



# Full wwPDB NMR Structure Validation Report ⓘ

Jun 12, 2024 – 05:05 PM EDT

PDB ID : 2LAI  
BMRB ID : 17525  
Title : Hyaloperonospora arabidopsidis Effector Protein ATR13  
Authors : Leonelli, L.; Pelton, J.G.; Wemmer, D.E.; Staskawicz, B.J.  
Deposited on : 2011-03-15

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 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)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

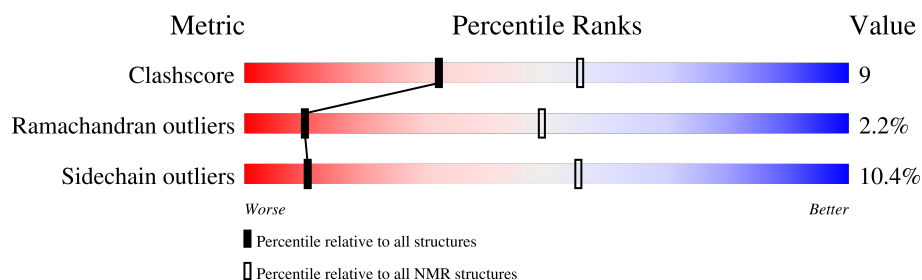
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 82%.

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	101	<div> <div>30%</div> <div>16%</div> <div>54%</div> </div>

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 6 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:78-A:88, A:116-A:150 (46)	1.02	6

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 and 2 single-model clusters were found.

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

### 3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1526 atoms, of which 729 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Avirulence protein ATR13.

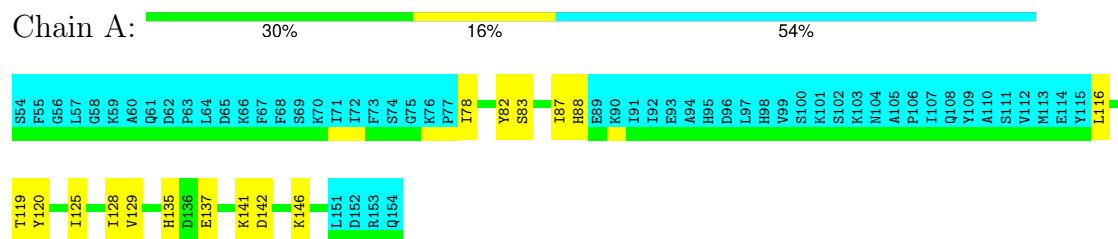
Mol	Chain	Residues	Atoms						Trace
1	A	101	Total	C	H	N	O	S	0
			1526	507	729	137	152	1	

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

### 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: Avirulence protein ATR13

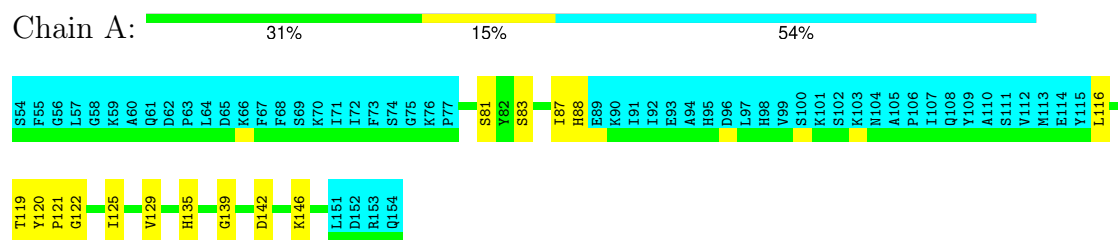


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

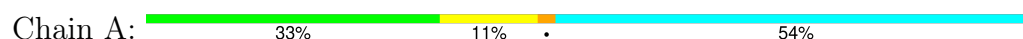
#### 4.2.1 Score per residue for model 1

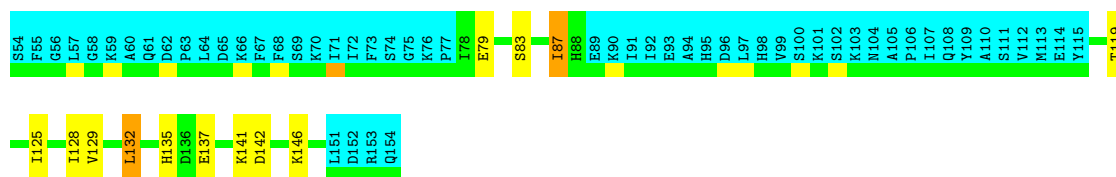
- Molecule 1: Avirulence protein ATR13



#### 4.2.2 Score per residue for model 2

- Molecule 1: Avirulence protein ATR13

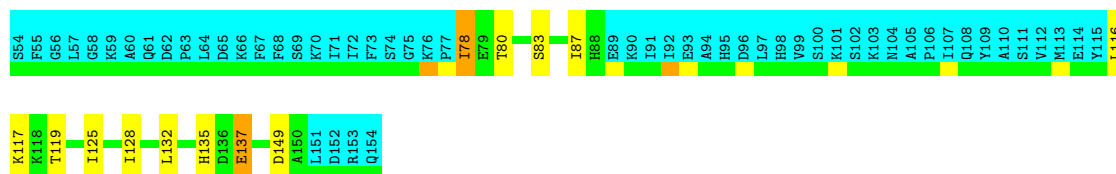




#### 4.2.3 Score per residue for model 3

- Molecule 1: Avirulence protein ATR13

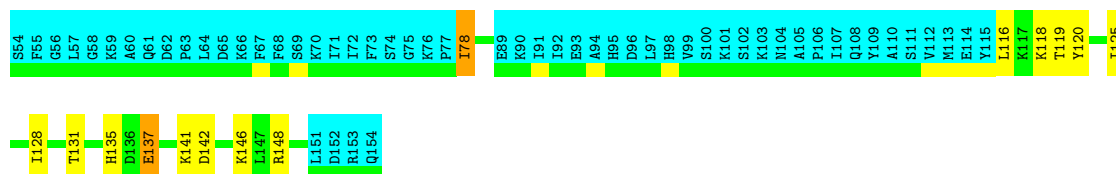
Chain A: 33% 11% 54%



#### 4.2.4 Score per residue for model 4

- Molecule 1: Avirulence protein ATR13

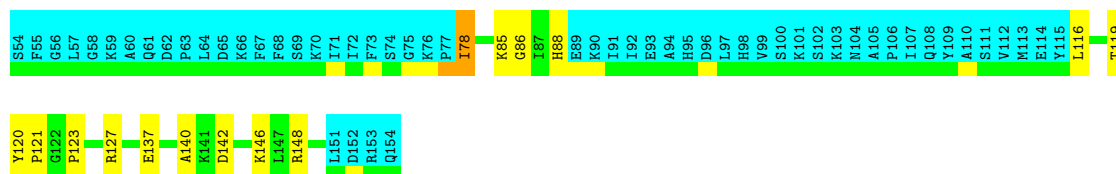
Chain A: 32% 12% 54%



#### 4.2.5 Score per residue for model 5

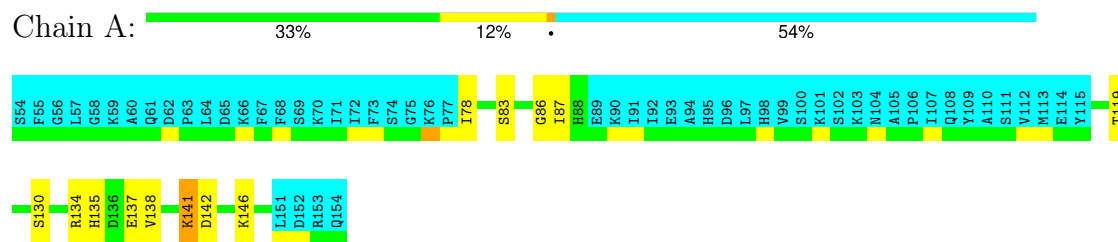
- Molecule 1: Avirulence protein ATR13

Chain A: 31% 14% 54%



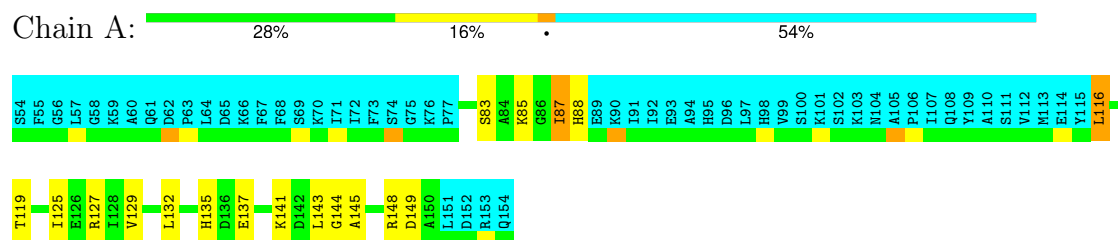
#### 4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Avirulence protein ATR13



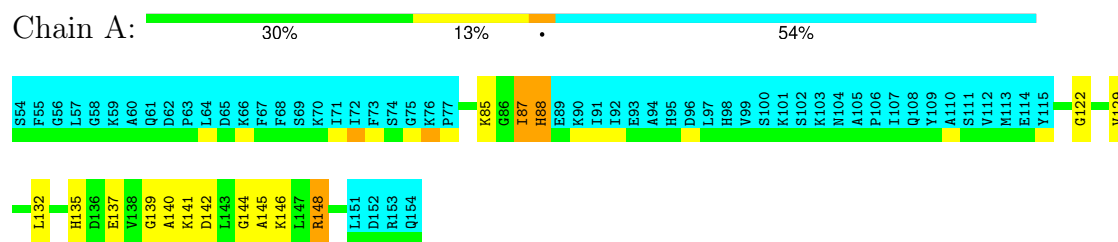
#### 4.2.7 Score per residue for model 7

- Molecule 1: Avirulence protein ATR13



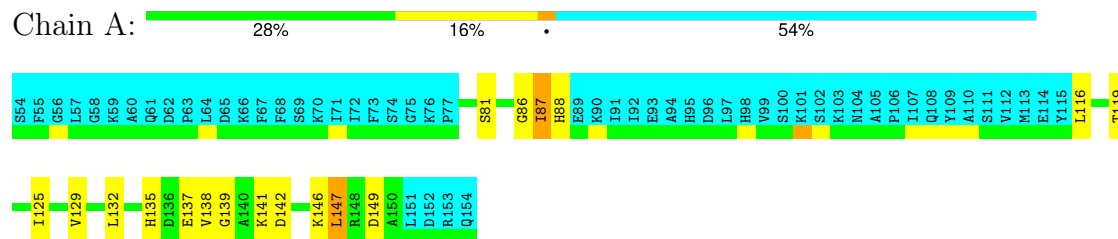
#### 4.2.8 Score per residue for model 8

- Molecule 1: Avirulence protein ATR13



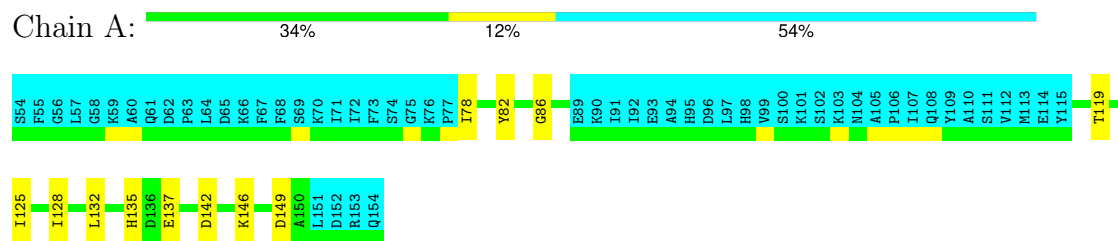
#### 4.2.9 Score per residue for model 9

- Molecule 1: Avirulence protein ATR13



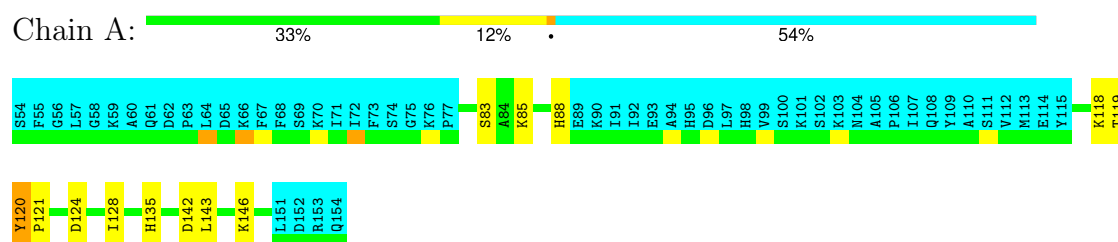
### 4.2.10 Score per residue for model 10

- Molecule 1: Avirulence protein ATR13



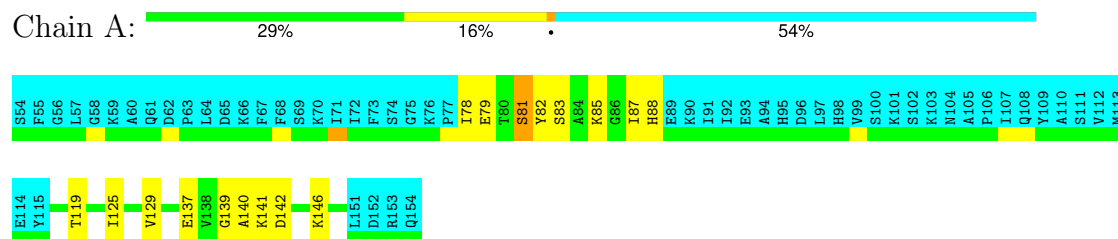
### 4.2.11 Score per residue for model 11

- Molecule 1: Avirulence protein ATR13



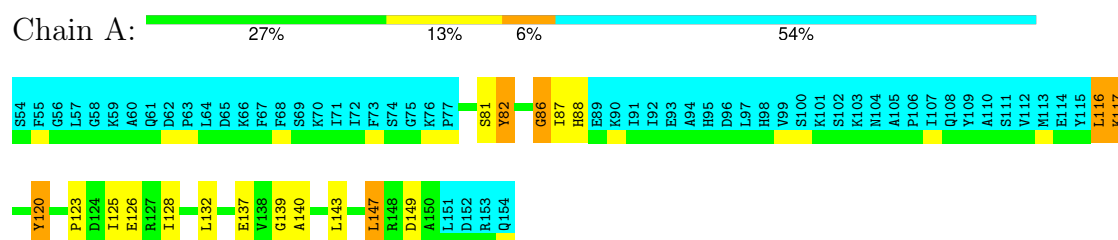
### 4.2.12 Score per residue for model 12

- Molecule 1: Avirulence protein ATR13



### 4.2.13 Score per residue for model 13

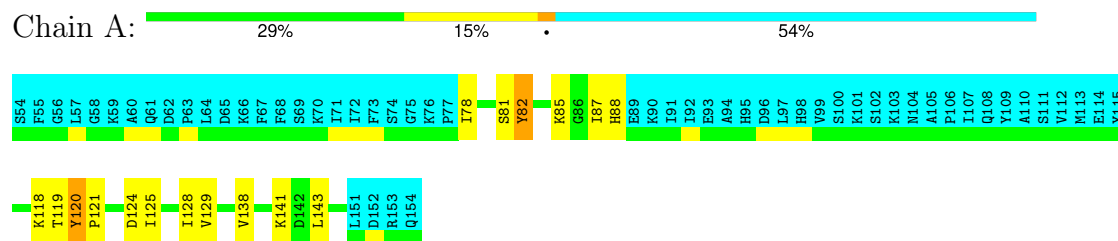
- Molecule 1: Avirulence protein ATR13





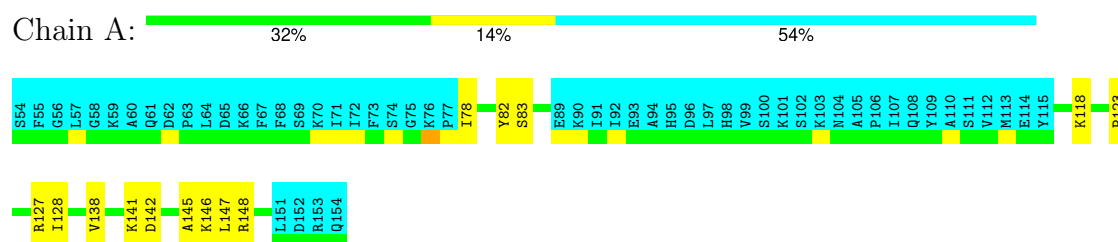
### 4.2.14 Score per residue for model 14

- Molecule 1: Avirulence protein ATR13



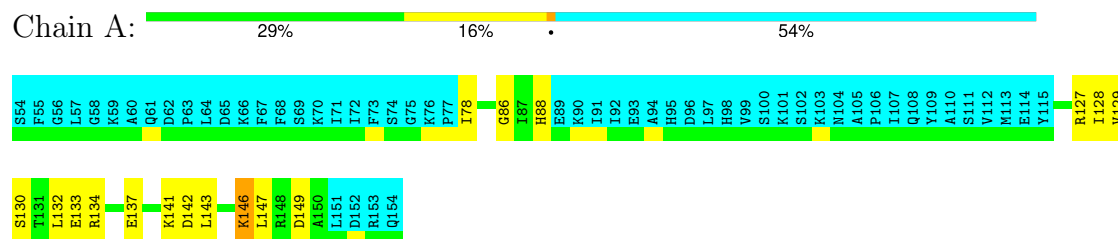
### 4.2.15 Score per residue for model 15

- Molecule 1: Avirulence protein ATR13



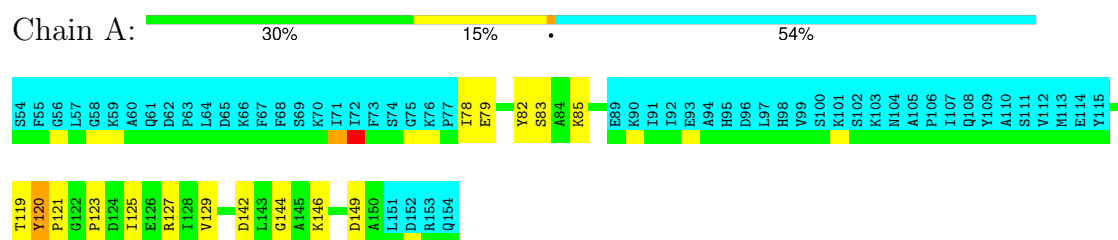
### 4.2.16 Score per residue for model 16

- Molecule 1: Avirulence protein ATR13



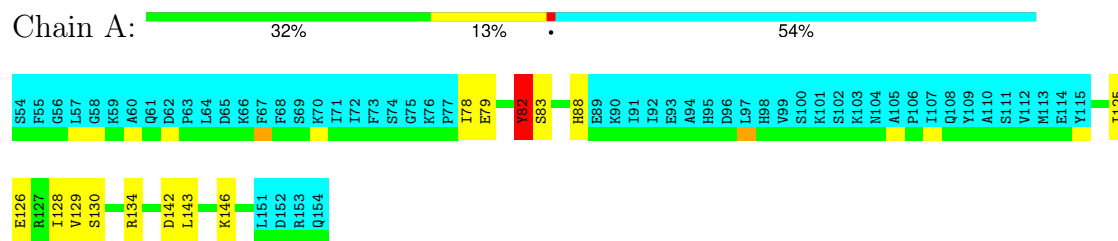
### 4.2.17 Score per residue for model 17

- Molecule 1: Avirulence protein ATR13



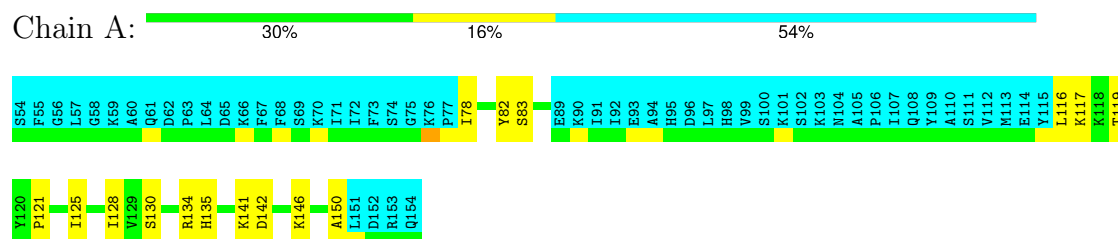
### 4.2.18 Score per residue for model 18

- Molecule 1: Avirulence protein ATR13



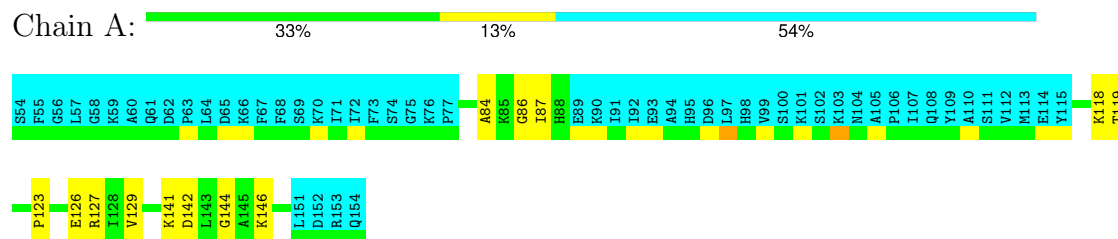
### 4.2.19 Score per residue for model 19

- Molecule 1: Avirulence protein ATR13



### 4.2.20 Score per residue for model 20

- Molecule 1: Avirulence protein ATR13



## 5 Refinement protocol and experimental data overview

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

Of the 200 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
CYANA	structure solution	2.1
CNS	structure solution	1.3
CYANA	refinement	2.1
CNS	refinement	1.3

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	876
Number of shifts mapped to atoms	810
Number of unparsed shifts	0
Number of shifts with mapping errors	66
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	82%

## 6 Model quality

### 6.1 Standard geometry

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	357	329	364	7±2
All	All	7140	6580	7280	135

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:137:GLU:O	1:A:141:LYS:HB2	0.74	1.83	8	2
1:A:137:GLU:HB2	1:A:140:ALA:HB3	0.65	1.65	8	2
1:A:88:HIS:HB3	1:A:140:ALA:HB2	0.65	1.69	12	2
1:A:132:LEU:HD11	1:A:140:ALA:HB1	0.58	1.75	13	1
1:A:132:LEU:HA	1:A:135:HIS:NE2	0.56	2.15	2	2
1:A:78:ILE:HD13	1:A:78:ILE:H	0.56	1.59	4	1
1:A:123:PRO:O	1:A:127:ARG:HG2	0.56	2.01	5	3
1:A:132:LEU:HD23	1:A:140:ALA:HB1	0.55	1.78	8	1
1:A:88:HIS:HB3	1:A:139:GLY:O	0.54	2.02	1	3
1:A:125:ILE:HA	1:A:128:ILE:HD12	0.53	1.80	3	6
1:A:79:GLU:O	1:A:83:SER:HB2	0.53	2.04	18	4
1:A:85:LYS:HA	1:A:137:GLU:OE1	0.52	2.05	7	1
1:A:142:ASP:O	1:A:146:LYS:HG2	0.52	2.04	16	2
1:A:128:ILE:O	1:A:132:LEU:HB2	0.52	2.05	3	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:129:VAL:O	1:A:133:GLU:HG2	0.52	2.04	16	1
1:A:83:SER:HA	1:A:135:HIS:CD2	0.51	2.39	11	1
1:A:120:TYR:N	1:A:121:PRO:CD	0.50	2.75	11	2
1:A:83:SER:HA	1:A:135:HIS:NE2	0.49	2.22	7	5
1:A:116:LEU:HD13	1:A:147:LEU:HD21	0.49	1.85	9	1
1:A:87:ILE:O	1:A:87:ILE:HD13	0.49	2.08	2	3
1:A:87:ILE:HG23	1:A:88:HIS:H	0.49	1.68	8	1
1:A:88:HIS:CE1	1:A:139:GLY:HA3	0.49	2.43	12	1
1:A:87:ILE:HG22	1:A:137:GLU:OE2	0.48	2.09	13	2
1:A:120:TYR:N	1:A:121:PRO:HD3	0.48	2.23	17	2
1:A:135:HIS:CE1	1:A:137:GLU:HB3	0.48	2.43	4	1
1:A:120:TYR:CD1	1:A:125:ILE:HG12	0.48	2.44	13	1
1:A:78:ILE:O	1:A:82:TYR:HB2	0.47	2.08	12	1
1:A:142:ASP:O	1:A:146:LYS:HD3	0.47	2.09	2	13
1:A:130:SER:O	1:A:134:ARG:HB2	0.47	2.09	16	4
1:A:88:HIS:ND1	1:A:143:LEU:HD22	0.47	2.25	18	2
1:A:125:ILE:O	1:A:129:VAL:HG22	0.47	2.10	9	8
1:A:145:ALA:HA	1:A:148:ARG:NE	0.47	2.25	15	1
1:A:143:LEU:O	1:A:147:LEU:HD12	0.46	2.10	13	1
1:A:78:ILE:HB	1:A:82:TYR:CD1	0.46	2.45	19	2
1:A:128:ILE:O	1:A:132:LEU:HD12	0.46	2.09	2	2
1:A:78:ILE:HG23	1:A:82:TYR:CG	0.46	2.46	18	1
1:A:124:ASP:O	1:A:128:ILE:HG13	0.46	2.11	11	2
1:A:82:TYR:CE1	1:A:128:ILE:HG23	0.46	2.45	13	1
1:A:88:HIS:O	1:A:139:GLY:HA3	0.46	2.11	8	1
1:A:135:HIS:ND1	1:A:137:GLU:HG2	0.46	2.26	10	2
1:A:88:HIS:ND1	1:A:143:LEU:HB2	0.45	2.25	11	3
1:A:81:SER:O	1:A:87:ILE:HD13	0.45	2.11	1	3
1:A:116:LEU:H	1:A:116:LEU:HD22	0.45	1.71	7	1
1:A:132:LEU:HA	1:A:135:HIS:CE1	0.45	2.47	10	1
1:A:82:TYR:CZ	1:A:128:ILE:HG23	0.45	2.47	15	1
1:A:135:HIS:NE2	1:A:137:GLU:HB3	0.44	2.27	4	1
1:A:82:TYR:CD2	1:A:87:ILE:HG12	0.44	2.47	14	1
1:A:142:ASP:O	1:A:146:LYS:HB2	0.44	2.13	15	4
1:A:116:LEU:HA	1:A:120:TYR:CD1	0.44	2.47	1	1
1:A:123:PRO:O	1:A:126:GLU:HG2	0.43	2.13	13	1
1:A:123:PRO:HA	1:A:126:GLU:OE1	0.43	2.14	13	1
1:A:135:HIS:CE1	1:A:137:GLU:HG2	0.43	2.48	9	3
1:A:145:ALA:O	1:A:149:ASP:HB2	0.43	2.13	7	1
1:A:87:ILE:HG22	1:A:137:GLU:OE1	0.43	2.12	12	2
1:A:145:ALA:O	1:A:148:ARG:HG3	0.43	2.13	8	1

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:88:HIS:CE1	1:A:143:LEU:HD13	0.42	2.50	16	1
1:A:116:LEU:O	1:A:117:LYS:HG2	0.42	2.14	3	1
1:A:116:LEU:HD23	1:A:120:TYR:CZ	0.42	2.50	1	2
1:A:129:VAL:HG12	1:A:144:GLY:O	0.41	2.16	17	3
1:A:116:LEU:O	1:A:120:TYR:HB3	0.41	2.16	5	1
1:A:132:LEU:HD22	1:A:144:GLY:N	0.41	2.31	7	1
1:A:78:ILE:HD13	1:A:78:ILE:O	0.41	2.16	3	1
1:A:78:ILE:O	1:A:131:THR:HG21	0.41	2.16	4	1
1:A:85:LYS:HA	1:A:135:HIS:NE2	0.41	2.30	8	1
1:A:81:SER:O	1:A:87:ILE:HG13	0.41	2.16	9	1
1:A:138:VAL:O	1:A:141:LYS:HD3	0.41	2.16	14	1
1:A:78:ILE:HG23	1:A:82:TYR:CD2	0.40	2.51	17	1
1:A:123:PRO:HA	1:A:126:GLU:OE2	0.40	2.17	20	1
1:A:80:THR:O	1:A:83:SER:HB2	0.40	2.17	3	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	46/101 (46%)	38±2 (83±5%)	7±2 (15±4%)	1±1 (2±2%)	10	49
All	All	920/2020 (46%)	766 (83%)	134 (15%)	20 (2%)	10	49

All 12 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	78	ILE	3
1	A	86	GLY	3
1	A	121	PRO	2
1	A	122	GLY	2
1	A	118	LYS	2
1	A	116	LEU	2
1	A	137	GLU	1
1	A	87	ILE	1

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	117	LYS	1
1	A	85	LYS	1
1	A	82	TYR	1
1	A	84	ALA	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	38/86 (44%)	34±2 (90±4%)	4±2 (10±4%)	10	55
All	All	760/1720 (44%)	681 (90%)	79 (10%)	10	55

All 22 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	119	THR	15
1	A	141	LYS	10
1	A	149	ASP	6
1	A	78	ILE	5
1	A	87	ILE	4
1	A	148	ARG	4
1	A	85	LYS	4
1	A	147	LEU	4
1	A	120	TYR	4
1	A	118	LYS	3
1	A	138	VAL	3
1	A	82	TYR	3
1	A	137	GLU	2
1	A	116	LEU	2
1	A	127	ARG	2
1	A	117	LYS	2
1	A	132	LEU	1
1	A	88	HIS	1
1	A	81	SER	1
1	A	83	SER	1
1	A	146	LYS	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	126	GLU	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 monosaccharides in this entry.

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

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 82% for the well-defined parts and 63% 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	876
Number of shifts mapped to atoms	810
Number of unparsed shifts	0
Number of shifts with mapping errors	66
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 66 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	56	GLY	H	8.382	0.02	1
1	A	57	LEU	H	8.139	0.02	1
1	A	58	GLY	H	8.51	0.02	1
1	A	59	LYS	H	8.136	0.02	1
1	A	61	GLN	H	8.386	0.02	1
1	A	62	ASP	H	8.979	0.02	1
1	A	64	LEU	H	9.121	0.02	1
1	A	65	ASP	H	7.321	0.02	1
1	A	66	LYS	H	8.621	0.02	1
1	A	67	PHE	H	7.595	0.02	1
1	A	68	PHE	H	8.67	0.02	1
1	A	69	SER	H	8.623	0.02	1
1	A	70	LYS	H	7.014	0.02	1
1	A	71	ILE	H	6.922	0.02	1

*Continued on next page...*

*Continued from previous page...*

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	72	ILE	H	8.726	0.02	1
1	A	73	PHE	H	8.293	0.02	1
1	A	74	SER	H	7.637	0.02	1
1	A	75	GLY	H	7.991	0.02	1
1	A	76	LYS	H	7.776	0.02	1
1	A	78	ILE	H	8.562	0.02	1
1	A	79	GLU	H	9.338	0.02	1
1	A	80	THR	H	7.595	0.02	1
1	A	81	SER	H	8.425	0.02	1
1	A	82	TYR	H	8.578	0.02	1
1	A	83	SER	H	7.059	0.02	1
1	A	85	LYS	H	8.815	0.02	1
1	A	86	GLY	H	11.209	0.02	1
1	A	87	ILE	H	7.544	0.02	1
1	A	88	HIS	H	9.372	0.02	1
1	A	89	GLU	H	5.886	0.02	1
1	A	90	LYS	H	7.076	0.02	1
1	A	91	ILE	H	7.755	0.02	1
1	A	93	GLU	H	7.928	0.02	1
1	A	95	HIS	H	8.259	0.02	1
1	A	96	ASP	H	9.181	0.02	1
1	A	104	ASN	H	8.468	0.02	1
1	A	116	LEU	H	8.611	0.02	1
1	A	117	LYS	H	8.43	0.02	1
1	A	118	LYS	H	7.059	0.02	1
1	A	119	THR	H	7.269	0.02	1
1	A	120	TYR	H	8.583	0.02	1
1	A	122	GLY	H	9.066	0.02	1
1	A	124	ASP	H	7.255	0.02	1
1	A	125	ILE	H	7.788	0.02	1
1	A	126	GLU	H	7.475	0.02	1
1	A	128	ILE	H	8.127	0.02	1
1	A	129	VAL	H	8.3	0.02	1
1	A	130	SER	H	8.293	0.02	1
1	A	131	THR	H	7.782	0.02	1
1	A	132	LEU	H	7.996	0.02	1
1	A	133	GLU	H	8.544	0.02	1
1	A	135	HIS	H	7.416	0.02	1
1	A	136	ASP	H	8.032	0.02	1
1	A	137	GLU	H	11.989	0.02	1
1	A	138	VAL	H	8.755	0.02	1

*Continued on next page...*

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	139	GLY	H	8.989	0.02	1
1	A	141	LYS	H	7.642	0.02	1
1	A	142	ASP	H	8.479	0.02	1
1	A	143	LEU	H	7.464	0.02	1
1	A	144	GLY	H	9.053	0.02	1
1	A	146	LYS	H	7.892	0.02	1
1	A	147	LEU	H	8.595	0.02	1
1	A	149	ASP	H	7.808	0.02	1
1	A	151	LEU	H	7.996	0.02	1
1	A	152	ASP	H	8.139	0.02	1
1	A	154	GLN	H	7.806	0.02	1

### 7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	77	$-0.73 \pm 0.17$	Should be checked
$^{13}\text{C}_\beta$	67	$-0.13 \pm 0.11$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	72	$-0.18 \pm 0.20$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	77	$-0.06 \pm 0.44$	None needed ( $< 0.5$ ppm)

### 7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 82%, i.e. 512 atoms were assigned a chemical shift out of a possible 624. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	224/230 (97%)	93/94 (99%)	87/92 (95%)	44/44 (100%)
Sidechain	276/360 (77%)	180/233 (77%)	96/113 (85%)	0/14 (0%)
Aromatic	12/34 (35%)	6/16 (38%)	6/14 (43%)	0/4 (0%)
Overall	512/624 (82%)	279/343 (81%)	189/219 (86%)	44/62 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 63%, i.e. 876 atoms were assigned a chemical shift out of a possible 1385. 0 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	386/502 (77%)	160/204 (78%)	149/202 (74%)	77/96 (80%)
Sidechain	468/775 (60%)	308/502 (61%)	160/245 (65%)	0/28 (0%)
Aromatic	22/108 (20%)	11/52 (21%)	11/48 (23%)	0/8 (0%)
Overall	876/1385 (63%)	479/758 (63%)	320/495 (65%)	77/132 (58%)

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

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.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	137	GLU	H	11.99	5.45 – 11.20	6.4

### 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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

