



# Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 08:13 am BST

PDB ID : 5JTR  
Title : The structure of chaperone SecB in complex with unstructured MBP binding site e  
Authors : Huang, C.; Saio, T.; Rossi, P.; Kalodimos, C.G.  
Deposited on : 2016-05-09

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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  
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)  
ShiftChecker : 2.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

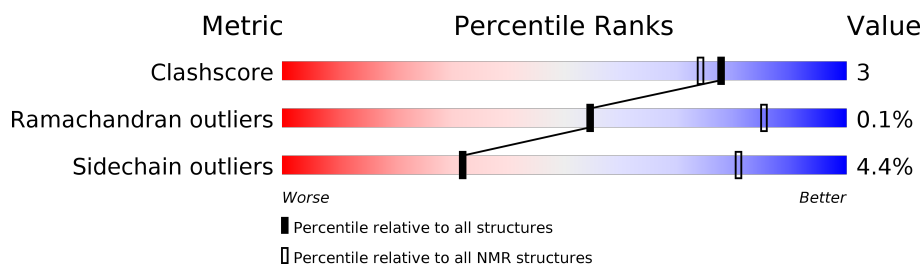
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 13%.

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  $\geq 3$ , 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	155	78% 20%
1	B	155	75% 5% 20%
1	C	155	72% 6% 22%
1	D	155	76% 21%
2	E	40	100%
2	F	40	100%
2	G	40	100%
2	H	40	100%

## 2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 9 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:10-A:133, B:10-B:133, C:10-C:89, C:93-C:133, D:10-D:132 (492)	0.53	9

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 1 single-model cluster was found.

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12032 atoms, of which 5880 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein-export protein SecB.

Mol	Chain	Residues	Atoms						Trace
1	A	155	Total	C	H	N	O	S	0
			2367	762	1155	198	243	9	
1	B	155	Total	C	H	N	O	S	0
			2367	762	1155	198	243	9	
1	C	155	Total	C	H	N	O	S	0
			2367	762	1155	198	243	9	
1	D	155	Total	C	H	N	O	S	0
			2367	762	1155	198	243	9	

- Molecule 2 is a protein called Maltose-binding periplasmic protein.

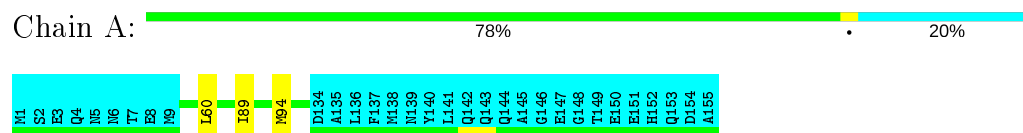
Mol	Chain	Residues	Atoms						Trace
2	E	40	Total	C	H	N	O	S	0
			641	216	315	49	60	1	
2	F	40	Total	C	H	N	O	S	0
			641	216	315	49	60	1	
2	G	40	Total	C	H	N	O	S	0
			641	216	315	49	60	1	
2	H	40	Total	C	H	N	O	S	0
			641	216	315	49	60	1	

## 4 Residue-property plots [i](#)

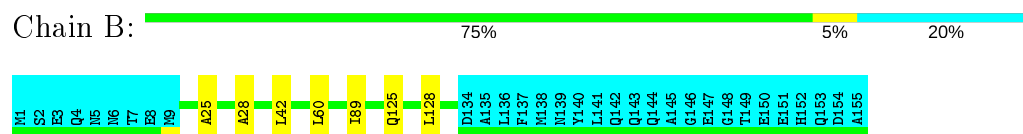
### 4.1 Average score per residue in the NMR ensemble

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.

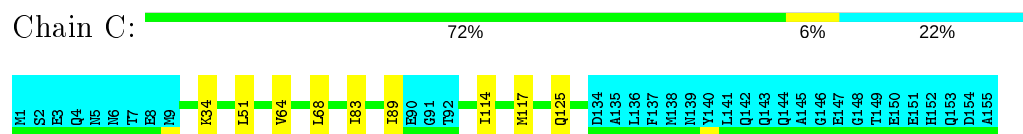
- Molecule 1: Protein-export protein SecB



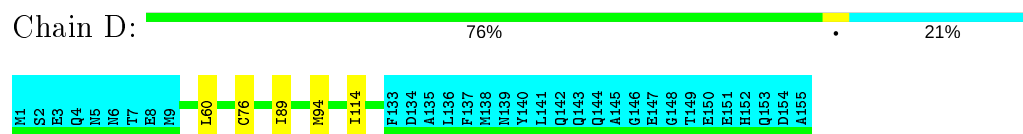
- Molecule 1: Protein-export protein SecB



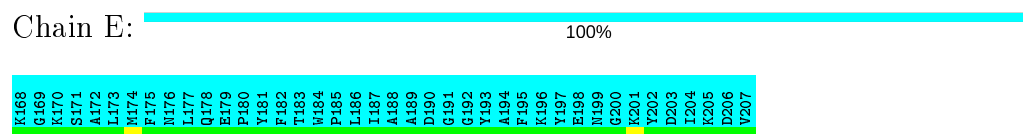
- Molecule 1: Protein-export protein SecB



- Molecule 1: Protein-export protein SecB

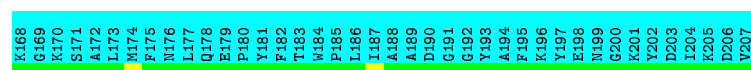


- Molecule 2: Maltose-binding periplasmic protein



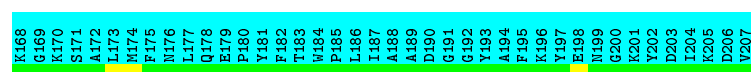
- Molecule 2: Maltose-binding periplasmic protein

Chain F:  100%



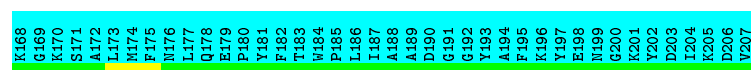
- Molecule 2: Maltose-binding periplasmic protein

Chain G:  100%



- Molecule 2: Maltose-binding periplasmic protein

Chain H:  100%



## 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

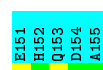
- Molecule 1: Protein-export protein SecB

Chain A:  73% 7% 20%



- Molecule 1: Protein-export protein SecB

Chain B:  69% 10% 20%



- Molecule 1: Protein-export protein SecB

Chain C:  68% 9% 22%





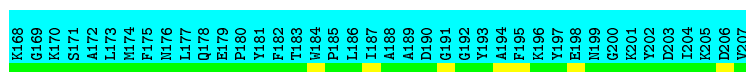
- Molecule 1: Protein-export protein SecB

Chain D: 72% 7% 21%



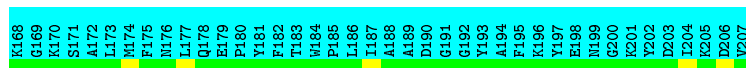
- Molecule 2: Maltose-binding periplasmic protein

Chain E: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain F: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%



- Molecule 2: Maltose-binding periplasmic protein

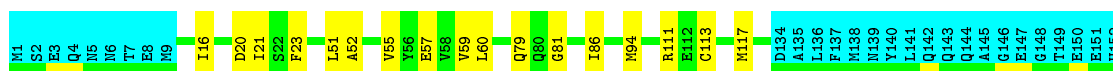
Chain H: 100%



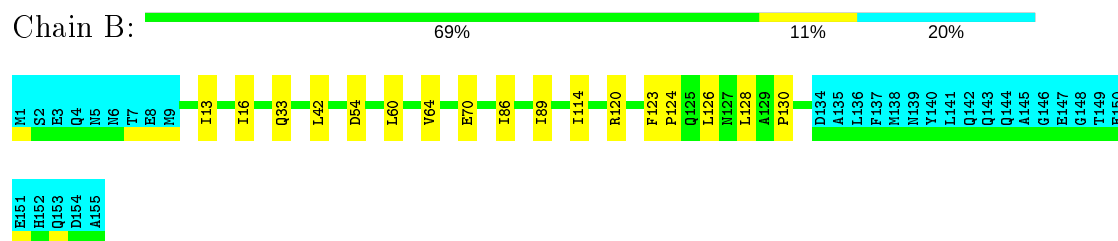
#### 4.2.2 Score per residue for model 2

- Molecule 1: Protein-export protein SecB

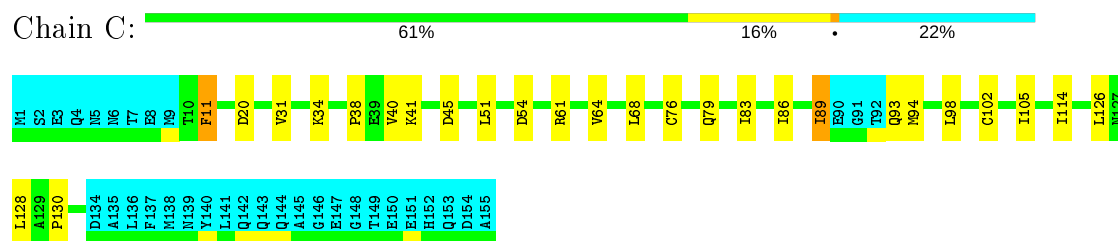
Chain A: 69% 11% 20%



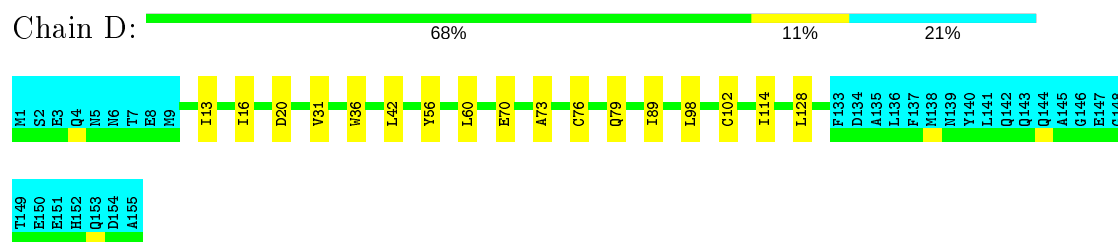
- Molecule 1: Protein-export protein SecB



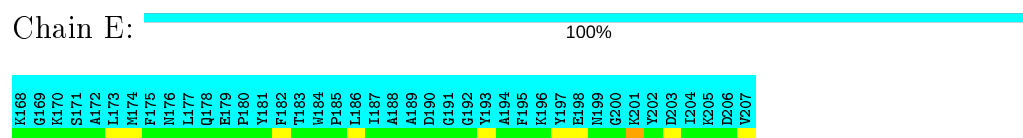
- Molecule 1: Protein-export protein SecB



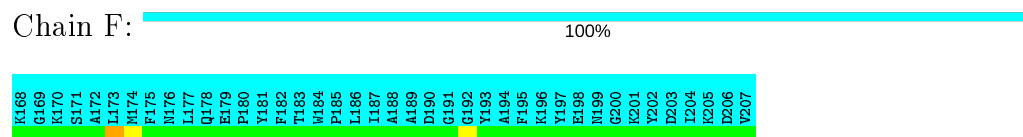
- Molecule 1: Protein-export protein SecB



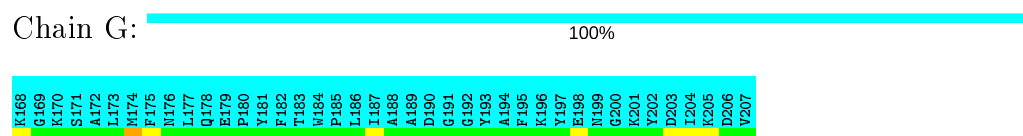
- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein

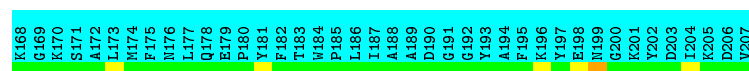


- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein

Chain H:  100%



#### 4.2.3 Score per residue for model 3

- Molecule 1: Protein-export protein SecB

Chain A:  75% 5% 20%



- Molecule 1: Protein-export protein SecB

Chain B:  73% 6% 20%



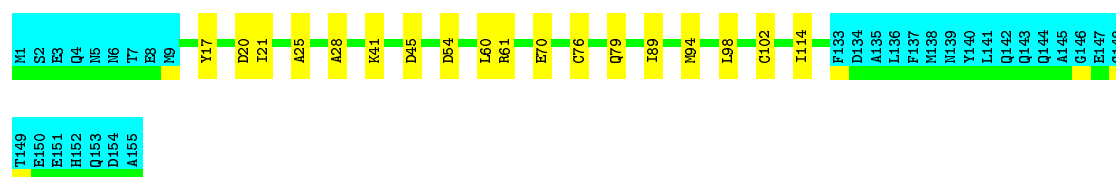
- Molecule 1: Protein-export protein SecB

Chain C:  70% 6% 22%



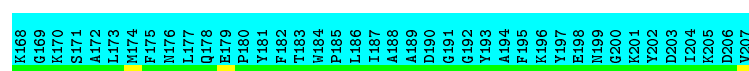
- Molecule 1: Protein-export protein SecB

Chain D:  68% 12% 21%



- Molecule 2: Maltose-binding periplasmic protein

Chain E:  100%



- Molecule 2: Maltose-binding periplasmic protein

Chain F:  100%



- Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%



- Molecule 2: Maltose-binding periplasmic protein

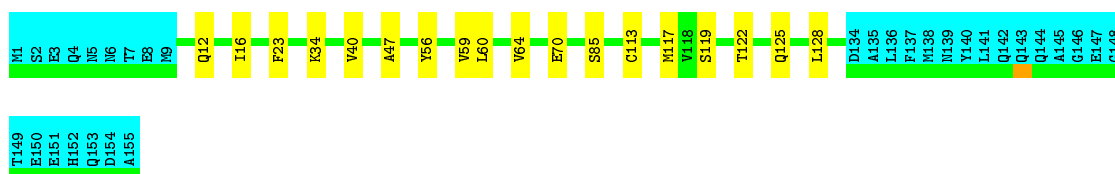
Chain H: 100%



#### 4.2.4 Score per residue for model 4

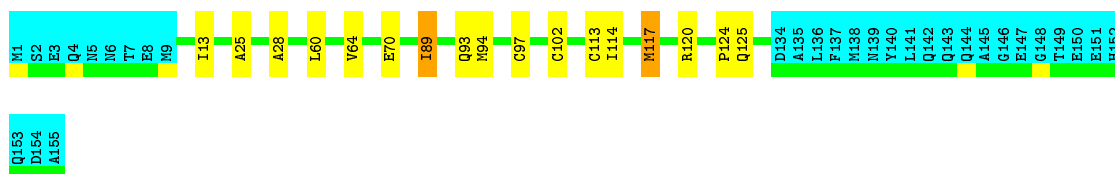
- Molecule 1: Protein-export protein SecB

Chain A: 68% 12% 20%



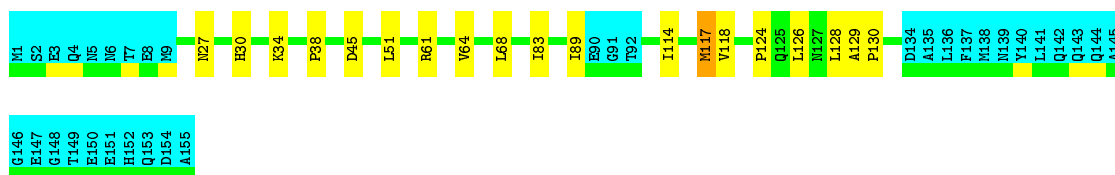
- Molecule 1: Protein-export protein SecB

Chain B: 69% 10% 20%

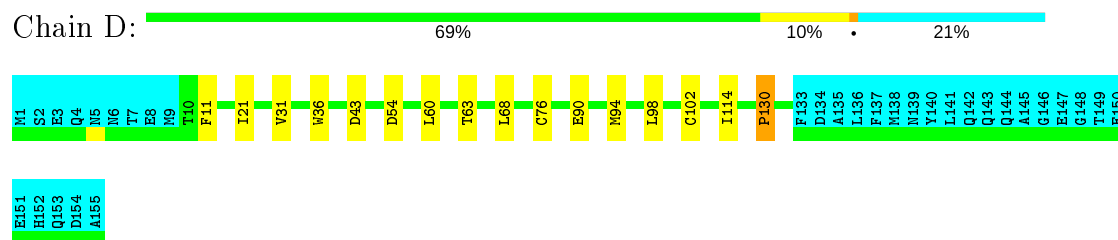


- Molecule 1: Protein-export protein SecB

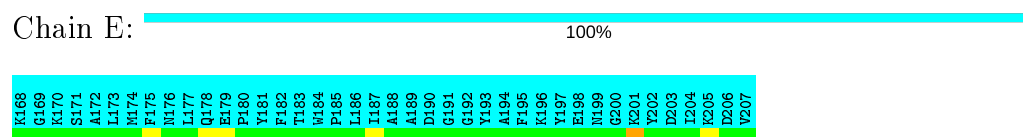
Chain C: 66% 12% 22%



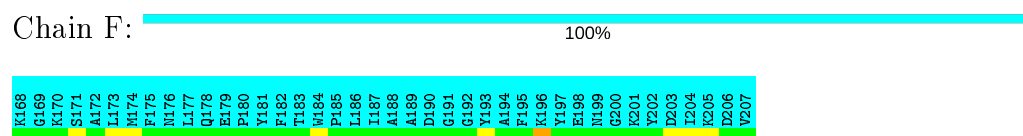
- Molecule 1: Protein-export protein SecB



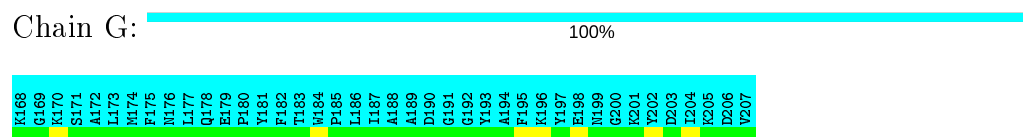
- Molecule 2: Maltose-binding periplasmic protein



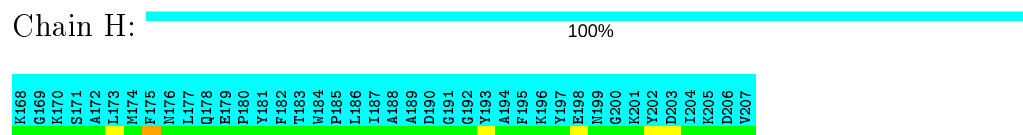
- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein

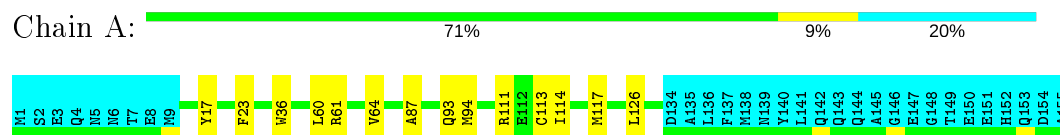


- Molecule 2: Maltose-binding periplasmic protein



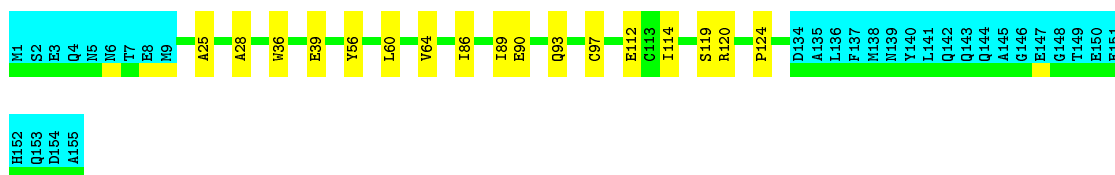
#### 4.2.5 Score per residue for model 5

- Molecule 1: Protein-export protein SecB



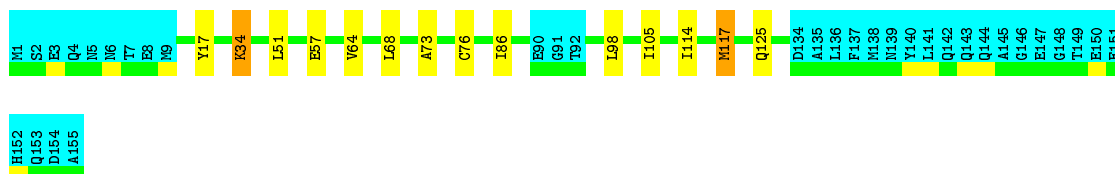
- Molecule 1: Protein-export protein SecB





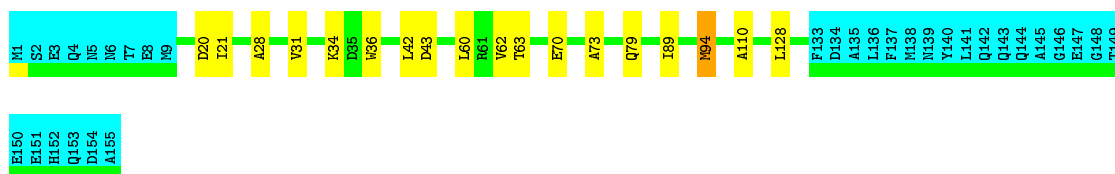
- Molecule 1: Protein-export protein SecB

Chain C: 69% 8% 22%



- Molecule 1: Protein-export protein SecB

Chain D: 68% 11% 21%



- Molecule 2: Maltose-binding periplasmic protein

Chain E: 100%



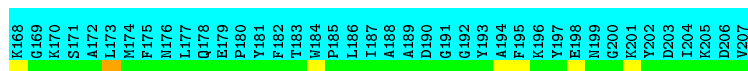
- Molecule 2: Maltose-binding periplasmic protein

Chain F: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%



- Molecule 2: Maltose-binding periplasmic protein

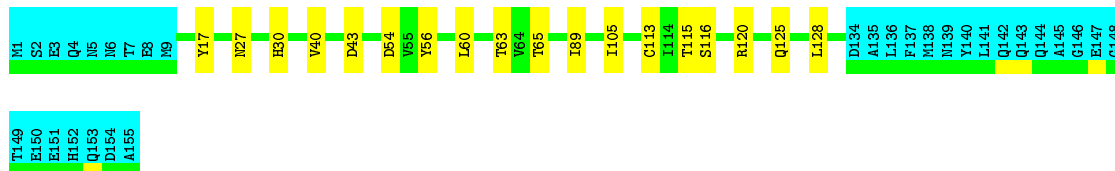
Chain H: 100%



#### 4.2.6 Score per residue for model 6

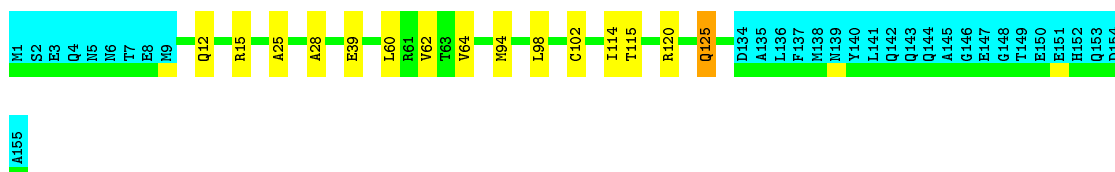
- Molecule 1: Protein-export protein SecB

Chain A: 68% 12% 20%



- Molecule 1: Protein-export protein SecB

Chain B: 70% 9% 20%



- Molecule 1: Protein-export protein SecB

Chain C: 70% 8% 22%



- Molecule 1: Protein-export protein SecB

Chain D: 76% 21%



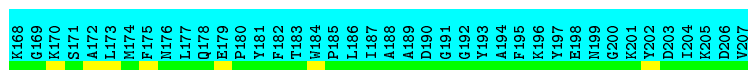
- Molecule 2: Maltose-binding periplasmic protein

Chain E: 100%



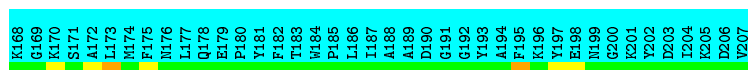
- Molecule 2: Maltose-binding periplasmic protein

Chain F: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain H: 100%



#### 4.2.7 Score per residue for model 7

- Molecule 1: Protein-export protein SecB

Chain A: 74% 6% 20%



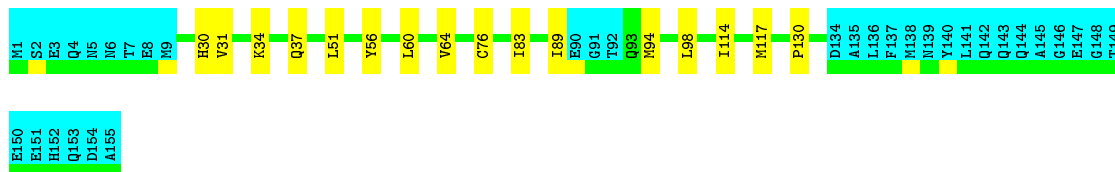
- Molecule 1: Protein-export protein SecB

Chain B: 71% 9% 20%



- Molecule 1: Protein-export protein SecB

Chain C: 68% 10% 22%



- Molecule 1: Protein-export protein SecB

Chain D: 70% 9% 21%



D154  
A155

- Molecule 2: Maltose-binding periplasmic protein

Chain E: 100%

K168 G169 K170 S171 A172 L173 M174 F175 M176 L177 Q178 E179 P180 Y181 F182 T183 M184 P185 L186 L187 A188 A189 D190 G191 G192 Y193 A194 F195 K196 Y197 E198 M199 G200 K201 Y202 D203 I204 K205 D206 V207

- Molecule 2: Maltose-binding periplasmic protein

Chain F: 100%

K168 G169 K170 S171 A172 L173 M174 F175 M176 L177 Q178 E179 P180 Y181 F182 T183 M184 P185 L186 L187 A188 A189 D190 G191 G192 Y193 A194 F195 K196 Y197 E198 M199 G200 K201 Y202 D203 I204 K205 D206 V207

- Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%

K168 G169 K170 S171 A172 L173 M174 F175 M176 L177 Q178 E179 P180 Y181 F182 T183 M184 P185 L186 L187 A188 A189 D190 G191 G192 Y193 A194 F195 K196 Y197 E198 M199 G200 K201 Y202 D203 I204 K205 D206 V207

- Molecule 2: Maltose-binding periplasmic protein

Chain H: 100%

K168 G169 K170 S171 A172 L173 M174 F175 M176 L177 Q178 E179 P180 Y181 F182 T183 M184 P185 L186 L187 A188 A189 D190 G191 G192 Y193 A194 F195 K196 Y197 E198 M199 G200 K201 Y202 D203 I204 K205 D206 V207

#### 4.2.8 Score per residue for model 8

- Molecule 1: Protein-export protein SecB

Chain A: 72% 7% 20%

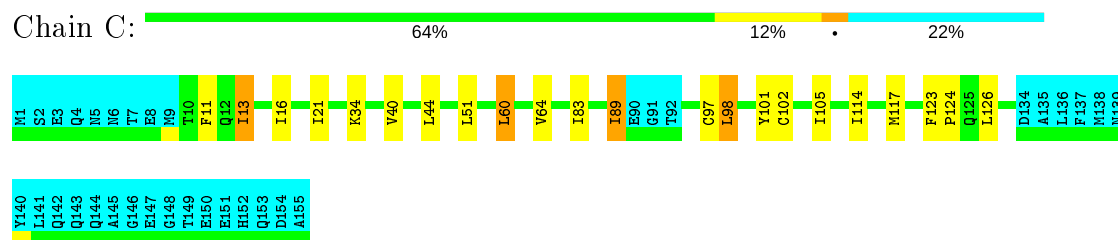
M1 S2 E3 Q4 N5 M6 T7 E8 M9 Y17 V31 D43 L60 T63 L68 I86 A87 G88 C97 C102 T115 Q125 D134 A135 L136 F137 M138 N139 Y140 L141 Q142 Q143 Q144 A145 G146 E147 G148 T149 E150 E151 H152 Q153 D154 A155

- Molecule 1: Protein-export protein SecB

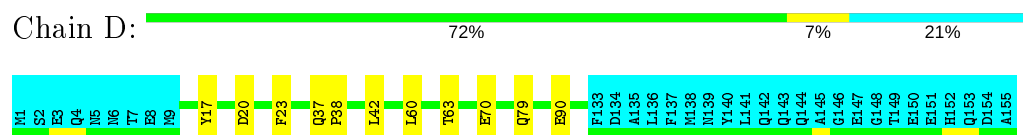
Chain B: 73% 7% 20%

M1 S2 E3 Q4 N5 M6 T7 E8 M9 D20 A28 Q37 L60 L68 A73 Q79 I89 E112 Q125 L126 N127 D134 A135 L136 F137 M138 N139 Y140 L141 Q142 Q143 Q144 A145 G146 E147 G148 T149 E150 E151 H152 Q153 D154 A155

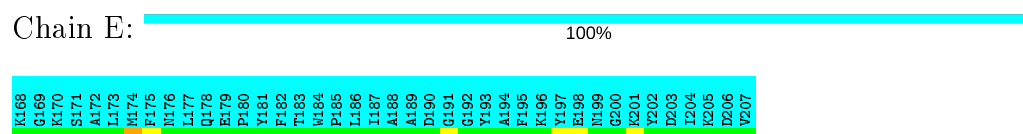
- Molecule 1: Protein-export protein SecB



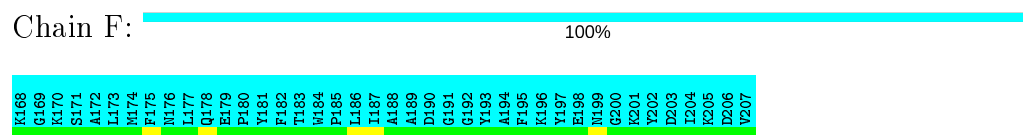
- Molecule 1: Protein-export protein SecB



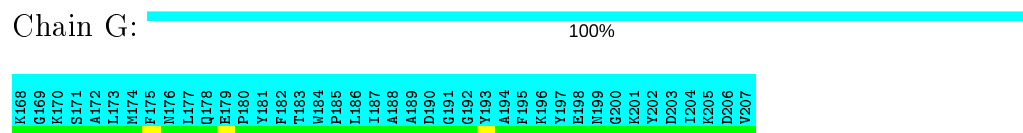
- Molecule 2: Maltose-binding periplasmic protein



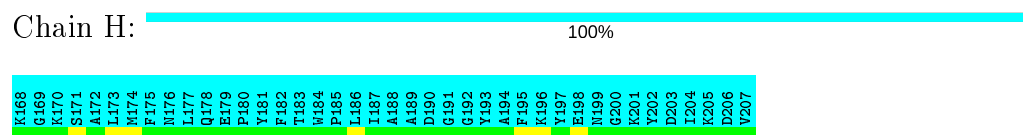
- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein



#### 4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: Protein-export protein SecB





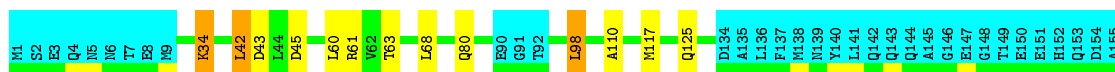
- Molecule 1: Protein-export protein SecB

Chain B: 75% 5% 20%



- Molecule 1: Protein-export protein SecB

Chain C: 70% 6% 22%



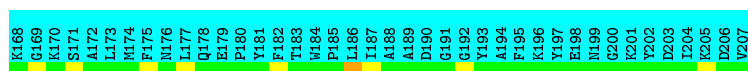
- Molecule 1: Protein-export protein SecB

Chain D: 75% 5% 21%



- Molecule 2: Maltose-binding periplasmic protein

Chain E: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain F: 100%



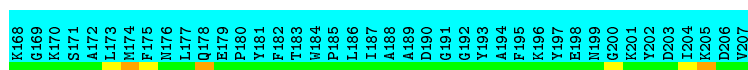
- Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%



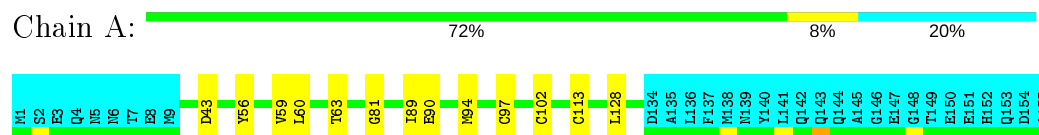
- Molecule 2: Maltose-binding periplasmic protein

Chain H: 100%

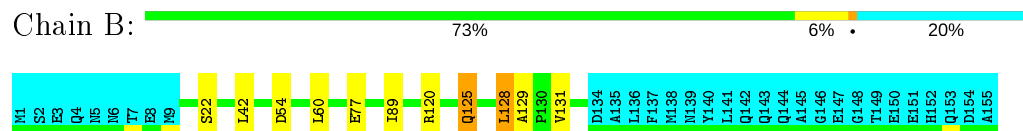


### 4.2.10 Score per residue for model 10

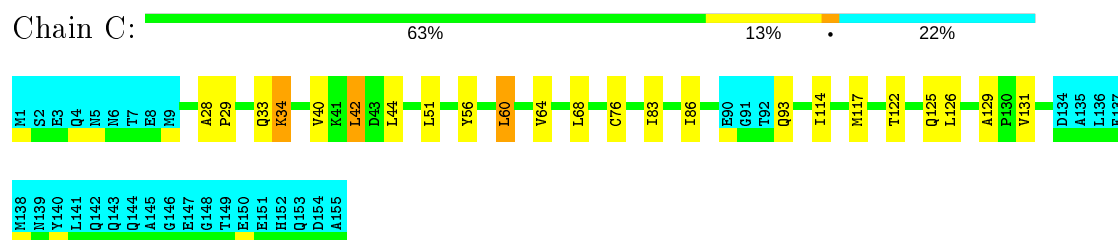
#### • Molecule 1: Protein-export protein SecB



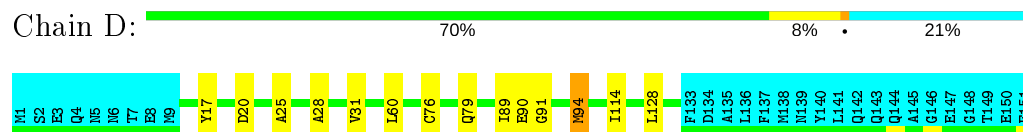
#### • Molecule 1: Protein-export protein SecB



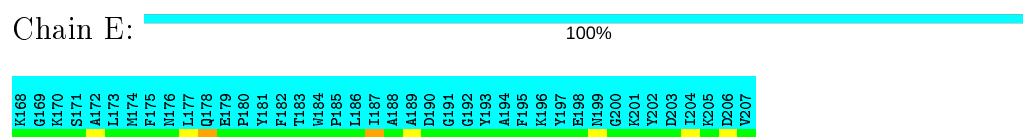
#### • Molecule 1: Protein-export protein SecB



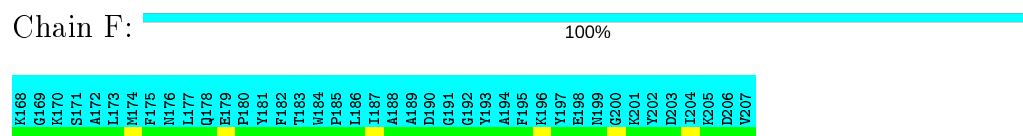
#### • Molecule 1: Protein-export protein SecB



#### • Molecule 2: Maltose-binding periplasmic protein



#### • Molecule 2: Maltose-binding periplasmic protein



#### • Molecule 2: Maltose-binding periplasmic protein





- Molecule 2: Maltose-binding periplasmic protein

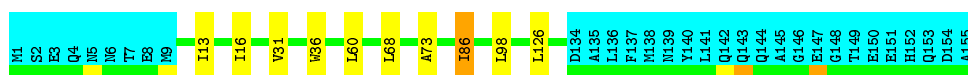
Chain H: 100%



#### 4.2.11 Score per residue for model 11

- Molecule 1: Protein-export protein SecB

Chain A: 74% 6% 20%



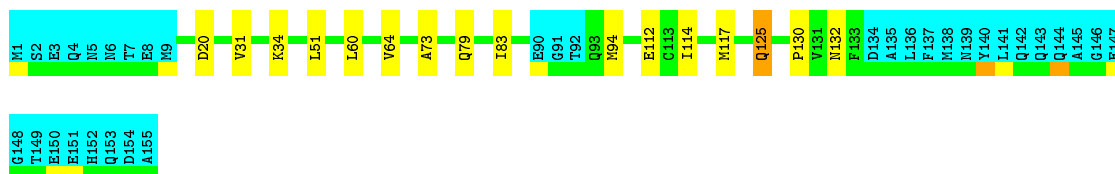
- Molecule 1: Protein-export protein SecB

Chain B: 74% 6% 20%



- Molecule 1: Protein-export protein SecB

Chain C: 68% 10% 22%



- Molecule 1: Protein-export protein SecB

Chain D: 71% 8% 21%

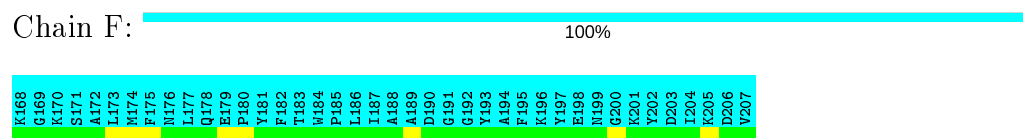


- Molecule 2: Maltose-binding periplasmic protein

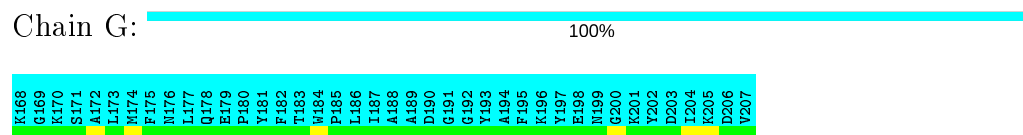
Chain E: 100%



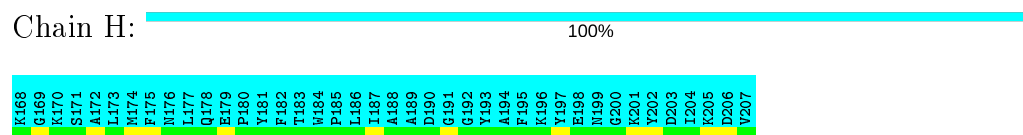
- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein

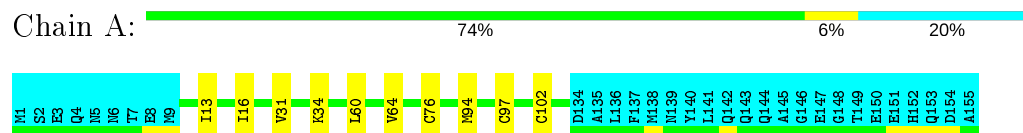


- Molecule 2: Maltose-binding periplasmic protein

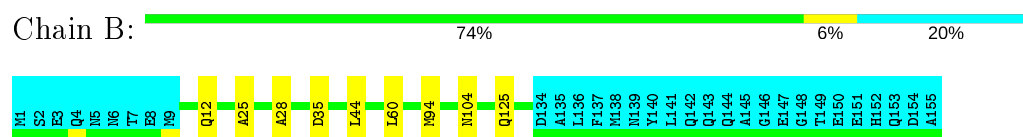


#### 4.2.12 Score per residue for model 12

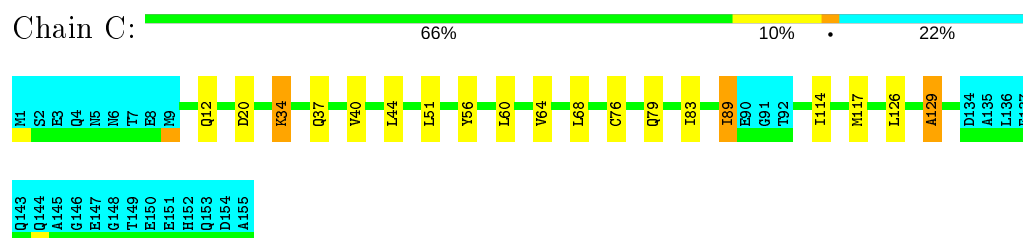
- Molecule 1: Protein-export protein SecB



- Molecule 1: Protein-export protein SecB



- Molecule 1: Protein-export protein SecB



- Molecule 1: Protein-export protein SecB





- Molecule 2: Maltose-binding periplasmic protein

Chain E: 100%



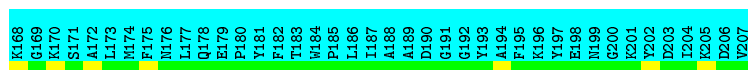
- Molecule 2: Maltose-binding periplasmic protein

Chain F: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain H: 100%



#### 4.2.13 Score per residue for model 13

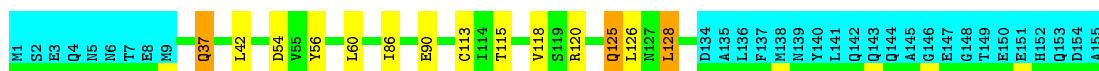
- Molecule 1: Protein-export protein SecB

Chain A: 70% 9% 20%

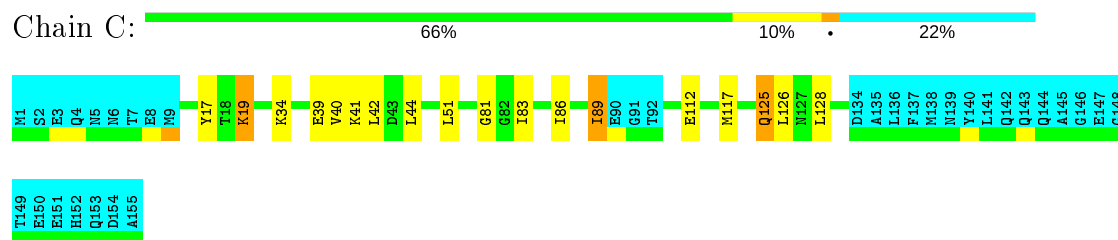


- Molecule 1: Protein-export protein SecB

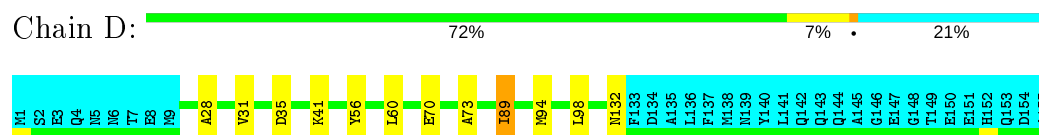
Chain B: 71% 7% 20%



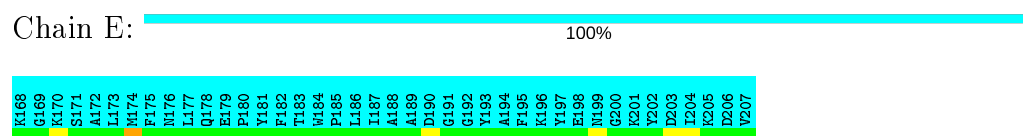
- Molecule 1: Protein-export protein SecB



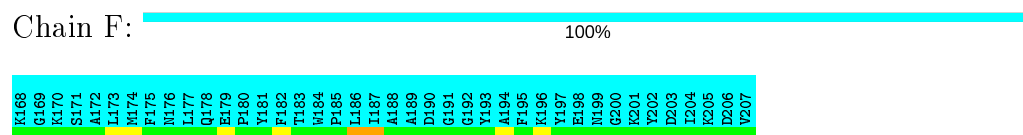
- Molecule 1: Protein-export protein SecB



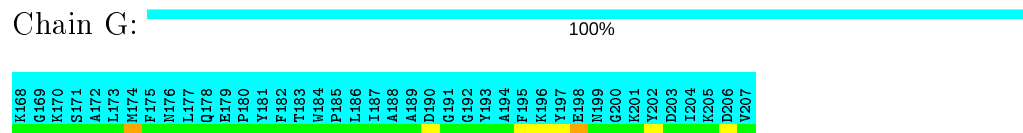
- Molecule 2: Maltose-binding periplasmic protein



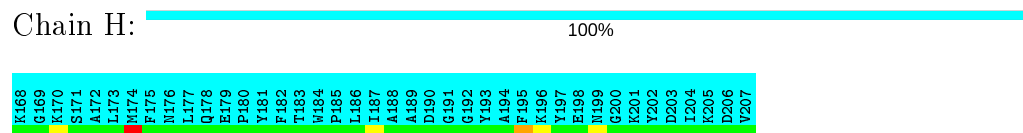
- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein



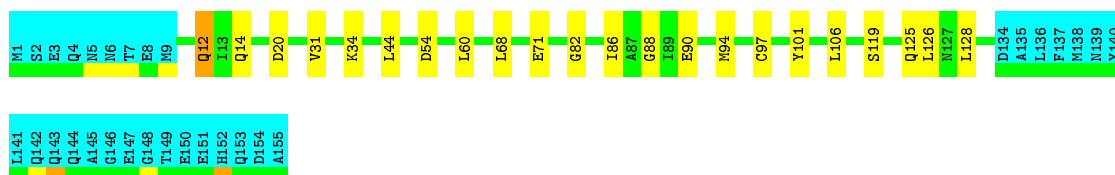
- Molecule 2: Maltose-binding periplasmic protein



#### 4.2.14 Score per residue for model 14

- Molecule 1: Protein-export protein SecB

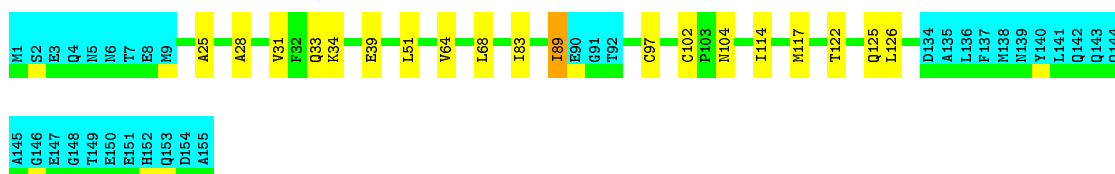




- Molecule 1: Protein-export protein SecB



- Molecule 1: Protein-export protein SecB



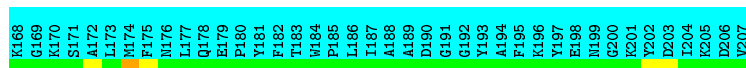
- Molecule 1: Protein-export protein SecB



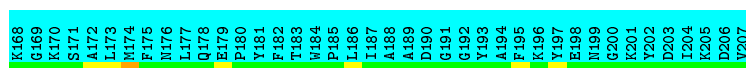
- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein

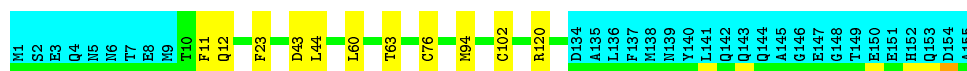
Chain H:  100%



#### 4.2.15 Score per residue for model 15

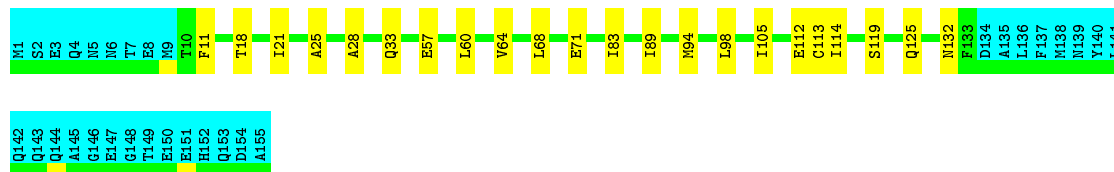
- Molecule 1: Protein-export protein SecB

Chain A:  73% 7% 20%



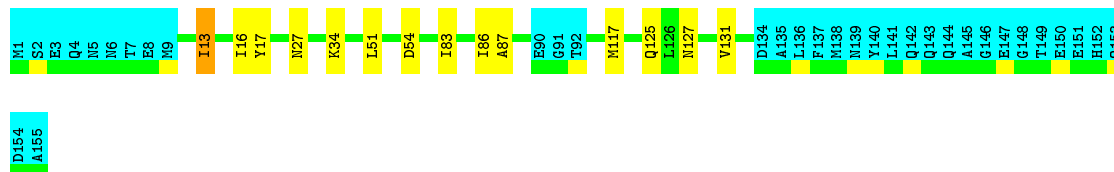
- Molecule 1: Protein-export protein SecB

Chain B:  66% 14% 20%



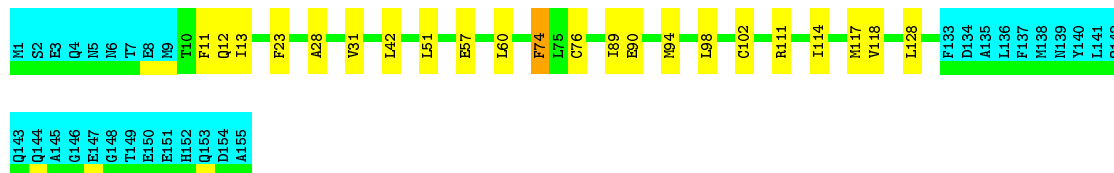
- Molecule 1: Protein-export protein SecB

Chain C:  69% 8% 22%



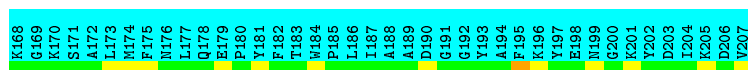
- Molecule 1: Protein-export protein SecB

Chain D:  65% 14% 21%



- Molecule 2: Maltose-binding periplasmic protein

Chain E:  100%



- Molecule 2: Maltose-binding periplasmic protein

Chain F: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain H: 100%



#### 4.2.16 Score per residue for model 16

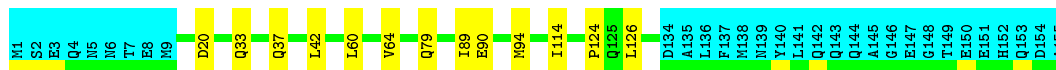
- Molecule 1: Protein-export protein SecB

Chain A: 74% 6% 20%



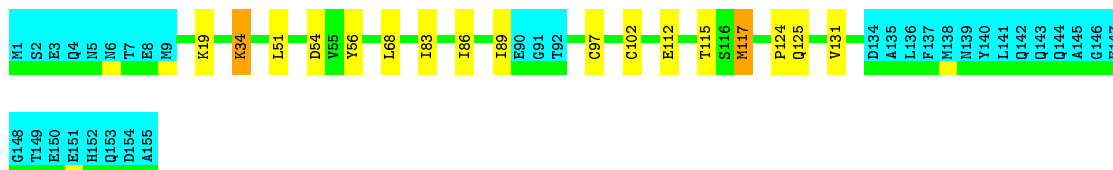
- Molecule 1: Protein-export protein SecB

Chain B: 72% 8% 20%

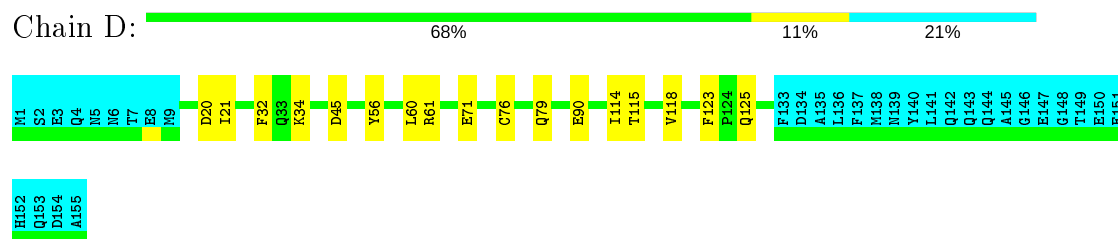


- Molecule 1: Protein-export protein SecB

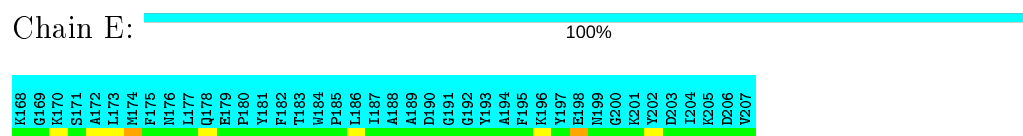
Chain C: 67% 10% 22%



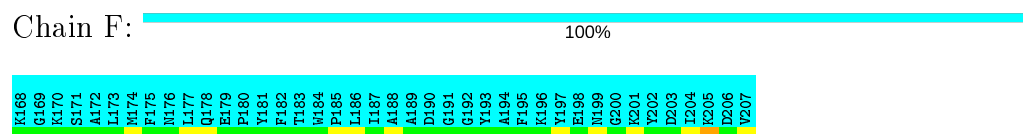
- Molecule 1: Protein-export protein SecB



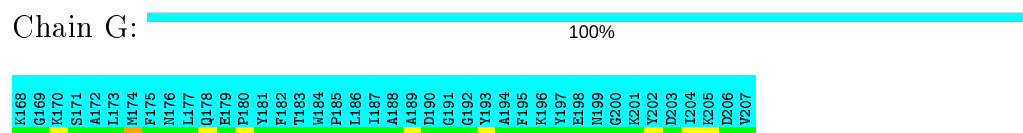
- Molecule 2: Maltose-binding periplasmic protein



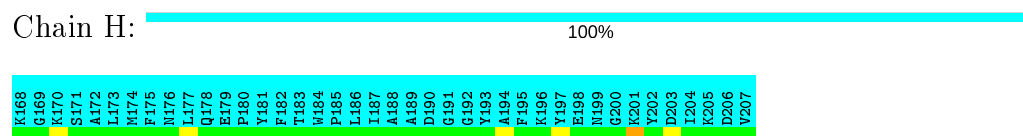
- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein

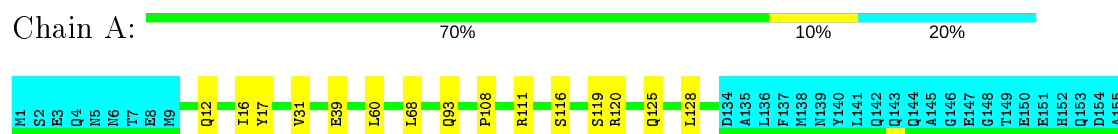


- Molecule 2: Maltose-binding periplasmic protein



#### 4.2.17 Score per residue for model 17

- Molecule 1: Protein-export protein SecB



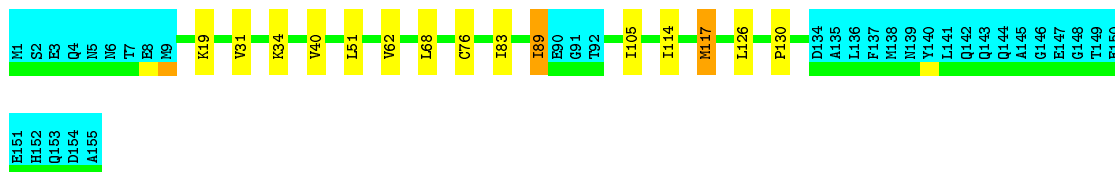
- Molecule 1: Protein-export protein SecB





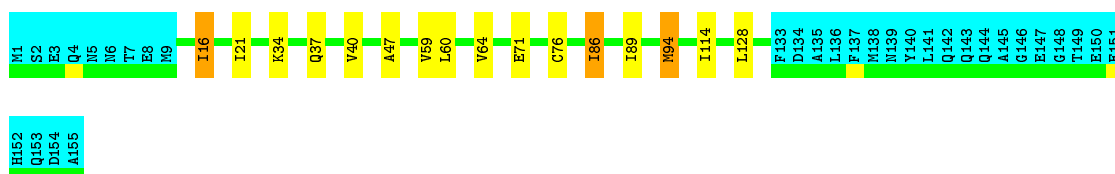
• Molecule 1: Protein-export protein SecB

Chain C: 68% 8% 22%



• Molecule 1: Protein-export protein SecB

Chain D: 69% 8% 21%



• Molecule 2: Maltose-binding periplasmic protein

Chain E: 100%



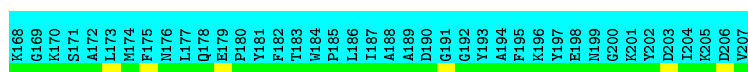
• Molecule 2: Maltose-binding periplasmic protein

Chain F: 100%



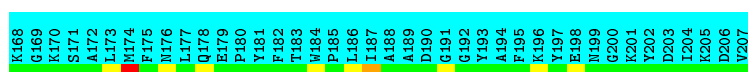
• Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%



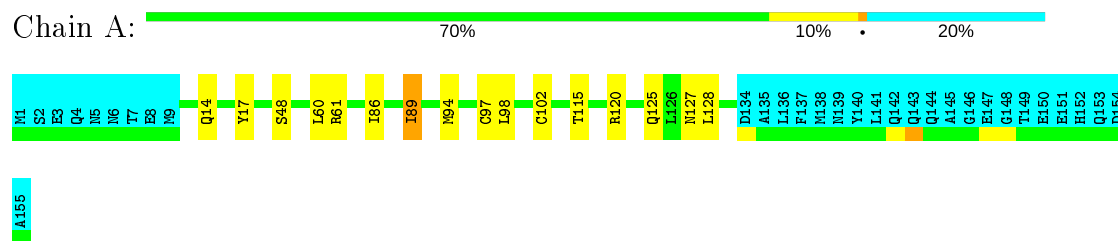
• Molecule 2: Maltose-binding periplasmic protein

Chain H: 100%

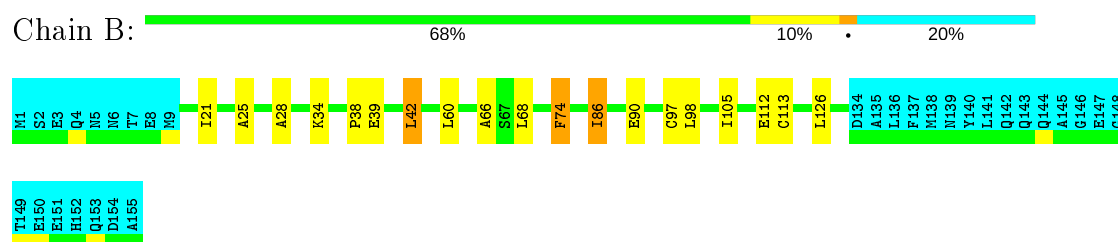


### 4.2.18 Score per residue for model 18

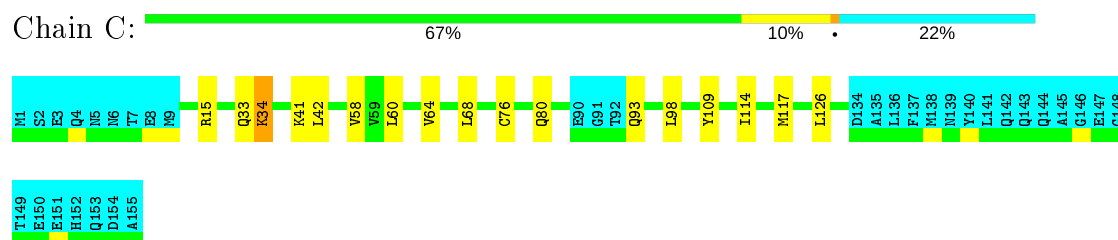
#### • Molecule 1: Protein-export protein SecB



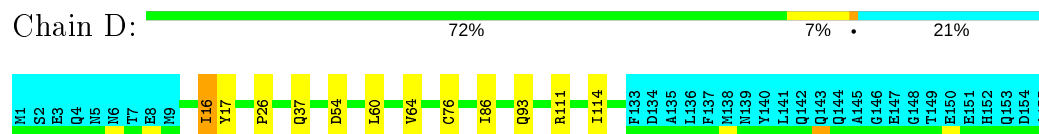
#### • Molecule 1: Protein-export protein SecB



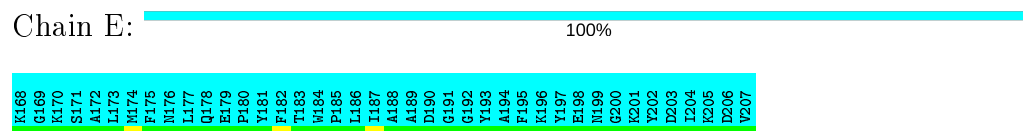
#### • Molecule 1: Protein-export protein SecB



#### • Molecule 1: Protein-export protein SecB



#### • Molecule 2: Maltose-binding periplasmic protein



#### • Molecule 2: Maltose-binding periplasmic protein





- Molecule 2: Maltose-binding periplasmic protein

Chain G: 100%



- Molecule 2: Maltose-binding periplasmic protein

Chain H: 100%



#### 4.2.19 Score per residue for model 19

- Molecule 1: Protein-export protein SecB

Chain A: 70% 9% 20%



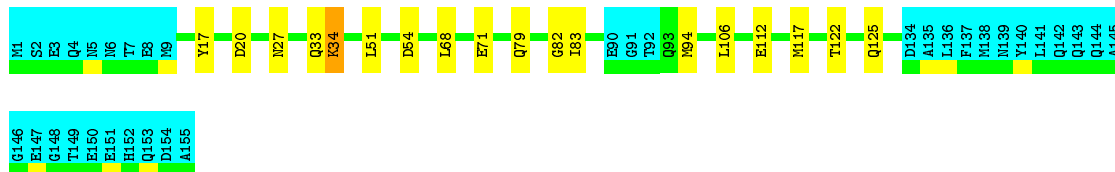
- Molecule 1: Protein-export protein SecB

Chain B: 72% 8% 20%



- Molecule 1: Protein-export protein SecB

Chain C: 66% 11% 22%



- Molecule 1: Protein-export protein SecB

Chain D: 70% 9% 21%



- Molecule 2: Maltose-binding periplasmic protein

Chain E:  100%



- Molecule 2: Maltose-binding periplasmic protein

Chain F:  100%



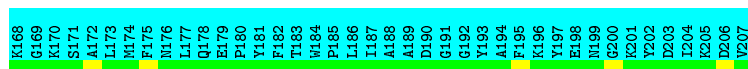
- Molecule 2: Maltose-binding periplasmic protein

Chain G:  100%



- Molecule 2: Maltose-binding periplasmic protein

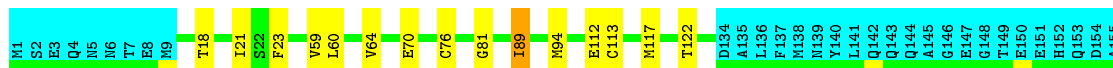
Chain H:  100%



#### 4.2.20 Score per residue for model 20

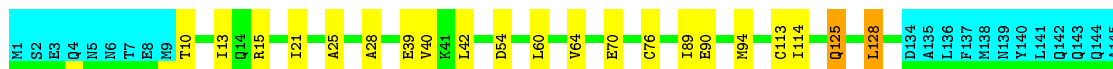
- Molecule 1: Protein-export protein SecB

Chain A:  70% 9% 20%

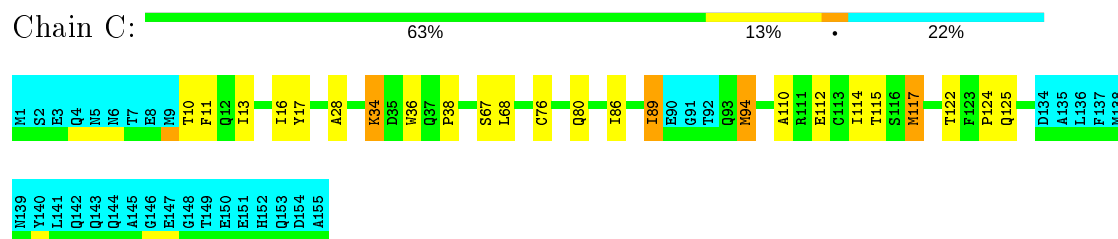


- Molecule 1: Protein-export protein SecB

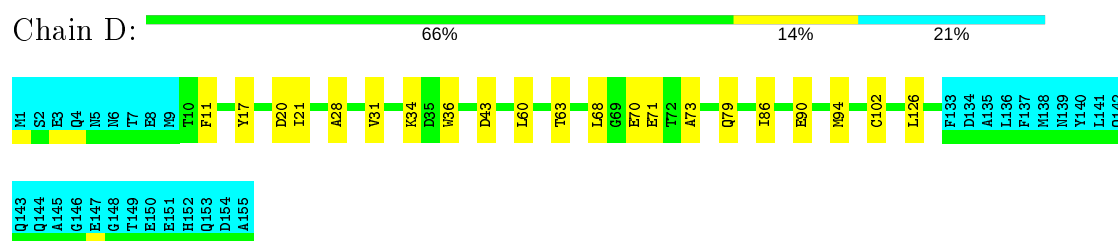
Chain B:  66% 12% 20%



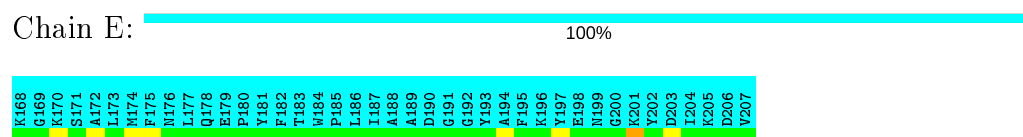
- Molecule 1: Protein-export protein SecB



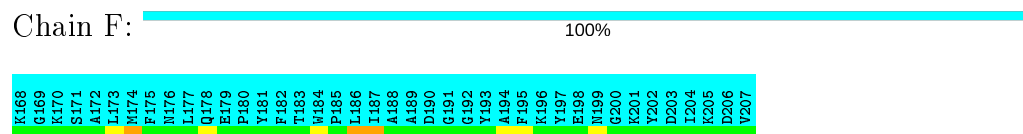
- Molecule 1: Protein-export protein SecB



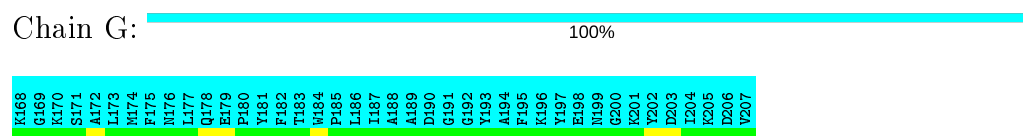
- Molecule 2: Maltose-binding periplasmic protein



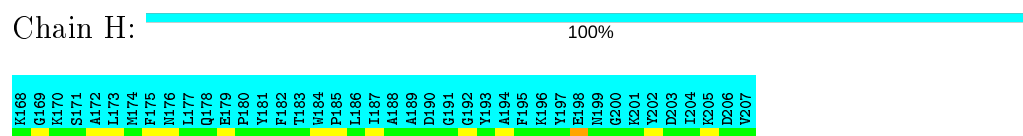
- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein



- Molecule 2: Maltose-binding periplasmic protein



## 5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CNS	refinement	
CYANA	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	8
Total number of shifts	5202
Number of shifts mapped to atoms	5202
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	13%

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

## 6 Model quality

### 6.1 Standard geometry

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

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	965	942	940	6±2
1	B	965	942	940	6±3
1	C	945	926	924	8±3
1	D	954	933	931	6±3
2	E	0	0	0	0±0
2	F	0	0	0	0±0
2	G	0	0	0	0±0
2	H	0	0	0	0±0
All	All	76580	74860	74700	440

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	
				Worst	Total
1:A:16:ILE:HB	1:C:130:PRO:HG2	0.66	1.67	7	4
1:B:25:ALA:HB1	1:B:28:ALA:HB2	0.65	1.66	3	5
1:D:98:LEU:HA	1:D:102:CYS:SG	0.65	2.32	15	4
1:C:94:MET:SD	1:C:98:LEU:HD21	0.64	2.32	7	1
1:C:34:LYS:HG2	1:C:68:LEU:HD13	0.64	1.68	5	9
1:A:16:ILE:HB	1:C:130:PRO:HG3	0.64	1.68	2	1
1:B:25:ALA:CB	1:B:28:ALA:HB2	0.62	2.24	3	11

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:40:VAL:HG12	1:B:126:LEU:HD22	0.62	1.71	11	1
1:D:94:MET:SD	1:D:98:LEU:HD23	0.62	2.34	7	1
1:A:23:PHE:HB2	1:A:117:MET:SD	0.61	2.35	16	8
1:B:66:ALA:HB3	1:B:74:PHE:HE2	0.61	1.53	18	1
1:A:97:CYS:SG	1:A:102:CYS:SG	0.60	2.98	12	4
1:C:31:VAL:HA	1:C:34:LYS:HE2	0.60	1.70	7	1
1:D:76:CYS:SG	1:D:114:ILE:HG23	0.60	2.37	18	7
1:B:118:VAL:HB	1:B:125:GLN:HG3	0.60	1.74	13	1
1:C:58:VAL:HG21	1:C:98:LEU:HB2	0.59	1.74	18	1
1:D:64:VAL:HG21	1:D:114:ILE:HG21	0.59	1.74	18	1
1:B:76:CYS:SG	1:B:114:ILE:HG23	0.58	2.38	20	1
1:C:117:MET:HE3	1:D:21:ILE:HD13	0.58	1.75	17	3
1:C:64:VAL:HG11	1:C:126:LEU:HG	0.58	1.75	3	2
1:C:27:ASN:HA	1:C:30:HIS:HB3	0.58	1.74	4	1
1:D:43:ASP:HB2	1:D:63:THR:HB	0.58	1.75	1	3
1:C:64:VAL:HG21	1:C:114:ILE:HG21	0.58	1.75	8	10
1:B:86:ILE:HD12	1:B:97:CYS:SG	0.58	2.39	7	1
1:B:125:GLN:HB2	1:C:125:GLN:HG2	0.57	1.76	13	1
1:A:17:TYR:HE2	1:B:28:ALA:HB1	0.57	1.57	8	4
1:C:38:PRO:HG2	1:C:124:PRO:HG3	0.56	1.78	4	1
1:B:58:VAL:HG11	1:B:98:LEU:HB2	0.55	1.79	7	1
1:B:119:SER:HB2	1:C:127:ASN:HB3	0.55	1.77	15	1
1:B:25:ALA:HB3	1:B:28:ALA:HB2	0.55	1.79	4	2
1:D:20:ASP:HB3	1:D:79:GLN:HB2	0.55	1.78	10	10
1:C:68:LEU:HD12	1:C:71:GLU:HG3	0.54	1.79	1	1
1:D:25:ALA:HB1	1:D:28:ALA:HB2	0.54	1.79	6	4
1:B:64:VAL:HG21	1:B:114:ILE:HG21	0.54	1.79	2	8
1:C:11:PHE:HA	1:C:86:ILE:HG22	0.54	1.79	20	1
1:C:40:VAL:HB	1:C:126:LEU:HD13	0.53	1.81	17	1
1:A:43:ASP:HB2	1:A:63:THR:HB	0.53	1.79	13	6
1:C:34:LYS:HE2	1:C:71:GLU:HG2	0.53	1.81	19	1
1:C:17:TYR:HE2	1:D:28:ALA:HB1	0.52	1.63	20	5
1:B:97:CYS:SG	1:B:102:CYS:SG	0.52	3.07	4	1
1:A:113:CYS:SG	1:B:120:ARG:HD3	0.52	2.45	10	6
1:A:89:ILE:HD13	1:A:94:MET:SD	0.52	2.44	20	1
1:B:42:LEU:HD22	1:B:126:LEU:HD11	0.52	1.80	16	1
1:B:45:ASP:HB2	1:B:61:ARG:HB3	0.52	1.82	14	1
1:D:31:VAL:HG21	1:D:73:ALA:HA	0.52	1.81	2	4
1:C:122:THR:HG23	1:D:17:TYR:HB3	0.51	1.82	20	3
1:D:42:LEU:HD21	1:D:128:LEU:HD22	0.51	1.82	2	2
1:B:86:ILE:HG13	1:B:97:CYS:SG	0.51	2.46	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:42:LEU:HD11	1:C:128:LEU:HD12	0.51	1.81	13	1
1:C:45:ASP:HB2	1:C:61:ARG:HB3	0.51	1.82	9	3
1:D:40:VAL:HG13	1:D:64:VAL:HG13	0.50	1.83	7	4
1:A:31:VAL:HG23	1:A:68:LEU:HD11	0.50	1.82	8	3
1:A:31:VAL:HA	1:A:34:LYS:HB2	0.50	1.83	12	1
1:A:105:ILE:HD12	1:C:132:ASN:HD21	0.50	1.66	6	1
1:D:62:VAL:HG21	1:D:110:ALA:HB1	0.50	1.84	14	3
1:B:40:VAL:HG11	1:B:125:GLN:HA	0.50	1.82	20	1
1:C:76:CYS:SG	1:C:114:ILE:HG23	0.50	2.47	17	9
1:C:51:LEU:HD11	1:C:83:ILE:HD12	0.50	1.83	8	13
1:A:120:ARG:HD3	1:B:113:CYS:SG	0.50	2.47	15	5
1:D:89:ILE:HD13	1:D:94:MET:SD	0.50	2.47	14	1
1:C:31:VAL:HG13	1:C:68:LEU:HD11	0.50	1.83	17	1
1:C:44:LEU:HG	1:C:60:LEU:HD21	0.49	1.84	8	2
1:A:64:VAL:HB	1:A:76:CYS:HB2	0.49	1.84	20	2
1:C:97:CYS:SG	1:C:102:CYS:SG	0.49	3.02	16	2
1:C:20:ASP:HB3	1:C:79:GLN:HB2	0.49	1.84	2	4
1:D:31:VAL:HG11	1:D:73:ALA:HA	0.49	1.84	12	1
1:D:34:LYS:NZ	1:D:71:GLU:HB3	0.49	2.22	17	2
1:C:89:ILE:HG12	1:C:94:MET:HG2	0.49	1.84	20	1
1:C:11:PHE:HE1	1:C:102:CYS:HG	0.49	1.50	1	1
1:C:40:VAL:HG11	1:C:126:LEU:HG	0.49	1.84	13	1
1:A:97:CYS:HA	1:A:101:TYR:HB3	0.49	1.83	19	2
1:D:76:CYS:SG	1:D:114:ILE:HG12	0.49	2.47	15	5
1:B:42:LEU:HD21	1:B:128:LEU:HD23	0.49	1.85	2	1
1:C:115:THR:HG23	1:C:125:GLN:HB2	0.49	1.83	3	2
1:C:43:ASP:HB2	1:C:63:THR:HB	0.49	1.85	9	1
1:B:125:GLN:HB3	1:C:125:GLN:HG3	0.49	1.85	11	1
1:A:34:LYS:HG3	1:A:71:GLU:HG2	0.49	1.83	14	2
1:A:119:SER:HB3	1:A:125:GLN:HB3	0.48	1.83	4	3
1:B:86:ILE:HG21	1:B:97:CYS:SG	0.48	2.48	5	1
1:C:89:ILE:HD12	1:C:94:MET:HA	0.48	1.85	7	1
1:A:115:THR:HG23	1:A:125:GLN:HB2	0.48	1.85	19	3
1:B:21:ILE:CD1	1:B:113:CYS:SG	0.48	3.01	20	4
1:C:98:LEU:HA	1:C:102:CYS:SG	0.48	2.48	8	2
1:D:36:TRP:HB2	1:D:68:LEU:HD22	0.48	1.85	20	2
1:B:115:THR:HA	1:B:125:GLN:HG3	0.48	1.85	6	2
1:D:51:LEU:HD11	1:D:57:GLU:HB2	0.48	1.85	15	2
1:B:66:ALA:HB3	1:B:74:PHE:CE2	0.48	2.40	18	1
1:D:118:VAL:HG13	1:D:123:PHE:HB2	0.48	1.86	16	1
1:A:48:SER:HB2	1:A:98:LEU:HD11	0.48	1.86	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:D:34:LYS:HZ2	1:D:71:GLU:HB3	0.48	1.69	20	1
1:C:51:LEU:HD11	1:C:57:GLU:HB2	0.48	1.86	5	2
1:B:20:ASP:HB3	1:B:79:GLN:HB2	0.48	1.85	16	2
1:B:13:ILE:HD11	1:B:16:ILE:HG13	0.47	1.84	2	1
1:A:82:GLY:HA3	1:A:106:LEU:HD21	0.47	1.84	14	1
1:B:105:ILE:HG23	1:D:111:ARG:NH2	0.47	2.24	18	2
1:A:20:ASP:HB3	1:A:79:GLN:HB2	0.47	1.87	3	4
1:D:94:MET:SD	1:D:95:ALA:N	0.47	2.87	12	1
1:B:115:THR:HA	1:B:125:GLN:HG2	0.47	1.85	13	1
1:D:74:PHE:CZ	1:D:118:VAL:HG22	0.47	2.44	15	1
1:D:13:ILE:HG12	1:D:16:ILE:HD11	0.47	1.86	2	1
1:D:89:ILE:HD12	1:D:94:MET:HG2	0.47	1.85	5	1
1:B:125:GLN:HA	1:C:125:GLN:HG2	0.47	1.87	15	1
1:B:132:ASN:H	1:D:13:ILE:HG21	0.47	1.69	15	1
1:B:18:THR:HG21	1:B:21:ILE:HD11	0.47	1.85	15	2
1:C:13:ILE:HD11	1:C:16:ILE:HG13	0.47	1.86	15	3
1:B:111:ARG:HH22	1:C:122:THR:HG22	0.47	1.68	19	1
1:B:130:PRO:HB2	1:D:16:ILE:HD13	0.47	1.85	2	1
1:A:42:LEU:HD21	1:A:128:LEU:HD22	0.47	1.87	9	1
1:C:115:THR:HG23	1:C:125:GLN:HB3	0.47	1.85	20	1
1:A:111:ARG:NH1	1:C:105:ILE:HG23	0.47	2.25	2	2
1:D:16:ILE:N	1:D:16:ILE:HD12	0.47	2.25	18	2
1:A:51:LEU:HD11	1:A:57:GLU:HB2	0.46	1.86	2	1
1:A:47:ALA:HB3	1:A:59:VAL:HB	0.46	1.86	4	1
1:A:40:VAL:HG23	1:A:64:VAL:HG13	0.46	1.87	4	1
1:B:130:PRO:HG3	1:D:16:ILE:HD11	0.46	1.87	17	1
1:A:18:THR:HG21	1:A:113:CYS:SG	0.46	2.50	20	1
1:B:21:ILE:HD11	1:B:113:CYS:SG	0.46	2.51	1	4
1:C:11:PHE:CE1	1:C:102:CYS:SG	0.46	3.04	2	1
1:A:40:VAL:HG21	1:A:128:LEU:HD21	0.46	1.86	4	1
1:D:89:ILE:HD13	1:D:94:MET:HG2	0.46	1.88	10	1
1:A:64:VAL:HG21	1:A:114:ILE:HG21	0.46	1.88	1	2
1:A:27:ASN:HB3	1:A:30:HIS:HB2	0.46	1.88	6	1
1:B:38:PRO:HB2	1:B:66:ALA:HB1	0.45	1.87	18	1
1:B:68:LEU:HG	1:B:73:ALA:HB2	0.45	1.87	1	2
1:B:119:SER:HB3	1:C:125:GLN:NE2	0.45	2.26	5	1
1:D:23:PHE:HB2	1:D:117:MET:SD	0.45	2.51	15	1
1:D:11:PHE:CZ	1:D:102:CYS:SG	0.45	3.09	15	1
1:B:42:LEU:HD11	1:B:128:LEU:HB2	0.45	1.87	11	1
1:C:34:LYS:HE3	1:C:68:LEU:CD1	0.45	2.42	1	1
1:B:42:LEU:HB3	1:B:64:VAL:HG22	0.45	1.89	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:89:ILE:H	1:C:89:ILE:HD13	0.45	1.72	2	2
1:C:89:ILE:HG12	1:C:94:MET:HB3	0.45	1.87	3	1
1:D:94:MET:HG3	1:D:98:LEU:HD23	0.45	1.87	13	1
1:C:118:VAL:HG21	1:C:126:LEU:HB2	0.45	1.86	4	1
1:D:31:VAL:HG13	1:D:68:LEU:HD12	0.45	1.87	20	2
1:D:115:THR:HG23	1:D:125:GLN:HG3	0.45	1.88	19	2
1:A:59:VAL:HA	1:A:81:GLY:HA2	0.44	1.90	2	4
1:A:21:ILE:CG2	1:A:117:MET:SD	0.44	3.05	20	2
1:D:37:GLN:HE21	1:D:38:PRO:HD2	0.44	1.72	8	1
1:A:12:GLN:HE21	1:A:12:GLN:HA	0.44	1.71	14	1
1:D:89:ILE:HD13	1:D:94:MET:HA	0.44	1.89	17	1
1:B:90:GLU:H	1:B:93:GLN:HB2	0.44	1.73	5	1
1:A:86:ILE:HG13	1:A:97:CYS:SG	0.44	2.51	8	1
1:B:130:PRO:HB2	1:D:16:ILE:HB	0.44	1.89	14	1
1:C:17:TYR:HB3	1:D:122:THR:HG23	0.44	1.89	19	1
1:C:34:LYS:HE2	1:C:73:ALA:HA	0.44	1.87	1	1
1:C:68:LEU:HG	1:C:73:ALA:HB2	0.44	1.90	5	1
1:C:60:LEU:HD21	1:C:103:PRO:HB3	0.44	1.89	6	1
1:A:17:TYR:CE2	1:B:28:ALA:HB1	0.44	2.44	8	2
1:C:11:PHE:CD1	1:C:97:CYS:SG	0.44	3.11	8	1
1:B:22:SER:HB3	1:B:77:GLU:HB3	0.44	1.90	10	1
1:C:40:VAL:HB	1:C:126:LEU:HD11	0.44	1.89	12	2
1:B:42:LEU:HB3	1:B:126:LEU:HD11	0.44	1.90	2	1
1:B:42:LEU:H	1:B:42:LEU:HD13	0.44	1.73	18	1
1:A:31:VAL:HG11	1:A:73:ALA:HA	0.44	1.88	11	1
1:B:86:ILE:HB	1:B:89:ILE:HD11	0.44	1.90	1	1
1:C:86:ILE:HD13	1:C:94:MET:HE3	0.44	1.87	2	1
1:C:28:ALA:HB3	1:C:29:PRO:HD3	0.44	1.89	10	1
1:A:52:ALA:HB3	1:A:55:VAL:HB	0.43	1.89	2	2
1:C:94:MET:SD	1:C:98:LEU:HB2	0.43	2.52	2	1
1:B:125:GLN:H	1:C:125:GLN:HG2	0.43	1.73	10	1
1:A:36:TRP:CE3	1:A:68:LEU:HD21	0.43	2.49	11	1
1:B:123:PHE:HB3	1:B:124:PRO:HD2	0.43	1.90	2	1
1:A:17:TYR:HB3	1:B:122:THR:HG23	0.43	1.88	3	1
1:D:45:ASP:HB3	1:D:61:ARG:HB3	0.43	1.91	3	2
1:A:40:VAL:HA	1:A:65:THR:O	0.43	2.13	6	1
1:A:16:ILE:HD12	1:C:130:PRO:HG3	0.43	1.90	11	1
1:C:117:MET:HE2	1:D:21:ILE:HG21	0.43	1.90	5	3
1:C:25:ALA:HB1	1:C:28:ALA:HB2	0.43	1.90	14	1
1:B:42:LEU:HB3	1:B:126:LEU:HD21	0.43	1.89	11	1
1:C:31:VAL:HG23	1:C:68:LEU:HD11	0.43	1.90	14	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:19:LYS:HD3	1:C:81:GLY:HA3	0.43	1.90	13	1
1:B:98:LEU:HA	1:B:102:CYS:SG	0.42	2.54	6	1
1:B:128:LEU:HD23	1:B:129:ALA:H	0.42	1.74	10	1
1:B:129:ALA:HB1	1:B:131:VAL:HG23	0.42	1.90	10	1
1:B:113:CYS:O	1:B:117:MET:HG2	0.42	2.14	1	1
1:B:125:GLN:NE2	1:C:124:PRO:HA	0.42	2.29	8	1
1:D:89:ILE:HG12	1:D:94:MET:HB2	0.42	1.92	13	1
1:B:12:GLN:HB3	1:B:85:SER:HB2	0.42	1.91	17	1
1:A:116:SER:O	1:A:120:ARG:HB2	0.42	2.14	6	3
1:C:115:THR:HG22	1:C:125:GLN:NE2	0.42	2.30	6	1
1:B:57:GLU:HG2	1:B:83:ILE:HG12	0.42	1.91	15	1
1:D:34:LYS:HZ1	1:D:71:GLU:HB3	0.42	1.74	17	1
1:B:34:LYS:HB3	1:B:68:LEU:HB3	0.42	1.91	18	1
1:A:43:ASP:HB3	1:A:63:THR:HB	0.42	1.91	8	1
1:A:23:PHE:HD1	1:A:76:CYS:SG	0.42	2.36	15	1
1:C:101:TYR:CE1	1:C:105:ILE:HG13	0.42	2.49	8	1
1:D:42:LEU:HA	1:D:63:THR:O	0.42	2.15	8	1
1:A:13:ILE:HD11	1:A:16:ILE:HG13	0.42	1.89	12	1
1:D:86:ILE:HD11	1:D:89:ILE:HD11	0.42	1.91	17	1
1:B:89:ILE:HB	1:B:93:GLN:HB2	0.42	1.91	4	1
1:D:34:LYS:NZ	1:D:71:GLU:HB2	0.42	2.29	16	1
1:D:11:PHE:HE2	1:D:102:CYS:HG	0.42	1.57	4	1
1:C:17:TYR:CE2	1:D:28:ALA:HB1	0.42	2.50	13	1
1:B:37:GLN:HB2	1:B:124:PRO:HG3	0.42	1.91	16	1
1:C:42:LEU:HB3	1:C:64:VAL:HG22	0.42	1.90	10	1
1:D:47:ALA:HB3	1:D:59:VAL:HB	0.42	1.89	17	1
1:A:12:GLN:HB3	1:A:85:SER:HB2	0.42	1.91	4	1
1:C:62:VAL:HB	1:C:114:ILE:HD11	0.42	1.90	17	1
1:C:28:ALA:HB1	1:D:17:TYR:HE2	0.42	1.75	20	1
1:B:12:GLN:HA	1:B:12:GLN:HE21	0.42	1.75	1	1
1:C:122:THR:HB	1:D:15:ARG:HH21	0.42	1.75	14	1
1:C:40:VAL:HG11	1:C:124:PRO:HG2	0.41	1.91	8	1
1:A:108:PRO:HA	1:A:111:ARG:NH1	0.41	2.30	17	1
1:C:40:VAL:HG11	1:C:128:LEU:HD21	0.41	1.91	2	1
1:B:68:LEU:O	1:B:71:GLU:HB2	0.41	2.16	15	1
1:D:114:ILE:O	1:D:118:VAL:HG23	0.41	2.14	15	1
1:C:38:PRO:HA	1:C:67:SER:O	0.41	2.14	20	1
1:C:80:GLN:HB2	1:C:110:ALA:HB2	0.41	1.92	20	2
1:A:23:PHE:HB3	1:B:21:ILE:HB	0.41	1.92	15	1
1:A:23:PHE:CD1	1:A:76:CYS:SG	0.41	3.14	15	1
1:B:54:ASP:HB3	1:B:86:ILE:O	0.41	2.16	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:13:ILE:HG13	1:D:130:PRO:HD3	0.41	1.92	4	1
1:A:11:PHE:CE2	1:A:102:CYS:SG	0.41	3.13	15	1
1:D:74:PHE:CE2	1:D:118:VAL:HG22	0.41	2.50	15	1
1:B:39:GLU:O	1:B:66:ALA:HA	0.41	2.16	1	1
1:A:20:ASP:HA	1:B:23:PHE:O	0.41	2.15	14	1
1:A:86:ILE:HD11	1:A:94:MET:HB2	0.41	1.93	19	1
1:D:111:ARG:HD3	1:D:128:LEU:O	0.41	2.15	11	1
1:C:123:PHE:HB3	1:C:124:PRO:HD2	0.41	1.92	8	1
1:B:58:VAL:HG21	1:B:98:LEU:HB2	0.41	1.92	14	1
1:C:31:VAL:HG21	1:C:73:ALA:HA	0.41	1.91	11	1
1:B:113:CYS:O	1:B:117:MET:SD	0.41	2.79	4	1
1:A:23:PHE:O	1:B:20:ASP:HA	0.41	2.16	7	1
1:B:117:MET:N	1:B:117:MET:SD	0.41	2.94	4	1
1:C:21:ILE:HB	1:D:23:PHE:HB3	0.41	1.92	8	1
1:B:125:GLN:HB3	1:C:125:GLN:NE2	0.41	2.31	10	1
1:C:80:GLN:NE2	1:C:109:TYR:HB3	0.41	2.31	18	1
1:D:43:ASP:HB3	1:D:63:THR:HB	0.41	1.92	20	1
1:A:86:ILE:HG21	1:A:98:LEU:HD21	0.41	1.92	11	1
1:A:111:ARG:HH12	1:C:105:ILE:HD12	0.41	1.76	5	1
1:A:115:THR:HG23	1:A:125:GLN:HG3	0.41	1.92	6	1
1:D:11:PHE:HA	1:D:85:SER:O	0.41	2.16	12	2
1:D:68:LEU:HG	1:D:73:ALA:HB2	0.41	1.93	20	1
1:C:23:PHE:HB3	1:D:21:ILE:HD12	0.40	1.94	3	1
1:B:62:VAL:HB	1:B:114:ILE:HD11	0.40	1.93	6	1
1:A:89:ILE:HD13	1:A:89:ILE:H	0.40	1.76	13	1
1:B:74:PHE:CE2	1:B:76:CYS:HB3	0.40	2.51	17	1
1:A:122:THR:HB	1:B:15:ARG:NH2	0.40	2.31	20	1
1:D:76:CYS:SG	1:D:117:MET:HE3	0.40	2.57	1	1
1:A:127:ASN:ND2	1:C:15:ARG:HA	0.40	2.32	18	1
1:D:11:PHE:CE2	1:D:102:CYS:SG	0.40	3.12	20	1
1:B:42:LEU:HG	1:B:128:LEU:HG	0.40	1.93	3	1
1:A:115:THR:CG2	1:A:125:GLN:HB2	0.40	2.47	8	1
1:B:130:PRO:HG2	1:D:16:ILE:O	0.40	2.16	14	1
1:C:82:GLY:HA3	1:C:106:LEU:HD21	0.40	1.93	19	1
1:C:30:HIS:CD2	1:C:34:LYS:HD3	0.40	2.52	7	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	124/155 (80%)	117±2 (94±2%)	7±2 (6±2%)	0±0 (0±0%)	100	100
1	B	124/155 (80%)	116±2 (93±2%)	8±2 (6±2%)	0±0 (0±0%)	50	82
1	C	121/155 (78%)	111±2 (92±2%)	10±2 (8±2%)	0±1 (0±0%)	44	80
1	D	123/155 (79%)	118±1 (96±1%)	5±1 (4±1%)	0±0 (0±0%)	54	85
2	E	0	-	-	-	-	-
2	F	0	-	-	-	-	-
2	G	0	-	-	-	-	-
2	H	0	-	-	-	-	-
All	All	9840/15600 (63%)	9233 (94%)	594 (6%)	13 (0%)	54	85

All 11 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	B	124	PRO	2
1	C	124	PRO	2
1	C	131	VAL	1
1	D	26	PRO	1
1	B	91	GLY	1
1	D	91	GLY	1
1	C	86	ILE	1
1	C	87	ALA	1
1	B	131	VAL	1
1	C	89	ILE	1
1	C	129	ALA	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	106/132 (80%)	102±2 (96±1%)	4±2 (4±1%)	38 86
1	B	106/132 (80%)	101±2 (95±2%)	5±2 (5±2%)	29 78
1	C	104/132 (79%)	99±2 (95±2%)	5±2 (5±2%)	27 76
1	D	105/132 (80%)	101±1 (96±1%)	4±1 (4±1%)	36 84
2	E	0	-	-	-
2	F	0	-	-	-
2	G	0	-	-	-
2	H	0	-	-	-
All	All	8420/13120 (64%)	8052 (96%)	368 (4%)	32 81

All 95 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	D	60	LEU	20
1	A	60	LEU	20
1	C	117	MET	19
1	B	60	LEU	19
1	C	34	LYS	16
1	B	89	ILE	11
1	D	70	GLU	10
1	A	89	ILE	10
1	C	89	ILE	9
1	B	125	GLN	8
1	D	90	GLU	8
1	C	60	LEU	7
1	A	128	LEU	7
1	B	42	LEU	7
1	D	56	TYR	6
1	C	86	ILE	6
1	D	89	ILE	6
1	A	94	MET	6
1	C	125	GLN	6
1	A	86	ILE	6
1	B	112	GLU	6
1	C	112	GLU	5
1	C	126	LEU	5
1	D	86	ILE	5
1	B	86	ILE	5
1	C	33	GLN	4
1	C	42	LEU	4
1	B	90	GLU	4

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Mol	Chain	Res	Type	Models (Total)
1	C	98	LEU	4
1	B	39	GLU	4
1	B	12	GLN	4
1	A	126	LEU	3
1	A	56	TYR	3
1	D	36	TRP	3
1	A	61	ARG	3
1	B	94	MET	3
1	C	93	GLN	3
1	B	128	LEU	3
1	B	126	LEU	3
1	B	98	LEU	3
1	C	41	LYS	3
1	C	56	TYR	3
1	D	94	MET	3
1	B	70	GLU	3
1	C	19	LYS	3
1	D	41	LYS	2
1	B	127	ASN	2
1	A	14	GLN	2
1	A	30	HIS	2
1	A	93	GLN	2
1	A	12	GLN	2
1	D	128	LEU	2
1	B	36	TRP	2
1	D	31	VAL	2
1	D	17	TYR	2
1	A	90	GLU	2
1	C	13	ILE	2
1	D	126	LEU	2
1	D	16	ILE	2
1	B	33	GLN	2
1	B	37	GLN	2
1	C	27	ASN	2
1	A	70	GLU	2
1	B	56	TYR	2
1	B	41	LYS	1
1	C	71	GLU	1
1	B	104	ASN	1
1	D	13	ILE	1
1	D	130	PRO	1
1	B	117	MET	1

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Mol	Chain	Res	Type	Models (Total)
1	D	132	ASN	1
1	D	93	GLN	1
1	C	37	GLN	1
1	A	122	THR	1
1	A	112	GLU	1
1	D	34	LYS	1
1	B	74	PHE	1
1	D	39	GLU	1
1	C	94	MET	1
1	B	11	PHE	1
1	C	132	ASN	1
1	C	44	LEU	1
1	B	30	HIS	1
1	B	54	ASP	1
1	B	118	VAL	1
1	C	11	PHE	1
1	A	127	ASN	1
1	A	132	ASN	1
1	D	74	PHE	1
1	C	104	ASN	1
1	A	13	ILE	1
1	B	13	ILE	1
1	A	34	LYS	1
1	B	44	LEU	1
1	C	54	ASP	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

There are no ligands in this entry.

## 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 13% for the well-defined parts and 12% for the entire structure.

### 7.1 Chemical shift list 1

File name: input\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_5*

#### 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	254
Number of shifts mapped to atoms	254
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
$^{13}\text{C}_\alpha$	40	$-0.25 \pm 0.14$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	36	$0.42 \pm 0.29$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	38	$-0.23 \pm 0.13$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	38	$-0.70 \pm 0.31$	Should be applied

#### 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 5893. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	0/2404 (0%)	0/956 (0%)	0/984 (0%)	0/464 (0%)
Sidechain	0/2970 (0%)	0/1732 (0%)	0/1126 (0%)	0/112 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	0/519 (0%)	0/275 (0%)	0/224 (0%)	0/20 (0%)
Overall	0/5893 (0%)	0/2963 (0%)	0/2334 (0%)	0/596 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 2%, i.e. 223 atoms were assigned a chemical shift out of a possible 9376. 0 out of 104 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	153/3828 (4%)	37/1524 (2%)	78/1560 (5%)	38/744 (5%)
Sidechain	70/4636 (2%)	15/2712 (1%)	55/1748 (3%)	0/176 (0%)
Aromatic	0/912 (0%)	0/480 (0%)	0/400 (0%)	0/32 (0%)
Overall	223/9376 (2%)	52/4716 (1%)	133/3708 (4%)	38/952 (4%)

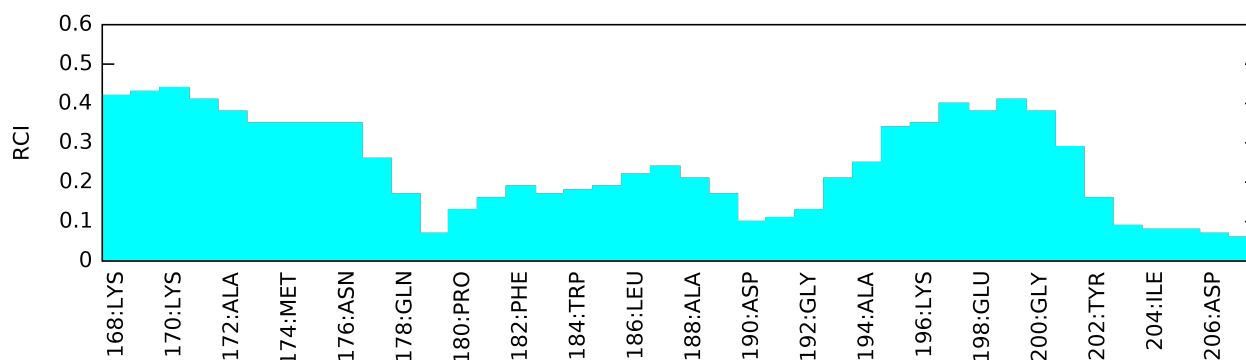
#### 7.1.4 Statistically unusual chemical shifts [i](#)

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 E:



## 7.2 Chemical shift list 2

File name: input\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_6*

### 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	254
Number of shifts mapped to atoms	254
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	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	40	$-0.25 \pm 0.07$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	36	$0.43 \pm 0.24$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	38	$-0.24 \pm 0.10$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	38	$-0.72 \pm 0.30$	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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 5893. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	0/2404 (0%)	0/956 (0%)	0/984 (0%)	0/464 (0%)
Sidechain	0/2970 (0%)	0/1732 (0%)	0/1126 (0%)	0/112 (0%)
Aromatic	0/519 (0%)	0/275 (0%)	0/224 (0%)	0/20 (0%)
Overall	0/5893 (0%)	0/2963 (0%)	0/2334 (0%)	0/596 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 2%, i.e. 223 atoms were assigned a chemical shift out of a possible 9376. 0 out of 104 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	153/3828 (4%)	37/1524 (2%)	78/1560 (5%)	38/744 (5%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Sidechain	70/4636 (2%)	15/2712 (1%)	55/1748 (3%)	0/176 (0%)
Aromatic	0/912 (0%)	0/480 (0%)	0/400 (0%)	0/32 (0%)
Overall	223/9376 (2%)	52/4716 (1%)	133/3708 (4%)	38/952 (4%)

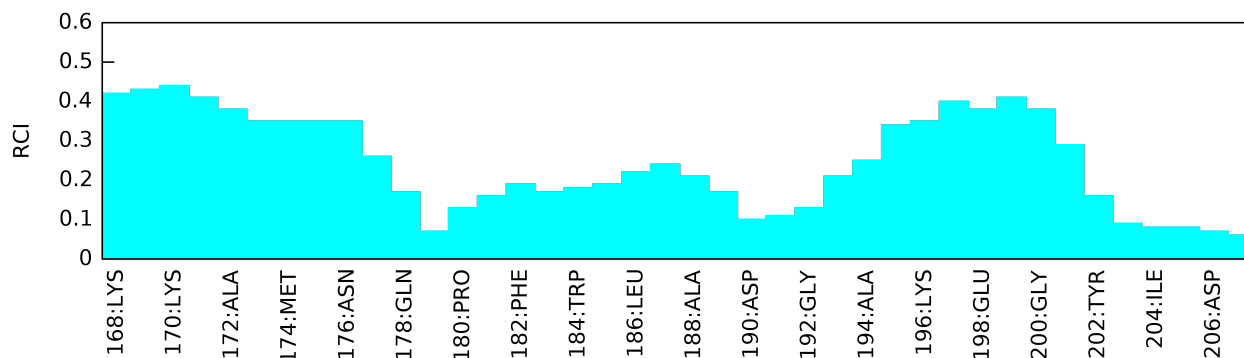
#### 7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 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.

Random coil index (RCI) for chain E:



### 7.3 Chemical shift list 3

File name: input\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_7*

#### 7.3.1 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	254
Number of shifts mapped to atoms	254

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

### 7.3.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	40	$-0.25 \pm 0.18$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	36	$0.45 \pm 0.28$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	38	$-0.24 \pm 0.15$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	38	$-0.71 \pm 0.30$	Should be applied

### 7.3.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 5893. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	0/2404 (0%)	0/956 (0%)	0/984 (0%)	0/464 (0%)
Sidechain	0/2970 (0%)	0/1732 (0%)	0/1126 (0%)	0/112 (0%)
Aromatic	0/519 (0%)	0/275 (0%)	0/224 (0%)	0/20 (0%)
Overall	0/5893 (0%)	0/2963 (0%)	0/2334 (0%)	0/596 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 2%, i.e. 223 atoms were assigned a chemical shift out of a possible 9376. 0 out of 104 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	153/3828 (4%)	37/1524 (2%)	78/1560 (5%)	38/744 (5%)
Sidechain	70/4636 (2%)	15/2712 (1%)	55/1748 (3%)	0/176 (0%)
Aromatic	0/912 (0%)	0/480 (0%)	0/400 (0%)	0/32 (0%)
Overall	223/9376 (2%)	52/4716 (1%)	133/3708 (4%)	38/952 (4%)

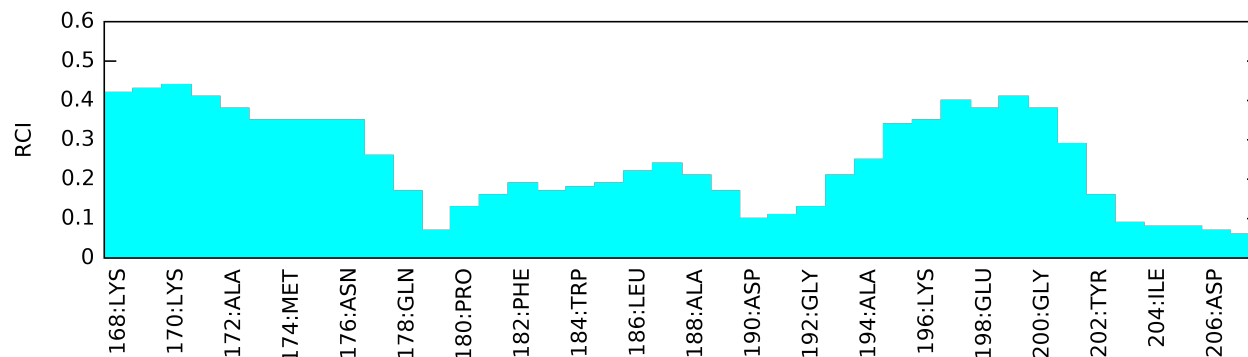
### 7.3.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

### 7.3.5 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 E:



## 7.4 Chemical shift list 4

File name: input\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_8*

### 7.4.1 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	254
Number of shifts mapped to atoms	254
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

### 7.4.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

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Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	40	$-0.25 \pm 0.08$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	36	$0.44 \pm 0.15$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	38	$-0.24 \pm 0.11$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	38	$-0.72 \pm 0.30$	Should be applied

### 7.4.3 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 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 5893. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	0/2404 (0%)	0/956 (0%)	0/984 (0%)	0/464 (0%)
Sidechain	0/2970 (0%)	0/1732 (0%)	0/1126 (0%)	0/112 (0%)
Aromatic	0/519 (0%)	0/275 (0%)	0/224 (0%)	0/20 (0%)
Overall	0/5893 (0%)	0/2963 (0%)	0/2334 (0%)	0/596 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 2%, i.e. 223 atoms were assigned a chemical shift out of a possible 9376. 0 out of 104 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	153/3828 (4%)	37/1524 (2%)	78/1560 (5%)	38/744 (5%)
Sidechain	70/4636 (2%)	15/2712 (1%)	55/1748 (3%)	0/176 (0%)
Aromatic	0/912 (0%)	0/480 (0%)	0/400 (0%)	0/32 (0%)
Overall	223/9376 (2%)	52/4716 (1%)	133/3708 (4%)	38/952 (4%)

### 7.4.4 Statistically unusual chemical shifts [i](#)

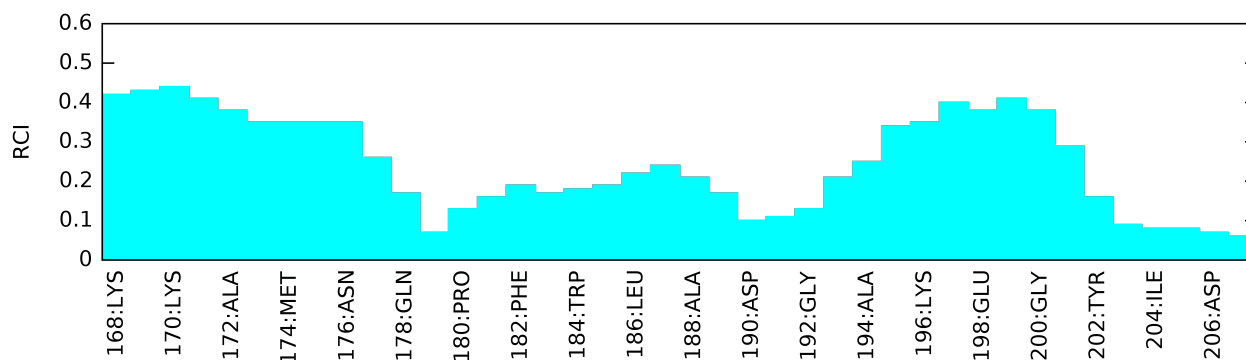
There are no statistically unusual chemical shifts.

### 7.4.5 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 E:



## 7.5 Chemical shift list 5

File name: input\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_list\_1*

### 7.5.1 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	1049
Number of shifts mapped to atoms	1049
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

### 7.5.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_{\alpha}$	139	$0.25 \pm 0.11$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_{\beta}$	128	$0.84 \pm 0.20$	Should be applied
$^{13}\text{C}'$	137	$0.29 \pm 0.10$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	133	$-1.16 \pm 0.30$	Should be applied

### 7.5.3 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 13%, i.e. 785 atoms were assigned a chemical shift out of a possible 5893. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	455/2404 (19%)	111/956 (12%)	233/984 (24%)	111/464 (24%)
Sidechain	217/2970 (7%)	60/1732 (3%)	157/1126 (14%)	0/112 (0%)
Aromatic	113/519 (22%)	57/275 (21%)	55/224 (25%)	1/20 (5%)
Overall	785/5893 (13%)	228/2963 (8%)	445/2334 (19%)	112/596 (19%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 10%, i.e. 930 atoms were assigned a chemical shift out of a possible 9376. 0 out of 104 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	542/3828 (14%)	133/1524 (9%)	276/1560 (18%)	133/744 (18%)
Sidechain	255/4636 (6%)	70/2712 (3%)	185/1748 (11%)	0/176 (0%)
Aromatic	133/912 (15%)	67/480 (14%)	65/400 (16%)	1/32 (3%)
Overall	930/9376 (10%)	270/4716 (6%)	526/3708 (14%)	134/952 (14%)

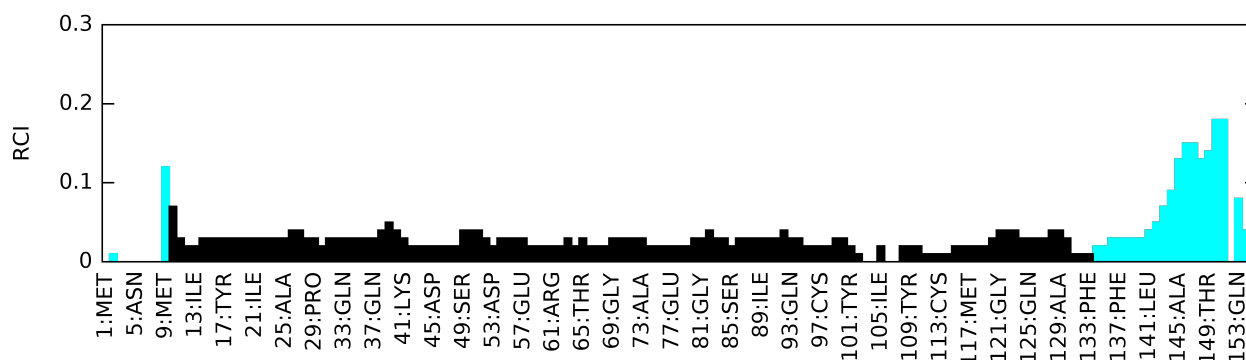
### 7.5.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

### 7.5.5 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:



## 7.6 Chemical shift list 6

File name: input\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_list\_2*

### 7.6.1 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	1044
Number of shifts mapped to atoms	1044
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

### 7.6.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	140	$0.27 \pm 0.12$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	126	$0.78 \pm 0.16$	Should be applied
$^{13}\text{C}'$	135	$0.26 \pm 0.12$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	132	$-1.09 \pm 0.27$	Should be applied

### 7.6.3 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 13%, i.e. 780 atoms were assigned a chemical shift out of a possible 5893. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned

stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	452/2404 (19%)	110/956 (12%)	232/984 (24%)	110/464 (24%)
Sidechain	215/2970 (7%)	60/1732 (3%)	155/1126 (14%)	0/112 (0%)
Aromatic	113/519 (22%)	57/275 (21%)	55/224 (25%)	1/20 (5%)
Overall	780/5893 (13%)	227/2963 (8%)	442/2334 (19%)	111/596 (19%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 10%, i.e. 925 atoms were assigned a chemical shift out of a possible 9376. 0 out of 104 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	539/3828 (14%)	132/1524 (9%)	275/1560 (18%)	132/744 (18%)
Sidechain	253/4636 (5%)	70/2712 (3%)	183/1748 (10%)	0/176 (0%)
Aromatic	133/912 (15%)	67/480 (14%)	65/400 (16%)	1/32 (3%)
Overall	925/9376 (10%)	269/4716 (6%)	523/3708 (14%)	133/952 (14%)

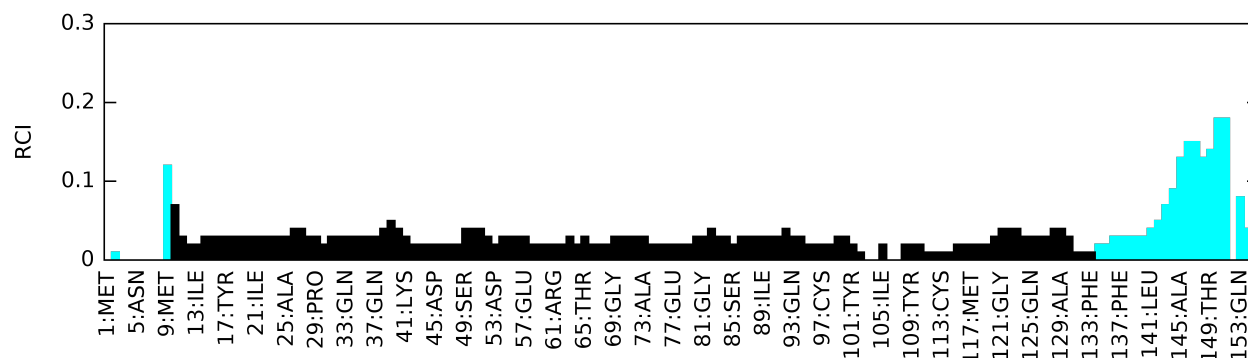
#### 7.6.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 7.6.5 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:



## 7.7 Chemical shift list 7

File name: input\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_list\_3*

### 7.7.1 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	1044
Number of shifts mapped to atoms	1044
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

### 7.7.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	140	$0.27 \pm 0.09$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	126	$0.79 \pm 0.20$	Should be applied
$^{13}\text{C}'$	135	$0.26 \pm 0.11$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	132	$-1.08 \pm 0.27$	Should be applied

### 7.7.3 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 13%, i.e. 780 atoms were assigned a chemical shift out of a possible 5893. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	452/2404 (19%)	110/956 (12%)	232/984 (24%)	110/464 (24%)
Sidechain	215/2970 (7%)	60/1732 (3%)	155/1126 (14%)	0/112 (0%)
Aromatic	113/519 (22%)	57/275 (21%)	55/224 (25%)	1/20 (5%)
Overall	780/5893 (13%)	227/2963 (8%)	442/2334 (19%)	111/596 (19%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 10%, i.e. 925 atoms were assigned a chemical shift out of a possible 9376. 0 out of 104 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	539/3828 (14%)	132/1524 (9%)	275/1560 (18%)	132/744 (18%)
Sidechain	253/4636 (5%)	70/2712 (3%)	183/1748 (10%)	0/176 (0%)
Aromatic	133/912 (15%)	67/480 (14%)	65/400 (16%)	1/32 (3%)
Overall	925/9376 (10%)	269/4716 (6%)	523/3708 (14%)	133/952 (14%)

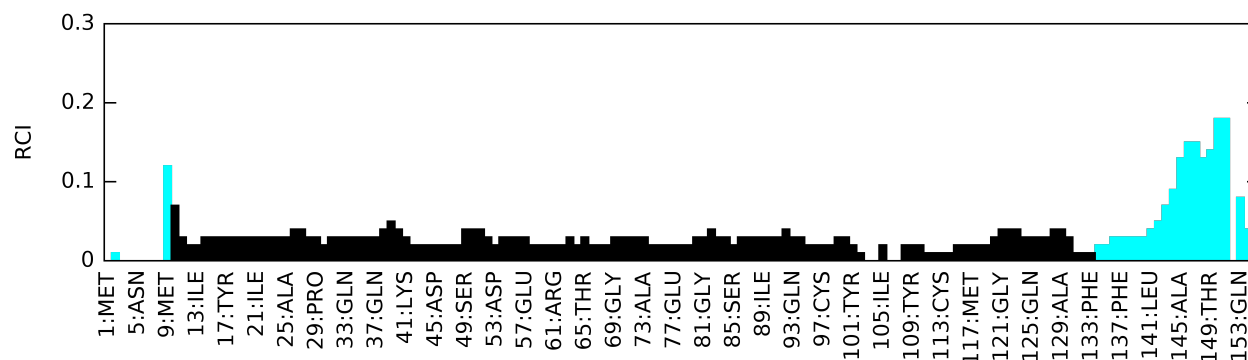
#### 7.7.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 7.7.5 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:



### 7.8 Chemical shift list 8

File name: input\_cs.cif

Chemical shift list name: *assigned\_chemical\_shift\_list\_4*

#### 7.8.1 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	1049
Number of shifts mapped to atoms	1049

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

### 7.8.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	139	$0.26 \pm 0.11$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	128	$0.85 \pm 0.17$	Should be applied
$^{13}\text{C}'$	137	$0.29 \pm 0.16$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	133	$-1.16 \pm 0.32$	Should be applied

### 7.8.3 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 13%, i.e. 785 atoms were assigned a chemical shift out of a possible 5893. 0 out of 80 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	455/2404 (19%)	111/956 (12%)	233/984 (24%)	111/464 (24%)
Sidechain	217/2970 (7%)	60/1732 (3%)	157/1126 (14%)	0/112 (0%)
Aromatic	113/519 (22%)	57/275 (21%)	55/224 (25%)	1/20 (5%)
Overall	785/5893 (13%)	228/2963 (8%)	445/2334 (19%)	112/596 (19%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 10%, i.e. 930 atoms were assigned a chemical shift out of a possible 9376. 0 out of 104 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	542/3828 (14%)	133/1524 (9%)	276/1560 (18%)	133/744 (18%)
Sidechain	255/4636 (6%)	70/2712 (3%)	185/1748 (11%)	0/176 (0%)
Aromatic	133/912 (15%)	67/480 (14%)	65/400 (16%)	1/32 (3%)
Overall	930/9376 (10%)	270/4716 (6%)	526/3708 (14%)	134/952 (14%)

### 7.8.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

### 7.8.5 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:

