

# Full wwPDB NMR Structure Validation Report (i)

### May 31, 2020 – 10:03 pm BST

PDB ID	:	6DSL
Title	:	Consensus engineered intein (Cat) with atypical split site
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Deposited on	:	2018-06-14

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 following versions of software and data (see references (1)) were used in the production of this report:

Cyrange	:	Kirchner and Güntert (2011)
$\operatorname{NmrClust}$	:	Kelley et al. (1996)
$\operatorname{MolProbity}$	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. $(2010)$
${ m ShiftChecker}$	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

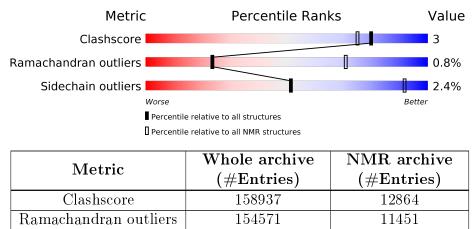
Sidechain outliers

# 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 89%.

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.



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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%

11428

Mol	Chain	Length	Quality of chain						
1	А	33	85%	6%	9%				
2	В	118	82%	6%	12%				



# 2 Ensemble composition and analysis (i)

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:1-A:30, B:32-B:135 (134)	0.29	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 2 clusters and 3 single-model clusters were found.

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



# 3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2411 atoms, of which 1195 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Consensus engineered intein CatN.

Mol	Chain	Residues	Atoms						Trace
1	Λ	22	Total	С	Η	Ν	Ο	S	0
	33	519	164	256	39	58	2	0	

• Molecule 2 is a protein called Consensus engineered intein CatC.

Mol	Chain	Residues	Atoms						Trace
0	D	110	Total	С	Η	Ν	Ο	S	0
2 B	118	1892	610	939	154	186	3	0	

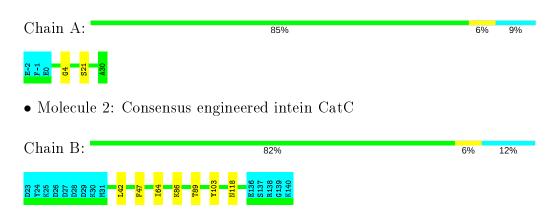


# 4 Residue-property plots (i)

## 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.

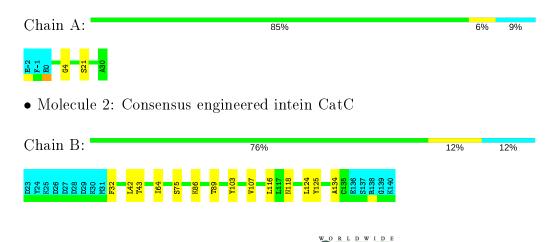
• Molecule 1: Consensus engineered intein CatN



## 4.2 Scores per residue for each member of the ensemble

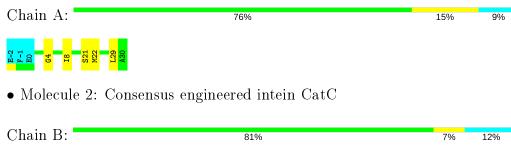
Colouring as in section 4.1 above.

### 4.2.1 Score per residue for model 1



### 4.2.2 Score per residue for model 2

• Molecule 1: Consensus engineered intein CatN





### 4.2.3 Score per residue for model 3

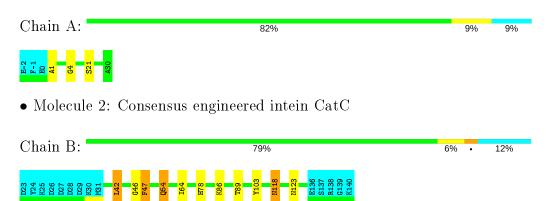
 $\bullet$  Molecule 1: Consensus engineered intein CatN

Chain A:	85%	6%	9%
1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2			

• Molecule 2: Consensus engineered intein CatC

Chain B:	79%	8%	•	12%
D23 724 825 D26 D27 D28 M31 M31 V41				

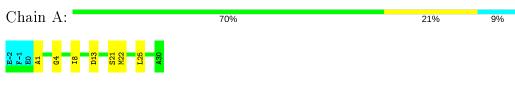
### 4.2.4 Score per residue for model 4





### 4.2.5 Score per residue for model 5

• Molecule 1: Consensus engineered intein CatN



• Molecule 2: Consensus engineered intein CatC

Chain B:	78%		10%	12%
D23 Y24 D26 D26 D28 D28 D28 M31 M31	L42 T43 F50 F50 S70 K82 K82 K82 V107 V107 V107 V113 M118	<u> </u>		

### 4.2.6 Score per residue for model 6

• Molecule 1: Consensus engineered intein CatN

Chain A:	82%	9%	9%
R-2 8-1 8-1 8-1 8-1 8-1 8-1 8-1 8-1 8-1 8-1			

• Molecule 2: Consensus engineered intein CatC

Chain B:			81%		5%	•	12%
724 724 726 726 726 728 729 729 730 730 731	4 0	164 K82 K86	T89 Y103 N118	E136 S137 R138 G139 K140			

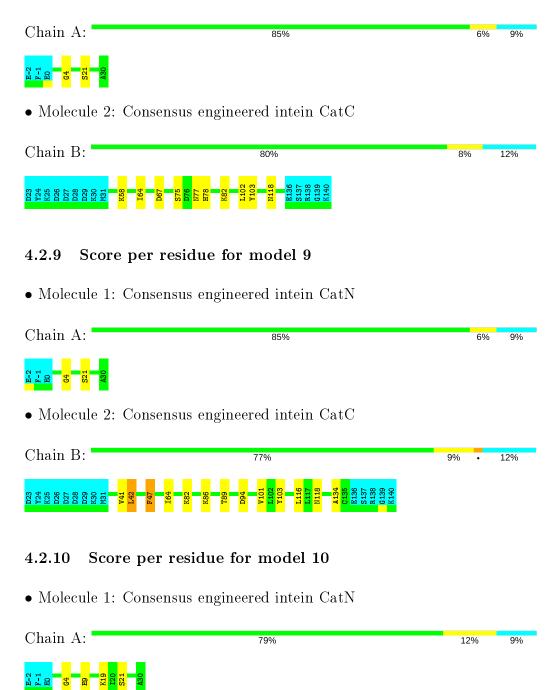
### 4.2.7 Score per residue for model 7

Chain A:	91%	9%
R- 2 8- 1 A30		
• Molecule 2: Consensus	engineered intein CatC	
Chain B:	81%	7% • 12%
Cham D.	0170	770 • 1270
123 123 123 123 123 123 123 123 124 14 150 150 151 150 151 151 151 151 151 151	K82 110 110 110 110 110 110 110 110 110 11	



### 4.2.8 Score per residue for model 8

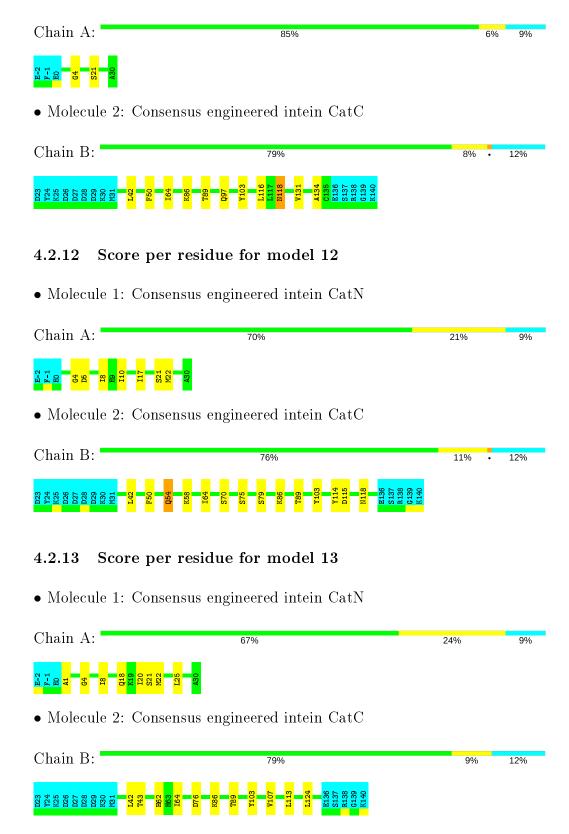
• Molecule 1: Consensus engineered intein CatN



Chain B:	80%	8%	•	12%	
123 124 125 126 127 127 128 130 143 143 143	138         111         113         111 <th 111<="" td="" th<=""><td></td><td></td><td></td></th>	<td></td> <td></td> <td></td>			



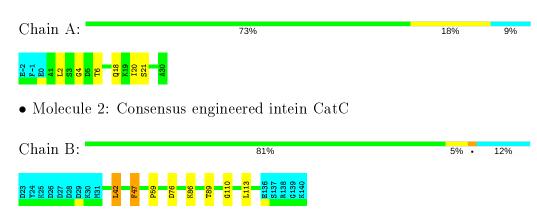
### 4.2.11 Score per residue for model 11





### 4.2.14 Score per residue for model 14

• Molecule 1: Consensus engineered intein CatN



### 4.2.15 Score per residue for model 15

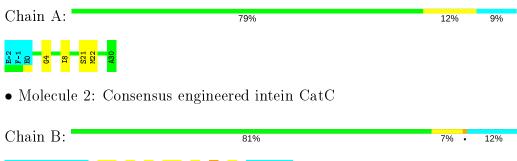
• Molecule 1: Consensus engineered intein CatN

Chain A:	82%	9%	9%
8월 11 11 12 13 14 14 14 14 14 14 14 14 14 14 14 14 14			

• Molecule 2: Consensus engineered intein CatC

Chain B:	77%	10%	• 12%	
023 124 125 026 027 028 129 129 129 129 131	L42 K55 F59 F59 F59 F59 F59 F55 F55 F55 F55 F			

### 4.2.16 Score per residue for model 16

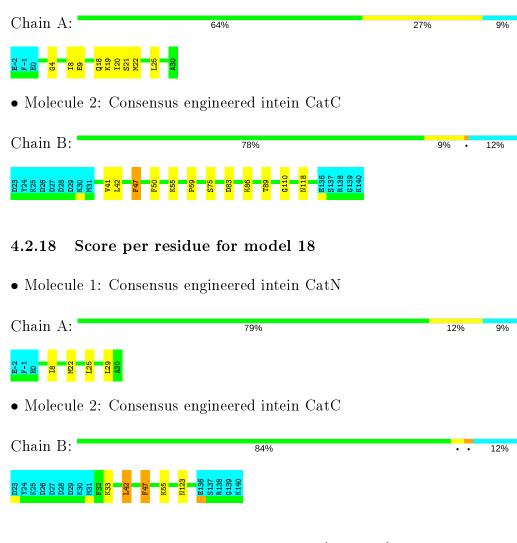




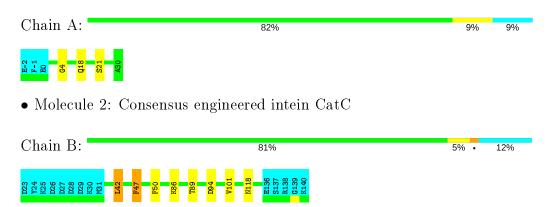


### 4.2.17 Score per residue for model 17

• Molecule 1: Consensus engineered intein CatN

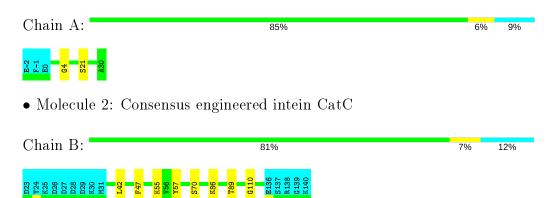


### 4.2.19 Score per residue for model 19 (medoid)





### 4.2.20 Score per residue for model 20





# 5 Refinement protocol and experimental data overview (i)

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

Of the 256 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
ARIA	refinement	
ARIA	structure calculation	

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)	input_cs.cif
Number of chemical shift lists	2
Total number of shifts	1772
Number of shifts mapped to atoms	1772
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	89%

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)

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	А	234	233	233	2±1
2	В	835	833	829	4±1
All	All	21380	21320	21240	116

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
2:B:42:LEU:HG	2:B:47:PHE:CZ	0.55	2.37	19	6
2:B:86:LYS:O	2:B:89:THR:HG22	0.54	2.02	1	14
2:B:50:PHE:HA	2:B:118:ASN:O	0.54	2.03	11	8
1:A:4:GLY:O	1:A:21:SER:HB2	0.53	2.03	8	18
2:B:116:LEU:O	2:B:134:ALA:HB1	0.53	2.04	11	4
2:B:97:GLN:OE1	2:B:131:VAL:HB	0.51	2.06	11	1
1:A:8:ILE:HD13	1:A:22:MET:SD	0.48	2.49	13	7
1:A:18:GLN:HG2	1:A:20:ILE:HG23	0.47	1.86	14	3
2:B:64:ILE:HA	2:B:103:TYR:O	0.47	2.09	8	11
2:B:41:VAL:O	2:B:47:PHE:HA	0.47	2.09	3	3
2:B:43:THR:HB	2:B:124:LEU:O	0.46	2.11	1	4
1:A:1:ALA:HB3	2:B:113:LEU:HB3	0.46	1.88	13	2
2:B:57:TYR:OH	2:B:110:GLY:HA3	0.46	2.10	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models		
Atom-1	Atom-2	$\operatorname{Clash}(\mathbf{A})$	Distance(A)	Worst	Total	
2:B:117:LEU:HA	2:B:135:CYS:O	0.46	2.11	10	1	
2:B:79:SER:HA	2:B:85:ILE:O	0.45	2.11	16	1	
1:A:9:GLU:OE1	1:A:19:LYS:HE2	0.44	2.11	17	2	
1:A:29:LEU:O	2:B:33:LYS:HD2	0.44	2.12	18	2	
2:B:59:PRO:HA	2:B:110:GLY:HA2	0.44	1.88	17	3	
2:B:58:LYS:HE2	2:B:75:SER:OG	0.44	2.12	8	2	
1:A:6:THR:O	1:A:21:SER:HA	0.44	2.13	14	1	
2:B:94:ASP:O	2:B:101:VAL:HG12	0.44	2.13	10	5	
1:A:2:LEU:HD21	1:A:6:THR:HG21	0.43	1.90	14	1	
2:B:125:TYR:N	2:B:125:TYR:CD1	0.43	2.86	3	1	
2:B:54:GLN:O	2:B:114:TYR:HA	0.43	2.14	12	1	
2:B:92:VAL:HA	2:B:101:VAL:HG13	0.43	1.90	15	1	
2:B:125:TYR:CD1	2:B:125:TYR:N	0.43	2.87	10	1	
2:B:62:HIS:CD2	2:B:76:ASP:HA	0.43	2.48	3	2	
1:A:13:ASP:HB2	2:B:37:LYS:O	0.43	2.13	5	1	
2:B:118:ASN:HA	2:B:123:ASN:OD1	0.42	2.14	4	1	
1:A:1:ALA:CB	2:B:113:LEU:HB3	0.41	2.45	13	1	
2:B:125:TYR:N	2:B:125:TYR:CD2	0.41	2.88	1	1	
2:B:67:ASP:HA	2:B:102:LEU:HD11	0.41	1.93	8	1	
1:A:1:ALA:N	2:B:78:HIS:HD2	0.41	2.14	4	1	
1:A:1:ALA:HA	2:B:115:ASP:HB2	0.41	1.93	15	1	
2:B:55:LYS:C	2:B:55:LYS:HD2	0.41	2.36	15	1	
2:B:117:LEU:CD1	2:B:135:CYS:HB3	0.40	2.47	15	1	
1:A:10:ILE:O	1:A:17:ILE:HA	0.40	2.15	12	1	

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# 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	Perce	entiles
1	А	29/33~(88%)	$29{\pm}0$ (100 ${\pm}1\%$ )	0±0 (0±1%)	0±0 (0±0%)	100	100
2	В	104/118~(88%)	$98\pm2~(94\pm2\%)$	$5\pm1 (5\pm1\%)$	$1\pm1 (1\pm1\%)$	20	68
All	All	2660/3020~(88%)	2537~(95%)	102~(4%)	21~(1%)	24	71

All 4 unique Ramachandran outliers are listed below. They are sorted by the frequency of occur-



rence in the ensemble.

Mol	Chain	$\mathbf{Res}$	Type	Models (Total)
2	В	47	PHE	10
2	В	118	ASN	9
2	В	46	GLY	1
2	В	32	PHE	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	Percentile	)S
1	А	26/29~(90%)	$26\pm0$ (99 $\pm2\%$ )	$0\pm0~(1\pm2\%)$	70 96	
2	В	93/106~(88%)	$91 \pm 1 (97 \pm 1\%)$	$3\pm1~(3\pm1\%)$	48 90	
All	All	2380/2700~(88%)	2323~(98%)	57 (2%)	51 92	

All 19 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	В	42	LEU	19
2	В	82	LYS	6
1	А	25	LEU	5
2	В	55	LYS	4
2	В	70	SER	4
2	В	107	VAL	3
2	В	125	TYR	2
2	В	54	GLN	2
2	В	77	ASN	2
2	В	76	ASP	1
2	В	75	SER	1
1	А	18	GLN	1
2	В	118	ASN	1
2	В	79	SER	1
2	В	113	LEU	1
2	В	86	LYS	1
2	В	83	ASP	1
1	А	5	ASP	1
2	В	32	PHE	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 carbohydrates 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 89% for the well-defined parts and 85% for the entire structure.

# 7.1 Chemical shift list 1

File name: input\_cs.cif

Chemical shift list name: assigned\_chemical\_shifts\_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	377
Number of shifts mapped to atoms	377
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

## 7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	${\bf Correction}\pm{\bf precision},ppm$	Suggested action
$^{13}C_{\alpha}$	30	$-0.28 \pm 0.30$	None needed ( $< 0.5$ ppm)
$^{13}C_{\beta}$	28	$-0.21 \pm 0.36$	None needed ( $< 0.5$ ppm)
$^{13}C'$	31	$2.42 \pm 0.40$	Should be applied
$^{15}N$	30	$0.77 \pm 0.70$	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 20%, i.e. 326 atoms were assigned a chemical shift out of a possible 1650. 4 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathbf{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Backbone	150/666~(23%)	60/266~(23%)	60/268~(22%)	30/132~(23%)
Sidechain	170/826~(21%)	103/481~(21%)	67/317~(21%)	0/28~(0%)

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	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Aromatic	6/158~(4%)	4/82~(5%)	2/68~(3%)	0/8~(0%)
Overall	326/1650~(20%)	167/829~(20%)	129/653~(20%)	30/168~(18%)

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The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 18%, i.e. 327 atoms were assigned a chemical shift out of a possible 1867. 4 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}$ N
Backbone	151/751~(20%)	60/300~(20%)	61/302~(20%)	30/149~(20%)
Sidechain	170/941~(18%)	103/549~(19%)	67/358~(19%)	0/34~(0%)
Aromatic	6/175~(3%)	4/91~(4%)	2/76~(3%)	0/8~(0%)
Overall	327/1867~(18%)	167/940~(18%)	130/736~(18%)	30/191~(16%)

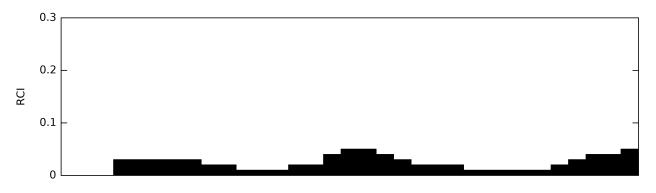
### 7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

### 7.1.5 Random Coil Index (RCI) plots (1)

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:



# 7.2 Chemical shift list 2

 $File name: input\_cs.cif$ 



Chemical shift list name: assigned chemical shifts 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	1395
Number of shifts mapped to atoms	1395
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

### 7.2.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	${\bf Correction}\pm{\bf precision},ppm$	Suggested action
$^{13}C_{\alpha}$	115	$-0.26 \pm 0.22$	None needed ( $< 0.5$ ppm)
$^{13}C_{\beta}$	106	$-0.02 \pm 0.13$	None needed ( $< 0.5$ ppm)
$^{13}C'$	113	$0.16 \pm 0.05$	None needed ( $< 0.5$ ppm)
<sup>15</sup> N	110	$0.40 \pm 0.45$	None needed ( $< 0.5$ ppm)

### 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 69%, i.e. 1138 atoms were assigned a chemical shift out of a possible 1650. 15 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Backbone	504/666~(76%)	202/266~(76%)	204/268~(76%)	98/132~(74%)
Sidechain	554/826~(67%)	345/481~(72%)	204/317~(64%)	5/28~(18%)
Aromatic	80/158~(51%)	53/82~(65%)	27/68~(40%)	0/8~(0%)
Overall	1138/1650~(69%)	600/829~(72%)	435/653~(67%)	103/168~(61%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 68%, i.e. 1265 atoms were assigned a chemical shift out of a possible 1867. 15 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

Backbone $563/751 (75\%)$ $225/300 (75\%)$ $228/302 (75\%)$ $110/149 (74\%)$		Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
	Backbone	563/751~(75%)	225/300~(75%)	228/302~(75%)	110/149~(74%)

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	Total	$^{1}\mathbf{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Sidechain	616/941~(65%)	386/549~(70%)	225/358~(63%)	5/34~(15%)
Aromatic	86/175~(49%)	57/91~(63%)	29/76~(38%)	0/8~(0%)
Overall	1265/1867~(68%)	668/940~(71%)	482/736~(65%)	115/191~(60%)

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### 7.2.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

## 7.2.5 Random Coil Index (RCI) plots (1)

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 B:

