



Full wwPDB NMR Structure Validation Report ⓘ

Jul 5, 2022 – 01:10 pm BST

PDB ID : 7P27
Title : NMR solution structure of Chikungunya virus macro domain
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Deposited on : 2021-07-04

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at 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 types of validation reports are described at <http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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	:	2.29
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

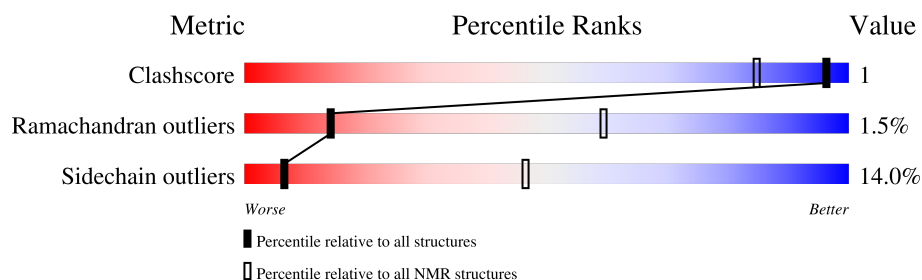
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR


The overall completeness of chemical shifts assignment is 78%.

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 ≥ 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	168	

2 Ensemble composition and analysis

This entry contains 21 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:3-A:160 (158)	0.39	1

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 2 clusters and 3 single-model clusters were found.

Cluster number	Models
1	1, 3, 4, 6, 8, 9, 10, 11, 13, 14, 15, 16, 17, 18, 19, 20
2	7, 12
Single-model clusters	2; 5; 21

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2444 atoms, of which 1216 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Polypeptide P1234.

Mol	Chain	Residues	Atoms						Trace
1	A	160	Total	C	H	N	O	S	0
			2444	765	1216	215	240	8	

There are 8 discrepancies between the modelled and reference sequences:

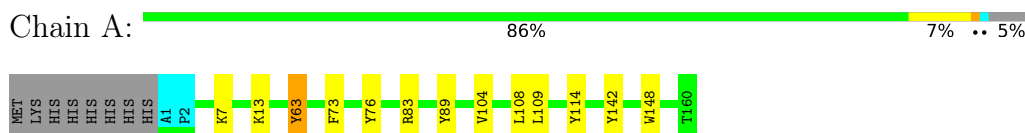
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP Q8JUX6
A	-6	LYS	-	expression tag	UNP Q8JUX6
A	-5	HIS	-	expression tag	UNP Q8JUX6
A	-4	HIS	-	expression tag	UNP Q8JUX6
A	-3	HIS	-	expression tag	UNP Q8JUX6
A	-2	HIS	-	expression tag	UNP Q8JUX6
A	-1	HIS	-	expression tag	UNP Q8JUX6
A	0	HIS	-	expression tag	UNP Q8JUX6

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: Polyprotein P1234

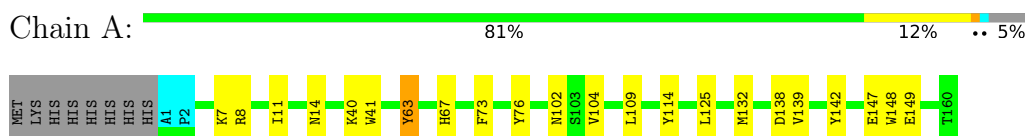


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

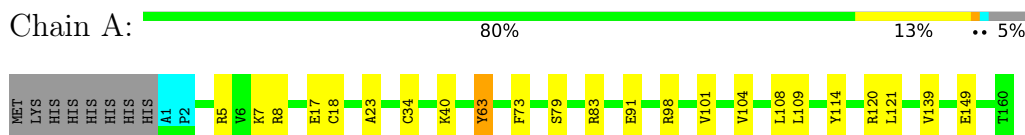
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Polyprotein P1234



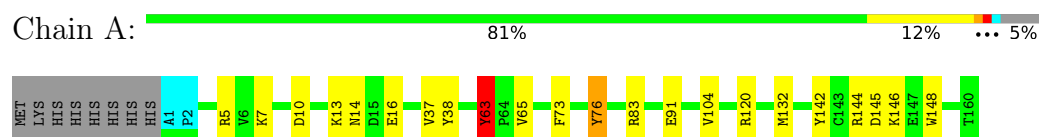
4.2.2 Score per residue for model 2

- Molecule 1: Polyprotein P1234



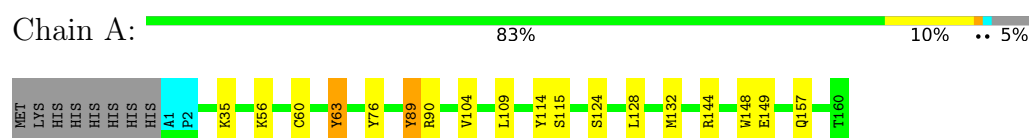
4.2.3 Score per residue for model 3

- Molecule 1: Polyprotein P1234



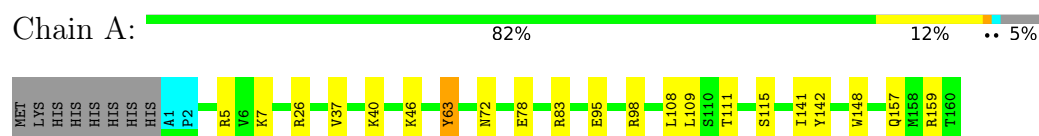
4.2.4 Score per residue for model 4

- Molecule 1: Polyprotein P1234



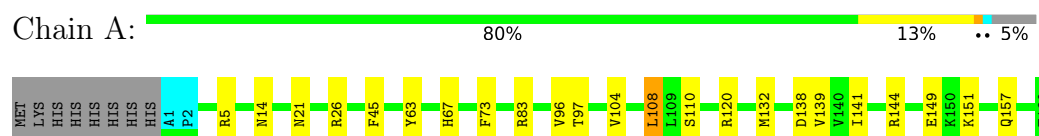
4.2.5 Score per residue for model 5

- Molecule 1: Polyprotein P1234



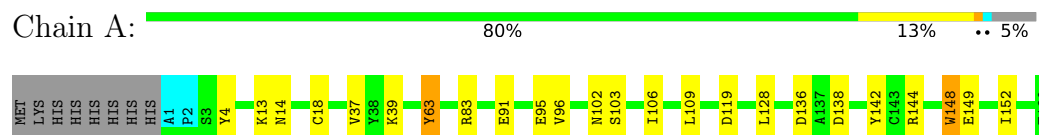
4.2.6 Score per residue for model 6

- Molecule 1: Polyprotein P1234




4.2.7 Score per residue for model 7

- Molecule 1: Polyprotein P1234



4.2.8 Score per residue for model 8


- Molecule 1: Polyprotein P1234

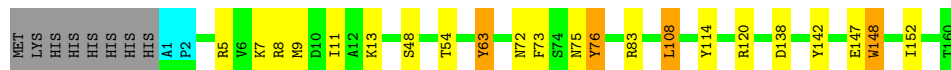
Chain A: 



4.2.9 Score per residue for model 9


- Molecule 1: Polyprotein P1234

Chain A: 



4.2.10 Score per residue for model 10


- Molecule 1: Polyprotein P1234

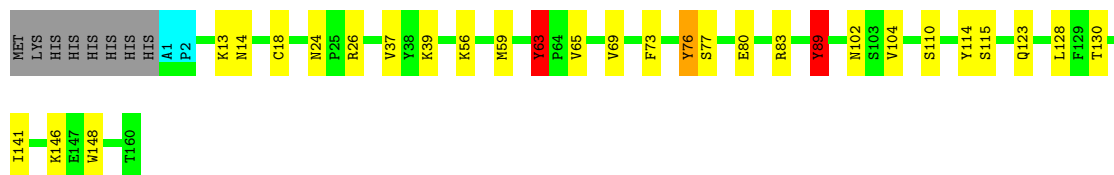
Chain A: 



4.2.11 Score per residue for model 11


- Molecule 1: Polyprotein P1234

Chain A: 



4.2.12 Score per residue for model 12

- Molecule 1: Polyprotein P1234

Chain A: 



4.2.13 Score per residue for model 13

- Molecule 1: Polyprotein P1234

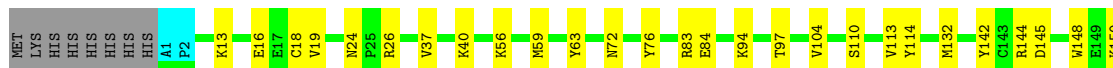
Chain A: 82% 11% 5%



4.2.14 Score per residue for model 14

- Molecule 1: Polyprotein P1234

Chain A: 78% 16% 5%



4.2.15 Score per residue for model 15

- Molecule 1: Polyprotein P1234

Chain A: 82% 11% 5%



4.2.16 Score per residue for model 16

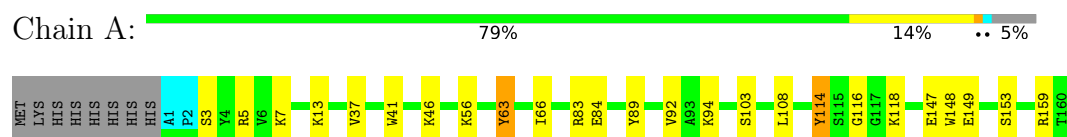
- Molecule 1: Polyprotein P1234

Chain A: 83% 11% 5%



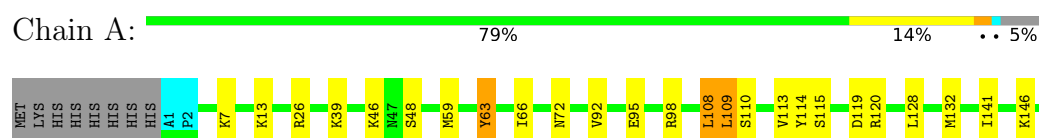
4.2.17 Score per residue for model 17

- Molecule 1: Polyprotein P1234



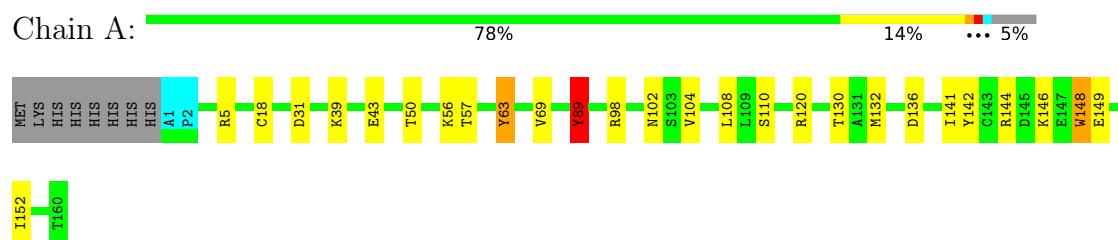
4.2.18 Score per residue for model 18

- Molecule 1: Polyprotein P1234



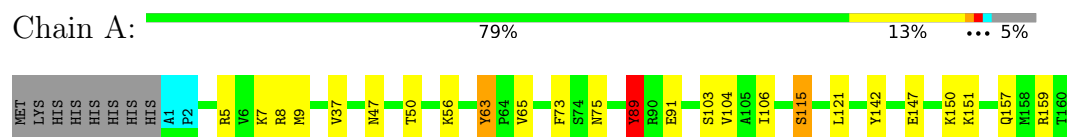
4.2.19 Score per residue for model 19

- Molecule 1: Polyprotein P1234



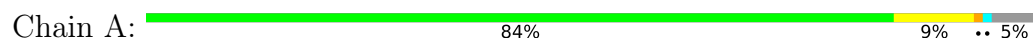
4.2.20 Score per residue for model 20

- Molecule 1: Polyprotein P1234



4.2.21 Score per residue for model 21

- Molecule 1: Polyprotein P1234



MET	LYS	HIS	HIS	HIS	HIS	HIS	HIS	A1	P2	K13	N24	K56	Y63	Y76	Y89	R90	E91	K94	N102	T130	Y142	D145	E146	E147	W148	E149	K150	K151	R159	T160
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5 Refinement protocol and experimental data overview

The models were refined using the following method: *molecular dynamics*.

Of the 21 calculated structures, 21 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
DYANA	structure calculation	
Amber	refinement	

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1670
Number of shifts mapped to atoms	1670
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	78%

6 Model quality

6.1 Standard geometry

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 (average) 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	0.57±0.01	0±0/1238 (0.0± 0.0%)	0.87±0.02	0±0/1674 (0.0± 0.0%)
All	All	0.57	0/25998 (0.0%)	0.87	4/35154 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	1.0±0.8
All	All	0	21

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	142	TYR	CB-CG-CD1	-6.34	117.20	121.00	20	2
1	A	67	HIS	CG-ND1-CE1	-5.97	97.94	105.70	1	1
1	A	114	TYR	CB-CG-CD1	-5.52	117.69	121.00	17	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	76	TYR	Sidechain	6
1	A	89	TYR	Sidechain	5
1	A	109	LEU	Peptide	4
1	A	8	ARG	Sidechain	2
1	A	4	TYR	Sidechain	2

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	120	ARG	Sidechain	1
1	A	159	ARG	Sidechain	1

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	1216	1204	1204	2±1
All	All	25536	25284	25284	41

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:63:TYR:CE2	1:A:65:VAL:HG22	0.67	2.23	3	3
1:A:70:GLY:CA	1:A:85:LEU:HD13	0.60	2.27	8	1
1:A:132:MET:HG2	1:A:139:VAL:HG11	0.57	1.75	6	2
1:A:23:ALA:HB2	1:A:34:CYS:SG	0.55	2.42	2	1
1:A:50:THR:HG23	1:A:69:VAL:CG2	0.52	2.34	19	1
1:A:66:ILE:HG21	1:A:92:VAL:HG23	0.52	1.81	18	1
1:A:89:TYR:CZ	1:A:130:THR:HG22	0.49	2.43	19	2
1:A:89:TYR:C	1:A:89:TYR:CD1	0.48	2.87	19	3
1:A:89:TYR:C	1:A:89:TYR:CD2	0.48	2.87	20	1
1:A:148:TRP:CZ3	1:A:152:ILE:HD11	0.46	2.46	7	3
1:A:70:GLY:HA3	1:A:85:LEU:HD13	0.46	1.86	8	1
1:A:108:LEU:HD21	1:A:141:ILE:HG23	0.46	1.87	18	2
1:A:96:VAL:HG13	1:A:104:VAL:HG11	0.45	1.87	6	1
1:A:125:LEU:HD21	1:A:155:ALA:HB1	0.45	1.87	8	1
1:A:70:GLY:HA2	1:A:85:LEU:HD13	0.45	1.87	8	1
1:A:89:TYR:CD1	1:A:89:TYR:C	0.44	2.90	21	1
1:A:89:TYR:CD2	1:A:89:TYR:C	0.44	2.91	10	2
1:A:105:ALA:HB1	1:A:142:TYR:CE1	0.44	2.47	12	1
1:A:116:GLY:O	1:A:118:LYS:CE	0.43	2.67	17	1
1:A:40:LYS:HB3	1:A:41:TRP:CD1	0.42	2.49	1	1
1:A:108:LEU:HD12	1:A:111:THR:CG2	0.42	2.44	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:4:TYR:CE1	1:A:141:ILE:HD13	0.42	2.49	13	1
1:A:21:ASN:HD21	1:A:67:HIS:CG	0.41	2.33	6	1
1:A:128:LEU:HD13	1:A:128:LEU:C	0.41	2.36	15	1
1:A:66:ILE:CG2	1:A:92:VAL:HG22	0.41	2.45	17	1
1:A:108:LEU:HD22	1:A:148:TRP:CZ3	0.41	2.51	9	1
1:A:17:GLU:O	1:A:101:VAL:HG11	0.41	2.16	2	1
1:A:66:ILE:CG2	1:A:92:VAL:HG23	0.41	2.46	18	1
1:A:66:ILE:N	1:A:66:ILE:HD12	0.41	2.31	15	1
1:A:147:GLU:OE2	1:A:151:LYS:NZ	0.40	2.53	10	1
1:A:18:CYS:HB3	1:A:104:VAL:HG23	0.40	1.93	14	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	157/168 (93%)	145±2 (92±1%)	10±2 (6±1%)	2±1 (1±1%)	14	59
All	All	3297/3528 (93%)	3041 (92%)	208 (6%)	48 (1%)	14	59

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	63	TYR	21
1	A	73	PHE	11
1	A	14	ASN	6
1	A	115	SER	6
1	A	110	SER	4

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	132/141 (94%)	114±3 (86±2%)	18±3 (14±2%)	6	46
All	All	2772/2961 (94%)	2385 (86%)	387 (14%)	6	46

