



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 03:39 PM BST

PDB ID : 1K85
Title : Solution structure of the fibronectin type III domain from *Bacillus circulans* WL-12 Chitinase A1.
Authors : Jee, J.G.; Ikegami, T.; Hashimoto, M.; Kawabata, T.; Ikeguchi, M.; Watanabe, T.; Shirakawa, M.
Deposited on : 2001-10-23

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

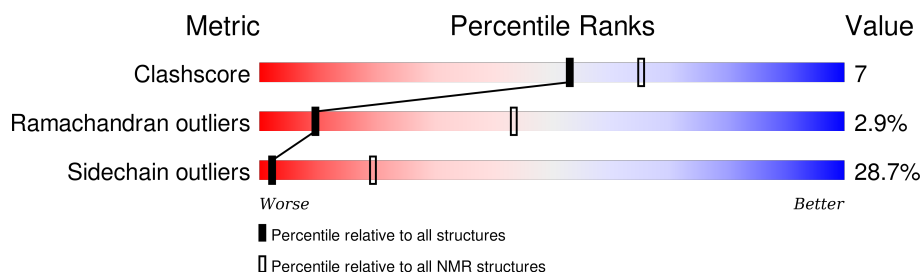
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 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 ≥ 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	88	 65% 32% ..

2 Ensemble composition and analysis ⓘ

This entry contains 30 models. Model 12 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:559-A:644 (86)	0.32	12

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 5 single-model clusters were found.

Cluster number	Models
1	1, 2, 4, 6, 8, 10, 11, 12, 14, 16, 17, 18, 19, 20, 23, 25, 26, 28
2	7, 9, 15
3	24, 30
4	13, 21
Single-model clusters	3; 5; 22; 27; 29

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1208 atoms, of which 598 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CHITINASE A1.

Mol	Chain	Residues	Atoms						Trace
1	A	88	Total	C	H	N	O	S	0
			1208	373	598	100	136	1	

There are 2 discrepancies between the modelled and reference sequences:

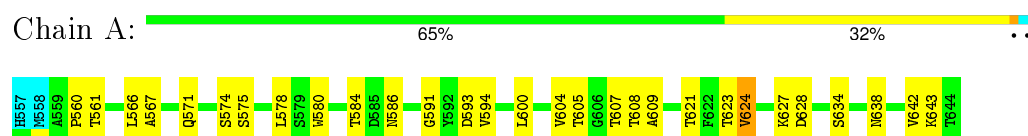
Chain	Residue	Modelled	Actual	Comment	Reference
A	557	HIS	-	CLONING ARTIFACT	UNP P20533
A	558	MET	-	CLONING ARTIFACT	UNP P20533

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: CHITINASE A1

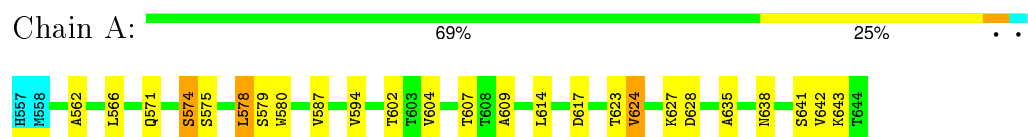


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

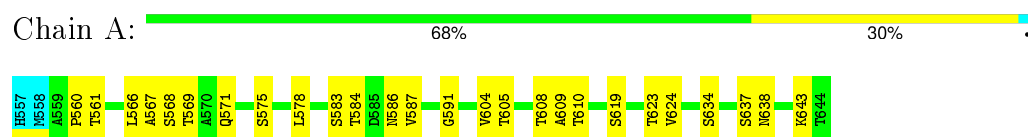
4.2.1 Score per residue for model 1

- Molecule 1: CHITINASE A1



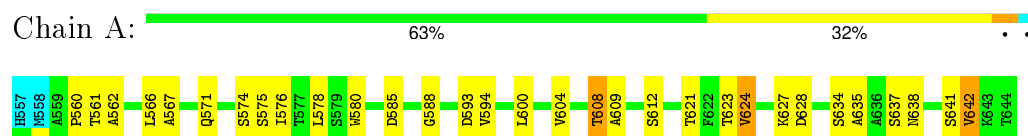
4.2.2 Score per residue for model 2

- Molecule 1: CHITINASE A1



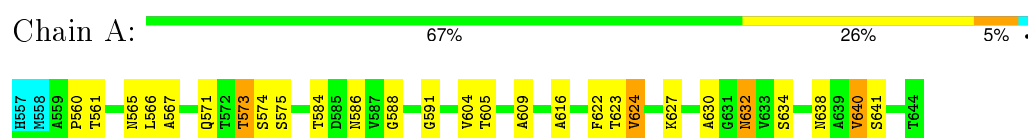
4.2.3 Score per residue for model 3

- Molecule 1: CHITINASE A1



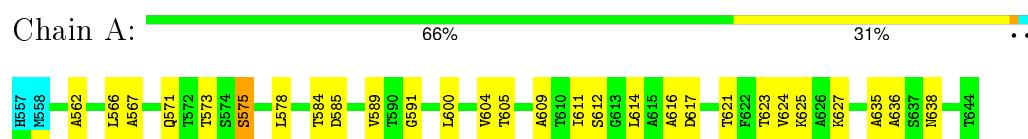
4.2.4 Score per residue for model 4

- Molecule 1: CHITINASE A1



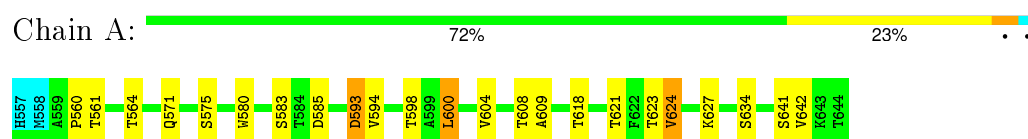
4.2.5 Score per residue for model 5

- Molecule 1: CHITINASE A1



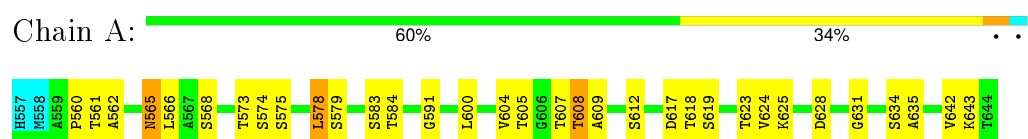
4.2.6 Score per residue for model 6

- Molecule 1: CHITINASE A1



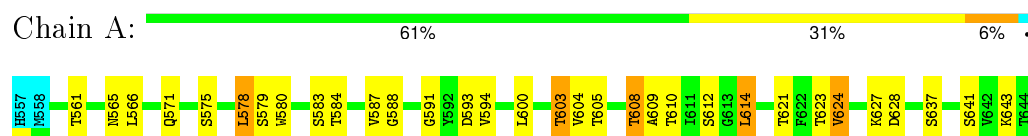
4.2.7 Score per residue for model 7

- Molecule 1: CHITINASE A1



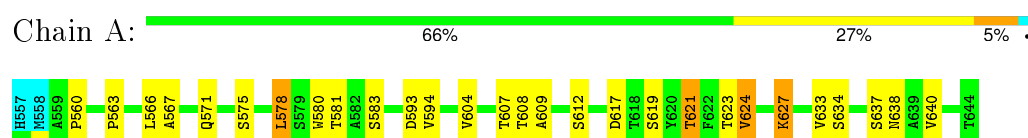
4.2.8 Score per residue for model 8

- Molecule 1: CHITINASE A1



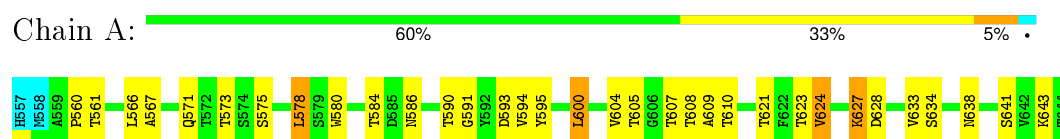
4.2.9 Score per residue for model 9

- Molecule 1: CHITINASE A1



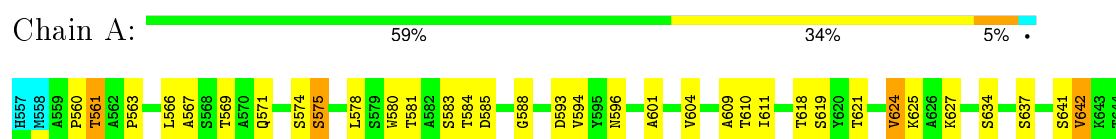
4.2.10 Score per residue for model 10

- Molecule 1: CHITINASE A1



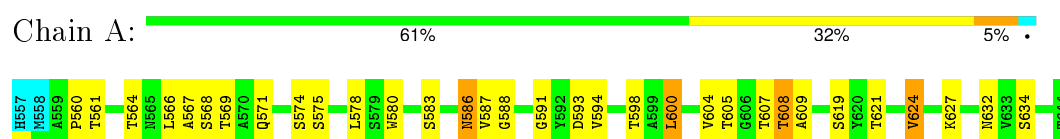
4.2.11 Score per residue for model 11

- Molecule 1: CHITINASE A1



4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: CHITINASE A1



4.2.13 Score per residue for model 13

- Molecule 1: CHITINASE A1

Chain A:  64% 32% •



4.2.14 Score per residue for model 14

- Molecule 1: CHITINASE A1

Chain A:  63% 28% 7%



4.2.15 Score per residue for model 15

- Molecule 1: CHITINASE A1

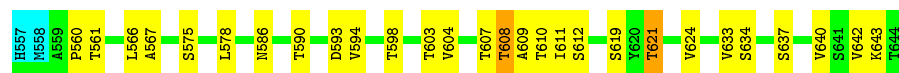
Chain A:  63% 33% •



4.2.16 Score per residue for model 16

- Molecule 1: CHITINASE A1

Chain A: 66% 30% 4%



4.2.17 Score per residue for model 17

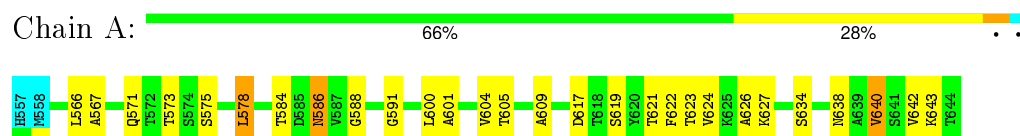
- Molecule 1: CHITINASE A1

Chain A: 56% 38% 5%



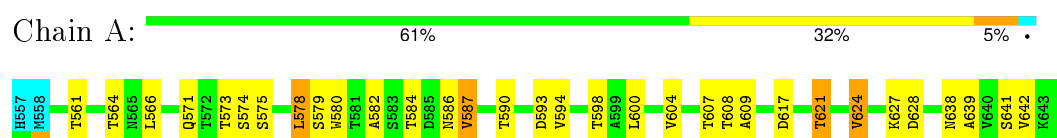
4.2.18 Score per residue for model 18

- Molecule 1: CHITINASE A1



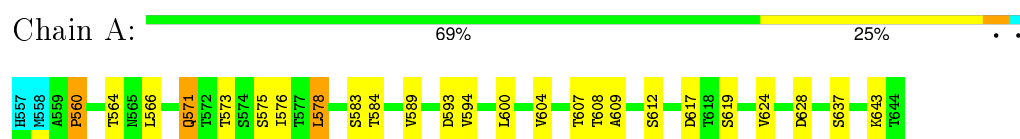
4.2.19 Score per residue for model 19

- Molecule 1: CHITINASE A1



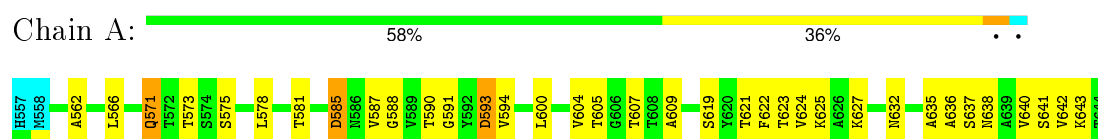
4.2.20 Score per residue for model 20

- Molecule 1: CHITINASE A1



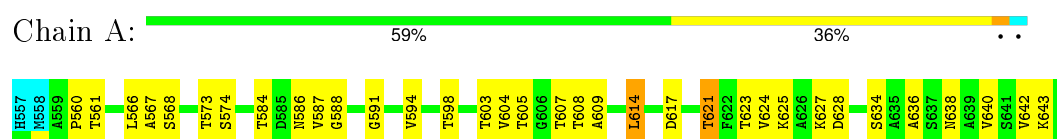
4.2.21 Score per residue for model 21

- Molecule 1: CHITINASE A1



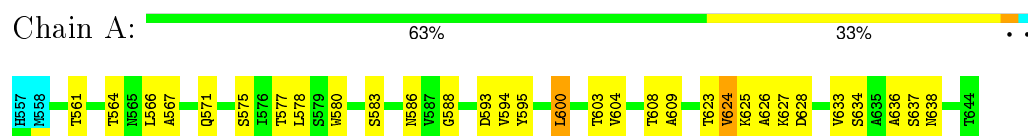
4.2.22 Score per residue for model 22

- Molecule 1: CHITINASE A1



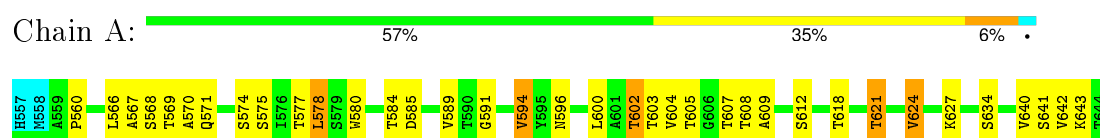
4.2.23 Score per residue for model 23

- Molecule 1: CHITINASE A1



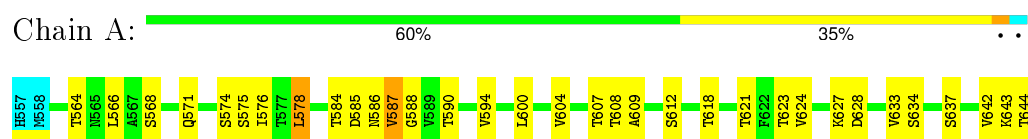
4.2.24 Score per residue for model 24

- Molecule 1: CHITINASE A1



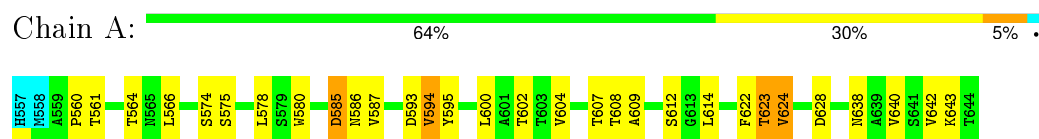
4.2.25 Score per residue for model 25

- Molecule 1: CHITINASE A1



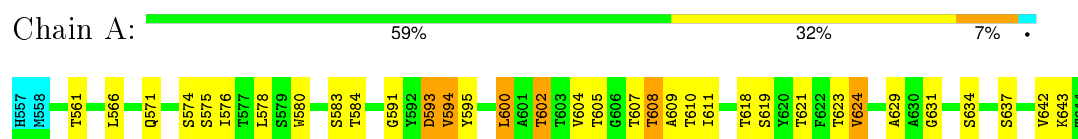
4.2.26 Score per residue for model 26

- Molecule 1: CHITINASE A1



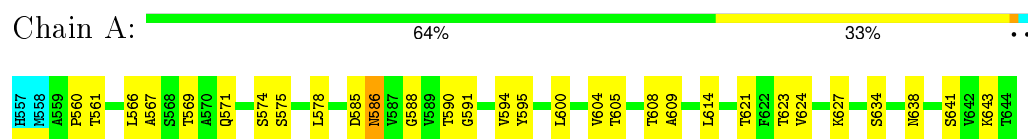
4.2.27 Score per residue for model 27

- Molecule 1: CHITINASE A1



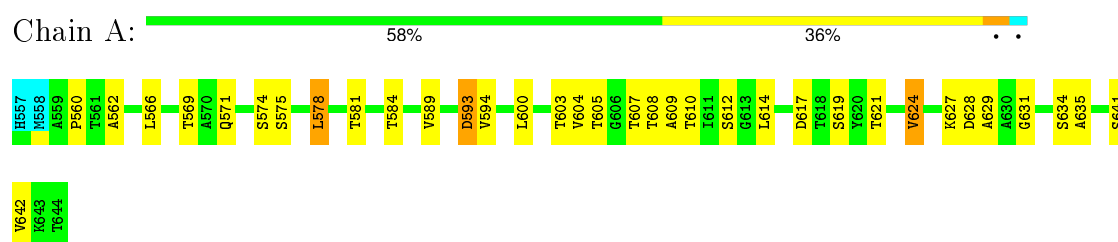
4.2.28 Score per residue for model 28

- Molecule 1: CHITINASE A1



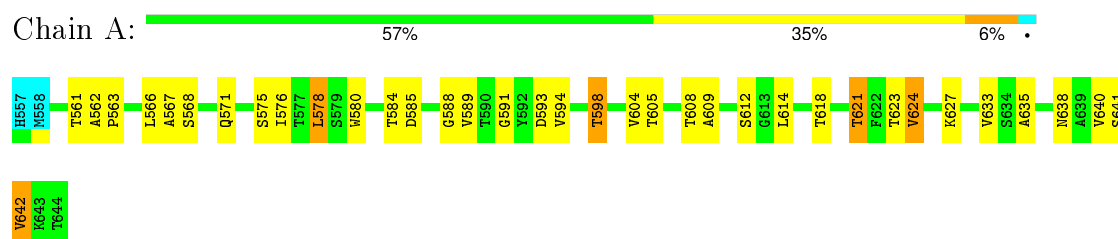
4.2.29 Score per residue for model 29

- Molecule 1: CHITINASE A1



4.2.30 Score per residue for model 30

- Molecule 1: CHITINASE A1



5 Refinement protocol and experimental data overview

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

Of the 150 calculated structures, 30 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
DYANA	structure solution	1.5
ARIA	structure solution	1.0
ARIA	refinement	1.0

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 5178
Number of chemical shift lists	1
Total number of shifts	906
Number of shifts mapped to atoms	906
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 ⓘ

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	592	579	579	8±2
All	All	17760	17370	17370	239

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:566:LEU:HD11	1:A:578:LEU:HG	0.71	1.63	10	21
1:A:604:VAL:HG11	1:A:609:ALA:HA	0.64	1.68	3	30
1:A:561:THR:HG23	1:A:585:ASP:HB2	0.62	1.72	26	1
1:A:566:LEU:HG	1:A:567:ALA:N	0.60	2.11	23	18
1:A:593:ASP:HB3	1:A:600:LEU:HD21	0.58	1.75	6	2
1:A:561:THR:HB	1:A:583:SER:HB2	0.58	1.76	27	5
1:A:566:LEU:HD21	1:A:578:LEU:HD22	0.57	1.75	26	2
1:A:591:GLY:HA2	1:A:605:THR:HA	0.56	1.77	2	17
1:A:573:THR:HG22	1:A:616:ALA:HB2	0.56	1.78	4	1
1:A:566:LEU:HD22	1:A:624:VAL:HG22	0.54	1.77	3	4
1:A:582:ALA:HB2	1:A:607:THR:HG22	0.54	1.79	19	1
1:A:561:THR:HB	1:A:583:SER:HB3	0.53	1.79	7	1
1:A:595:TYR:HA	1:A:600:LEU:HA	0.52	1.80	10	6
1:A:625:LYS:HE3	1:A:636:ALA:N	0.52	2.20	23	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:595:TYR:HE2	1:A:625:LYS:HG3	0.52	1.65	23	2
1:A:562:ALA:HB2	1:A:635:ALA:H	0.51	1.64	1	9
1:A:593:ASP:OD1	1:A:600:LEU:HD12	0.51	2.05	29	1
1:A:580:TRP:CD2	1:A:624:VAL:HG11	0.50	2.41	19	11
1:A:626:ALA:HB3	1:A:634:SER:OG	0.50	2.06	17	3
1:A:585:ASP:O	1:A:589:VAL:HG23	0.49	2.07	24	3
1:A:622:PHE:H	1:A:640:VAL:HG12	0.49	1.67	4	2
1:A:586:ASN:HD22	1:A:587:VAL:HG23	0.49	1.67	14	1
1:A:573:THR:HB	1:A:616:ALA:HB2	0.49	1.83	5	1
1:A:627:LYS:HB3	1:A:633:VAL:HG12	0.49	1.84	10	3
1:A:622:PHE:N	1:A:640:VAL:HG12	0.48	2.23	4	2
1:A:594:VAL:HG13	1:A:602:THR:HB	0.48	1.85	24	1
1:A:604:VAL:HG11	1:A:608:THR:O	0.48	2.09	17	10
1:A:621:THR:HA	1:A:640:VAL:O	0.47	2.10	22	6
1:A:578:LEU:O	1:A:608:THR:HA	0.47	2.09	3	8
1:A:594:VAL:HB	1:A:624:VAL:HG13	0.47	1.86	13	1
1:A:593:ASP:HB3	1:A:600:LEU:HD11	0.47	1.85	12	3
1:A:575:SER:HA	1:A:611:ILE:O	0.47	2.10	16	4
1:A:625:LYS:HE2	1:A:636:ALA:N	0.47	2.25	22	3
1:A:566:LEU:HD23	1:A:640:VAL:HB	0.46	1.85	13	1
1:A:576:ILE:HD11	1:A:642:VAL:HG11	0.46	1.86	3	1
1:A:571:GLN:HB2	1:A:576:ILE:HG13	0.46	1.87	30	2
1:A:580:TRP:CE2	1:A:624:VAL:HG11	0.46	2.46	1	3
1:A:560:PRO:HD3	1:A:628:ASP:HB3	0.46	1.88	17	1
1:A:630:ALA:HB3	1:A:632:ASN:HD21	0.45	1.71	4	1
1:A:622:PHE:HB2	1:A:640:VAL:CG1	0.45	2.41	26	4
1:A:604:VAL:HG21	1:A:608:THR:O	0.44	2.13	13	3
1:A:570:ALA:HB3	1:A:577:THR:OG1	0.44	2.11	17	2
1:A:594:VAL:CG1	1:A:602:THR:HG23	0.44	2.42	27	2
1:A:596:ASN:HB2	1:A:601:ALA:HB2	0.44	1.89	11	1
1:A:566:LEU:HD13	1:A:624:VAL:CG2	0.44	2.42	23	3
1:A:571:GLN:HG3	1:A:642:VAL:HG21	0.44	1.90	30	1
1:A:576:ILE:HD12	1:A:642:VAL:HG11	0.44	1.87	25	1
1:A:590:THR:HG23	1:A:591:GLY:H	0.44	1.73	14	1
1:A:571:GLN:NE2	1:A:642:VAL:HG13	0.44	2.28	21	1
1:A:621:THR:HG22	1:A:639:ALA:HB1	0.43	1.90	19	1
1:A:585:ASP:HB3	1:A:587:VAL:HG22	0.43	1.89	21	1
1:A:566:LEU:CD1	1:A:640:VAL:HB	0.43	2.43	26	2
1:A:571:GLN:NE2	1:A:644:THR:HA	0.43	2.27	25	1
1:A:560:PRO:HB3	1:A:589:VAL:HG22	0.43	1.91	29	2
1:A:574:SER:O	1:A:614:LEU:HD12	0.43	2.13	14	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:580:TRP:CZ2	1:A:624:VAL:HG11	0.43	2.49	14	3
1:A:594:VAL:HG13	1:A:602:THR:HG23	0.42	1.91	26	1
1:A:574:SER:O	1:A:614:LEU:HB2	0.42	2.13	22	1
1:A:577:THR:HA	1:A:609:ALA:O	0.42	2.14	23	1
1:A:626:ALA:O	1:A:633:VAL:HA	0.42	2.15	23	1
1:A:576:ILE:HG22	1:A:611:ILE:HB	0.41	1.92	27	1
1:A:586:ASN:O	1:A:587:VAL:HG12	0.41	2.16	25	1
1:A:600:LEU:HD13	1:A:601:ALA:N	0.41	2.29	18	1
1:A:622:PHE:O	1:A:623:THR:HG23	0.41	2.16	26	1
1:A:622:PHE:O	1:A:640:VAL:HG12	0.41	2.16	26	1
1:A:585:ASP:CG	1:A:586:ASN:N	0.41	2.74	28	1
1:A:571:GLN:NE2	1:A:642:VAL:HB	0.41	2.31	11	1
1:A:593:ASP:OD1	1:A:603:THR:HG22	0.41	2.15	8	1
1:A:594:VAL:HB	1:A:602:THR:HG22	0.40	1.92	1	1
1:A:563:PRO:HB3	1:A:580:TRP:CD1	0.40	2.51	30	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	85/88 (97%)	69±2 (81±3%)	13±2 (16±2%)	2±1 (3±1%)	9	43
All	All	2550/2640 (97%)	2076 (81%)	401 (16%)	73 (3%)	9	43

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	560	PRO	17
1	A	574	SER	16
1	A	588	GLY	14
1	A	587	VAL	7
1	A	586	ASN	7
1	A	631	GLY	3
1	A	629	ALA	2

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Mol	Chain	Res	Type	Models (Total)
1	A	614	LEU	2
1	A	563	PRO	2
1	A	634	SER	1
1	A	565	ASN	1
1	A	598	THR	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	64/66 (97%)	46±3 (71±4%)	18±3 (29±4%)	2	19
All	All	1920/1980 (97%)	1369 (71%)	551 (29%)	2	19

All 49 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	624	VAL	30
1	A	575	SER	28
1	A	594	VAL	24
1	A	571	GLN	23
1	A	627	LYS	21
1	A	623	THR	20
1	A	621	THR	19
1	A	584	THR	19
1	A	634	SER	18
1	A	643	LYS	17
1	A	638	ASN	16
1	A	628	ASP	16
1	A	593	ASP	15
1	A	607	THR	15
1	A	641	SER	15
1	A	561	THR	15
1	A	612	SER	14
1	A	600	LEU	14
1	A	608	THR	14
1	A	642	VAL	14

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Mol	Chain	Res	Type	Models (Total)
1	A	637	SER	13
1	A	578	LEU	13
1	A	619	SER	12
1	A	618	THR	10
1	A	564	THR	9
1	A	590	THR	9
1	A	617	ASP	9
1	A	569	THR	9
1	A	610	THR	9
1	A	573	THR	8
1	A	568	SER	8
1	A	583	SER	8
1	A	603	THR	7
1	A	586	ASN	7
1	A	585	ASP	6
1	A	598	THR	6
1	A	614	LEU	6
1	A	579	SER	5
1	A	581	THR	5
1	A	565	ASN	5
1	A	640	VAL	3
1	A	587	VAL	3
1	A	633	VAL	3
1	A	632	ASN	3
1	A	602	THR	2
1	A	625	LYS	2
1	A	605	THR	2
1	A	577	THR	1
1	A	596	ASN	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 [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 87% for the well-defined parts and 85% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5178

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	906
Number of shifts mapped to atoms	906
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	87	-0.21 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	81	-0.06 ± 0.15	None needed (< 0.5 ppm)
$^{13}\text{C}'$	84	0.01 ± 0.25	None needed (< 0.5 ppm)
^{15}N	84	0.31 ± 0.36	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. 741 atoms were assigned a chemical shift out of a possible 848. 9 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	423/426 (99%)	170/170 (100%)	169/172 (98%)	84/84 (100%)
Sidechain	294/377 (78%)	170/210 (81%)	124/158 (78%)	0/9 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	24/45 (53%)	23/23 (100%)	0/21 (0%)	1/1 (100%)
Overall	741/848 (87%)	363/403 (90%)	293/351 (83%)	85/94 (90%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 85%, i.e. 749 atoms were assigned a chemical shift out of a possible 877. 9 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	425/436 (97%)	170/174 (98%)	171/176 (97%)	84/86 (98%)
Sidechain	300/388 (77%)	174/217 (80%)	126/162 (78%)	0/9 (0%)
Aromatic	24/53 (45%)	23/27 (85%)	0/23 (0%)	1/3 (33%)
Overall	749/877 (85%)	367/418 (88%)	297/361 (82%)	85/98 (87%)

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	580	TRP	HE1	5.80	12.85 – 7.35	-7.8

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:

