



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:56 AM GMT

PDB ID : 3NLK
Title : Structure of neuronal nitric oxide synthase R349A 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 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

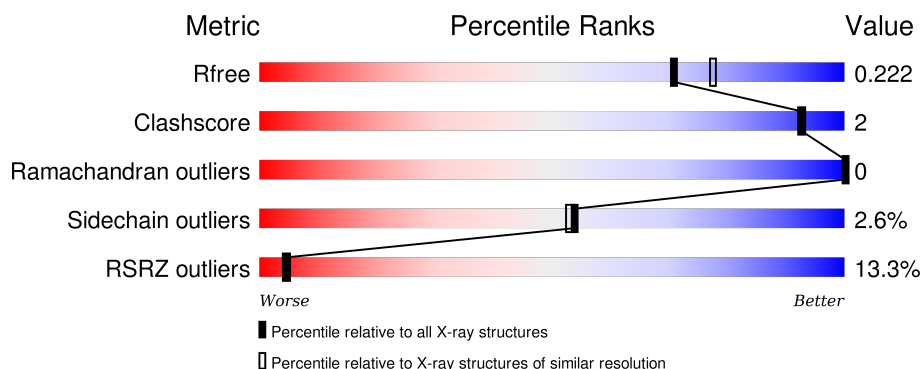
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	91344	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (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 ≥ 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
5	ACT	B	860	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7210 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.

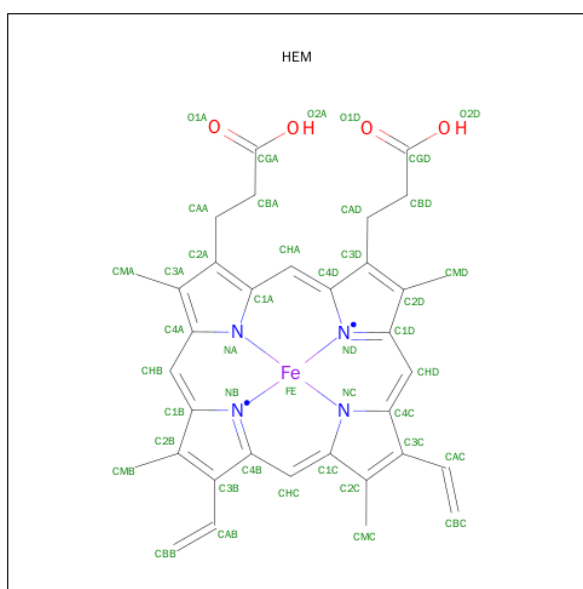
- Molecule 1 is a protein called Nitric oxide synthase, brain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	0	0
			3313	2121	566	605	21			
1	B	411	Total	C	N	O	S	0	0	0
			3339	2137	571	610	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	349	ALA	ARG	ENGINEERED MUTATION	UNP P29476
B	349	ALA	ARG	ENGINEERED MUTATION	UNP P29476

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



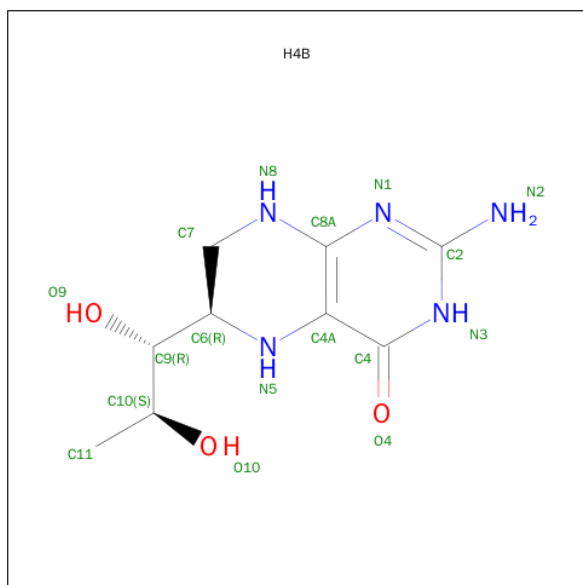
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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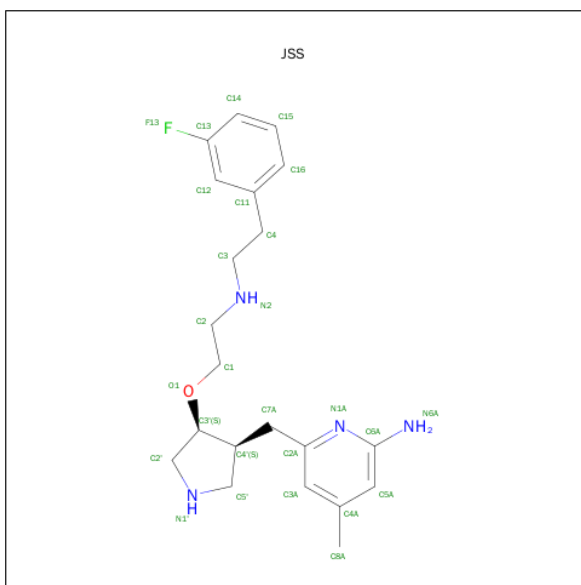
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



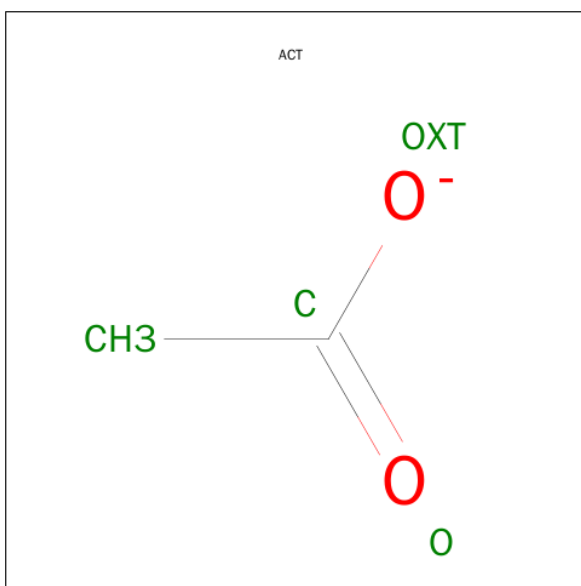
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is 6-[[[(3S,4S)-4-(2-[[2-(3-FLUOROPHENYL)ETHYL]AMINO}ETHOXY)PYRROLIDIN-3-YL]METHYL]-4-METHYLPYRIDIN-2-AMINE (three-letter code: JSS) (formula: $C_{21}H_{29}FN_4O$).



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

- 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 1	Zn 1	0	0

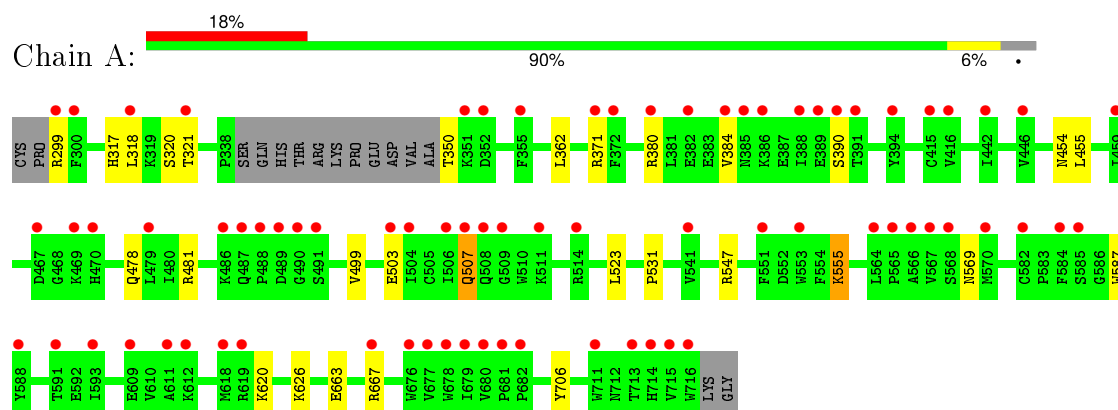
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	148	Total 148	O 148	0	0
7	B	227	Total 227	O 227	0	0

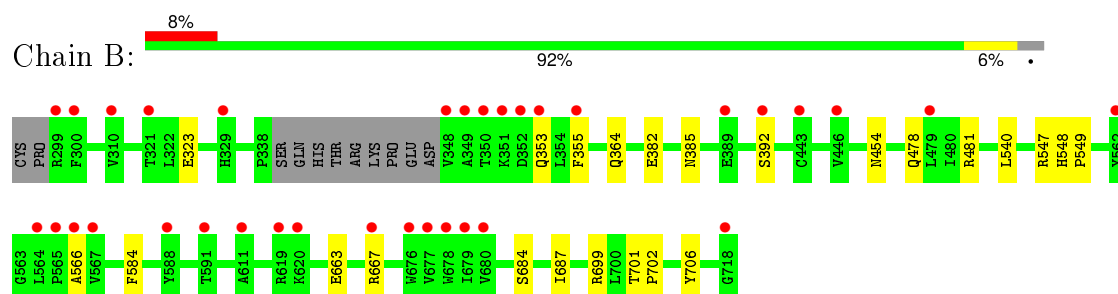
3 Residue-property plots [i](#)

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 ($RSRZ > 2$). 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	52.06Å 112.14Å 164.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.96 – 2.02 40.96 – 2.02	Depositor EDS
% Data completeness (in resolution range)	98.7 (40.96-2.02) 98.7 (40.96-2.02)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.174 , 0.211 0.195 , 0.222	Depositor DCC
R_{free} test set	3190 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	39.1	Xtriage
Anisotropy	0.287	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 62922 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7210	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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, JSS, 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	0.65	0/3406	0.64	0/4621
1	B	0.70	0/3432	0.67	0/4654
All	All	0.68	0/6838	0.66	0/9275

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	3313	0	3221	13	0
1	B	3339	0	3251	11	0
2	A	43	0	30	3	0
2	B	43	0	30	4	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	27	0	29	1	0
4	B	27	0	29	1	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	148	0	0	0	0
7	B	227	0	0	0	0
All	All	7210	0	6626	27	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 2.

All (27) 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:706:TYR:OH	2:B:750:HEM:O1D	1.96	0.81
2:A:750:HEM:HHC	2:A:750:HEM:HBB2	1.67	0.74
1:A:706:TYR:OH	2:A:750:HEM:O1D	2.05	0.73
2:A:750:HEM:HBA1	4:A:800:JSS:H7AA	1.87	0.55
1:B:663:GLU:HB3	1:B:667:ARG:NH1	2.23	0.54
1:B:355:PHE:CE1	1:B:385:ASN:HB2	2.43	0.54
1:A:499:VAL:O	1:A:503:GLU:HG3	2.09	0.53
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.92	0.52
1:A:362:LEU:HD11	1:A:384:VAL:HG21	1.93	0.50
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.95	0.48
1:A:663:GLU:O	1:A:667:ARG:HG2	2.14	0.46
1:A:626:LYS:HB3	1:B:687:ILE:HD12	1.98	0.46
2:B:750:HEM:HBA1	4:B:800:JSS:H7AA	1.98	0.45
1:A:299:ARG:O	1:A:317:HIS:CE1	2.69	0.45
1:A:455:LEU:HD12	1:A:587:TRP:CB	2.47	0.45
1:B:584:PHE:CD1	2:B:750:HEM:CAC	3.00	0.45
1:B:548:HIS:CG	1:B:549:PRO:HD2	2.54	0.43
1:A:299:ARG:HG3	1:A:318:LEU:HD11	2.00	0.43
1:B:478:GLN:HB2	1:B:481:ARG:HG3	2.01	0.42
1:A:507:GLN:O	1:A:507:GLN:HG2	2.18	0.42
1:B:684:SER:HB3	1:B:687:ILE:HG12	2.01	0.42
1:B:701:THR:HA	1:B:702:PRO:C	2.40	0.41
1:A:555:LYS:HB3	1:A:555:LYS:NZ	2.35	0.41
1:B:566:ALA:HA	1:B:584:PHE:O	2.21	0.41
2:B:750:HEM:HBB2	2:B:750:HEM:HHC	2.02	0.41
1:A:455:LEU:HD12	1:A:587:TRP:HB3	2.02	0.41
1:B:323:GLU:O	1:B:699:ARG:HD3	2.21	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%)	395 (98%)	8 (2%)	0	100	100
1	B	407/422 (96%)	403 (99%)	4 (1%)	0	100	100
All	All	810/844 (96%)	798 (98%)	12 (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	363/376 (96%)	351 (97%)	12 (3%)	45	42
1	B	365/376 (97%)	358 (98%)	7 (2%)	65	66
All	All	728/752 (97%)	709 (97%)	19 (3%)	54	53

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	320	SER
1	A	321	THR
1	A	350	THR
1	A	371	ARG
1	A	380	ARG
1	A	390	SER
1	A	454	ASN
1	A	507	GLN

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Mol	Chain	Res	Type
1	A	547	ARG
1	A	555	LYS
1	A	569	ASN
1	A	620	LYS
1	B	353	GLN
1	B	364	GLN
1	B	382	GLU
1	B	392	SER
1	B	454	ASN
1	B	540	LEU
1	B	547	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	454	ASN
1	A	507	GLN
1	A	527	ASN
1	A	569	ASN
1	A	605	ASN
1	A	642	GLN
1	A	697	ASN
1	B	454	ASN
1	B	507	GLN
1	B	508	GLN
1	B	529	ASN
1	B	535	GLN
1	B	601	ASN
1	B	605	ASN
1	B	628	GLN
1	B	642	GLN
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 [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	750	1	30,50,50	2.28	10 (33%)	24,82,82	2.59	11 (45%)
3	H4B	A	760	-	13,18,18	0.95	0	11,26,26	2.46	6 (54%)
4	JSS	A	800	-	26,29,29	0.69	0	27,38,38	1.33	3 (11%)
5	ACT	A	860	-	1,3,3	1.18	0	0,3,3	0.00	-
2	HEM	B	750	1	30,50,50	2.02	9 (30%)	24,82,82	2.38	12 (50%)
3	H4B	B	760	-	13,18,18	1.00	1 (7%)	11,26,26	2.65	5 (45%)
4	JSS	B	800	-	26,29,29	0.79	0	27,38,38	1.56	2 (7%)
5	ACT	B	860	-	1,3,3	1.13	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	-	0/10/54/54	0/0/8/8
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2
4	JSS	A	800	-	-	0/13/23/23	0/3/3/3
5	ACT	A	860	-	-	0/0/0/0	0/0/0/0
2	HEM	B	750	1	-	0/10/54/54	0/0/8/8
3	H4B	B	760	-	-	0/8/17/17	0/2/2/2
4	JSS	B	800	-	-	0/13/23/23	0/3/3/3
5	ACT	B	860	-	-	0/0/0/0	0/0/0/0

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C3D-C4D	-6.38	1.43	1.51
2	A	750	HEM	C3B-C4B	-5.83	1.46	1.51
2	B	750	HEM	C3B-C4B	-5.69	1.46	1.51
2	B	750	HEM	C3D-C4D	-4.76	1.45	1.51
2	A	750	HEM	C2C-C1C	-3.98	1.45	1.52
2	B	750	HEM	C2C-C1C	-3.53	1.45	1.52
2	B	750	HEM	C2B-C1B	-2.25	1.44	1.51
2	A	750	HEM	C2D-C1D	-2.12	1.44	1.51
2	B	750	HEM	C2D-C1D	-2.05	1.45	1.51
2	A	750	HEM	C2B-C1B	-2.05	1.45	1.51
2	A	750	HEM	CMA-C3A	2.21	1.56	1.51
2	B	750	HEM	CAA-C2A	2.23	1.55	1.52
2	B	750	HEM	C1C-NC	2.23	1.38	1.36
2	B	750	HEM	C3C-CAC	2.40	1.55	1.51
2	A	750	HEM	FE-NB	2.49	2.10	1.97
2	B	750	HEM	FE-ND	2.55	2.11	1.97
2	A	750	HEM	FE-NC	2.57	2.05	1.95
3	B	760	H4B	C7-N8	2.60	1.49	1.46
2	A	750	HEM	FE-ND	2.90	2.12	1.97
2	A	750	HEM	C1C-NC	3.16	1.39	1.36

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	750	HEM	CBD-CAD-C3D	-4.20	101.33	113.55
4	B	800	JSS	C3A-C2A-N1A	-3.74	118.73	122.96
2	A	750	HEM	CAA-C2A-C1A	-3.54	123.17	127.01
4	A	800	JSS	C3A-C2A-N1A	-3.33	119.20	122.96
3	A	760	H4B	N3-C2-N1	-3.19	120.30	125.53
2	B	750	HEM	C3C-CAC-CBC	-3.00	119.85	124.46
2	A	750	HEM	CMA-C3A-C4A	-2.48	124.26	128.36
2	B	750	HEM	CAA-C2A-C1A	-2.47	124.33	127.01
3	B	760	H4B	N3-C2-N1	-2.42	121.56	125.53
2	A	750	HEM	C3B-C4B-NB	-2.34	107.16	111.63
2	B	750	HEM	CBD-CAD-C3D	-2.31	106.82	113.55
2	B	750	HEM	C3B-C4B-NB	-2.13	107.55	111.63
2	B	750	HEM	CMA-C3A-C4A	-2.10	124.90	128.36
3	A	760	H4B	C4A-C8A-N8	2.00	120.79	118.43
3	B	760	H4B	C2-N1-C8A	2.02	119.07	114.54
3	A	760	H4B	N2-C2-N3	2.06	120.61	117.20
4	A	800	JSS	C3-N2-C2	2.18	121.09	113.35
3	A	760	H4B	C2-N1-C8A	2.42	119.99	114.54
2	B	750	HEM	C2D-C3D-C4D	2.54	105.80	101.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	750	HEM	C2D-C3D-C4D	2.61	105.93	101.50
3	B	760	H4B	C4A-C8A-N8	2.73	121.64	118.43
2	A	750	HEM	CMD-C2D-C3D	2.95	127.39	114.35
2	B	750	HEM	CMD-C2D-C3D	3.01	127.66	114.35
2	B	750	HEM	C3B-C4B-CHC	3.08	127.50	123.16
2	A	750	HEM	C3B-C4B-CHC	3.32	127.83	123.16
2	B	750	HEM	CMB-C2B-C3B	3.52	125.31	116.53
4	A	800	JSS	C6A-N1A-C2A	3.83	120.95	118.23
3	A	760	H4B	C4-N3-C2	3.95	121.42	115.94
2	A	750	HEM	CAD-C3D-C4D	3.99	126.56	112.47
3	B	760	H4B	C4-N3-C2	4.13	121.67	115.94
2	B	750	HEM	CMC-C2C-C3C	4.19	126.98	116.53
2	B	750	HEM	CAD-C3D-C4D	4.36	127.86	112.47
2	A	750	HEM	CMB-C2B-C3B	4.50	127.77	116.53
2	B	750	HEM	CAD-C3D-C2D	4.56	126.32	113.22
4	B	800	JSS	C6A-N1A-C2A	4.66	121.54	118.23
2	A	750	HEM	CMC-C2C-C3C	4.78	128.47	116.53
2	A	750	HEM	CAD-C3D-C2D	4.94	127.43	113.22
3	A	760	H4B	C4-C4A-C8A	5.00	119.08	114.56
3	B	760	H4B	C4-C4A-C8A	6.17	120.15	114.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	750	HEM	3	0
4	A	800	JSS	1	0
2	B	750	HEM	4	0
4	B	800	JSS	1	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%)	0.93	75 (18%) 2 2	30, 54, 102, 128	0
1	B	411/422 (97%)	0.43	34 (8%) 14 15	29, 44, 69, 93	0
All	All	818/844 (96%)	0.68	109 (13%) 4 5	29, 48, 94, 128	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	716	TRP	8.2
1	B	300	PHE	7.1
1	A	506	ILE	5.5
1	B	350	THR	5.3
1	A	390	SER	5.0
1	A	355	PHE	4.9
1	B	348	VAL	4.8
1	A	486	LYS	4.8
1	A	389	GLU	4.7
1	A	488	PRO	4.5
1	A	567	VAL	4.2
1	A	352	ASP	4.2
1	A	714	HIS	4.1
1	B	349	ALA	4.1
1	A	619	ARG	4.1
1	B	619	ARG	4.0
1	B	351	LYS	3.9
1	A	611	ALA	3.8
1	A	715	VAL	3.8
1	A	678	TRP	3.7
1	B	299	ARG	3.7
1	B	677	VAL	3.7
1	A	479	LEU	3.6
1	A	677	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	487	GLN	3.5
1	B	718	GLY	3.5
1	A	553	TRP	3.4
1	A	491	SER	3.4
1	B	567	VAL	3.4
1	A	713	THR	3.4
1	A	388	ILE	3.4
1	B	321	THR	3.3
1	A	514	ARG	3.3
1	B	389	GLU	3.1
1	A	490	GLY	3.1
1	A	566	ALA	3.0
1	A	386	LYS	3.0
1	A	584	PHE	3.0
1	A	507	GLN	2.9
1	B	352	ASP	2.9
1	A	591	THR	2.9
1	A	351	LYS	2.9
1	A	682	PRO	2.9
1	A	551	PHE	2.8
1	A	679	ILE	2.8
1	A	711	TRP	2.8
1	A	503	GLU	2.8
1	B	446	VAL	2.8
1	B	566	ALA	2.7
1	A	489	ASP	2.7
1	A	382	GLU	2.7
1	A	299	ARG	2.6
1	B	479	LEU	2.6
1	A	415	CYS	2.6
1	A	667	ARG	2.6
1	A	446	VAL	2.6
1	A	511	LYS	2.6
1	A	582	CYS	2.5
1	B	355	PHE	2.5
1	A	470	HIS	2.5
1	B	620	LYS	2.5
1	A	300	PHE	2.5
1	A	508	GLN	2.5
1	A	318	LEU	2.5
1	B	564	LEU	2.5
1	A	593	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	676	TRP	2.5
1	A	609	GLU	2.4
1	B	611	ALA	2.4
1	B	678	TRP	2.4
1	A	565	PRO	2.4
1	A	681	PRO	2.4
1	A	321	THR	2.4
1	A	391	THR	2.4
1	A	469	LYS	2.3
1	A	385	ASN	2.3
1	B	591	THR	2.3
1	B	667	ARG	2.3
1	A	588	TYR	2.3
1	A	568	SER	2.3
1	B	392	SER	2.3
1	A	564	LEU	2.3
1	A	416	VAL	2.3
1	A	618	MET	2.3
1	A	442	ILE	2.3
1	A	372	PHE	2.2
1	A	394	TYR	2.2
1	A	585	SER	2.2
1	A	371	ARG	2.2
1	A	384	VAL	2.2
1	B	329	HIS	2.2
1	A	459	ILE	2.1
1	B	353	GLN	2.1
1	A	680	VAL	2.1
1	B	565	PRO	2.1
1	A	570	MET	2.1
1	A	380	ARG	2.1
1	A	612	LYS	2.1
1	B	588	TYR	2.1
1	A	504	ILE	2.1
1	B	562	TYR	2.1
1	A	541	VAL	2.1
1	B	310	VAL	2.1
1	B	443	CYS	2.1
1	B	680	VAL	2.1
1	A	509	GLY	2.0
1	A	467	ASP	2.0
1	B	676	TRP	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	679	ILE	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	B	860	4/4	0.97	0.17	5.29	62,63,63,63	0
5	ACT	A	860	4/4	0.94	0.17	1.57	72,72,73,74	0
4	JSS	B	800	27/27	0.95	0.22	0.96	32,38,55,57	0
4	JSS	A	800	27/27	0.94	0.26	0.81	29,41,65,69	0
3	H4B	B	760	17/17	0.97	0.21	0.78	32,36,37,38	0
3	H4B	A	760	17/17	0.96	0.21	0.64	35,39,44,44	0
2	HEM	A	750	43/43	0.97	0.22	0.62	29,34,48,50	0
2	HEM	B	750	43/43	0.97	0.18	0.53	31,35,44,48	0
6	ZN	A	900	1/1	0.99	0.10	-0.52	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.