



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 27, 2017 – 04:46 PM EDT

PDB ID : 3JX2  
Title : Structure of rat neuronal nitric oxide synthase D597N/M336V mutant heme domain in complex with N1-{(3'S,4'S)-4'-[(6"-amino-4"-methylpyridin-2"-yl)methyl]pyrrolidin-3'-yl}-N2-(3'-fluorophenethyl)ethane-1,2-diamine  
Authors : Delker, S.L.; Li, H.; Poulos, T.L.  
Deposited on : unknown  
Resolution : 2.10 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](mailto: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.

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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

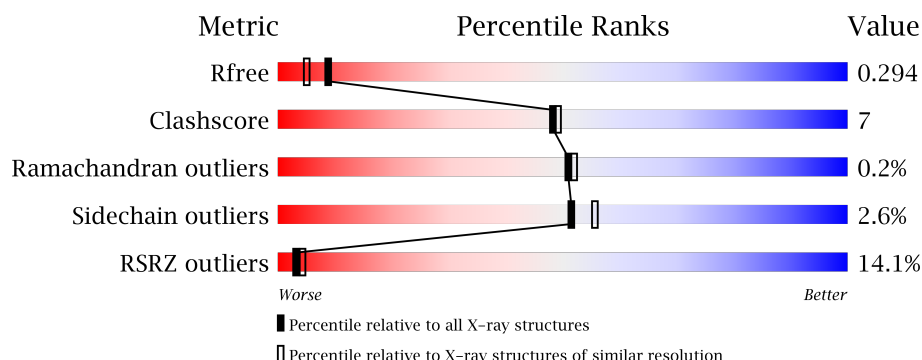
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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  $\geq 3$ , 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>82%</div> <div>15%</div> <div></div> </div> </div>
1	B	422	<div> <div>8%</div> <div> <div></div> <div>79%</div> <div>18%</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
5	ACT	A	860	-	-	X	-
6	GOL	A	880	-	-	-	X
6	GOL	B	880	-	-	-	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7190 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	409	Total	C	N	O	S	0	0	0
			3330	2132	572	606	20			
1	B	411	Total	C	N	O	S	0	0	0
			3344	2140	575	609	20			

There are 4 discrepancies between the modelled and reference sequences:

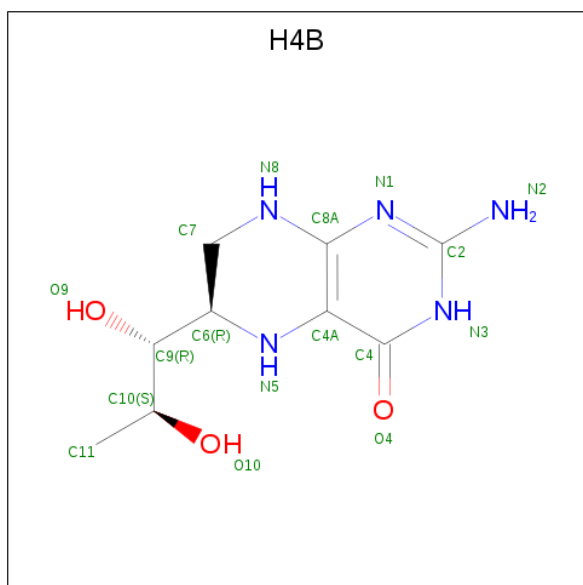
Chain	Residue	Modelled	Actual	Comment	Reference
A	336	VAL	MET	ENGINEERED	UNP P29476
A	597	ASN	ASP	ENGINEERED	UNP P29476
B	336	VAL	MET	ENGINEERED	UNP P29476
B	597	ASN	ASP	ENGINEERED	UNP P29476

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



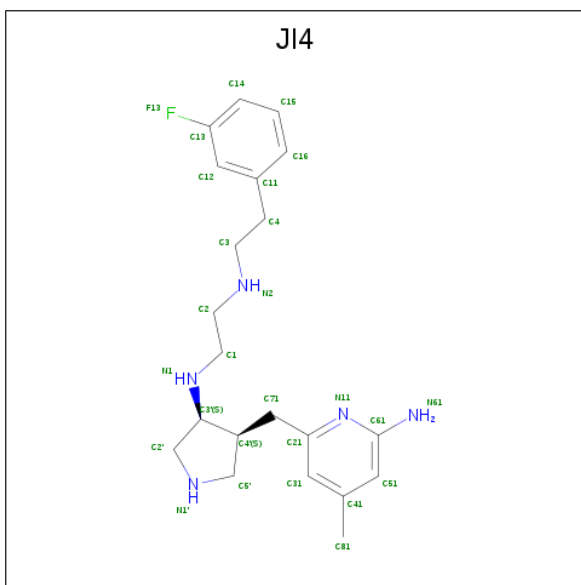
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



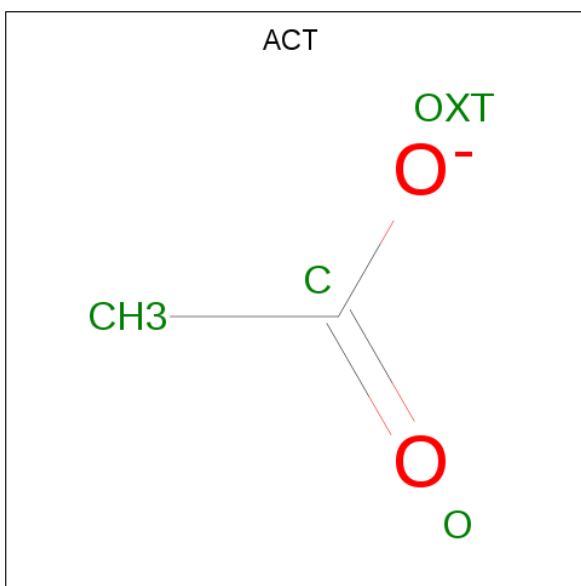
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is N-{(3S,4S)-4-[(6-amino-4-methylpyridin-2-yl)methyl]pyrrolidin-3-yl}-N'-[2-(3-fluorophenyl)ethyl]ethane-1,2-diamine (three-letter code: JI4) (formula:  $C_{21}H_{30}FN_5$ ).



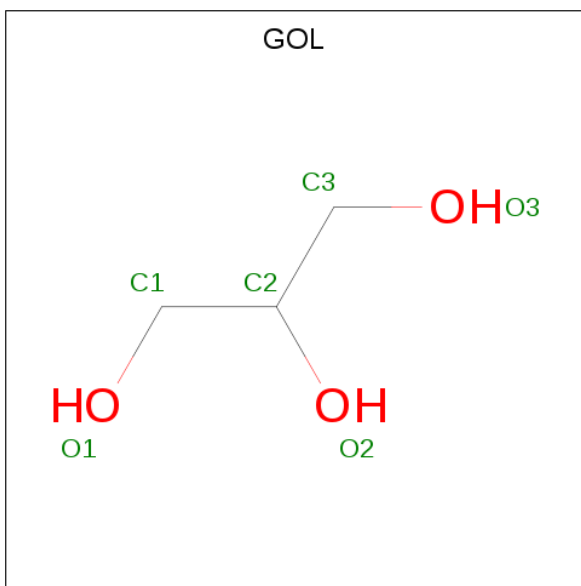
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	F	N	0	0
			27	21	1	5		
4	B	1	Total	C	F	N	0	0
			27	21	1	5		

- 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 GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula:  $Zn$ ).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Zn	0	0
			1	1		

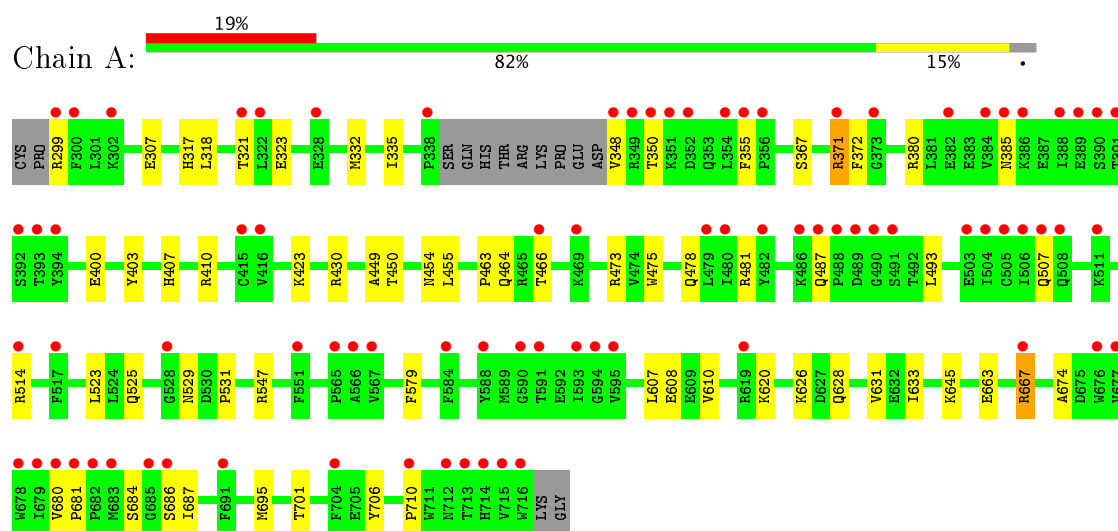
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	126	Total	O	0	0
			126	126		
8	B	195	Total	O	0	0
			195	195		

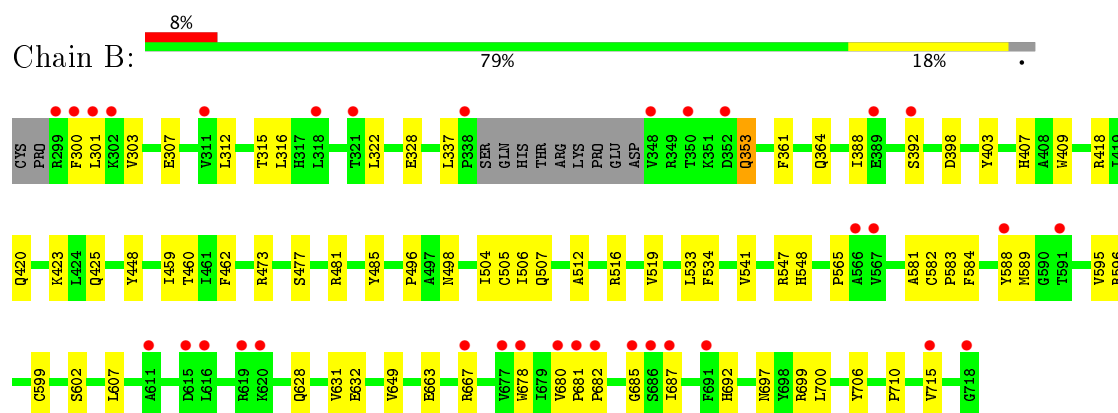
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ( $RSRZ > 2$ ). 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, $\alpha$ , $\beta$ , $\gamma$	51.69Å 110.80Å 164.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.83 – 2.10 38.53 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (46.83-2.10) 99.5 (38.53-2.10)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.73 (at 2.10Å)	Xtriage
Refinement program	CNS, REFMAC 5.5.0089	Depositor
R, $R_{free}$	0.197 , 0.248 0.246 , 0.294	Depositor DCC
$R_{free}$ test set	2768 reflections (5.22%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.4	Xtriage
Anisotropy	0.828	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7190	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.97% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, H4B, JI4, ACT, HEM

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	0.63	0/3423	0.69	1/4645 (0.0%)
1	B	0.79	1/3437 (0.0%)	0.77	1/4661 (0.0%)
All	All	0.71	1/6860 (0.0%)	0.73	2/9306 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	678	TRP	CB-CG	5.34	1.59	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	337	LEU	CA-CB-CG	7.89	133.45	115.30
1	A	410	ARG	NE-CZ-NH2	5.47	123.04	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	3330	0	3245	41	0
1	B	3344	0	3261	49	0
2	A	43	0	30	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	43	0	30	8	0
3	A	17	0	15	0	0
3	B	17	0	15	1	0
4	A	27	0	30	1	0
4	B	27	0	30	2	0
5	A	4	0	3	2	0
5	B	4	0	3	0	0
6	A	6	0	8	0	0
6	B	6	0	8	2	0
7	A	1	0	0	0	0
8	A	126	0	0	2	0
8	B	195	0	0	4	0
All	All	7190	0	6678	93	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 (93) 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)
2:B:750:HEM:HHC	2:B:750:HEM:HBB2	1.59	0.82
2:A:750:HEM:HBB2	2:A:750:HEM:HHC	1.65	0.78
1:A:371:ARG:CG	1:A:371:ARG:HH21	2.00	0.74
1:A:348:VAL:HG11	1:A:466:THR:O	1.87	0.74
3:B:760:H4B:HN5	6:B:880:GOL:H32	1.53	0.72
1:A:371:ARG:HG3	1:A:371:ARG:HH21	1.58	0.69
1:A:706:TYR:OH	2:A:750:HEM:O1D	2.06	0.68
2:A:750:HEM:HMC2	2:A:750:HEM:HBC2	1.77	0.67
1:A:473:ARG:NH2	1:A:710:PRO:HD3	2.10	0.67
1:B:460:THR:O	1:B:583:PRO:HD2	1.97	0.63
1:B:595:VAL:O	1:B:599:CYS:HB2	2.01	0.61
2:B:750:HEM:O2A	8:B:1039:HOH:O	2.16	0.60
1:A:525:GLN:HG3	1:A:529:ASN:O	2.02	0.59
2:A:750:HEM:HBA1	4:A:800:JI4:H71A	1.84	0.58
1:B:706:TYR:CZ	4:B:800:JI4:H12	2.38	0.58
2:A:750:HEM:HBB2	2:A:750:HEM:CHC	2.34	0.57
1:B:425:GLN:HG2	1:B:448:TYR:CZ	2.40	0.57
1:B:322:LEU:HD13	1:B:699:ARG:HH21	1.69	0.57
2:A:750:HEM:HMB3	5:A:860:ACT:H3	1.87	0.56
1:B:398:ASP:HB2	8:B:1103:HOH:O	2.05	0.56
1:A:323:GLU:HG2	1:B:328:GLU:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:663:GLU:O	1:A:667:ARG:HG2	2.07	0.55
1:B:462:PHE:HB2	1:B:581:ALA:HB3	1.89	0.54
1:B:596:ARG:HH22	6:B:880:GOL:H2	1.72	0.54
1:A:380:ARG:HD3	1:A:400:GLU:OE1	2.08	0.53
2:B:750:HEM:HBA1	4:B:800:JI4:H71A	1.91	0.52
1:A:684:SER:HB3	1:A:687:ILE:HG12	1.90	0.52
1:A:631:VAL:HG11	1:B:628:GLN:HG2	1.92	0.52
1:A:478:GLN:HB2	1:A:481:ARG:HG3	1.91	0.52
1:A:450:THR:HA	1:A:455:LEU:HD22	1.93	0.51
1:B:505:CYS:O	1:B:506:ILE:C	2.49	0.51
1:B:533:LEU:O	1:B:534:PHE:CG	2.63	0.51
1:A:307:GLU:HG3	8:B:1052:HOH:O	2.10	0.51
1:B:485:TYR:HE2	1:B:512:ALA:HB1	1.76	0.50
1:A:371:ARG:CG	1:A:371:ARG:NH2	2.67	0.50
1:B:409:TRP:CZ3	2:B:750:HEM:HMC3	2.48	0.49
1:A:684:SER:HB3	1:A:687:ILE:CG1	2.43	0.48
1:A:475:TRP:CZ2	1:A:531:PRO:HG3	2.47	0.48
2:A:750:HEM:HMB3	5:A:860:ACT:CH3	2.43	0.48
1:B:459:ILE:HD11	1:B:582:CYS:HB2	1.96	0.48
1:B:303:VAL:HG23	1:B:312:LEU:HB2	1.95	0.47
1:B:584:PHE:CD1	2:B:750:HEM:HAC	2.50	0.47
1:B:519:VAL:HG21	1:B:541:VAL:HG11	1.96	0.47
2:A:750:HEM:O2A	8:A:1021:HOH:O	2.21	0.47
1:A:626:LYS:HB3	1:B:687:ILE:HD12	1.97	0.47
1:A:628:GLN:HG2	1:B:631:VAL:HG11	1.97	0.47
1:B:425:GLN:HG2	1:B:448:TYR:CE2	2.49	0.46
1:A:607:LEU:HD13	1:A:626:LYS:HG2	1.97	0.46
1:A:674:ALA:HB3	1:A:695:MET:HB3	1.96	0.46
1:B:481:ARG:NE	1:B:498:ASN:HD21	2.14	0.46
1:B:403:TYR:CE1	1:B:407:HIS:CE1	3.04	0.45
1:A:523:LEU:HD22	1:A:531:PRO:HB2	1.98	0.45
1:B:316:LEU:HD21	1:B:700:LEU:HD11	1.98	0.45
2:A:750:HEM:CBB	2:A:750:HEM:HHC	2.42	0.45
1:B:663:GLU:O	1:B:667:ARG:HD2	2.17	0.45
1:A:403:TYR:CE1	1:A:407:HIS:CE1	3.06	0.44
1:A:355:PHE:CE1	1:A:385:ASN:HB2	2.52	0.44
1:B:473:ARG:CZ	1:B:710:PRO:HG3	2.48	0.44
1:A:430:ARG:O	1:A:463:PRO:HG3	2.18	0.44
1:B:353:GLN:HB3	1:B:353:GLN:HE21	1.63	0.43
1:A:299:ARG:HA	8:A:1034:HOH:O	2.18	0.43
1:B:307:GLU:HG2	1:B:692:HIS:CG	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:565:PRO:HB3	1:B:588:TYR:CZ	2.53	0.43
1:B:409:TRP:CH2	2:B:750:HEM:HMC3	2.54	0.43
1:A:686:SER:OG	1:B:595:VAL:HG12	2.19	0.43
1:A:299:ARG:O	1:A:317:HIS:CE1	2.72	0.43
1:B:361:PHE:HA	1:B:364:GLN:HE21	1.84	0.43
1:A:680:VAL:HA	1:A:681:PRO:HD3	1.90	0.42
1:A:686:SER:HB3	1:B:682:PRO:HB2	2.00	0.42
1:A:332:MET:HE2	1:B:301:LEU:HD22	2.01	0.42
1:B:589:MET:HA	1:B:649:VAL:O	2.19	0.42
1:B:584:PHE:CD1	2:B:750:HEM:CAC	3.03	0.42
1:A:367:SER:HA	1:A:372:PHE:HB2	2.01	0.42
1:A:449:ALA:O	1:A:455:LEU:HA	2.20	0.42
1:A:610:VAL:HG21	1:A:633:ILE:HD11	2.01	0.41
1:A:487:GLN:HE22	1:A:493:LEU:HD22	1.85	0.41
1:B:418:ARG:C	1:B:420:GLN:N	2.73	0.41
1:B:388:ILE:O	1:B:392:SER:N	2.47	0.41
1:A:332:MET:HB3	1:A:335:ILE:HG13	2.03	0.41
1:A:332:MET:CE	1:B:301:LEU:HD22	2.50	0.41
1:B:496:PRO:HB2	1:B:602:SER:O	2.20	0.41
1:A:464:GLN:HB3	1:A:579:PHE:CE2	2.55	0.41
1:A:423:LYS:HE2	1:A:423:LYS:HB2	1.87	0.41
1:B:300:PHE:CD2	1:B:315:THR:HG22	2.56	0.41
1:B:680:VAL:HA	1:B:681:PRO:HD3	1.95	0.41
1:B:473:ARG:HD2	1:B:473:ARG:HA	1.83	0.41
1:A:323:GLU:HA	1:B:328:GLU:O	2.21	0.41
1:B:303:VAL:CG2	1:B:312:LEU:HB2	2.51	0.41
1:B:697:ASN:HD22	1:B:697:ASN:HA	1.70	0.41
1:B:607:LEU:HB2	8:B:1023:HOH:O	2.21	0.40
1:B:409:TRP:CZ2	2:B:750:HEM:CHC	3.05	0.40
1:A:299:ARG:HG3	1:A:318:LEU:HD11	2.03	0.40
1:B:548:HIS:NE2	1:B:632:GLU:OE1	2.54	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	405/422 (96%)	390 (96%)	15 (4%)	0	100	100
1	B	407/422 (96%)	390 (96%)	15 (4%)	2 (0%)	32	28
All	All	812/844 (96%)	780 (96%)	30 (4%)	2 (0%)	51	52

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	685	GLY
1	B	504	ILE

### 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%)	353 (97%)	12 (3%)	43	45
1	B	366/377 (97%)	359 (98%)	7 (2%)	62	68
All	All	731/754 (97%)	712 (97%)	19 (3%)	51	55

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

Mol	Chain	Res	Type
1	A	321	THR
1	A	350	THR
1	A	371	ARG
1	A	454	ASN
1	A	507	GLN
1	A	514	ARG
1	A	547	ARG
1	A	608	GLU
1	A	620	LYS
1	A	645	LYS
1	A	667	ARG

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Mol	Chain	Res	Type
1	A	701	THR
1	B	353	GLN
1	B	423	LYS
1	B	477	SER
1	B	507	GLN
1	B	516	ARG
1	B	547	ARG
1	B	715	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	364	GLN
1	A	454	ASN
1	A	642	GLN
1	A	697	ASN
1	B	364	GLN
1	B	385	ASN
1	B	420	GLN
1	B	454	ASN
1	B	508	GLN
1	B	601	ASN
1	B	605	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 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	2.23	8 (28%)	17,82,82	2.62	7 (41%)
3	H4B	A	760	-	14,18,18	0.76	0	12,26,26	2.29	4 (33%)
4	JI4	A	800	-	25,29,29	0.77	2 (8%)	30,38,38	1.72	8 (26%)
5	ACT	A	860	-	1,3,3	1.73	0	0,3,3	0.00	-
6	GOL	A	880	-	5,5,5	0.42	0	5,5,5	0.18	0
2	HEM	B	750	1	28,50,50	2.21	10 (35%)	17,82,82	2.60	8 (47%)
3	H4B	B	760	-	14,18,18	0.66	0	12,26,26	2.26	4 (33%)
4	JI4	B	800	-	25,29,29	0.72	0	30,38,38	1.60	7 (23%)
5	ACT	B	860	-	1,3,3	1.44	0	0,3,3	0.00	-
6	GOL	B	880	-	5,5,5	0.33	0	5,5,5	0.15	0

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	JI4	A	800	-	-	0/13/23/23	0/3/3/3
5	ACT	A	860	-	-	0/0/0/0	0/0/0/0
6	GOL	A	880	-	-	0/4/4/4	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	JI4	B	800	-	-	0/13/23/23	0/3/3/3
5	ACT	B	860	-	-	0/0/0/0	0/0/0/0
6	GOL	B	880	-	-	0/4/4/4	0/0/0/0

All (20) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	750	HEM	C3B-C2B	-5.86	1.32	1.40
2	B	750	HEM	C3C-C2C	-4.48	1.34	1.40
2	A	750	HEM	C3C-C2C	-4.01	1.35	1.40
2	B	750	HEM	C3B-C2B	-3.12	1.36	1.40
2	B	750	HEM	C4A-CHB	-2.11	1.34	1.40
4	A	800	JI4	C14-C13	2.06	1.41	1.37
4	A	800	JI4	C12-C13	2.07	1.41	1.37
2	B	750	HEM	CMA-C3A	2.24	1.56	1.51
2	A	750	HEM	C1D-ND	2.28	1.41	1.36
2	A	750	HEM	C3C-CAC	2.54	1.52	1.47
2	B	750	HEM	CMB-C2B	2.61	1.57	1.51
2	B	750	HEM	C4D-ND	2.63	1.39	1.36
2	A	750	HEM	CMC-C2C	2.82	1.57	1.51
2	A	750	HEM	C4D-ND	2.82	1.40	1.36
2	B	750	HEM	C3B-CAB	3.01	1.53	1.47
2	A	750	HEM	C3B-CAB	3.39	1.54	1.47
2	B	750	HEM	C1B-NB	3.46	1.40	1.36
2	B	750	HEM	C3C-CAC	3.58	1.54	1.47
2	B	750	HEM	C3D-C2D	4.84	1.52	1.37
2	A	750	HEM	C3D-C2D	5.11	1.52	1.37

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	750	HEM	CBA-CAA-C2A	-6.64	99.78	112.48
2	B	750	HEM	CBA-CAA-C2A	-6.32	100.39	112.48
2	A	750	HEM	CBD-CAD-C3D	-5.02	102.90	112.47
2	B	750	HEM	C1D-C2D-C3D	-4.43	103.91	107.00
4	B	800	JI4	C31-C21-N11	-3.46	119.16	122.91
2	B	750	HEM	CAD-CBD-CGD	-3.31	107.00	112.66
4	A	800	JI4	C31-C21-N11	-3.20	119.44	122.91
4	A	800	JI4	C14-C13-C12	-2.88	119.51	123.29
4	A	800	JI4	C2-C1-N1	-2.80	106.53	111.03
3	A	760	H4B	N3-C2-N1	-2.61	121.22	125.45
2	A	750	HEM	C3C-C4C-NC	-2.60	106.04	110.94
2	B	750	HEM	CMA-C3A-C4A	-2.57	124.52	128.46
4	B	800	JI4	C3-C4-C11	-2.53	107.51	112.81
4	B	800	JI4	C14-C13-C12	-2.43	120.10	123.29
4	A	800	JI4	C81-C41-C31	-2.41	117.39	120.94
3	B	760	H4B	N3-C2-N1	-2.37	121.61	125.45
2	A	750	HEM	CAD-CBD-CGD	-2.35	108.64	112.66
4	A	800	JI4	C3-C4-C11	-2.09	108.44	112.81
2	A	750	HEM	C1D-C2D-C3D	-2.08	105.55	107.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	750	HEM	CBD-CAD-C3D	-2.06	108.54	112.47
2	B	750	HEM	CMA-C3A-C2A	2.05	128.81	124.94
4	B	800	JI4	C2'-C3'-N1	2.18	117.64	113.95
2	A	750	HEM	CMC-C2C-C3C	2.37	129.29	124.89
4	B	800	JI4	C3-N2-C2	2.53	122.53	113.33
3	B	760	H4B	C2-N1-C8A	2.54	120.23	114.51
2	B	750	HEM	C4C-C3C-C2C	2.54	108.67	106.90
2	B	750	HEM	CMB-C2B-C3B	2.58	129.69	124.89
4	B	800	JI4	C5'-N1'-C2'	2.58	111.42	105.40
4	A	800	JI4	C71-C21-N11	2.59	121.20	117.12
3	A	760	H4B	C2-N1-C8A	2.78	120.77	114.51
3	A	760	H4B	C4-N3-C2	3.27	120.77	116.06
3	B	760	H4B	C4-N3-C2	3.31	120.82	116.06
4	A	800	JI4	C61-N11-C21	3.56	120.69	118.17
4	A	800	JI4	C5'-N1'-C2'	3.58	113.72	105.40
4	B	800	JI4	C61-N11-C21	4.02	121.01	118.17
2	A	750	HEM	C4C-C3C-C2C	4.06	109.73	106.90
3	A	760	H4B	C4-C4A-C8A	4.90	119.00	114.56
3	B	760	H4B	C4-C4A-C8A	5.39	119.44	114.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	750	HEM	9	0
4	A	800	JI4	1	0
5	A	860	ACT	2	0
2	B	750	HEM	8	0
3	B	760	H4B	1	0
4	B	800	JI4	2	0
6	B	880	GOL	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	409/422 (96%)	1.02	82 (20%) 1 1	29, 57, 107, 131	0
1	B	411/422 (97%)	0.49	34 (8%) 12 15	25, 45, 76, 98	0
All	All	820/844 (97%)	0.75	116 (14%) 3 4	25, 50, 98, 131	0

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	PHE	9.0
1	A	348	VAL	7.2
1	A	488	PRO	6.9
1	A	300	PHE	6.5
1	A	716	TRP	6.2
1	B	718	GLY	6.0
1	A	715	VAL	6.0
1	B	348	VAL	5.6
1	A	352	ASP	4.9
1	A	503	GLU	4.8
1	A	349	ARG	4.8
1	A	355	PHE	4.7
1	A	490	GLY	4.5
1	A	390	SER	4.4
1	B	619	ARG	4.1
1	B	302	LYS	4.0
1	A	391	THR	4.0
1	A	506	ILE	4.0
1	B	350	THR	3.9
1	A	350	THR	3.8
1	B	616	LEU	3.8
1	A	713	THR	3.7
1	B	352	ASP	3.7
1	B	715	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	712	ASN	3.6
1	A	567	VAL	3.5
1	A	619	ARG	3.4
1	A	392	SER	3.3
1	A	299	ARG	3.3
1	A	351	LYS	3.3
1	A	588	TYR	3.3
1	A	393	THR	3.3
1	A	322	LEU	3.3
1	A	302	LYS	3.2
1	A	486	LYS	3.2
1	A	389	GLU	3.2
1	B	691	PHE	3.2
1	B	611	ALA	3.1
1	A	682	PRO	3.1
1	A	388	ILE	3.1
1	A	679	ILE	3.1
1	A	566	ALA	3.1
1	A	507	GLN	3.1
1	B	311	VAL	3.1
1	A	678	TRP	3.0
1	A	677	VAL	3.0
1	A	591	THR	3.0
1	A	479	LEU	2.9
1	B	677	VAL	2.9
1	A	321	THR	2.9
1	A	511	LYS	2.8
1	B	591	THR	2.8
1	A	487	GLN	2.8
1	A	683	MET	2.8
1	A	489	ASP	2.8
1	A	382	GLU	2.8
1	A	704	PHE	2.8
1	A	595	VAL	2.7
1	A	356	PRO	2.7
1	A	528	GLY	2.7
1	A	551	PHE	2.7
1	A	714	HIS	2.7
1	A	691	PHE	2.7
1	A	685	GLY	2.7
1	A	482	TYR	2.7
1	B	620	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	593	ILE	2.6
1	B	615	ASP	2.6
1	A	469	LYS	2.6
1	A	681	PRO	2.6
1	A	385	ASN	2.6
1	A	565	PRO	2.5
1	A	415	CYS	2.5
1	A	584	PHE	2.5
1	A	680	VAL	2.5
1	B	299	ARG	2.5
1	A	517	PHE	2.5
1	B	566	ALA	2.4
1	A	373	GLY	2.4
1	B	588	TYR	2.4
1	B	680	VAL	2.4
1	A	466	THR	2.4
1	A	394	TYR	2.4
1	A	328	GLU	2.3
1	B	389	GLU	2.3
1	A	386	LYS	2.3
1	A	676	TRP	2.3
1	B	567	VAL	2.3
1	B	301	LEU	2.3
1	B	685	GLY	2.3
1	A	505	CYS	2.3
1	B	667	ARG	2.3
1	B	321	THR	2.3
1	A	667	ARG	2.3
1	A	384	VAL	2.2
1	A	491	SER	2.2
1	B	338	PRO	2.2
1	B	392	SER	2.2
1	A	504	ILE	2.2
1	A	508	GLN	2.2
1	A	338	PRO	2.2
1	A	594	GLY	2.2
1	B	681	PRO	2.2
1	A	480	ILE	2.1
1	B	318	LEU	2.1
1	B	678	TRP	2.1
1	A	371	ARG	2.1
1	B	682	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	687	ILE	2.1
1	A	590	GLY	2.1
1	A	354	LEU	2.1
1	A	686	SER	2.1
1	B	686	SER	2.1
1	A	416	VAL	2.1
1	A	514	ARG	2.0
1	A	710	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
6	GOL	B	880	6/6	0.81	0.35	3.43	88,89,89,89	0
6	GOL	A	880	6/6	0.76	0.34	3.20	58,61,63,64	0
4	J14	A	800	27/27	0.82	0.30	1.70	34,44,69,71	0
4	J14	B	800	27/27	0.89	0.25	1.52	29,41,72,73	0
2	HEM	A	750	43/43	0.96	0.24	0.99	30,35,46,50	0
2	HEM	B	750	43/43	0.96	0.19	0.58	30,35,42,49	0
3	H4B	B	760	17/17	0.94	0.21	0.52	24,30,40,43	0
3	H4B	A	760	17/17	0.94	0.18	0.04	31,34,40,41	0
5	ACT	B	860	4/4	0.94	0.11	-0.25	59,60,60,61	0
5	ACT	A	860	4/4	0.95	0.11	-0.85	64,66,66,67	0
7	ZN	A	900	1/1	0.99	0.10	-1.34	41,41,41,41	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.