



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:02 PM GMT

PDB ID : 4KCJ
Title : Structure of neuronal nitric oxide synthase heme domain in complex with N, N'-((ethane-1,2-diylbis(oxy))bis(3,1-phenylene))bis(thiophene-2-carboximide)
Authors : Li, H.; Poulos, T.L.
Deposited on : 2013-04-24
Resolution : 2.05 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

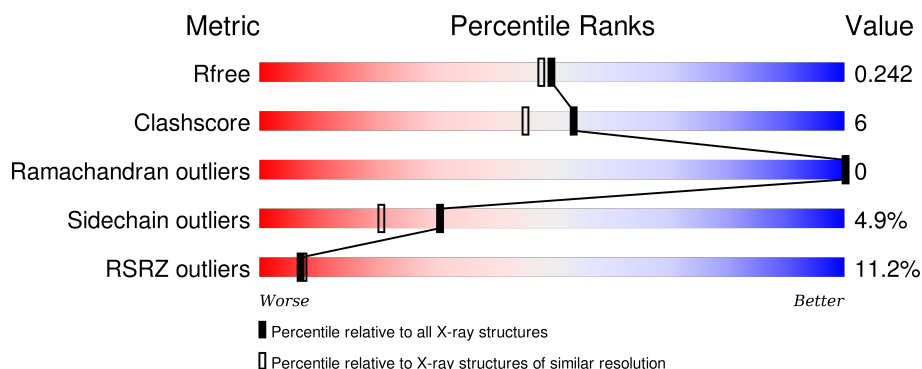
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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	ACT	A	803	-	-	-	X
4	ACT	B	803	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7116 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	1	0
			3319	2125	566	607	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: $C_9H_{15}N_5O_3$).



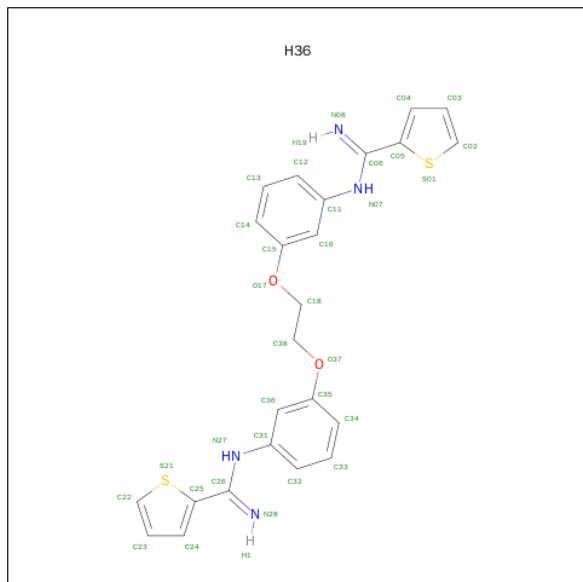
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 17	C 9	N 5	O 3	0	0
3	B	1	Total 17	C 9	N 5	O 3	0	0

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



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

- Molecule 5 is N,N'-[ETHANE-1,2-DIYLBIS(OXYBENZENE-3,1-DIYL)]DITHIOPHENE-2-CARBOXIMIDAMIDE (three-letter code: H36) (formula: C₂₄H₂₂N₄O₂S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			32	24	4	2	2		
5	B	1	Total	C	N	O	S	0	0
			32	24	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		

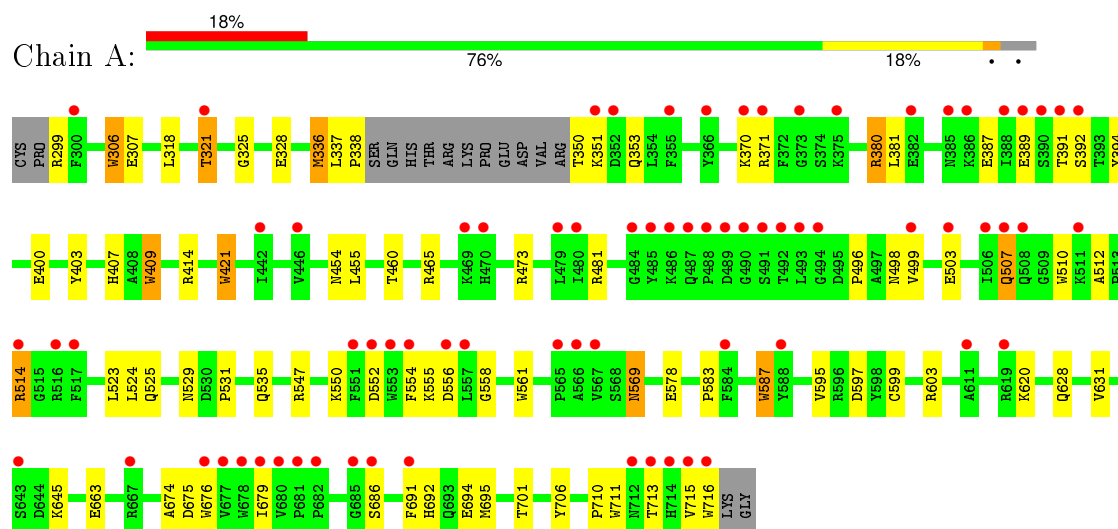
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	107	Total	O	0	0
			107	107		
7	B	152	Total	O	0	0
			152	152		

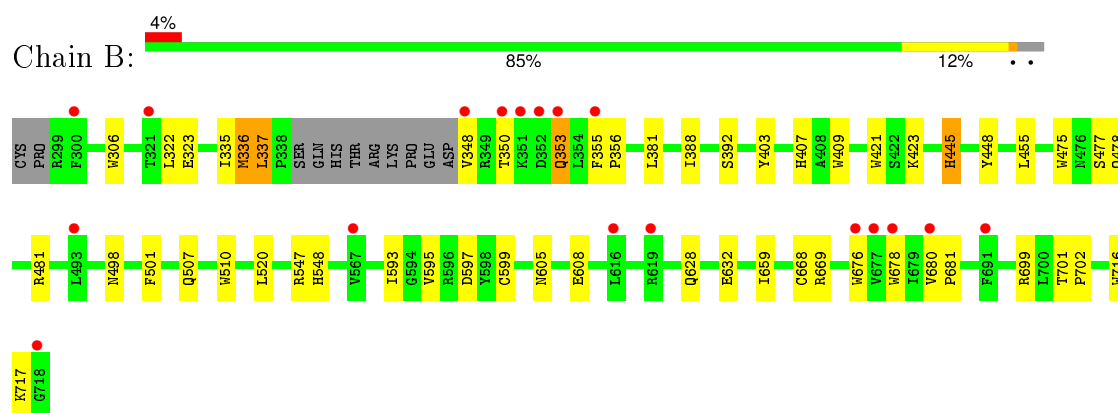
3 Residue-property plots

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: 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	51.80Å 111.03Å 164.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	92.19 – 2.05 41.18 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.6 (92.19-2.05) 99.2 (41.18-2.04)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.195 , 0.242 0.194 , 0.242	Depositor DCC
R_{free} test set	2989 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	36.4	Xtriage
Anisotropy	0.795	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	4 of 61000 reflections (0.007%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7116	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, ZN, H36, 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	0.75	9/3415 (0.3%)	0.75	0/4633
1	B	0.78	7/3438 (0.2%)	0.74	1/4661 (0.0%)
All	All	0.76	16/6853 (0.2%)	0.74	1/9294 (0.0%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	421	TRP	CD2-CE2	5.83	1.48	1.41
1	A	561	TRP	CD2-CE2	5.71	1.48	1.41
1	B	676	TRP	CD2-CE2	5.66	1.48	1.41
1	B	678	TRP	CD2-CE2	5.54	1.48	1.41
1	A	510	TRP	CD2-CE2	5.54	1.48	1.41
1	A	409	TRP	CD2-CE2	5.47	1.48	1.41
1	B	716	TRP	CD2-CE2	5.43	1.47	1.41
1	A	711	TRP	CD2-CE2	5.41	1.47	1.41
1	B	409	TRP	CD2-CE2	5.40	1.47	1.41
1	B	475	TRP	CD2-CE2	5.33	1.47	1.41
1	A	716	TRP	CD2-CE2	5.30	1.47	1.41
1	A	587	TRP	CD2-CE2	5.30	1.47	1.41
1	B	510	TRP	CD2-CE2	5.30	1.47	1.41
1	A	306	TRP	CD2-CE2	5.29	1.47	1.41
1	A	676	TRP	CD2-CE2	5.04	1.47	1.41
1	A	421	TRP	CD2-CE2	5.02	1.47	1.41

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	669	ARG	NE-CZ-NH2	-5.82	117.39	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3319	0	3227	56	0
1	B	3345	0	3259	29	0
2	A	43	0	30	5	0
2	B	43	0	30	4	0
3	A	17	0	15	0	0
3	B	17	0	15	1	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0
5	A	32	0	20	1	0
5	B	32	0	20	2	0
6	A	1	0	0	0	0
7	A	107	0	0	7	0
7	B	152	0	0	2	0
All	All	7116	0	6622	87	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (87) 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:A:321:THR:HG21	1:A:701:THR:HG22	1.54	0.90
2:A:801:HEM:HMC2	2:A:801:HEM:HBC2	1.60	0.83
1:A:523:LEU:CD2	1:A:531:PRO:HB2	2.09	0.82
1:A:523:LEU:HD23	1:A:531:PRO:HB2	1.63	0.81
1:A:351:LYS:HE2	1:A:392:SER:HB3	1.62	0.80
1:B:605:ASN:ND2	7:B:1049:HOH:O	2.13	0.78
2:B:801:HEM:HBC2	2:B:801:HEM:HMC2	1.65	0.77
1:A:414:ARG:NH1	1:A:706:TYR:OH	2.28	0.65
1:A:380:ARG:HD3	1:A:400:GLU:OE1	1.97	0.65
2:B:801:HEM:HBB2	2:B:801:HEM:HHC	1.79	0.64
1:A:554:PHE:HB3	7:A:968:HOH:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:LEU:HD21	1:A:531:PRO:HB2	1.84	0.60
1:B:595:VAL:O	1:B:599:CYS:HB2	2.02	0.59
1:A:555:LYS:N	7:A:968:HOH:O	2.29	0.58
1:A:692:HIS:ND1	7:A:1004:HOH:O	2.32	0.58
1:B:481:ARG:NH2	7:B:997:HOH:O	2.35	0.57
1:A:523:LEU:CD2	1:A:531:PRO:CB	2.82	0.57
1:A:481:ARG:NH2	7:A:983:HOH:O	2.37	0.57
1:A:525:GLN:HG3	1:A:529:ASN:O	2.05	0.56
1:A:473:ARG:NH2	1:A:710:PRO:HD3	2.21	0.55
1:B:477:SER:OG	5:B:804:H36:H8	2.06	0.55
1:A:371:ARG:HG3	1:A:371:ARG:HH21	1.72	0.55
1:A:706:TYR:OH	2:A:801:HEM:O2D	2.19	0.54
1:A:631:VAL:HG11	1:B:628:GLN:HG2	1.89	0.54
1:A:496:PRO:HA	1:A:499:VAL:HG23	1.90	0.54
1:B:323:GLU:O	1:B:699:ARG:HD3	2.08	0.53
1:A:387:GLU:OE1	1:A:394:TYR:HA	2.08	0.53
1:B:336:MET:HE2	3:B:802:H4B:H9	1.90	0.53
2:B:801:HEM:CBB	2:B:801:HEM:HHC	2.39	0.52
1:A:555:LYS:HG3	1:A:556:ASP:N	2.25	0.52
1:A:535:GLN:NE2	7:A:947:HOH:O	2.41	0.50
1:A:465:ARG:HD2	1:A:578:GLU:OE1	2.11	0.50
1:A:299:ARG:HG2	1:A:318:LEU:HD11	1.92	0.50
2:A:801:HEM:CMC	2:A:801:HEM:HBC2	2.35	0.50
1:A:306:TRP:CE2	1:B:336:MET:HE3	2.47	0.49
1:A:465:ARG:NH1	1:A:465:ARG:HB2	2.27	0.49
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.00	0.49
2:A:801:HEM:HHC	2:A:801:HEM:HBB2	1.95	0.49
1:A:523:LEU:HD21	1:A:531:PRO:CB	2.41	0.49
5:A:804:H36:H2	1:B:306:TRP:O	2.12	0.49
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.00	0.48
1:A:523:LEU:HD23	1:A:531:PRO:CB	2.39	0.48
1:A:628:GLN:NE2	1:B:632:GLU:OE2	2.47	0.48
1:A:465:ARG:HH11	1:A:465:ARG:HB2	1.79	0.47
1:A:350:THR:HB	1:A:353:GLN:NE2	2.29	0.47
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.97	0.47
1:A:336:MET:HB3	1:A:336:MET:HE2	1.82	0.46
1:A:686:SER:OG	1:B:595:VAL:CG1	2.63	0.46
1:A:674:ALA:HB3	1:A:695:MET:HB3	1.98	0.46
1:A:336:MET:HG3	1:B:306:TRP:NE1	2.30	0.46
1:A:694:GLU:HB3	1:B:335:ILE:HD13	1.98	0.46
1:A:558:GLY:HA2	7:A:936:HOH:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:524:LEU:O	1:A:531:PRO:HA	2.16	0.45
1:A:595:VAL:O	1:A:599:CYS:HB2	2.16	0.45
1:B:445:HIS:C	1:B:445:HIS:CD2	2.90	0.45
1:B:322:LEU:HD13	1:B:699:ARG:NH2	2.32	0.45
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.49	0.45
1:A:350:THR:HB	1:A:353:GLN:HG3	1.99	0.44
1:A:507:GLN:O	1:A:507:GLN:HG2	2.16	0.44
1:A:391:THR:O	1:A:392:SER:OG	2.33	0.44
1:A:460:THR:O	1:A:583:PRO:HD2	2.18	0.44
1:B:481:ARG:HD3	1:B:498:ASN:HD21	1.81	0.43
1:B:593:ILE:HA	1:B:597:ASP:HB2	2.00	0.43
1:A:686:SER:HA	1:A:691:PHE:CG	2.53	0.43
1:A:597:ASP:OD1	1:A:603:ARG:NH1	2.51	0.43
1:A:675:ASP:O	1:A:679:ILE:HG12	2.17	0.43
1:B:448:TYR:CD2	1:B:448:TYR:C	2.91	0.43
2:B:801:HEM:CHC	2:B:801:HEM:HBB2	2.48	0.43
1:A:512:ALA:C	1:A:514:ARG:H	2.21	0.43
1:B:701:THR:HA	1:B:702:PRO:C	2.39	0.43
1:B:478:GLN:HB2	1:B:481:ARG:HG3	2.00	0.43
1:A:481:ARG:NH1	1:A:498:ASN:OD1	2.51	0.43
1:A:325:GLY:HA3	1:A:338:PRO:HB2	2.00	0.43
2:A:801:HEM:HHC	2:A:801:HEM:CBB	2.49	0.42
1:A:512:ALA:C	1:A:514:ARG:N	2.73	0.42
1:A:569:ASN:H	1:A:569:ASN:HD22	1.67	0.42
1:B:659:ILE:HD13	1:B:659:ILE:HA	1.90	0.42
1:A:409:TRP:CE3	1:A:421:TRP:HA	2.54	0.42
1:B:353:GLN:H	1:B:353:GLN:HE21	1.67	0.41
1:B:680:VAL:HA	1:B:681:PRO:HD3	1.91	0.41
1:A:523:LEU:HD23	1:A:523:LEU:C	2.41	0.41
7:A:949:HOH:O	1:B:337:LEU:HD12	2.20	0.41
1:B:388:ILE:O	1:B:392:SER:N	2.50	0.41
1:B:501:PHE:HD2	1:B:520:LEU:HD13	1.86	0.41
1:B:355:PHE:HB2	1:B:356:PRO:CD	2.51	0.41
1:A:306:TRP:O	5:B:804:H36:H2	2.21	0.40
1:A:350:THR:HB	1:A:353:GLN:CG	2.51	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%)	393 (97%)	11 (3%)	0	100	100
1	B	407/422 (96%)	400 (98%)	7 (2%)	0	100	100
All	All	811/844 (96%)	793 (98%)	18 (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	364/377 (97%)	341 (94%)	23 (6%)	22	12
1	B	366/377 (97%)	352 (96%)	14 (4%)	40	31
All	All	730/754 (97%)	693 (95%)	37 (5%)	31	19

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	307[A]	GLU
1	A	307[B]	GLU
1	A	321	THR
1	A	328	GLU
1	A	336	MET
1	A	337	LEU
1	A	370	LYS
1	A	380	ARG

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Mol	Chain	Res	Type
1	A	381	LEU
1	A	389	GLU
1	A	454	ASN
1	A	503	GLU
1	A	507	GLN
1	A	514	ARG
1	A	547	ARG
1	A	550	LYS
1	A	552	ASP
1	A	569	ASN
1	A	620	LYS
1	A	645	LYS
1	A	663	GLU
1	A	713	THR
1	A	715	VAL
1	B	336	MET
1	B	337	LEU
1	B	348	VAL
1	B	350	THR
1	B	353	GLN
1	B	381	LEU
1	B	423	LYS
1	B	445	HIS
1	B	455	LEU
1	B	507	GLN
1	B	547	ARG
1	B	608	GLU
1	B	668	CYS
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	353	GLN
1	A	454	ASN
1	A	508	GLN
1	A	527	ASN
1	A	569	ASN
1	A	605	ASN
1	A	697	ASN
1	B	353	GLN
1	B	385	ASN

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Mol	Chain	Res	Type
1	B	454	ASN
1	B	535	GLN
1	B	601	ASN
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 ⓘ

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	801	1	30,50,50	2.86	13 (43%)	24,82,82	2.97	11 (45%)
3	H4B	A	802	-	13,18,18	0.88	0	11,26,26	2.98	6 (54%)
4	ACT	A	803	-	1,3,3	0.41	0	0,3,3	0.00	-
5	H36	A	804	-	33,35,35	1.27	5 (15%)	32,46,46	1.92	4 (12%)
2	HEM	B	801	1	30,50,50	2.70	13 (43%)	24,82,82	2.92	12 (50%)
3	H4B	B	802	-	13,18,18	1.06	0	11,26,26	2.45	6 (54%)
4	ACT	B	803	-	1,3,3	1.69	0	0,3,3	0.00	-
5	H36	B	804	-	33,35,35	1.51	5 (15%)	32,46,46	1.96	4 (12%)

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	ACT	A	803	-	-	0/0/0/0	0/0/0/0
5	H36	A	804	-	-	0/15/23/23	0/4/4/4
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	ACT	B	803	-	-	0/0/0/0	0/0/0/0
5	H36	B	804	-	-	0/15/23/23	0/4/4/4

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C3D-C4D	-3.93	1.46	1.51
2	B	801	HEM	C3D-C4D	-3.61	1.47	1.51
2	A	801	HEM	C3B-C4B	-3.34	1.48	1.51
2	B	801	HEM	C3B-C4B	-2.87	1.49	1.51
2	B	801	HEM	C2D-C3D	-2.67	1.46	1.54
5	A	804	H36	C06-N07	-2.48	1.34	1.39
5	B	804	H36	C06-N07	-2.41	1.34	1.39
5	A	804	H36	C31-N27	-2.38	1.37	1.41
2	A	801	HEM	C2D-C3D	-2.36	1.47	1.54
5	A	804	H36	C26-N27	-2.25	1.34	1.39
2	B	801	HEM	C4A-CHB	2.15	1.45	1.39
5	A	804	H36	C05-C06	2.17	1.48	1.45
5	B	804	H36	C25-S21	2.25	1.75	1.72
2	B	801	HEM	FE-ND	2.40	2.10	1.97
2	A	801	HEM	CHD-C1D	2.49	1.45	1.38
2	B	801	HEM	C1A-CHA	2.57	1.46	1.39
5	B	804	H36	C05-S01	2.67	1.75	1.72
2	A	801	HEM	FE-ND	2.70	2.11	1.97
2	B	801	HEM	FE-NB	2.75	2.12	1.97
2	B	801	HEM	CHC-C4B	2.80	1.46	1.38
5	B	804	H36	C05-C06	2.84	1.49	1.45
2	A	801	HEM	C4A-CHB	2.97	1.48	1.39
2	A	801	HEM	FE-NB	3.00	2.13	1.97
2	A	801	HEM	CHC-C4B	3.10	1.47	1.38
2	A	801	HEM	C2A-C3A	3.19	1.47	1.37
5	A	804	H36	C25-C26	3.20	1.50	1.45
2	B	801	HEM	C2A-C3A	3.25	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	HEM	CHD-C4C	3.49	1.44	1.36
2	A	801	HEM	CHC-C1C	3.88	1.45	1.36
2	B	801	HEM	CHC-C1C	4.61	1.47	1.36
2	A	801	HEM	CHD-C4C	4.79	1.47	1.36
5	B	804	H36	C25-C26	4.91	1.52	1.45
2	B	801	HEM	C1C-NC	6.73	1.44	1.36
2	A	801	HEM	C4C-NC	7.33	1.45	1.36
2	B	801	HEM	C4C-NC	7.36	1.45	1.36
2	A	801	HEM	C1C-NC	7.52	1.45	1.36

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	804	H36	C03-C02-S01	-7.15	105.32	113.23
5	B	804	H36	C23-C22-S21	-6.61	105.91	113.23
2	B	801	HEM	CBA-CAA-C2A	-6.30	101.25	112.53
5	B	804	H36	C03-C02-S01	-6.24	106.33	113.23
5	A	804	H36	C23-C22-S21	-5.75	106.87	113.23
2	A	801	HEM	CBA-CAA-C2A	-5.20	103.21	112.53
2	A	801	HEM	C3C-CAC-CBC	-5.04	116.72	124.46
3	B	802	H4B	N3-C2-N1	-3.52	119.76	125.53
2	B	801	HEM	C3C-CAC-CBC	-3.43	119.19	124.46
3	A	802	H4B	N3-C2-N1	-3.39	119.97	125.53
2	B	801	HEM	C3B-CAB-CBB	-2.82	120.14	124.46
5	A	804	H36	C11-N07-C06	-2.31	122.64	128.32
2	A	801	HEM	C3B-CAB-CBB	-2.30	120.93	124.46
2	A	801	HEM	CAD-CBD-CGD	-2.26	103.82	113.02
2	B	801	HEM	C3B-C4B-CHC	-2.19	120.08	123.16
3	B	802	H4B	N2-C2-N1	2.04	120.57	117.20
2	A	801	HEM	C3B-C4B-NB	2.13	115.69	111.63
5	A	804	H36	C25-C26-N27	2.18	121.30	115.07
5	B	804	H36	C18-O17-C15	2.22	123.38	117.91
2	B	801	HEM	C2C-C1C-NC	2.22	113.95	110.21
3	B	802	H4B	C4A-C8A-N8	2.22	121.05	118.43
2	A	801	HEM	CAA-CBA-CGA	2.39	117.12	112.75
2	B	801	HEM	C3B-C4B-NB	2.40	116.21	111.63
2	B	801	HEM	CAA-CBA-CGA	2.53	117.39	112.75
3	B	802	H4B	C2-N1-C8A	2.87	121.00	114.54
3	B	802	H4B	C4-N3-C2	3.01	120.12	115.94
2	B	801	HEM	CMD-C2D-C3D	3.07	127.94	114.35
2	A	801	HEM	CMD-C2D-C3D	3.11	128.12	114.35
3	A	802	H4B	C4-N3-C2	3.38	120.63	115.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	804	H36	C25-C26-N27	3.39	124.75	115.07
3	A	802	H4B	C2-N1-C8A	3.52	122.45	114.54
2	A	801	HEM	CAD-C3D-C4D	3.70	125.53	112.47
3	A	802	H4B	N2-C2-N3	3.82	123.52	117.20
3	A	802	H4B	C4A-C8A-N8	4.55	123.79	118.43
3	B	802	H4B	C4-C4A-C8A	4.86	118.96	114.56
2	B	801	HEM	CAD-C3D-C4D	4.86	129.60	112.47
2	B	801	HEM	CMC-C2C-C3C	5.11	129.29	116.53
2	B	801	HEM	CAD-C3D-C2D	5.12	127.93	113.22
3	A	802	H4B	C4-C4A-C8A	5.13	119.20	114.56
2	A	801	HEM	CMB-C2B-C3B	5.30	129.75	116.53
2	B	801	HEM	CMB-C2B-C3B	5.61	130.53	116.53
2	A	801	HEM	CMC-C2C-C3C	5.91	131.28	116.53
2	A	801	HEM	CAD-C3D-C2D	6.14	130.88	113.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEM	5	0
5	A	804	H36	1	0
2	B	801	HEM	4	0
3	B	802	H4B	1	0
5	B	804	H36	2	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%)	0.84	74 (18%) 2 2	30, 56, 101, 139	0
1	B	411/422 (97%)	0.17	18 (4%) 38 43	28, 44, 70, 99	0
All	All	818/844 (96%)	0.50	92 (11%) 7 7	28, 49, 94, 139	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	488	PRO	9.5
1	B	300	PHE	7.9
1	A	486	LYS	6.5
1	A	716	TRP	5.6
1	A	352	ASP	5.6
1	A	715	VAL	5.5
1	B	718	GLY	5.4
1	A	506	ILE	5.3
1	A	551	PHE	5.3
1	B	348	VAL	4.7
1	A	493	LEU	4.5
1	A	507	GLN	4.5
1	A	503	GLU	4.3
1	A	712	ASN	4.2
1	A	491	SER	4.0
1	A	553	TRP	3.9
1	A	499	VAL	3.9
1	B	619	ARG	3.9
1	A	321	THR	3.8
1	A	489	ASP	3.7
1	A	508	GLN	3.7
1	A	713	THR	3.7
1	A	492	THR	3.7
1	B	350	THR	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	514	ARG	3.6
1	A	677	VAL	3.4
1	B	353	GLN	3.4
1	A	355	PHE	3.4
1	A	351	LYS	3.3
1	A	300	PHE	3.3
1	B	677	VAL	3.3
1	A	487	GLN	3.3
1	A	511	LYS	3.2
1	B	355	PHE	3.2
1	A	678	TRP	3.1
1	A	714	HIS	3.1
1	A	373	GLY	3.1
1	A	386	LYS	3.1
1	A	390	SER	3.0
1	A	479	LEU	3.0
1	A	370	LYS	3.0
1	A	516	ARG	2.9
1	B	352	ASP	2.9
1	A	485	TYR	2.9
1	A	679	ILE	2.9
1	A	567	VAL	2.8
1	A	490	GLY	2.8
1	A	611	ALA	2.8
1	A	389	GLU	2.8
1	A	667	ARG	2.7
1	A	554	PHE	2.7
1	A	442	ILE	2.7
1	A	588	TYR	2.7
1	A	392	SER	2.7
1	A	480	ILE	2.6
1	B	616	LEU	2.6
1	A	676	TRP	2.6
1	A	584	PHE	2.6
1	A	557	LEU	2.6
1	B	321	THR	2.6
1	B	351	LYS	2.6
1	A	680	VAL	2.5
1	A	385	ASN	2.5
1	A	691	PHE	2.5
1	A	391	THR	2.5
1	A	619	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	680	VAL	2.4
1	A	565	PRO	2.4
1	A	371	ARG	2.4
1	A	681	PRO	2.3
1	B	493	LEU	2.3
1	A	484	GLY	2.3
1	A	685	GLY	2.3
1	A	682	PRO	2.3
1	A	517	PHE	2.3
1	A	366	TYR	2.3
1	A	382	GLU	2.3
1	B	567	VAL	2.3
1	A	469	LYS	2.3
1	A	446	VAL	2.2
1	A	643	SER	2.2
1	A	556	ASP	2.2
1	A	388	ILE	2.2
1	A	552	ASP	2.2
1	A	566	ALA	2.2
1	A	375	LYS	2.1
1	B	676	TRP	2.1
1	B	691	PHE	2.1
1	A	470	HIS	2.1
1	A	494	GLY	2.1
1	B	678	TRP	2.0
1	A	686	SER	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(\AA^2)	Q<0.9
4	ACT	B	803	4/4	0.98	0.24	7.48	42,47,49,53	0
4	ACT	A	803	4/4	0.99	0.23	3.53	41,43,47,48	0
3	H4B	B	802	17/17	0.90	0.23	1.17	39,43,48,55	0
2	HEM	B	801	43/43	0.98	0.16	0.88	28,31,43,50	0
3	H4B	A	802	17/17	0.94	0.19	0.37	35,38,42,43	0
2	HEM	A	801	43/43	0.97	0.18	0.37	30,33,42,44	0
5	H36	A	804	32/32	0.88	0.18	0.28	21,34,66,70	0
5	H36	B	804	32/32	0.93	0.14	-0.14	18,45,61,71	0
6	ZN	A	805	1/1	0.98	0.08	-1.21	41,41,41,41	0

6.5 Other polymers

There are no such residues in this entry.