



# Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 11:11 pm BST

PDB ID : 2LN0  
Title : Structure of MOZ  
Authors : Qiu, Y.  
Deposited on : 2011-12-15

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

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

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:

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : 2.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

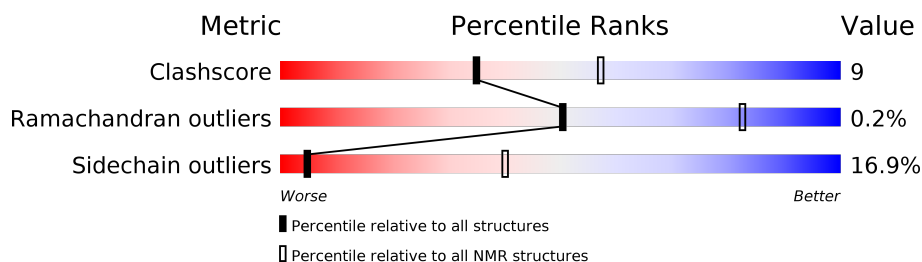
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 83%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	112	

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:207-A:313 (107)	0.53	10

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 4 clusters. No single-model clusters were found.

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1691 atoms, of which 828 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Histone acetyltransferase KAT6A.

Mol	Chain	Residues	Atoms						Trace
1	A	110	Total	C	H	N	O	S	0
			1687	525	828	156	159	19	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	202	HIS	-	EXPRESSION TAG	UNP Q92794
A	203	MET	-	EXPRESSION TAG	UNP Q92794

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

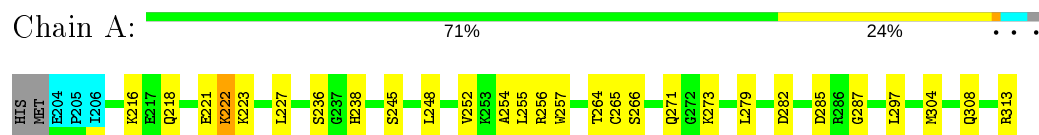
Mol	Chain	Residues	Atoms	
2	A	4	Total	Zn
			4	4

## 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: Histone acetyltransferase KAT6A

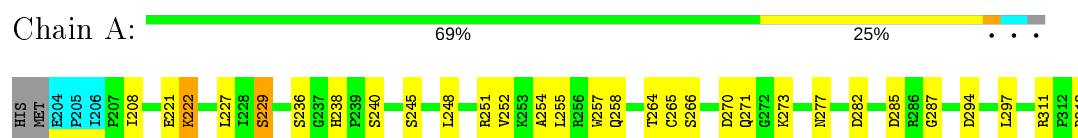


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

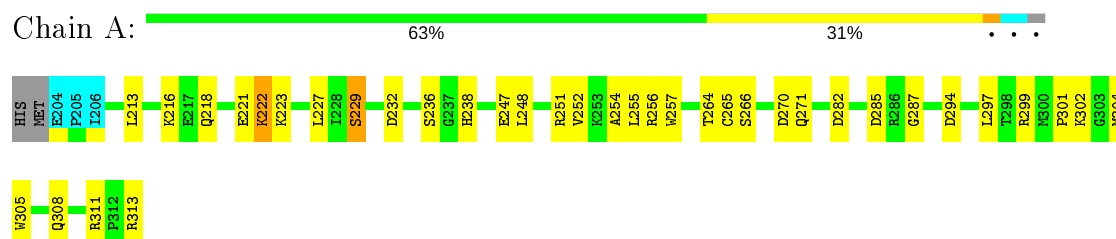
#### 4.2.1 Score per residue for model 1

- Molecule 1: Histone acetyltransferase KAT6A



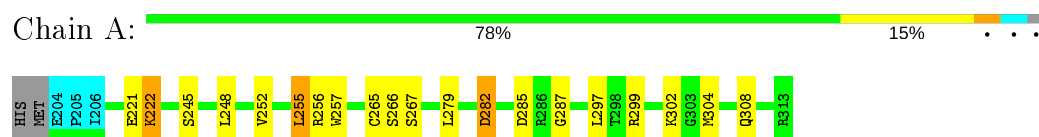
#### 4.2.2 Score per residue for model 2

- Molecule 1: Histone acetyltransferase KAT6A



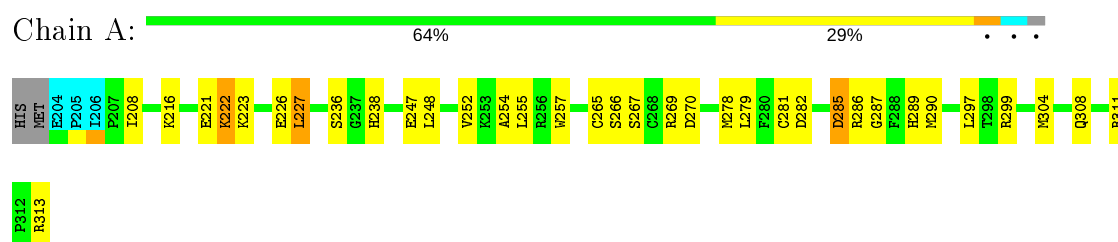
### 4.2.3 Score per residue for model 3

- Molecule 1: Histone acetyltransferase KAT6A



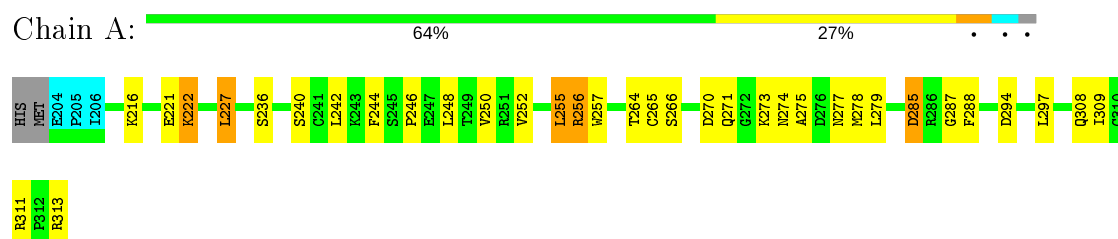
### 4.2.4 Score per residue for model 4

- Molecule 1: Histone acetyltransferase KAT6A



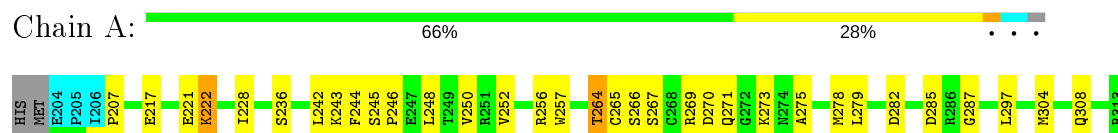
### 4.2.5 Score per residue for model 5

- Molecule 1: Histone acetyltransferase KAT6A



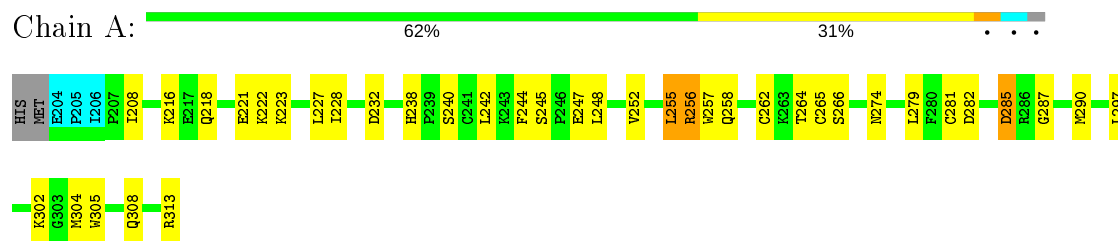
### 4.2.6 Score per residue for model 6

- Molecule 1: Histone acetyltransferase KAT6A



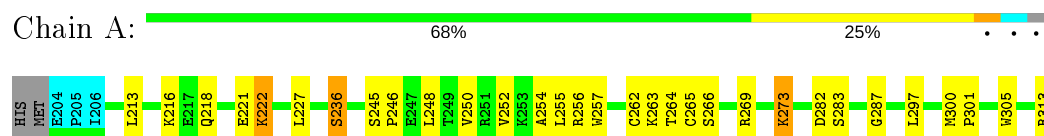
### 4.2.7 Score per residue for model 7

- Molecule 1: Histone acetyltransferase KAT6A



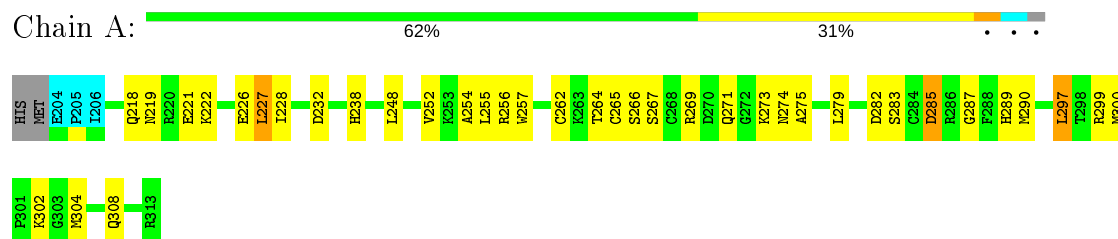
### 4.2.8 Score per residue for model 8

- Molecule 1: Histone acetyltransferase KAT6A



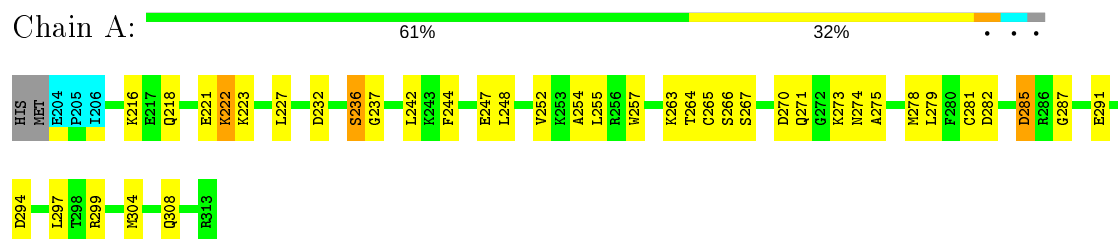
### 4.2.9 Score per residue for model 9

- Molecule 1: Histone acetyltransferase KAT6A



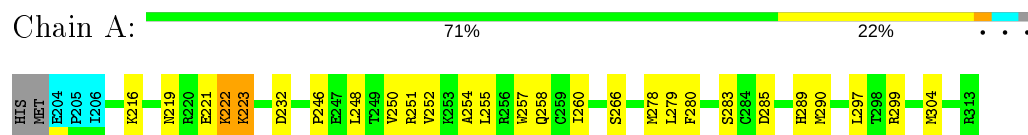
### 4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: Histone acetyltransferase KAT6A



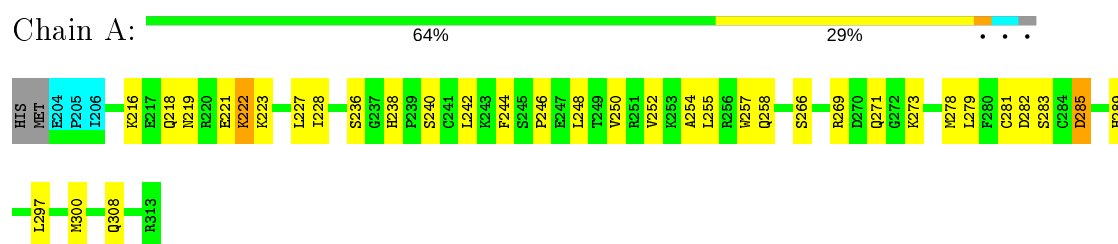
### 4.2.11 Score per residue for model 11

- Molecule 1: Histone acetyltransferase KAT6A



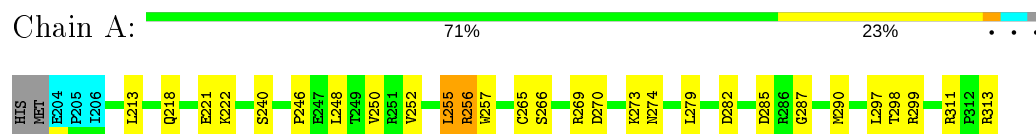
### 4.2.12 Score per residue for model 12

- Molecule 1: Histone acetyltransferase KAT6A



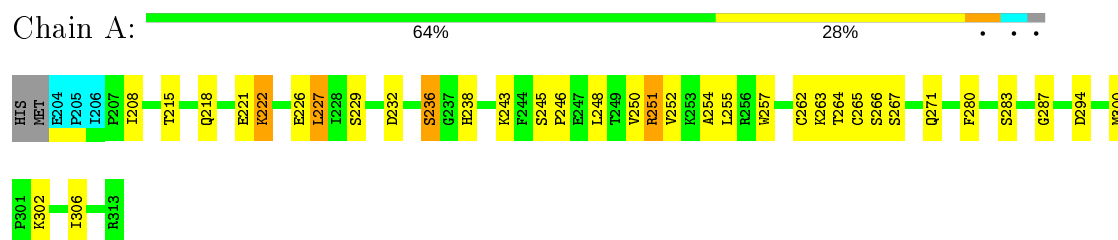
### 4.2.13 Score per residue for model 13

- Molecule 1: Histone acetyltransferase KAT6A



### 4.2.14 Score per residue for model 14

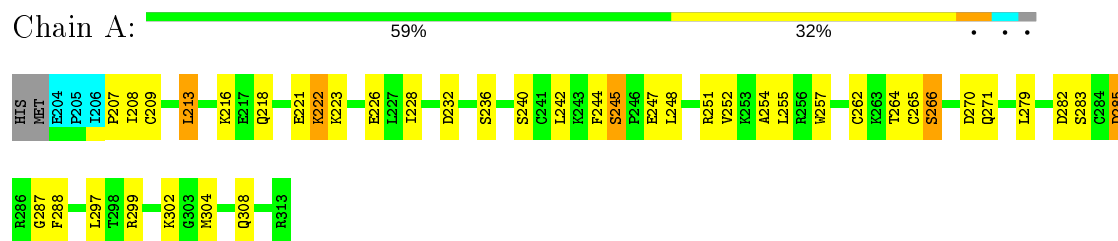
- Molecule 1: Histone acetyltransferase KAT6A





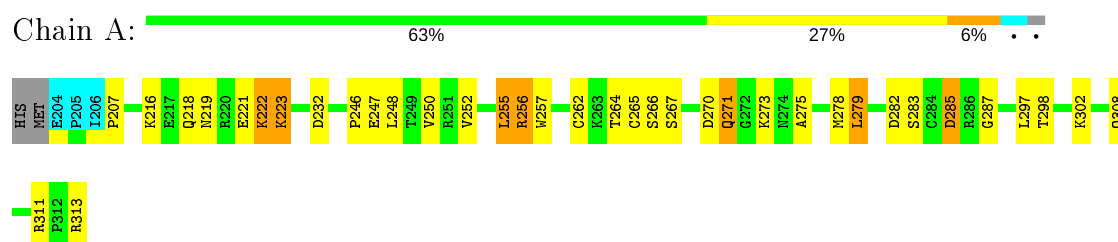
### 4.2.15 Score per residue for model 15

- Molecule 1: Histone acetyltransferase KAT6A



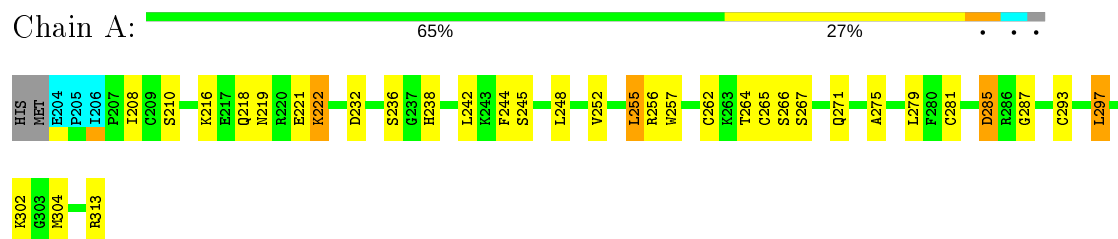
### 4.2.16 Score per residue for model 16

- Molecule 1: Histone acetyltransferase KAT6A



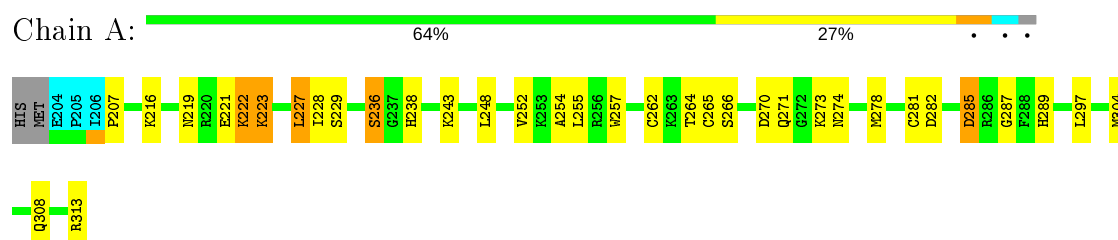
### 4.2.17 Score per residue for model 17

- Molecule 1: Histone acetyltransferase KAT6A



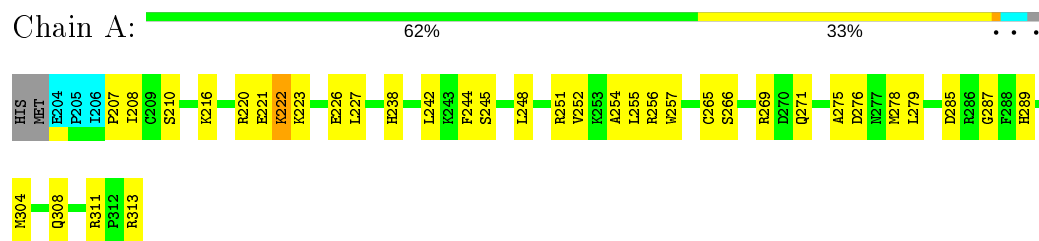
### 4.2.18 Score per residue for model 18

- Molecule 1: Histone acetyltransferase KAT6A



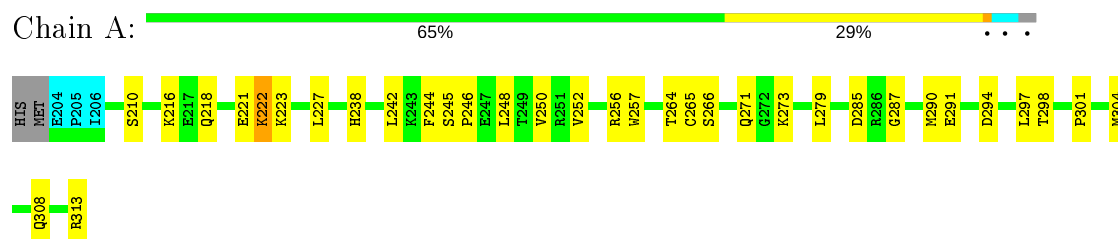
#### 4.2.19 Score per residue for model 19

- Molecule 1: Histone acetyltransferase KAT6A



#### 4.2.20 Score per residue for model 20

- Molecule 1: Histone acetyltransferase KAT6A



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 500 calculated structures, 20 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
CNS	refinement	
CNS	structure solution	

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1181
Number of shifts mapped to atoms	1181
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

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:  
ZN

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	835	804	804	14±3
All	All	16780	16080	16080	286

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 9.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:275:ALA:HB1	1:A:289:HIS:NE2	0.78	1.93	9	1
1:A:252:VAL:HA	1:A:255:LEU:HD23	0.71	1.62	7	6
1:A:227:LEU:HD23	1:A:236:SER:HB2	0.69	1.63	18	3
1:A:264:THR:HG21	1:A:271:GLN:CG	0.69	2.17	5	1
1:A:227:LEU:HD23	1:A:238:HIS:CD2	0.65	2.27	4	2
1:A:279:LEU:HD22	1:A:297:LEU:HD11	0.64	1.68	10	2
1:A:227:LEU:HD13	1:A:236:SER:OG	0.64	1.93	1	1
1:A:264:THR:HG22	1:A:271:GLN:NE2	0.62	2.09	14	3
1:A:252:VAL:HG13	1:A:257:TRP:HB2	0.62	1.70	3	6
1:A:264:THR:HG22	1:A:271:GLN:HG2	0.60	1.72	10	2
1:A:275:ALA:HB1	1:A:289:HIS:HE2	0.59	1.53	9	1
1:A:248:LEU:HD21	1:A:282:ASP:C	0.59	2.16	15	2

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:264:THR:HG22	1:A:271:GLN:CG	0.59	2.27	10	3
1:A:297:LEU:HD11	1:A:305:TRP:CD1	0.59	2.31	8	3
1:A:271:GLN:O	1:A:275:ALA:HB3	0.58	1.98	9	1
1:A:227:LEU:HD12	1:A:236:SER:HB2	0.58	1.75	14	1
1:A:271:GLN:O	1:A:275:ALA:HB2	0.58	1.98	19	1
1:A:248:LEU:HD21	1:A:285:ASP:OD2	0.57	1.98	7	4
1:A:246:PRO:O	1:A:250:VAL:HG23	0.57	1.99	14	9
1:A:275:ALA:HB1	1:A:289:HIS:CD2	0.57	2.34	9	1
1:A:262:CYS:O	1:A:264:THR:HG23	0.57	1.99	8	8
1:A:248:LEU:HD21	1:A:285:ASP:OD1	0.56	2.00	10	2
1:A:227:LEU:HD22	1:A:238:HIS:CD2	0.56	2.35	14	1
1:A:248:LEU:HD21	1:A:282:ASP:O	0.56	2.00	3	2
1:A:279:LEU:HD11	1:A:297:LEU:HD12	0.55	1.77	17	3
1:A:255:LEU:HD12	1:A:256:ARG:N	0.55	2.17	7	6
1:A:279:LEU:CD2	1:A:297:LEU:HD12	0.55	2.31	19	1
1:A:227:LEU:N	1:A:227:LEU:HD23	0.55	2.17	14	1
1:A:278:MET:CG	1:A:289:HIS:CD2	0.55	2.90	4	5
1:A:279:LEU:CD1	1:A:297:LEU:HD11	0.54	2.32	4	3
1:A:275:ALA:HB1	1:A:278:MET:CE	0.53	2.33	6	4
1:A:290:MET:HA	1:A:297:LEU:HD12	0.53	1.79	4	1
1:A:227:LEU:HD23	1:A:236:SER:CB	0.53	2.34	12	3
1:A:254:ALA:O	1:A:255:LEU:HD23	0.53	2.03	14	12
1:A:248:LEU:O	1:A:252:VAL:HG23	0.52	2.03	14	17
1:A:265:CYS:HA	1:A:287:GLY:O	0.52	2.04	2	18
1:A:279:LEU:HD13	1:A:297:LEU:HD12	0.52	1.82	7	3
1:A:208:ILE:HG22	1:A:215:THR:HG22	0.52	1.82	14	1
1:A:248:LEU:HD13	1:A:285:ASP:OD2	0.52	2.05	15	1
1:A:228:ILE:HG22	1:A:257:TRP:CE3	0.52	2.40	12	6
1:A:264:THR:HG22	1:A:271:GLN:HG3	0.52	1.81	17	2
1:A:242:LEU:HB3	1:A:244:PHE:CE1	0.51	2.40	20	8
1:A:221:GLU:O	1:A:222:LYS:HG2	0.51	2.06	17	20
1:A:279:LEU:HD11	1:A:297:LEU:HD11	0.51	1.80	3	1
1:A:271:GLN:HA	1:A:275:ALA:HB2	0.51	1.82	16	2
1:A:227:LEU:CD2	1:A:238:HIS:CD2	0.50	2.94	2	4
1:A:264:THR:HG21	1:A:271:GLN:HG2	0.50	1.83	5	1
1:A:279:LEU:HD12	1:A:293:CYS:SG	0.50	2.47	17	1
1:A:264:THR:HG21	1:A:271:GLN:HG3	0.49	1.84	5	2
1:A:265:CYS:HB2	1:A:289:HIS:CE1	0.49	2.42	9	1
1:A:279:LEU:CD1	1:A:297:LEU:HD12	0.48	2.38	7	7
1:A:227:LEU:HD21	1:A:238:HIS:CD2	0.48	2.42	1	1
1:A:216:LYS:HA	1:A:227:LEU:HD21	0.48	1.85	7	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:283:SER:HB2	1:A:306:ILE:HD12	0.47	1.86	14	1
1:A:252:VAL:CG1	1:A:257:TRP:CD1	0.47	2.98	12	14
1:A:219:ASN:CG	1:A:238:HIS:CD2	0.47	2.88	9	2
1:A:245:SER:H	1:A:248:LEU:HD12	0.47	1.69	15	1
1:A:248:LEU:HD13	1:A:282:ASP:C	0.47	2.29	12	1
1:A:275:ALA:HB1	1:A:278:MET:HE3	0.47	1.87	5	1
1:A:227:LEU:CD1	1:A:238:HIS:CD2	0.47	2.98	12	4
1:A:219:ASN:HB3	1:A:223:LYS:HG3	0.47	1.86	18	3
1:A:242:LEU:HB3	1:A:244:PHE:CZ	0.46	2.45	20	2
1:A:252:VAL:HA	1:A:255:LEU:CD2	0.46	2.39	5	6
1:A:227:LEU:HD23	1:A:236:SER:OG	0.46	2.11	12	1
1:A:266:SER:HB3	1:A:288:PHE:CZ	0.46	2.46	15	1
1:A:269:ARG:HD3	1:A:269:ARG:N	0.45	2.26	6	1
1:A:275:ALA:HB1	1:A:278:MET:HE1	0.45	1.87	6	1
1:A:227:LEU:HD13	1:A:236:SER:HB3	0.45	1.87	10	2
1:A:297:LEU:HD11	1:A:305:TRP:NE1	0.45	2.25	2	1
1:A:251:ARG:O	1:A:255:LEU:HG	0.45	2.11	14	4
1:A:219:ASN:CB	1:A:223:LYS:HG3	0.45	2.42	16	1
1:A:252:VAL:HG13	1:A:257:TRP:CD1	0.44	2.47	12	3
1:A:288:PHE:HZ	1:A:309:ILE:HD11	0.44	1.73	5	1
1:A:248:LEU:HD11	1:A:285:ASP:HB2	0.43	1.90	9	1
1:A:260:ILE:HD12	1:A:280:PHE:CE2	0.43	2.49	11	1
1:A:281:CYS:O	1:A:285:ASP:HA	0.43	2.13	17	6
1:A:264:THR:HG22	1:A:271:GLN:HB3	0.43	1.91	16	1
1:A:297:LEU:HD13	1:A:301:PRO:CG	0.42	2.44	8	1
1:A:219:ASN:HA	1:A:238:HIS:CE1	0.42	2.49	12	1
1:A:271:GLN:NE2	1:A:275:ALA:HB1	0.42	2.29	17	1
1:A:227:LEU:HD22	1:A:237:GLY:N	0.42	2.29	10	1
1:A:227:LEU:HD12	1:A:238:HIS:CD2	0.42	2.49	18	1
1:A:229:SER:OG	1:A:236:SER:HB3	0.42	2.14	1	1
1:A:270:ASP:O	1:A:271:GLN:HB2	0.42	2.14	18	2
1:A:297:LEU:HD13	1:A:301:PRO:HG3	0.41	1.92	2	2
1:A:288:PHE:CZ	1:A:309:ILE:HD11	0.41	2.50	5	1
1:A:278:MET:HG3	1:A:289:HIS:CD2	0.41	2.51	4	1
1:A:229:SER:HA	1:A:236:SER:HA	0.41	1.92	2	1
1:A:265:CYS:O	1:A:269:ARG:HD3	0.41	2.14	9	1
1:A:209:CYS:O	1:A:213:LEU:HA	0.41	2.16	15	1
1:A:227:LEU:HD23	1:A:238:HIS:NE2	0.41	2.31	4	1
1:A:263:LYS:HD2	1:A:280:PHE:CE1	0.41	2.51	14	1
1:A:207:PRO:O	1:A:227:LEU:HD22	0.41	2.16	18	1
1:A:264:THR:CG2	1:A:271:GLN:HG3	0.40	2.45	5	1

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:227:LEU:HD13	1:A:236:SER:CB	0.40	2.46	10	1
1:A:219:ASN:HB2	1:A:223:LYS:O	0.40	2.16	12	1
1:A:264:THR:HG22	1:A:271:GLN:CD	0.40	2.37	18	1
1:A:264:THR:CG2	1:A:271:GLN:HA	0.40	2.47	6	1
1:A:252:VAL:HG13	1:A:257:TRP:CB	0.40	2.42	3	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	106/112 (95%)	97±2 (92±2%)	9±2 (8±2%)	0±0 (0±0%)	50	82
All	All	2120/2240 (95%)	1941 (92%)	174 (8%)	5 (0%)	50	82

All 3 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	207	PRO	3
1	A	301	PRO	1
1	A	273	LYS	1

### 6.3.2 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 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	98/103 (95%)	81±3 (83±3%)	17±3 (17±3%)	5	40
All	All	1960/2060 (95%)	1628 (83%)	332 (17%)	5	40

All 50 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	266	SER	20
1	A	285	ASP	18
1	A	222	LYS	17
1	A	308	GLN	14
1	A	216	LYS	13
1	A	304	MET	13
1	A	313	ARG	12
1	A	218	GLN	12
1	A	282	ASP	11
1	A	273	LYS	11
1	A	245	SER	10
1	A	256	ARG	10
1	A	223	LYS	10
1	A	232	ASP	9
1	A	302	LYS	9
1	A	299	ARG	8
1	A	236	SER	8
1	A	270	ASP	8
1	A	267	SER	8
1	A	311	ARG	7
1	A	274	ASN	6
1	A	247	GLU	6
1	A	255	LEU	6
1	A	283	SER	6
1	A	294	ASP	6
1	A	240	SER	6
1	A	290	MET	5
1	A	227	LEU	5
1	A	226	GLU	5
1	A	269	ARG	5
1	A	258	GLN	4
1	A	300	MET	4
1	A	213	LEU	4
1	A	229	SER	4
1	A	297	LEU	4
1	A	251	ARG	3
1	A	298	THR	3
1	A	210	SER	3
1	A	243	LYS	3
1	A	271	GLN	2
1	A	263	LYS	2
1	A	291	GLU	2

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	208	ILE	2
1	A	277	ASN	2
1	A	276	ASP	1
1	A	286	ARG	1
1	A	264	THR	1
1	A	220	ARG	1
1	A	217	GLU	1
1	A	279	LEU	1

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

### 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 83% for the well-defined parts and 81% for the entire structure.

### 7.1 Chemical shift list 1

File name: input\_cs.cif

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	1181
Number of shifts mapped to atoms	1181
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	109	$-0.65 \pm 0.22$	Should be applied
$^{13}\text{C}_\beta$	102	$0.24 \pm 0.18$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	100	$-2.20 \pm 0.28$	Should be applied
$^{15}\text{N}$	97	$-0.07 \pm 0.33$	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 83%, i.e. 1094 atoms were assigned a chemical shift out of a possible 1321. 1 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	506/519 (97%)	203/206 (99%)	207/214 (97%)	96/99 (97%)
Sidechain	558/728 (77%)	369/439 (84%)	182/249 (73%)	7/40 (18%)

*Continued on next page...*

Continued from previous page...

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	30/74 (41%)	28/40 (70%)	0/30 (0%)	2/4 (50%)
Overall	1094/1321 (83%)	600/685 (88%)	389/493 (79%)	105/143 (73%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 81%, i.e. 1094 atoms were assigned a chemical shift out of a possible 1359. 1 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	506/532 (95%)	203/211 (96%)	207/220 (94%)	96/101 (95%)
Sidechain	558/753 (74%)	369/454 (81%)	182/259 (70%)	7/40 (18%)
Aromatic	30/74 (41%)	28/40 (70%)	0/30 (0%)	2/4 (50%)
Overall	1094/1359 (81%)	600/705 (85%)	389/509 (76%)	105/145 (72%)

#### 7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 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:

