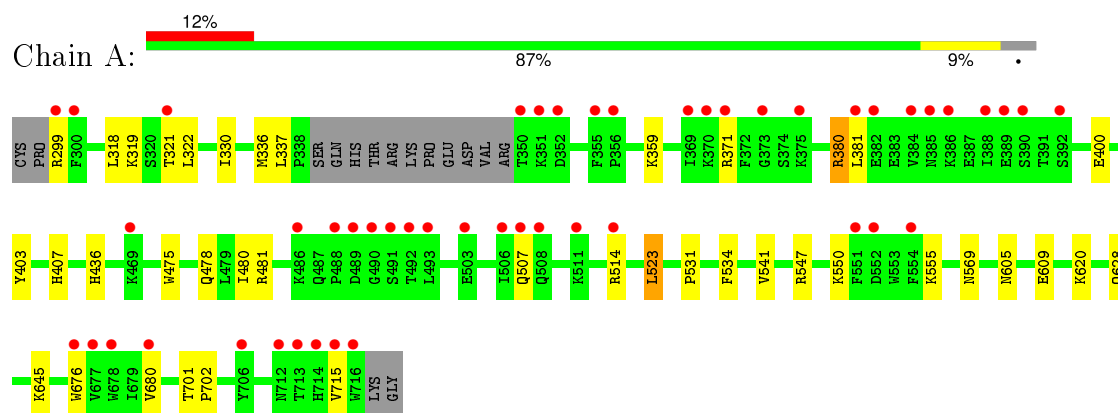
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	146	Total	O	0	0
			146	146		
7	B	233	Total	O	0	0
			233	233		

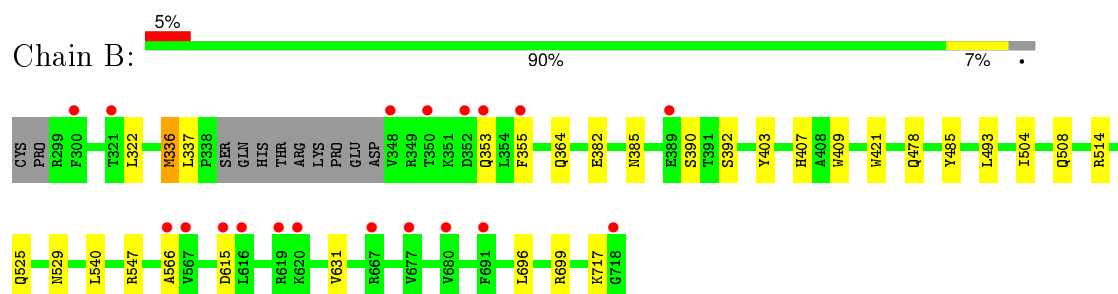
3 Residue-property plots [i](#)

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 ($RSRZ > 2$). 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, α , β , γ	52.13Å 110.73Å 164.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.06 – 1.85 44.02 – 1.85	Depositor EDS
% Data completeness (in resolution range)	97.9 (44.06-1.85) 98.0 (44.02-1.85)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.185 , 0.219 0.185 , 0.218	Depositor DCC
R_{free} test set	3986 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.766	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 80491 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7238	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, ZN, H4B, Q13, 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	0.52	0/3422	0.65	0/4644
1	B	0.58	0/3459	0.68	0/4689
All	All	0.56	0/6881	0.67	0/9333

There are no bond length outliers.

There are no bond angle outliers.

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	3323	0	3234	21	0
1	B	3357	0	3275	17	0
2	A	43	0	30	4	0
2	B	43	0	30	4	0
3	A	17	0	15	0	0
3	B	17	0	15	1	0
4	A	25	0	27	3	0
4	B	25	0	27	4	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	146	0	0	4	0
7	B	233	0	0	2	0
All	All	7238	0	6659	43	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (43) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:801:HEM:HBA2	4:B:803:Q13:H20	1.54	0.89
2:A:801:HEM:HMC2	2:A:801:HEM:HBC2	1.70	0.72
1:A:609:GLU:HG3	7:A:935:HOH:O	1.89	0.71
2:B:801:HEM:CBA	4:B:803:Q13:H20	2.26	0.62
1:A:337:LEU:HD21	4:A:803:Q13:H3	1.81	0.62
1:B:364:GLN:NE2	7:B:1095:HOH:O	2.28	0.59
1:A:701[B]:THR:HG22	1:A:702:PRO:HA	1.84	0.58
1:A:321:THR:HG23	1:A:322:LEU:HG	1.88	0.55
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.88	0.54
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.91	0.52
1:A:701[B]:THR:CG2	1:A:702:PRO:HA	2.40	0.50
2:A:801:HEM:HBA2	4:A:803:Q13:H21	1.93	0.50
1:A:330:ILE:HD11	1:B:696:LEU:HD22	1.95	0.49
1:A:480:ILE:HD13	1:A:541:VAL:HG13	1.96	0.48
1:A:605:ASN:ND2	7:A:921:HOH:O	2.44	0.47
2:A:801:HEM:CBA	4:A:803:Q13:H21	2.44	0.47
1:A:380:ARG:HD3	1:A:400:GLU:OE1	2.15	0.47
1:A:676:TRP:CE2	1:A:680:VAL:HG21	2.50	0.47
1:A:436:HIS:CD2	1:A:534:PHE:HE2	2.32	0.46
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.50	0.46
2:B:801:HEM:HBA2	4:B:803:Q13:C08	2.37	0.46
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.97	0.46
1:A:330:ILE:HD11	1:B:696:LEU:HB3	1.98	0.45
1:A:701[B]:THR:HG22	7:A:928:HOH:O	2.17	0.44
1:B:615:ASP:HA	7:B:1060:HOH:O	2.18	0.44
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.06	0.44
1:B:336:MET:HE1	3:B:802:H4B:H9	2.00	0.43
1:B:336:MET:HB2	1:B:336:MET:HE2	1.71	0.43
1:B:337:LEU:HD21	4:B:803:Q13:H3	2.01	0.42
1:B:485:TYR:CE1	1:B:514:ARG:HA	2.54	0.42
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:801:HEM:HHC	2:A:801:HEM:HBB2	2.02	0.42
1:A:701[A]:THR:HG23	7:A:1006:HOH:O	2.19	0.41
1:B:525:GLN:HG3	1:B:529:ASN:O	2.20	0.41
1:A:628:GLN:HG2	1:B:631:VAL:HG11	2.02	0.41
1:B:355:PHE:CE1	1:B:385:ASN:HB2	2.55	0.41
1:B:493:LEU:HD21	1:B:514:ARG:O	2.21	0.40
1:A:359:LYS:HA	1:A:381:LEU:HD11	2.02	0.40
1:A:478:GLN:HB2	1:A:481:ARG:HG3	2.03	0.40
1:B:478:GLN:HA	1:B:566:ALA:O	2.22	0.40
1:B:504:ILE:O	1:B:508:GLN:HG2	2.21	0.40
1:A:299:ARG:HG3	1:A:318:LEU:HD21	2.03	0.40
1:B:322:LEU:HD12	1:B:699:ARG: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	405/422 (96%)	394 (97%)	11 (3%)	0	100	100
1	B	410/422 (97%)	404 (98%)	6 (2%)	0	100	100
All	All	815/844 (97%)	798 (98%)	17 (2%)	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	365/377 (97%)	351 (96%)	14 (4%)	40	19
1	B	369/377 (98%)	361 (98%)	8 (2%)	60	43
All	All	734/754 (97%)	712 (97%)	22 (3%)	48	29

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	319	LYS
1	A	336	MET
1	A	371	ARG
1	A	380	ARG
1	A	507	GLN
1	A	514	ARG
1	A	523	LEU
1	A	547	ARG
1	A	550	LYS
1	A	555	LYS
1	A	569	ASN
1	A	620	LYS
1	A	645	LYS
1	A	715	VAL
1	B	336	MET
1	B	353	GLN
1	B	382	GLU
1	B	390	SER
1	B	392	SER
1	B	540	LEU
1	B	547	ARG
1	B	717	LYS

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	454	ASN
1	A	527	ASN
1	A	569	ASN
1	A	605	ASN
1	A	697	ASN
1	B	425	GLN

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Mol	Chain	Res	Type
1	B	440	ASN
1	B	454	ASN
1	B	507	GLN
1	B	527	ASN
1	B	535	GLN
1	B	601	ASN
1	B	605	ASN
1	B	697	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 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	801	1	30,50,50	2.08	7 (23%)	24,82,82	2.33	9 (37%)
3	H4B	A	802	-	13,18,18	1.13	3 (23%)	11,26,26	2.54	6 (54%)
4	Q13	A	803	-	26,26,26	1.02	1 (3%)	29,35,35	2.43	7 (24%)
5	ACT	A	804	-	1,3,3	1.54	0	0,3,3	0.00	-
2	HEM	B	801	1	30,50,50	2.15	7 (23%)	24,82,82	2.55	11 (45%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	H4B	B	802	-	13,18,18	1.21	1 (7%)	11,26,26	2.40	5 (45%)
4	Q13	B	803	-	26,26,26	0.98	2 (7%)	29,35,35	2.62	9 (31%)
5	ACT	B	804	-	1,3,3	1.22	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	H4B	A	802	-	-	0/8/17/17	0/2/2/2
4	Q13	A	803	-	-	0/14/15/15	0/2/2/2
5	ACT	A	804	-	-	0/0/0/0	0/0/0/0
2	HEM	B	801	1	-	0/10/54/54	0/0/8/8
3	H4B	B	802	-	-	0/8/17/17	0/2/2/2
4	Q13	B	803	-	-	0/14/15/15	0/2/2/2
5	ACT	B	804	-	-	0/0/0/0	0/0/0/0

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	HEM	C2D-C3D	-6.68	1.34	1.54
2	A	801	HEM	C2D-C3D	-6.51	1.35	1.54
2	B	801	HEM	C2C-C1C	-6.26	1.40	1.52
2	A	801	HEM	C2C-C1C	-5.55	1.42	1.52
2	A	801	HEM	C3D-C4D	-3.59	1.47	1.51
2	B	801	HEM	C3D-C4D	-2.94	1.47	1.51
2	B	801	HEM	C2B-C1B	-2.56	1.43	1.51
2	A	801	HEM	C2B-C1B	-2.35	1.44	1.51
3	A	802	H4B	C7-N8	2.00	1.48	1.46
4	B	803	Q13	C08-C06	2.02	1.55	1.50
4	B	803	Q13	O15-C13	2.07	1.45	1.43
2	B	801	HEM	FE-NB	2.07	2.08	1.97
3	A	802	H4B	C4-N3	2.10	1.37	1.33
3	A	802	H4B	C2-N2	2.15	1.38	1.34
3	B	802	H4B	C7-N8	2.20	1.49	1.46
4	A	803	Q13	C08-C06	2.30	1.56	1.50
2	A	801	HEM	FE-NB	2.36	2.10	1.97
2	A	801	HEM	C1C-NC	2.61	1.39	1.36
2	B	801	HEM	C1C-NC	2.95	1.39	1.36
2	A	801	HEM	FE-NC	2.98	2.07	1.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	HEM	FE-NC	3.02	2.07	1.95

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	803	Q13	C05-C06-N01	-4.81	117.53	122.96
2	B	801	HEM	C1D-CHD-C4C	-4.21	118.79	125.82
4	A	803	Q13	C05-C06-N01	-4.11	118.32	122.96
2	B	801	HEM	CBA-CAA-C2A	-3.77	105.77	112.53
3	A	802	H4B	N3-C2-N1	-3.60	119.64	125.53
4	B	803	Q13	C25-C26-N21	-3.58	118.92	122.96
2	A	801	HEM	C1D-CHD-C4C	-3.57	119.85	125.82
4	A	803	Q13	C25-C26-N21	-3.27	119.27	122.96
3	B	802	H4B	N3-C2-N1	-3.26	120.19	125.53
2	A	801	HEM	CBD-CAD-C3D	-2.99	104.85	113.55
2	A	801	HEM	CBA-CAA-C2A	-2.94	107.27	112.53
2	B	801	HEM	CBD-CAD-C3D	-2.49	106.30	113.55
4	B	803	Q13	C07-C04-C05	-2.38	117.33	120.95
2	B	801	HEM	CAA-C2A-C1A	-2.26	124.55	127.01
2	B	801	HEM	C3B-C4B-NB	-2.24	107.35	111.63
3	B	802	H4B	N2-C2-N3	2.06	120.60	117.20
4	A	803	Q13	C16-C26-N21	2.25	120.56	115.83
2	B	801	HEM	C2D-C3D-C4D	2.27	105.35	101.50
4	B	803	Q13	C16-C26-N21	2.29	120.63	115.83
3	A	802	H4B	N2-C2-N3	2.34	121.08	117.20
2	A	801	HEM	C2D-C3D-C4D	2.40	105.57	101.50
4	B	803	Q13	N22-C22-N21	2.51	121.07	116.50
4	A	803	Q13	N22-C22-N21	2.62	121.28	116.50
4	B	803	Q13	C08-C06-N01	2.65	121.40	115.83
2	A	801	HEM	CMD-C2D-C3D	2.71	126.35	114.35
2	A	801	HEM	CMB-C2B-C3B	2.76	123.42	116.53
4	A	803	Q13	C08-C06-C05	2.83	124.59	120.75
2	B	801	HEM	CMD-C2D-C3D	2.87	127.05	114.35
3	A	802	H4B	C4-N3-C2	2.92	119.99	115.94
3	B	802	H4B	C2-N1-C8A	3.03	121.35	114.54
3	B	802	H4B	C4-N3-C2	3.21	120.39	115.94
3	A	802	H4B	C4-C4A-C8A	3.52	117.75	114.56
3	A	802	H4B	C2-N1-C8A	3.77	123.02	114.54
3	A	802	H4B	C4A-C8A-N8	3.81	122.92	118.43
4	B	803	Q13	O09-C10-C11	4.04	117.17	108.49
2	B	801	HEM	CMB-C2B-C3B	4.36	127.41	116.53
2	B	801	HEM	CAD-C3D-C4D	4.40	128.00	112.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	HEM	CAD-C3D-C2D	4.47	126.07	113.22
2	A	801	HEM	CAD-C3D-C4D	4.49	128.29	112.47
2	B	801	HEM	CAD-C3D-C2D	4.67	126.63	113.22
2	B	801	HEM	CMC-C2C-C3C	4.84	128.60	116.53
2	A	801	HEM	CMC-C2C-C3C	4.97	128.93	116.53
3	B	802	H4B	C4-C4A-C8A	5.08	119.16	114.56
4	A	803	Q13	C02-N01-C06	7.32	123.44	118.23
4	B	803	Q13	C22-N21-C26	7.39	123.48	118.23
4	A	803	Q13	C22-N21-C26	7.46	123.53	118.23
4	B	803	Q13	C02-N01-C06	7.51	123.56	118.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEM	4	0
4	A	803	Q13	3	0
2	B	801	HEM	4	0
3	B	802	H4B	1	0
4	B	803	Q13	4	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, 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	407/422 (96%)	0.56	49 (12%) 6 6	20, 40, 72, 92	0
1	B	411/422 (97%)	0.19	19 (4%) 36 34	19, 32, 57, 76	0
All	All	818/844 (96%)	0.37	68 (8%) 14 14	19, 36, 69, 92	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	488	PRO	6.5
1	A	355	PHE	6.4
1	A	715	VAL	6.2
1	B	300	PHE	6.0
1	A	716	TRP	5.5
1	B	718	GLY	4.6
1	A	352	ASP	4.5
1	B	350	THR	4.3
1	A	486	LYS	4.3
1	A	507	GLN	4.3
1	A	351	LYS	4.1
1	A	321	THR	3.8
1	A	300	PHE	3.8
1	A	388	ILE	3.3
1	A	713	THR	3.3
1	B	619	ARG	3.3
1	B	348	VAL	3.2
1	A	386	LYS	3.2
1	A	370	LYS	3.2
1	B	321	THR	3.2
1	A	490	GLY	3.0
1	A	390	SER	2.8
1	A	469	LYS	2.8
1	A	551	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	491	SER	2.7
1	B	680	VAL	2.7
1	A	511	LYS	2.7
1	B	677	VAL	2.6
1	A	373	GLY	2.6
1	B	616	LEU	2.6
1	A	385	ASN	2.5
1	A	381	LEU	2.5
1	A	350	THR	2.5
1	A	676	TRP	2.5
1	B	566	ALA	2.5
1	B	620	LYS	2.5
1	A	299	ARG	2.5
1	A	706	TYR	2.5
1	A	508	GLN	2.5
1	B	352	ASP	2.5
1	B	567	VAL	2.4
1	A	714	HIS	2.4
1	A	552	ASP	2.4
1	A	677	VAL	2.4
1	B	691	PHE	2.4
1	A	489	ASP	2.4
1	A	392	SER	2.4
1	B	615	ASP	2.3
1	A	493	LEU	2.3
1	A	369	ILE	2.3
1	A	389	GLU	2.3
1	B	389	GLU	2.2
1	A	382	GLU	2.2
1	B	355	PHE	2.2
1	A	356	PRO	2.2
1	A	503	GLU	2.2
1	A	680	VAL	2.2
1	A	678	TRP	2.1
1	A	371	ARG	2.1
1	A	514	ARG	2.1
1	A	554	PHE	2.1
1	A	506	ILE	2.1
1	B	353	GLN	2.1
1	A	384	VAL	2.0
1	A	492	THR	2.0
1	A	712	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	667	ARG	2.0
1	A	375	LYS	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, 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	ACT	A	804	4/4	0.87	0.29	8.12	66,71,72,75	0
5	ACT	B	804	4/4	0.89	0.17	6.50	49,56,58,60	0
4	Q13	A	803	25/25	0.88	0.20	2.33	25,44,60,62	0
4	Q13	B	803	25/25	0.90	0.21	2.00	26,41,50,51	0
2	HEM	B	801	43/43	0.98	0.14	0.68	20,22,29,32	0
2	HEM	A	801	43/43	0.97	0.14	0.68	23,25,30,31	0
3	H4B	B	802	17/17	0.95	0.17	0.52	24,26,30,30	0
3	H4B	A	802	17/17	0.96	0.12	-0.36	25,26,28,30	0
6	ZN	A	805	1/1	1.00	0.09	-0.89	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.