All 97 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	63	TYR	16
1	A	148	TRP	15
1	A	83	ARG	13
1	A	114	TYR	12
1	A	13	LYS	12
1	A	7	LYS	11
1	A	104	VAL	11
1	A	142	TYR	11
1	A	149	GLU	10
1	A	5	ARG	10
1	A	56	LYS	10
1	A	157	GLN	10
1	A	108	LEU	9
1	A	37	VAL	9
1	A	120	ARG	8
1	A	132	MET	8
1	A	102	ASN	7
1	A	109	LEU	7
1	A	89	TYR	7
1	A	147	GLU	6
1	A	91	GLU	6
1	A	98	ARG	6
1	A	144	ARG	6
1	A	146	LYS	6
1	A	26	ARG	6
1	A	39	LYS	6
1	A	138	ASP	5
1	A	18	CYS	5
1	A	76	TYR	5
1	A	128	LEU	5
1	A	141	ILE	5
1	A	40	LYS	4
1	A	145	ASP	4
1	A	72	ASN	4
1	A	95	GLU	4
1	A	84	GLU	4

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Mol	Chain	Res	Type	Models (Total)
1	A	11	ILE	3
1	A	121	LEU	3
1	A	16	GLU	3
1	A	46	LYS	3
1	A	159	ARG	3
1	A	151	LYS	3
1	A	103	SER	3
1	A	48	SER	3
1	A	75	ASN	3
1	A	3	SER	3
1	A	24	ASN	3
1	A	59	MET	3
1	A	110	SER	3
1	A	94	LYS	3
1	A	8	ARG	2
1	A	79	SER	2
1	A	90	ARG	2
1	A	45	PHE	2
1	A	97	THR	2
1	A	4	TYR	2
1	A	106	ILE	2
1	A	119	ASP	2
1	A	136	ASP	2
1	A	9	MET	2
1	A	43	GLU	2
1	A	80	GLU	2
1	A	113	VAL	2
1	A	150	LYS	2
1	A	153	SER	2
1	A	125	LEU	1
1	A	139	VAL	1
1	A	10	ASP	1
1	A	38	TYR	1
1	A	35	LYS	1
1	A	60	CYS	1
1	A	124	SER	1
1	A	78	GLU	1
1	A	111	THR	1
1	A	96	VAL	1
1	A	127	HIS	1
1	A	154	GLU	1
1	A	54	THR	1

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Mol	Chain	Res	Type	Models (Total)
1	A	17	GLU	1
1	A	92	VAL	1
1	A	134	SER	1
1	A	69	VAL	1
1	A	77	SER	1
1	A	123	GLN	1
1	A	82	ASP	1
1	A	118	LYS	1
1	A	14	ASN	1
1	A	19	VAL	1
1	A	33	VAL	1
1	A	41	TRP	1
1	A	31	ASP	1
1	A	57	THR	1
1	A	47	ASN	1
1	A	50	THR	1
1	A	65	VAL	1
1	A	115	SER	1
1	A	130	THR	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 monosaccharides in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 78% for the well-defined parts and 78% for the entire structure.

7.1 Chemical shift list 1

File name: working_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	1670
Number of shifts mapped to atoms	1670
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	152	-0.00 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	143	0.12 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}'$	146	0.05 ± 0.14	None needed (< 0.5 ppm)
^{15}N	137	0.27 ± 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 78%, i.e. 1472 atoms were assigned a chemical shift out of a possible 1881. 24 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	723/776 (93%)	291/309 (94%)	296/316 (94%)	136/151 (90%)
Sidechain	749/984 (76%)	453/576 (79%)	296/359 (82%)	0/49 (0%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	0/121 (0%)	0/63 (0%)	0/54 (0%)	0/4 (0%)
Overall	1472/1881 (78%)	744/948 (78%)	592/729 (81%)	136/204 (67%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 1479 atoms were assigned a chemical shift out of a possible 1900. 24 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	728/784 (93%)	293/312 (94%)	298/320 (93%)	137/152 (90%)
Sidechain	751/995 (75%)	454/583 (78%)	297/363 (82%)	0/49 (0%)
Aromatic	0/121 (0%)	0/63 (0%)	0/54 (0%)	0/4 (0%)
Overall	1479/1900 (78%)	747/958 (78%)	595/737 (81%)	137/205 (67%)

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	40	LYS	HG3	-0.63	2.76 – -0.04	-7.1
1	A	40	LYS	HG2	-0.38	2.67 – 0.07	-6.7
1	A	159	ARG	HD2	1.97	4.27 – 1.97	-5.0

7.1.5 Random Coil Index (RCI) plots ⓘ

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:

