



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 13, 2017 – 12:54 am GMT

PDB ID : 2M33  
Title : Solution NMR structure of full-length oxidized microsomal rabbit cytochrome b5  
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Deposited on : 2013-01-08

This is a Full wwPDB NMR 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/NMRValidationReportHelp>

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:

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

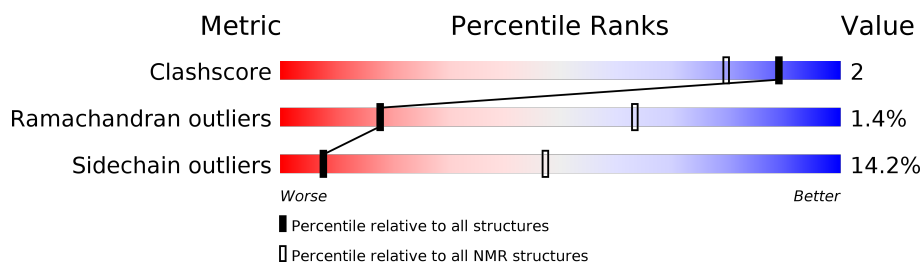
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 59%.

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)	NMR archive (#Entries)
Clashscore	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	134	 69% 7% • 22%

## 2 Ensemble composition and analysis

This entry contains 23 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *minimized average structure*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:2-A:104 (103)	0.36	7

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 5 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 5, 7, 13, 14, 20, 23
2	2, 3, 4, 12, 15, 19
3	6, 11, 16, 18, 21
4	8, 9, 10
5	17, 22

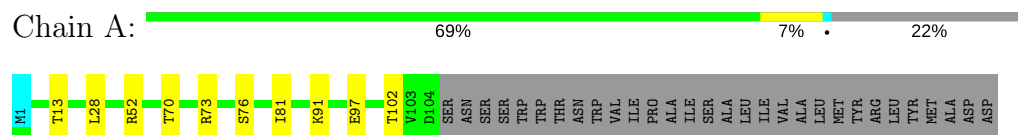


## 4 Residue-property plots [i](#)

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Cytochrome b5

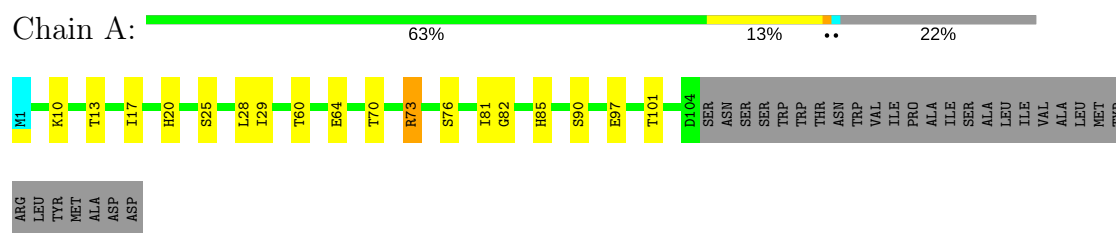


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

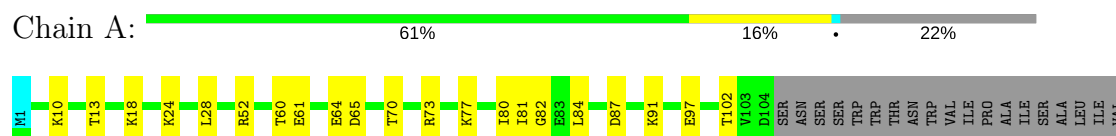
#### 4.2.1 Score per residue for model 1

- Molecule 1: Cytochrome b5



#### 4.2.2 Score per residue for model 2

- Molecule 1: Cytochrome b5



ALA  
LEU  
MET  
TYR  
ARG  
LEU  
TYR  
MET  
ALA  
ASP  
ASP

### 4.2.3 Score per residue for model 3

- Molecule 1: Cytochrome b5

Chain A: 



ILE  
VAL  
ALA  
LEU  
MET  
TYR  
ARG  
LEU  
TYR  
MET  
ALA  
ASP  
ASP

### 4.2.4 Score per residue for model 4

- Molecule 1: Cytochrome b5

Chain A: 

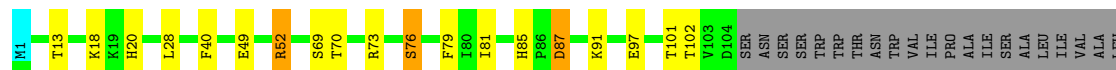


TYR  
MET  
ALA  
ASP  
ASP

### 4.2.5 Score per residue for model 5

- Molecule 1: Cytochrome b5

Chain A: 

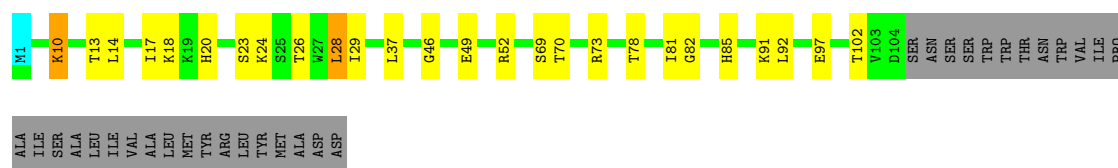


MET  
TYR  
ARG  
LEU  
TYR  
MET  
ALA  
ASP  
ASP

### 4.2.6 Score per residue for model 6

- Molecule 1: Cytochrome b5

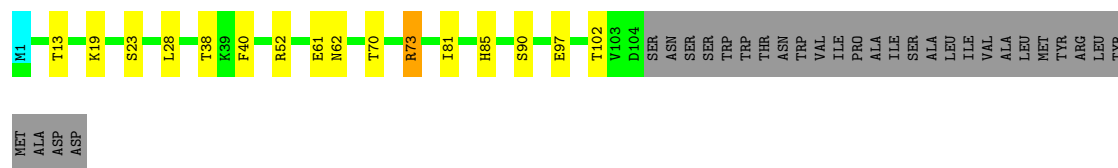
Chain A: 



#### 4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Cytochrome b5

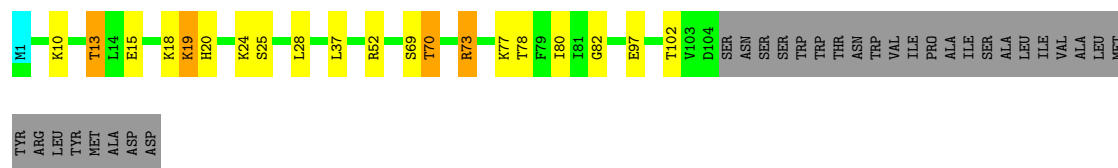
Chain A: 



#### 4.2.8 Score per residue for model 8

- Molecule 1: Cytochrome b5

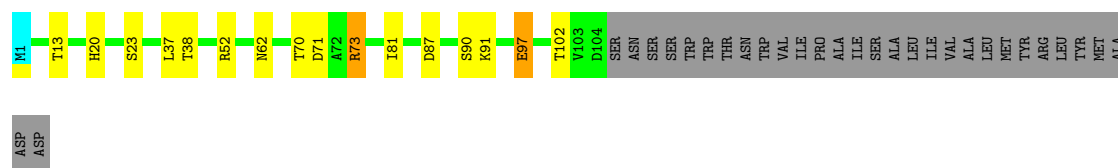
Chain A: 



#### 4.2.9 Score per residue for model 9

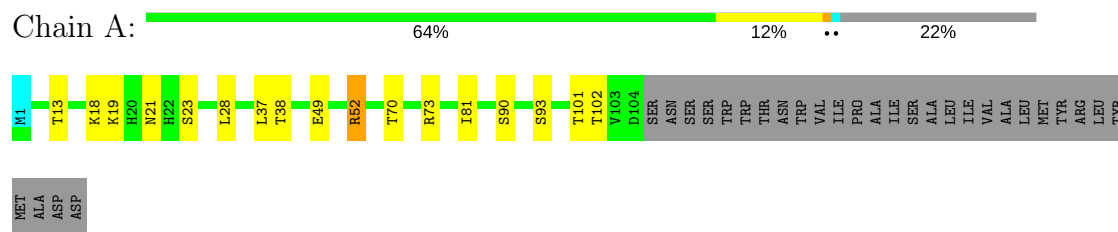
- Molecule 1: Cytochrome b5

Chain A: 



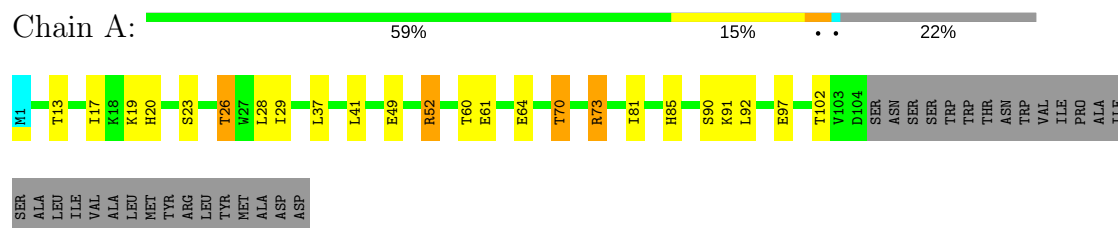
#### 4.2.10 Score per residue for model 10

- Molecule 1: Cytochrome b5



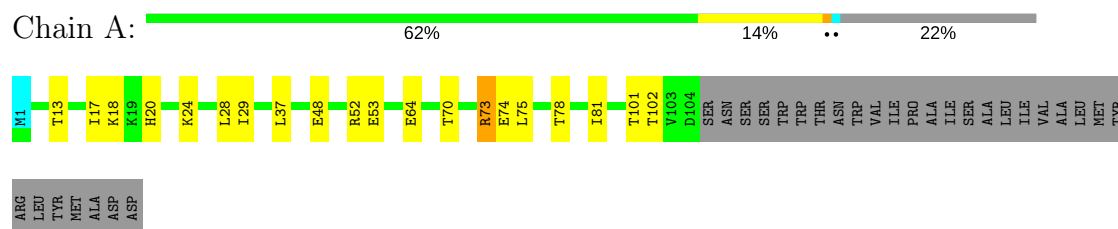
#### 4.2.11 Score per residue for model 11

- Molecule 1: Cytochrome b5



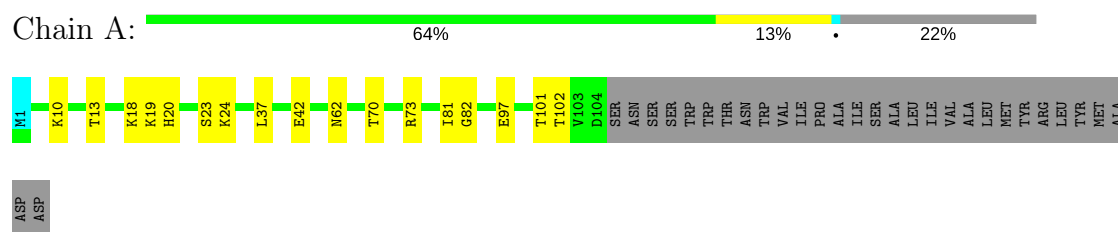
#### 4.2.12 Score per residue for model 12

- Molecule 1: Cytochrome b5



#### 4.2.13 Score per residue for model 13

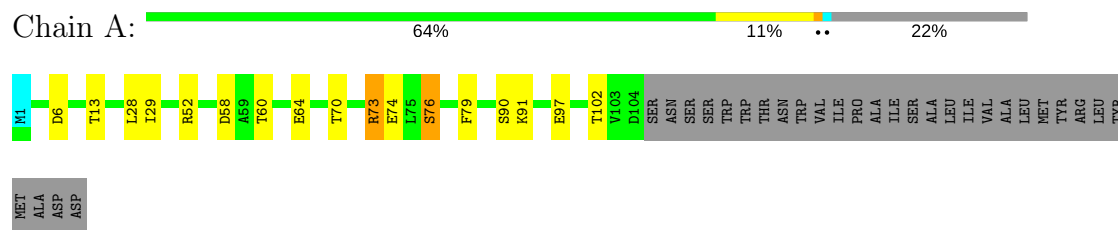
- Molecule 1: Cytochrome b5





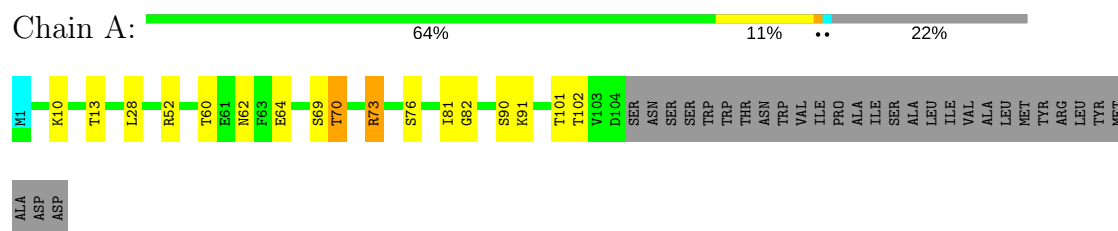
#### 4.2.14 Score per residue for model 14

- Molecule 1: Cytochrome b5



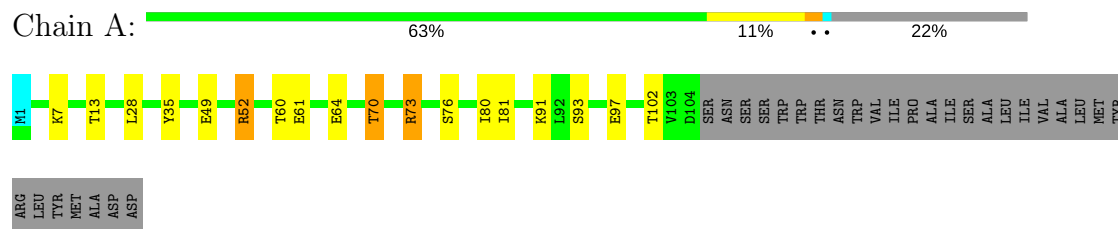
#### 4.2.15 Score per residue for model 15

- Molecule 1: Cytochrome b5



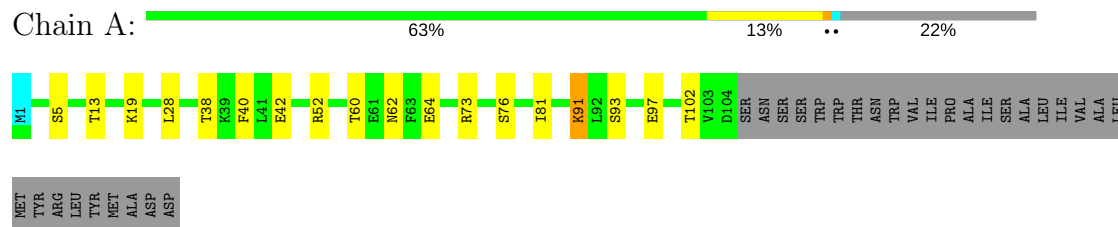
#### 4.2.16 Score per residue for model 16

- Molecule 1: Cytochrome b5



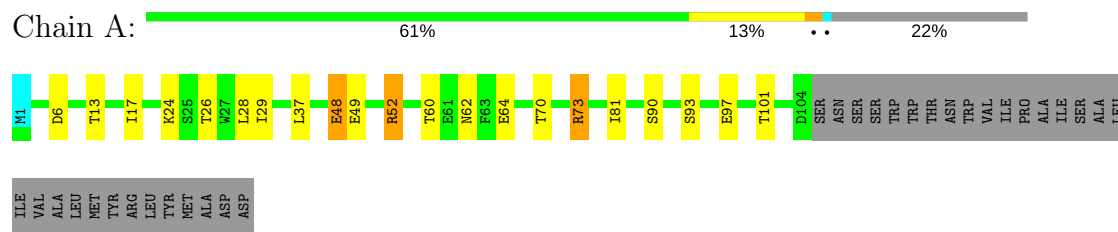
#### 4.2.17 Score per residue for model 17

- Molecule 1: Cytochrome b5



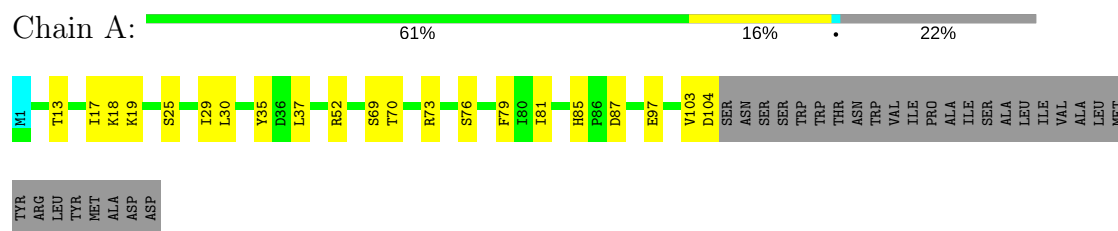
#### 4.2.18 Score per residue for model 18

- Molecule 1: Cytochrome b5



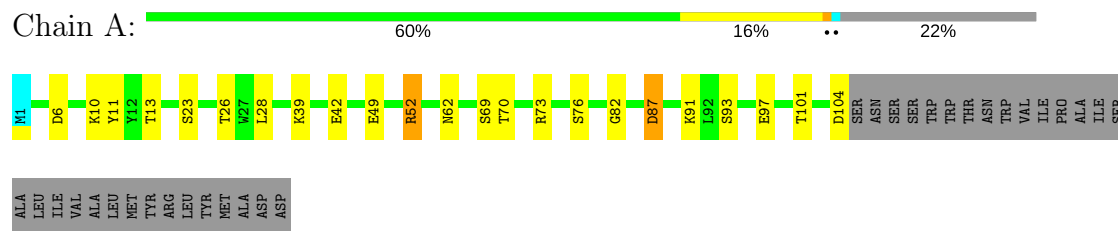
#### 4.2.19 Score per residue for model 19

- Molecule 1: Cytochrome b5



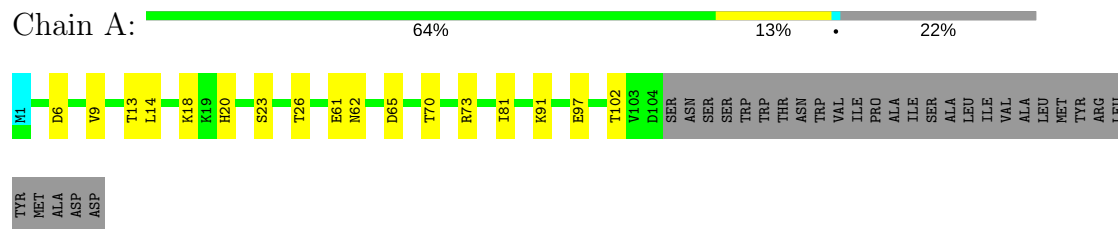
#### 4.2.20 Score per residue for model 20

- Molecule 1: Cytochrome b5



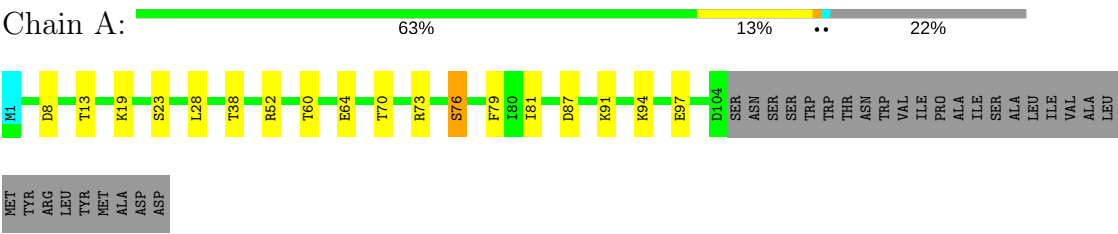
#### 4.2.21 Score per residue for model 21

- Molecule 1: Cytochrome b5



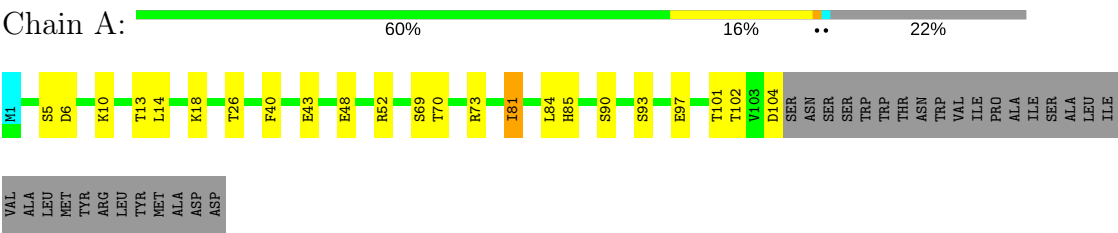
4.2.22 Score per residue for model 22

- Molecule 1: Cytochrome b5



4.2.23 Score per residue for model 23

- Molecule 1: Cytochrome b5



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry, torsion angle dynamics, simulated annealing*.

Of the 50 calculated structures, 23 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	structure solution	2.1
HADDOCK	refinement	
CYANA	refinement	2.1

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	2m33_cs.str
Number of chemical shift lists	1
Total number of shifts	939
Number of shifts mapped to atoms	939
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	59%

No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	828	804	799	4±1
2	A	43	30	30	0±1
All	All	20033	19182	19067	82

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 2.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:ILE:HD13	1:A:29:ILE:HD11	0.60	1.71	6	6
1:A:60:THR:O	1:A:64:GLU:HG2	0.54	2.02	14	10
1:A:62:ASN:OD1	2:A:400:HEM:HAC	0.54	2.02	21	7
1:A:70:THR:O	1:A:73:ARG:HG3	0.51	2.05	18	9
1:A:49:GLU:OE1	1:A:52:ARG:HD2	0.50	2.06	16	2
1:A:61:GLU:O	1:A:65:ASP:HB2	0.50	2.07	2	2
1:A:37:LEU:HG	1:A:37:LEU:O	0.49	2.07	9	1
1:A:26:THR:HG21	1:A:41:LEU:HD21	0.49	1.85	11	1
1:A:87:ASP:O	1:A:91:LYS:HB3	0.48	2.08	9	3
1:A:10:LYS:O	1:A:82:GLY:HA3	0.48	2.09	6	7
1:A:35:TYR:CE1	1:A:80:ILE:HB	0.48	2.43	16	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:76:SER:HA	1:A:79:PHE:CD2	0.46	2.45	19	4
1:A:28:LEU:HD12	1:A:37:LEU:HD21	0.45	1.88	12	1
1:A:49:GLU:O	1:A:52:ARG:HG3	0.45	2.12	20	3
1:A:20:HIS:O	1:A:25:SER:HB2	0.45	2.11	1	2
1:A:14:LEU:O	1:A:18:LYS:HG2	0.44	2.13	21	3
2:A:400:HEM:HBA1	2:A:400:HEM:CMA	0.44	2.43	3	1
1:A:87:ASP:O	1:A:91:LYS:HB2	0.44	2.13	20	2
1:A:29:ILE:O	1:A:58:ASP:HA	0.43	2.13	14	1
1:A:49:GLU:OE2	1:A:52:ARG:HD2	0.43	2.13	5	1
1:A:28:LEU:HB2	1:A:37:LEU:HD21	0.43	1.91	6	1
1:A:48:GLU:O	1:A:52:ARG:HG3	0.43	2.14	18	1
1:A:75:LEU:O	1:A:78:THR:HG22	0.43	2.13	12	1
1:A:77:LYS:O	1:A:80:ILE:HG22	0.42	2.14	2	2
1:A:73:ARG:HD3	1:A:74:GLU:OE2	0.42	2.15	12	1
1:A:81:ILE:H	1:A:81:ILE:HD13	0.42	1.73	23	1
1:A:15:GLU:O	1:A:19:LYS:HB2	0.42	2.15	8	1
1:A:52:ARG:HD3	1:A:53:GLU:N	0.41	2.31	4	1
1:A:13:THR:HB	1:A:15:GLU:OE1	0.41	2.16	8	1
1:A:33:LYS:HB2	1:A:35:TYR:CE2	0.41	2.50	4	1
1:A:28:LEU:HD13	2:A:400:HEM:HMC3	0.41	1.93	12	1
1:A:73:ARG:HD3	1:A:74:GLU:OE1	0.40	2.17	14	1
1:A:30:LEU:HB2	1:A:35:TYR:CE1	0.40	2.52	19	1

## 6.3 Torsion angles [i](#)

### 6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	102/134 (76%)	91±2 (90±2%)	9±2 (9±2%)	1±1 (1±1%)	18	63
All	All	2346/3082 (76%)	2100 (90%)	214 (9%)	32 (1%)	18	63

All 5 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	97	GLU	19
1	A	91	LYS	9
1	A	9	VAL	2
1	A	46	GLY	1
1	A	103	VAL	1

### 6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	92/119 (77%)	79±3 (86±3%)	13±3 (14±3%)	8	47
All	All	2116/2737 (77%)	1815 (86%)	301 (14%)	8	47

All 49 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	13	THR	23
1	A	73	ARG	23
1	A	81	ILE	20
1	A	52	ARG	20
1	A	102	THR	18
1	A	28	LEU	17
1	A	70	THR	16
1	A	101	THR	10
1	A	90	SER	9
1	A	19	LYS	9
1	A	76	SER	9
1	A	23	SER	9
1	A	20	HIS	8
1	A	85	HIS	7
1	A	18	LYS	7
1	A	69	SER	7
1	A	24	LYS	6
1	A	37	LEU	6
1	A	93	SER	6
1	A	26	THR	6
1	A	6	ASP	6

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Mol	Chain	Res	Type	Models (Total)
1	A	38	THR	6
1	A	87	ASP	5
1	A	61	GLU	4
1	A	84	LEU	4
1	A	40	PHE	4
1	A	92	LEU	3
1	A	104	ASP	3
1	A	42	GLU	3
1	A	48	GLU	3
1	A	10	LYS	2
1	A	5	SER	2
1	A	78	THR	2
1	A	97	GLU	2
1	A	62	ASN	2
1	A	64	GLU	1
1	A	43	GLU	1
1	A	21	ASN	1
1	A	25	SER	1
1	A	39	LYS	1
1	A	8	ASP	1
1	A	91	LYS	1
1	A	94	LYS	1
1	A	11	TYR	1
1	A	53	GLU	1
1	A	49	GLU	1
1	A	88	ASP	1
1	A	71	ASP	1
1	A	7	LYS	1

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

### 6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.



## 6.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	HEM	A	400	1	28,50,50	2.01±0.01	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	HEM	A	400	1	17,82,82	1.08±0.02	0±0 (0±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	400	1	-	0±0,6,54,54	0±0,0,8,8

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 59% for the well-defined parts and 58% for the entire structure.

### 7.1 Chemical shift list 1

File name: 2m33\_cs.str

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	939
Number of shifts mapped to atoms	939
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	29

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	74	$0.06 \pm 0.39$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	46	$0.12 \pm 0.17$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
$^{15}\text{N}$	95	$0.35 \pm 0.21$	None needed ( $< 0.5$ ppm)

#### 7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 59%, i.e. 747 atoms were assigned a chemical shift out of a possible 1273. 3 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	350/509 (69%)	192/203 (95%)	70/206 (34%)	88/100 (88%)
Sidechain	366/647 (57%)	288/377 (76%)	74/247 (30%)	4/23 (17%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	31/117 (26%)	30/61 (49%)	0/43 (0%)	1/13 (8%)
Overall	747/1273 (59%)	510/641 (80%)	144/496 (29%)	93/136 (68%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 58%, i.e. 747 atoms were assigned a chemical shift out of a possible 1286. 3 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	350/514 (68%)	192/205 (94%)	70/208 (34%)	88/101 (87%)
Sidechain	366/655 (56%)	288/382 (75%)	74/250 (30%)	4/23 (17%)
Aromatic	31/117 (26%)	30/61 (49%)	0/43 (0%)	1/13 (8%)
Overall	747/1286 (58%)	510/648 (79%)	144/501 (29%)	93/137 (68%)

#### 7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	123	VAL	HG11	-2.40	2.13 – -0.47	-12.4
1	A	123	VAL	HG12	-2.40	2.13 – -0.47	-12.4
1	A	123	VAL	HG13	-2.40	2.13 – -0.47	-12.4
1	A	30	LEU	HD11	-2.33	2.16 – -0.64	-11.0
1	A	30	LEU	HD12	-2.33	2.16 – -0.64	-11.0
1	A	30	LEU	HD13	-2.33	2.16 – -0.64	-11.0
1	A	44	HIS	HB3	7.26	5.00 – 1.10	10.8
1	A	81	ILE	HD12	-1.38	2.13 – -0.77	-7.1
1	A	81	ILE	HD13	-1.38	2.13 – -0.77	-7.1
1	A	81	ILE	HD11	-1.38	2.13 – -0.77	-7.1
1	A	30	LEU	HD21	-1.08	2.14 – -0.66	-6.5
1	A	30	LEU	HD23	-1.08	2.14 – -0.66	-6.5
1	A	30	LEU	HD22	-1.08	2.14 – -0.66	-6.5
1	A	63	PHE	HB3	0.56	4.85 – 1.05	-6.3
1	A	28	LEU	HD23	-0.99	2.14 – -0.66	-6.2
1	A	28	LEU	HD21	-0.99	2.14 – -0.66	-6.2
1	A	28	LEU	HD22	-0.99	2.14 – -0.66	-6.2
1	A	59	ALA	HB3	-0.17	2.61 – 0.11	-6.1
1	A	59	ALA	HB2	-0.17	2.61 – 0.11	-6.1
1	A	59	ALA	HB1	-0.17	2.61 – 0.11	-6.1
1	A	86	PRO	HD3	1.34	5.52 – 1.72	-6.0
1	A	30	LEU	HG	-0.41	3.16 – -0.14	-5.8

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Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	69	SER	H	11.65	11.23 – 5.33	5.7
1	A	28	LEU	HD13	-0.81	2.16 – -0.64	-5.6
1	A	28	LEU	HD12	-0.81	2.16 – -0.64	-5.6
1	A	28	LEU	HD11	-0.81	2.16 – -0.64	-5.6
1	A	29	ILE	CG1	18.21	36.54 – 18.94	-5.4
1	A	54	GLN	HB3	0.57	3.37 – 0.67	-5.4
1	A	47	GLY	HA2	5.98	5.87 – 2.07	5.3

### 7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

