



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:30 PM GMT

PDB ID : 4CDT
Title : Structure of rat neuronal nitric oxide synthase heme domain in complex with
7-((3-Fluorophenethylamino)ethyl)quinolin-2-amine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2013-11-05
Resolution : 2.00 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

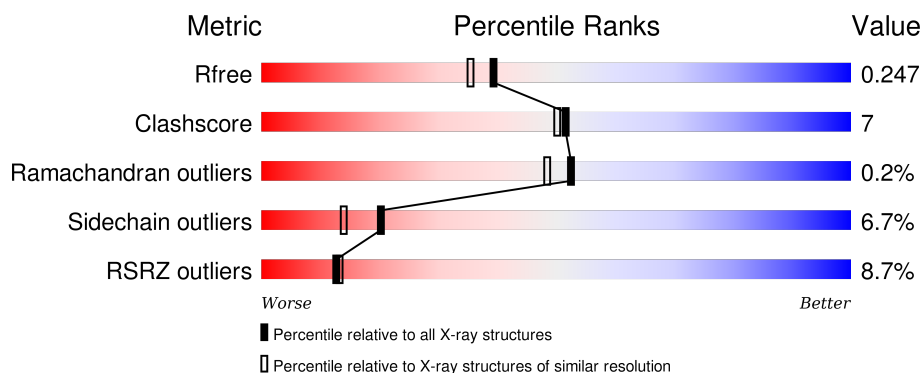
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	<div> <div>12%</div> <div>79%</div> <div>14%</div> <div>• •</div> </div>
1	B	422	<div> <div>5%</div> <div>81%</div> <div>14%</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
5	ACT	A	860	-	-	-	X

2 Entry composition [i](#)

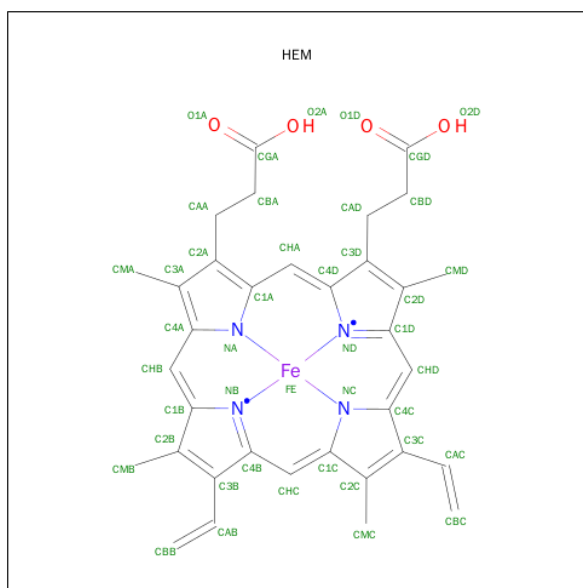
There are 7 unique types of molecules in this entry. The entry contains 7017 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

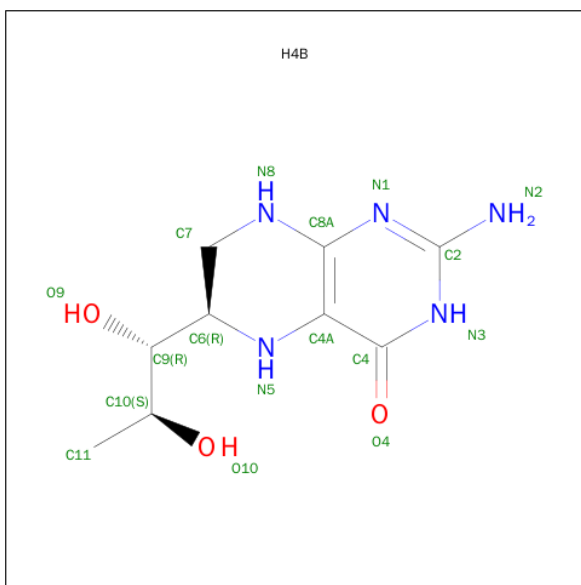
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	0	1
			3314	2121	567	605	21			
1	B	411	Total	C	N	O	S	0	0	0
			3345	2140	574	610	21			

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



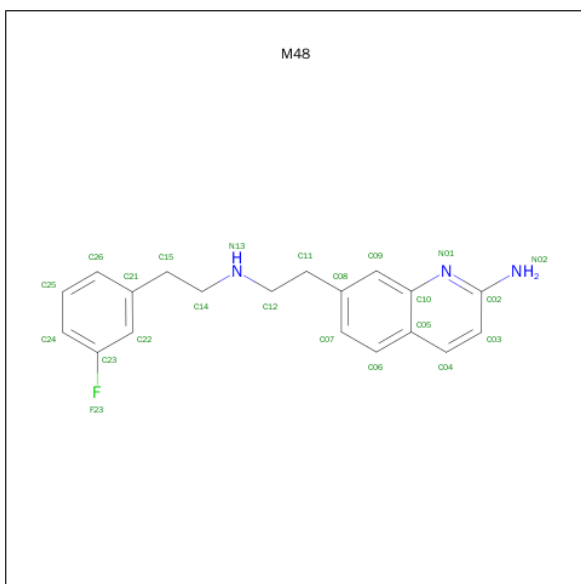
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



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

- Molecule 4 is 7-[2-[2-(3-FLUOROPHENYL)ETHYLAMINO]ETHYL]QUINOLIN-2-AMINE (three-letter code: M48) (formula: $C_{19}H_{20}FN_3$).



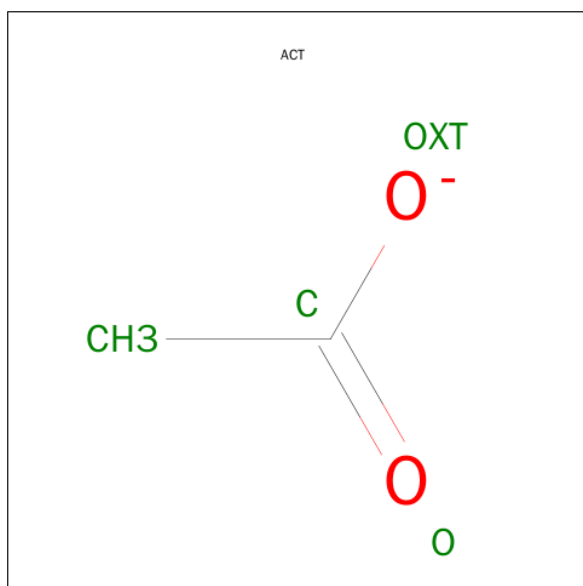
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	F	N	0	0
			23	19	1	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	F	N	0	0
			23	19	1	3		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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		

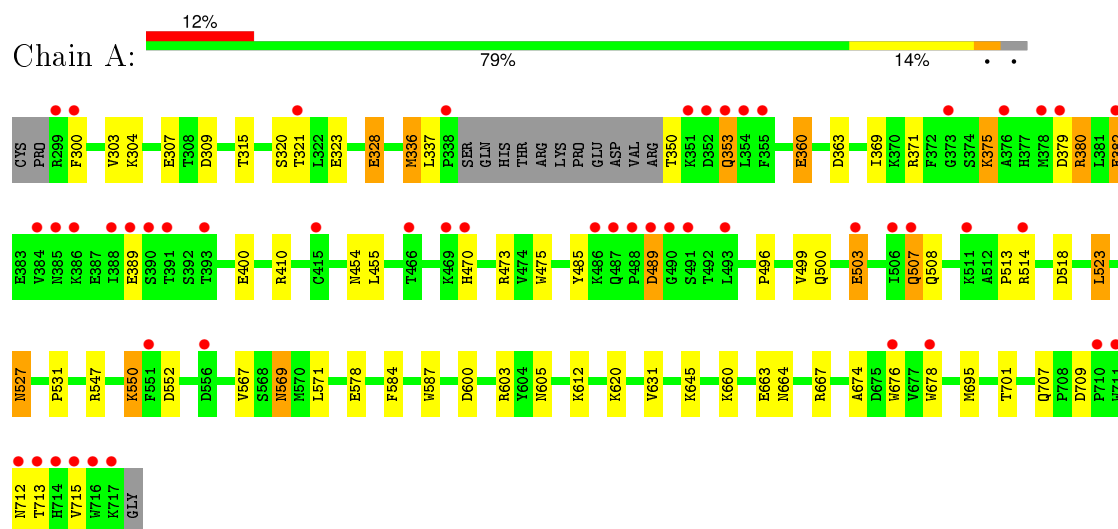
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	91	Total	O	0	0
			91	91		
7	B	92	Total	O	0	0
			92	92		

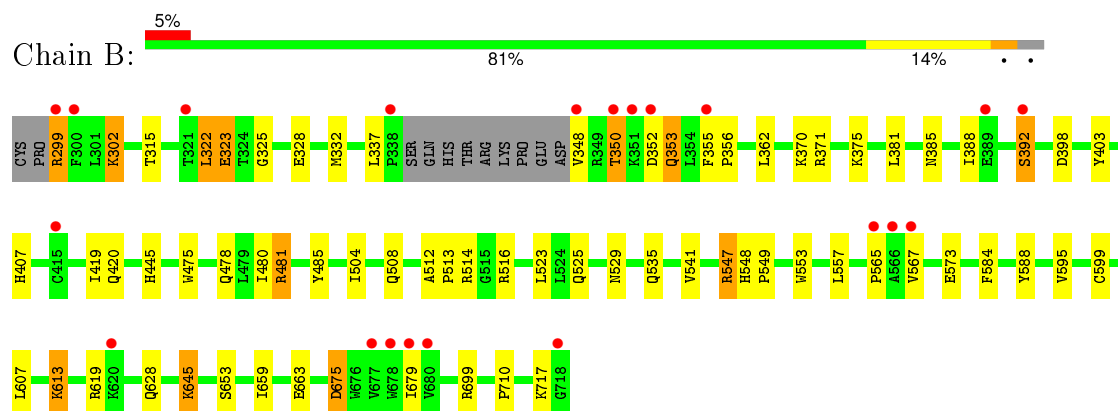
3 Residue-property plots [i](#)

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	52.37Å 111.82Å 165.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	92.65 – 2.00 46.32 – 2.00	Depositor EDS
% Data completeness (in resolution range)	92.4 (92.65-2.00) 92.5 (46.32-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.74 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.196 , 0.247 0.197 , 0.247	Depositor DCC
R_{free} test set	3085 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.632	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 53.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	3 of 61671 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7017	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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, M48, 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	0.84	2/3407 (0.1%)	0.91	5/4623 (0.1%)
1	B	0.85	0/3438	0.89	3/4661 (0.1%)
All	All	0.84	2/6845 (0.0%)	0.90	8/9284 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	360	GLU	CG-CD	6.52	1.61	1.51
1	A	676	TRP	CE3-CZ3	5.24	1.47	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	410	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	B	675	ASP	CB-CG-OD1	6.33	124.00	118.30
1	A	410	ARG	NE-CZ-NH2	-6.27	117.17	120.30
1	A	603	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	A	363	ASP	CB-CG-OD1	5.72	123.44	118.30
1	A	600	ASP	CB-CG-OD1	5.44	123.20	118.30
1	B	557	LEU	CB-CG-CD1	-5.42	101.79	111.00
1	B	371	ARG	NE-CZ-NH1	5.27	122.94	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3314	0	3221	45	0
1	B	3345	0	3259	43	0
2	A	43	0	30	4	0
2	B	43	0	30	3	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	23	0	20	4	0
4	B	23	0	20	2	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	1	0	0	0	0
7	A	91	0	0	2	0
7	B	92	0	0	2	0
All	All	7017	0	6616	92	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 (92) 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:500:GLN:HA	1:A:503:GLU:OE2	1.47	1.11
1:A:336:MET:HE1	1:A:678:TRP:HZ2	1.39	0.88
1:A:336:MET:CE	1:A:678:TRP:HZ2	2.00	0.73
2:A:750:HEM:HMC2	2:A:750:HEM:HBC2	1.72	0.71
1:A:350:THR:N	1:A:353:GLN:HE22	1.88	0.70
1:A:470:HIS:O	1:A:527:ASN:HA	1.92	0.69
1:B:325:GLY:O	1:B:332:MET:HG3	1.93	0.68
1:A:328:GLU:HB2	1:B:323:GLU:HG3	1.73	0.68
1:B:619:ARG:HH11	1:B:619:ARG:CB	2.08	0.67
1:B:350:THR:HG23	1:B:352:ASP:HB3	1.77	0.66
1:A:631:VAL:HG11	1:B:628:GLN:HG2	1.77	0.65
1:A:369:ILE:HG13	1:A:371:ARG:HG3	1.79	0.65
1:B:659:ILE:O	1:B:663:GLU:HG3	2.00	0.61
1:A:336:MET:HE1	1:A:678:TRP:CZ2	2.28	0.61
2:B:750:HEM:HH1	2:B:750:HEM:HBB2	1.82	0.60
1:A:379:ASP:O	1:A:382:GLU:HG3	2.02	0.59
1:B:355:PHE:CE1	1:B:385:ASN:HB2	2.37	0.59
1:B:299:ARG:HB3	1:B:299:ARG:CZ	2.32	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:500:GLN:HA	1:A:503:GLU:CD	2.20	0.58
1:B:619:ARG:HH11	1:B:619:ARG:HB2	1.69	0.58
1:A:350:THR:N	1:A:353:GLN:NE2	2.52	0.57
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.87	0.57
1:A:567:VAL:HG21	4:A:801:M48:C07	2.36	0.56
1:B:619:ARG:NH1	1:B:619:ARG:HB2	2.21	0.56
1:B:504:ILE:O	1:B:508:GLN:HG2	2.06	0.56
1:A:328:GLU:H	1:A:328:GLU:CD	2.09	0.56
1:B:350:THR:O	1:B:353:GLN:HG2	2.06	0.56
1:B:567:VAL:HG21	4:B:801:M48:C07	2.39	0.53
1:A:660:LYS:HE2	1:A:664:ASN:HD21	1.73	0.53
1:A:307:GLU:HG3	7:B:2078:HOH:O	2.09	0.52
1:B:398:ASP:HB2	7:B:2015:HOH:O	2.08	0.52
2:A:750:HEM:HBB2	2:A:750:HEM:HHC	1.91	0.51
1:B:553:TRP:HB2	1:B:613:LYS:HE3	1.91	0.51
1:A:513:PRO:HG2	1:A:518:ASP:CG	2.30	0.51
1:B:322:LEU:HD13	1:B:699:ARG:HH21	1.75	0.51
1:A:375:LYS:HD3	1:A:379:ASP:OD2	2.09	0.50
1:B:362:LEU:HD12	1:B:381:LEU:HD23	1.92	0.50
1:B:478:GLN:HB2	1:B:481:ARG:HG3	1.94	0.50
1:A:605:ASN:ND2	7:A:2062:HOH:O	2.44	0.49
1:B:350:THR:CG2	1:B:352:ASP:HB3	2.40	0.49
1:A:500:GLN:CA	1:A:503:GLU:OE2	2.40	0.49
1:A:455:LEU:HD12	1:A:587:TRP:HB3	1.95	0.49
1:A:701:THR:HG22	7:A:2006:HOH:O	2.13	0.48
1:B:348:VAL:HG13	1:B:348:VAL:O	2.14	0.48
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.02	0.48
2:A:750:HEM:HBA2	4:A:801:M48:C09	2.43	0.48
1:B:645:LYS:HB2	1:B:645:LYS:HE2	1.63	0.47
1:B:548:HIS:CG	1:B:549:PRO:HD2	2.50	0.47
1:B:475:TRP:HB2	1:B:523:LEU:HB3	1.97	0.47
1:B:607:LEU:HA	1:B:607:LEU:HD23	1.82	0.46
1:B:584:PHE:HE1	4:B:801:M48:H06	1.79	0.46
1:A:503:GLU:O	1:A:507:GLN:HB3	2.17	0.45
1:B:355:PHE:N	1:B:356:PRO:HD2	2.31	0.45
1:B:480:ILE:HD13	1:B:541:VAL:HG13	1.98	0.45
1:A:584:PHE:HE1	4:A:801:M48:H06	1.81	0.45
1:A:667:ARG:HG3	1:A:667:ARG:NH1	2.32	0.45
1:B:547:ARG:H	1:B:547:ARG:HD3	1.81	0.45
1:B:619:ARG:NH1	1:B:619:ARG:CB	2.78	0.45
1:A:380:ARG:HD3	1:A:400:GLU:OE2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:388:ILE:O	1:B:392:SER:N	2.46	0.44
1:A:328:GLU:N	1:A:328:GLU:CD	2.70	0.44
1:A:508:GLN:HA	1:A:508:GLN:NE2	2.33	0.44
1:A:304:LYS:HE3	1:A:309:ASP:OD1	2.18	0.44
2:A:750:HEM:HBA2	4:A:801:M48:H09	2.00	0.44
1:B:675:ASP:O	1:B:679:ILE:HG12	2.18	0.43
1:A:674:ALA:HB3	1:A:695:MET:HB3	1.99	0.43
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.99	0.43
1:A:709:ASP:HB2	1:A:712:ASN:ND2	2.33	0.43
1:A:496:PRO:HA	1:A:499:VAL:HG23	2.00	0.43
1:A:508:GLN:NE2	1:A:508:GLN:CA	2.80	0.43
1:B:485:TYR:CZ	1:B:514:ARG:HA	2.54	0.43
1:B:565:PRO:HB3	1:B:588:TYR:CZ	2.54	0.42
1:A:455:LEU:HD12	1:A:587:TRP:CB	2.49	0.42
1:A:323:GLU:HG2	1:B:328:GLU:HB3	2.00	0.42
1:B:512:ALA:HA	1:B:513:PRO:HD2	1.65	0.42
1:A:569:ASN:H	1:A:569:ASN:HD22	1.66	0.42
2:B:750:HEM:HHC	2:B:750:HEM:CBB	2.49	0.42
1:A:571:LEU:HD21	1:A:578:GLU:HG2	2.02	0.42
1:B:619:ARG:HH11	1:B:619:ARG:HB3	1.83	0.41
1:B:595:VAL:O	1:B:599:CYS:HB2	2.21	0.41
1:A:667:ARG:HG3	1:A:667:ARG:HH11	1.86	0.41
1:A:485:TYR:CZ	1:A:514:ARG:HA	2.55	0.41
1:A:300:PHE:HD1	1:A:315:THR:HG22	1.86	0.41
1:B:547:ARG:HD3	1:B:547:ARG:N	2.35	0.41
1:B:302:LYS:HE3	1:B:302:LYS:HB2	1.21	0.41
2:B:750:HEM:HBC2	2:B:750:HEM:CMC	2.51	0.40
1:A:571:LEU:HD12	1:A:707:GLN:OE1	2.21	0.40
1:A:550:LYS:HB2	1:A:550:LYS:HE3	1.67	0.40
1:A:473:ARG:HH11	1:A:473:ARG:HD3	1.75	0.40
1:B:419:ILE:HG23	1:B:420:GLN:HG2	2.03	0.40
1:B:525:GLN:HG3	1:B:529:ASN:O	2.21	0.40
1:B:353:GLN:HB3	1:B:353:GLN:HE21	1.71	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%)	382 (95%)	21 (5%)	1 (0%)	52	48
1	B	407/422 (96%)	398 (98%)	8 (2%)	1 (0%)	52	48
All	All	811/844 (96%)	780 (96%)	29 (4%)	2 (0%)	52	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	489	ASP
1	B	322	LEU

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	363/377 (96%)	335 (92%)	28 (8%)	16	10
1	B	366/377 (97%)	345 (94%)	21 (6%)	25	19
All	All	729/754 (97%)	680 (93%)	49 (7%)	20	14

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	303	VAL
1	A	320	SER
1	A	321	THR
1	A	328	GLU

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Mol	Chain	Res	Type
1	A	336	MET
1	A	337	LEU
1	A	353	GLN
1	A	360	GLU
1	A	375	LYS
1	A	380	ARG
1	A	382	GLU
1	A	389	GLU
1	A	454	ASN
1	A	489	ASP
1	A	503	GLU
1	A	507	GLN
1	A	523	LEU
1	A	527	ASN
1	A	547	ARG
1	A	550	LYS
1	A	552	ASP
1	A	569	ASN
1	A	612	LYS
1	A	620	LYS
1	A	645	LYS
1	A	663	GLU
1	A	713	THR
1	A	715	VAL
1	B	299	ARG
1	B	302	LYS
1	B	315	THR
1	B	323	GLU
1	B	337	LEU
1	B	350	THR
1	B	353	GLN
1	B	370	LYS
1	B	375	LYS
1	B	392	SER
1	B	445	HIS
1	B	481	ARG
1	B	516	ARG
1	B	535	GLN
1	B	547	ARG
1	B	573	GLU
1	B	613	LYS
1	B	645	LYS

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Mol	Chain	Res	Type
1	B	653	SER
1	B	710	PRO
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	364	GLN
1	A	454	ASN
1	A	507	GLN
1	A	508	GLN
1	A	569	ASN
1	A	642	GLN
1	A	697	ASN
1	A	712	ASN
1	B	454	ASN
1	B	507	GLN
1	B	605	ASN
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 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	2.35	9 (30%)	24,82,82	2.56	9 (37%)
3	H4B	A	760	-	13,18,18	1.25	2 (15%)	11,26,26	2.67	7 (63%)
4	M48	A	801	-	25,25,25	1.16	2 (8%)	31,33,33	1.52	5 (16%)
5	ACT	A	860	-	1,3,3	1.24	0	0,3,3	0.00	-
2	HEM	B	750	1	30,50,50	2.16	6 (20%)	24,82,82	2.62	11 (45%)
3	H4B	B	760	-	13,18,18	1.43	2 (15%)	11,26,26	2.55	6 (54%)
4	M48	B	801	-	25,25,25	1.12	3 (12%)	31,33,33	1.75	8 (25%)
5	ACT	B	860	-	1,3,3	1.03	0	0,3,3	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	750	1	-	0/10/54/54	0/0/8/8
3	H4B	A	760	-	-	0/8/17/17	0/2/2/2
4	M48	A	801	-	-	0/8/8/8	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	M48	B	801	-	-	0/8/8/8	0/3/3/3
5	ACT	B	860	-	-	0/0/0/0	0/0/0/0

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	750	HEM	C2D-C3D	-6.63	1.34	1.54
2	A	750	HEM	C2D-C3D	-5.88	1.36	1.54
2	B	750	HEM	C2C-C1C	-5.82	1.41	1.52
2	A	750	HEM	C2C-C1C	-4.85	1.43	1.52
2	A	750	HEM	C3B-C4B	-4.66	1.47	1.51
2	A	750	HEM	C3D-C4D	-4.40	1.45	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C2B-C1B	-3.09	1.41	1.51
2	B	750	HEM	C3D-C4D	-2.81	1.48	1.51
2	B	750	HEM	C2B-C1B	-2.72	1.42	1.51
3	B	760	H4B	C2-N1	2.04	1.39	1.35
4	B	801	M48	C24-C23	2.12	1.41	1.37
3	A	760	H4B	C6-N5	2.12	1.50	1.45
2	A	750	HEM	CHC-C1C	2.13	1.41	1.36
4	A	801	M48	C22-C23	2.15	1.41	1.37
3	A	760	H4B	C2-N1	2.17	1.39	1.35
4	B	801	M48	C22-C23	2.30	1.41	1.37
2	B	750	HEM	C1C-NC	2.42	1.39	1.36
4	B	801	M48	C04-C03	2.43	1.41	1.36
2	A	750	HEM	FE-NB	2.67	2.11	1.97
4	A	801	M48	C06-C07	2.69	1.42	1.36
2	A	750	HEM	C1C-NC	3.27	1.40	1.36
3	B	760	H4B	C6-N5	3.46	1.52	1.45
2	A	750	HEM	FE-NC	3.90	2.11	1.95
2	B	750	HEM	FE-NC	3.96	2.11	1.95

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	750	HEM	C3C-CAC-CBC	-4.86	117.00	124.46
2	A	750	HEM	CBA-CAA-C2A	-4.55	104.38	112.53
2	B	750	HEM	CBA-CAA-C2A	-4.40	104.64	112.53
3	A	760	H4B	N3-C2-N1	-3.87	119.20	125.53
2	B	750	HEM	C1D-CHD-C4C	-3.12	120.60	125.82
4	B	801	M48	C24-C23-C22	-2.98	119.50	123.35
2	B	750	HEM	C3C-CAC-CBC	-2.89	120.02	124.46
4	A	801	M48	C24-C23-C22	-2.82	119.72	123.35
4	B	801	M48	C03-C04-C05	-2.75	116.56	120.83
2	A	750	HEM	C1D-CHD-C4C	-2.72	121.27	125.82
3	B	760	H4B	N3-C2-N1	-2.67	121.16	125.53
2	B	750	HEM	C3B-CAB-CBB	-2.61	120.45	124.46
2	B	750	HEM	C3B-C4B-NB	-2.59	106.68	111.63
4	B	801	M48	C03-C02-N01	-2.39	119.58	122.20
4	B	801	M48	C04-C03-C02	2.03	121.54	119.55
2	A	750	HEM	CMD-C2D-C3D	2.09	123.60	114.35
3	A	760	H4B	C8A-C4A-N5	2.21	121.64	118.85
2	B	750	HEM	C2D-C3D-C4D	2.21	105.25	101.50
4	A	801	M48	C14-C15-C21	2.33	117.66	112.83
2	A	750	HEM	CMB-C2B-C3B	2.36	122.42	116.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	801	M48	C21-C22-C23	2.47	120.89	118.84
4	B	801	M48	C12-N13-C14	2.54	122.36	113.35
3	B	760	H4B	C2-N1-C8A	2.65	120.50	114.54
3	A	760	H4B	N2-C2-N1	2.66	121.61	117.20
2	B	750	HEM	CMD-C2D-C3D	2.75	126.52	114.35
3	A	760	H4B	C4A-C8A-N8	2.83	121.76	118.43
3	B	760	H4B	N2-C2-N1	2.93	122.05	117.20
3	A	760	H4B	C2-N1-C8A	2.96	121.20	114.54
3	B	760	H4B	C4-N3-C2	3.04	120.16	115.94
4	A	801	M48	C12-N13-C14	3.10	124.32	113.35
4	A	801	M48	C12-C11-C08	3.20	119.48	112.83
4	B	801	M48	C02-N01-C10	3.33	121.75	117.78
4	A	801	M48	C21-C22-C23	3.36	121.63	118.84
2	A	750	HEM	C2D-C3D-C4D	3.43	107.32	101.50
3	B	760	H4B	C4A-C8A-N8	3.65	122.72	118.43
3	A	760	H4B	C4-N3-C2	3.75	121.15	115.94
2	A	750	HEM	CAD-C3D-C4D	3.87	126.11	112.47
4	B	801	M48	N02-C02-N01	3.92	120.58	118.03
3	A	760	H4B	C4-C4A-C8A	4.13	118.31	114.56
2	B	750	HEM	CAD-C3D-C4D	4.33	127.75	112.47
2	B	750	HEM	CMC-C2C-C3C	4.50	127.78	116.53
3	B	760	H4B	C4-C4A-C8A	4.51	118.65	114.56
2	A	750	HEM	CAD-C3D-C2D	4.64	126.56	113.22
2	B	750	HEM	CMB-C2B-C3B	4.71	128.28	116.53
2	B	750	HEM	CAD-C3D-C2D	4.79	126.99	113.22
2	A	750	HEM	CMC-C2C-C3C	5.48	130.21	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	750	HEM	4	0
4	A	801	M48	4	0
2	B	750	HEM	3	0
4	B	801	M48	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	408/422 (96%)	0.67	50 (12%) 5 6	25, 51, 89, 127	0
1	B	411/422 (97%)	0.36	21 (5%) 32 33	27, 42, 73, 101	0
All	All	819/844 (97%)	0.51	71 (8%) 13 13	25, 46, 85, 127	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	PHE	8.0
1	A	355	PHE	5.6
1	A	299	ARG	5.3
1	A	716	TRP	5.2
1	A	715	VAL	5.0
1	B	348	VAL	4.9
1	B	350	THR	4.7
1	A	506	ILE	4.6
1	A	489	ASP	4.4
1	B	718	GLY	4.4
1	A	338	PRO	4.2
1	A	488	PRO	4.2
1	A	385	ASN	4.1
1	A	352	ASP	3.9
1	B	352	ASP	3.9
1	A	503	GLU	3.8
1	A	378	MET	3.7
1	A	717	LYS	3.5
1	B	321	THR	3.4
1	A	491	SER	3.3
1	A	490	GLY	3.3
1	A	351	LYS	3.3
1	A	382	GLU	3.2
1	B	299	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	493	LEU	3.2
1	B	677	VAL	3.1
1	A	711	TRP	3.1
1	A	713	THR	3.1
1	A	514	ARG	3.1
1	B	338	PRO	3.1
1	A	487	GLN	3.0
1	A	714	HIS	3.0
1	A	469	LYS	2.9
1	A	388	ILE	2.9
1	A	390	SER	2.8
1	A	551	PHE	2.8
1	A	373	GLY	2.7
1	A	511	LYS	2.7
1	A	300	PHE	2.7
1	B	678	TRP	2.7
1	B	567	VAL	2.6
1	A	415	CYS	2.6
1	A	712	ASN	2.6
1	A	376	ALA	2.6
1	B	389	GLU	2.6
1	B	566	ALA	2.6
1	A	354	LEU	2.6
1	A	470	HIS	2.5
1	A	389	GLU	2.5
1	B	351	LYS	2.5
1	A	466	THR	2.5
1	B	679	ILE	2.4
1	A	486	LYS	2.4
1	A	391	THR	2.4
1	B	680	VAL	2.3
1	A	353	GLN	2.3
1	A	678	TRP	2.3
1	A	676	TRP	2.2
1	A	386	LYS	2.2
1	A	710	PRO	2.2
1	A	379	ASP	2.1
1	B	392	SER	2.1
1	A	393	THR	2.1
1	B	355	PHE	2.1
1	A	384	VAL	2.1
1	A	321	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	556	ASP	2.1
1	B	620	LYS	2.0
1	A	507	GLN	2.0
1	B	415	CYS	2.0
1	B	565	PRO	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	860	4/4	0.94	0.21	4.54	67,73,74,75	0
2	HEM	B	750	43/43	0.98	0.20	1.14	24,30,40,49	0
2	HEM	A	750	43/43	0.98	0.17	0.53	27,32,41,43	0
3	H4B	B	760	17/17	0.97	0.19	0.49	28,30,37,38	0
6	ZN	A	1717	1/1	0.99	0.13	0.22	40,40,40,40	0
5	ACT	B	860	4/4	0.97	0.15	0.09	54,58,58,62	0
3	H4B	A	760	17/17	0.98	0.14	-0.26	28,32,40,43	0
4	M48	A	801	23/23	0.95	0.14	-0.58	13,22,81,84	0
4	M48	B	801	23/23	0.93	0.15	-0.70	16,26,76,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.