Full wwPDB NMR Structure Validation Report (i)

Dec 13, 2023 – 06:03 PM EST

PDB ID	:	2JQ4
BMRB ID	:	15269
Title	:	Complete resonance assignments and solution structure calculation of ATC2521 (NESG ID: AtT6) from Agrobacterium tumefaciens
Authors	:	Srisailam, S.; Lemak, A.; Yee, A.; Karra, M.D.; Lukin, J.A.; Arrowsmith, C.H.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2007-05-29

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 (i) 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 (i)) were used in the production of this report:

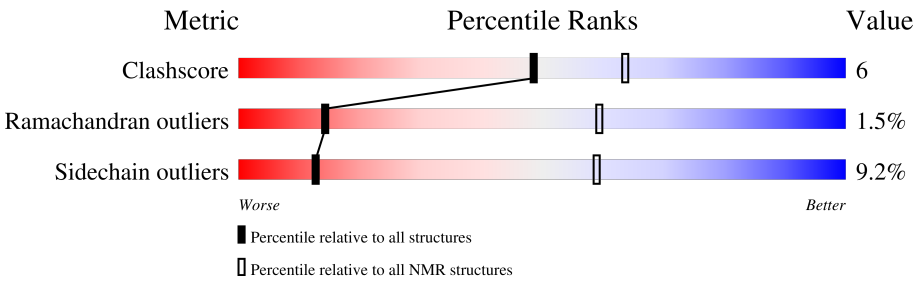
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 88%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	105	63% 12% • 21%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	A:1-A:79 (79)	0.70	6

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 5 clusters and 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1269 atoms, of which 637 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Hypothetical protein Atu2571.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	83	1269	404	637	99	127	2	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	cloning artifact	UNP Q8UCC7
A	-20	GLY	-	cloning artifact	UNP Q8UCC7
A	-19	SER	-	cloning artifact	UNP Q8UCC7
A	-18	SER	-	cloning artifact	UNP Q8UCC7
A	-17	HIS	-	expression tag	UNP Q8UCC7
A	-16	HIS	-	expression tag	UNP Q8UCC7
A	-15	HIS	-	expression tag	UNP Q8UCC7
A	-14	HIS	-	expression tag	UNP Q8UCC7
A	-13	HIS	-	expression tag	UNP Q8UCC7
A	-12	HIS	-	expression tag	UNP Q8UCC7
A	-11	SER	-	cloning artifact	UNP Q8UCC7
A	-10	SER	-	cloning artifact	UNP Q8UCC7
A	-9	GLY	-	cloning artifact	UNP Q8UCC7
A	-8	ARG	-	cloning artifact	UNP Q8UCC7
A	-7	GLU	-	cloning artifact	UNP Q8UCC7
A	-6	ASN	-	cloning artifact	UNP Q8UCC7
A	-5	LEU	-	cloning artifact	UNP Q8UCC7
A	-4	TYR	-	cloning artifact	UNP Q8UCC7
A	-3	PHE	-	cloning artifact	UNP Q8UCC7
A	-2	GLN	-	cloning artifact	UNP Q8UCC7
A	-1	GLY	-	cloning artifact	UNP Q8UCC7
A	0	HIS	-	cloning artifact	UNP Q8UCC7

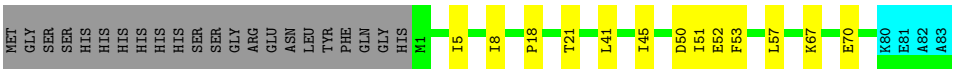
4 Residue-property plots (i)

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: Hypothetical protein Atu2571

Chain A:



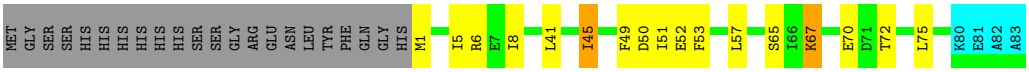
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Hypothetical protein Atu2571

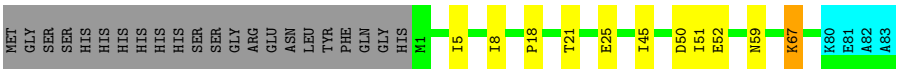
Chain A:



4.2.2 Score per residue for model 2

• Molecule 1: Hypothetical protein Atu2571

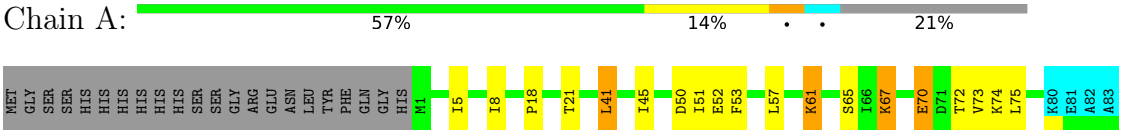
Chain A:



4.2.3 Score per residue for model 3

- Molecule 1: Hypothetical protein Atu2571

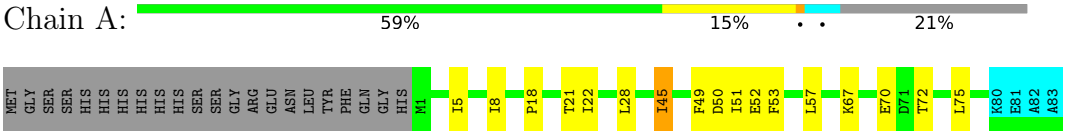
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Hypothetical protein Atu2571

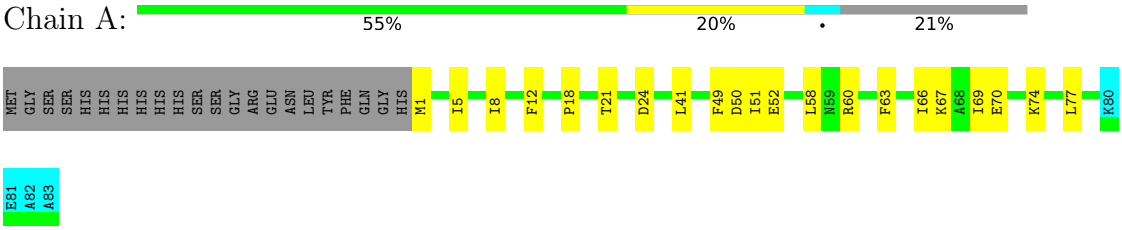
Chain A:



4.2.5 Score per residue for model 5

- Molecule 1: Hypothetical protein Atu2571

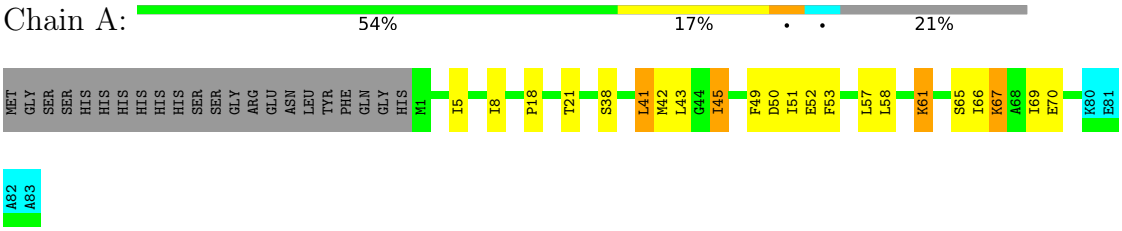
Chain A:



4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Hypothetical protein Atu2571

Chain A:



4.2.7 Score per residue for model 7

- Molecule 1: Hypothetical protein Atu2571

Chain A: 62% 11% • • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 I8 P18 T21 S38 L41 I45 F49 D50 I51 E52 N59 K67 E70 K80 E81 A82 A83

4.2.8 Score per residue for model 8

• Molecule 1: Hypothetical protein Atu2571

Chain A: 59% 15% • • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 I8 P18 T21 S35 S38 V39 Q40 L41 D50 I51 E52 F53 L57 I66 K67 A68 I69 E70 K80 E81 A82 A83

4.2.9 Score per residue for model 9

• Molecule 1: Hypothetical protein Atu2571

Chain A: 55% 18% • • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 I8 Q14 L15 P16 T17 P18 T21 S38 L41 I45 F49 D50 I51 E52 F53 L57 L58 N59 R60 K67 E70 K80 E81 A82

A83

4.2.10 Score per residue for model 10

• Molecule 1: Hypothetical protein Atu2571

Chain A: 62% 13% • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 I8 P18 T21 V39 Q40 L41 M42 D50 I51 E52 F53 L57 K67 E70 K80 E81 A82 A83

4.2.11 Score per residue for model 11

• Molecule 1: Hypothetical protein Atu2571

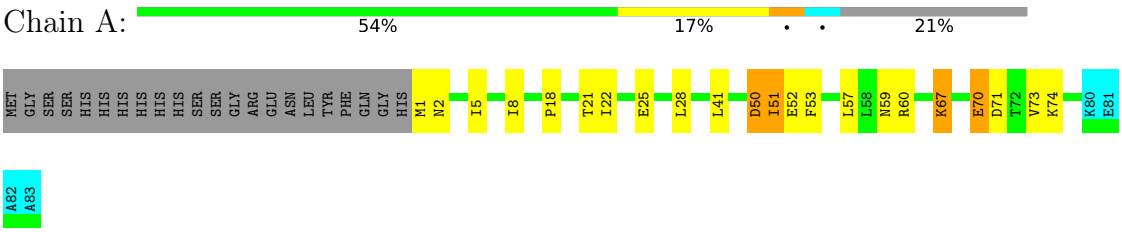
Chain A: 57% 16% • • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 I8 L9 F12 G13 P18 T21 S38 V39 Q40 L41 M42 D50 I51 E52 L58 K67 E70 D71 K74 K80 E81 A82 A83

4.2.12 Score per residue for model 12

- Molecule 1: Hypothetical protein Atu2571

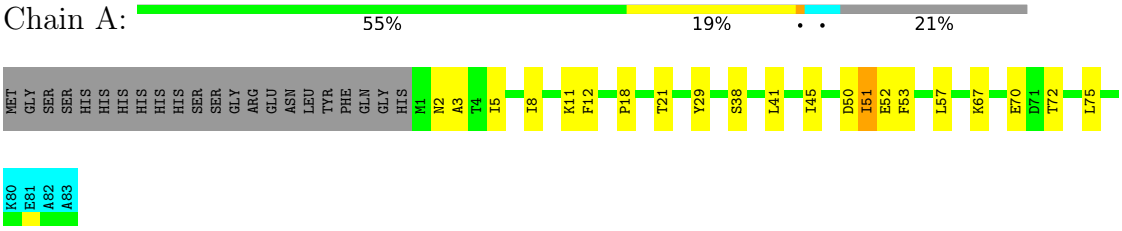
Chain A:



4.2.13 Score per residue for model 13

- Molecule 1: Hypothetical protein Atu2571

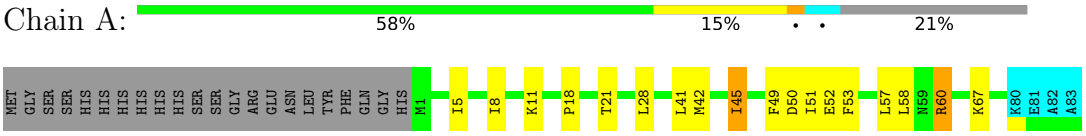
Chain A:



4.2.14 Score per residue for model 14

- Molecule 1: Hypothetical protein Atu2571

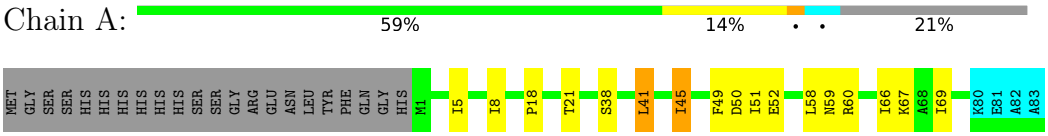
Chain A:



4.2.15 Score per residue for model 15

- Molecule 1: Hypothetical protein Atu2571

Chain A:



4.2.16 Score per residue for model 16

- Molecule 1: Hypothetical protein Atu2571

Chain A: 59% 15% • • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 I8 P18 T21 A26 D27 L28 S38 L41 I45 D50 I51 E52 F53 L57 K67 E70 V73 K80 E81 A82 A83

4.2.17 Score per residue for model 17

• Molecule 1: Hypothetical protein Atu2571

Chain A: 58% 17% • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 I8 F12 P18 T21 D27 L41 D50 I51 E52 F53 L57 L58 F63 A64 K67 E70 K74 K80 E81 A82 A83

4.2.18 Score per residue for model 18

• Molecule 1: Hypothetical protein Atu2571

Chain A: 54% 19% • • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 I8 F12 P18 T21 L41 I45 F49 D50 I51 E52 F53 L57 S65 I66 K67 A68 I69 E70 D71 T72 V73 K74 L75 K80 E81

A82 A83

4.2.19 Score per residue for model 19

• Molecule 1: Hypothetical protein Atu2571

Chain A: 60% 10% 5% • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 I8 F12 L41 M42 I45 F49 D50 I51 E52 F53 L57 K67 E70 K74 K80 E81 A82 A83

4.2.20 Score per residue for model 20

• Molecule 1: Hypothetical protein Atu2571

Chain A: 53% 20% • • 21%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY ARG GLU ASN LEU TYR PHE GLN GLY HIS M1 I5 R6 E7 I8 P18 T21 S38 L41 M42 L43 G44 D50 I51 E52 F53 L57 L58 N59 R60 I66 K67 A68 I69 E70 K80 E81 A82 A83

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *DGSA-distance geometry simulated annealing.*

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy.*

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

Software name	**Classification**	**Version**
CYANA	structure solution	
CNS	refinement	

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	972
Number of shifts mapped to atoms	972
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

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	603	608	611	8±2
All	All	12060	12160	12220	150

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:53:PHE:HB3	1:A:57:LEU:HD11	0.67	1.67	18	15
1:A:2:ASN:HB3	1:A:70:GLU:HG2	0.61	1.73	12	1
1:A:5:ILE:O	1:A:8:ILE:HG22	0.57	1.99	12	20
1:A:61:LYS:HB2	1:A:61:LYS:HZ2	0.57	1.59	6	1
1:A:70:GLU:O	1:A:73:VAL:HG12	0.56	1.99	12	3
1:A:38:SER:HA	1:A:41:LEU:HD23	0.56	1.76	20	9
1:A:1:MET:SD	1:A:1:MET:N	0.53	2.81	12	1
1:A:72:THR:O	1:A:75:LEU:HG	0.51	2.06	13	4
1:A:22:ILE:HD12	1:A:28:LEU:HG	0.51	1.83	12	1
1:A:1:MET:SD	1:A:49:PHE:CE1	0.50	3.04	5	2
1:A:18:PRO:O	1:A:21:THR:HG22	0.50	2.07	9	16
1:A:1:MET:SD	1:A:77:LEU:HD11	0.50	2.47	5	1
1:A:42:MET:SD	1:A:53:PHE:HD2	0.50	2.29	14	1
1:A:61:LYS:HB2	1:A:61:LYS:NZ	0.49	2.23	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:39:VAL:O	1:A:42:MET:HG2	0.49	2.08	10	1
1:A:42:MET:SD	1:A:58:LEU:HD21	0.49	2.48	20	1
1:A:42:MET:SD	1:A:58:LEU:HD22	0.49	2.48	6	1
1:A:60:ARG:HE	1:A:60:ARG:HA	0.48	1.68	5	1
1:A:45:ILE:HG23	1:A:49:PHE:CE2	0.46	2.45	15	9
1:A:66:ILE:HA	1:A:69:ILE:HG22	0.46	1.87	15	6
1:A:70:GLU:O	1:A:74:LYS:HG3	0.46	2.11	19	4
1:A:27:ASP:HA	1:A:64:ALA:O	0.45	2.11	17	1
1:A:1:MET:SD	1:A:73:VAL:HG13	0.45	2.51	18	1
1:A:71:ASP:HA	1:A:74:LYS:NZ	0.45	2.27	12	1
1:A:43:LEU:HD12	1:A:44:GLY:N	0.45	2.26	20	1
1:A:22:ILE:HD12	1:A:28:LEU:HD22	0.44	1.90	4	1
1:A:8:ILE:HG12	1:A:12:PHE:HB2	0.44	1.90	5	6
1:A:42:MET:O	1:A:52:GLU:HB3	0.44	2.12	19	1
1:A:59:ASN:OD1	1:A:60:ARG:N	0.43	2.51	9	3
1:A:35:SER:O	1:A:39:VAL:HG23	0.43	2.13	8	1
1:A:28:LEU:H	1:A:28:LEU:HD22	0.43	1.73	14	1
1:A:1:MET:SD	1:A:49:PHE:CD1	0.43	3.12	19	1
1:A:58:LEU:HA	1:A:63:PHE:CE1	0.43	2.48	17	2
1:A:18:PRO:O	1:A:21:THR:HB	0.43	2.13	2	2
1:A:25:GLU:HG2	1:A:67:LYS:HD2	0.42	1.90	12	2
1:A:2:ASN:OD1	1:A:3:ALA:N	0.42	2.52	13	1
1:A:8:ILE:HD13	1:A:41:LEU:O	0.42	2.14	13	4
1:A:65:SER:HB3	1:A:67:LYS:HE3	0.42	1.91	6	3
1:A:15:LEU:HD12	1:A:16:PRO:HD2	0.42	1.92	9	1
1:A:50:ASP:OD2	1:A:51:ILE:HG23	0.42	2.15	12	1
1:A:59:ASN:OD1	1:A:60:ARG:HG2	0.42	2.13	9	1
1:A:26:ALA:O	1:A:28:LEU:HD22	0.42	2.15	16	1
1:A:71:ASP:HA	1:A:74:LYS:HE3	0.42	1.91	11	1
1:A:71:ASP:O	1:A:75:LEU:HG	0.42	2.15	18	1
1:A:61:LYS:NZ	1:A:61:LYS:HB2	0.41	2.29	3	1
1:A:42:MET:SD	1:A:58:LEU:HD13	0.41	2.55	11	1
1:A:5:ILE:HD13	1:A:53:PHE:HZ	0.41	1.75	16	1
1:A:1:MET:O	1:A:5:ILE:HG13	0.41	2.15	20	2
1:A:9:LEU:HA	1:A:13:GLY:HA3	0.41	1.92	11	1
1:A:24:ASP:HB2	1:A:66:ILE:HB	0.41	1.92	5	1
1:A:60:ARG:HA	1:A:60:ARG:NE	0.41	2.31	14	1
1:A:65:SER:HB3	1:A:67:LYS:HE2	0.41	1.92	1	1
1:A:50:ASP:OD1	1:A:51:ILE:HG23	0.40	2.16	19	1
1:A:51:ILE:HD13	1:A:51:ILE:H	0.40	1.76	18	2
1:A:51:ILE:H	1:A:51:ILE:HD13	0.40	1.77	19	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	78/105 (74%)	72±2 (92±2%)	5±2 (7±2%)	1±0 (1±0%)	14 59
All	All	1560/2100 (74%)	1435 (92%)	102 (7%)	23 (1%)	14 59

All 3 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	50	ASP	20
1	A	58	LEU	2
1	A	59	ASN	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	65/86 (76%)	59±1 (91±2%)	6±1 (9±2%)	13 59
All	All	1300/1720 (76%)	1180 (91%)	120 (9%)	13 59

All 17 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	51	ILE	20
1	A	52	GLU	20
1	A	67	LYS	20
1	A	41	LEU	17
1	A	70	GLU	14
1	A	45	ILE	12
1	A	6	ARG	2

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Mol	Chain	Res	Type	Models (Total)
1	A	61	LYS	2
1	A	59	ASN	2
1	A	60	ARG	2
1	A	11	LYS	2
1	A	58	LEU	2
1	A	74	LYS	1
1	A	43	LEU	1
1	A	14	GLN	1
1	A	40	GLN	1
1	A	29	TYR	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 88% for the well-defined parts and 88% 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 (i)

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	972
Number of shifts mapped to atoms	972
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	81	-0.38 ± 0.21	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	76	0.10 ± 0.21	None needed (< 0.5 ppm)
$^{13}C'$	75	-0.09 ± 0.21	None needed (< 0.5 ppm)
^{15}N	73	0.07 ± 0.43	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 88%, i.e. 927 atoms were assigned a chemical shift out of a possible 1059. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	368/393 (94%)	150/159 (94%)	149/158 (94%)	69/76 (91%)
Sidechain	532/607 (88%)	366/399 (92%)	162/193 (84%)	4/15 (27%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	27/59 (46%)	18/29 (62%)	9/30 (30%)	0/0 (—%)
Overall	927/1059 (88%)	534/587 (91%)	320/381 (84%)	73/91 (80%)

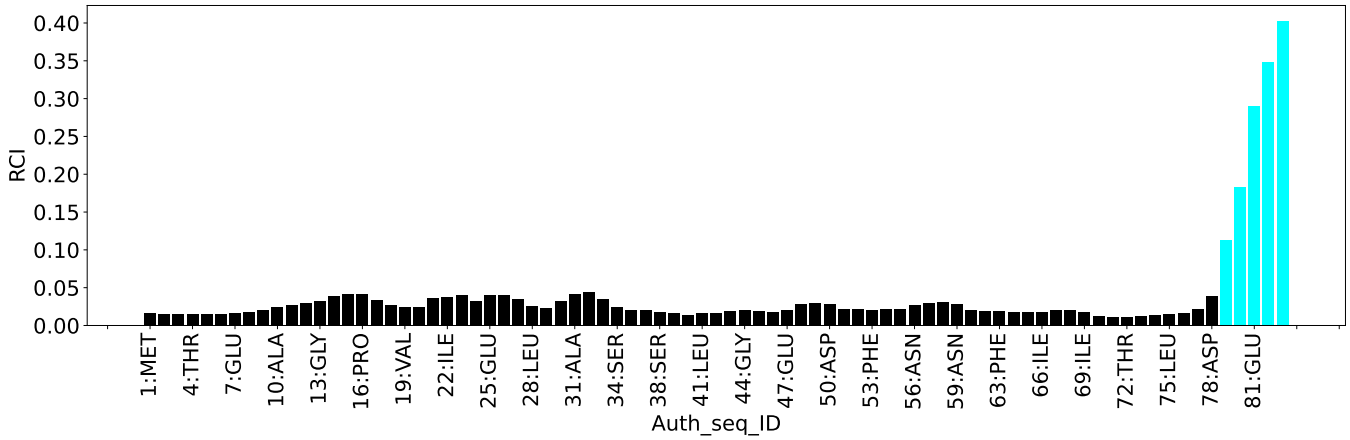
The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 88%, i.e. 972 atoms were assigned a chemical shift out of a possible 1107. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	387/413 (94%)	158/167 (95%)	156/166 (94%)	73/80 (91%)
Sidechain	558/635 (88%)	384/417 (92%)	170/202 (84%)	4/16 (25%)
Aromatic	27/59 (46%)	18/29 (62%)	9/30 (30%)	0/0 (—%)
Overall	972/1107 (88%)	560/613 (91%)	335/398 (84%)	77/96 (80%)

7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

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: