



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 02:02 AM BST

PDB ID : 2LU5
Title : Structure and chemical shifts of Cu(I),Zn(II) superoxide dismutase by solid-state NMR
Authors : Knight, M.J.; Pell, A.J.; Bertini, I.; Felli, I.C.; Gonnelli, L.; Pierattelli, R.; Herrmann, T.; Emsley, L.; Pintacuda, G.
Deposited on : 2012-06-08

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
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

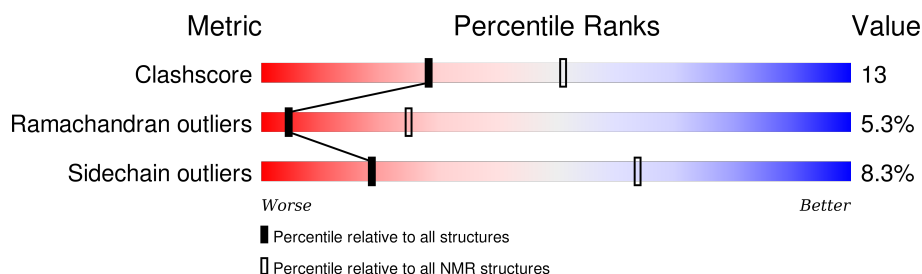
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLID-STATE NMR

The overall completeness of chemical shifts assignment is 30%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	153	

2 Ensemble composition and analysis

This entry contains 19 models. Model 14 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 target function*.

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:80, A:84-A:153 (150)	1.18	14

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 12 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2195 atoms, of which 1085 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Superoxide dismutase [Cu-Zn].

Mol	Chain	Residues	Atoms						Trace
1	A	153	Total	C	H	N	O	S	0
			2194	679	1085	203	225	2	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	ALA	CYS	ENGINEERED MUTATION	UNP P00441
A	111	SER	CYS	ENGINEERED MUTATION	UNP P00441

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

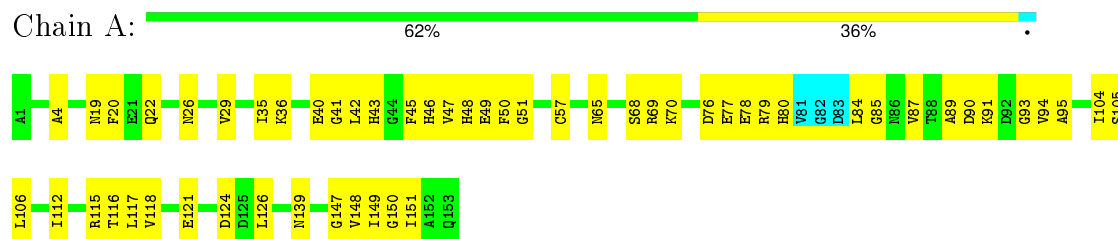
Mol	Chain	Residues	Atoms	
2	A	1	Total	Cu
			1	1

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: Superoxide dismutase [Cu-Zn]

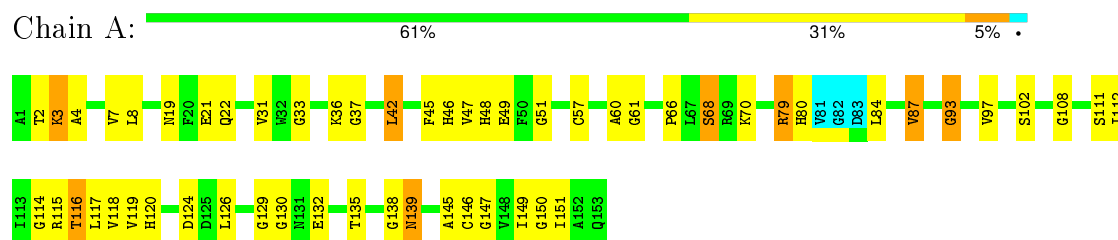


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

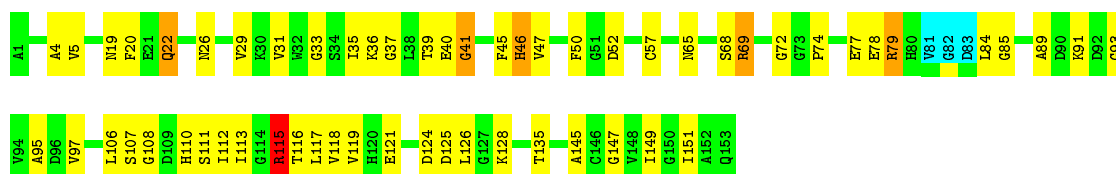
- Molecule 1: Superoxide dismutase [Cu-Zn]



4.2.2 Score per residue for model 2

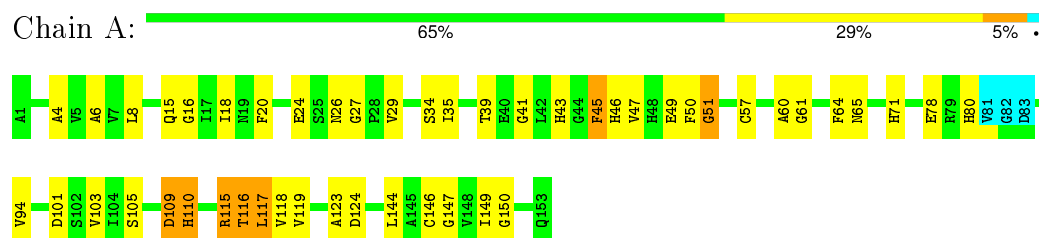
- Molecule 1: Superoxide dismutase [Cu-Zn]





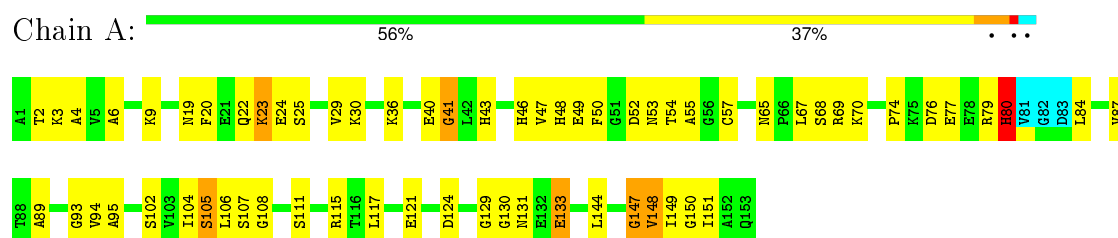
4.2.3 Score per residue for model 3

- Molecule 1: Superoxide dismutase [Cu-Zn]



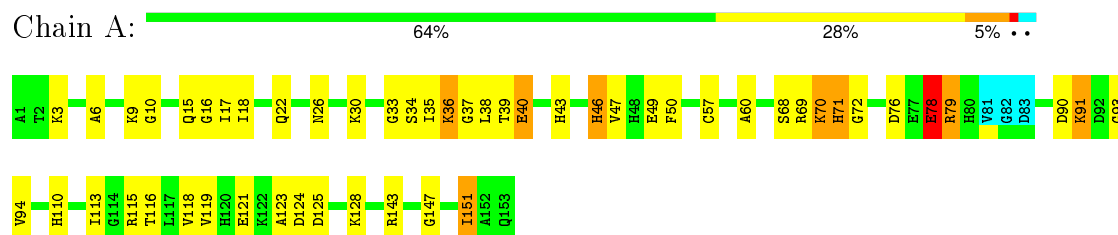
4.2.4 Score per residue for model 4

- Molecule 1: Superoxide dismutase [Cu-Zn]



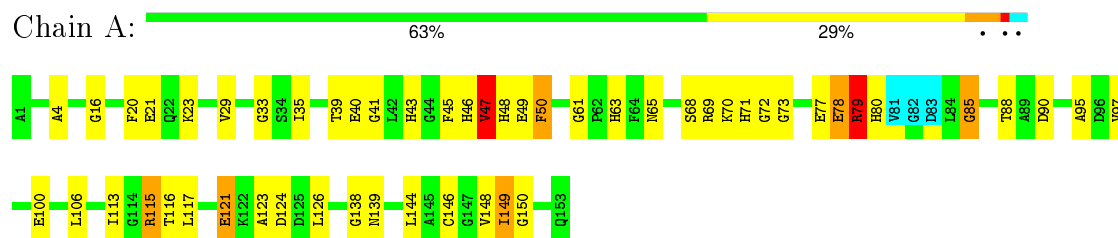
4.2.5 Score per residue for model 5

- Molecule 1: Superoxide dismutase [Cu-Zn]



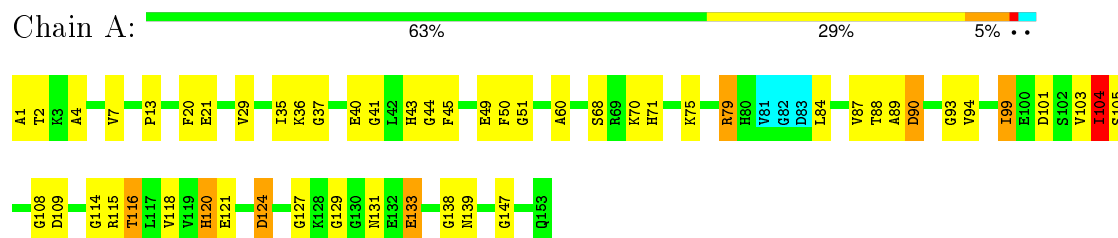
4.2.6 Score per residue for model 6

- Molecule 1: Superoxide dismutase [Cu-Zn]



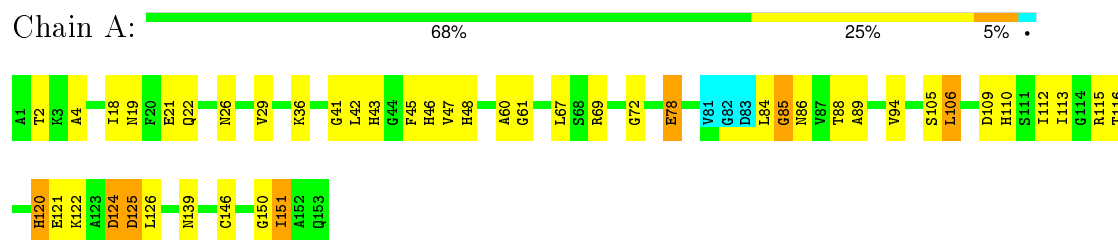
4.2.7 Score per residue for model 7

- Molecule 1: Superoxide dismutase [Cu-Zn]



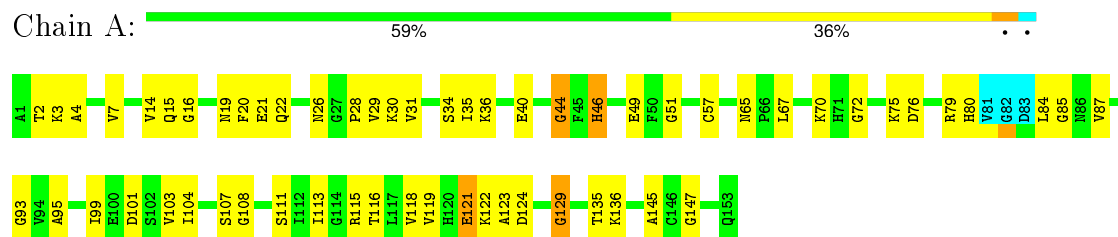
4.2.8 Score per residue for model 8

- Molecule 1: Superoxide dismutase [Cu-Zn]



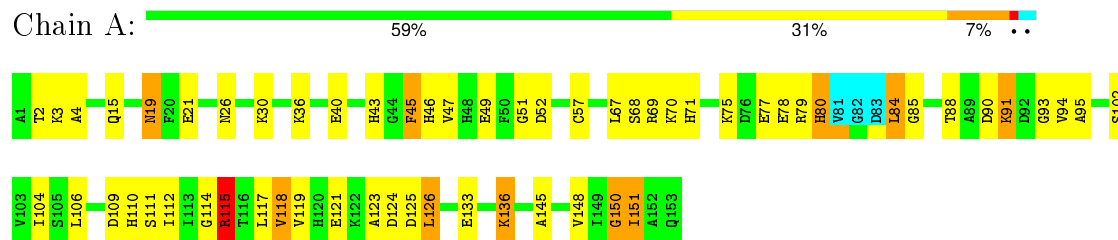
4.2.9 Score per residue for model 9

- Molecule 1: Superoxide dismutase [Cu-Zn]



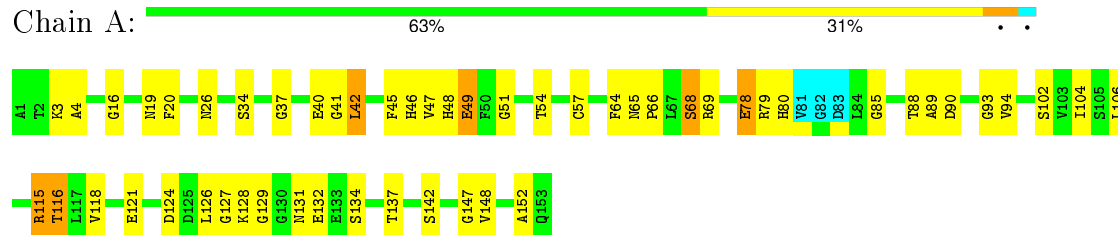
4.2.10 Score per residue for model 10

- Molecule 1: Superoxide dismutase [Cu-Zn]



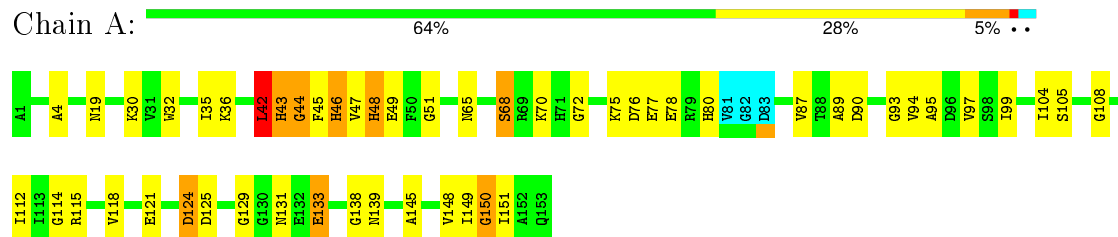
4.2.11 Score per residue for model 11

- Molecule 1: Superoxide dismutase [Cu-Zn]



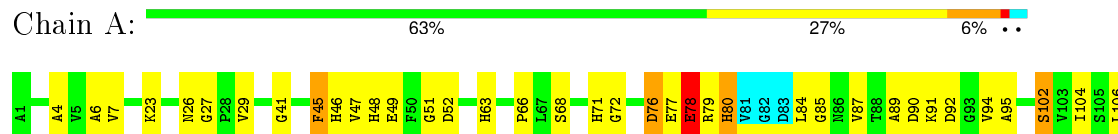
4.2.12 Score per residue for model 12

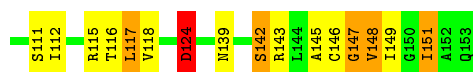
- Molecule 1: Superoxide dismutase [Cu-Zn]



4.2.13 Score per residue for model 13

- Molecule 1: Superoxide dismutase [Cu-Zn]

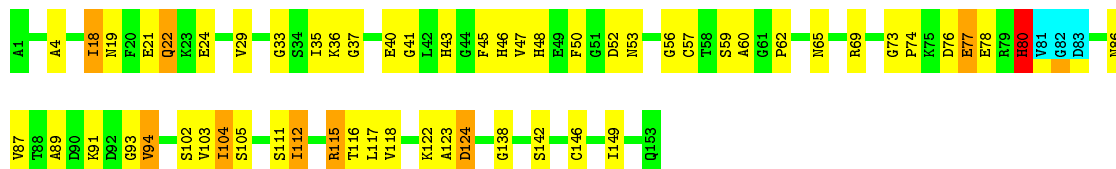




4.2.14 Score per residue for model 14 (medoid)

- Molecule 1: Superoxide dismutase [Cu-Zn]

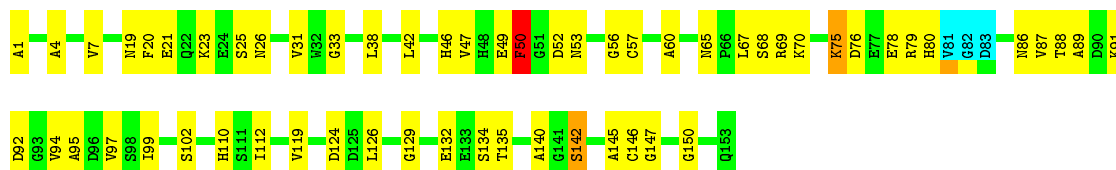
Chain A: 61% 31% 5% ..



4.2.15 Score per residue for model 15

- Molecule 1: Superoxide dismutase [Cu-Zn]

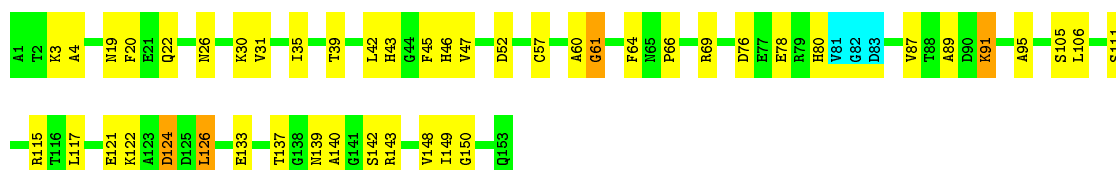
Chain A: 60% 36% ...



4.2.16 Score per residue for model 16

- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain A: 67% 28% ..

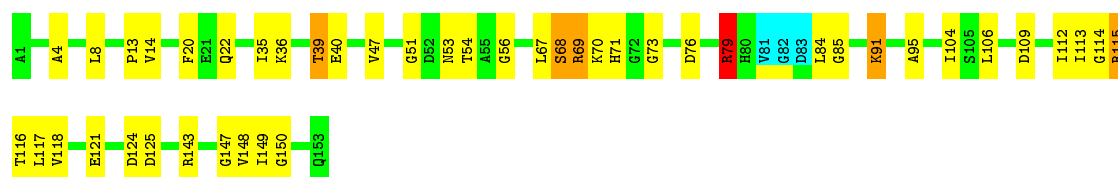


4.2.17 Score per residue for model 17

- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain A: 69% 25% ...

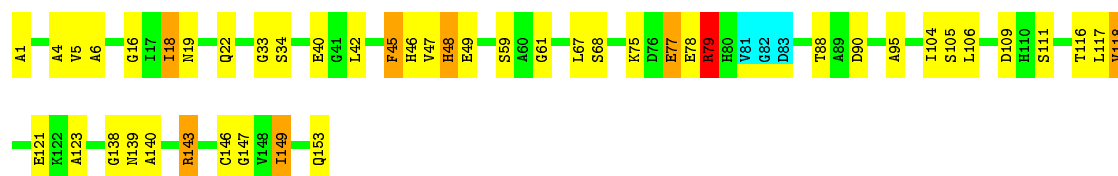




4.2.18 Score per residue for model 18

- Molecule 1: Superoxide dismutase [Cu-Zn]

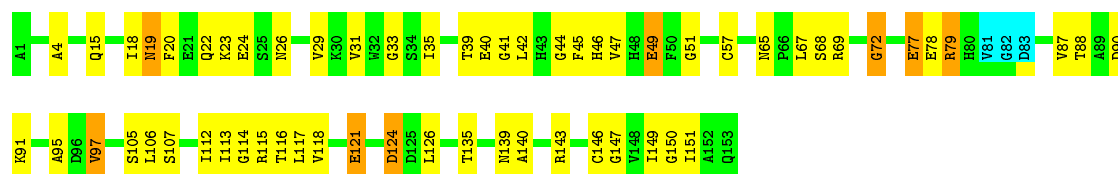
Chain A: 68% 25% 5% ..



4.2.19 Score per residue for model 19

- Molecule 1: Superoxide dismutase [Cu-Zn]

Chain A: 59% 34% 5% .



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 80 calculated structures, 19 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
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)	2lu5_cs.str
Number of chemical shift lists	1
Total number of shifts	517
Number of shifts mapped to atoms	517
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	30%

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.14±0.04	3±2/1108 (0.3±0.1%)	0.93±0.03	3±1/1493 (0.2±0.1%)
All	All	1.14	53/21052 (0.3%)	0.93	48/28367 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.3±0.6
All	All	0	6

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	138	GLY	C-O	9.85	1.39	1.23	18	2
1	A	118	VAL	C-O	7.93	1.38	1.23	18	5
1	A	45	PHE	C-O	6.48	1.35	1.23	18	3
1	A	108	GLY	N-CA	-6.38	1.36	1.46	4	2
1	A	150	GLY	N-CA	-6.37	1.36	1.46	12	4
1	A	150	GLY	CA-C	-6.19	1.42	1.51	16	5
1	A	46	HIS	C-O	5.90	1.34	1.23	9	3
1	A	105	SER	C-N	-5.73	1.20	1.34	18	2
1	A	37	GLY	N-CA	-5.71	1.37	1.46	5	1
1	A	106	LEU	N-CA	-5.64	1.35	1.46	8	2
1	A	139	ASN	C-O	5.62	1.34	1.23	7	3
1	A	108	GLY	CA-C	-5.55	1.43	1.51	7	1
1	A	78	GLU	CD-OE2	-5.47	1.19	1.25	13	1
1	A	145	ALA	N-CA	-5.46	1.35	1.46	13	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	107	SER	N-CA	-5.45	1.35	1.46	9	2
1	A	114	GLY	N-CA	-5.39	1.38	1.46	7	1
1	A	90	ASP	C-N	-5.38	1.21	1.34	7	1
1	A	105	SER	N-CA	-5.37	1.35	1.46	4	1
1	A	41	GLY	N-CA	-5.34	1.38	1.46	2	1
1	A	106	LEU	C-N	-5.33	1.21	1.34	8	1
1	A	114	GLY	CA-C	-5.32	1.43	1.51	7	1
1	A	140	ALA	C-O	5.31	1.33	1.23	15	1
1	A	68	SER	N-CA	-5.15	1.36	1.46	11	1
1	A	40	GLU	C-N	-5.15	1.23	1.33	2	1
1	A	124	ASP	CB-CG	5.14	1.62	1.51	13	1
1	A	85	GLY	N-CA	-5.13	1.38	1.46	17	1
1	A	147	GLY	N-CA	-5.12	1.38	1.46	2	1
1	A	115	ARG	NE-CZ	5.08	1.39	1.33	10	1
1	A	107	SER	C-N	-5.08	1.24	1.33	2	1
1	A	79	ARG	N-CA	-5.06	1.36	1.46	17	1
1	A	68	SER	CA-CB	-5.00	1.45	1.52	12	1

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	124	ASP	CB-CG-OD1	10.70	127.93	118.30	12	17
1	A	124	ASP	CB-CG-OD2	8.81	126.23	118.30	16	14
1	A	124	ASP	OD1-CG-OD2	-8.03	108.04	123.30	13	17

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	115	ARG	Sidechain	2
1	A	69	ARG	Sidechain	1
1	A	80	HIS	Peptide	1
1	A	45	PHE	Mainchain	1
1	A	79	ARG	Sidechain	1

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	1090	1069	1061	27±5
All	All	20729	20311	20157	512

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 13.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:116:THR:HB	1:A:146:CYS:SG	0.77	2.19	6	3
1:A:60:ALA:HB2	1:A:116:THR:HB	0.76	1.57	7	1
1:A:87:VAL:HB	1:A:95:ALA:HB1	0.75	1.58	9	4
1:A:57:CYS:SG	1:A:143:ARG:HA	0.73	2.22	19	3
1:A:67:LEU:O	1:A:78:GLU:HA	0.71	1.86	10	1
1:A:41:GLY:HA3	1:A:89:ALA:O	0.70	1.86	13	5
1:A:57:CYS:SG	1:A:118:VAL:HG21	0.70	2.26	10	1
1:A:4:ALA:HB3	1:A:20:PHE:H	0.70	1.45	3	10
1:A:115:ARG:HD3	1:A:149:ILE:O	0.69	1.86	6	2
1:A:116:THR:HA	1:A:147:GLY:O	0.68	1.89	5	8
1:A:51:GLY:HA2	1:A:114:GLY:O	0.66	1.91	17	4
1:A:35:ILE:O	1:A:94:VAL:HA	0.65	1.92	5	4
1:A:36:LYS:HA	1:A:93:GLY:O	0.64	1.92	10	8
1:A:37:GLY:O	1:A:93:GLY:HA3	0.64	1.92	11	5
1:A:75:LYS:O	1:A:102:SER:HA	0.63	1.94	15	1
1:A:4:ALA:O	1:A:19:ASN:HA	0.63	1.94	8	9
1:A:110:HIS:HA	1:A:115:ARG:NE	0.63	2.08	10	1
1:A:143:ARG:HA	1:A:146:CYS:SG	0.62	2.35	18	1
1:A:43:HIS:O	1:A:123:ALA:HA	0.62	1.94	3	5
1:A:115:ARG:NH1	1:A:148:VAL:HB	0.62	2.10	6	1
1:A:67:LEU:O	1:A:79:ARG:HA	0.61	1.95	18	2
1:A:46:HIS:HB2	1:A:124:ASP:OD1	0.61	1.95	14	1
1:A:78:GLU:O	1:A:79:ARG:HG2	0.60	1.95	2	1
1:A:51:GLY:HA3	1:A:114:GLY:O	0.60	1.95	10	1
1:A:33:GLY:O	1:A:97:VAL:HB	0.60	1.97	1	2
1:A:48:HIS:CE1	1:A:60:ALA:HB3	0.60	2.31	8	1
1:A:117:LEU:HB3	1:A:149:ILE:HG21	0.60	1.74	17	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:68:SER:OG	1:A:76:ASP:HA	0.60	1.97	12	1
1:A:117:LEU:HD22	1:A:149:ILE:HB	0.59	1.72	16	1
1:A:87:VAL:HG22	1:A:95:ALA:HB1	0.59	1.73	15	1
1:A:40:GLU:HB3	1:A:90:ASP:C	0.59	2.18	10	2
1:A:57:CYS:HB2	1:A:60:ALA:HB3	0.59	1.73	16	3
1:A:39:THR:OG1	1:A:91:LYS:HA	0.59	1.97	17	2
1:A:68:SER:HA	1:A:79:ARG:O	0.59	1.98	1	4
1:A:79:ARG:HA	1:A:79:ARG:NE	0.59	2.13	13	1
1:A:46:HIS:CE1	1:A:85:GLY:HA3	0.58	2.34	6	1
1:A:72:GLY:HA3	1:A:80:HIS:C	0.58	2.19	6	1
1:A:118:VAL:HA	1:A:146:CYS:HB3	0.58	1.74	13	1
1:A:22:GLN:HG2	1:A:105:SER:O	0.57	1.99	16	1
1:A:46:HIS:HA	1:A:118:VAL:O	0.57	2.00	5	1
1:A:119:VAL:O	1:A:145:ALA:HB3	0.57	1.99	1	5
1:A:115:ARG:HD3	1:A:116:THR:N	0.57	2.15	11	1
1:A:115:ARG:O	1:A:115:ARG:HD2	0.57	2.00	6	1
1:A:115:ARG:O	1:A:148:VAL:HA	0.57	1.99	16	3
1:A:88:THR:O	1:A:95:ALA:HA	0.57	2.00	15	5
1:A:129:GLY:HA2	1:A:134:SER:O	0.57	2.00	15	1
1:A:47:VAL:HB	1:A:49:GLU:OE2	0.57	2.00	12	1
1:A:53:ASN:HB3	1:A:56:GLY:O	0.56	2.01	17	3
1:A:48:HIS:ND1	1:A:60:ALA:HB3	0.56	2.14	8	1
1:A:112:ILE:HG13	1:A:151:ILE:O	0.56	2.00	2	1
1:A:51:GLY:H	1:A:115:ARG:HD3	0.56	1.60	10	1
1:A:112:ILE:O	1:A:150:GLY:HA2	0.56	2.00	8	3
1:A:29:VAL:HG12	1:A:31:VAL:HG13	0.55	1.76	19	1
1:A:9:LYS:O	1:A:55:ALA:HA	0.55	2.01	4	1
1:A:7:VAL:O	1:A:147:GLY:HA3	0.55	2.01	7	4
1:A:48:HIS:CG	1:A:60:ALA:HB3	0.55	2.36	8	1
1:A:111:SER:HB3	1:A:115:ARG:CZ	0.55	2.31	1	1
1:A:2:THR:O	1:A:3:LYS:HD2	0.55	2.02	4	1
1:A:124:ASP:HA	1:A:139:ASN:O	0.55	2.02	8	1
1:A:131:ASN:HB3	1:A:133:GLU:OE1	0.55	2.02	7	3
1:A:18:ILE:HG22	1:A:33:GLY:HA3	0.55	1.78	14	2
1:A:48:HIS:HB2	1:A:116:THR:O	0.54	2.02	13	1
1:A:115:ARG:O	1:A:149:ILE:HG12	0.54	2.01	1	1
1:A:2:THR:O	1:A:21:GLU:HB3	0.54	2.02	1	2
1:A:68:SER:HA	1:A:79:ARG:HB2	0.54	1.76	18	1
1:A:43:HIS:HA	1:A:87:VAL:O	0.54	2.01	14	1
1:A:3:LYS:HG3	1:A:152:ALA:O	0.54	2.02	11	1
1:A:60:ALA:HB2	1:A:116:THR:CB	0.54	2.30	7	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:131:ASN:N	1:A:134:SER:HB2	0.54	2.17	11	1
1:A:115:ARG:O	1:A:149:ILE:HB	0.54	2.02	4	1
1:A:29:VAL:HG11	1:A:103:VAL:HG12	0.54	1.79	14	1
1:A:22:GLN:HG3	1:A:106:LEU:HB3	0.54	1.78	2	1
1:A:68:SER:HA	1:A:78:GLU:OE1	0.54	2.03	13	1
1:A:65:ASN:OD1	1:A:66:PRO:HD2	0.54	2.03	11	1
1:A:27:GLY:O	1:A:102:SER:HB3	0.54	2.02	13	1
1:A:111:SER:O	1:A:115:ARG:HD3	0.54	2.03	16	1
1:A:64:PHE:O	1:A:66:PRO:HD3	0.53	2.03	16	1
1:A:68:SER:O	1:A:80:HIS:HA	0.53	2.03	10	1
1:A:68:SER:HB2	1:A:79:ARG:O	0.53	2.02	5	1
1:A:45:PHE:CG	1:A:124:ASP:HB3	0.53	2.39	13	1
1:A:115:ARG:NH2	1:A:148:VAL:HG13	0.53	2.18	17	1
1:A:115:ARG:N	1:A:115:ARG:HD2	0.53	2.19	1	1
1:A:128:LYS:HD3	1:A:128:LYS:O	0.53	2.04	5	1
1:A:45:PHE:CE1	1:A:47:VAL:HB	0.53	2.39	2	1
1:A:57:CYS:SG	1:A:118:VAL:HG22	0.53	2.43	9	3
1:A:125:ASP:HB3	1:A:128:LYS:HB3	0.53	1.79	5	1
1:A:46:HIS:CB	1:A:119:VAL:HA	0.53	2.33	15	1
1:A:44:GLY:HA2	1:A:87:VAL:N	0.53	2.19	12	1
1:A:2:THR:O	1:A:21:GLU:HA	0.53	2.03	8	1
1:A:33:GLY:H	1:A:97:VAL:HG11	0.53	1.63	6	2
1:A:19:ASN:O	1:A:31:VAL:HB	0.52	2.03	16	2
1:A:15:GLN:O	1:A:35:ILE:HA	0.52	2.03	5	2
1:A:16:GLY:HA2	1:A:34:SER:O	0.52	2.04	5	3
1:A:76:ASP:HA	1:A:80:HIS:CG	0.52	2.39	16	1
1:A:1:ALA:HA	1:A:22:GLN:O	0.52	2.05	18	1
1:A:7:VAL:N	1:A:148:VAL:HG11	0.52	2.20	13	1
1:A:77:GLU:O	1:A:78:GLU:HB3	0.52	2.04	12	1
1:A:35:ILE:HB	1:A:95:ALA:HB3	0.52	1.81	17	1
1:A:61:GLY:HA2	1:A:142:SER:HB3	0.52	1.82	16	1
1:A:57:CYS:SG	1:A:142:SER:HA	0.52	2.45	15	2
1:A:5:VAL:HA	1:A:18:ILE:O	0.52	2.05	18	1
1:A:47:VAL:CB	1:A:117:LEU:HD23	0.52	2.35	16	1
1:A:6:ALA:HB2	1:A:149:ILE:HA	0.51	1.82	18	1
1:A:57:CYS:SG	1:A:116:THR:HB	0.51	2.45	2	1
1:A:6:ALA:HB3	1:A:18:ILE:H	0.51	1.64	5	2
1:A:22:GLN:HE21	1:A:106:LEU:HG	0.51	1.65	19	1
1:A:45:PHE:O	1:A:124:ASP:HB3	0.51	2.05	7	1
1:A:42:LEU:HD23	1:A:43:HIS:N	0.51	2.21	16	1
1:A:20:PHE:CE1	1:A:106:LEU:HG	0.51	2.40	4	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:42:LEU:HG	1:A:120:HIS:O	0.51	2.06	1	1
1:A:112:ILE:HD13	1:A:112:ILE:H	0.51	1.66	14	1
1:A:69:ARG:N	1:A:79:ARG:HB2	0.51	2.21	17	1
1:A:42:LEU:HD22	1:A:87:VAL:HB	0.51	1.82	16	1
1:A:6:ALA:HA	1:A:148:VAL:O	0.51	2.06	4	1
1:A:80:HIS:NE2	1:A:105:SER:HB2	0.51	2.20	14	1
1:A:87:VAL:CB	1:A:95:ALA:HB1	0.51	2.35	9	1
1:A:51:GLY:HA2	1:A:115:ARG:N	0.51	2.21	7	1
1:A:6:ALA:HA	1:A:148:VAL:HG21	0.51	1.83	13	1
1:A:68:SER:HA	1:A:77:GLU:OE1	0.51	2.06	19	1
1:A:42:LEU:HB2	1:A:123:ALA:HB2	0.50	1.84	18	1
1:A:118:VAL:HA	1:A:146:CYS:CB	0.50	2.36	13	1
1:A:49:GLU:HA	1:A:49:GLU:OE1	0.50	2.04	19	1
1:A:73:GLY:O	1:A:77:GLU:HG3	0.50	2.07	14	1
1:A:69:ARG:O	1:A:70:LYS:HB2	0.50	2.06	5	1
1:A:113:ILE:HA	1:A:150:GLY:HA3	0.50	1.83	19	1
1:A:51:GLY:N	1:A:115:ARG:HD3	0.50	2.22	19	2
1:A:84:LEU:HD23	1:A:85:GLY:N	0.50	2.21	13	2
1:A:72:GLY:HA3	1:A:80:HIS:O	0.50	2.07	12	1
1:A:46:HIS:CD2	1:A:117:LEU:HD12	0.50	2.41	3	1
1:A:49:GLU:N	1:A:115:ARG:HD2	0.49	2.22	11	1
1:A:89:ALA:HA	1:A:94:VAL:O	0.49	2.07	3	2
1:A:67:LEU:O	1:A:78:GLU:HB3	0.49	2.07	19	1
1:A:113:ILE:HA	1:A:115:ARG:NH1	0.49	2.22	17	1
1:A:45:PHE:CG	1:A:84:LEU:HB3	0.49	2.42	8	1
1:A:69:ARG:HB2	1:A:78:GLU:HA	0.49	1.83	11	1
1:A:9:LYS:HD3	1:A:10:GLY:N	0.49	2.21	5	1
1:A:129:GLY:CA	1:A:135:THR:HA	0.49	2.36	15	1
1:A:80:HIS:CD2	1:A:126:LEU:HG	0.49	2.42	10	1
1:A:46:HIS:CD2	1:A:126:LEU:HB2	0.49	2.43	19	1
1:A:84:LEU:HD23	1:A:85:GLY:H	0.49	1.68	13	1
1:A:49:GLU:CD	1:A:65:ASN:HB3	0.49	2.27	4	1
1:A:29:VAL:HG12	1:A:104:ILE:HG23	0.49	1.83	7	1
1:A:16:GLY:HA3	1:A:34:SER:O	0.49	2.07	9	2
1:A:70:LYS:CB	1:A:79:ARG:HB2	0.49	2.38	15	1
1:A:99:ILE:H	1:A:99:ILE:HD13	0.49	1.67	7	1
1:A:121:GLU:O	1:A:122:LYS:HG2	0.49	2.08	8	1
1:A:66:PRO:O	1:A:70:LYS:HA	0.48	2.08	1	1
1:A:38:LEU:HA	1:A:92:ASP:OD1	0.48	2.08	15	1
1:A:40:GLU:HG3	1:A:121:GLU:O	0.48	2.08	11	1
1:A:3:LYS:O	1:A:151:ILE:HG12	0.48	2.08	10	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:GLN:HG3	1:A:105:SER:C	0.48	2.29	19	1
1:A:48:HIS:O	1:A:115:ARG:HG3	0.48	2.09	8	1
1:A:49:GLU:HG3	1:A:109:ASP:OD1	0.48	2.09	10	1
1:A:51:GLY:HA2	1:A:115:ARG:HA	0.48	1.86	11	4
1:A:2:THR:C	1:A:21:GLU:HG3	0.48	2.28	9	1
1:A:49:GLU:HB3	1:A:109:ASP:OD2	0.48	2.08	3	1
1:A:124:ASP:OD2	1:A:140:ALA:HB2	0.48	2.09	19	1
1:A:117:LEU:HD22	1:A:148:VAL:O	0.48	2.09	13	1
1:A:57:CYS:SG	1:A:118:VAL:HB	0.48	2.49	11	1
1:A:39:THR:HB	1:A:90:ASP:O	0.48	2.09	6	1
1:A:45:PHE:O	1:A:47:VAL:HG12	0.48	2.09	3	1
1:A:22:GLN:CG	1:A:106:LEU:HB3	0.48	2.38	2	1
1:A:19:ASN:O	1:A:31:VAL:HA	0.47	2.09	1	3
1:A:24:GLU:H	1:A:24:GLU:CD	0.47	2.13	14	2
1:A:40:GLU:O	1:A:90:ASP:HA	0.47	2.09	11	1
1:A:51:GLY:HA3	1:A:115:ARG:HA	0.47	1.86	13	1
1:A:45:PHE:HB3	1:A:85:GLY:C	0.47	2.28	2	1
1:A:75:LYS:O	1:A:104:ILE:HG13	0.47	2.09	12	1
1:A:21:GLU:O	1:A:29:VAL:HG23	0.47	2.09	6	1
1:A:65:ASN:O	1:A:70:LYS:HA	0.47	2.09	6	2
1:A:33:GLY:O	1:A:97:VAL:HG22	0.47	2.09	19	1
1:A:69:ARG:HA	1:A:78:GLU:HA	0.47	1.86	8	1
1:A:110:HIS:HB3	1:A:113:ILE:O	0.47	2.10	2	2
1:A:68:SER:HA	1:A:80:HIS:HB3	0.47	1.87	4	1
1:A:111:SER:O	1:A:115:ARG:HG3	0.47	2.09	9	1
1:A:86:ASN:O	1:A:97:VAL:HA	0.47	2.10	15	1
1:A:35:ILE:HG22	1:A:95:ALA:HB2	0.47	1.87	2	1
1:A:117:LEU:HB3	1:A:149:ILE:CD1	0.47	2.40	13	1
1:A:28:PRO:HB3	1:A:101:ASP:N	0.47	2.24	9	1
1:A:46:HIS:CB	1:A:119:VAL:HB	0.47	2.39	5	1
1:A:75:LYS:C	1:A:105:SER:HB3	0.46	2.31	12	1
1:A:22:GLN:HA	1:A:104:ILE:O	0.46	2.10	14	1
1:A:44:GLY:HA2	1:A:85:GLY:O	0.46	2.10	9	1
1:A:67:LEU:C	1:A:79:ARG:HB2	0.46	2.31	19	1
1:A:57:CYS:O	1:A:142:SER:HB2	0.46	2.10	14	1
1:A:45:PHE:HA	1:A:85:GLY:O	0.46	2.09	11	1
1:A:40:GLU:O	1:A:121:GLU:HB3	0.46	2.09	4	4
1:A:117:LEU:HD13	1:A:149:ILE:HB	0.46	1.87	16	1
1:A:112:ILE:HG22	1:A:150:GLY:HA2	0.46	1.88	15	1
1:A:112:ILE:O	1:A:115:ARG:HG2	0.46	2.10	19	1
1:A:89:ALA:HB3	1:A:121:GLU:HG2	0.46	1.88	11	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:50:PHE:CD2	1:A:59:SER:HB3	0.46	2.45	14	1
1:A:21:GLU:O	1:A:29:VAL:HB	0.46	2.10	9	1
1:A:77:GLU:HB2	1:A:79:ARG:HD2	0.46	1.86	18	1
1:A:40:GLU:OE2	1:A:122:LYS:HG2	0.46	2.09	14	1
1:A:84:LEU:HD13	1:A:85:GLY:N	0.46	2.26	10	1
1:A:69:ARG:CB	1:A:78:GLU:HA	0.46	2.41	11	1
1:A:115:ARG:HD3	1:A:149:ILE:C	0.46	2.31	6	2
1:A:14:VAL:HA	1:A:36:LYS:O	0.46	2.11	9	2
1:A:35:ILE:H	1:A:95:ALA:HB3	0.46	1.70	16	1
1:A:116:THR:HB	1:A:147:GLY:HA2	0.45	1.88	13	1
1:A:22:GLN:NE2	1:A:106:LEU:HG	0.45	2.26	19	1
1:A:42:LEU:HA	1:A:87:VAL:O	0.45	2.11	19	1
1:A:69:ARG:C	1:A:78:GLU:HA	0.45	2.32	2	1
1:A:67:LEU:C	1:A:69:ARG:H	0.45	2.14	15	3
1:A:111:SER:O	1:A:115:ARG:HD2	0.45	2.11	14	1
1:A:45:PHE:CD1	1:A:45:PHE:O	0.45	2.70	13	1
1:A:68:SER:HB2	1:A:79:ARG:C	0.45	2.32	5	1
1:A:117:LEU:O	1:A:146:CYS:HA	0.45	2.11	3	1
1:A:72:GLY:HA2	1:A:77:GLU:CG	0.45	2.41	19	1
1:A:42:LEU:CB	1:A:88:THR:HA	0.45	2.41	8	1
1:A:2:THR:O	1:A:21:GLU:HB2	0.45	2.12	10	1
1:A:40:GLU:N	1:A:90:ASP:HA	0.45	2.27	18	2
1:A:76:ASP:HB3	1:A:78:GLU:OE1	0.45	2.11	5	1
1:A:46:HIS:O	1:A:47:VAL:HG23	0.45	2.12	13	1
1:A:49:GLU:OE2	1:A:64:PHE:HA	0.45	2.12	3	1
1:A:46:HIS:O	1:A:47:VAL:HG13	0.45	2.12	6	1
1:A:68:SER:HA	1:A:77:GLU:C	0.45	2.31	6	1
1:A:3:LYS:HB3	1:A:3:LYS:NZ	0.45	2.27	1	1
1:A:13:PRO:HB3	1:A:120:HIS:HA	0.45	1.88	7	1
1:A:113:ILE:HA	1:A:115:ARG:NE	0.45	2.26	6	1
1:A:4:ALA:HA	1:A:151:ILE:HA	0.45	1.88	19	4
1:A:121:GLU:CD	1:A:121:GLU:H	0.45	2.15	5	2
1:A:23:LYS:HG3	1:A:24:GLU:H	0.45	1.72	4	1
1:A:107:SER:O	1:A:112:ILE:HA	0.45	2.11	19	1
1:A:54:THR:O	1:A:147:GLY:HA2	0.44	2.12	17	1
1:A:46:HIS:HB2	1:A:125:ASP:HA	0.44	1.89	2	1
1:A:49:GLU:HB3	1:A:110:HIS:HB2	0.44	1.88	5	1
1:A:57:CYS:HB2	1:A:60:ALA:CB	0.44	2.42	5	1
1:A:116:THR:HG22	1:A:146:CYS:HB3	0.44	1.89	8	1
1:A:47:VAL:HG13	1:A:117:LEU:HA	0.44	1.90	1	1
1:A:125:ASP:HB3	1:A:128:LYS:CB	0.44	2.43	5	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:110:HIS:CG	1:A:115:ARG:HG2	0.44	2.47	3	1
1:A:22:GLN:HG3	1:A:105:SER:O	0.44	2.12	19	1
1:A:120:HIS:CD2	1:A:124:ASP:HB2	0.44	2.48	8	1
1:A:22:GLN:HG3	1:A:29:VAL:HG12	0.44	1.89	4	1
1:A:42:LEU:HB3	1:A:88:THR:HG22	0.44	1.89	19	1
1:A:60:ALA:HB1	1:A:118:VAL:HG13	0.44	1.89	7	1
1:A:88:THR:HA	1:A:121:GLU:OE1	0.44	2.12	7	1
1:A:21:GLU:O	1:A:104:ILE:HA	0.44	2.13	14	1
1:A:47:VAL:HA	1:A:117:LEU:HA	0.44	1.89	14	1
1:A:40:GLU:HB3	1:A:91:LYS:N	0.44	2.28	10	1
1:A:115:ARG:HH21	1:A:148:VAL:HG13	0.44	1.72	17	1
1:A:68:SER:HA	1:A:79:ARG:C	0.44	2.33	17	1
1:A:75:LYS:O	1:A:101:ASP:HA	0.44	2.13	7	1
1:A:133:GLU:O	1:A:136:LYS:HG3	0.44	2.13	10	1
1:A:116:THR:CB	1:A:147:GLY:HA2	0.44	2.43	13	1
1:A:124:ASP:OD2	1:A:140:ALA:HA	0.44	2.13	16	1
1:A:45:PHE:CD1	1:A:85:GLY:HA3	0.44	2.48	2	1
1:A:4:ALA:HB3	1:A:20:PHE:N	0.44	2.28	16	1
1:A:74:PRO:HA	1:A:84:LEU:HG	0.44	1.90	2	1
1:A:57:CYS:O	1:A:142:SER:HB3	0.43	2.13	11	1
1:A:40:GLU:O	1:A:121:GLU:HB2	0.43	2.13	6	1
1:A:49:GLU:CG	1:A:60:ALA:HB2	0.43	2.43	1	1
1:A:39:THR:HB	1:A:91:LYS:HB3	0.43	1.90	16	1
1:A:22:GLN:HB2	1:A:106:LEU:HA	0.43	1.89	8	1
1:A:48:HIS:NE2	1:A:65:ASN:HB2	0.43	2.28	4	1
1:A:1:ALA:O	1:A:21:GLU:HA	0.43	2.12	7	2
1:A:113:ILE:HD12	1:A:113:ILE:H	0.43	1.72	19	1
1:A:45:PHE:CE1	1:A:126:LEU:HA	0.43	2.48	6	1
1:A:112:ILE:O	1:A:149:ILE:HG22	0.43	2.13	13	1
1:A:46:HIS:CE1	1:A:138:GLY:HA3	0.43	2.47	1	1
1:A:49:GLU:CB	1:A:110:HIS:HB2	0.43	2.44	5	1
1:A:121:GLU:H	1:A:121:GLU:CD	0.43	2.13	12	2
1:A:48:HIS:NE2	1:A:118:VAL:HG23	0.43	2.29	12	1
1:A:89:ALA:CB	1:A:121:GLU:HB3	0.43	2.43	8	1
1:A:42:LEU:HA	1:A:88:THR:HA	0.43	1.89	11	1
1:A:38:LEU:HD23	1:A:39:THR:N	0.43	2.29	5	1
1:A:48:HIS:CD2	1:A:118:VAL:HB	0.43	2.48	18	1
1:A:42:LEU:O	1:A:43:HIS:HB2	0.43	2.13	12	1
1:A:44:GLY:HA3	1:A:87:VAL:H	0.43	1.73	7	1
1:A:126:LEU:HA	1:A:135:THR:O	0.43	2.14	2	1
1:A:50:PHE:HA	1:A:111:SER:OG	0.43	2.13	4	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:40:GLU:OE2	1:A:122:LYS:HD3	0.43	2.14	9	1
1:A:129:GLY:HA2	1:A:135:THR:HA	0.43	1.91	15	1
1:A:39:THR:HA	1:A:91:LYS:N	0.43	2.29	19	1
1:A:52:ASP:OD1	1:A:57:CYS:HA	0.43	2.13	14	1
1:A:5:VAL:O	1:A:149:ILE:HA	0.43	2.14	2	1
1:A:57:CYS:N	1:A:146:CYS:SG	0.43	2.87	15	3
1:A:31:VAL:HG13	1:A:99:ILE:HG21	0.43	1.91	15	1
1:A:79:ARG:NH1	1:A:80:HIS:HB2	0.43	2.29	6	1
1:A:46:HIS:O	1:A:47:VAL:HB	0.43	2.13	5	1
1:A:89:ALA:CB	1:A:121:GLU:HB2	0.43	2.44	16	1
1:A:50:PHE:CZ	1:A:60:ALA:HA	0.43	2.49	15	1
1:A:65:ASN:HB3	1:A:68:SER:OG	0.43	2.14	2	1
1:A:110:HIS:HA	1:A:115:ARG:HE	0.43	1.72	10	1
1:A:115:ARG:HH11	1:A:115:ARG:CA	0.43	2.26	10	1
1:A:7:VAL:H	1:A:148:VAL:HG11	0.42	1.74	13	1
1:A:49:GLU:CB	1:A:108:GLY:HA2	0.42	2.43	12	1
1:A:117:LEU:HB3	1:A:149:ILE:CG2	0.42	2.44	6	2
1:A:4:ALA:CB	1:A:151:ILE:HA	0.42	2.44	13	1
1:A:117:LEU:N	1:A:117:LEU:HD12	0.42	2.28	16	1
1:A:90:ASP:CG	1:A:91:LYS:H	0.42	2.17	19	1
1:A:42:LEU:HB3	1:A:87:VAL:O	0.42	2.14	16	1
1:A:17:ILE:O	1:A:33:GLY:HA2	0.42	2.15	5	1
1:A:74:PRO:O	1:A:84:LEU:HD13	0.42	2.14	4	1
1:A:41:GLY:N	1:A:90:ASP:HA	0.42	2.29	7	1
1:A:46:HIS:HB2	1:A:117:LEU:HD12	0.42	1.90	13	1
1:A:147:GLY:O	1:A:148:VAL:HG23	0.42	2.14	4	1
1:A:104:ILE:HD12	1:A:105:SER:N	0.42	2.30	4	1
1:A:71:HIS:O	1:A:127:GLY:HA2	0.42	2.14	7	1
1:A:68:SER:OG	1:A:80:HIS:HB2	0.42	2.15	13	1
1:A:54:THR:HA	1:A:147:GLY:O	0.42	2.14	4	1
1:A:70:LYS:HE2	1:A:76:ASP:OD2	0.42	2.14	4	1
1:A:68:SER:N	1:A:79:ARG:HB2	0.42	2.28	19	1
1:A:116:THR:CG2	1:A:146:CYS:HB3	0.42	2.44	8	1
1:A:18:ILE:HG12	1:A:46:HIS:HE2	0.42	1.74	8	1
1:A:29:VAL:HG23	1:A:102:SER:HA	0.42	1.91	13	1
1:A:39:THR:HA	1:A:91:LYS:HA	0.42	1.89	5	1
1:A:29:VAL:HG22	1:A:101:ASP:H	0.42	1.74	3	1
1:A:50:PHE:N	1:A:115:ARG:HG3	0.42	2.29	5	1
1:A:134:SER:HA	1:A:137:THR:HG22	0.42	1.91	11	1
1:A:117:LEU:O	1:A:146:CYS:HB2	0.42	2.13	13	1
1:A:129:GLY:HA3	1:A:135:THR:HA	0.42	1.90	9	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:90:ASP:OD2	1:A:91:LYS:HG2	0.42	2.14	3	1
1:A:115:ARG:NE	1:A:150:GLY:HA3	0.42	2.30	6	1
1:A:59:SER:O	1:A:62:PRO:HD3	0.42	2.15	14	1
1:A:49:GLU:O	1:A:50:PHE:HB2	0.42	2.15	6	1
1:A:42:LEU:HA	1:A:122:LYS:C	0.42	2.35	16	1
1:A:46:HIS:HB3	1:A:119:VAL:HB	0.42	1.90	5	1
1:A:84:LEU:H	1:A:103:VAL:HG11	0.42	1.74	9	1
1:A:47:VAL:HB	1:A:63:HIS:CD2	0.41	2.50	6	1
1:A:57:CYS:HB2	1:A:60:ALA:HB2	0.41	1.92	5	1
1:A:79:ARG:O	1:A:80:HIS:HB2	0.41	2.15	4	1
1:A:2:THR:HA	1:A:21:GLU:HG3	0.41	1.92	10	1
1:A:127:GLY:C	1:A:128:LYS:HD2	0.41	2.35	11	1
1:A:44:GLY:HA2	1:A:87:VAL:H	0.41	1.73	12	1
1:A:103:VAL:C	1:A:105:SER:H	0.41	2.19	7	1
1:A:41:GLY:N	1:A:90:ASP:HB3	0.41	2.31	6	1
1:A:106:LEU:HG	1:A:112:ILE:HG22	0.41	1.92	17	1
1:A:21:GLU:HB2	1:A:29:VAL:HG23	0.41	1.91	8	1
1:A:69:ARG:HA	1:A:79:ARG:H	0.41	1.75	2	1
1:A:16:GLY:HA3	1:A:35:ILE:HD13	0.41	1.93	6	1
1:A:90:ASP:C	1:A:92:ASP:H	0.41	2.19	13	1
1:A:74:PRO:C	1:A:76:ASP:H	0.41	2.19	14	1
1:A:72:GLY:C	1:A:126:LEU:HB3	0.41	2.36	6	1
1:A:67:LEU:O	1:A:79:ARG:HB2	0.41	2.15	17	1
1:A:27:GLY:H	1:A:103:VAL:HG22	0.41	1.75	3	1
1:A:68:SER:HB3	1:A:78:GLU:H	0.41	1.75	12	1
1:A:45:PHE:HB3	1:A:124:ASP:CB	0.41	2.45	10	1
1:A:48:HIS:HB2	1:A:115:ARG:HB3	0.41	1.92	11	1
1:A:54:THR:HA	1:A:148:VAL:HG23	0.41	1.92	11	1
1:A:3:LYS:N	1:A:21:GLU:HG3	0.41	2.30	9	1
1:A:8:LEU:HB3	1:A:117:LEU:HD21	0.41	1.92	3	1
1:A:22:GLN:O	1:A:22:GLN:HG3	0.41	2.14	8	1
1:A:72:GLY:HA2	1:A:79:ARG:HB2	0.41	1.92	2	1
1:A:90:ASP:HB3	1:A:93:GLY:HA3	0.41	1.93	5	1
1:A:68:SER:HA	1:A:77:GLU:CD	0.41	2.35	19	1
1:A:110:HIS:O	1:A:115:ARG:HB2	0.41	2.15	10	1
1:A:69:ARG:HB3	1:A:79:ARG:HA	0.41	1.93	6	1
1:A:108:GLY:HA3	1:A:111:SER:O	0.41	2.16	1	1
1:A:132:GLU:O	1:A:135:THR:HB	0.41	2.16	1	1
1:A:39:THR:HB	1:A:91:LYS:CA	0.41	2.45	16	1
1:A:34:SER:HA	1:A:95:ALA:O	0.41	2.16	9	1
1:A:16:GLY:HA3	1:A:35:ILE:HG22	0.41	1.93	9	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:ASN:ND2	1:A:108:GLY:HA2	0.41	2.31	9	1
1:A:65:ASN:HB2	1:A:109:ASP:OD2	0.41	2.15	3	1
1:A:115:ARG:O	1:A:149:ILE:HG22	0.41	2.16	19	1
1:A:68:SER:CB	1:A:78:GLU:H	0.41	2.28	12	1
1:A:87:VAL:HB	1:A:95:ALA:CB	0.41	2.45	12	1
1:A:125:ASP:O	1:A:138:GLY:HA2	0.41	2.16	12	1
1:A:76:ASP:HB2	1:A:102:SER:O	0.41	2.16	14	1
1:A:69:ARG:HB3	1:A:78:GLU:OE1	0.41	2.16	14	1
1:A:67:LEU:CB	1:A:109:ASP:HB2	0.41	2.46	8	1
1:A:22:GLN:HA	1:A:29:VAL:HG12	0.41	1.92	2	1
1:A:79:ARG:O	1:A:80:HIS:HB3	0.41	2.15	10	1
1:A:69:ARG:HD2	1:A:69:ARG:O	0.41	2.16	10	1
1:A:149:ILE:O	1:A:149:ILE:HG23	0.41	2.16	6	1
1:A:42:LEU:HD22	1:A:87:VAL:HG23	0.41	1.92	1	1
1:A:68:SER:HA	1:A:79:ARG:CB	0.41	2.45	18	1
1:A:69:ARG:O	1:A:71:HIS:N	0.41	2.52	10	1
1:A:66:PRO:HB3	1:A:69:ARG:NH2	0.40	2.31	16	1
1:A:118:VAL:HA	1:A:145:ALA:O	0.40	2.16	12	1
1:A:46:HIS:NE2	1:A:117:LEU:HG	0.40	2.30	10	1
1:A:45:PHE:HB3	1:A:124:ASP:HB2	0.40	1.93	10	1
1:A:32:TRP:HA	1:A:97:VAL:O	0.40	2.17	12	1
1:A:45:PHE:CD2	1:A:124:ASP:HB3	0.40	2.51	13	1
1:A:22:GLN:HB2	1:A:104:ILE:HB	0.40	1.93	9	1
1:A:118:VAL:HG22	1:A:140:ALA:HB3	0.40	1.92	18	1
1:A:89:ALA:HB1	1:A:93:GLY:HA2	0.40	1.94	7	1
1:A:115:ARG:NH1	1:A:150:GLY:HA3	0.40	2.32	17	1
1:A:53:ASN:O	1:A:147:GLY:HA3	0.40	2.16	4	1
1:A:47:VAL:HG22	1:A:117:LEU:CD1	0.40	2.45	4	1
1:A:126:LEU:HD12	1:A:135:THR:O	0.40	2.17	19	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	148/153 (97%)	113±4 (76±3%)	27±5 (19±3%)	8±3 (5±2%)	4 25

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2812/2907 (97%)	2141 (76%)	522 (19%)	149 (5%)	4	25

All 42 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	ASN	10
1	A	129	GLY	6
1	A	80	HIS	6
1	A	79	ARG	6
1	A	52	ASP	6
1	A	139	ASN	6
1	A	61	GLY	6
1	A	78	GLU	6
1	A	94	VAL	6
1	A	50	PHE	5
1	A	77	GLU	5
1	A	91	LYS	5
1	A	70	LYS	5
1	A	76	ASP	4
1	A	104	ILE	4
1	A	47	VAL	4
1	A	102	SER	4
1	A	109	ASP	4
1	A	41	GLY	4
1	A	111	SER	4
1	A	42	LEU	3
1	A	44	GLY	3
1	A	72	GLY	3
1	A	71	HIS	3
1	A	23	LYS	3
1	A	85	GLY	2
1	A	147	GLY	2
1	A	93	GLY	2
1	A	151	ILE	2
1	A	125	ASP	2
1	A	130	GLY	2
1	A	142	SER	2
1	A	148	VAL	2
1	A	43	HIS	2
1	A	68	SER	2
1	A	138	GLY	2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	73	GLY	1
1	A	123	ALA	1
1	A	63	HIS	1
1	A	90	ASP	1
1	A	126	LEU	1
1	A	51	GLY	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	115/117 (98%)	105±2 (92±2%)	10±2 (8±2%)	19	64
All	All	2185/2223 (98%)	2004 (92%)	181 (8%)	19	64

All 72 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	49	GLU	7
1	A	115	ARG	7
1	A	30	LYS	6
1	A	78	GLU	6
1	A	22	GLN	5
1	A	79	ARG	5
1	A	48	HIS	5
1	A	121	GLU	5
1	A	126	LEU	5
1	A	133	GLU	4
1	A	45	PHE	4
1	A	116	THR	4
1	A	75	LYS	4
1	A	84	LEU	4
1	A	104	ILE	4
1	A	149	ILE	4
1	A	46	HIS	3
1	A	15	GLN	3
1	A	99	ILE	3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	151	ILE	3
1	A	117	LEU	3
1	A	143	ARG	3
1	A	36	LYS	3
1	A	106	LEU	3
1	A	19	ASN	3
1	A	80	HIS	3
1	A	18	ILE	3
1	A	71	HIS	3
1	A	144	LEU	3
1	A	8	LEU	2
1	A	40	GLU	2
1	A	136	LYS	2
1	A	86	ASN	2
1	A	25	SER	2
1	A	42	LEU	2
1	A	65	ASN	2
1	A	3	LYS	2
1	A	57	CYS	2
1	A	77	GLU	2
1	A	120	HIS	2
1	A	112	ILE	2
1	A	91	LYS	2
1	A	43	HIS	2
1	A	132	GLU	2
1	A	124	ASP	2
1	A	23	LYS	2
1	A	110	HIS	2
1	A	39	THR	2
1	A	113	ILE	2
1	A	35	ILE	1
1	A	47	VAL	1
1	A	69	ARG	1
1	A	119	VAL	1
1	A	67	LEU	1
1	A	153	GLN	1
1	A	102	SER	1
1	A	125	ASP	1
1	A	97	VAL	1
1	A	118	VAL	1
1	A	26	ASN	1
1	A	142	SER	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	24	GLU	1
1	A	59	SER	1
1	A	13	PRO	1
1	A	76	ASP	1
1	A	137	THR	1
1	A	68	SER	1
1	A	87	VAL	1
1	A	66	PRO	1
1	A	128	LYS	1
1	A	100	GLU	1
1	A	50	PHE	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 30% for the well-defined parts and 30% for the entire structure.

7.1 Chemical shift list 1

File name: 2lu5_cs.str

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	517
Number of shifts mapped to atoms	517
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	125	3.23 ± 0.17	Should be applied
$^{13}\text{C}_\beta$	0	—	—
$^{13}\text{C}'$	120	3.48 ± 0.14	Should be applied
^{15}N	136	1.03 ± 0.65	None needed (imprecise)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 30%, i.e. 508 atoms were assigned a chemical shift out of a possible 1673. 0 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	508/740 (69%)	134/295 (45%)	240/300 (80%)	134/145 (92%)
Sidechain	0/821 (0%)	0/476 (0%)	0/312 (0%)	0/33 (0%)

Continued on next page...

Continued from previous page...

	Total	¹ H	¹³ C	¹⁵ N
Aromatic	0/112 (0%)	0/58 (0%)	0/37 (0%)	0/17 (0%)
Overall	508/1673 (30%)	134/829 (16%)	240/649 (37%)	134/195 (69%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 30%, i.e. 517 atoms were assigned a chemical shift out of a possible 1698. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	517/755 (68%)	136/301 (45%)	245/306 (80%)	136/148 (92%)
Sidechain	0/831 (0%)	0/481 (0%)	0/317 (0%)	0/33 (0%)
Aromatic	0/112 (0%)	0/58 (0%)	0/37 (0%)	0/17 (0%)
Overall	517/1698 (30%)	136/840 (16%)	245/660 (37%)	136/198 (69%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

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.

Random coil index (RCI) for chain A:

