



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 07:09 PM UTC

PDB ID : 2BZT / pdb_00002bzt
BMRB ID : 6776
Title : NMR structure of the bacterial protein YFHJ from E. coli
Authors : Pastore, C.; Kelly, G.; Adinolfi, S.; Mc Cormick, J.E.; Pastore, A.
Deposited on : 2005-08-22

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 : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
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) : 2.49

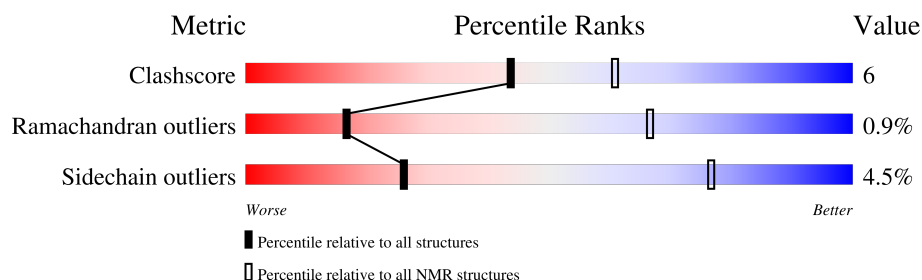
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 94%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	66	 80% 15% . .

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:65 (64)	0.56	4

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 8 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 965 atoms, of which 421 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN ISCX.

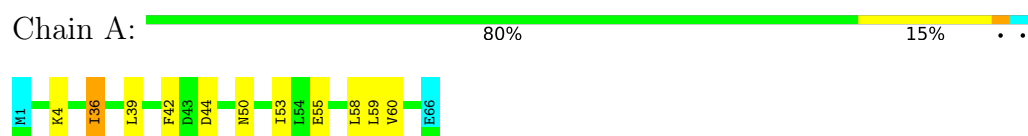
Mol	Chain	Residues	Atoms						Trace
1	A	66	Total	C	H	N	O	S	0
			965	345	421	83	113	3	

4 Residue-property plots

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: PROTEIN ISCX

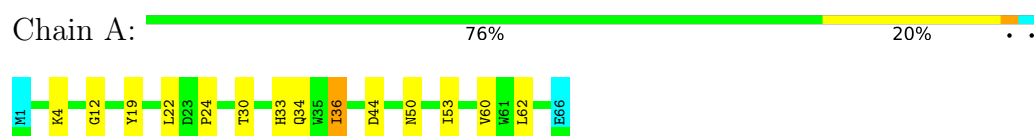


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

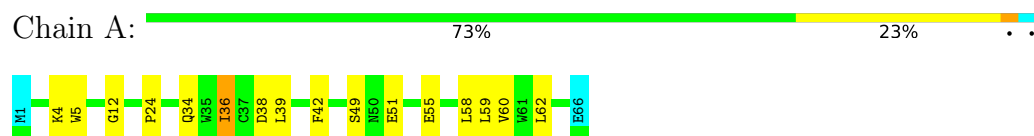
4.2.1 Score per residue for model 1

- Molecule 1: PROTEIN ISCX



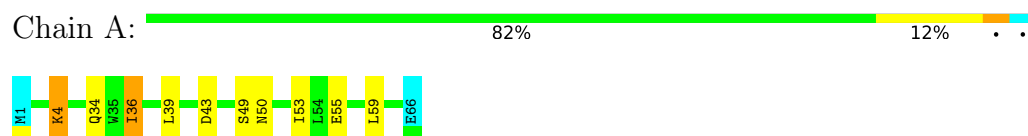
4.2.2 Score per residue for model 2

- Molecule 1: PROTEIN ISCX



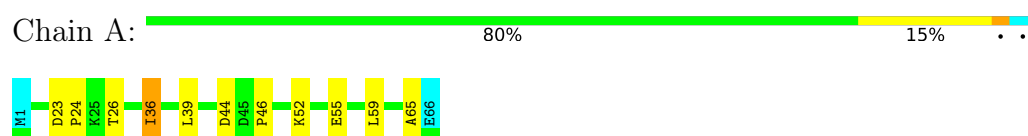
4.2.3 Score per residue for model 3

- Molecule 1: PROTEIN ISCX



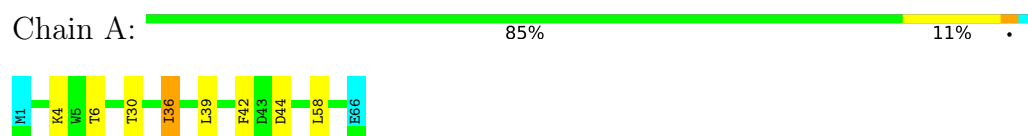
4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: PROTEIN ISCX



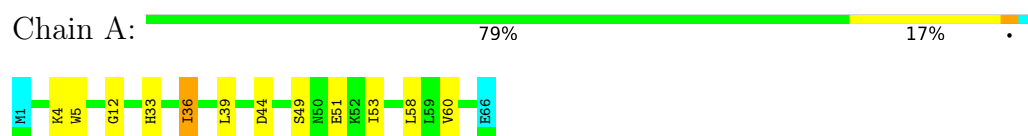
4.2.5 Score per residue for model 5

- Molecule 1: PROTEIN ISCX



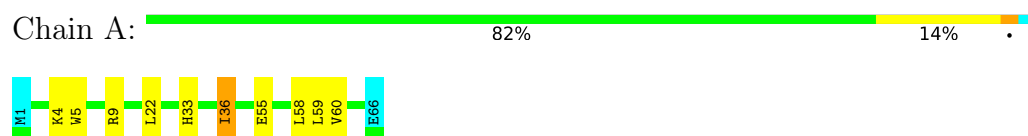
4.2.6 Score per residue for model 6

- Molecule 1: PROTEIN ISCX



4.2.7 Score per residue for model 7

- Molecule 1: PROTEIN ISCX



4.2.8 Score per residue for model 8

- Molecule 1: PROTEIN ISCX

Chain A:  77% 18% . .



4.2.9 Score per residue for model 9

- Molecule 1: PROTEIN ISCX

Chain A:  82% 14% . .



4.2.10 Score per residue for model 10

- Molecule 1: PROTEIN ISCX

Chain A:  74% 21% . .



4.2.11 Score per residue for model 11

- Molecule 1: PROTEIN ISCX

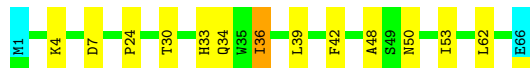
Chain A:  83% 12% . .



4.2.12 Score per residue for model 12

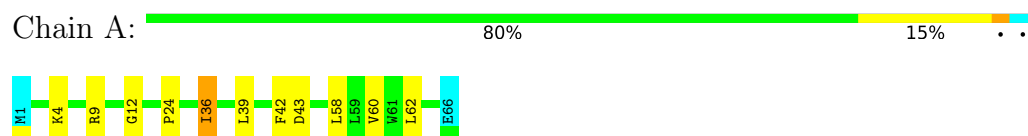
- Molecule 1: PROTEIN ISCX

Chain A:  77% 18% . .



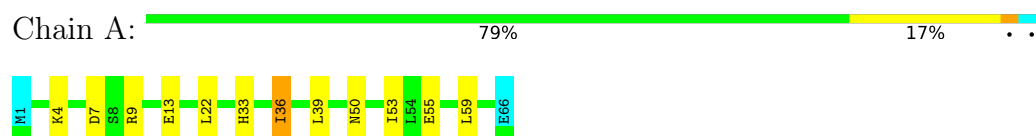
4.2.13 Score per residue for model 13

- Molecule 1: PROTEIN ISCX



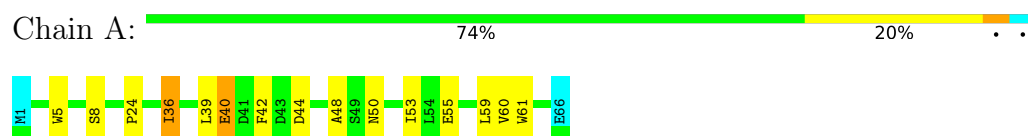
4.2.14 Score per residue for model 14

- Molecule 1: PROTEIN ISCX



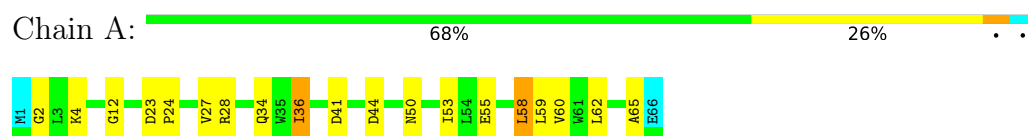
4.2.15 Score per residue for model 15

- Molecule 1: PROTEIN ISCX



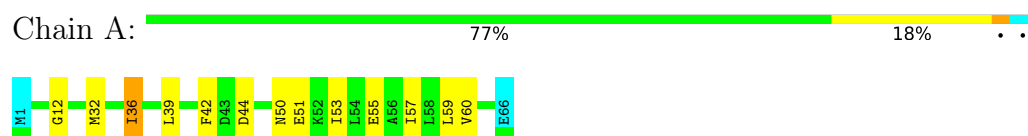
4.2.16 Score per residue for model 16

- Molecule 1: PROTEIN ISCX



4.2.17 Score per residue for model 17

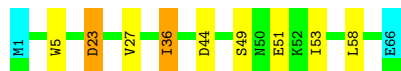
- Molecule 1: PROTEIN ISCX



4.2.18 Score per residue for model 18

- Molecule 1: PROTEIN ISCX

Chain A:  83% 11% . .



4.2.19 Score per residue for model 19

- Molecule 1: PROTEIN ISCX

Chain A:  79% 17% . .



4.2.20 Score per residue for model 20

- Molecule 1: PROTEIN ISCX

Chain A:  79% 14% 5% .



5 Refinement protocol and experimental data overview

The models were refined using the following method: *ARIA 1.2*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *LOWEST ENERGY*.

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

Software name	Classification	Version
ARIA	refinement	1.2
XEASY	structure solution	
NMRDraw	structure solution	
NMRPipe	structure solution	

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	843
Number of shifts mapped to atoms	758
Number of unparsed shifts	0
Number of shifts with mapping errors	85
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	94%

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	526	408	487	7±2
All	All	10520	8160	9740	131

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:TYR:HB3	1:A:22:LEU:HD13	0.67	1.65	1	1
1:A:50:ASN:HB2	1:A:53:ILE:HG12	0.65	1.69	15	1
1:A:5:TRP:CZ2	1:A:49:SER:HB3	0.62	2.29	18	4
1:A:12:GLY:HA3	1:A:60:VAL:HG13	0.60	1.73	10	7
1:A:33:HIS:HA	1:A:36:ILE:HG22	0.56	1.77	12	9
1:A:36:ILE:HA	1:A:39:LEU:HG	0.56	1.78	4	11
1:A:39:LEU:HB2	1:A:42:PHE:HB2	0.55	1.77	17	2
1:A:39:LEU:HB2	1:A:42:PHE:HB3	0.53	1.80	13	6
1:A:52:LYS:HE2	1:A:52:LYS:HA	0.52	1.81	4	1
1:A:4:LYS:HD2	1:A:44:ASP:OD2	0.51	2.05	6	1
1:A:24:PRO:HG3	1:A:65:ALA:HB3	0.50	1.83	16	2
1:A:4:LYS:HA	1:A:44:ASP:HB2	0.50	1.82	5	1
1:A:39:LEU:HB2	1:A:42:PHE:CB	0.50	2.36	13	3
1:A:4:LYS:HD2	1:A:44:ASP:HB2	0.50	1.82	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:4:LYS:HG2	1:A:7:ASP:OD2	0.49	2.07	12	1
1:A:36:ILE:O	1:A:36:ILE:HD13	0.49	2.07	17	17
1:A:9:ARG:HA	1:A:60:VAL:HG21	0.49	1.83	13	3
1:A:55:GLU:O	1:A:59:LEU:HG	0.49	2.08	4	14
1:A:50:ASN:O	1:A:53:ILE:HB	0.48	2.08	12	10
1:A:5:TRP:HB3	1:A:53:ILE:HG21	0.48	1.86	18	2
1:A:4:LYS:HE3	1:A:44:ASP:OD2	0.48	2.09	16	1
1:A:24:PRO:HG2	1:A:62:LEU:HD23	0.47	1.86	1	4
1:A:2:GLY:N	1:A:43:ASP:HB3	0.47	2.24	10	1
1:A:37:CYS:HA	1:A:42:PHE:CD2	0.47	2.45	9	1
1:A:51:GLU:H	1:A:51:GLU:CD	0.47	2.18	17	1
1:A:32:MET:HE1	1:A:57:ILE:HB	0.46	1.87	17	1
1:A:2:GLY:HA3	1:A:41:ASP:O	0.46	2.11	16	1
1:A:9:ARG:O	1:A:13:GLU:HG3	0.46	2.10	14	1
1:A:30:THR:O	1:A:34:GLN:HG2	0.45	2.11	12	1
1:A:40:GLU:H	1:A:40:GLU:CD	0.45	2.19	15	1
1:A:23:ASP:O	1:A:26:THR:HG22	0.45	2.12	4	1
1:A:34:GLN:HA	1:A:34:GLN:OE1	0.45	2.12	2	1
1:A:44:ASP:O	1:A:46:PRO:HD3	0.44	2.12	4	1
1:A:2:GLY:H	1:A:43:ASP:HB3	0.44	1.72	10	1
1:A:23:ASP:OD2	1:A:25:LYS:HB2	0.44	2.13	10	1
1:A:4:LYS:HD2	1:A:44:ASP:CG	0.44	2.38	5	1
1:A:58:LEU:O	1:A:62:LEU:HG	0.43	2.13	16	2
1:A:23:ASP:O	1:A:27:VAL:HG23	0.43	2.13	20	3
1:A:12:GLY:HA3	1:A:60:VAL:CG1	0.43	2.44	16	1
1:A:24:PRO:HB3	1:A:61:TRP:CG	0.42	2.50	15	1
1:A:8:SER:O	1:A:60:VAL:HG11	0.42	2.14	15	1
1:A:28:ARG:HA	1:A:28:ARG:HE	0.42	1.75	16	1
1:A:3:LEU:HB2	1:A:42:PHE:HA	0.42	1.92	8	1
1:A:30:THR:O	1:A:34:GLN:HG3	0.41	2.15	1	1
1:A:24:PRO:HB2	1:A:62:LEU:HD23	0.41	1.91	13	1
1:A:5:TRP:CE3	1:A:53:ILE:HG21	0.41	2.51	15	1
1:A:4:LYS:HB2	1:A:7:ASP:OD2	0.41	2.16	14	1
1:A:5:TRP:CE3	1:A:5:TRP:HA	0.40	2.51	7	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	64/66 (97%)	59±1 (92±2%)	4±1 (7±2%)	1±1 (1±1%)	16	66
All	All	1280/1320 (97%)	1182 (92%)	87 (7%)	11 (1%)	16	66

All 4 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	44	ASP	6
1	A	48	ALA	3
1	A	49	SER	1
1	A	6	THR	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	57/59 (97%)	54±1 (96±2%)	3±1 (4±2%)	26	77
All	All	1140/1180 (97%)	1089 (96%)	51 (4%)	26	77

All 12 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	36	ILE	20
1	A	58	LEU	9
1	A	4	LYS	6
1	A	51	GLU	3
1	A	22	LEU	3
1	A	34	GLN	2
1	A	6	THR	2
1	A	30	THR	2
1	A	38	ASP	1
1	A	40	GLU	1
1	A	23	ASP	1
1	A	41	ASP	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 oligosaccharides 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 94% for the well-defined parts and 94% 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	843
Number of shifts mapped to atoms	758
Number of unparsed shifts	0
Number of shifts with mapping errors	85
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

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

- No matching atom found in the structure. All 85 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	MET	H	8.248	0.003	1
1	A	1	MET	HB3	1.978	0.011	2
1	A	1	MET	HG3	2.532	0.001	2
1	A	3	LEU	HB3	1.282	0.000	2
1	A	4	LYS	HB3	1.635	0.001	2
1	A	4	LYS	HD3	1.443	0.001	2
1	A	4	LYS	HE3	2.879	0.006	2
1	A	4	LYS	HG3	1.385	0.000	2
1	A	5	TRP	HB3	3.171	0.000	2
1	A	7	ASP	HB3	3.073	0.002	2
1	A	8	SER	HB3	3.716	0.002	2
1	A	9	ARG	HB3	1.823	0.002	2
1	A	9	ARG	HD3	3.231	0.001	2
1	A	9	ARG	HG3	1.579	0.008	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	10	GLU	HB3	1.916	0.004	2
1	A	10	GLU	HG3	2.273	0.001	2
1	A	11	ILE	HG13	0.661	0.002	2
1	A	13	GLU	HB3	2.054	0.001	1
1	A	13	GLU	HG3	2.216	0.003	2
1	A	15	LEU	HB3	-0.153	0.003	2
1	A	16	TYR	HB3	2.981	0.004	2
1	A	17	ASP	HB3	2.503	0.000	2
1	A	19	TYR	HB3	3.036	0.018	2
1	A	20	PRO	HB3	1.852	0.000	2
1	A	20	PRO	HD3	3.241	0.001	2
1	A	20	PRO	HG3	1.89	0.001	2
1	A	21	ASP	HB3	2.78	0.000	2
1	A	22	LEU	HB3	1.542	0.002	2
1	A	23	ASP	HB3	2.696	0.000	2
1	A	24	PRO	HB3	0.444	0.001	2
1	A	24	PRO	HD3	3.814	0.000	2
1	A	24	PRO	HG3	0.925	0.002	2
1	A	25	LYS	HB3	1.778	0.001	2
1	A	25	LYS	HD3	1.721	0.004	2
1	A	25	LYS	HE3	3.04	0.003	1
1	A	25	LYS	HG3	1.421	0.003	1
1	A	28	ARG	HB3	1.752	0.002	2
1	A	28	ARG	HD3	3.189	0.001	2
1	A	28	ARG	HG3	1.698	0.004	2
1	A	29	PHE	HB3	3.197	0.000	2
1	A	31	ASP	HB3	1.8	0.003	2
1	A	32	MET	HB3	2.067	0.002	2
1	A	32	MET	HG3	2.7	0.006	2
1	A	33	HIS	HB3	3.134	0.001	1
1	A	34	GLN	HB3	2.111	0.000	2
1	A	34	GLN	HG3	2.452	0.002	2
1	A	35	TRP	HB3	3.076	0.003	2
1	A	36	ILE	HG13	0.721	0.005	2
1	A	37	CYS	HB3	2.698	0.002	2
1	A	38	ASP	HB3	2.724	0.000	2
1	A	39	LEU	HB3	1.573	0.005	2
1	A	40	GLU	HB3	1.968	0.004	2
1	A	40	GLU	HG3	2.32	0.003	1
1	A	41	ASP	HB3	2.421	0.000	2
1	A	42	PHE	HB3	2.96	0.004	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	43	ASP	HB3	2.175	0.004	2
1	A	44	ASP	HB3	2.125	0.002	2
1	A	45	ASP	HB3	2.877	0.002	2
1	A	46	PRO	HB3	2.355	0.007	2
1	A	46	PRO	HD3	4.232	0.001	2
1	A	46	PRO	HG3	2.348	0.002	1
1	A	47	GLN	HB3	2.165	0.000	2
1	A	47	GLN	HG3	2.437	0.000	2
1	A	49	SER	HB3	2.05	0.003	2
1	A	50	ASN	HB3	2.99	0.001	1
1	A	51	GLU	HB3	2.032	0.005	1
1	A	51	GLU	HG3	2.239	0.000	1
1	A	52	LYS	HB3	1.859	0.002	2
1	A	52	LYS	HD3	1.704	0.002	1
1	A	52	LYS	HE3	2.993	0.000	1
1	A	52	LYS	HG3	1.486	0.000	2
1	A	53	ILE	HG13	1.201	0.004	2
1	A	54	LEU	HB3	0.979	0.003	2
1	A	55	GLU	HB3	2.201	0.000	2
1	A	55	GLU	HG3	2.339	0.002	2
1	A	57	ILE	HG13	1.29	0.004	2
1	A	58	LEU	HB3	1.678	0.001	2
1	A	59	LEU	HB3	1.64	0.000	2
1	A	61	TRP	HB3	3.339	0.002	2
1	A	62	LEU	HB3	1.538	0.000	2
1	A	63	ASP	HB3	2.721	0.000	2
1	A	64	GLU	HB3	1.609	0.005	2
1	A	64	GLU	HG3	2.077	0.000	2
1	A	66	GLU	HB3	2.061	0.003	1
1	A	66	GLU	HG3	2.33	0.010	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
$^{13}\text{C}_\alpha$	66	-0.25 ± 0.37	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	64	0.15 ± 0.18	None needed (< 0.5 ppm)
$^{13}\text{C}'$	60	-0.01 ± 0.24	None needed (< 0.5 ppm)
^{15}N	63	0.85 ± 0.29	Should be applied

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 94%, i.e. 818 atoms were assigned a chemical shift out of a possible 870. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	311/316 (98%)	127/127 (100%)	123/128 (96%)	61/61 (100%)
Sidechain	431/472 (91%)	294/304 (97%)	134/156 (86%)	3/12 (25%)
Aromatic	76/82 (93%)	38/40 (95%)	35/37 (95%)	3/5 (60%)
Overall	818/870 (94%)	459/471 (97%)	292/321 (91%)	67/78 (86%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 94%, i.e. 843 atoms were assigned a chemical shift out of a possible 897. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	320/326 (98%)	131/131 (100%)	126/132 (95%)	63/63 (100%)
Sidechain	447/489 (91%)	305/315 (97%)	139/162 (86%)	3/12 (25%)
Aromatic	76/82 (93%)	38/40 (95%)	35/37 (95%)	3/5 (60%)
Overall	843/897 (94%)	474/486 (98%)	300/331 (91%)	69/80 (86%)

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	61	TRP	CZ2	45.45	107.20 – 121.33	-48.7
1	A	58	LEU	N	58.15	102.77 – 140.89	-16.7
1	A	49	SER	HB3	2.05	2.49 – 5.20	-6.6
1	A	44	ASP	H	5.29	5.52 – 11.08	-5.4

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:

