



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 09:37 PM BST

PDB ID : 2JZD  
Title : NMR structure of the domain 527-651 of the SARS-CoV nonstructural protein nsp3  
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Deposited on : 2008-01-04

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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	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

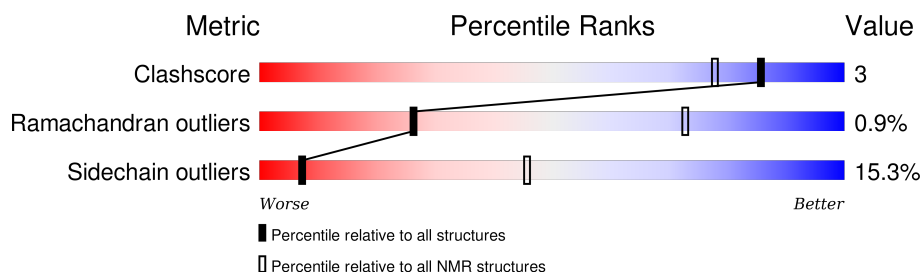
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 87%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	129	 84% 10% 5%

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 6 as representative, based on the following criterion: *closest to the average*.

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:527-A:648 (122)	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 3 clusters and 2 single-model clusters were found.

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

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2026 atoms, of which 1023 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Replicase polypeptide 1ab.

Mol	Chain	Residues	Atoms						Trace
1	A	129	Total	C	H	N	O	S	0
			2026	638	1023	171	185	9	

There are 4 discrepancies between the modelled and reference sequences:

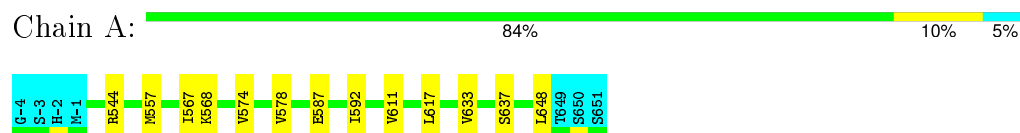
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	LEADER SEQUENCE	UNP P59641
A	-3	SER	-	LEADER SEQUENCE	UNP P59641
A	-2	HIS	-	LEADER SEQUENCE	UNP P59641
A	-1	MET	-	LEADER SEQUENCE	UNP P59641

## 4 Residue-property plots

### 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: Replicase polypeptide 1ab

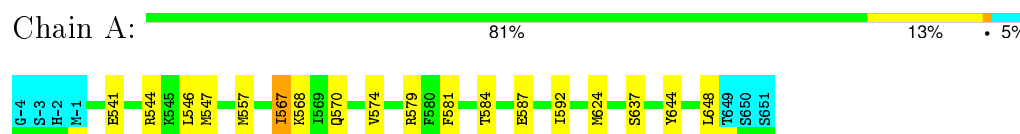


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

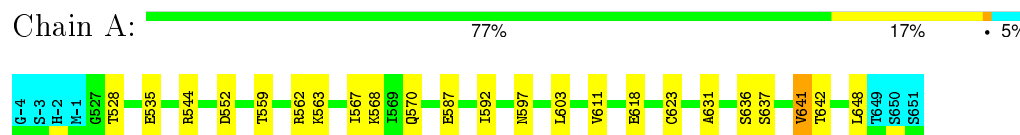
#### 4.2.1 Score per residue for model 1

- Molecule 1: Replicase polypeptide 1ab



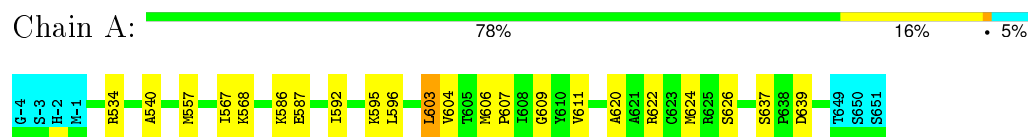
#### 4.2.2 Score per residue for model 2

- Molecule 1: Replicase polypeptide 1ab



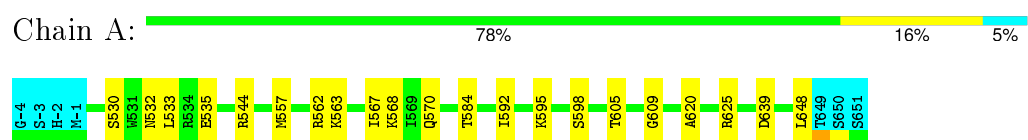
### 4.2.3 Score per residue for model 3

- Molecule 1: Replicase polypeptide 1ab



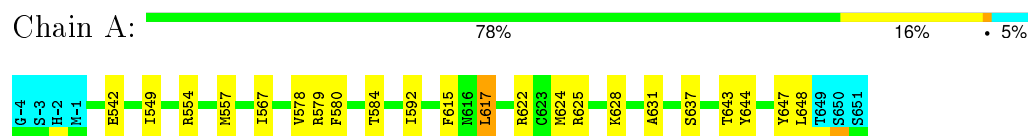
### 4.2.4 Score per residue for model 4

- Molecule 1: Replicase polypeptide 1ab



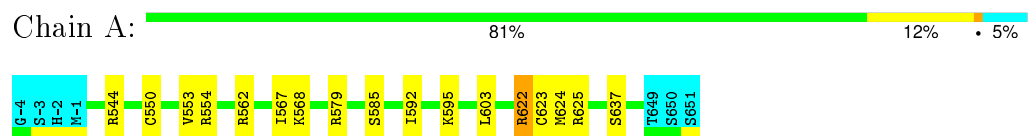
### 4.2.5 Score per residue for model 5

- Molecule 1: Replicase polypeptide 1ab



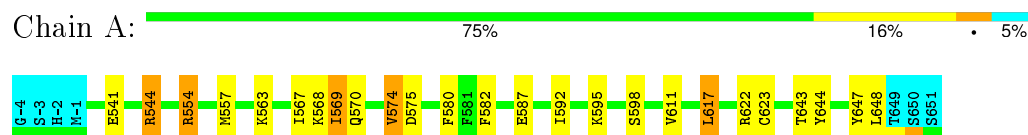
### 4.2.6 Score per residue for model 6

- Molecule 1: Replicase polypeptide 1ab



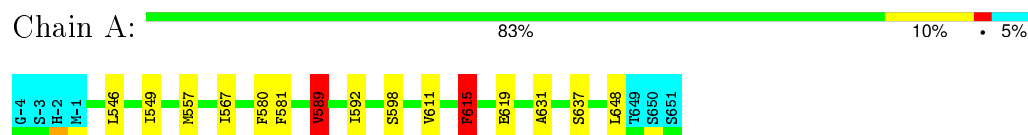
### 4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Replicase polypeptide 1ab



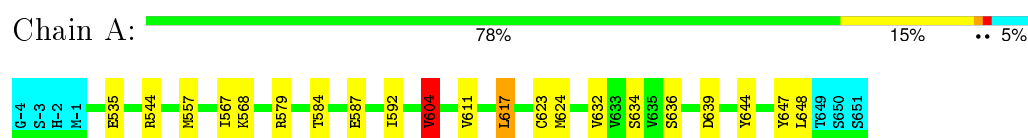
### 4.2.8 Score per residue for model 8

- Molecule 1: Replicase polypeptide 1ab



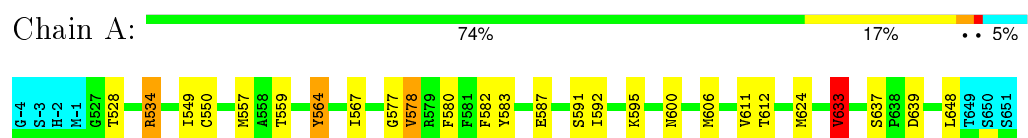
### 4.2.9 Score per residue for model 9

- Molecule 1: Replicase polypeptide 1ab



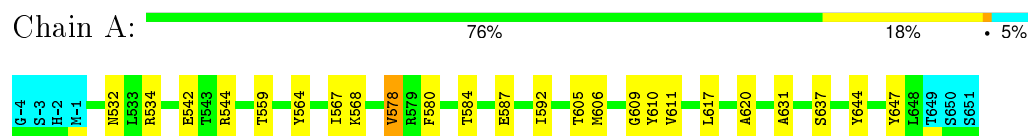
### 4.2.10 Score per residue for model 10

- Molecule 1: Replicase polypeptide 1ab



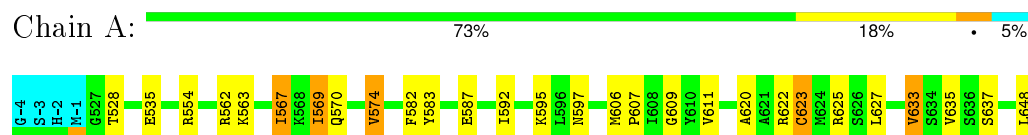
### 4.2.11 Score per residue for model 11

- Molecule 1: Replicase polypeptide 1ab



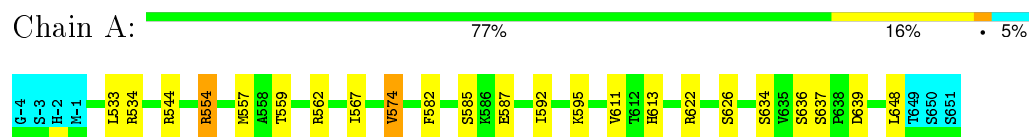
### 4.2.12 Score per residue for model 12

- Molecule 1: Replicase polypeptide 1ab



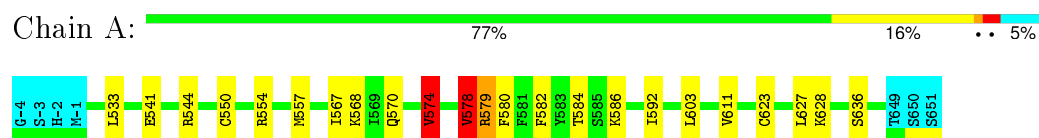
### 4.2.13 Score per residue for model 13

- Molecule 1: Replicase polypeptide 1ab



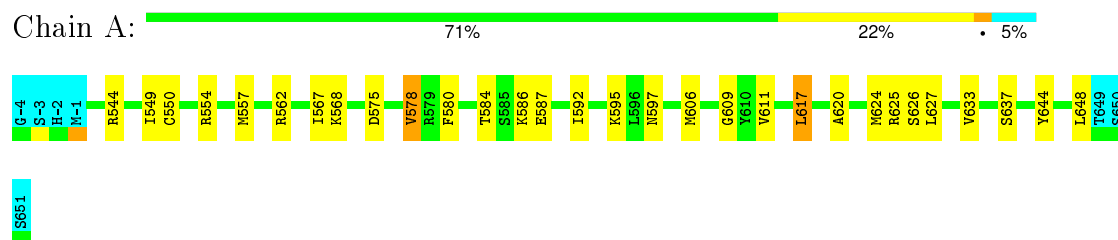
### 4.2.14 Score per residue for model 14

- Molecule 1: Replicase polypeptide 1ab



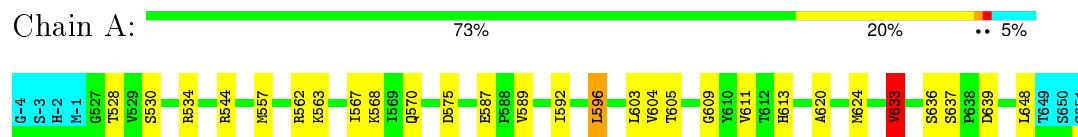
### 4.2.15 Score per residue for model 15

- Molecule 1: Replicase polypeptide 1ab



### 4.2.16 Score per residue for model 16

- Molecule 1: Replicase polypeptide 1ab

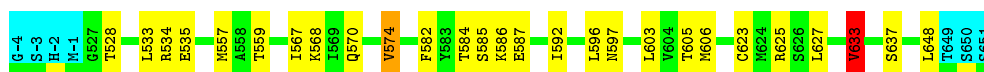


### 4.2.17 Score per residue for model 17

- Molecule 1: Replicase polypeptide 1ab







#### 4.2.18 Score per residue for model 18

- Molecule 1: Replicase polypeptide 1ab

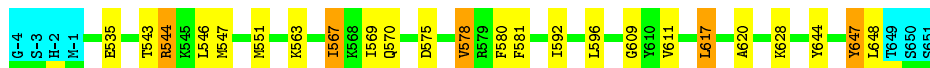
Chain A: 79% 14% 5%



#### 4.2.19 Score per residue for model 19

- Molecule 1: Replicase polypeptide 1ab

Chain A: 76% 15% 5%



#### 4.2.20 Score per residue for model 20

- Molecule 1: Replicase polypeptide 1ab

Chain A: 72% 21% 5%



## 5 Refinement protocol and experimental data overview

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

Of the 80 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure solution	1.2
CYANA	refinement	1.2

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)	BMRB entry 15618
Number of chemical shift lists	1
Total number of shifts	1536
Number of shifts mapped to atoms	1536
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

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

## 6 Model quality i

### 6.1 Standard geometry i

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	0.60±0.01	0±0/976 (0.0±0.0%)	1.07±0.04	1±1/1323 (0.1±0.1%)
All	All	0.60	0/19520 (0.0%)	1.07	27/26460 (0.1%)

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	1.4±1.2
All	All	0	29

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	641	VAL	CA-CB-CG1	9.29	124.83	110.90	2	1
1	A	578	VAL	CA-CB-CG1	8.43	123.54	110.90	14	1
1	A	633	VAL	CA-CB-CG1	8.36	123.44	110.90	10	4
1	A	625	ARG	NE-CZ-NH2	-6.31	117.14	120.30	12	3
1	A	564	TYR	CB-CG-CD2	-6.28	117.23	121.00	10	1
1	A	641	VAL	CG1-CB-CG2	-6.18	101.01	110.90	2	1
1	A	577	GLY	C-N-CA	6.09	136.94	121.70	10	1
1	A	615	PHE	CB-CG-CD2	-6.06	116.56	120.80	5	2
1	A	579	ARG	NE-CZ-NH2	-6.03	117.28	120.30	14	1
1	A	603	LEU	CB-CG-CD2	5.99	121.18	111.00	3	1
1	A	554	ARG	NE-CZ-NH1	5.94	123.27	120.30	15	1
1	A	562	ARG	NE-CZ-NH2	-5.76	117.42	120.30	15	2
1	A	574	VAL	CA-CB-CG1	5.54	119.20	110.90	14	1
1	A	554	ARG	NE-CZ-NH2	-5.51	117.55	120.30	18	1
1	A	562	ARG	NE-CZ-NH1	5.47	123.03	120.30	4	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	644	TYR	CB-CG-CD1	-5.27	117.84	121.00	1	1
1	A	625	ARG	NE-CZ-NH1	5.18	122.89	120.30	20	1
1	A	604	VAL	CA-CB-CG1	5.11	118.57	110.90	9	1
1	A	534	ARG	NE-CZ-NH2	-5.03	117.78	120.30	17	1
1	A	579	ARG	NE-CZ-NH1	5.01	122.81	120.30	1	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	622	ARG	Sidechain	5
1	A	631	ALA	Peptide	4
1	A	625	ARG	Sidechain	4
1	A	554	ARG	Sidechain	2
1	A	583	TYR	Sidechain	2
1	A	534	ARG	Sidechain	2
1	A	579	ARG	Sidechain	2
1	A	564	TYR	Sidechain	2
1	A	615	PHE	Sidechain	1
1	A	610	TYR	Sidechain	1
1	A	647	TYR	Sidechain	1
1	A	544	ARG	Sidechain	1
1	A	562	ARG	Sidechain	1
1	A	580	PHE	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	956	981	979	5±4
All	All	19120	19620	19580	103

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:574:VAL:HG11	1:A:582:PHE:CE2	0.79	2.12	17	5
1:A:617:LEU:HD11	1:A:644:TYR:CD2	0.77	2.15	19	7
1:A:549:ILE:HD11	1:A:580:PHE:CD1	0.68	2.24	10	5
1:A:528:THR:HA	1:A:633:VAL:HG13	0.63	1.70	17	4
1:A:570:GLN:NE2	1:A:574:VAL:HG12	0.60	2.12	17	1
1:A:578:VAL:HG13	1:A:580:PHE:CZ	0.55	2.35	11	4
1:A:578:VAL:CG1	1:A:580:PHE:CZ	0.54	2.90	15	4
1:A:528:THR:CA	1:A:633:VAL:HG13	0.54	2.32	17	3
1:A:609:GLY:O	1:A:620:ALA:HB2	0.53	2.03	16	8
1:A:589:VAL:HG11	1:A:615:PHE:CZ	0.52	2.39	8	1
1:A:540:ALA:HB2	1:A:604:VAL:CG1	0.52	2.34	3	1
1:A:617:LEU:HD11	1:A:644:TYR:HD2	0.52	1.64	19	3
1:A:569:ILE:HD12	1:A:582:PHE:CZ	0.52	2.40	7	1
1:A:578:VAL:HG13	1:A:580:PHE:CE2	0.52	2.40	14	3
1:A:574:VAL:HG11	1:A:582:PHE:CD2	0.51	2.40	17	1
1:A:617:LEU:HD12	1:A:647:TYR:CE2	0.50	2.41	19	5
1:A:617:LEU:HD13	1:A:617:LEU:C	0.50	2.27	15	4
1:A:567:ILE:CD1	1:A:569:ILE:HD13	0.50	2.37	18	2
1:A:546:LEU:HD23	1:A:547:MET:N	0.50	2.22	1	2
1:A:578:VAL:CG1	1:A:580:PHE:CE2	0.49	2.95	10	1
1:A:617:LEU:C	1:A:617:LEU:HD13	0.48	2.29	9	2
1:A:567:ILE:HD13	1:A:569:ILE:H	0.47	1.68	12	1
1:A:546:LEU:HD21	1:A:581:PHE:HB2	0.46	1.86	19	2
1:A:597:ASN:OD1	1:A:627:LEU:HD12	0.46	2.10	17	3
1:A:596:LEU:HD11	1:A:603:LEU:HD21	0.46	1.87	16	1
1:A:617:LEU:HD13	1:A:617:LEU:O	0.46	2.10	9	4
1:A:617:LEU:HD12	1:A:647:TYR:CD2	0.46	2.46	11	6
1:A:548:PRO:HG2	1:A:605:THR:HG21	0.45	1.89	20	1
1:A:617:LEU:CD1	1:A:644:TYR:CD2	0.45	2.98	15	5
1:A:549:ILE:HD11	1:A:580:PHE:HD1	0.44	1.69	10	1
1:A:599:LEU:HD12	1:A:599:LEU:H	0.44	1.72	20	1
1:A:604:VAL:HG13	1:A:632:VAL:HB	0.41	1.92	9	1
1:A:567:ILE:HG13	1:A:574:VAL:CG1	0.41	2.45	1	1
1:A:546:LEU:HD11	1:A:581:PHE:HB2	0.41	1.92	8	1
1:A:596:LEU:HD12	1:A:603:LEU:HD21	0.41	1.93	17	1
1:A:606:MET:HB3	1:A:607:PRO:HD2	0.41	1.92	12	1
1:A:536:MET:CE	1:A:634:SER:HB3	0.41	2.45	20	1
1:A:620:ALA:HA	1:A:623:CYS:SG	0.41	2.56	12	1
1:A:549:ILE:HD13	1:A:582:PHE:CE1	0.41	2.50	10	1
1:A:607:PRO:HA	1:A:624:MET:SD	0.40	2.56	3	1
1:A:589:VAL:CG2	1:A:613:HIS:CD2	0.40	3.03	16	1
1:A:617:LEU:C	1:A:617:LEU:CD1	0.40	2.89	15	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	122/129 (95%)	110±3 (90±2%)	11±3 (9±2%)	1±1 (1±1%)	26	73
All	All	2440/2580 (95%)	2193 (90%)	224 (9%)	23 (1%)	26	73

All 7 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	611	VAL	15
1	A	604	VAL	2
1	A	569	ILE	2
1	A	543	THR	1
1	A	544	ARG	1
1	A	589	VAL	1
1	A	579	ARG	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	105/111 (95%)	89±3 (85±3%)	16±3 (15±3%)	7	46
All	All	2100/2220 (95%)	1779 (85%)	321 (15%)	7	46

All 65 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	567	ILE	20
1	A	592	ILE	20
1	A	648	LEU	16

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Mol	Chain	Res	Type	Models (Total)
1	A	568	LYS	14
1	A	637	SER	14
1	A	587	GLU	13
1	A	557	MET	13
1	A	544	ARG	12
1	A	584	THR	9
1	A	570	GLN	9
1	A	623	CYS	8
1	A	595	LYS	8
1	A	639	ASP	7
1	A	578	VAL	7
1	A	624	MET	7
1	A	554	ARG	6
1	A	636	SER	6
1	A	617	LEU	6
1	A	535	GLU	6
1	A	563	LYS	6
1	A	606	MET	6
1	A	550	CYS	5
1	A	603	LEU	5
1	A	541	GLU	5
1	A	574	VAL	5
1	A	559	THR	5
1	A	633	VAL	4
1	A	533	LEU	4
1	A	628	LYS	4
1	A	534	ARG	4
1	A	575	ASP	4
1	A	605	THR	4
1	A	586	LYS	4
1	A	598	SER	4
1	A	626	SER	3
1	A	562	ARG	3
1	A	585	SER	3
1	A	596	LEU	3
1	A	579	ARG	3
1	A	553	VAL	2
1	A	634	SER	2
1	A	643	THR	2
1	A	542	GLU	2
1	A	532	ASN	2
1	A	635	VAL	2

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Mol	Chain	Res	Type	Models (Total)
1	A	622	ARG	2
1	A	604	VAL	2
1	A	530	SER	2
1	A	627	LEU	2
1	A	641	VAL	1
1	A	616	ASN	1
1	A	551	MET	1
1	A	589	VAL	1
1	A	642	THR	1
1	A	552	ASP	1
1	A	618	GLU	1
1	A	591	SER	1
1	A	597	ASN	1
1	A	565	LYS	1
1	A	528	THR	1
1	A	613	HIS	1
1	A	612	THR	1
1	A	619	GLU	1
1	A	600	ASN	1
1	A	625	ARG	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 ⓘ

There are no ligands in this entry.



## 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 87% for the well-defined parts and 86% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 15618

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	1536
Number of shifts mapped to atoms	1536
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	128	$0.28 \pm 0.21$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	121	$0.49 \pm 0.10$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	44	$0.04 \pm 0.19$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	122	$-0.34 \pm 0.32$	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 87%, i.e. 1305 atoms were assigned a chemical shift out of a possible 1505. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	517/598 (86%)	238/238 (100%)	163/244 (67%)	116/116 (100%)
Sidechain	689/795 (87%)	422/466 (91%)	260/294 (88%)	7/35 (20%)

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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	99/112 (88%)	51/58 (88%)	47/49 (96%)	1/5 (20%)
Overall	1305/1505 (87%)	711/762 (93%)	470/587 (80%)	124/156 (79%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 86%, i.e. 1355 atoms were assigned a chemical shift out of a possible 1572. 0 out of 20 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	543/633 (86%)	249/252 (99%)	172/258 (67%)	122/123 (99%)
Sidechain	711/819 (87%)	436/481 (91%)	268/303 (88%)	7/35 (20%)
Aromatic	101/120 (84%)	52/62 (84%)	48/51 (94%)	1/7 (14%)
Overall	1355/1572 (86%)	737/795 (93%)	488/612 (80%)	130/165 (79%)

#### 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	529	VAL	HG21	-0.95	2.20 – -0.60	-6.2
1	A	529	VAL	HG23	-0.95	2.20 – -0.60	-6.2
1	A	529	VAL	HG22	-0.95	2.20 – -0.60	-6.2
1	A	618	GLU	HB3	0.80	3.10 – 0.90	-5.5

#### 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:

