



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2017 – 06:55 PM EDT

PDB ID : 3JT8
Title : Structure of neuronal nitric oxide synthase heme domain complexed with N 5
-{3-[(1-methylethyl)sulfanyl]propanimidoyl}-L-ornithine
Authors : Li, H.; Poulos, T.L.
Deposited on : unknown
Resolution : 1.95 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

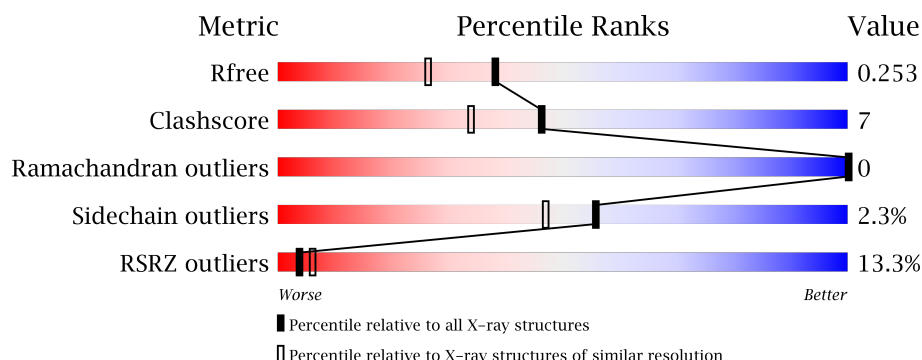
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	100719	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (1.96-1.96)

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	<div> <div>19%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>• •</div> </div> </div>
1	B	422	<div> <div>7%</div> <div> <div></div> <div>90%</div> <div>8%</div> <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
4	JM4	A	800[A]	-	-	X	X
4	JM4	A	800[B]	-	-	X	X
4	JM4	B	800[A]	-	-	X	X
4	JM4	B	800[B]	-	-	X	X
5	ACT	A	860	-	-	-	X
5	ACT	B	860	-	-	-	X

2 Entry composition [i](#)

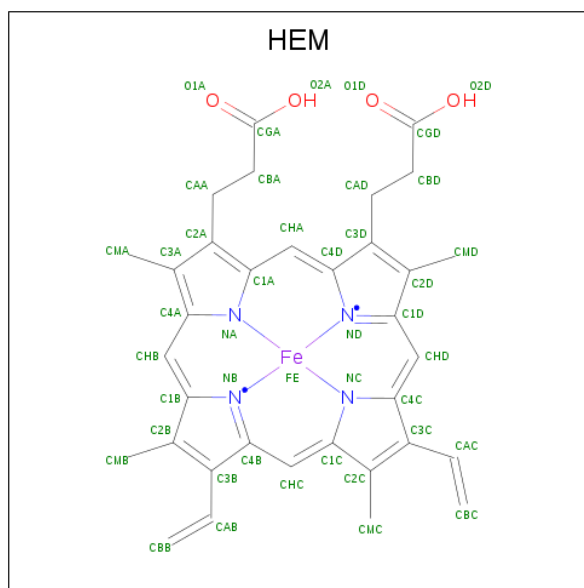
There are 7 unique types of molecules in this entry. The entry contains 7241 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			3319	2125	566	606	22			
1	B	411	Total	C	N	O	S	0	3	0
			3354	2146	574	612	22			

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



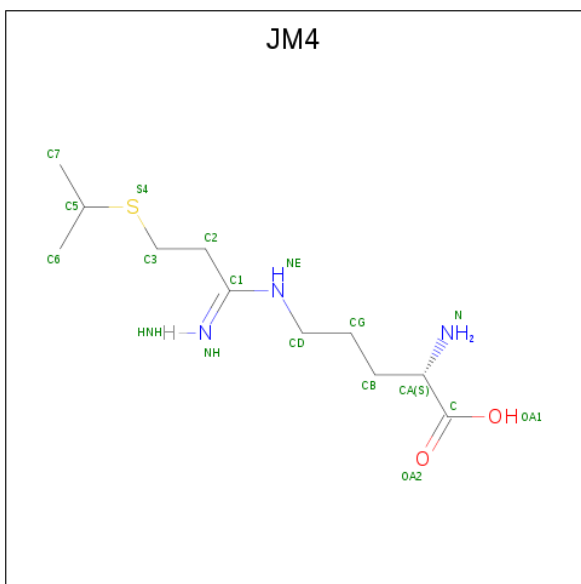
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- 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 N 5 -{3-[(1-methylethyl)sulfanyl]propanimidoyl}-L-ornithine (three-letter code: JM4) (formula: C₁₁H₂₃N₃O₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	1
			29	20	5	2	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	1
			29	20	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		

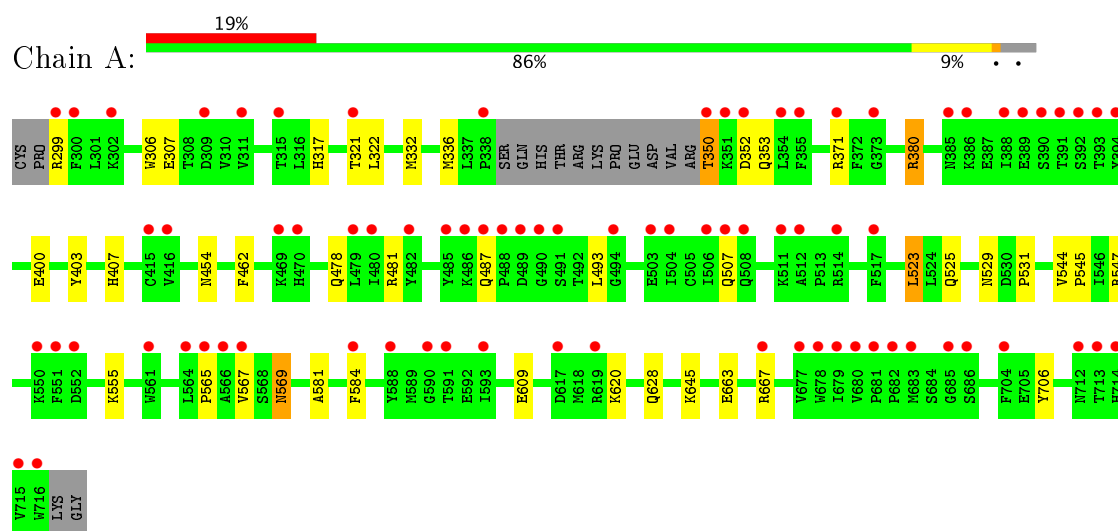
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	151	Total	O	0	0
			151	151		
7	B	230	Total	O	0	0
			230	230		

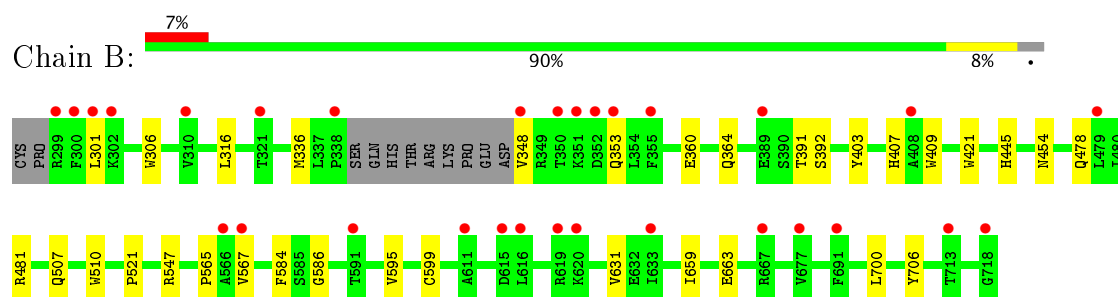
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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, α , β , γ	52.19Å 111.37Å 164.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.11 – 1.95 37.82 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.0 (38.11-1.95) 99.0 (37.82-1.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 1.95Å)	Xtriage
Refinement program	CNS, REFMAC 5.5.0089	Depositor
R, R_{free}	0.187 , 0.222 0.223 , 0.253	Depositor DCC
R_{free} test set	3483 reflections (5.22%)	DCC
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7241	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 4.37% 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, 0.333 respectively for untwinned datasets, and 0.375, 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, JM4, 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	0.54	0/3418	0.61	0/4637
1	B	0.61	0/3456	0.61	0/4685
All	All	0.58	0/6874	0.61	0/9322

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	3319	0	3231	32	0
1	B	3354	0	3274	31	0
2	A	43	0	30	6	0
2	B	43	0	30	4	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	29	0	38	33	0
4	B	29	0	38	27	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	151	0	0	2	0
7	B	230	0	0	4	0
All	All	7241	0	6677	98	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 7.

All (98) 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)
4:B:800[B]:JM4:NE	4:B:800[B]:JM4:H6B	1.39	1.32
4:A:800[B]:JM4:C1	4:A:800[B]:JM4:H6B	1.70	1.21
4:A:800[B]:JM4:H6B	4:A:800[B]:JM4:C2	1.75	1.17
4:B:800[B]:JM4:NE	4:B:800[B]:JM4:C6	2.08	1.16
1:A:565:PRO:HB2	4:A:800[B]:JM4:H2A	1.28	1.10
4:B:800[B]:JM4:CD	4:B:800[B]:JM4:H6B	1.81	1.10
4:B:800[B]:JM4:H6A	4:B:800[B]:JM4:C1	1.80	1.10
4:A:800[B]:JM4:C6	4:A:800[B]:JM4:C2	2.34	1.03
4:A:800[B]:JM4:C6	4:A:800[B]:JM4:C1	2.35	1.02
4:B:800[B]:JM4:C6	4:B:800[B]:JM4:C1	2.38	1.01
4:A:800[B]:JM4:H6B	4:A:800[B]:JM4:H2	1.42	1.01
1:B:584:PHE:CE1	4:B:800[B]:JM4:H7B	2.01	0.96
1:B:584:PHE:HE1	4:B:800[B]:JM4:H7B	1.34	0.86
4:B:800[B]:JM4:HDA	4:B:800[B]:JM4:H6B	1.60	0.83
4:A:800[B]:JM4:CD	4:A:800[B]:JM4:H6B	2.08	0.82
1:B:586:GLY:H	4:B:800[B]:JM4:H3	1.49	0.77
4:A:800[B]:JM4:HD	4:A:800[B]:JM4:H6B	1.66	0.77
4:A:800[B]:JM4:H6B	4:A:800[B]:JM4:NE	1.99	0.76
1:A:567:VAL:HG21	4:A:800[A]:JM4:H6	1.69	0.73
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.71	0.71
1:A:584:PHE:CE1	4:A:800[B]:JM4:H7B	2.26	0.71
1:B:565:PRO:HB2	4:B:800[B]:JM4:H2	1.73	0.69
1:A:350:THR:N	1:A:353:GLN:HE21	1.93	0.66
1:A:584:PHE:HE1	4:A:800[B]:JM4:H7B	1.58	0.65
4:A:800[A]:JM4:HDA	4:A:800[A]:JM4:H6B	1.79	0.65
1:A:307:GLU:HG3	7:B:1069:HOH:O	1.98	0.63
4:A:800[B]:JM4:H6A	4:A:800[B]:JM4:C1	2.25	0.62
4:B:800[B]:JM4:HNE	4:B:800[B]:JM4:H6B	1.56	0.62
1:B:565:PRO:HG2	4:B:800[B]:JM4:H2A	1.83	0.61
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.82	0.61
1:B:584:PHE:HE1	4:B:800[A]:JM4:H5	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:565:PRO:CB	4:A:800[B]:JM4:H2A	2.19	0.61
1:B:584:PHE:HE1	4:B:800[B]:JM4:C7	2.11	0.61
2:B:750:HEM:C4D	4:B:800[A]:JM4:H6A	2.36	0.60
4:A:800[A]:JM4:H7A	4:A:800[A]:JM4:CD	2.31	0.60
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.86	0.57
1:A:663:GLU:O	1:A:667:ARG:HG2	2.04	0.56
2:B:750:HEM:C4B	4:B:800[A]:JM4:H3A	2.40	0.56
1:A:584:PHE:HE1	4:A:800[A]:JM4:H5	1.70	0.56
1:B:565:PRO:HG2	4:B:800[B]:JM4:C2	2.35	0.56
2:A:750:HEM:C4B	4:A:800[A]:JM4:H3A	2.41	0.55
4:B:800[A]:JM4:HDA	4:B:800[A]:JM4:H6B	1.88	0.55
1:A:567:VAL:HG21	4:A:800[B]:JM4:H7A	1.88	0.55
1:A:565:PRO:HG2	4:A:800[A]:JM4:H2A	1.89	0.54
1:A:567:VAL:HG21	4:A:800[A]:JM4:C6	2.37	0.54
1:B:567:VAL:HG21	4:B:800[A]:JM4:H6	1.88	0.53
4:A:800[A]:JM4:H7A	4:A:800[A]:JM4:H2	1.90	0.53
4:B:800[B]:JM4:C6	4:B:800[B]:JM4:HNE	2.17	0.53
1:A:380:ARG:HD3	1:A:400:GLU:OE1	2.10	0.52
1:A:299:ARG:O	1:A:317:HIS:CE1	2.63	0.52
2:A:750:HEM:HBB2	2:A:750:HEM:HHC	1.93	0.51
4:A:800[A]:JM4:H7A	4:A:800[A]:JM4:HDA	1.91	0.51
2:A:750:HEM:CMC	2:A:750:HEM:HBC2	2.41	0.51
4:A:800[A]:JM4:H7A	4:A:800[A]:JM4:HD	1.93	0.50
1:A:567:VAL:CG2	4:A:800[B]:JM4:H7A	2.43	0.49
2:A:750:HEM:HMC1	2:A:750:HEM:HBC2	1.94	0.49
1:B:364:GLN:NE2	7:B:1218:HOH:O	2.26	0.49
2:B:750:HEM:HHC	2:B:750:HEM:HBB2	1.94	0.49
2:A:750:HEM:C4D	4:A:800[A]:JM4:H6A	2.47	0.49
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.01	0.49
1:B:391:THR:O	1:B:392:SER:HB2	2.13	0.48
1:B:567:VAL:HG21	4:B:800[A]:JM4:C6	2.43	0.48
1:B:507:GLN:NE2	7:B:1079:HOH:O	2.46	0.48
1:A:332:MET:HE3	1:B:301:LEU:HD22	1.95	0.47
1:B:445:HIS:C	1:B:445:HIS:CD2	2.88	0.47
1:A:336:MET:HG3	1:B:306:TRP:NE1	2.29	0.47
4:A:800[B]:JM4:H7A	4:A:800[B]:JM4:HD	1.96	0.46
1:B:595:VAL:O	1:B:599:CYS:HB2	2.16	0.46
1:B:706:TYR:OH	2:B:750:HEM:O1D	2.22	0.46
1:A:569:ASN:H	1:A:569:ASN:HD22	1.63	0.46
1:A:609:GLU:HG3	7:A:1148:HOH:O	2.16	0.45
4:A:800[A]:JM4:H3	4:A:800[A]:JM4:H7B	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.52	0.45
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.05	0.45
1:A:493:LEU:HA	7:A:1103:HOH:O	2.17	0.45
4:A:800[B]:JM4:HD	4:A:800[B]:JM4:H2	1.76	0.45
1:A:706:TYR:OH	2:A:750:HEM:O1D	2.26	0.44
1:B:586:GLY:N	4:B:800[B]:JM4:H3	2.25	0.44
4:B:800[A]:JM4:H7B	4:B:800[A]:JM4:H3	1.68	0.44
1:A:321:THR:HG23	1:A:322:LEU:HG	2.00	0.44
4:A:800[B]:JM4:HBA	4:A:800[B]:JM4:HNE	1.61	0.44
4:A:800[A]:JM4:H2	4:A:800[A]:JM4:C7	2.48	0.43
1:B:565:PRO:HG2	4:B:800[A]:JM4:H2A	2.01	0.43
1:B:567:VAL:HG21	4:B:800[B]:JM4:H7A	2.00	0.43
1:B:510:TRP:CE2	1:B:521:PRO:HD3	2.53	0.43
1:B:348:VAL:HG12	7:B:1168:HOH:O	2.19	0.43
1:A:628:GLN:HG2	1:B:631:VAL:HG11	2.00	0.43
1:B:316:LEU:HD21	1:B:700:LEU:HD11	2.01	0.42
1:B:567:VAL:CG2	4:B:800[B]:JM4:H7A	2.50	0.42
1:A:306:TRP:CD2	1:B:336:MET:HE3	2.54	0.42
1:A:525:GLN:HG3	1:A:529:ASN:O	2.19	0.42
1:A:350:THR:N	1:A:353:GLN:NE2	2.66	0.41
1:A:567:VAL:CG2	4:A:800[A]:JM4:H6	2.43	0.41
1:A:462:PHE:HB2	1:A:581:ALA:HB3	2.03	0.41
4:B:800[A]:JM4:HDA	4:B:800[A]:JM4:H7A	2.03	0.40
1:A:544:VAL:HA	1:A:545:PRO:HD2	1.93	0.40
4:A:800[B]:JM4:H6A	4:A:800[B]:JM4:NH	2.37	0.40
1:B:659:ILE:O	1:B:663:GLU:HG3	2.22	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%)	396 (98%)	9 (2%)	0	100	100
1	B	410/422 (97%)	402 (98%)	8 (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%)	352 (96%)	13 (4%)	40	26
1	B	369/377 (98%)	365 (99%)	4 (1%)	78	75
All	All	734/754 (97%)	717 (98%)	17 (2%)	56	47

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	371	ARG
1	A	380	ARG
1	A	454	ASN
1	A	487	GLN
1	A	507	GLN
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	B	353	GLN
1	B	360	GLU
1	B	454	ASN
1	B	547	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	385	ASN
1	A	454	ASN
1	A	508	GLN
1	A	569	ASN
1	A	628	GLN
1	A	642	GLN
1	A	697	ASN
1	B	454	ASN
1	B	507	GLN
1	B	508	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 [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 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	A	750	1	28,50,50	2.16	7 (25%)	17,82,82	2.22	5 (29%)
3	H4B	A	760	-	14,18,18	0.87	0	12,26,26	2.55	6 (50%)
4	JM4	A	800[A]	-	10,16,16	6.73	3 (30%)	7,19,19	0.89	0
4	JM4	A	800[B]	-	10,16,16	6.85	3 (30%)	7,19,19	0.82	0
5	ACT	A	860	-	1,3,3	1.49	0	0,3,3	0.00	-
2	HEM	B	750	1	28,50,50	2.24	9 (32%)	17,82,82	2.13	3 (17%)
3	H4B	B	760	-	14,18,18	1.07	1 (7%)	12,26,26	2.42	5 (41%)
4	JM4	B	800[A]	-	10,16,16	6.57	3 (30%)	7,19,19	0.78	0
4	JM4	B	800[B]	-	10,16,16	6.80	3 (30%)	7,19,19	0.76	0
5	ACT	B	860	-	1,3,3	1.33	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	-	0/6/54/54	0/0/8/8
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2
4	JM4	A	800[A]	-	-	0/12/17/17	0/0/0/0
4	JM4	A	800[B]	-	-	0/12/17/17	0/0/0/0
5	ACT	A	860	-	-	0/0/0/0	0/0/0/0
2	HEM	B	750	1	-	0/6/54/54	0/0/8/8
3	H4B	B	760	-	-	0/8/17/17	0/2/2/2
4	JM4	B	800[A]	-	-	0/12/17/17	0/0/0/0
4	JM4	B	800[B]	-	-	0/12/17/17	0/0/0/0
5	ACT	B	860	-	-	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)
4	A	800[B]	JM4	C2-C1	-21.02	1.34	1.51
4	B	800[B]	JM4	C2-C1	-20.94	1.34	1.51
4	A	800[A]	JM4	C2-C1	-20.66	1.34	1.51
4	B	800[A]	JM4	C2-C1	-20.27	1.34	1.51
2	A	750	HEM	C3B-C2B	-4.94	1.33	1.40
2	B	750	HEM	C3B-C2B	-4.59	1.34	1.40
2	B	750	HEM	C3C-C2C	-4.43	1.34	1.40
4	A	800[B]	JM4	C3-S4	-4.25	1.75	1.81
4	A	800[A]	JM4	C3-S4	-4.24	1.75	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	800[B]	JM4	C3-S4	-3.99	1.76	1.81
4	B	800[A]	JM4	C3-S4	-3.39	1.77	1.81
2	A	750	HEM	C3C-C2C	-3.25	1.36	1.40
2	B	750	HEM	CMB-C2B	2.00	1.55	1.51
2	B	750	HEM	CMD-C2D	2.09	1.55	1.51
2	B	750	HEM	CMC-C2C	2.13	1.56	1.51
4	A	800[A]	JM4	C1-NH	2.27	1.33	1.27
4	B	800[B]	JM4	C1-NH	2.36	1.33	1.27
3	B	760	H4B	C4-N3	2.38	1.37	1.33
4	B	800[A]	JM4	C1-NH	2.43	1.33	1.27
2	A	750	HEM	C1B-NB	2.47	1.39	1.36
2	A	750	HEM	C1C-NC	2.57	1.39	1.36
4	A	800[B]	JM4	C1-NH	2.78	1.34	1.27
2	A	750	HEM	C3C-CAC	3.13	1.54	1.47
2	B	750	HEM	C4D-ND	3.28	1.40	1.36
2	B	750	HEM	C3B-CAB	3.40	1.54	1.47
2	A	750	HEM	C3B-CAB	3.55	1.54	1.47
2	B	750	HEM	C3C-CAC	3.61	1.54	1.47
2	B	750	HEM	C3D-C2D	4.54	1.51	1.37
2	A	750	HEM	C3D-C2D	5.15	1.52	1.37

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	750	HEM	CBA-CAA-C2A	-5.97	101.06	112.48
2	A	750	HEM	CBA-CAA-C2A	-5.07	102.78	112.48
2	A	750	HEM	CBD-CAD-C3D	-4.44	103.99	112.47
2	B	750	HEM	CBD-CAD-C3D	-4.34	104.19	112.47
3	B	760	H4B	N3-C2-N1	-3.50	119.78	125.45
3	A	760	H4B	N3-C2-N1	-3.49	119.79	125.45
2	A	750	HEM	C1D-C2D-C3D	-2.55	105.22	107.00
2	B	750	HEM	C1D-C2D-C3D	-2.40	105.33	107.00
3	A	760	H4B	C4A-N5-C6	-2.02	115.66	121.16
3	B	760	H4B	N2-C2-N3	2.31	120.93	117.24
3	A	760	H4B	N2-C2-N3	2.48	121.21	117.24
3	B	760	H4B	C2-N1-C8A	2.67	120.52	114.51
2	A	750	HEM	C4C-C3C-C2C	2.77	108.83	106.90
2	A	750	HEM	CMC-C2C-C3C	2.98	130.42	124.89
3	A	760	H4B	C2-N1-C8A	3.21	121.74	114.51
3	A	760	H4B	C4-N3-C2	3.58	121.21	116.06
3	B	760	H4B	C4-N3-C2	3.87	121.62	116.06
3	B	760	H4B	C4-C4A-C8A	4.39	118.54	114.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	760	H4B	C4-C4A-C8A	4.92	119.02	114.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 66 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	750	HEM	6	0
4	A	800[A]	JM4	14	0
4	A	800[B]	JM4	19	0
2	B	750	HEM	4	0
4	B	800[A]	JM4	9	0
4	B	800[B]	JM4	18	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%)	1.08	79 (19%) 1 1	25, 52, 94, 123	0
1	B	411/422 (97%)	0.55	30 (7%) 16 25	25, 40, 63, 81	0
All	All	818/844 (96%)	0.81	109 (13%) 4 6	25, 45, 88, 123	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	PHE	8.8
1	A	716	TRP	7.5
1	A	715	VAL	7.5
1	A	352	ASP	6.7
1	A	355	PHE	6.4
1	B	348	VAL	5.9
1	B	718	GLY	5.3
1	A	488	PRO	5.0
1	A	486	LYS	4.7
1	A	351	LYS	4.7
1	A	300	PHE	4.4
1	A	350	THR	4.2
1	A	507	GLN	4.1
1	B	619	ARG	4.0
1	A	390	SER	4.0
1	A	619	ARG	3.9
1	A	388	ILE	3.8
1	B	299	ARG	3.8
1	A	511	LYS	3.8
1	A	506	ILE	3.7
1	A	514	ARG	3.7
1	B	352	ASP	3.7
1	A	712	ASN	3.6
1	A	392	SER	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	350	THR	3.6
1	A	678	TRP	3.6
1	A	491	SER	3.6
1	A	667	ARG	3.6
1	A	593	ILE	3.6
1	A	503	GLU	3.5
1	B	338	PRO	3.4
1	A	489	ASP	3.4
1	A	299	ARG	3.4
1	A	386	LYS	3.3
1	A	385	ASN	3.3
1	A	567	VAL	3.3
1	A	490	GLY	3.3
1	A	714	HIS	3.2
1	A	485	TYR	3.2
1	A	487	GLN	3.2
1	A	389	GLU	3.1
1	B	620	LYS	3.1
1	B	615	ASP	3.1
1	A	394	TYR	3.0
1	B	310	VAL	3.0
1	A	504	ILE	2.9
1	A	584	PHE	2.9
1	A	469	LYS	2.9
1	B	351	LYS	2.9
1	A	680	VAL	2.9
1	B	389	GLU	2.9
1	B	616	LEU	2.9
1	A	551	PHE	2.9
1	B	355	PHE	2.9
1	A	338	PRO	2.9
1	A	508	GLN	2.8
1	A	470	HIS	2.8
1	A	588	TYR	2.8
1	B	321	THR	2.8
1	A	679	ILE	2.7
1	A	321	THR	2.7
1	A	565	PRO	2.7
1	A	391	THR	2.7
1	B	567	VAL	2.6
1	A	713	THR	2.6
1	A	494	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	704	PHE	2.6
1	B	667	ARG	2.6
1	A	591	THR	2.6
1	B	566	ALA	2.5
1	A	682	PRO	2.5
1	B	611	ALA	2.5
1	A	479	LEU	2.5
1	A	393	THR	2.5
1	A	677	VAL	2.4
1	B	677	VAL	2.4
1	A	517	PHE	2.4
1	A	415	CYS	2.4
1	A	686	SER	2.4
1	B	591	THR	2.4
1	B	408	ALA	2.4
1	A	552	ASP	2.3
1	A	550	LYS	2.3
1	A	564	LEU	2.3
1	A	681	PRO	2.3
1	A	302	LYS	2.3
1	A	315	THR	2.3
1	A	617	ASP	2.2
1	A	590	GLY	2.2
1	B	302	LYS	2.2
1	B	301	LEU	2.2
1	A	482	TYR	2.2
1	A	309	ASP	2.2
1	B	479	LEU	2.2
1	B	353	GLN	2.2
1	A	371	ARG	2.1
1	A	373	GLY	2.1
1	A	566	ALA	2.1
1	A	512	ALA	2.1
1	A	416	VAL	2.1
1	A	480	ILE	2.1
1	A	685	GLY	2.1
1	A	354	LEU	2.1
1	B	713	THR	2.0
1	B	633	ILE	2.0
1	A	311	VAL	2.0
1	B	691	PHE	2.0
1	A	561	TRP	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	683	MET	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	0.95	0.15	5.68	50,50,51,51	0
5	ACT	A	860	4/4	0.95	0.19	2.73	65,67,67,68	0
4	JM4	A	800[A]	17/17	0.84	0.30	2.67	42,47,51,53	12
4	JM4	A	800[B]	17/17	0.84	0.30	2.67	48,49,51,53	12
4	JM4	B	800[B]	17/17	0.83	0.26	1.86	47,51,62,63	12
4	JM4	B	800[A]	17/17	0.83	0.26	1.86	43,47,49,50	12
2	HEM	A	750	43/43	0.97	0.20	0.56	26,30,35,37	0
2	HEM	B	750	43/43	0.98	0.16	0.47	24,29,35,37	0
3	H4B	B	760	17/17	0.96	0.16	0.46	27,30,34,34	0
3	H4B	A	760	17/17	0.96	0.15	-0.02	27,29,35,36	0
6	ZN	A	900	1/1	0.99	0.08	-1.39	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.