Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 09:50 AM GMT

PDB ID : 3JX6

Title : Structure of neuronal nitric oxide synthase D597N/M336V/Y706A mutant heme domain complexed with N1-[(3' R,4' R)-4'-((6"-amino-4"-methylpy ridin-2"-yl)methyl)pyrrolidin-3'-yl]-N2-(3'-fluorophenethyl)ethane-1,2-diamin e tetrahydrochloride

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Deposited on : 2009-09-18

Resolution : 2.35 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 (i) symbol.

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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.
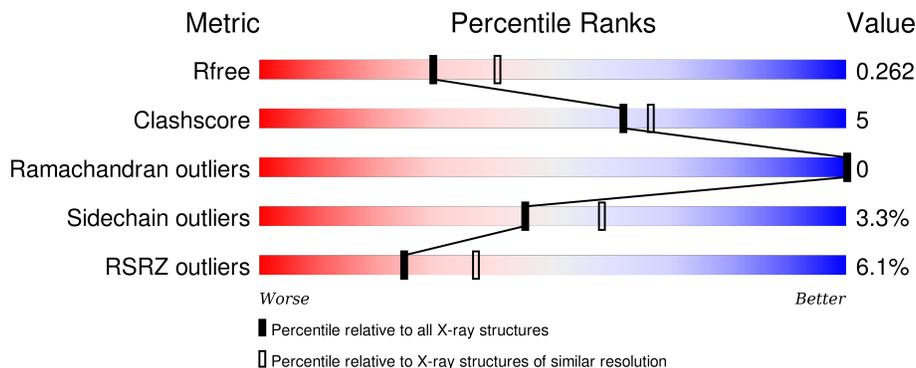
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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 <=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	JI5	A	800	-	-	-	X
4	JI5	B	800	-	-	-	X
5	ACT	A	860	-	-	-	X
5	ACT	B	861	-	-	-	X

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7014 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
			3305	2115	567	603	20			
1	B	411	Total	C	N	O	S	0	0	0
			3337	2134	575	608	20			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	336	VAL	MET	ENGINEERED	UNP P29476
A	597	ASN	ASP	ENGINEERED	UNP P29476
A	706	ALA	TYR	ENGINEERED	UNP P29476
B	336	VAL	MET	ENGINEERED	UNP P29476
B	597	ASN	ASP	ENGINEERED	UNP P29476
B	706	ALA	TYR	ENGINEERED	UNP P29476

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).
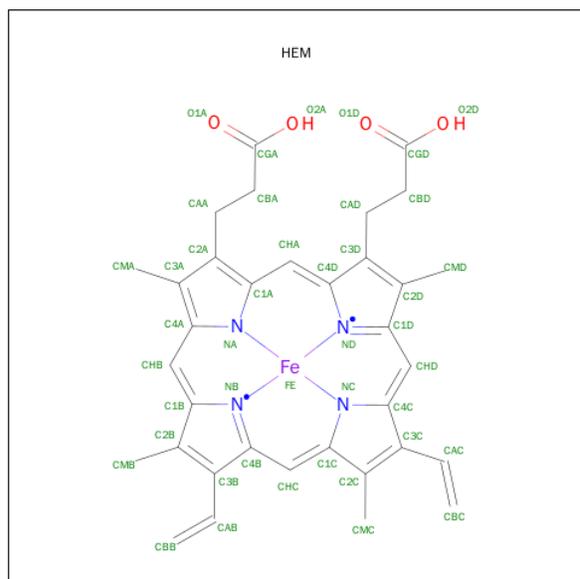
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $C_9H_{15}N_5O_3$).
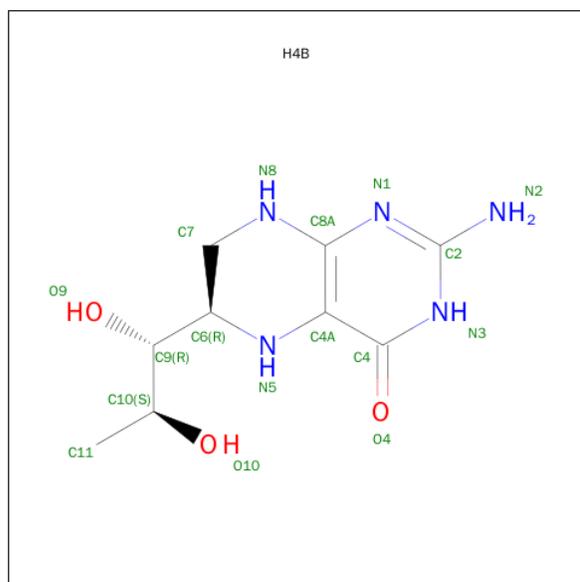
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is N-{(3R,4R)-4-[(6-AMINO-4-METHYLPYRIDIN-2-YL)METHYL]PYRRO LIDIN-3-YL}-N'-[2-(3-FLUOROPHENYL)ETHYL]ETHANE-1,2-DIAMINE (three-letter code: JI5) (formula: $C_{21}H_{30}FN_5$).
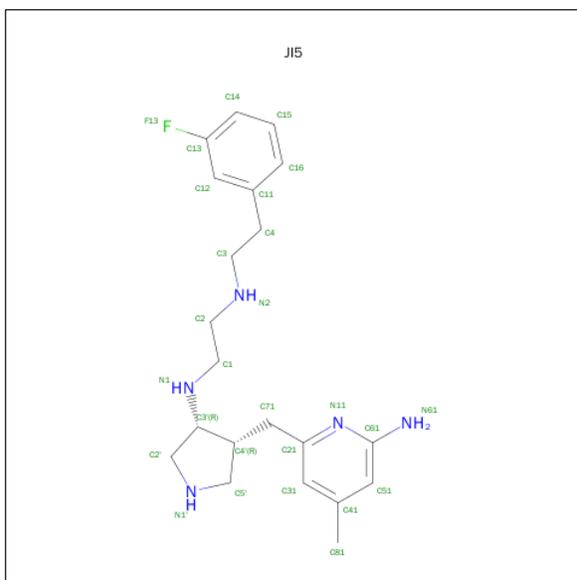
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	F	N	0	0
			27	21	1	5		
4	B	1	Total	C	F	N	0	0
			27	21	1	5		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).
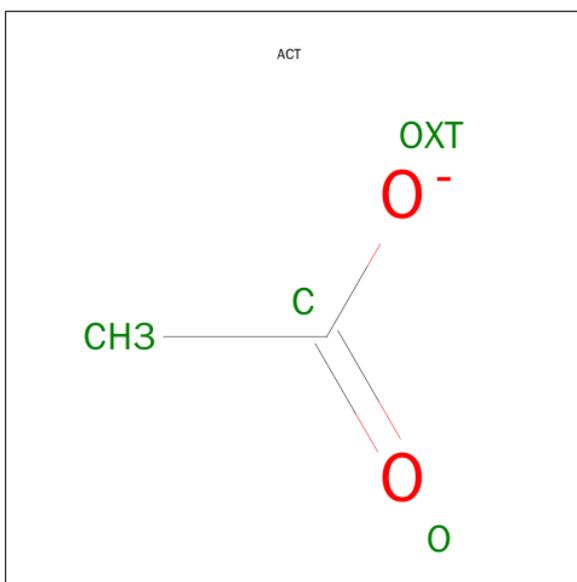
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

- 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	77	Total 77	O 77	0	0
7	B	112	Total 112	O 112	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
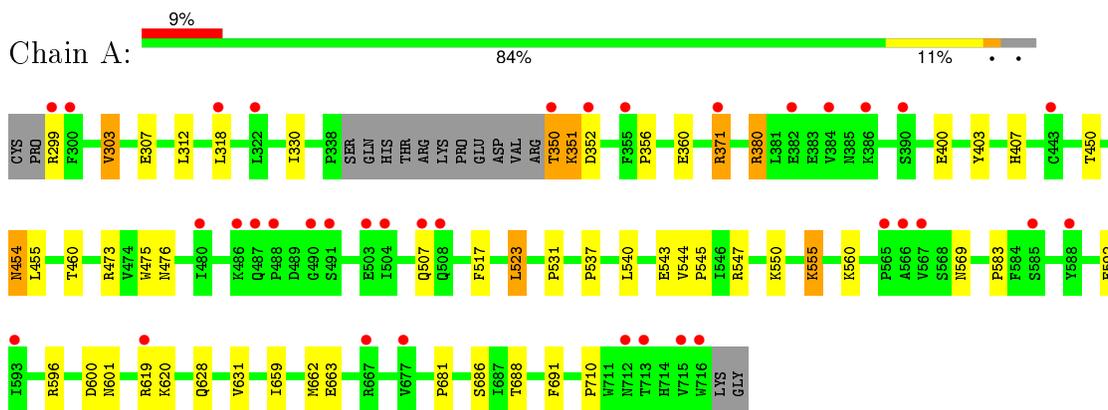
• Molecule 1: Nitric oxide synthase, brain
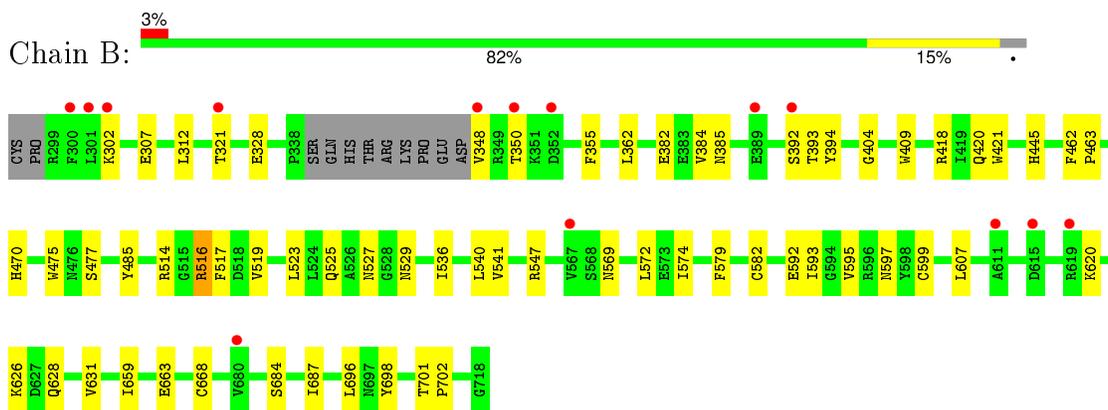
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	51.92Å 111.00Å 164.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.81 – 2.35 40.81 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.4 (40.81-2.35) 98.4 (40.81-2.35)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$<I/\sigma(I)>$ [1]	1.17 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0089	Depositor
R, R_{free}	0.188 , 0.245 0.208 , 0.262	Depositor DCC
R_{free} test set	1964 reflections (5.21%)	DCC
Wilson B-factor (Å^2)	45.7	Xtriage
Anisotropy	0.388	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 46.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$<|L|> = 0.49$, $<L^2> = 0.32$	Xtriage
Outliers	1 of 39665 reflections (0.003%)	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7014	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.40% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.

[2] Theoretical values of $<|L|>$, $<L^2>$ 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, JI5, 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	0.61	0/3397	0.66	0/4610
1	B	0.68	0/3429	0.71	0/4650
All	All	0.65	0/6826	0.69	0/9260

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 (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	3305	0	3219	37	0
1	B	3337	0	3257	35	0
2	A	43	0	30	4	0
2	B	43	0	30	1	0
3	A	17	0	15	0	0
3	B	17	0	15	0	0
4	A	27	0	30	2	0
4	B	27	0	30	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	77	0	0	3	0
7	B	112	0	0	3	0
All	All	7014	0	6632	73	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 5.

All (73) 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:668:CYS:HB3	7:B:1081:HOH:O	1.67	0.92
1:A:371:ARG:HH21	1:A:371:ARG:HG2	1.39	0.88
1:A:371:ARG:CG	1:A:371:ARG:HH21	1.91	0.83
2:A:750:HEM:HMC2	2:A:750:HEM:HBC2	1.60	0.81
1:A:601:ASN:HB2	7:A:1017:HOH:O	1.81	0.79
1:A:475:TRP:HB2	1:A:523:LEU:HB3	1.71	0.73
1:A:380:ARG:HD3	1:A:400:GLU:OE1	1.89	0.72
1:A:371:ARG:HG2	1:A:371:ARG:NH2	2.05	0.71
1:A:592:GLU:OE1	4:A:800:JI5:H16	1.91	0.69
1:A:303:VAL:HG23	1:A:312:LEU:HB2	1.77	0.67
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.78	0.66
1:A:307:GLU:HG3	7:B:1003:HOH:O	1.96	0.64
1:B:525:GLN:HG3	1:B:529:ASN:O	1.99	0.63
1:A:350:THR:HG22	1:A:351:LYS:H	1.63	0.63
1:B:536:ILE:HG13	7:B:1099:HOH:O	2.00	0.61
2:A:750:HEM:CMC	2:A:750:HEM:HBC2	2.29	0.59
1:A:620:LYS:HB2	1:A:620:LYS:NZ	2.17	0.59
1:A:299:ARG:HG3	1:A:318:LEU:HD21	1.86	0.58
1:B:409:TRP:CE3	1:B:421:TRP:HA	2.39	0.58
2:A:750:HEM:HBB2	2:A:750:HEM:HHC	1.86	0.57
1:A:659:ILE:O	1:A:663:GLU:HG3	2.05	0.56
1:B:659:ILE:O	1:B:663:GLU:HG3	2.06	0.55
2:A:750:HEM:HBA1	4:A:800:JI5:H4	1.88	0.54
1:B:470:HIS:HB3	1:B:527:ASN:ND2	2.22	0.53
1:B:572:LEU:HB3	1:B:579:PHE:HB2	1.92	0.51
1:B:684:SER:HB3	1:B:687:ILE:HD11	1.93	0.50
1:A:330:ILE:HD11	1:B:696:LEU:HB3	1.93	0.49
1:A:686:SER:HA	1:A:691:PHE:CG	2.47	0.49
7:A:1001:HOH:O	1:B:307:GLU:HG3	2.12	0.49
1:B:595:VAL:O	1:B:599:CYS:HB2	2.13	0.48
1:A:460:THR:O	1:A:583:PRO:HD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:THR:HA	1:A:455:LEU:HD22	1.95	0.48
1:B:607:LEU:HD13	1:B:626:LYS:HG2	1.96	0.47
1:A:631:VAL:HG11	1:B:628:GLN:HG2	1.97	0.47
1:B:516:ARG:HG2	1:B:517:PHE:CE1	2.50	0.47
1:A:628:GLN:HG2	1:B:631:VAL:HG11	1.96	0.47
1:A:543:GLU:OE2	1:A:560:LYS:HE3	2.15	0.46
1:A:475:TRP:CZ2	1:A:531:PRO:HG3	2.50	0.46
1:A:555:LYS:HB3	1:A:555:LYS:NZ	2.32	0.45
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.05	0.45
1:B:445:HIS:C	1:B:445:HIS:CD2	2.91	0.45
1:B:477:SER:HA	1:B:569:ASN:HB3	1.98	0.44
1:B:418:ARG:C	1:B:420:GLN:N	2.70	0.44
1:A:523:LEU:HA	1:A:523:LEU:HD23	1.84	0.44
1:A:596:ARG:NH2	1:A:600:ASP:OD2	2.44	0.44
1:B:302:LYS:HA	1:B:312:LEU:O	2.18	0.44
1:A:537:PRO:HB2	1:A:540:LEU:HG	1.99	0.44
1:B:485:TYR:CE1	1:B:514:ARG:HA	2.54	0.43
1:A:352:ASP:O	1:A:356:PRO:HD2	2.19	0.43
1:B:362:LEU:HA	1:B:362:LEU:HD23	1.91	0.43
1:B:355:PHE:CE1	1:B:385:ASN:HB2	2.53	0.42
1:B:582:CYS:O	1:B:582:CYS:SG	2.76	0.42
1:A:681:PRO:HG2	1:A:688:THR:HG21	2.01	0.42
1:A:454:ASN:ND2	7:A:1019:HOH:O	2.53	0.42
1:B:418:ARG:C	1:B:420:GLN:H	2.22	0.42
1:A:473:ARG:NH2	1:A:710:PRO:HD3	2.35	0.42
1:A:475:TRP:CE3	1:A:523:LEU:HD13	2.55	0.42
1:B:462:PHE:HB3	1:B:463:PRO:CD	2.50	0.42
1:B:592:GLU:OE1	4:B:800:JI5:H16	2.20	0.42
1:A:303:VAL:CG2	1:A:312:LEU:HB2	2.47	0.41
1:B:519:VAL:HG21	1:B:541:VAL:HG11	2.02	0.41
1:A:517:PHE:CB	1:A:560:LYS:HE2	2.50	0.41
1:B:593:ILE:HA	1:B:597:ASN:HB2	2.03	0.41
1:B:362:LEU:HD11	1:B:384:VAL:HG21	2.03	0.41
1:B:404:GLY:HA3	1:B:574:ILE:HD13	2.02	0.41
1:B:393:THR:OG1	1:B:394:TYR:N	2.53	0.41
1:B:475:TRP:HB2	1:B:523:LEU:HB3	2.03	0.41
1:A:330:ILE:HD12	1:B:698:TYR:CD2	2.55	0.41
1:B:701:THR:HA	1:B:702:PRO:C	2.40	0.41
1:A:544:VAL:HA	1:A:545:PRO:HD3	1.89	0.41
1:B:382:GLU:HA	1:B:382:GLU:OE1	2.20	0.41
2:B:750:HEM:CMC	2:B:750:HEM:HBC2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:550:LYS:HB2	1:A:550:LYS:HE3	1.89	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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%)	387 (96%)	16 (4%)	0	100	100
1	B	407/422 (96%)	395 (97%)	12 (3%)	0	100	100
All	All	810/844 (96%)	782 (96%)	28 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	362/376 (96%)	347 (96%)	15 (4%)	37	48
1	B	365/376 (97%)	356 (98%)	9 (2%)	55	70
All	All	727/752 (97%)	703 (97%)	24 (3%)	45	58

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	303	VAL
1	A	350	THR
1	A	351	LYS
1	A	360	GLU
1	A	371	ARG
1	A	380	ARG
1	A	454	ASN
1	A	476	ASN
1	A	507	GLN
1	A	523	LEU
1	A	547	ARG
1	A	555	LYS
1	A	569	ASN
1	A	619	ARG
1	A	662	MET
1	B	321	THR
1	B	328	GLU
1	B	348	VAL
1	B	350	THR
1	B	392	SER
1	B	516	ARG
1	B	540	LEU
1	B	547	ARG
1	B	620	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	317	HIS
1	A	353	GLN
1	A	436	HIS
1	A	454	ASN
1	A	569	ASN
1	A	605	ASN
1	A	642	GLN
1	A	697	ASN
1	A	712	ASN
1	B	329	HIS
1	B	364	GLN
1	B	385	ASN
1	B	425	GLN
1	B	436	HIS
1	B	454	ASN

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Mol	Chain	Res	Type
1	B	527	ASN
1	B	601	ASN
1	B	605	ASN
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	750	1	30,50,50	2.16	10 (33%)	24,82,82	2.68	11 (45%)
3	H4B	A	760	-	13,18,18	0.69	0	11,26,26	2.64	6 (54%)
4	JI5	A	800	-	26,29,29	0.69	0	30,38,38	1.75	6 (20%)
5	ACT	A	860	-	1,3,3	1.27	0	0,3,3	0.00	-
2	HEM	B	750	1	30,50,50	2.23	7 (23%)	24,82,82	2.71	10 (41%)
3	H4B	B	761	-	13,18,18	0.90	0	11,26,26	2.56	4 (36%)
4	JI5	B	800	-	26,29,29	0.69	0	30,38,38	1.82	6 (20%)
5	ACT	B	861	-	1,3,3	1.26	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	JI5	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	761	-	-	0/8/17/17	0/2/2/2
4	JI5	B	800	-	-	0/13/23/23	0/3/3/3
5	ACT	B	861	-	-	0/0/0/0	0/0/0/0

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	750	HEM	C3B-C4B	-7.27	1.45	1.51
2	A	750	HEM	C3D-C4D	-6.26	1.43	1.51
2	A	750	HEM	C3B-C4B	-5.80	1.46	1.51
2	B	750	HEM	C3D-C4D	-5.66	1.44	1.51
2	B	750	HEM	C2C-C1C	-4.49	1.44	1.52
2	A	750	HEM	C2C-C1C	-3.00	1.46	1.52
2	A	750	HEM	C2D-C1D	-2.80	1.42	1.51
2	B	750	HEM	C2B-C1B	-2.34	1.44	1.51
2	B	750	HEM	C2D-C1D	-2.08	1.45	1.51
2	A	750	HEM	C2B-C1B	-2.06	1.45	1.51
2	B	750	HEM	C1C-NC	2.02	1.38	1.36
2	A	750	HEM	FE-ND	2.02	2.08	1.97
2	A	750	HEM	FE-NC	2.09	2.04	1.95
2	A	750	HEM	FE-NB	2.24	2.09	1.97
2	A	750	HEM	C3B-CAB	2.34	1.55	1.51
2	B	750	HEM	CMA-C3A	2.47	1.56	1.51
2	A	750	HEM	C1C-NC	2.65	1.39	1.36

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	750	HEM	CBA-CAA-C2A	-5.69	102.33	112.53
2	A	750	HEM	CBD-CAD-C3D	-5.12	98.64	113.55
4	A	800	JI5	C3-C4-C11	-3.95	104.63	112.83
2	A	750	HEM	CBA-CAA-C2A	-3.86	105.62	112.53
3	A	760	H4B	N3-C2-N1	-3.81	119.28	125.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	750	HEM	CAA-C2A-C1A	-3.20	123.53	127.01
4	B	800	JI5	C3-C4-C11	-3.18	106.24	112.83
2	B	750	HEM	C3C-CAC-CBC	-3.10	119.71	124.46
2	B	750	HEM	CBD-CAD-C3D	-3.02	104.76	113.55
2	A	750	HEM	C3C-CAC-CBC	-3.02	119.83	124.46
4	A	800	JI5	C14-C13-C12	-2.67	119.91	123.35
4	A	800	JI5	C31-C21-N11	-2.39	120.27	122.96
3	B	761	H4B	N3-C2-N1	-2.23	121.88	125.53
4	B	800	JI5	C31-C21-N11	-2.18	120.50	122.96
4	B	800	JI5	C21-C71-C4'	-2.14	107.35	115.57
4	B	800	JI5	C41-C31-C21	-2.09	118.97	120.28
3	A	760	H4B	N2-C2-N1	2.02	120.54	117.20
3	B	761	H4B	N2-C2-N1	2.12	120.71	117.20
2	A	750	HEM	C2C-C1C-CHC	2.25	127.11	123.68
2	B	750	HEM	C3B-C4B-CHC	2.37	126.50	123.16
4	A	800	JI5	C2-C1-N1	2.40	114.11	110.67
2	B	750	HEM	CMD-C2D-C3D	2.57	125.72	114.35
3	A	760	H4B	C4A-C8A-N8	2.89	121.83	118.43
2	A	750	HEM	CMD-C2D-C3D	2.99	127.56	114.35
2	A	750	HEM	C2D-C3D-C4D	3.02	106.62	101.50
3	A	760	H4B	C2-N1-C8A	3.10	121.51	114.54
2	A	750	HEM	C3B-C4B-CHC	3.54	128.15	123.16
3	B	761	H4B	C4-N3-C2	3.78	121.19	115.94
2	B	750	HEM	CMC-C2C-C3C	4.06	126.68	116.53
4	A	800	JI5	C1-N1-C3'	4.07	120.03	113.89
3	A	760	H4B	C4-C4A-C8A	4.16	118.33	114.56
4	B	800	JI5	C61-N11-C21	4.17	121.19	118.23
2	A	750	HEM	CMB-C2B-C3B	4.24	127.11	116.53
2	A	750	HEM	CMC-C2C-C3C	4.24	127.12	116.53
2	A	750	HEM	CAD-C3D-C4D	4.25	127.45	112.47
3	A	760	H4B	C4-N3-C2	4.28	121.88	115.94
4	A	800	JI5	C61-N11-C21	4.32	121.30	118.23
2	A	750	HEM	CAD-C3D-C2D	4.39	125.83	113.22
2	B	750	HEM	CAD-C3D-C4D	4.50	128.33	112.47
2	B	750	HEM	CAD-C3D-C2D	4.71	126.75	113.22
2	B	750	HEM	CMB-C2B-C3B	4.93	128.84	116.53
4	B	800	JI5	C1-N1-C3'	5.82	122.66	113.89
3	B	761	H4B	C4-C4A-C8A	6.34	120.30	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	4	0
4	A	800	JI5	2	0
2	B	750	HEM	1	0
4	B	800	JI5	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 (i)

6.1 Protein, DNA and RNA chains (i)

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%)	0.58	36 (8%)	12	20	32, 55, 93, 119	0
1	B	411/422 (97%)	0.19	14 (3%)	49	62	26, 44, 70, 86	0
All	All	818/844 (96%)	0.38	50 (6%)	25	37	26, 49, 85, 119	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	715	VAL	7.0
1	A	488	PRO	5.5
1	B	300	PHE	5.3
1	A	300	PHE	4.3
1	B	352	ASP	4.3
1	A	716	TRP	4.2
1	B	619	ARG	3.7
1	B	350	THR	3.4
1	A	713	THR	3.3
1	A	566	ALA	3.3
1	A	355	PHE	3.2
1	A	371	ARG	2.8
1	A	504	ILE	2.8
1	A	352	ASP	2.8
1	A	486	LYS	2.7
1	A	567	VAL	2.7
1	B	301	LEU	2.7
1	A	503	GLU	2.7
1	B	302	LYS	2.7
1	A	565	PRO	2.7
1	A	386	LYS	2.6
1	A	712	ASN	2.6
1	B	348	VAL	2.6
1	B	321	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	390	SER	2.6
1	B	611	ALA	2.6
1	A	588	TYR	2.5
1	A	480	ILE	2.5
1	B	615	ASP	2.5
1	A	487	GLN	2.3
1	A	322	LEU	2.3
1	A	299	ARG	2.2
1	A	318	LEU	2.2
1	A	667	ARG	2.2
1	A	593	ILE	2.2
1	A	490	GLY	2.2
1	A	507	GLN	2.2
1	A	585	SER	2.1
1	A	677	VAL	2.1
1	B	392	SER	2.1
1	A	443	CYS	2.1
1	A	384	VAL	2.1
1	B	680	VAL	2.0
1	A	350	THR	2.0
1	A	382	GLU	2.0
1	A	491	SER	2.0
1	B	389	GLU	2.0
1	A	619	ARG	2.0
1	A	508	GLN	2.0
1	B	567	VAL	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(Å²)	Q<0.9
5	ACT	B	861	4/4	0.94	0.18	5.75	69,70,70,70	0
4	JI5	A	800	27/27	0.88	0.34	2.71	52,73,79,82	0
5	ACT	A	860	4/4	0.90	0.22	2.51	80,81,81,81	0
4	JI5	B	800	27/27	0.89	0.25	2.06	53,57,63,65	0
2	HEM	A	750	43/43	0.98	0.20	0.42	30,37,52,54	0
2	HEM	B	750	43/43	0.98	0.17	0.36	29,37,46,50	0
3	H4B	A	760	17/17	0.95	0.18	0.33	39,45,48,51	0
3	H4B	B	761	17/17	0.96	0.16	-0.30	33,38,41,42	0
6	ZN	A	900	1/1	0.99	0.08	-1.56	48,48,48,48	0

6.5 Other polymers (i)

There are no such residues in this entry.