



Full wwPDB NMR Structure Validation Report ⓘ

Apr 21, 2024 – 04:46 PM EDT

PDB ID : 2RVB
BMRB ID : 11594
Title : Solution structure of the complex between XPC acidic domain and TFIIH p62 PH domain
Authors : Okuda, M.; Nishimura, Y.
Deposited on : 2015-07-01

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) : 2.36.2

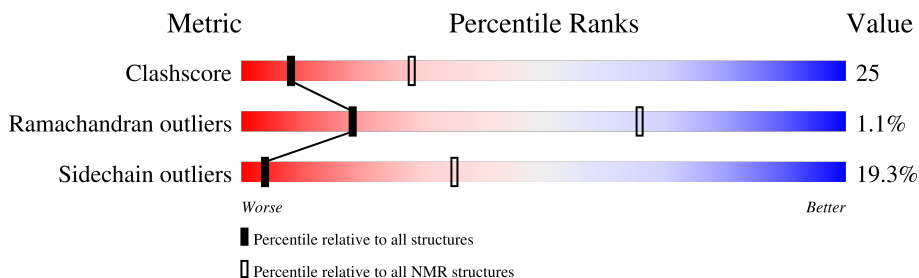
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 82%.

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	52	
2	B	110	

2 Ensemble composition and analysis

This entry contains 20 models. Model 19 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:132-A:139, B:8-B:35, B:43-B:103 (97)	0.40	19

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. No single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2481 atoms, of which 1232 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DNA repair protein complementing XP-C cells.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	48	720	227	334	66	92	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	GLY	-	expression tag	UNP Q01831
A	106	SER	-	expression tag	UNP Q01831
A	107	HIS	-	expression tag	UNP Q01831
A	108	MET	-	expression tag	UNP Q01831

- Molecule 2 is a protein called General transcription factor IIH subunit 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	B	108	1761	547	898	154	158	4	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP P32780
B	0	SER	-	expression tag	UNP P32780

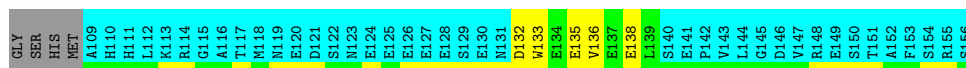
4 Residue-property plots

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.

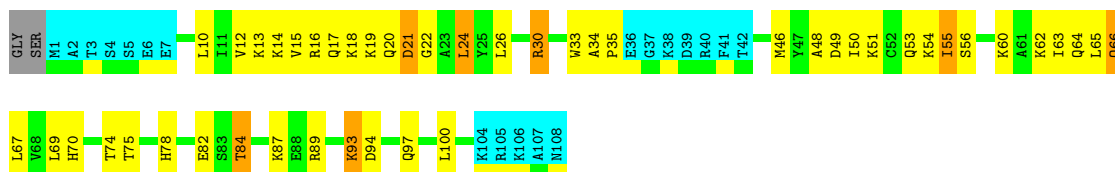
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 



- Molecule 2: General transcription factor IIIH subunit 1

Chain B: 



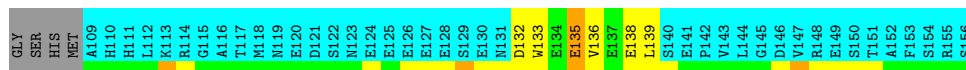
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

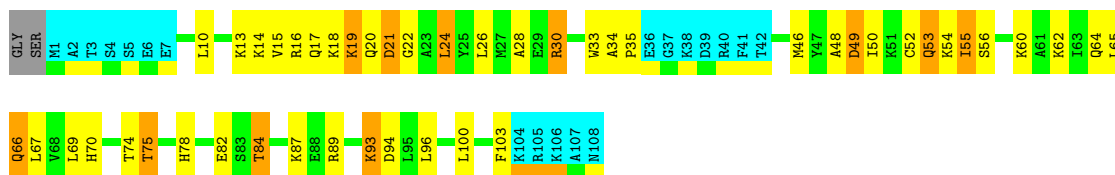
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 



- Molecule 2: General transcription factor IIIH subunit 1

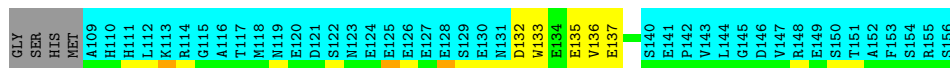
Chain B: 



4.2.2 Score per residue for model 2

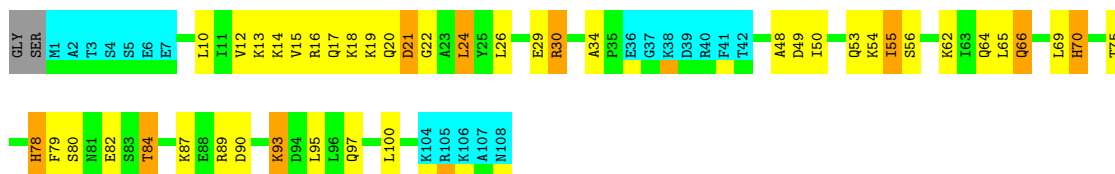
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 6% 10% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

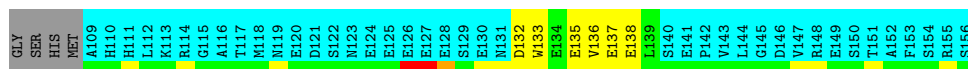
Chain B: 42% 31% 8% 17% .



4.2.3 Score per residue for model 3

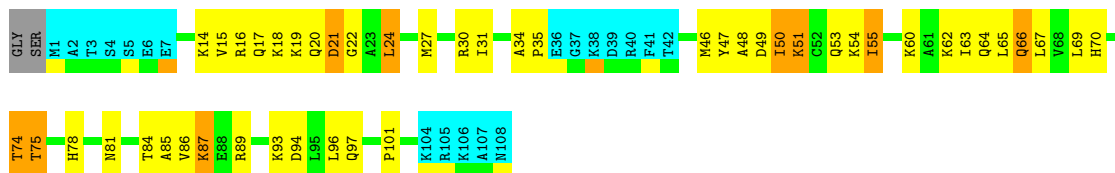
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: . 12% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

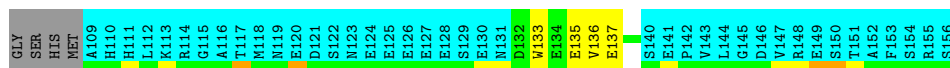
Chain B: 38% 35% 8% 17% .



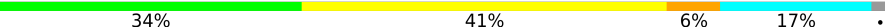
4.2.4 Score per residue for model 4

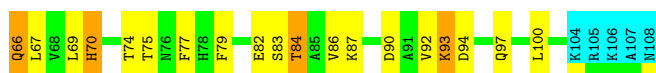
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 



- Molecule 2: General transcription factor IIIH subunit 1

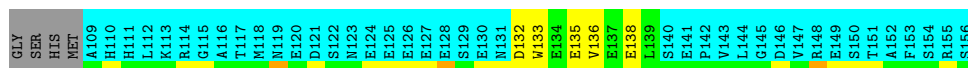
Chain B: 



4.2.5 Score per residue for model 5

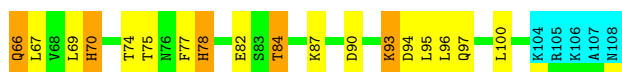
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 



- Molecule 2: General transcription factor IIIH subunit 1

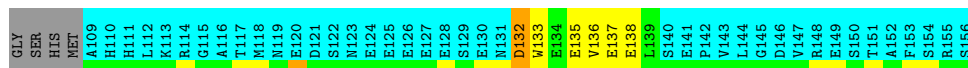
Chain B: 



4.2.6 Score per residue for model 6

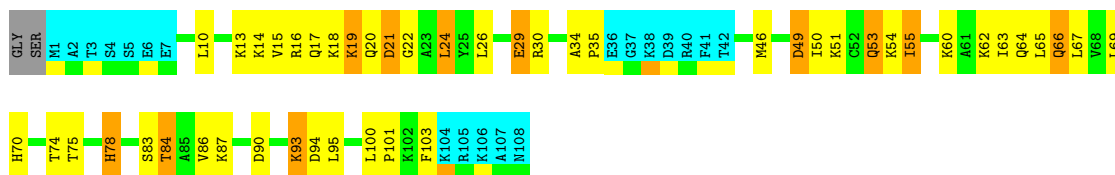
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 



- Molecule 2: General transcription factor IIIH subunit 1

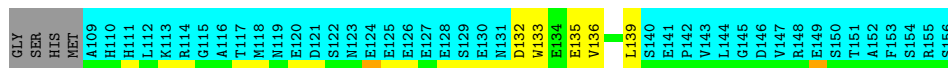
Chain B: 



4.2.7 Score per residue for model 7

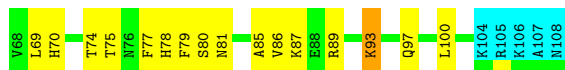
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 6% 10% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

Chain B: 34% 39% 8% 17%



4.2.8 Score per residue for model 8

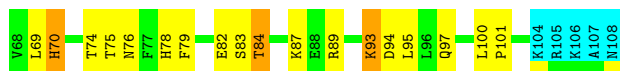
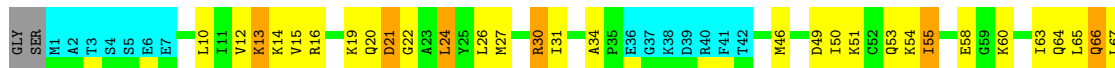
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 6% 8% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

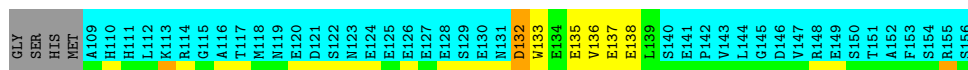
Chain B: 37% 35% 8% 17%



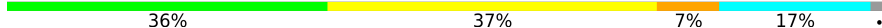
4.2.9 Score per residue for model 9

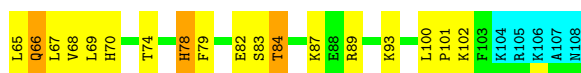
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A:  10% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

Chain B:  36% 37% 7% 17%



4.2.10 Score per residue for model 10

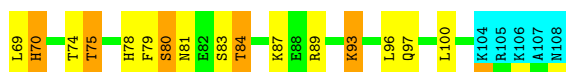
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A:  6% 10% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

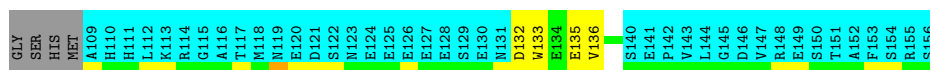
Chain B:  42% 27% 12% 17%



4.2.11 Score per residue for model 11

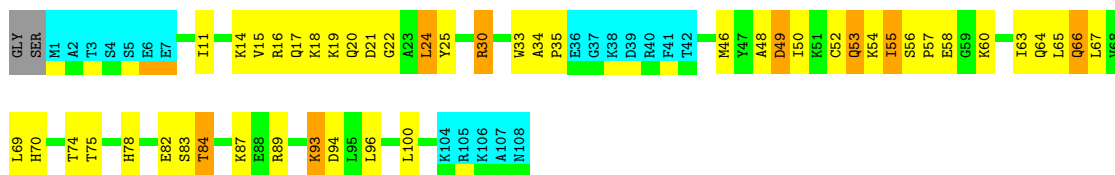
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A:  8% 8% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

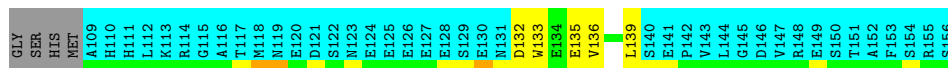
Chain B:  38% 35% 7% 17%



4.2.12 Score per residue for model 12

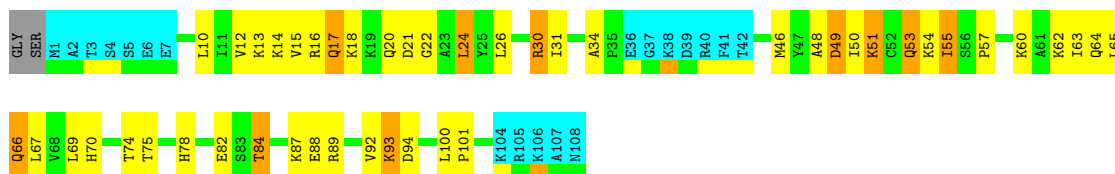
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 6% 10% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

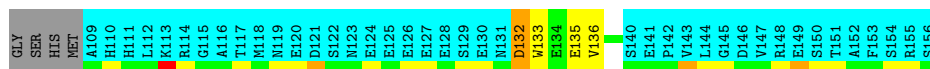
Chain B: 38% 34% 9% 17%



4.2.13 Score per residue for model 13

- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 8% 6% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

Chain B: 35% 40% 6% 17%



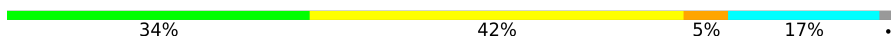
4.2.14 Score per residue for model 14

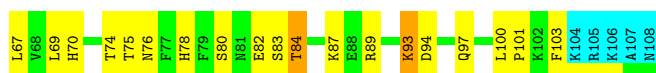
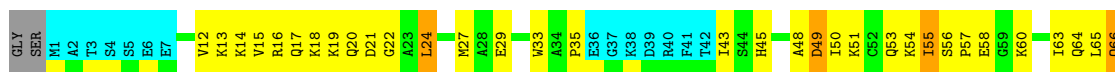
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A:  12% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

Chain B:  34% 42% 5% 17%



4.2.15 Score per residue for model 15

- Molecule 1: DNA repair protein complementing XP-C cells

Chain A:  13% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

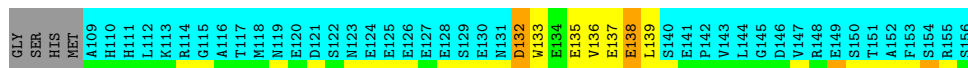
Chain B:  35% 38% 7% 17%



4.2.16 Score per residue for model 16

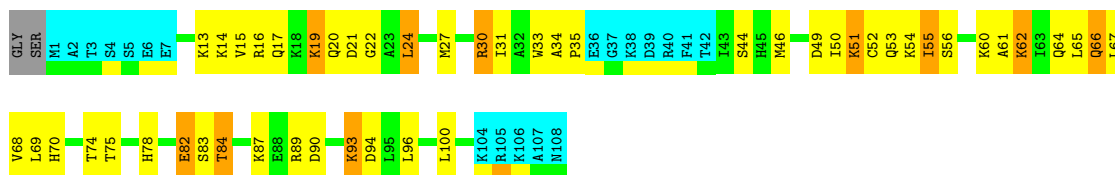
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A:  10% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

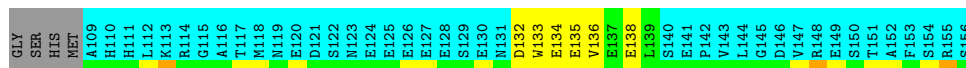
Chain B:  36% 35% 9% 17%



4.2.17 Score per residue for model 17

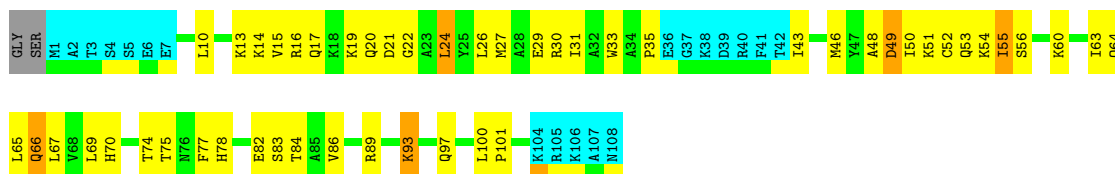
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: . 12% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

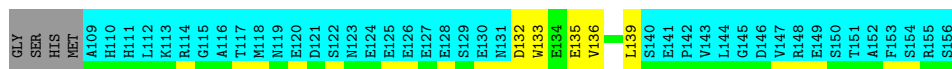
Chain B: 35% 41% 5% 17% .



4.2.18 Score per residue for model 18

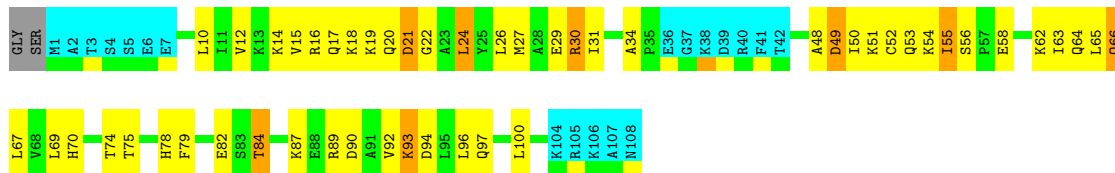
- Molecule 1: DNA repair protein complementing XP-C cells

Chain A: 6% 10% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

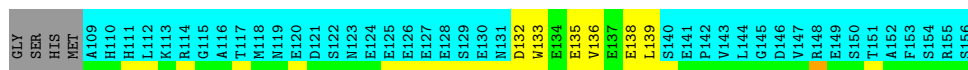
Chain B: 35% 39% 7% 17% .



4.2.19 Score per residue for model 19 (medoid)

- Molecule 1: DNA repair protein complementing XP-C cells

Chain A:  12% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

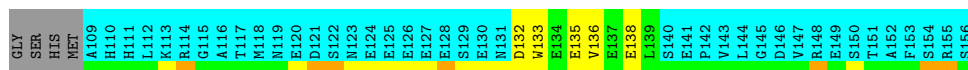
Chain B:  40% 33% 8% 17%



4.2.20 Score per residue for model 20

- Molecule 1: DNA repair protein complementing XP-C cells

Chain A:  6% 10% 77% 8%



- Molecule 2: General transcription factor IIIH subunit 1

Chain B:  32% 42% 7% 17%



5 Refinement protocol and experimental data overview

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
X-PLOR NIH	structure solution	
X-PLOR NIH	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	2
Total number of shifts	1721
Number of shifts mapped to atoms	1721
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	82%

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	73	58	58	12±2
2	B	711	750	750	39±3
All	All	15680	16160	16160	784

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 25.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:64:GLN:HG2	2:B:78:HIS:HA	0.86	1.48	6	19
2:B:22:GLY:HA2	2:B:35:PRO:HA	0.84	1.46	11	9
2:B:50:ILE:HB	2:B:100:LEU:HD21	0.78	1.54	2	16
2:B:55:ILE:HG22	2:B:65:LEU:HD12	0.75	1.59	8	20
1:A:136:VAL:HB	2:B:53:GLN:HG2	0.74	1.58	4	9
2:B:51:LYS:HE3	2:B:52:CYS:SG	0.74	2.23	5	5
2:B:63:ILE:HG22	2:B:89:ARG:HG3	0.74	1.60	14	2
2:B:49:ASP:HA	2:B:70:HIS:NE2	0.73	1.98	18	20
1:A:132:ASP:HB2	2:B:60:LYS:HE2	0.73	1.61	6	5
2:B:63:ILE:HG21	2:B:86:VAL:HA	0.72	1.61	7	5
1:A:136:VAL:HB	2:B:53:GLN:O	0.71	1.85	6	16
2:B:15:VAL:HG21	2:B:24:LEU:HB2	0.70	1.62	2	18
1:A:132:ASP:HB2	2:B:60:LYS:CE	0.67	2.20	7	4

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:86:VAL:HB	2:B:87:LYS:HE2	0.67	1.67	7	1
2:B:16:ARG:HG2	2:B:21:ASP:HA	0.66	1.65	6	7
2:B:50:ILE:HB	2:B:100:LEU:CD2	0.65	2.21	13	18
2:B:56:SER:HB2	2:B:60:LYS:HD2	0.65	1.67	7	3
1:A:132:ASP:O	2:B:57:PRO:HD2	0.65	1.91	10	8
2:B:13:LYS:HA	2:B:13:LYS:HE2	0.64	1.69	12	9
2:B:16:ARG:HA	2:B:20:GLN:O	0.64	1.92	8	20
2:B:67:LEU:O	2:B:74:THR:HA	0.64	1.93	1	19
2:B:22:GLY:CA	2:B:35:PRO:HA	0.63	2.23	11	7
2:B:84:THR:HB	2:B:88:GLU:HG3	0.62	1.69	20	3
2:B:53:GLN:HE21	2:B:97:GLN:HB3	0.62	1.55	2	4
2:B:18:LYS:HA	2:B:18:LYS:HE2	0.61	1.71	10	3
2:B:51:LYS:HB2	2:B:70:HIS:HB3	0.61	1.71	15	8
1:A:136:VAL:HG21	2:B:93:LYS:HG3	0.61	1.71	5	6
2:B:55:ILE:HB	2:B:89:ARG:HD2	0.61	1.71	3	2
1:A:138:GLU:HG2	2:B:100:LEU:HB3	0.61	1.72	6	1
1:A:136:VAL:O	2:B:52:CYS:HB2	0.60	1.97	20	7
2:B:84:THR:HG22	2:B:87:LYS:HD2	0.60	1.71	6	7
2:B:12:VAL:HB	2:B:24:LEU:HB3	0.60	1.73	19	8
2:B:10:LEU:HB3	2:B:26:LEU:HD12	0.59	1.74	1	8
2:B:22:GLY:HA2	2:B:35:PRO:CA	0.59	2.26	11	4
1:A:138:GLU:HB2	2:B:101:PRO:HG3	0.59	1.75	9	1
2:B:63:ILE:HG23	2:B:89:ARG:HD3	0.59	1.73	18	4
2:B:16:ARG:HD2	2:B:21:ASP:HA	0.59	1.75	17	2
2:B:50:ILE:HA	2:B:69:LEU:HD22	0.58	1.74	14	13
1:A:133:TRP:CZ3	2:B:64:GLN:HB2	0.58	2.34	14	15
2:B:65:LEU:HB2	2:B:79:PHE:HE2	0.58	1.59	8	3
1:A:133:TRP:HB2	2:B:54:LYS:CB	0.57	2.29	7	17
2:B:63:ILE:CG2	2:B:89:ARG:HD3	0.57	2.29	20	3
1:A:136:VAL:HG21	2:B:93:LYS:CG	0.57	2.29	7	19
2:B:63:ILE:HG22	2:B:89:ARG:HD3	0.56	1.76	20	2
1:A:132:ASP:HB3	2:B:60:LYS:CE	0.56	2.31	13	7
2:B:31:ILE:HD13	2:B:67:LEU:HD11	0.56	1.76	16	8
2:B:16:ARG:O	2:B:78:HIS:HB3	0.56	2.01	9	12
2:B:84:THR:HA	2:B:87:LYS:HD2	0.55	1.77	20	9
2:B:18:LYS:O	2:B:19:LYS:HB2	0.54	2.02	13	4
2:B:22:GLY:HA3	2:B:33:TRP:CZ2	0.54	2.37	16	10
1:A:137:GLU:HG3	1:A:138:GLU:N	0.54	2.17	16	2
2:B:16:ARG:HG2	2:B:21:ASP:HB3	0.54	1.79	20	1
2:B:63:ILE:HG12	2:B:86:VAL:HG22	0.54	1.80	7	3
2:B:57:PRO:HA	2:B:89:ARG:NH2	0.54	2.18	7	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:30:ARG:CB	2:B:46:MET:HA	0.54	2.33	7	3
2:B:62:LYS:HG3	2:B:64:GLN:NE2	0.53	2.18	12	1
2:B:50:ILE:HG23	2:B:69:LEU:CD2	0.53	2.33	9	17
2:B:87:LYS:N	2:B:87:LYS:HD2	0.53	2.18	3	1
1:A:133:TRP:HB2	2:B:54:LYS:HB3	0.53	1.79	18	17
2:B:96:LEU:O	2:B:100:LEU:HG	0.53	2.04	20	6
2:B:54:LYS:HD2	2:B:66:GLN:OE1	0.53	2.04	18	8
2:B:30:ARG:HB2	2:B:46:MET:HA	0.52	1.82	16	2
2:B:62:LYS:HG3	2:B:64:GLN:OE1	0.52	2.04	3	1
2:B:54:LYS:HB2	2:B:66:GLN:HG2	0.52	1.81	9	11
2:B:14:LYS:NZ	2:B:81:ASN:HA	0.52	2.19	10	1
2:B:26:LEU:HD11	2:B:92:VAL:HG13	0.52	1.81	4	3
2:B:47:TYR:CE2	2:B:96:LEU:HD23	0.52	2.39	19	4
2:B:99:LEU:HA	2:B:102:LYS:HD2	0.51	1.81	20	1
2:B:43:ILE:HG23	2:B:45:HIS:CD2	0.51	2.41	7	4
2:B:30:ARG:HB3	2:B:46:MET:SD	0.51	2.46	10	11
2:B:49:ASP:HA	2:B:70:HIS:CE1	0.51	2.39	14	1
1:A:136:VAL:HG11	2:B:53:GLN:HE21	0.51	1.65	15	1
2:B:12:VAL:HG11	2:B:79:PHE:HE1	0.51	1.65	4	2
2:B:29:GLU:HA	2:B:103:PHE:CZ	0.51	2.41	6	1
2:B:48:ALA:HA	2:B:103:PHE:O	0.50	2.05	1	2
1:A:132:ASP:CB	2:B:60:LYS:HE2	0.50	2.35	6	3
2:B:30:ARG:HB3	2:B:46:MET:HG2	0.50	1.83	8	3
2:B:20:GLN:HG2	2:B:33:TRP:HH2	0.50	1.65	17	2
2:B:62:LYS:HD2	2:B:78:HIS:CE1	0.50	2.41	18	2
2:B:13:LYS:HD2	2:B:13:LYS:H	0.50	1.66	7	1
2:B:16:ARG:NH1	2:B:21:ASP:HB3	0.50	2.21	7	4
1:A:135:GLU:HB3	2:B:54:LYS:HD3	0.49	1.83	13	15
2:B:10:LEU:HB3	2:B:26:LEU:HB2	0.49	1.82	18	4
2:B:47:TYR:HA	2:B:50:ILE:HG12	0.49	1.85	13	1
1:A:133:TRP:HZ3	2:B:65:LEU:N	0.49	2.05	15	7
2:B:53:GLN:NE2	2:B:97:GLN:HB3	0.49	2.23	10	5
2:B:49:ASP:HA	2:B:70:HIS:HE2	0.49	1.67	13	1
1:A:136:VAL:HG13	2:B:97:GLN:NE2	0.49	2.23	14	11
2:B:43:ILE:HG21	2:B:77:PHE:HZ	0.49	1.67	5	4
2:B:55:ILE:HB	2:B:89:ARG:HD3	0.49	1.84	19	2
2:B:66:GLN:O	2:B:66:GLN:HG3	0.49	2.07	7	9
2:B:81:ASN:O	2:B:85:ALA:HB2	0.48	2.09	7	2
2:B:21:ASP:O	2:B:35:PRO:HA	0.48	2.08	7	2
2:B:84:THR:HA	2:B:87:LYS:HD3	0.48	1.84	9	3
1:A:132:ASP:HB3	2:B:60:LYS:HE3	0.48	1.85	17	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:17:GLN:O	2:B:20:GLN:HG2	0.48	2.08	12	2
2:B:53:GLN:OE1	2:B:93:LYS:HA	0.48	2.09	17	6
1:A:134:GLU:HG3	2:B:57:PRO:HD3	0.48	1.84	10	2
1:A:133:TRP:CE3	2:B:56:SER:N	0.48	2.81	13	12
2:B:52:CYS:HB3	2:B:68:VAL:HB	0.47	1.86	16	1
1:A:136:VAL:HB	2:B:53:GLN:HG3	0.47	1.87	5	4
2:B:17:GLN:O	2:B:17:GLN:HG3	0.47	2.10	2	3
2:B:46:MET:HB2	2:B:49:ASP:OD2	0.47	2.10	8	5
2:B:18:LYS:HA	2:B:18:LYS:CE	0.47	2.40	10	1
2:B:62:LYS:HB3	2:B:78:HIS:CD2	0.47	2.44	16	1
2:B:93:LYS:HZ2	2:B:93:LYS:HB3	0.47	1.69	4	5
2:B:64:GLN:HG2	2:B:78:HIS:CA	0.46	2.32	6	1
2:B:50:ILE:O	2:B:100:LEU:HD22	0.46	2.10	20	1
2:B:51:LYS:HE2	2:B:70:HIS:HA	0.46	1.87	3	1
2:B:62:LYS:HB2	2:B:78:HIS:CD2	0.46	2.46	1	1
2:B:13:LYS:N	2:B:13:LYS:HD3	0.46	2.25	8	2
1:A:134:GLU:OE2	2:B:55:ILE:HG13	0.46	2.11	17	1
2:B:26:LEU:HD13	2:B:95:LEU:HD23	0.45	1.88	8	4
2:B:66:GLN:HA	2:B:75:THR:O	0.45	2.10	10	4
2:B:51:LYS:HB2	2:B:70:HIS:CB	0.45	2.41	15	2
1:A:135:GLU:HB3	2:B:54:LYS:CD	0.45	2.41	18	15
2:B:84:THR:HG22	2:B:87:LYS:CD	0.44	2.43	16	5
2:B:16:ARG:HG3	2:B:80:SER:OG	0.44	2.12	2	4
1:A:136:VAL:CG2	2:B:55:ILE:HD13	0.44	2.42	19	3
2:B:11:ILE:HG23	2:B:25:TYR:CE1	0.44	2.47	11	1
2:B:16:ARG:HG2	2:B:21:ASP:CB	0.44	2.42	2	1
2:B:29:GLU:HB2	2:B:30:ARG:NH1	0.44	2.27	2	1
2:B:63:ILE:C	2:B:64:GLN:HG3	0.44	2.32	7	1
2:B:53:GLN:O	2:B:53:GLN:HG2	0.44	2.13	12	2
2:B:12:VAL:HG11	2:B:79:PHE:CE2	0.44	2.48	7	4
2:B:50:ILE:CB	2:B:100:LEU:HD21	0.44	2.37	2	1
1:A:132:ASP:OD1	1:A:132:ASP:N	0.44	2.50	19	1
1:A:133:TRP:CZ2	2:B:66:GLN:HB3	0.43	2.48	4	4
1:A:136:VAL:N	2:B:53:GLN:O	0.43	2.51	4	4
1:A:139:LEU:HB3	2:B:97:GLN:HG3	0.43	1.90	18	2
2:B:69:LEU:N	2:B:69:LEU:HD23	0.43	2.29	8	8
1:A:136:VAL:CB	2:B:53:GLN:O	0.43	2.65	9	1
2:B:64:GLN:NE2	2:B:78:HIS:HB2	0.43	2.29	1	1
2:B:43:ILE:HG23	2:B:45:HIS:NE2	0.43	2.29	14	1
2:B:12:VAL:HA	2:B:88:GLU:OE2	0.43	2.13	15	1
1:A:133:TRP:CE2	2:B:66:GLN:HB3	0.42	2.49	3	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:136:VAL:HB	2:B:53:GLN:CG	0.42	2.37	4	1
2:B:27:MET:HB2	2:B:30:ARG:O	0.42	2.13	5	4
2:B:24:LEU:HD21	2:B:31:ILE:HD11	0.42	1.91	16	1
2:B:61:ALA:C	2:B:62:LYS:HG3	0.42	2.35	16	1
2:B:47:TYR:HB2	2:B:103:PHE:HB2	0.42	1.92	19	1
2:B:56:SER:HB2	2:B:60:LYS:CD	0.42	2.40	7	1
1:A:132:ASP:HB3	2:B:60:LYS:HE2	0.42	1.90	12	1
2:B:63:ILE:HD12	2:B:63:ILE:N	0.42	2.30	13	1
1:A:138:GLU:HB2	2:B:101:PRO:HB3	0.42	1.90	3	2
2:B:30:ARG:HD3	2:B:46:MET:SD	0.42	2.55	3	1
2:B:50:ILE:HG12	2:B:69:LEU:HD22	0.42	1.90	18	3
1:A:133:TRP:CB	2:B:54:LYS:HB2	0.42	2.44	12	1
2:B:30:ARG:HB2	2:B:45:HIS:O	0.42	2.15	13	1
1:A:133:TRP:HZ3	2:B:64:GLN:C	0.41	2.19	13	5
2:B:84:THR:HG22	2:B:87:LYS:HD3	0.41	1.92	11	1
2:B:19:LYS:N	2:B:19:LYS:HD3	0.41	2.29	1	2
2:B:93:LYS:HD2	2:B:93:LYS:C	0.41	2.34	3	1
1:A:133:TRP:HB2	2:B:54:LYS:HB2	0.41	1.92	12	1
1:A:132:ASP:O	2:B:60:LYS:HE2	0.41	2.16	15	1
2:B:31:ILE:HD12	2:B:96:LEU:HD11	0.41	1.91	16	1
2:B:53:GLN:HE22	2:B:93:LYS:HA	0.41	1.75	5	1
1:A:133:TRP:HZ2	2:B:76:ASN:ND2	0.41	2.13	14	1
2:B:53:GLN:OE1	2:B:96:LEU:HB3	0.41	2.16	11	1
2:B:51:LYS:HG3	2:B:70:HIS:HB3	0.41	1.93	9	1
2:B:13:LYS:O	2:B:15:VAL:HG23	0.41	2.15	9	1
1:A:135:GLU:HB3	2:B:54:LYS:CE	0.40	2.46	12	1
2:B:33:TRP:HB3	2:B:43:ILE:HB	0.40	1.93	5	1
1:A:136:VAL:HG21	2:B:93:LYS:CD	0.40	2.46	9	1
2:B:46:MET:O	2:B:50:ILE:HG13	0.40	2.16	19	1
2:B:68:VAL:HA	2:B:74:THR:HG22	0.40	1.94	9	1
2:B:88:GLU:O	2:B:92:VAL:HG23	0.40	2.17	12	1
2:B:30:ARG:HD3	2:B:46:MET:HG2	0.40	1.92	8	1
2:B:87:LYS:N	2:B:87:LYS:HD3	0.40	2.29	13	1
2:B:55:ILE:O	2:B:57:PRO:HD3	0.40	2.15	14	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	8/52 (15%)	6±0 (78±5%)	2±0 (22±5%)	0±0 (1±3%)	29	74
2	B	89/110 (81%)	85±1 (95±1%)	3±1 (3±1%)	1±0 (1±0%)	18	66
All	All	1940/3240 (60%)	1823 (94%)	96 (5%)	21 (1%)	18	66

All 2 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	14	LYS	20
1	A	132	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	8/46 (17%)	7±1 (84±11%)	1±1 (16±11%)	5	43
2	B	77/94 (82%)	62±2 (80±3%)	15±2 (20±3%)	4	34
All	All	1700/2800 (61%)	1372 (81%)	328 (19%)	4	35

All 41 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)
2	B	24	LEU	20
2	B	55	ILE	20
2	B	66	GLN	20
2	B	75	THR	19
2	B	84	THR	19
2	B	93	LYS	18
2	B	21	ASP	16
2	B	82	GLU	16
2	B	17	GLN	15
2	B	19	LYS	15
2	B	30	ARG	14

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
2	B	94	ASP	14
2	B	83	SER	10
2	B	49	ASP	9
1	A	137	GLU	8
2	B	53	GLN	7
2	B	90	ASP	7
2	B	18	LYS	7
2	B	58	GLU	7
2	B	89	ARG	6
1	A	132	ASP	6
2	B	70	HIS	6
2	B	51	LYS	6
2	B	13	LYS	6
1	A	138	GLU	5
1	A	139	LEU	5
2	B	78	HIS	4
2	B	62	LYS	3
2	B	29	GLU	3
2	B	50	ILE	2
2	B	87	LYS	2
2	B	31	ILE	2
2	B	80	SER	2
2	B	44	SER	2
1	A	135	GLU	1
2	B	74	THR	1
2	B	102	LYS	1
2	B	20	GLN	1
2	B	60	LYS	1
2	B	97	GLN	1
2	B	27	MET	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 82% 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	473
Number of shifts mapped to atoms	473
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 \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	48	-0.05 ± 0.05	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	46	0.06 ± 0.06	None needed (< 0.5 ppm)
$^{13}\text{C}'$	45	-0.11 ± 0.05	None needed (< 0.5 ppm)
^{15}N	46	-2.76 ± 0.14	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 7%, i.e. 94 atoms were assigned a chemical shift out of a possible 1386. 0 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	40/482 (8%)	16/194 (8%)	16/194 (8%)	8/94 (9%)
Sidechain	42/811 (5%)	25/527 (5%)	17/255 (7%)	0/29 (0%)

Continued on next page...

Continued from previous page...

	Total	¹ H	¹³ C	¹⁵ N
Aromatic	12/93 (13%)	6/47 (13%)	5/41 (12%)	1/5 (20%)
Overall	94/1386 (7%)	47/768 (6%)	38/490 (8%)	9/128 (7%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 22%, i.e. 473 atoms were assigned a chemical shift out of a possible 2137. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	232/778 (30%)	93/314 (30%)	93/312 (30%)	46/152 (30%)
Sidechain	219/1232 (18%)	129/791 (16%)	87/389 (22%)	3/52 (6%)
Aromatic	22/127 (17%)	11/65 (17%)	10/55 (18%)	1/7 (14%)
Overall	473/2137 (22%)	233/1170 (20%)	190/756 (25%)	50/211 (24%)

7.1.4 Statistically unusual chemical shifts [i](#)

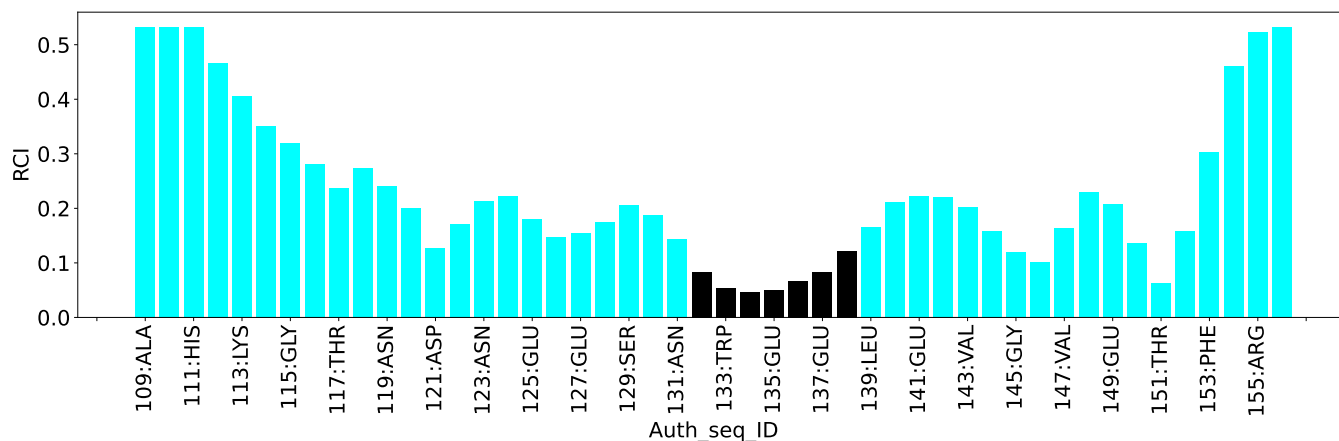
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	151	THR	CB	32.31	61.12 – 78.27	-21.8

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:



7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 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	1248
Number of shifts mapped to atoms	1248
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	108	-0.14 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	104	0.13 ± 0.24	None needed (< 0.5 ppm)
$^{13}\text{C}'$	108	0.17 ± 0.17	None needed (< 0.5 ppm)
^{15}N	104	-1.35 ± 0.43	Should be applied

7.2.3 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 76%, i.e. 1049 atoms were assigned a chemical shift out of a possible 1386. 0 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	442/482 (92%)	178/194 (92%)	178/194 (92%)	86/94 (91%)
Sidechain	560/811 (69%)	339/527 (64%)	212/255 (83%)	9/29 (31%)
Aromatic	47/93 (51%)	24/47 (51%)	22/41 (54%)	1/5 (20%)
Overall	1049/1386 (76%)	541/768 (70%)	412/490 (84%)	96/128 (75%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 58%, i.e. 1248 atoms were assigned a chemical shift out of a possible 2137. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	536/778 (69%)	216/314 (69%)	216/312 (69%)	104/152 (68%)
Sidechain	659/1232 (53%)	400/791 (51%)	249/389 (64%)	10/52 (19%)
Aromatic	53/127 (42%)	27/65 (42%)	25/55 (45%)	1/7 (14%)
Overall	1248/2137 (58%)	643/1170 (55%)	490/756 (65%)	115/211 (55%)

7.2.4 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
2	B	66	GLN	HB2	0.36	0.80 – 3.29	-6.8
2	B	17	GLN	HB2	0.43	0.80 – 3.29	-6.5
2	B	17	GLN	HB3	0.40	0.71 – 3.33	-6.2
2	B	64	GLN	HA	6.44	2.17 – 6.35	5.2
2	B	64	GLN	CB	38.11	20.34 – 37.98	5.1

7.2.5 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 B:

