



Full wwPDB NMR Structure Validation Report ⓘ

Jun 24, 2024 – 08:23 AM EDT

PDB ID : 6GCJ
BMRB ID : 19782
Title : Solution structure of the RodA hydrophobin from *Aspergillus fumigatus*
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Deposited on : 2018-04-18

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
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) : 2.37.1

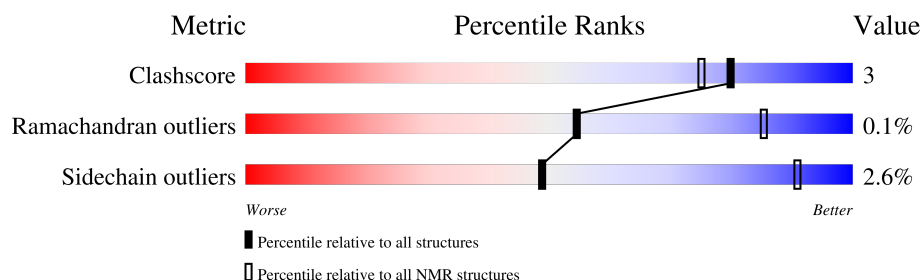
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 97%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	142	

2 Ensemble composition and analysis

This entry contains 10 models. Model 8 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:39-A:110, A:121-A:136, A:148-A:159 (100)	0.78	8

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, 4, 8, 10
2	2, 3
3	7, 9
Single-model clusters	5; 6

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1744 atoms, of which 876 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Hydrophobin.

Mol	Chain	Residues	Atoms						Trace
1	A	121	Total	C	H	N	O	S	0
			1744	538	876	146	176	8	

There is a discrepancy between the modelled and reference sequences:

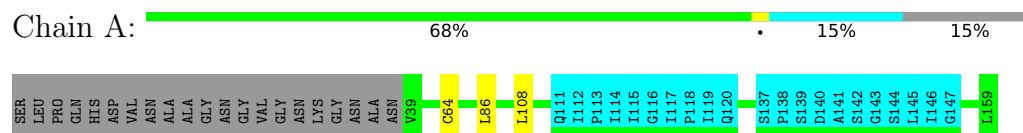
Chain	Residue	Modelled	Actual	Comment	Reference
A	18	SER	ALA	conflict	UNP B0Y4B1

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: Hydrophobin

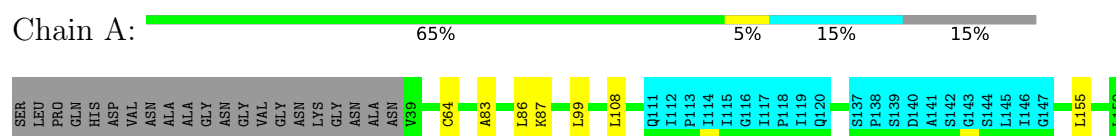


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

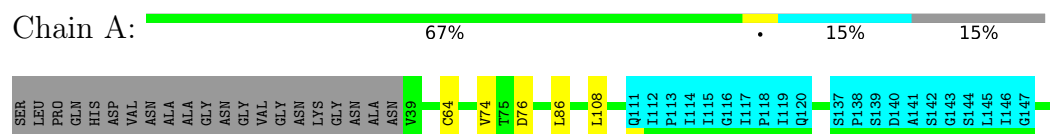
4.2.1 Score per residue for model 1

- Molecule 1: Hydrophobin



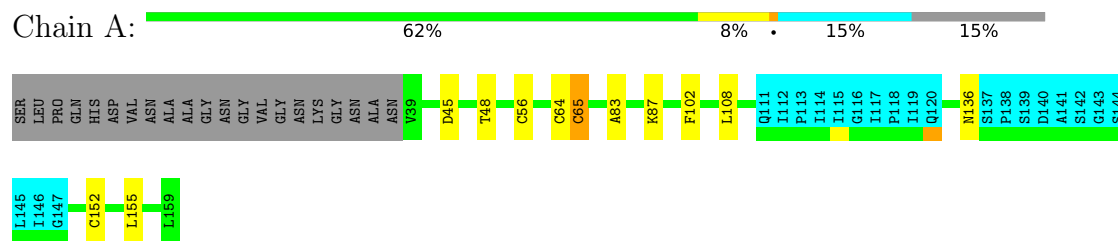
4.2.2 Score per residue for model 2

- Molecule 1: Hydrophobin



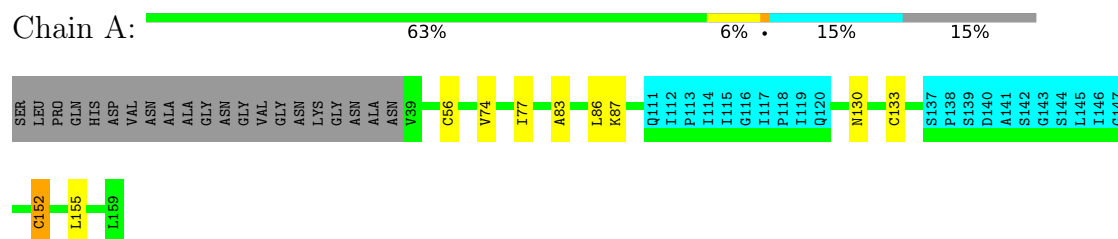
4.2.3 Score per residue for model 3

- Molecule 1: Hydrophobin



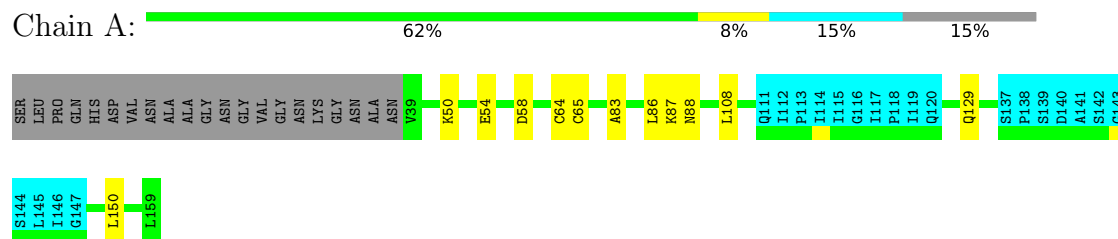
4.2.4 Score per residue for model 4

- Molecule 1: Hydrophobin



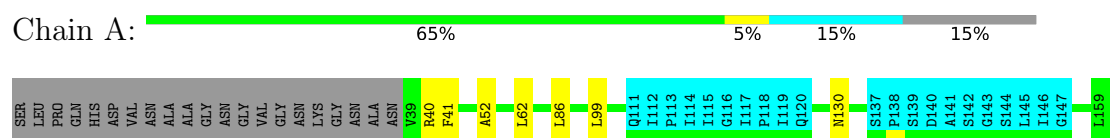
4.2.5 Score per residue for model 5

- Molecule 1: Hydrophobin



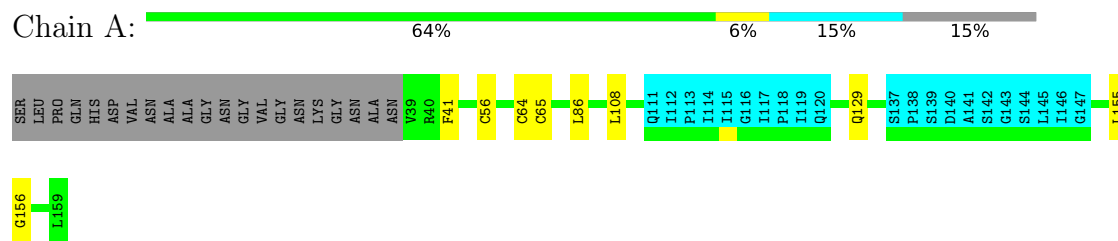
4.2.6 Score per residue for model 6

- Molecule 1: Hydrophobin



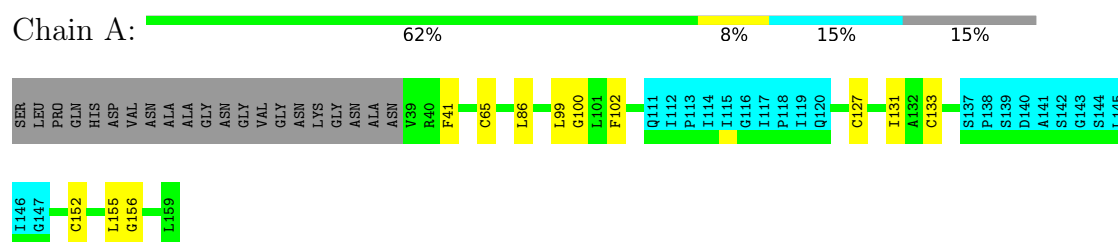
4.2.7 Score per residue for model 7

- Molecule 1: Hydrophobin



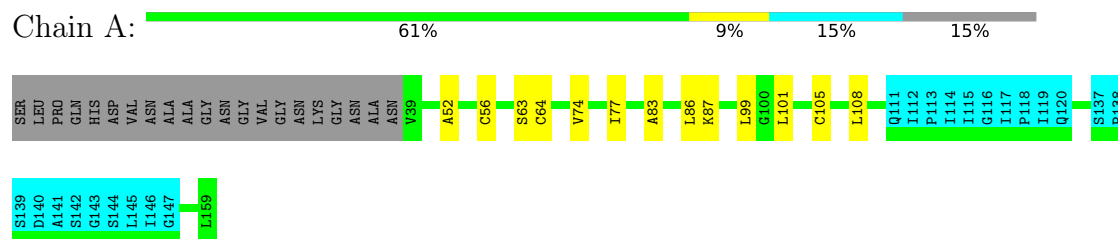
4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: Hydrophobin



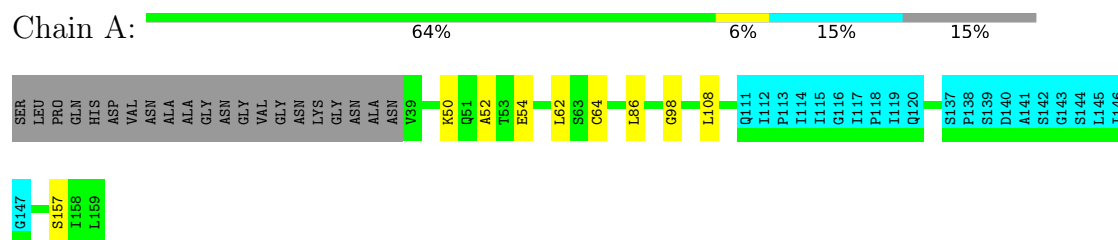
4.2.9 Score per residue for model 9

- Molecule 1: Hydrophobin



4.2.10 Score per residue for model 10

- Molecule 1: Hydrophobin



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 500 calculated structures, 10 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
ARIA	structure calculation	2.3
CNS	refinement	
TALOS-N	structure calculation	

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	1685
Number of shifts mapped to atoms	1471
Number of unparsed shifts	0
Number of shifts with mapping errors	214
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	97%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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 [i](#)

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	724	724	723	4±1
All	All	7240	7240	7230	39

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:64:CYS:SG	1:A:108:LEU:HD11	0.59	2.36	5	5
1:A:127:CYS:SG	1:A:131:ILE:HG12	0.53	2.44	8	1
1:A:56:CYS:SG	1:A:155:LEU:HD13	0.53	2.44	7	3
1:A:50:LYS:O	1:A:54:GLU:HG2	0.51	2.06	5	2
1:A:52:ALA:HB3	1:A:62:LEU:HD11	0.49	1.84	10	1
1:A:133:CYS:SG	1:A:155:LEU:HD13	0.48	2.49	8	1
1:A:64:CYS:SG	1:A:108:LEU:HD21	0.48	2.48	3	2
1:A:65:CYS:SG	1:A:102:PHE:HB3	0.47	2.50	8	2
1:A:40:ARG:HD2	1:A:41:PHE:CE1	0.47	2.45	6	1
1:A:155:LEU:O	1:A:155:LEU:HD23	0.46	2.10	1	1
1:A:83:ALA:O	1:A:87:LYS:HB2	0.46	2.11	1	5
1:A:74:VAL:HB	1:A:76:ASP:OD1	0.45	2.11	2	1
1:A:102:PHE:CD2	1:A:152:CYS:HB3	0.43	2.48	3	1
1:A:63:SER:OG	1:A:105:CYS:HB3	0.42	2.14	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:CYS:O	1:A:129:GLN:HB3	0.42	2.14	5	1
1:A:74:VAL:HG21	1:A:77:ILE:HD12	0.42	1.90	9	2
1:A:98:GLY:HA3	1:A:157:SER:OG	0.42	2.14	10	1
1:A:41:PHE:HB3	1:A:156:GLY:C	0.41	2.36	8	1
1:A:52:ALA:CB	1:A:62:LEU:HD11	0.41	2.46	6	1
1:A:77:ILE:HD13	1:A:101:LEU:HD23	0.41	1.92	9	1
1:A:86:LEU:HD22	1:A:99:LEU:HD13	0.41	1.93	9	1
1:A:133:CYS:C	1:A:152:CYS:SG	0.41	2.98	4	1
1:A:41:PHE:O	1:A:156:GLY:HA3	0.41	2.16	7	1
1:A:99:LEU:HD23	1:A:100:GLY:N	0.41	2.30	8	1
1:A:52:ALA:O	1:A:56:CYS:HB2	0.40	2.17	9	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	98/142 (69%)	94±2 (96±2%)	4±1 (4±2%)	0±0 (0±0%)	54	85
All	All	980/1420 (69%)	943 (96%)	36 (4%)	1 (0%)	54	85

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	58	ASP	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	81/112 (72%)	79±1 (97±1%)	2±1 (3±1%)	49 91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	810/1120 (72%)	789 (97%)	21 (3%)	49 91

All 10 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	86	LEU	8
1	A	99	LEU	2
1	A	65	CYS	2
1	A	130	ASN	2
1	A	152	CYS	2
1	A	45	ASP	1
1	A	136	ASN	1
1	A	88	ASN	1
1	A	150	LEU	1
1	A	129	GLN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 97% for the well-defined parts and 97% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *RodA*

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	1685
Number of shifts mapped to atoms	1471
Number of unparsed shifts	0
Number of shifts with mapping errors	214
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

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

- No matching atom found in the structure. All 214 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	18	SER	C	170.489	.	1
1	A	18	SER	CA	57.199	.	1
1	A	18	SER	CB	63.049	.	1
1	A	18	SER	HA	4.143	.	1
1	A	18	SER	HB2	3.926	.	2
1	A	18	SER	HB3	3.981	.	2
1	A	19	LEU	C	175.122	.	1
1	A	19	LEU	CA	53.306	.	1
1	A	19	LEU	CB	41.661	.	1
1	A	19	LEU	CD1	23.246	.	1
1	A	19	LEU	CD2	25.018	.	1
1	A	19	LEU	CG	27.014	.	1
1	A	19	LEU	H	8.668	.	1
1	A	19	LEU	HA	4.669	.	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	19	LEU	HB2	1.575	.	2
1	A	19	LEU	HB3	1.692	.	2
1	A	19	LEU	HG	1.696	.	1
1	A	19	LEU	N	123.818	.	1
1	A	19	LEU	HD12	0.928	.	2
1	A	19	LEU	HD11	0.928	.	2
1	A	19	LEU	HD13	0.928	.	2
1	A	19	LEU	HD23	0.934	.	2
1	A	19	LEU	HD21	0.934	.	2
1	A	19	LEU	HD22	0.934	.	2
1	A	20	PRO	C	176.726	.	1
1	A	20	PRO	CA	63.135	.	1
1	A	20	PRO	CB	31.98	.	1
1	A	20	PRO	CD	50.528	.	1
1	A	20	PRO	CG	27.355	.	1
1	A	20	PRO	HA	4.38	.	1
1	A	20	PRO	HB2	1.819	.	2
1	A	20	PRO	HB3	2.276	.	2
1	A	20	PRO	HD2	3.648	.	2
1	A	20	PRO	HD3	3.845	.	2
1	A	20	PRO	HG2	2.023	.	2
1	A	20	PRO	HG3	2.023	.	2
1	A	21	GLN	C	175.803	.	1
1	A	21	GLN	CA	55.806	.	1
1	A	21	GLN	CB	29.575	.	1
1	A	21	GLN	CG	33.699	.	1
1	A	21	GLN	H	8.477	.	1
1	A	21	GLN	HA	4.244	.	1
1	A	21	GLN	HB2	1.957	.	2
1	A	21	GLN	HB3	2.017	.	2
1	A	21	GLN	HG2	2.337	.	2
1	A	21	GLN	HG3	2.337	.	2
1	A	21	GLN	N	120.661	.	1
1	A	22	HIS	C	173.821	.	1
1	A	22	HIS	CA	55.191	.	1
1	A	22	HIS	CB	29.255	.	1
1	A	22	HIS	CD2	119.969	.	1
1	A	22	HIS	CE1	136.317	.	1
1	A	22	HIS	H	8.523	.	1
1	A	22	HIS	HA	4.69	.	1
1	A	22	HIS	HB2	3.156	.	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	22	HIS	HB3	3.235	.	2
1	A	22	HIS	HD2	7.268	.	1
1	A	22	HIS	HE1	8.586	.	1
1	A	22	HIS	N	119.285	.	1
1	A	23	ASP	C	176.211	.	1
1	A	23	ASP	CA	54.018	.	1
1	A	23	ASP	CB	40.754	.	1
1	A	23	ASP	H	8.479	.	1
1	A	23	ASP	HA	4.635	.	1
1	A	23	ASP	HB2	2.628	.	2
1	A	23	ASP	HB3	2.748	.	2
1	A	23	ASP	N	121.852	.	1
1	A	24	VAL	C	176.022	.	1
1	A	24	VAL	CA	62.669	.	1
1	A	24	VAL	CB	32.473	.	1
1	A	24	VAL	CG1	20.097	.	1
1	A	24	VAL	CG2	20.927	.	1
1	A	24	VAL	H	8.21	.	1
1	A	24	VAL	HA	4.066	.	1
1	A	24	VAL	HB	2.106	.	1
1	A	24	VAL	N	120.603	.	1
1	A	24	VAL	HG13	0.893	.	2
1	A	24	VAL	HG12	0.893	.	2
1	A	24	VAL	HG11	0.893	.	2
1	A	24	VAL	HG22	0.929	.	2
1	A	24	VAL	HG23	0.929	.	2
1	A	24	VAL	HG21	0.929	.	2
1	A	25	ASN	C	175.071	.	1
1	A	25	ASN	CA	53.218	.	1
1	A	25	ASN	CB	38.86	.	1
1	A	25	ASN	H	8.471	.	1
1	A	25	ASN	HA	4.701	.	1
1	A	25	ASN	HB2	2.836	.	2
1	A	25	ASN	HB3	2.74	.	2
1	A	25	ASN	HD21	6.904	.	2
1	A	25	ASN	HD22	7.576	.	2
1	A	25	ASN	N	121.313	.	1
1	A	25	ASN	ND2	112.514	.	1
1	A	26	ALA	C	177.547	.	1
1	A	26	ALA	CA	52.777	.	1
1	A	26	ALA	CB	19.109	.	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	26	ALA	H	8.135	.	1
1	A	26	ALA	HA	4.261	.	1
1	A	26	ALA	N	124.727	.	1
1	A	26	ALA	HB3	1.375	.	2
1	A	26	ALA	HB1	1.375	.	2
1	A	26	ALA	HB2	1.375	.	2
1	A	27	ALA	C	178.365	.	1
1	A	27	ALA	CA	52.655	.	1
1	A	27	ALA	CB	19.161	.	1
1	A	27	ALA	H	8.226	.	1
1	A	27	ALA	HA	4.293	.	1
1	A	27	ALA	N	122.631	.	1
1	A	27	ALA	HB3	1.387	.	2
1	A	27	ALA	HB1	1.387	.	2
1	A	27	ALA	HB2	1.387	.	2
1	A	28	GLY	C	174.136	.	1
1	A	28	GLY	CA	45.402	.	1
1	A	28	GLY	H	8.237	.	1
1	A	28	GLY	HA2	3.93	.	2
1	A	28	GLY	HA3	3.93	.	2
1	A	28	GLY	N	107.621	.	1
1	A	29	ASN	C	175.879	.	1
1	A	29	ASN	CA	53.231	.	1
1	A	29	ASN	CB	38.948	.	1
1	A	29	ASN	H	8.294	.	1
1	A	29	ASN	HA	4.727	.	1
1	A	29	ASN	HB2	2.775	.	2
1	A	29	ASN	HB3	2.863	.	2
1	A	29	ASN	N	118.48	.	1
1	A	30	GLY	C	174.295	.	1
1	A	30	GLY	CA	45.442	.	1
1	A	30	GLY	H	8.431	.	1
1	A	30	GLY	HA2	3.967	.	2
1	A	30	GLY	HA3	3.967	.	2
1	A	30	GLY	N	109.29	.	1
1	A	31	VAL	C	176.872	.	1
1	A	31	VAL	CA	62.484	.	1
1	A	31	VAL	CB	32.472	.	1
1	A	31	VAL	CG1	20.256	.	1
1	A	31	VAL	CG2	20.997	.	1
1	A	31	VAL	H	7.983	.	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	31	VAL	HA	4.117	.	1
1	A	31	VAL	HB	2.112	.	1
1	A	31	VAL	N	118.961	.	1
1	A	31	VAL	HG13	0.918	.	2
1	A	31	VAL	HG12	0.918	.	2
1	A	31	VAL	HG11	0.918	.	2
1	A	31	VAL	HG22	0.918	.	2
1	A	31	VAL	HG23	0.918	.	2
1	A	31	VAL	HG21	0.918	.	2
1	A	32	GLY	C	173.957	.	1
1	A	32	GLY	CA	45.358	.	1
1	A	32	GLY	H	8.498	.	1
1	A	32	GLY	HA2	3.931	.	2
1	A	32	GLY	HA3	3.935	.	2
1	A	32	GLY	N	111.919	.	1
1	A	33	ASN	C	175.465	.	1
1	A	33	ASN	CA	53.248	.	1
1	A	33	ASN	CB	38.876	.	1
1	A	33	ASN	H	8.287	.	1
1	A	33	ASN	HA	4.705	.	1
1	A	33	ASN	HB2	2.757	.	2
1	A	33	ASN	HB3	2.817	.	2
1	A	33	ASN	N	118.773	.	1
1	A	34	LYS	C	177.087	.	1
1	A	34	LYS	CA	56.429	.	1
1	A	34	LYS	CB	32.699	.	1
1	A	34	LYS	CD	28.914	.	1
1	A	34	LYS	CE	42.058	.	1
1	A	34	LYS	CG	24.625	.	1
1	A	34	LYS	H	8.374	.	1
1	A	34	LYS	HA	4.305	.	1
1	A	34	LYS	HB2	1.882	.	2
1	A	34	LYS	HB3	1.75	.	2
1	A	34	LYS	HD2	1.627	.	2
1	A	34	LYS	HD3	1.615	.	2
1	A	34	LYS	HE2	3.007	.	2
1	A	34	LYS	HE3	3.017	.	2
1	A	34	LYS	HG2	1.422	.	2
1	A	34	LYS	HG3	1.422	.	2
1	A	34	LYS	N	121.483	.	1
1	A	35	GLY	C	173.666	.	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	35	GLY	CA	45.255	.	1
1	A	35	GLY	H	8.356	.	1
1	A	35	GLY	HA2	3.932	.	2
1	A	35	GLY	HA3	3.932	.	2
1	A	35	GLY	N	109.226	.	1
1	A	36	ASN	C	175.207	.	1
1	A	36	ASN	CA	52.889	.	1
1	A	36	ASN	CB	39.072	.	1
1	A	36	ASN	H	8.266	.	1
1	A	36	ASN	HA	4.715	.	1
1	A	36	ASN	HB2	2.787	.	2
1	A	36	ASN	HB3	2.85	.	2
1	A	36	ASN	HD21	6.902	.	2
1	A	36	ASN	HD22	7.573	.	2
1	A	36	ASN	N	118.756	.	1
1	A	36	ASN	ND2	112.829	.	1
1	A	37	ALA	C	177.589	.	1
1	A	37	ALA	CA	53.004	.	1
1	A	37	ALA	CB	19.133	.	1
1	A	37	ALA	H	8.417	.	1
1	A	37	ALA	HA	4.27	.	1
1	A	37	ALA	N	124.511	.	1
1	A	37	ALA	HB3	1.391	.	2
1	A	37	ALA	HB1	1.391	.	2
1	A	37	ALA	HB2	1.391	.	2
1	A	38	ASN	C	174.723	.	1
1	A	38	ASN	CA	53.805	.	1
1	A	38	ASN	CB	39.092	.	1
1	A	38	ASN	H	8.418	.	1
1	A	38	ASN	HA	4.668	.	1
1	A	38	ASN	HB2	2.759	.	2
1	A	38	ASN	HB3	2.87	.	2
1	A	38	ASN	HD21	7.008	.	2
1	A	38	ASN	HD22	7.619	.	2
1	A	38	ASN	N	116.935	.	1
1	A	38	ASN	ND2	113.412	.	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
$^{13}\text{C}_\alpha$	142	-0.12 ± 0.17	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	123	0.41 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}'$	142	-0.13 ± 0.13	None needed (< 0.5 ppm)
^{15}N	134	0.30 ± 0.23	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 97%, i.e. 1216 atoms were assigned a chemical shift out of a possible 1255. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	506/506 (100%)	209/209 (100%)	200/200 (100%)	97/97 (100%)
Sidechain	684/720 (95%)	465/469 (99%)	203/228 (89%)	16/23 (70%)
Aromatic	26/29 (90%)	13/14 (93%)	13/15 (87%)	0/0 (—%)
Overall	1216/1255 (97%)	687/692 (99%)	416/443 (94%)	113/120 (94%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 97%, i.e. 1470 atoms were assigned a chemical shift out of a possible 1515. 0 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	608/608 (100%)	251/251 (100%)	242/242 (100%)	115/115 (100%)
Sidechain	836/878 (95%)	569/575 (99%)	250/278 (90%)	17/25 (68%)
Aromatic	26/29 (90%)	13/14 (93%)	13/15 (87%)	0/0 (—%)
Overall	1470/1515 (97%)	833/840 (99%)	505/535 (94%)	132/140 (94%)

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	48	THR	HG1	5.90	0.08 – 2.19	22.6
1	A	157	SER	HB2	2.17	2.61 – 5.13	-6.7

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:

