



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 09:50 PM BST

PDB ID : 2JZ4
Title : Putative 32 kDa myrosinase binding protein At3g16450.1 from *Arabidopsis thaliana*
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Deposited on : 2007-12-28

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
<http://wwpdb.org/validation/2016/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
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

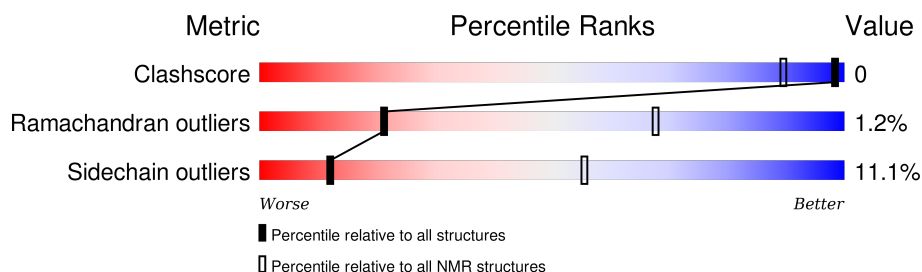
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 66%.

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 ≥ 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	299	

2 Ensemble composition and analysis ⓘ

This entry contains 20 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:2-A:18, A:22-A:144 (140)	0.98	3
2	A:153-A:297 (145)	0.75	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 6 clusters. No single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 4427 atoms, of which 2171 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Jasmonate inducible protein isolog.

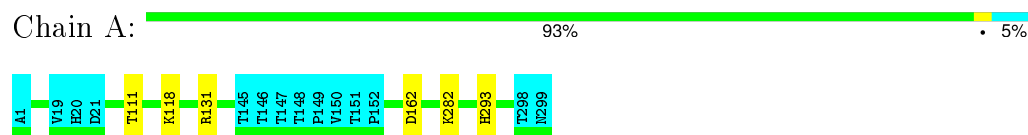
Mol	Chain	Residues	Atoms						Trace
1	A	299	Total	C	H	N	O	S	0
			4427	1433	2171	372	449	2	

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: Jasmonate inducible protein isolog

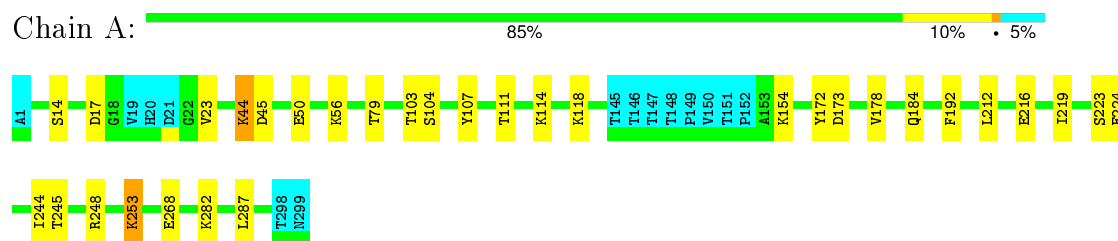


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

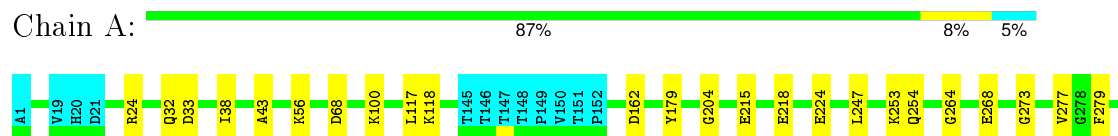
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Jasmonate inducible protein isolog



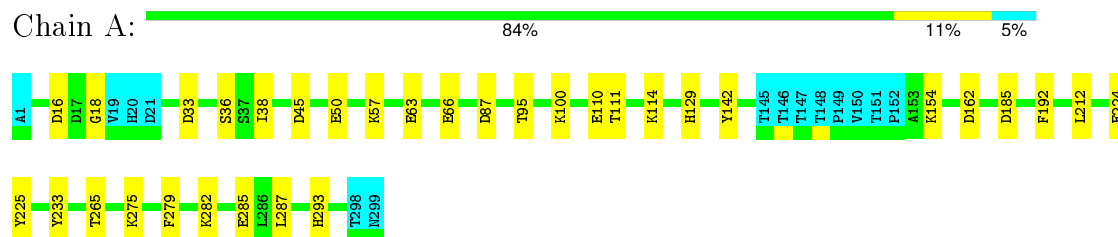
4.2.2 Score per residue for model 2

- Molecule 1: Jasmonate inducible protein isolog



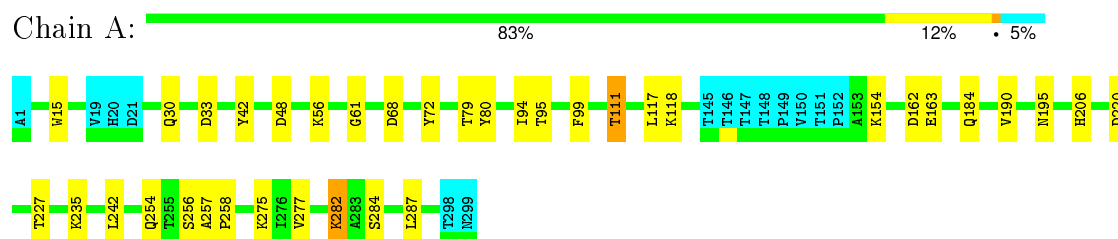
4.2.3 Score per residue for model 3

- Molecule 1: Jasmonate inducible protein isolog



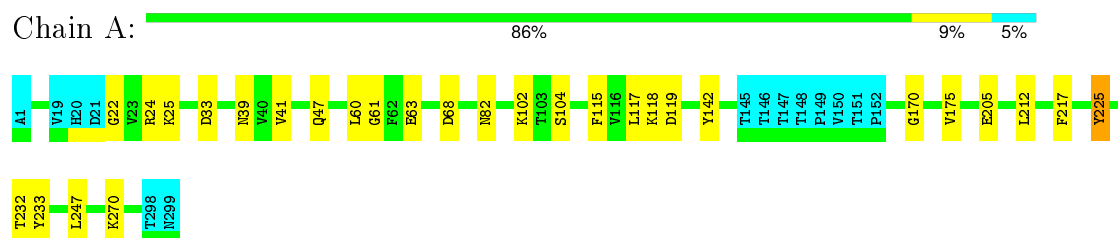
4.2.4 Score per residue for model 4

- Molecule 1: Jasmonate inducible protein isolog



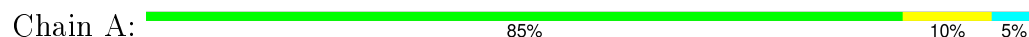
4.2.5 Score per residue for model 5

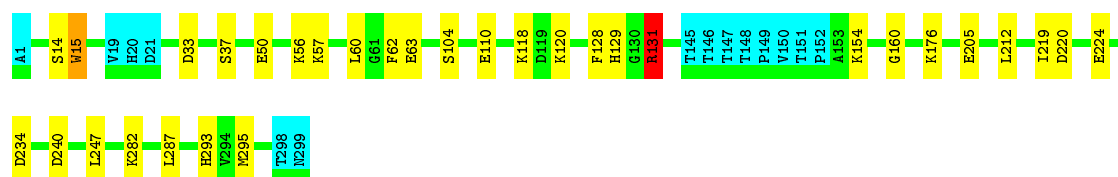
- Molecule 1: Jasmonate inducible protein isolog



4.2.6 Score per residue for model 6

- Molecule 1: Jasmonate inducible protein isolog

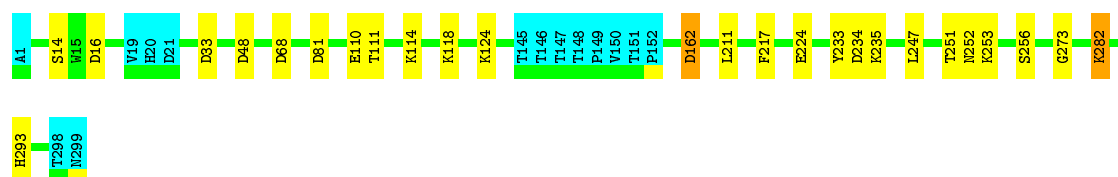




4.2.7 Score per residue for model 7

- Molecule 1: Jasmonate inducible protein isolog

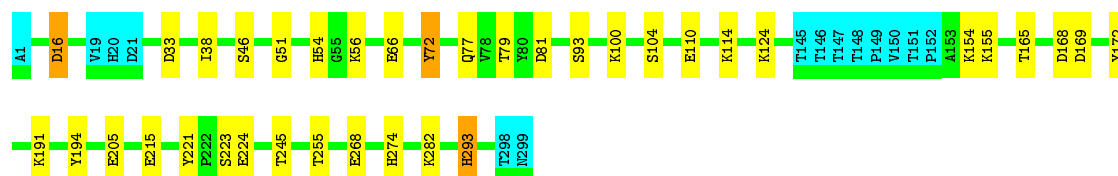
Chain A: 87% 8% 5%



4.2.8 Score per residue for model 8

- Molecule 1: Jasmonate inducible protein isolog

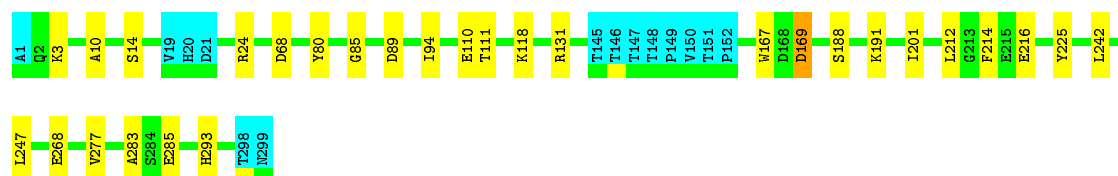
Chain A: 83% 11% 5%



4.2.9 Score per residue for model 9

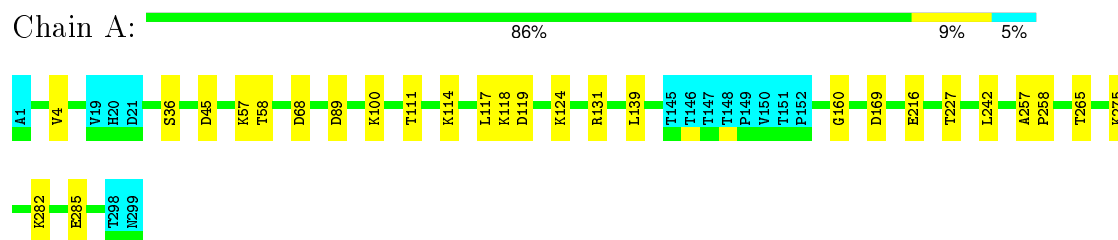
- Molecule 1: Jasmonate inducible protein isolog

Chain A: 86% 9% 5%



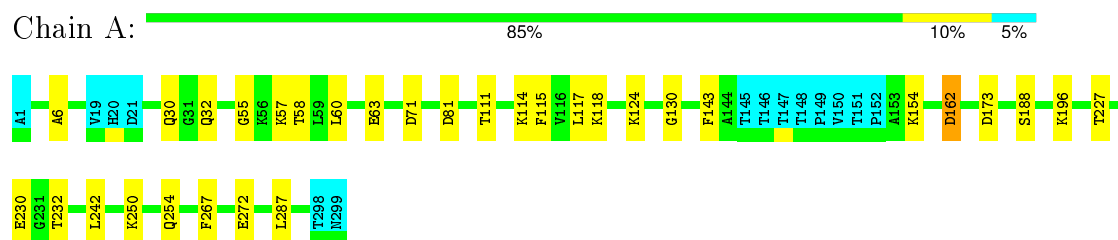
4.2.10 Score per residue for model 10

- Molecule 1: Jasmonate inducible protein isolog



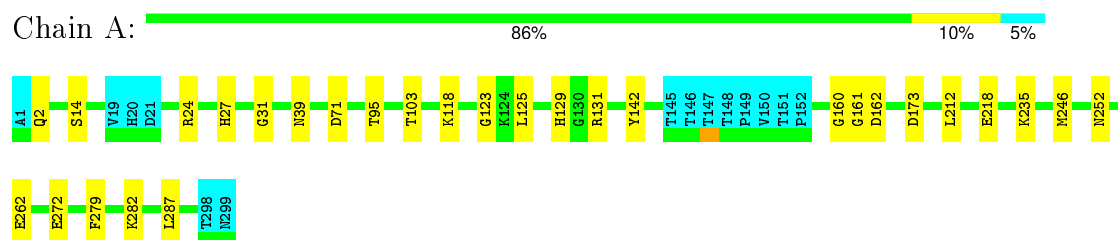
4.2.11 Score per residue for model 11

- Molecule 1: Jasmonate inducible protein isolog



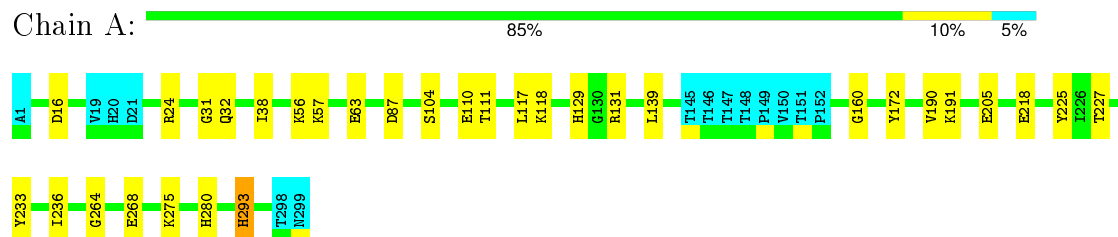
4.2.12 Score per residue for model 12

- Molecule 1: Jasmonate inducible protein isolog



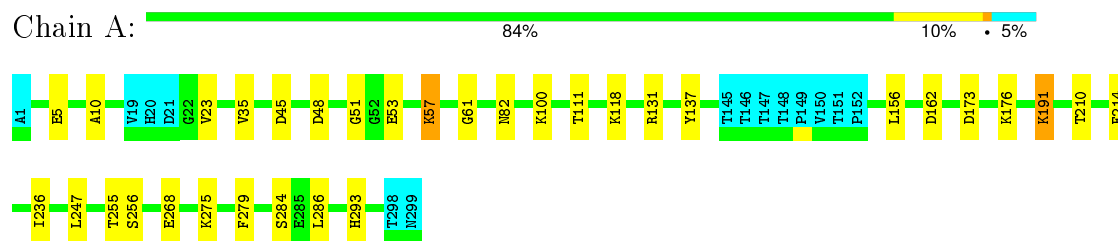
4.2.13 Score per residue for model 13

- Molecule 1: Jasmonate inducible protein isolog



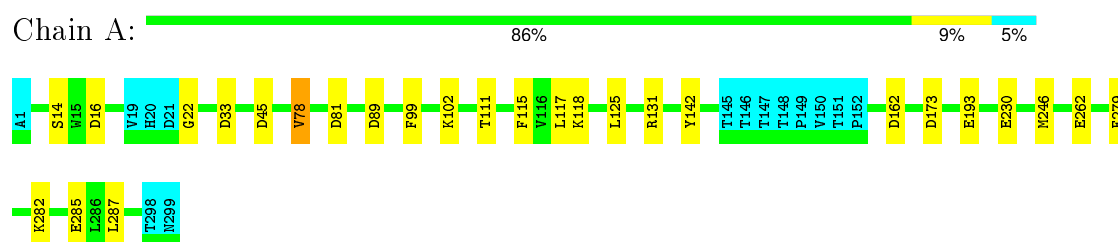
4.2.14 Score per residue for model 14

- Molecule 1: Jasmonate inducible protein isolog



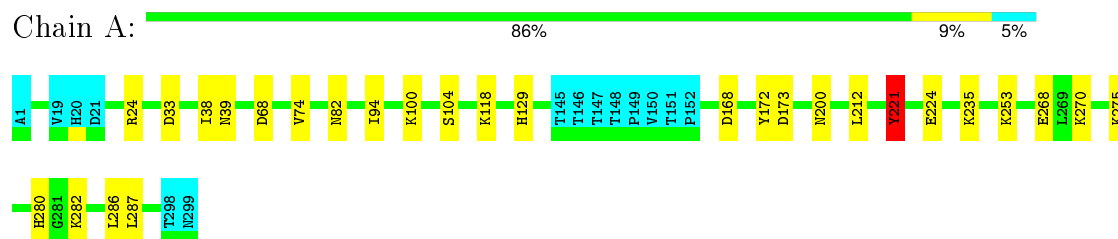
4.2.15 Score per residue for model 15

- Molecule 1: Jasmonate inducible protein isolog



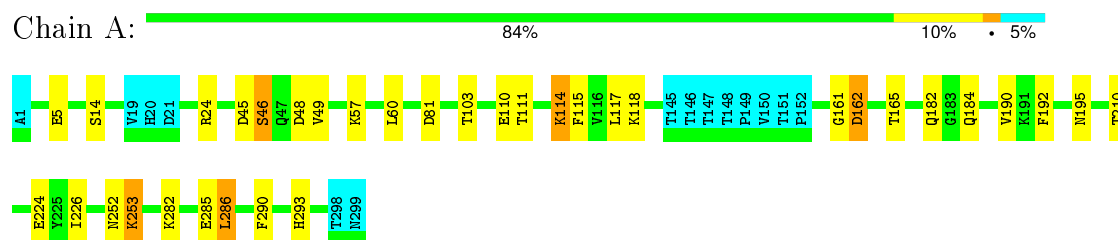
4.2.16 Score per residue for model 16

- Molecule 1: Jasmonate inducible protein isolog



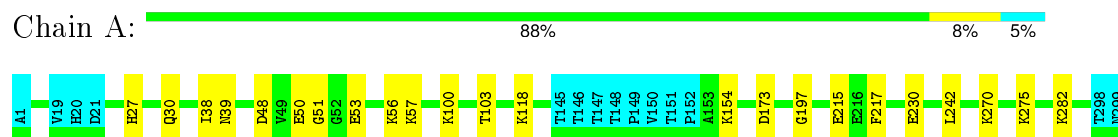
4.2.17 Score per residue for model 17

- Molecule 1: Jasmonate inducible protein isolog



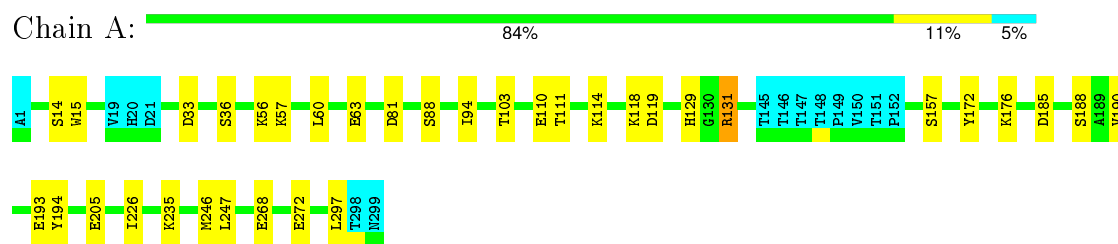
4.2.18 Score per residue for model 18

- Molecule 1: Jasmonate inducible protein isolog



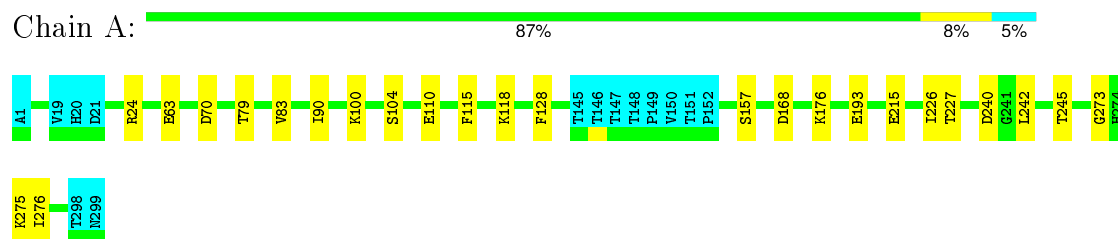
4.2.19 Score per residue for model 19

- Molecule 1: Jasmonate inducible protein isolog



4.2.20 Score per residue for model 20

- Molecule 1: Jasmonate inducible protein isolog



5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS*.

Of the 100 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	2.2
OPALP	refinement	1.4

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 15607
Number of chemical shift lists	1
Total number of shifts	2463
Number of shifts mapped to atoms	2463
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	66%

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	0.64±0.01	0±0/2202 (0.0±0.0%)	1.01±0.02	0±1/2968 (0.0±0.0%)
All	All	0.64	0/44040 (0.0%)	1.01	7/59360 (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	0.9±1.0
All	All	0	19

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	131	ARG	NE-CZ-NH2	-6.73	116.93	120.30	6	1
1	A	225	TYR	CB-CG-CD2	-5.68	117.59	121.00	5	1
1	A	44	LYS	C-N-CA	5.66	135.85	121.70	1	1
1	A	172	TYR	CB-CG-CD2	-5.66	117.61	121.00	1	1
1	A	24	ARG	NE-CZ-NH2	-5.13	117.74	120.30	20	1
1	A	131	ARG	CD-NE-CZ	5.11	130.75	123.60	6	1
1	A	32	GLN	C-N-CA	5.08	134.39	121.70	11	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	142	TYR	Sidechain	3

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	80	TYR	Sidechain	2
1	A	72	TYR	Sidechain	2
1	A	221	TYR	Sidechain	2
1	A	131	ARG	Sidechain	2
1	A	172	TYR	Sidechain	2
1	A	248	ARG	Sidechain	1
1	A	179	TYR	Sidechain	1
1	A	42	TYR	Sidechain	1
1	A	225	TYR	Sidechain	1
1	A	233	TYR	Sidechain	1
1	A	107	TYR	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	2155	2076	2076	2±1
All	All	43100	41520	41520	34

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:167:TRP:HE1	1:A:283:ALA:HB2	0.61	1.55	9	1
1:A:162:ASP:C	1:A:282:LYS:HE3	0.55	2.22	4	1
1:A:191:LYS:HE2	1:A:214:PHE:CE2	0.54	2.37	14	1
1:A:79:THR:HG21	1:A:110:GLU:HA	0.53	1.80	20	1
1:A:191:LYS:HE2	1:A:214:PHE:CZ	0.50	2.41	14	1
1:A:162:ASP:HA	1:A:282:LYS:CE	0.49	2.38	7	1
1:A:79:THR:HG21	1:A:111:THR:H	0.49	1.66	1	2
1:A:178:VAL:HG13	1:A:192:PHE:CE2	0.48	2.44	1	1
1:A:257:ALA:HB1	1:A:258:PRO:HD2	0.48	1.86	10	2
1:A:191:LYS:HE3	1:A:214:PHE:CE2	0.47	2.45	9	1
1:A:115:PHE:CE2	1:A:117:LEU:HD22	0.46	2.45	5	2
1:A:191:LYS:CE	1:A:214:PHE:CZ	0.46	2.98	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:155:LYS:HE2	1:A:293:HIS:CE1	0.46	2.46	8	1
1:A:72:TYR:CG	1:A:124:LYS:HE3	0.45	2.47	8	1
1:A:78:VAL:HG13	1:A:115:PHE:CE1	0.45	2.47	15	1
1:A:110:GLU:OE1	1:A:114:LYS:NZ	0.43	2.51	19	1
1:A:226:ILE:HG22	1:A:276:ILE:HD12	0.43	1.91	20	1
1:A:57:LYS:HE3	1:A:62:PHE:CZ	0.43	2.49	6	1
1:A:15:TRP:CE3	1:A:129:HIS:CB	0.43	3.02	19	1
1:A:172:TYR:CD1	1:A:194:TYR:CE2	0.43	3.07	19	1
1:A:10:ALA:HB3	1:A:137:TYR:CG	0.42	2.49	14	1
1:A:117:LEU:N	1:A:117:LEU:HD23	0.42	2.30	11	1
1:A:191:LYS:HE3	1:A:214:PHE:CZ	0.41	2.50	9	1
1:A:162:ASP:HA	1:A:282:LYS:HE3	0.41	1.92	3	1
1:A:24:ARG:CG	1:A:43:ALA:HB2	0.41	2.46	2	1
1:A:15:TRP:CD1	1:A:131:ARG:HG3	0.41	2.51	6	1
1:A:25:LYS:HE3	1:A:41:VAL:HG21	0.41	1.92	5	1
1:A:280:HIS:CD2	1:A:293:HIS:HD1	0.41	2.34	13	1
1:A:53:GLU:OE2	1:A:57:LYS:HE2	0.41	2.16	14	1
1:A:27:HIS:CD2	1:A:39:ASN:HD22	0.40	2.35	18	1
1:A:25:LYS:HE3	1:A:41:VAL:CG2	0.40	2.47	5	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	285/299 (95%)	251±4 (88±1%)	31±3 (11±1%)	3±2 (1±1%)	21	68
All	All	5700/5980 (95%)	5023 (88%)	610 (11%)	67 (1%)	21	68

All 42 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	253	LYS	5
1	A	160	GLY	4
1	A	61	GLY	3

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Mol	Chain	Res	Type	Models (Total)
1	A	14	SER	3
1	A	273	GLY	3
1	A	51	GLY	3
1	A	162	ASP	3
1	A	31	GLY	2
1	A	284	SER	2
1	A	114	LYS	2
1	A	285	GLU	2
1	A	264	GLY	2
1	A	46	SER	2
1	A	161	GLY	2
1	A	22	GLY	2
1	A	45	ASP	1
1	A	169	ASP	1
1	A	232	THR	1
1	A	6	ALA	1
1	A	35	VAL	1
1	A	182	GLN	1
1	A	87	ASP	1
1	A	10	ALA	1
1	A	287	LEU	1
1	A	60	LEU	1
1	A	85	GLY	1
1	A	170	GLY	1
1	A	277	VAL	1
1	A	131	ARG	1
1	A	204	GLY	1
1	A	286	LEU	1
1	A	226	ILE	1
1	A	30	GLN	1
1	A	55	GLY	1
1	A	16	ASP	1
1	A	156	LEU	1
1	A	130	GLY	1
1	A	221	TYR	1
1	A	227	THR	1
1	A	18	GLY	1
1	A	197	GLY	1
1	A	123	GLY	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	218/231 (94%)	194±4 (89±2%)	24±4 (11±2%)	12	55
All	All	4360/4620 (94%)	3878 (89%)	482 (11%)	12	55

All 149 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	118	LYS	18
1	A	282	LYS	11
1	A	111	THR	11
1	A	33	ASP	10
1	A	293	HIS	8
1	A	100	LYS	8
1	A	275	LYS	8
1	A	268	GLU	8
1	A	56	LYS	8
1	A	224	GLU	8
1	A	57	LYS	8
1	A	104	SER	7
1	A	110	GLU	7
1	A	212	LEU	7
1	A	63	GLU	7
1	A	173	ASP	7
1	A	68	ASP	7
1	A	154	LYS	7
1	A	247	LEU	7
1	A	287	LEU	7
1	A	114	LYS	6
1	A	242	LEU	6
1	A	162	ASP	6
1	A	24	ARG	6
1	A	131	ARG	6
1	A	38	ILE	6
1	A	117	LEU	6
1	A	81	ASP	6
1	A	235	LYS	5

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Mol	Chain	Res	Type	Models (Total)
1	A	103	THR	5
1	A	279	PHE	5
1	A	45	ASP	5
1	A	205	GLU	5
1	A	14	SER	5
1	A	129	HIS	5
1	A	16	ASP	5
1	A	48	ASP	5
1	A	50	GLU	4
1	A	190	VAL	4
1	A	215	GLU	4
1	A	176	LYS	4
1	A	227	THR	4
1	A	94	ILE	4
1	A	60	LEU	4
1	A	256	SER	3
1	A	252	ASN	3
1	A	169	ASP	3
1	A	272	GLU	3
1	A	246	MET	3
1	A	191	LYS	3
1	A	233	TYR	3
1	A	193	GLU	3
1	A	168	ASP	3
1	A	82	ASN	3
1	A	245	THR	3
1	A	285	GLU	3
1	A	95	THR	3
1	A	39	ASN	3
1	A	218	GLU	3
1	A	124	LYS	3
1	A	216	GLU	3
1	A	230	GLU	3
1	A	286	LEU	3
1	A	254	GLN	3
1	A	119	ASP	3
1	A	225	TYR	3
1	A	188	SER	3
1	A	89	ASP	3
1	A	270	LYS	3
1	A	217	PHE	3
1	A	184	GLN	3

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Mol	Chain	Res	Type	Models (Total)
1	A	36	SER	3
1	A	71	ASP	2
1	A	220	ASP	2
1	A	165	THR	2
1	A	262	GLU	2
1	A	58	THR	2
1	A	192	PHE	2
1	A	30	GLN	2
1	A	15	TRP	2
1	A	234	ASP	2
1	A	236	ILE	2
1	A	255	THR	2
1	A	23	VAL	2
1	A	5	GLU	2
1	A	128	PHE	2
1	A	210	THR	2
1	A	195	ASN	2
1	A	219	ILE	2
1	A	99	PHE	2
1	A	66	GLU	2
1	A	240	ASP	2
1	A	265	THR	2
1	A	32	GLN	2
1	A	253	LYS	2
1	A	139	LEU	2
1	A	115	PHE	2
1	A	125	LEU	2
1	A	277	VAL	2
1	A	185	ASP	2
1	A	102	LYS	2
1	A	223	SER	2
1	A	157	SER	2
1	A	274	HIS	1
1	A	2	GLN	1
1	A	280	HIS	1
1	A	267	PHE	1
1	A	79	THR	1
1	A	93	SER	1
1	A	172	TYR	1
1	A	70	ASP	1
1	A	46	SER	1
1	A	244	ILE	1

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Mol	Chain	Res	Type	Models (Total)
1	A	53	GLU	1
1	A	90	ILE	1
1	A	175	VAL	1
1	A	3	LYS	1
1	A	83	VAL	1
1	A	297	LEU	1
1	A	201	ILE	1
1	A	295	MET	1
1	A	194	TYR	1
1	A	196	LYS	1
1	A	290	PHE	1
1	A	4	VAL	1
1	A	120	LYS	1
1	A	232	THR	1
1	A	17	ASP	1
1	A	87	ASP	1
1	A	78	VAL	1
1	A	163	GLU	1
1	A	142	TYR	1
1	A	37	SER	1
1	A	211	LEU	1
1	A	44	LYS	1
1	A	251	THR	1
1	A	47	GLN	1
1	A	77	GLN	1
1	A	200	ASN	1
1	A	143	PHE	1
1	A	49	VAL	1
1	A	88	SER	1
1	A	221	TYR	1
1	A	226	ILE	1
1	A	206	HIS	1
1	A	27	HIS	1
1	A	74	VAL	1
1	A	250	LYS	1
1	A	54	HIS	1

6.3.3 RNA ⓘ

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](#)

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 66% for the well-defined parts and 65% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 15607

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	2463
Number of shifts mapped to atoms	2463
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	11

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	261	0.02 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	240	-0.10 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	—
^{15}N	285	0.13 ± 0.23	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 66%, i.e. 2157 atoms were assigned a chemical shift out of a possible 3264. 0 out of 41 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	1085/1413 (77%)	557/564 (99%)	253/570 (44%)	275/279 (99%)
Sidechain	948/1522 (62%)	499/882 (57%)	435/588 (74%)	14/52 (27%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	124/329 (38%)	65/177 (37%)	58/142 (41%)	1/10 (10%)
Overall	2157/3264 (66%)	1121/1623 (69%)	746/1300 (57%)	290/341 (85%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 65%, i.e. 2230 atoms were assigned a chemical shift out of a possible 3407. 0 out of 43 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	1125/1479 (76%)	579/590 (98%)	261/598 (44%)	285/291 (98%)
Sidechain	981/1592 (62%)	516/921 (56%)	451/618 (73%)	14/53 (26%)
Aromatic	124/336 (37%)	65/181 (36%)	58/144 (40%)	1/11 (9%)
Overall	2230/3407 (65%)	1160/1692 (69%)	770/1360 (57%)	300/355 (85%)

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	191	LYS	HE2	0.89	3.87 – 1.97	-10.7
1	A	7	GLY	HA3	1.33	5.80 – 2.00	-6.8
1	A	3	LYS	HE2	1.71	3.87 – 1.97	-6.4
1	A	254	GLN	HE22	9.57	9.27 – 4.77	5.7
1	A	195	ASN	HB2	1.06	4.36 – 1.26	-5.6
1	A	78	VAL	HB	0.21	3.59 – 0.39	-5.6
1	A	3	LYS	HG3	-0.19	2.76 – -0.04	-5.5
1	A	155	LYS	HE2	1.87	3.87 – 1.97	-5.5
1	A	155	LYS	HG3	-0.15	2.76 – -0.04	-5.4
1	A	163	GLU	HB2	0.93	3.08 – 0.98	-5.3
1	A	191	LYS	HD3	0.43	2.75 – 0.45	-5.1

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:

