Full wwPDB NMR Structure Validation Report (i)

Jun 12, 2024 – 04:12 AM EDT

PDB ID	:	2KJ5
BMRB ID	:	16312
Title	:	Solution NMR structure of a domain from a putative phage integrase protein Nmul_A0064 from Nitrosospira multiformis, Northeast Structural Genomics Consortium Target NmR46C
Authors	:	Mills, J.L.; Eletsky, A.; Ghosh, A.; Wang, D.; Lee, H.; Ciccosanti, C.; Jiang, M.; Nair, R.; Rost, B.; Swapna, G.V.T.; Acton, T.B.; Xiao, R.; Everett, J.K.; Prestegard, J.H.; Montelione, G.T.; Szyperski, T.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2009-05-21

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:

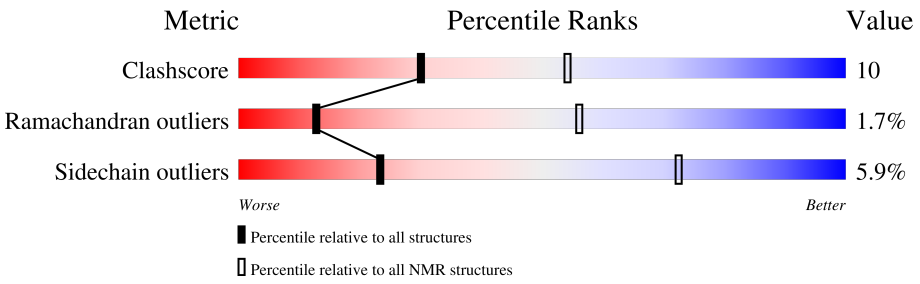
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 84%.

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	116	66% 15% 19%

2 Ensemble composition and analysis (i)

This entry contains 20 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:7-A:100 (94)	1.16	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 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1897 atoms, of which 954 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Phage integrase.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	116	1897	598	954	180	161	4	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q2YCZ8
A	109	LEU	-	expression tag	UNP Q2YCZ8
A	110	GLU	-	expression tag	UNP Q2YCZ8
A	111	HIS	-	expression tag	UNP Q2YCZ8
A	112	HIS	-	expression tag	UNP Q2YCZ8
A	113	HIS	-	expression tag	UNP Q2YCZ8
A	114	HIS	-	expression tag	UNP Q2YCZ8
A	115	HIS	-	expression tag	UNP Q2YCZ8
A	116	HIS	-	expression tag	UNP Q2YCZ8

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: Phage integrase

Chain A: 66% 15% 19%

M1 A2 E3 K4 N5 A6 F17 I21 W25 K26 H27 P28 I35 E36 K37 D38 I39 K40 P41 K47 L60 K61 A62 V63 M64 K65 R66 K80 D101 P102 G103 D104 A105 G106 G107 K108 L109 E110 H111 H112 H113 H114 H115 H116

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: Phage integrase

Chain A: 59% 22% • 19%

M1 A2 E3 K4 N5 A6 Y7 F17 I21 R24 W25 K26 H27 P28 R32 I35 E36 I39 K40 P41 A42 I43 I56 D57 D58 V59 R66 T75 L79 Y85 K88 Y94 N95 P96 F100 D101 P102 G103 D104 A105 G106 G107 K108 L109 E110 H111 H112 H113 H114 H115 H116

4.2.2 Score per residue for model 2

• Molecule 1: Phage integrase

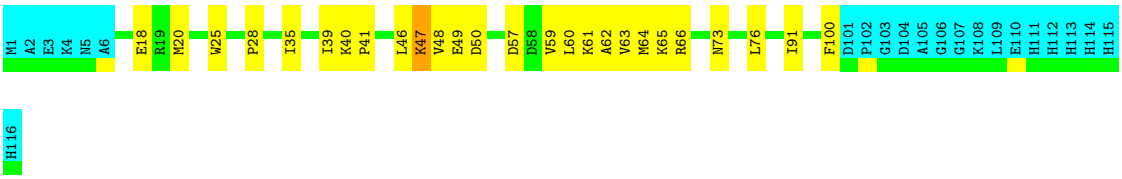
Chain A: 60% 20% • 19%

M1 A2 E3 K4 N5 A6 A10 Q11 E15 R19 K26 R32 I35 I39 K40 P41 A42 I43 V48 V51 D58 K61 T75 L76 L79 N84 I87 K88 E93 Y94 N95 F100 D101 P102 G103 D104 A105 G106 G107 K108 L109 E110 H111

4.2.3 Score per residue for model 3

- Molecule 1: Phage integrase

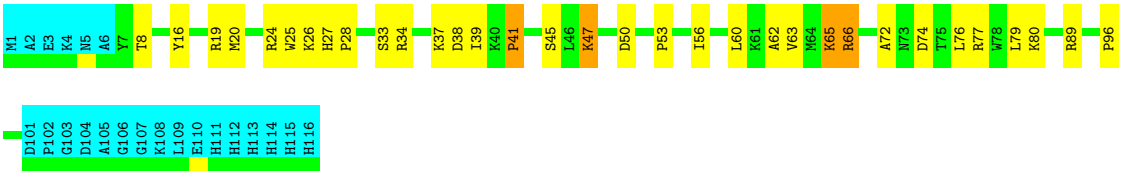
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Phage integrase

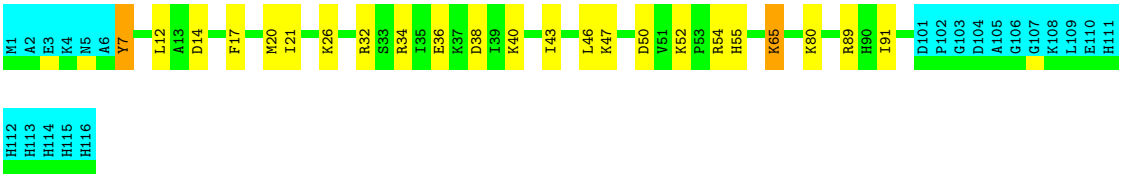
Chain A:



4.2.5 Score per residue for model 5

- Molecule 1: Phage integrase

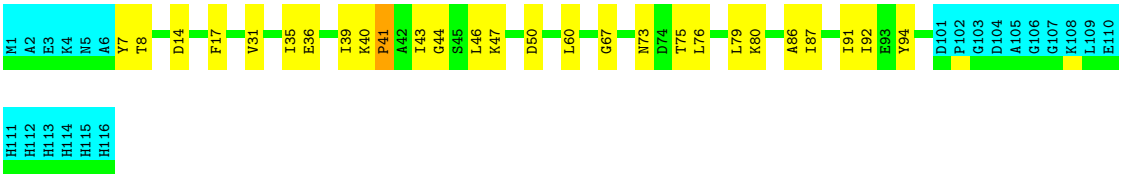
Chain A:



4.2.6 Score per residue for model 6

- Molecule 1: Phage integrase

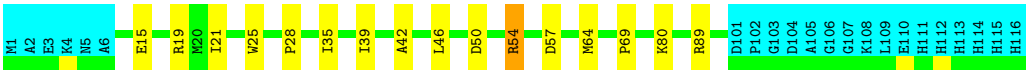
Chain A:



4.2.7 Score per residue for model 7

- Molecule 1: Phage integrase

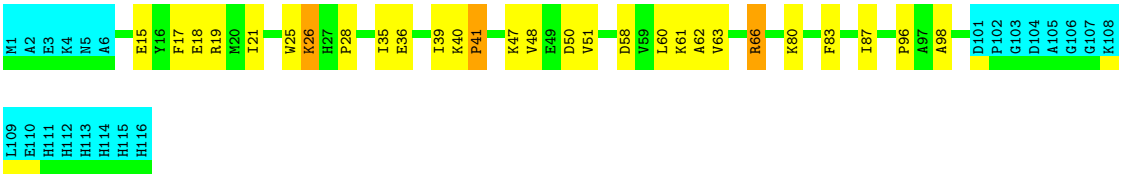
Chain A:



4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: Phage integrase

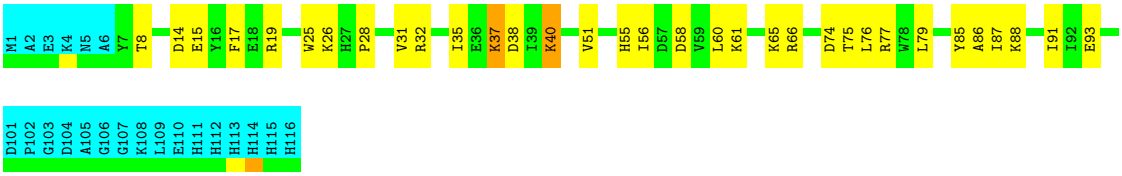
Chain A:



4.2.9 Score per residue for model 9

- Molecule 1: Phage integrase

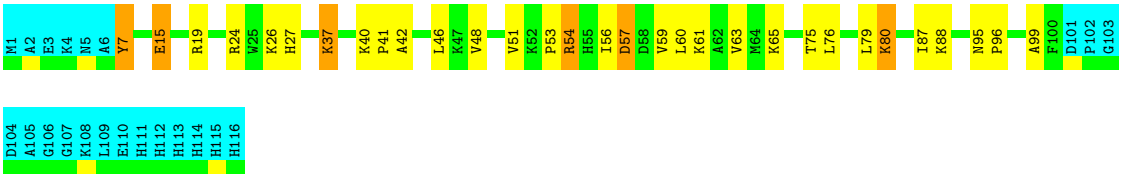
Chain A:



4.2.10 Score per residue for model 10

- Molecule 1: Phage integrase

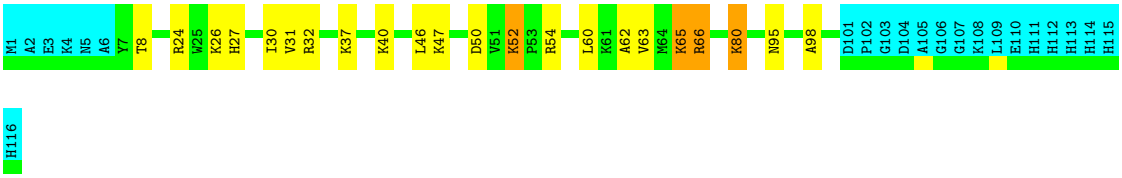
Chain A:



4.2.11 Score per residue for model 11

- Molecule 1: Phage integrase

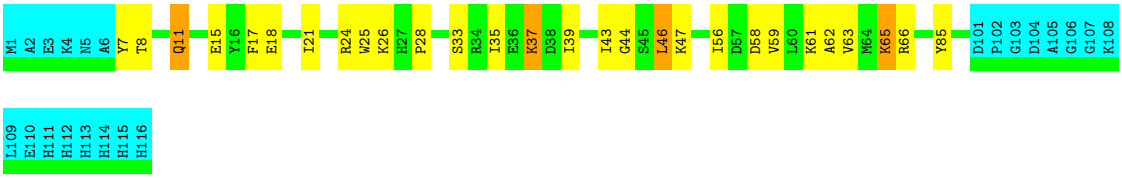
Chain A:



4.2.12 Score per residue for model 12

- Molecule 1: Phage integrase

Chain A:



4.2.13 Score per residue for model 13

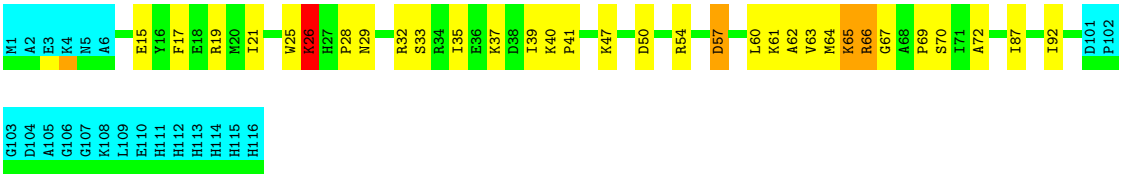
- Molecule 1: Phage integrase

Chain A:

4.2.14 Score per residue for model 14

- Molecule 1: Phage integrase

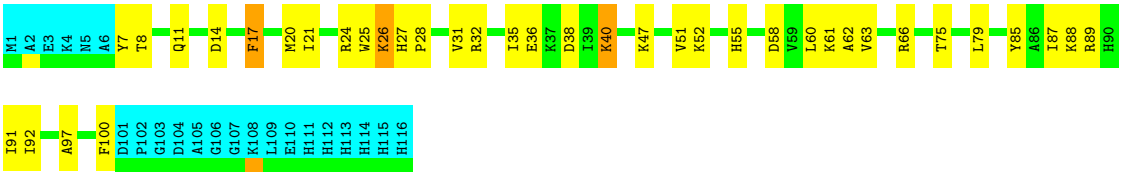
Chain A:



4.2.15 Score per residue for model 15

- Molecule 1: Phage integrase

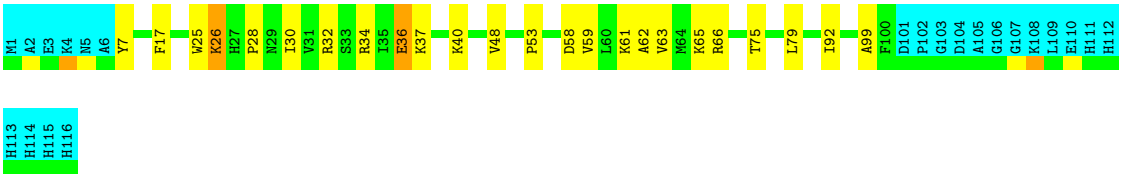
Chain A:



4.2.16 Score per residue for model 16

- Molecule 1: Phage integrase

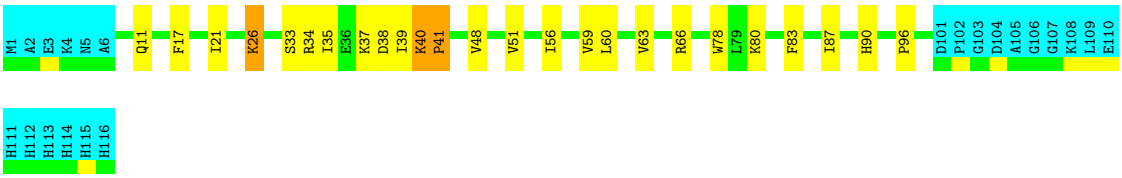
Chain A:



4.2.17 Score per residue for model 17

- Molecule 1: Phage integrase

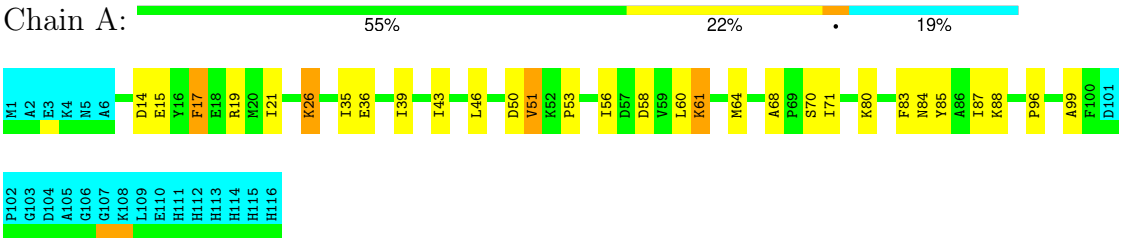
Chain A:



4.2.18 Score per residue for model 18

- Molecule 1: Phage integrase

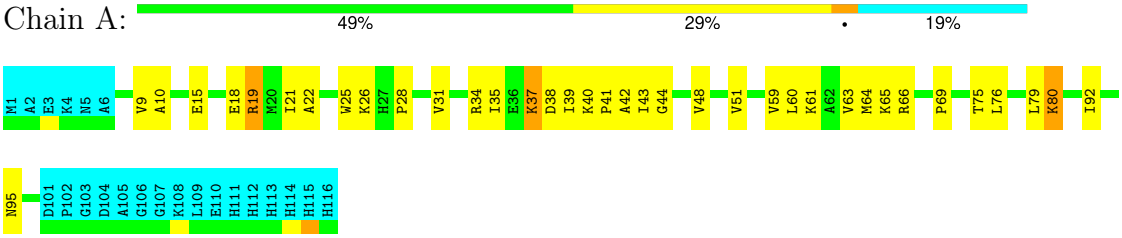
Chain A:



4.2.19 Score per residue for model 19

- Molecule 1: Phage integrase

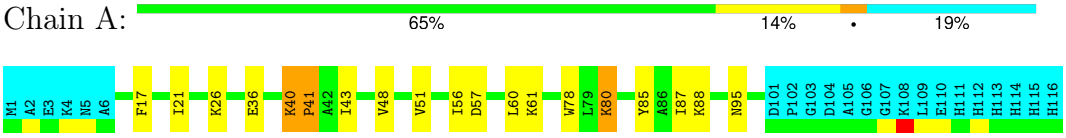
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: Phage integrase

Chain A:



5 Refinement protocol and experimental data overview (i)

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

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
TALOS	geometry optimization	
CYANA	structure solution	
CYANA	refinement	
CNS	structure solution	
CNS	refinement	
MOLMOL	refinement	
MOLMOL	structure solution	
AutoStructure	structure solution	
AutoStructure	refinement	
PSVS	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	1346
Number of shifts mapped to atoms	1346
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	84%

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	773	801	798	16±5
All	All	15460	16020	15960	314

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 10.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:ASP:HA	1:A:61:LYS:HE2	0.98	1.30	8	4
1:A:58:ASP:HA	1:A:61:LYS:HD2	0.93	1.39	18	1
1:A:17:PHE:HA	1:A:21:ILE:HD13	0.93	1.41	17	5
1:A:47:LYS:HG2	1:A:49:GLU:HG2	0.88	1.45	3	1
1:A:26:LYS:HA	1:A:26:LYS:HE3	0.86	1.47	1	3
1:A:58:ASP:HA	1:A:61:LYS:HD3	0.85	1.47	12	1
1:A:47:LYS:HB2	1:A:50:ASP:HB2	0.80	1.50	11	2
1:A:8:THR:HA	1:A:47:LYS:HA	0.78	1.51	15	4
1:A:17:PHE:HB2	1:A:21:ILE:HD12	0.77	1.56	15	3
1:A:87:ILE:HG13	1:A:93:GLU:HA	0.76	1.57	9	1
1:A:37:LYS:HE3	1:A:66:ARG:HD2	0.76	1.57	17	1
1:A:35:ILE:HG22	1:A:40:LYS:HD2	0.74	1.57	15	1
1:A:85:TYR:HA	1:A:88:LYS:HD3	0.72	1.61	15	3
1:A:36:GLU:HA	1:A:40:LYS:HD3	0.71	1.62	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:87:ILE:HD11	1:A:95:ASN:HB2	0.71	1.62	10	3
1:A:41:PRO:HG2	1:A:59:VAL:HB	0.70	1.63	10	1
1:A:25:TRP:CD1	1:A:28:PRO:HG3	0.69	2.23	7	3
1:A:41:PRO:HB3	1:A:59:VAL:HB	0.66	1.67	19	1
1:A:25:TRP:HE1	1:A:28:PRO:HG3	0.66	1.50	9	6
1:A:64:MET:HG2	1:A:69:PRO:HA	0.65	1.68	14	4
1:A:35:ILE:HG23	1:A:39:ILE:HD12	0.65	1.69	18	2
1:A:17:PHE:O	1:A:21:ILE:HB	0.63	1.93	1	4
1:A:41:PRO:HG3	1:A:59:VAL:HG23	0.63	1.68	17	1
1:A:36:GLU:HA	1:A:40:LYS:HG3	0.62	1.69	8	2
1:A:26:LYS:HE2	1:A:26:LYS:HA	0.62	1.69	18	3
1:A:35:ILE:HA	1:A:39:ILE:HD13	0.62	1.71	8	1
1:A:35:ILE:HG12	1:A:39:ILE:HD12	0.61	1.70	3	1
1:A:53:PRO:HB3	1:A:99:ALA:HB2	0.61	1.72	18	3
1:A:27:HIS:HB2	1:A:30:ILE:HB	0.61	1.71	11	1
1:A:37:LYS:HA	1:A:37:LYS:HE3	0.61	1.71	9	1
1:A:46:LEU:O	1:A:50:ASP:HB2	0.60	1.97	5	2
1:A:60:LEU:HD11	1:A:76:LEU:HD21	0.60	1.73	9	3
1:A:35:ILE:O	1:A:40:LYS:HG2	0.59	1.96	6	1
1:A:46:LEU:HB2	1:A:50:ASP:HB2	0.59	1.74	7	1
1:A:54:ARG:O	1:A:54:ARG:HD3	0.59	1.98	7	1
1:A:74:ASP:O	1:A:77:ARG:HG2	0.58	1.98	4	2
1:A:76:LEU:O	1:A:80:LYS:HD2	0.58	1.97	19	1
1:A:87:ILE:HA	1:A:92:ILE:O	0.58	1.97	14	3
1:A:36:GLU:HA	1:A:40:LYS:HE2	0.58	1.74	5	1
1:A:15:GLU:O	1:A:19:ARG:HD3	0.57	1.99	14	1
1:A:80:LYS:HG2	1:A:95:ASN:HD21	0.56	1.60	11	1
1:A:48:VAL:O	1:A:51:VAL:HG12	0.56	2.00	10	6
1:A:53:PRO:HG3	1:A:96:PRO:HA	0.56	1.77	4	1
1:A:75:THR:O	1:A:79:LEU:HG	0.56	2.01	6	8
1:A:89:ARG:HD3	1:A:91:ILE:HD11	0.56	1.78	5	1
1:A:39:ILE:HG23	1:A:79:LEU:HD21	0.55	1.77	4	1
1:A:65:LYS:HE2	1:A:65:LYS:HA	0.55	1.78	5	1
1:A:35:ILE:O	1:A:39:ILE:HB	0.54	2.02	19	4
1:A:97:ALA:HA	1:A:100:PHE:HD2	0.54	1.62	15	1
1:A:36:GLU:HA	1:A:40:LYS:CG	0.54	2.32	8	2
1:A:7:TYR:CE1	1:A:12:LEU:HA	0.54	2.38	5	1
1:A:14:ASP:HA	1:A:17:PHE:CD1	0.54	2.37	9	3
1:A:26:LYS:HE3	1:A:26:LYS:HA	0.54	1.79	14	1
1:A:8:THR:HB	1:A:45:SER:HA	0.54	1.78	4	1
1:A:52:LYS:H	1:A:52:LYS:HD2	0.54	1.63	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:48:VAL:HG12	1:A:92:ILE:HD13	0.54	1.80	19	2
1:A:10:ALA:HA	1:A:40:LYS:CD	0.53	2.34	2	1
1:A:68:ALA:HB3	1:A:71:ILE:HD13	0.53	1.80	18	1
1:A:51:VAL:HG22	1:A:96:PRO:HG3	0.53	1.79	17	2
1:A:24:ARG:O	1:A:24:ARG:HD2	0.53	2.03	10	1
1:A:26:LYS:HA	1:A:26:LYS:CE	0.53	2.32	8	5
1:A:62:ALA:O	1:A:65:LYS:HG3	0.53	2.03	11	3
1:A:35:ILE:HA	1:A:39:ILE:CG1	0.53	2.33	19	2
1:A:15:GLU:O	1:A:19:ARG:HG2	0.52	2.04	10	6
1:A:21:ILE:HG23	1:A:25:TRP:HB2	0.52	1.81	7	1
1:A:54:ARG:HA	1:A:57:ASP:OD2	0.52	2.03	14	2
1:A:33:SER:O	1:A:37:LYS:HG3	0.52	2.04	12	1
1:A:61:LYS:O	1:A:64:MET:HG2	0.52	2.04	3	1
1:A:92:ILE:HG12	1:A:94:TYR:H	0.52	1.64	6	1
1:A:29:ASN:HA	1:A:32:ARG:HB2	0.52	1.82	14	1
1:A:39:ILE:O	1:A:41:PRO:HD3	0.51	2.05	1	3
1:A:25:TRP:HE1	1:A:28:PRO:HB3	0.51	1.65	12	3
1:A:76:LEU:HG	1:A:100:PHE:HD2	0.51	1.65	2	1
1:A:60:LEU:HA	1:A:63:VAL:HG22	0.51	1.82	19	10
1:A:60:LEU:HD22	1:A:72:ALA:HB1	0.51	1.82	4	1
1:A:54:ARG:HA	1:A:57:ASP:HB3	0.51	1.82	7	1
1:A:21:ILE:HG21	1:A:31:VAL:HG21	0.51	1.82	13	1
1:A:56:ILE:O	1:A:59:VAL:HG22	0.51	2.05	12	1
1:A:34:ARG:O	1:A:38:ASP:HB2	0.51	2.05	17	1
1:A:87:ILE:HA	1:A:93:GLU:HA	0.51	1.82	2	1
1:A:53:PRO:HB3	1:A:99:ALA:CB	0.51	2.36	18	1
1:A:41:PRO:HA	1:A:66:ARG:HH22	0.50	1.65	1	1
1:A:80:LYS:HA	1:A:80:LYS:HE3	0.50	1.83	5	2
1:A:10:ALA:HA	1:A:40:LYS:HE2	0.50	1.83	19	1
1:A:61:LYS:O	1:A:65:LYS:HG3	0.50	2.06	3	1
1:A:76:LEU:HG	1:A:100:PHE:CD2	0.50	2.41	2	1
1:A:33:SER:O	1:A:37:LYS:HB3	0.50	2.06	17	3
1:A:76:LEU:HD23	1:A:79:LEU:HD12	0.50	1.83	10	2
1:A:58:ASP:CA	1:A:61:LYS:HD2	0.50	2.25	18	1
1:A:17:PHE:CD2	1:A:21:ILE:HD12	0.50	2.41	5	1
1:A:15:GLU:O	1:A:19:ARG:HD2	0.49	2.07	19	1
1:A:89:ARG:HE	1:A:89:ARG:HA	0.49	1.68	7	1
1:A:80:LYS:HE2	1:A:80:LYS:O	0.49	2.08	20	1
1:A:65:LYS:HD2	1:A:65:LYS:C	0.49	2.28	19	2
1:A:60:LEU:O	1:A:64:MET:HG3	0.49	2.08	19	3
1:A:7:TYR:CD1	1:A:11:GLN:HB3	0.49	2.43	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:ASP:O	1:A:61:LYS:HG2	0.49	2.07	16	1
1:A:35:ILE:HA	1:A:39:ILE:HB	0.49	1.83	3	2
1:A:35:ILE:HG22	1:A:40:LYS:HE2	0.49	1.85	17	3
1:A:32:ARG:HE	1:A:36:GLU:CD	0.49	2.11	16	1
1:A:56:ILE:O	1:A:60:LEU:HG	0.49	2.08	20	5
1:A:83:PHE:O	1:A:87:ILE:HG13	0.49	2.08	8	3
1:A:39:ILE:HD13	1:A:75:THR:HG23	0.48	1.84	1	1
1:A:55:HIS:HA	1:A:58:ASP:OD2	0.48	2.09	9	1
1:A:89:ARG:HG3	1:A:91:ILE:HG13	0.48	1.85	15	1
1:A:57:ASP:O	1:A:61:LYS:HD3	0.48	2.08	20	1
1:A:52:LYS:HB2	1:A:54:ARG:HG2	0.48	1.85	5	1
1:A:21:ILE:HD11	1:A:78:TRP:CZ2	0.48	2.43	20	2
1:A:40:LYS:HE2	1:A:44:GLY:HA2	0.48	1.85	6	1
1:A:56:ILE:HA	1:A:59:VAL:HG22	0.48	1.86	1	1
1:A:57:ASP:HB2	1:A:100:PHE:HZ	0.48	1.69	1	1
1:A:41:PRO:HD2	1:A:43:ILE:HG12	0.47	1.86	2	3
1:A:51:VAL:HG13	1:A:96:PRO:HG2	0.47	1.84	8	1
1:A:46:LEU:HG	1:A:50:ASP:HB2	0.47	1.86	6	1
1:A:43:ILE:HG13	1:A:44:GLY:H	0.46	1.70	19	1
1:A:62:ALA:O	1:A:66:ARG:HG3	0.46	2.10	8	3
1:A:25:TRP:NE1	1:A:28:PRO:HG3	0.46	2.23	9	3
1:A:35:ILE:HA	1:A:39:ILE:HD12	0.46	1.88	12	2
1:A:37:LYS:HD2	1:A:37:LYS:C	0.46	2.31	19	2
1:A:14:ASP:HA	1:A:17:PHE:HD1	0.46	1.69	9	1
1:A:65:LYS:HD3	1:A:66:ARG:N	0.46	2.26	14	2
1:A:51:VAL:HA	1:A:55:HIS:HD2	0.46	1.71	9	2
1:A:95:ASN:ND2	1:A:98:ALA:HB2	0.45	2.25	11	1
1:A:31:VAL:O	1:A:35:ILE:HG13	0.45	2.11	9	3
1:A:63:VAL:HA	1:A:66:ARG:HG2	0.45	1.89	19	1
1:A:21:ILE:HD11	1:A:78:TRP:HZ2	0.45	1.71	17	1
1:A:14:ASP:HA	1:A:17:PHE:CD2	0.45	2.46	6	1
1:A:9:VAL:HG21	1:A:43:ILE:HD12	0.45	1.87	19	1
1:A:76:LEU:O	1:A:80:LYS:HG3	0.45	2.12	6	1
1:A:56:ILE:HG13	1:A:96:PRO:HB2	0.44	1.89	10	1
1:A:46:LEU:HB2	1:A:50:ASP:CB	0.44	2.42	7	1
1:A:32:ARG:HD3	1:A:32:ARG:O	0.44	2.13	2	1
1:A:76:LEU:HA	1:A:79:LEU:HD12	0.44	1.90	19	1
1:A:47:LYS:HB2	1:A:50:ASP:OD2	0.44	2.13	8	1
1:A:35:ILE:HA	1:A:39:ILE:HG12	0.44	1.90	19	1
1:A:85:TYR:HA	1:A:88:LYS:HE2	0.44	1.90	20	1
1:A:7:TYR:HB3	1:A:11:GLN:HB2	0.44	1.88	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:ALA:O	1:A:66:ARG:HG2	0.43	2.13	16	3
1:A:52:LYS:N	1:A:55:HIS:HD2	0.43	2.11	5	1
1:A:34:ARG:HD3	1:A:38:ASP:OD2	0.43	2.13	4	1
1:A:80:LYS:O	1:A:84:ASN:HB2	0.43	2.13	13	1
1:A:25:TRP:HD1	1:A:28:PRO:HG3	0.43	1.69	7	1
1:A:86:ALA:HA	1:A:91:ILE:HD12	0.43	1.90	9	2
1:A:62:ALA:O	1:A:65:LYS:HG2	0.43	2.13	16	1
1:A:20:MET:HA	1:A:20:MET:CE	0.43	2.42	15	1
1:A:26:LYS:O	1:A:27:HIS:HB2	0.43	2.14	15	1
1:A:20:MET:CE	1:A:20:MET:HA	0.43	2.44	3	1
1:A:27:HIS:HD2	1:A:31:VAL:HB	0.43	1.74	11	1
1:A:46:LEU:O	1:A:46:LEU:HG	0.43	2.13	11	2
1:A:51:VAL:HG13	1:A:96:PRO:HG3	0.43	1.91	18	1
1:A:15:GLU:OE2	1:A:19:ARG:HD3	0.43	2.14	19	1
1:A:68:ALA:HB3	1:A:71:ILE:CD1	0.42	2.44	18	1
1:A:85:TYR:HA	1:A:88:LYS:HG2	0.42	1.90	1	1
1:A:34:ARG:HA	1:A:38:ASP:OD1	0.42	2.14	19	1
1:A:47:LYS:HB3	1:A:50:ASP:HB2	0.42	1.92	3	1
1:A:47:LYS:HB3	1:A:50:ASP:OD2	0.42	2.14	14	1
1:A:11:GLN:NE2	1:A:14:ASP:HB3	0.42	2.30	15	1
1:A:57:ASP:HB2	1:A:100:PHE:CZ	0.42	2.49	1	2
1:A:10:ALA:HA	1:A:40:LYS:HD2	0.42	1.90	2	1
1:A:32:ARG:O	1:A:36:GLU:HG3	0.42	2.13	5	1
1:A:43:ILE:HA	1:A:46:LEU:HD21	0.42	1.92	12	1
1:A:60:LEU:HD22	1:A:72:ALA:HA	0.42	1.91	14	1
1:A:63:VAL:HA	1:A:66:ARG:CG	0.42	2.45	14	1
1:A:18:GLU:O	1:A:22:ALA:HB2	0.42	2.14	19	1
1:A:65:LYS:HE3	1:A:66:ARG:HB3	0.41	1.92	11	1
1:A:43:ILE:HG13	1:A:44:GLY:N	0.41	2.29	19	1
1:A:84:ASN:O	1:A:88:LYS:HD3	0.41	2.14	2	1
1:A:89:ARG:HA	1:A:89:ARG:NE	0.41	2.30	7	1
1:A:15:GLU:HG3	1:A:85:TYR:HE2	0.41	1.75	12	1
1:A:19:ARG:N	1:A:19:ARG:HD2	0.41	2.30	4	1
1:A:21:ILE:HG22	1:A:21:ILE:O	0.41	2.16	14	1
1:A:21:ILE:HD13	1:A:31:VAL:HG11	0.41	1.92	19	1
1:A:41:PRO:HG3	1:A:59:VAL:HB	0.41	1.90	3	1
1:A:94:TYR:O	1:A:96:PRO:HD3	0.41	2.16	1	1
1:A:51:VAL:O	1:A:51:VAL:HG13	0.41	2.15	10	1
1:A:43:ILE:HA	1:A:46:LEU:HD13	0.41	1.92	18	1
1:A:39:ILE:C	1:A:41:PRO:HD3	0.41	2.36	8	1
1:A:24:ARG:HG3	1:A:24:ARG:O	0.41	2.16	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:LYS:HE2	1:A:61:LYS:HB3	0.41	1.80	15	1
1:A:24:ARG:HD3	1:A:24:ARG:O	0.40	2.16	12	1
1:A:59:VAL:O	1:A:63:VAL:HG13	0.40	2.15	16	1
1:A:16:TYR:CZ	1:A:20:MET:HG3	0.40	2.51	4	1
1:A:34:ARG:HA	1:A:38:ASP:OD2	0.40	2.16	5	1
1:A:63:VAL:HA	1:A:66:ARG:CZ	0.40	2.46	12	1
1:A:52:LYS:H	1:A:55:HIS:CD2	0.40	2.35	15	1
1:A:26:LYS:HD3	1:A:26:LYS:HA	0.40	1.82	16	1
1:A:36:GLU:HA	1:A:40:LYS:HE3	0.40	1.93	20	1
1:A:84:ASN:O	1:A:88:LYS:HG3	0.40	2.15	18	1
1:A:47:LYS:HG3	1:A:48:VAL:N	0.40	2.32	3	1
1:A:65:LYS:HG3	1:A:66:ARG:N	0.40	2.31	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	94/116 (81%)	84±2 (89±2%)	8±2 (9±2%)	2±1 (2±1%)	13	56
All	All	1880/2320 (81%)	1678 (89%)	170 (9%)	32 (2%)	13	56

All 9 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	26	LYS	12
1	A	41	PRO	6
1	A	42	ALA	4
1	A	47	LYS	3
1	A	43	ILE	2
1	A	67	GLY	2
1	A	44	GLY	1
1	A	24	ARG	1
1	A	51	VAL	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	80/96 (83%)	75±3 (94±3%)	5±3 (6±3%)	23	72
All	All	1600/1920 (83%)	1505 (94%)	95 (6%)	23	72

All 35 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	80	LYS	10
1	A	40	LYS	8
1	A	37	LYS	7
1	A	65	LYS	6
1	A	26	LYS	5
1	A	32	ARG	5
1	A	66	ARG	4
1	A	54	ARG	4
1	A	61	LYS	4
1	A	17	PHE	4
1	A	18	GLU	3
1	A	7	TYR	3
1	A	36	GLU	3
1	A	24	ARG	2
1	A	27	HIS	2
1	A	38	ASP	2
1	A	57	ASP	2
1	A	52	LYS	2
1	A	11	GLN	2
1	A	70	SER	2
1	A	73	ASN	1
1	A	89	ARG	1
1	A	14	ASP	1
1	A	20	MET	1
1	A	8	THR	1
1	A	15	GLU	1
1	A	88	LYS	1
1	A	46	LEU	1
1	A	84	ASN	1

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Mol	Chain	Res	Type	Models (Total)
1	A	30	ILE	1
1	A	34	ARG	1
1	A	90	HIS	1
1	A	50	ASP	1
1	A	19	ARG	1
1	A	95	ASN	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 84% for the well-defined parts and 81% 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	1346
Number of shifts mapped to atoms	1346
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 (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	115	-0.08 ± 0.16	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	109	0.48 ± 0.12	None needed (< 0.5 ppm)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	109	0.78 ± 0.51	None needed (imprecise)

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 84%, i.e. 1157 atoms were assigned a chemical shift out of a possible 1384. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	369/463 (80%)	186/186 (100%)	94/188 (50%)	89/89 (100%)
Sidechain	715/807 (89%)	486/524 (93%)	217/242 (90%)	12/41 (29%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	73/114 (64%)	43/55 (78%)	28/51 (55%)	2/8 (25%)
Overall	1157/1384 (84%)	715/765 (93%)	339/481 (70%)	103/138 (75%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 81%, i.e. 1346 atoms were assigned a chemical shift out of a possible 1660. 0 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	454/574 (79%)	230/232 (99%)	115/232 (50%)	109/110 (99%)
Sidechain	819/924 (89%)	557/599 (93%)	249/281 (89%)	13/44 (30%)
Aromatic	73/162 (45%)	43/79 (54%)	28/63 (44%)	2/20 (10%)
Overall	1346/1660 (81%)	830/910 (91%)	392/576 (68%)	124/174 (71%)

7.1.4 Statistically unusual chemical shifts (i)

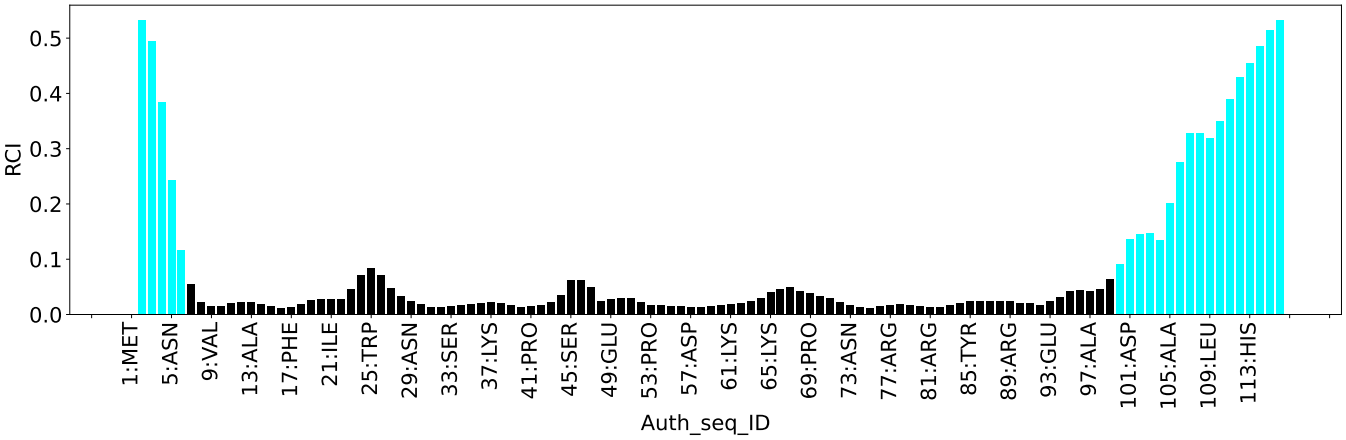
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	52	LYS	H	11.84	5.24 – 11.12	6.2

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:


RCI
0.0
0.1
0.2
0.3
0.4
0.5
1:MET
5:ASN
9:VAL
13:ALA
17:PHE
21:ILE
25:TRP
29:ASN
33:SER
37:LYS
41:PRO
45:SER
49:GLU
53:PRO
57:ASP
61:LYS
65:LYS
69:PRO
73:ASN
77:ARG
81:ARG
85:TYR
89:ARG
93:GLU
97:ALA
101:ASP
105:ALA
109:LEU
113:HIS
Auth_seq_ID