



# Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 11:57 pm BST

PDB ID : 2M1K  
Title : Interaction of Human S100A6 (C3S) with V domain of Receptor for Advanced Glycation End products (RAGE)  
Authors : Gupta, A.A.; Yu, C.  
Deposited on : 2012-11-29

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

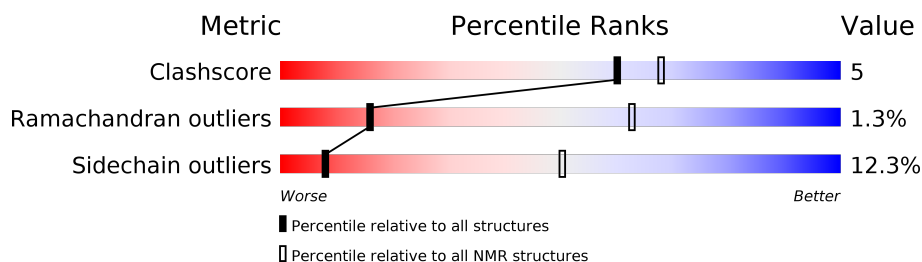
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 8%.

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	B	90	 96%
1	D	90	 96%
2	A	101	 76% 24%
2	C	101	 73% 26%

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 6 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	B:2-B:90, D:2-D:90, A:21-A:121, C:21-C:121 (380)	0.62	6

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters. No single-model clusters were found.

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6060 atoms, of which 3070 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein S100-A6.

Mol	Chain	Residues	Atoms						Trace
1	B	89	Total	C	H	N	O	S	0
			1431	449	724	119	138	1	
1	D	89	Total	C	H	N	O	S	0
			1431	449	724	119	138	1	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	3	SER	CYS	ENGINEERED MUTATION	UNP P06703
D	3	SER	CYS	ENGINEERED MUTATION	UNP P06703

- Molecule 2 is a protein called Advanced glycosylation end product-specific receptor.

Mol	Chain	Residues	Atoms						Trace
2	A	101	Total	C	H	N	O	S	0
			1599	498	811	148	138	4	
2	C	101	Total	C	H	N	O	S	0
			1599	498	811	148	138	4	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	ALA	-	EXPRESSION TAG	UNP Q15109
A	22	MET	-	EXPRESSION TAG	UNP Q15109
C	21	ALA	-	EXPRESSION TAG	UNP Q15109
C	22	MET	-	EXPRESSION TAG	UNP Q15109

## 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 S100-A6

Chain B:  96%



- Molecule 1: Protein S100-A6

Chain D:  96%



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A:  76% 24%



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain C:  73% 26%



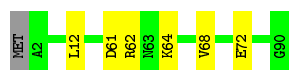
### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

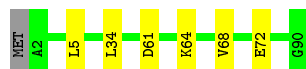
- Molecule 1: Protein S100-A6

Chain B:  92% 7%



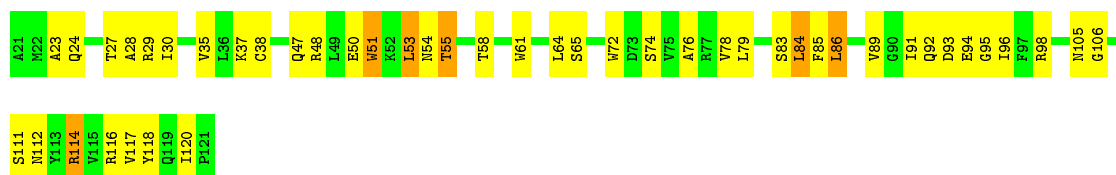
- Molecule 1: Protein S100-A6

Chain D:  92% 7%



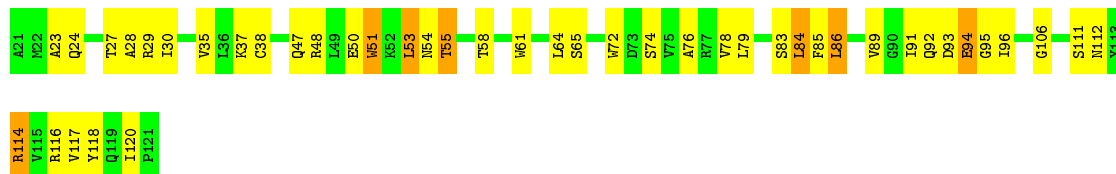
- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A:  54% 40% 6%



- Molecule 2: Advanced glycosylation end product-specific receptor

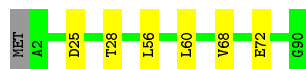
Chain C:  56% 37% 7%



#### 4.2.2 Score per residue for model 2

- Molecule 1: Protein S100-A6

Chain B:  92% 7%

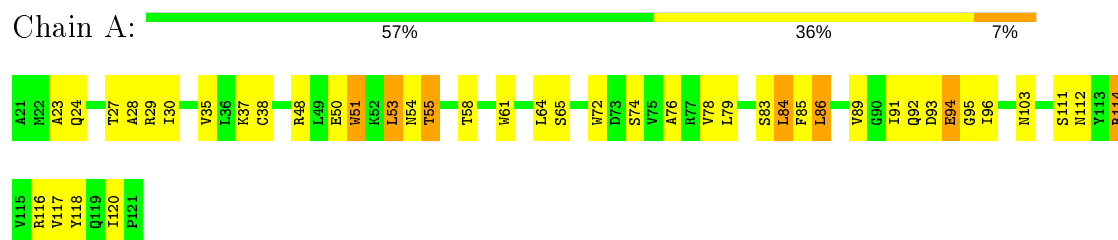


- Molecule 1: Protein S100-A6

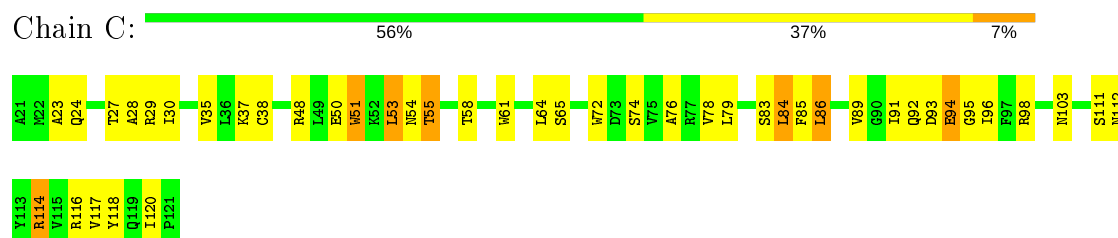
Chain D:  92% 7%



- Molecule 2: Advanced glycosylation end product-specific receptor

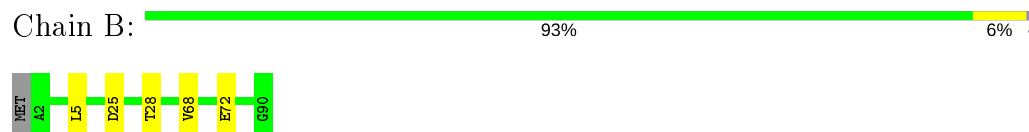


- Molecule 2: Advanced glycosylation end product-specific receptor

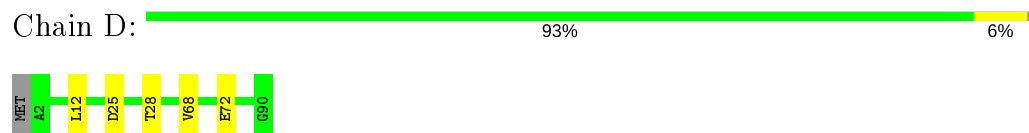


#### 4.2.3 Score per residue for model 3

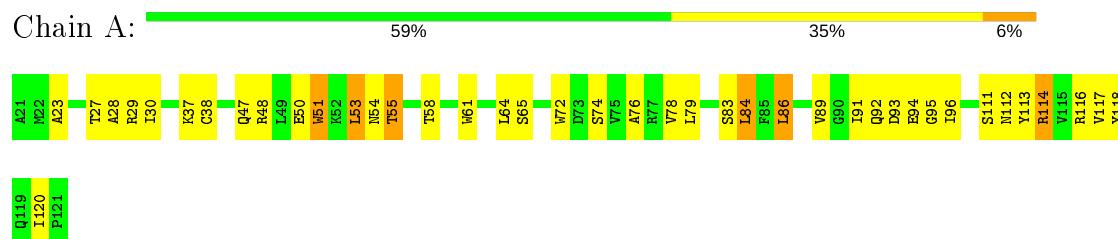
- Molecule 1: Protein S100-A6



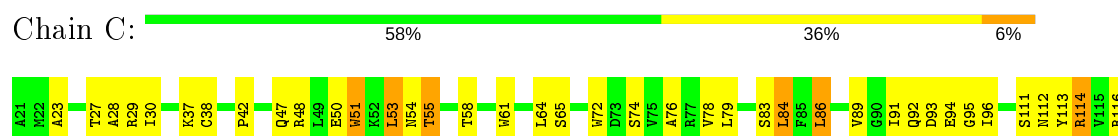
- Molecule 1: Protein S100-A6



- Molecule 2: Advanced glycosylation end product-specific receptor



- Molecule 2: Advanced glycosylation end product-specific receptor





#### 4.2.4 Score per residue for model 4

- Molecule 1: Protein S100-A6

Chain B: 99%



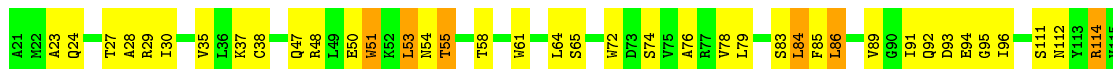
- Molecule 1: Protein S100-A6

Chain D: 97%



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A: 57% 37% 6%



- Molecule 2: Advanced glycosylation end product-specific receptor

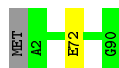
Chain C: 56% 37% 7%



#### 4.2.5 Score per residue for model 5

- Molecule 1: Protein S100-A6

Chain B: 98%



- Molecule 1: Protein S100-A6

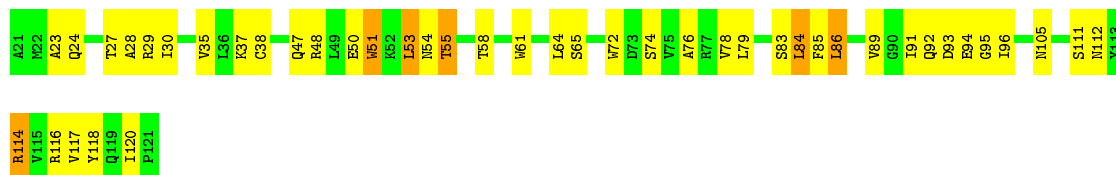


Chain D:  99%



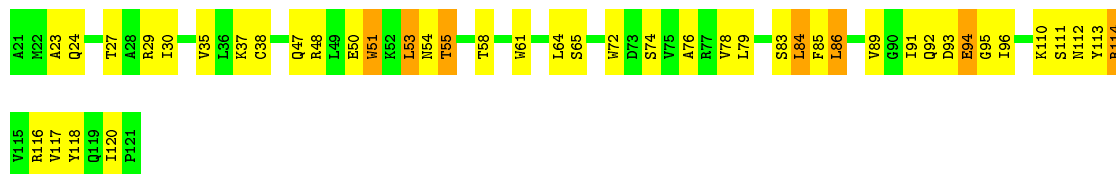
- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A:  56% 38% 6%



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain C:  56% 37% 7%



#### 4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Protein S100-A6

Chain B:  97%



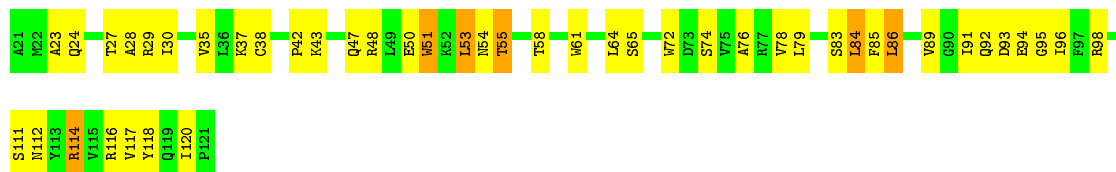
- Molecule 1: Protein S100-A6

Chain D:  94%

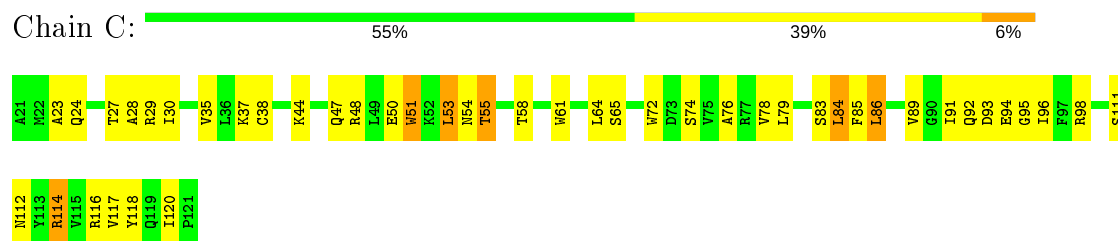


- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A:  54% 40% 6%

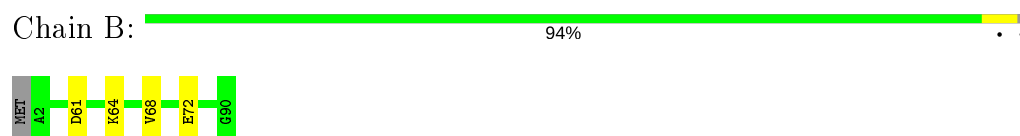


- Molecule 2: Advanced glycosylation end product-specific receptor

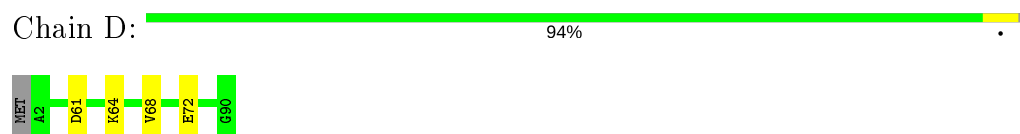


#### 4.2.7 Score per residue for model 7

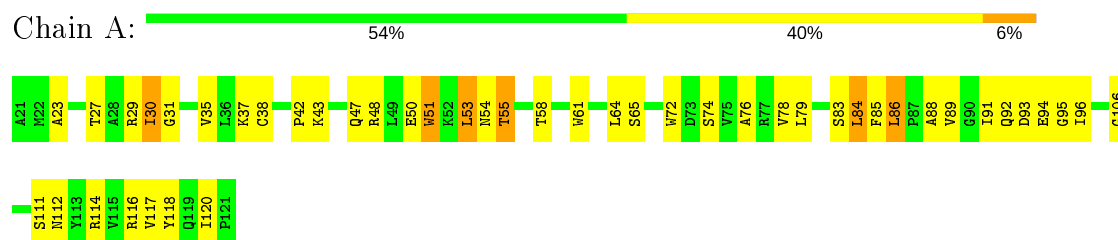
- Molecule 1: Protein S100-A6



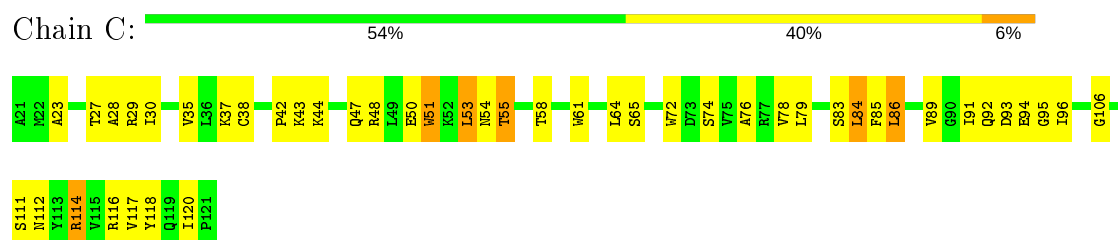
- Molecule 1: Protein S100-A6



- Molecule 2: Advanced glycosylation end product-specific receptor




- Molecule 2: Advanced glycosylation end product-specific receptor



#### 4.2.8 Score per residue for model 8

- Molecule 1: Protein S100-A6

Chain B:  90% 9%



- Molecule 1: Protein S100-A6

Chain D:  94%



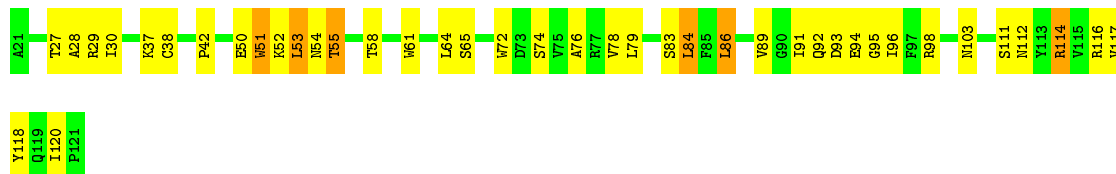
- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A:  60% 35% 5%



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain C:  59% 35% 6%




#### 4.2.9 Score per residue for model 9

- Molecule 1: Protein S100-A6

Chain B:  92% 7%

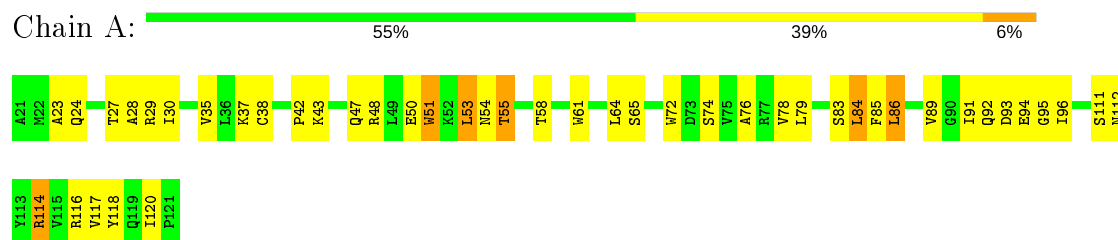


- Molecule 1: Protein S100-A6

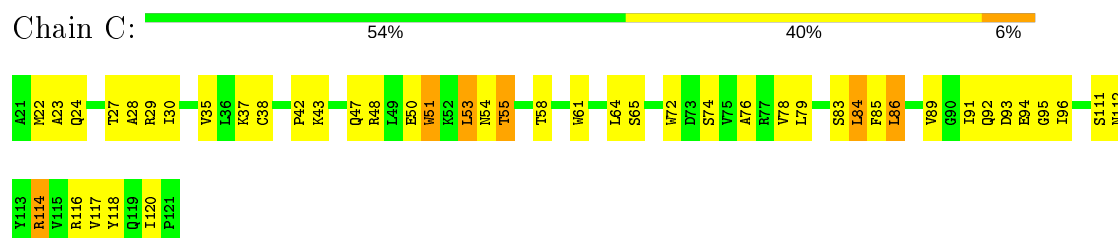
Chain D:  90% 9%



- Molecule 2: Advanced glycosylation end product-specific receptor

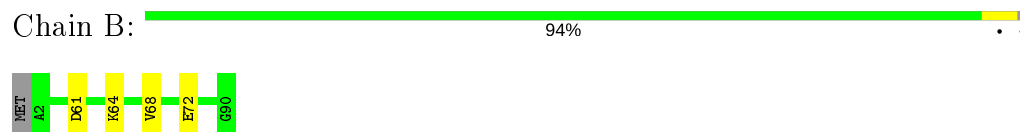


- Molecule 2: Advanced glycosylation end product-specific receptor

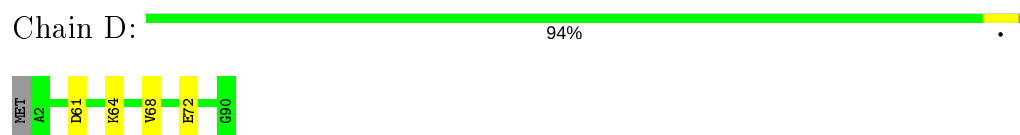


#### 4.2.10 Score per residue for model 10

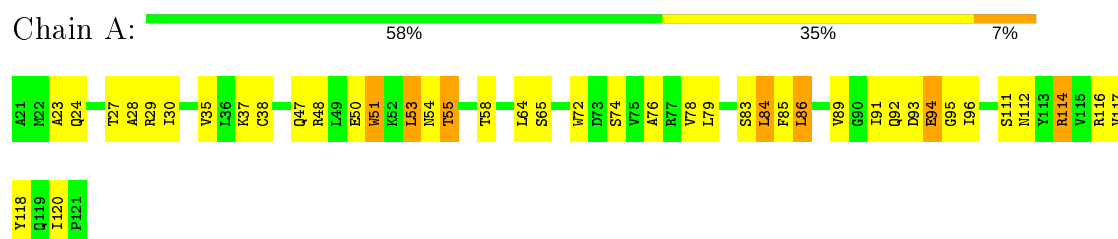
- Molecule 1: Protein S100-A6



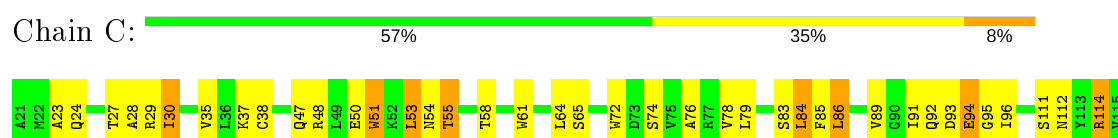
- Molecule 1: Protein S100-A6



- Molecule 2: Advanced glycosylation end product-specific receptor



- Molecule 2: Advanced glycosylation end product-specific receptor





#### 4.2.11 Score per residue for model 11

- Molecule 1: Protein S100-A6

Chain B: 86% 12% ..



- Molecule 1: Protein S100-A6

Chain D: 86% 12% ..



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A: 82% 18%



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain C: 87% 12% .



#### 4.2.12 Score per residue for model 12

- Molecule 1: Protein S100-A6

Chain B: 86% 12% ..

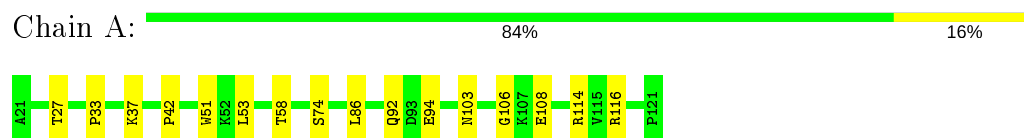


- Molecule 1: Protein S100-A6

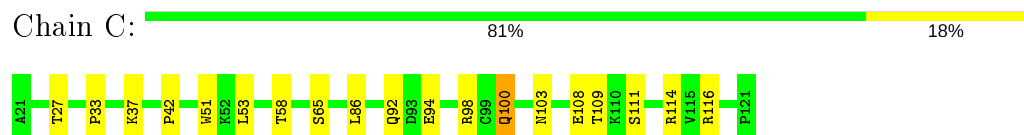
Chain D: 83% 14% ..



- Molecule 2: Advanced glycosylation end product-specific receptor

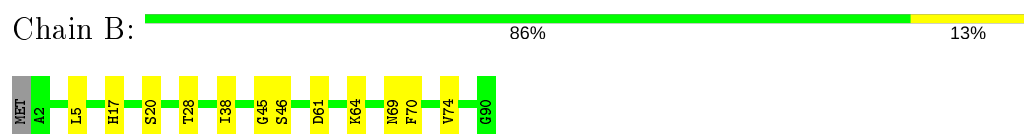


- Molecule 2: Advanced glycosylation end product-specific receptor

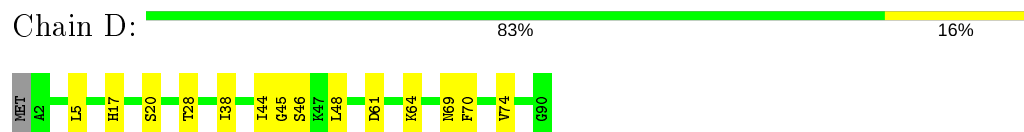


#### 4.2.13 Score per residue for model 13

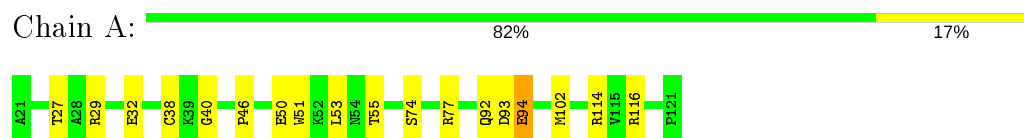
- Molecule 1: Protein S100-A6



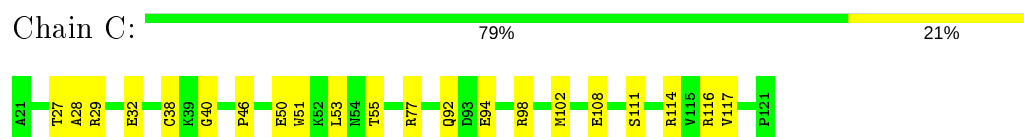
- Molecule 1: Protein S100-A6



- Molecule 2: Advanced glycosylation end product-specific receptor



- Molecule 2: Advanced glycosylation end product-specific receptor



#### 4.2.14 Score per residue for model 14

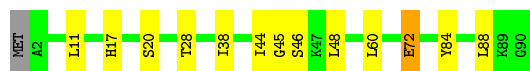
- Molecule 1: Protein S100-A6





- Molecule 1: Protein S100-A6

Chain D: 84% 13% ..



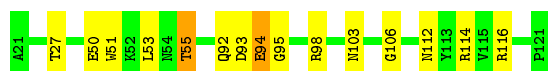
- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A: 87% 12% .



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain C: 85% 13% .



#### 4.2.15 Score per residue for model 15

- Molecule 1: Protein S100-A6

Chain B: 87% 12% .



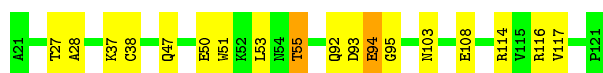
- Molecule 1: Protein S100-A6

Chain D: 89% 10% .



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A: 82% 16% .



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain C: 81% 18% .



#### 4.2.16 Score per residue for model 16

- Molecule 1: Protein S100-A6

Chain B: 88% 10% ..



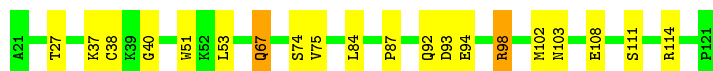
- Molecule 1: Protein S100-A6

Chain D: 88% 10% ..



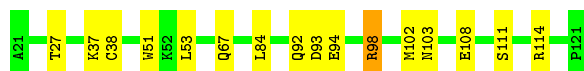
- Molecule 2: Advanced glycosylation end product-specific receptor

Chain A: 80% 18% .



- Molecule 2: Advanced glycosylation end product-specific receptor

Chain C: 84% 15% .



#### 4.2.17 Score per residue for model 17

- Molecule 1: Protein S100-A6

Chain B: 91% 8% .



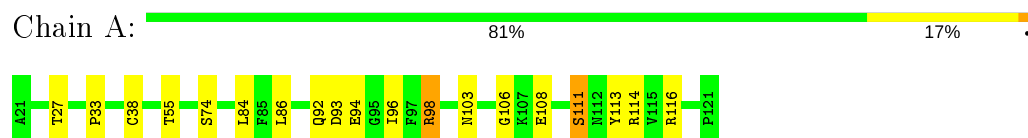
- Molecule 1: Protein S100-A6

Chain D: 88% 11% .

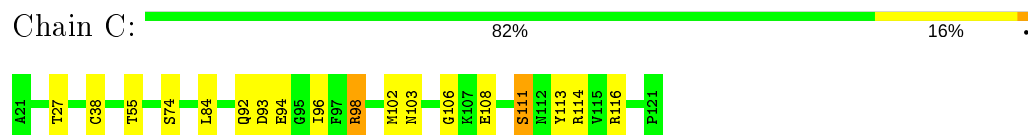




- Molecule 2: Advanced glycosylation end product-specific receptor

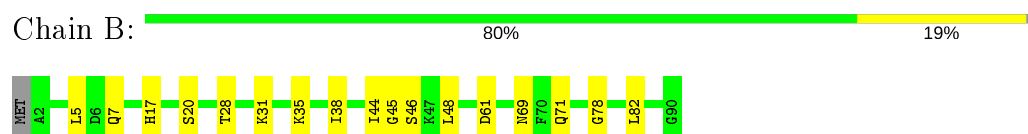


- Molecule 2: Advanced glycosylation end product-specific receptor

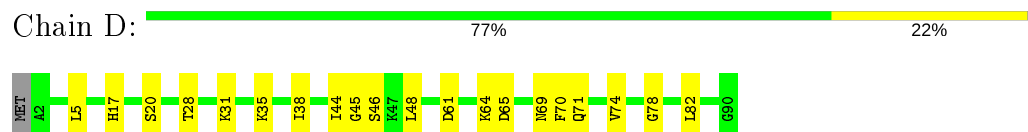


#### 4.2.18 Score per residue for model 18

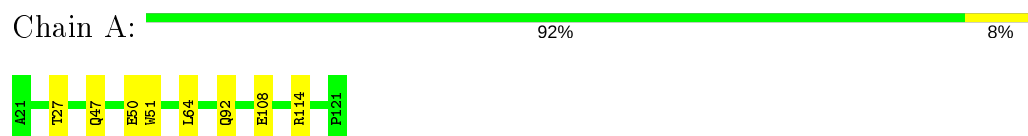
- Molecule 1: Protein S100-A6



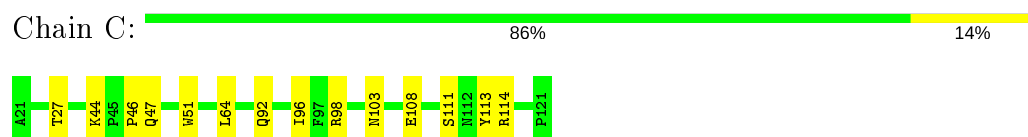
- Molecule 1: Protein S100-A6



- Molecule 2: Advanced glycosylation end product-specific receptor

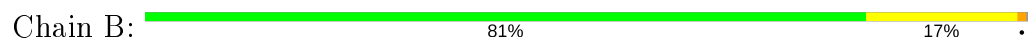


- Molecule 2: Advanced glycosylation end product-specific receptor



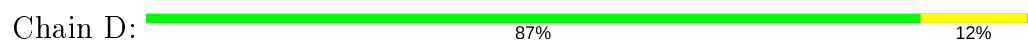
#### 4.2.19 Score per residue for model 19

- Molecule 1: Protein S100-A6

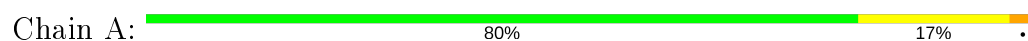




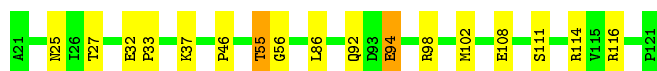
- Molecule 1: Protein S100-A6



- Molecule 2: Advanced glycosylation end product-specific receptor

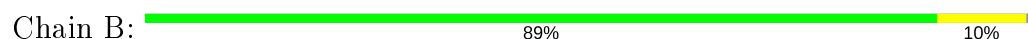


- Molecule 2: Advanced glycosylation end product-specific receptor



#### 4.2.20 Score per residue for model 20

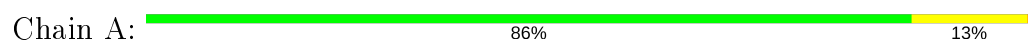
- Molecule 1: Protein S100-A6



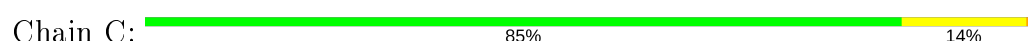
- Molecule 1: Protein S100-A6

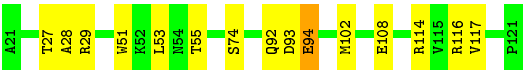


- Molecule 2: Advanced glycosylation end product-specific receptor



- Molecule 2: Advanced glycosylation end product-specific receptor





## 5 Refinement protocol and experimental data overview

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

Of the 200 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
HADDOCK	structure solution	
HADDOCK	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	5
Total number of shifts	441
Number of shifts mapped to atoms	441
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	8%

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	B	707	724	721	3±2
1	D	707	724	721	3±2
2	A	788	811	808	11±9
2	C	788	811	808	12±9
All	All	59800	61400	61160	571

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:64:LEU:HD21	2:C:72:TRP:CZ3	0.76	2.16	4	10
2:A:64:LEU:HD21	2:A:72:TRP:CZ3	0.76	2.16	7	10
2:C:35:VAL:HG22	2:C:85:PHE:CD1	0.71	2.21	2	8
2:A:35:VAL:HG22	2:A:85:PHE:CD1	0.70	2.20	9	8
2:A:78:VAL:HG13	2:A:83:SER:O	0.70	1.87	1	10
2:C:78:VAL:HG13	2:C:83:SER:O	0.70	1.87	1	10
1:B:68:VAL:HA	1:B:72:GLU:OE1	0.66	1.91	7	8
1:D:68:VAL:HA	1:D:72:GLU:OE1	0.61	1.96	7	8
1:D:60:LEU:O	1:D:72:GLU:HG2	0.60	1.96	14	1
2:C:23:ALA:HA	2:C:112:ASN:O	0.60	1.97	4	9
2:A:23:ALA:HA	2:A:112:ASN:O	0.60	1.97	7	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:28:ALA:O	2:C:117:VAL:HA	0.60	1.97	3	12
2:C:94:GLU:OE2	2:C:116:ARG:HD2	0.59	1.98	15	7
2:A:64:LEU:HD21	2:A:72:TRP:CE3	0.59	2.33	9	10
2:C:64:LEU:HD21	2:C:72:TRP:CE3	0.59	2.33	2	10
2:A:72:TRP:CZ2	2:A:84:LEU:HD21	0.58	2.34	4	10
2:C:72:TRP:CZ2	2:C:84:LEU:HD21	0.57	2.34	4	10
2:A:96:ILE:HG23	2:A:113:TYR:O	0.57	2.00	8	2
1:D:17:HIS:HA	1:D:20:SER:OG	0.57	1.99	18	9
2:A:55:THR:HG23	2:A:95:GLY:HA3	0.57	1.77	8	10
2:C:55:THR:HG23	2:C:95:GLY:HA3	0.56	1.77	1	10
1:B:61:ASP:OD2	1:B:64:LYS:HA	0.56	2.01	16	6
1:D:61:ASP:OD2	1:D:64:LYS:HA	0.56	2.00	16	6
1:B:60:LEU:O	1:B:72:GLU:HG2	0.55	2.02	14	1
2:A:28:ALA:O	2:A:117:VAL:HA	0.55	2.01	9	10
2:A:98:ARG:HA	2:A:111:SER:O	0.54	2.01	17	3
2:A:89:VAL:HG13	2:A:93:ASP:CB	0.54	2.33	9	10
2:C:89:VAL:HG13	2:C:93:ASP:CB	0.54	2.33	8	10
1:B:17:HIS:HA	1:B:20:SER:OG	0.53	2.02	11	9
2:C:51:TRP:HB2	2:C:64:LEU:HD23	0.53	1.81	8	10
2:A:76:ALA:HB2	2:A:86:LEU:HG	0.53	1.80	10	10
2:C:76:ALA:HB2	2:C:86:LEU:HG	0.53	1.80	4	10
2:A:51:TRP:HB2	2:A:64:LEU:HD23	0.53	1.81	9	10
2:C:94:GLU:OE2	2:C:116:ARG:HD3	0.53	2.03	17	1
1:B:38:ILE:O	1:B:45:GLY:HA3	0.52	2.04	16	9
2:A:96:ILE:HG23	2:A:113:TYR:C	0.52	2.24	8	2
2:C:94:GLU:OE2	2:C:117:VAL:HG22	0.52	2.04	5	5
1:D:38:ILE:O	1:D:45:GLY:HA3	0.51	2.05	16	10
2:A:94:GLU:OE2	2:A:116:ARG:HD2	0.51	2.04	15	5
2:A:57:ARG:HB3	2:A:59:GLU:OE2	0.50	2.06	11	1
2:C:98:ARG:HA	2:C:111:SER:O	0.50	2.06	17	6
1:B:5:LEU:HG	1:D:12:LEU:CD2	0.49	2.37	9	2
1:B:78:GLY:O	1:B:82:LEU:HG	0.49	2.08	18	1
2:A:94:GLU:OE2	2:A:117:VAL:HG22	0.49	2.07	10	2
2:C:98:ARG:HB2	2:C:112:ASN:ND2	0.49	2.23	6	3
2:C:89:VAL:HG13	2:C:93:ASP:HB3	0.49	1.85	3	10
2:A:89:VAL:HG13	2:A:93:ASP:HB3	0.49	1.85	9	10
2:C:57:ARG:HB3	2:C:59:GLU:OE2	0.48	2.08	11	1
2:A:79:LEU:N	2:A:79:LEU:HD22	0.48	2.24	9	7
2:C:79:LEU:HD22	2:C:79:LEU:N	0.48	2.24	2	6
2:C:79:LEU:N	2:C:79:LEU:HD22	0.48	2.24	3	4
1:D:64:LYS:O	2:C:44:LYS:HD3	0.48	2.09	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:33:PRO:HA	2:C:86:LEU:O	0.48	2.09	19	2
2:A:79:LEU:HD22	2:A:79:LEU:N	0.48	2.24	10	3
2:A:55:THR:CG2	2:A:95:GLY:HA3	0.47	2.39	14	2
2:A:96:ILE:HG22	2:A:112:ASN:HD22	0.47	1.69	7	7
2:A:24:GLN:O	2:A:114:ARG:N	0.47	2.47	4	7
2:A:98:ARG:HB2	2:A:112:ASN:ND2	0.47	2.24	6	2
2:A:96:ILE:HA	2:A:113:TYR:O	0.47	2.09	17	2
1:D:34:LEU:HD22	1:D:68:VAL:HG21	0.47	1.87	1	1
2:C:96:ILE:CG1	2:C:114:ARG:HG2	0.47	2.40	4	10
2:A:96:ILE:CG1	2:A:114:ARG:HG2	0.46	2.40	10	8
1:B:12:LEU:CD2	1:D:5:LEU:HG	0.46	2.40	9	3
2:A:75:VAL:O	2:A:87:PRO:HD2	0.46	2.11	16	1
1:D:31:LYS:O	1:D:35:LYS:HB2	0.46	2.11	18	1
2:C:24:GLN:O	2:C:114:ARG:N	0.46	2.49	9	7
1:B:65:ASP:OD1	1:B:67:GLU:HB2	0.46	2.10	12	1
1:D:44:ILE:O	1:D:48:LEU:HG	0.46	2.11	18	6
2:C:96:ILE:HG22	2:C:112:ASN:HD22	0.45	1.71	1	4
1:D:78:GLY:O	1:D:82:LEU:HG	0.45	2.12	18	1
1:D:65:ASP:O	1:D:66:GLN:HB2	0.45	2.11	12	1
1:D:70:PHE:O	1:D:74:VAL:HG23	0.45	2.11	11	4
1:B:44:ILE:O	1:B:48:LEU:HG	0.45	2.12	18	4
2:C:100:GLN:HG3	2:C:109:THR:O	0.45	2.12	12	1
1:B:72:GLU:HG2	2:A:105:ASN:ND2	0.44	2.27	5	1
1:B:69:ASN:HB3	2:A:107:LYS:CE	0.44	2.43	19	1
2:C:53:LEU:HD11	2:C:58:THR:HG23	0.44	1.88	12	1
2:A:31:GLY:HA2	2:A:88:ALA:HB1	0.43	1.90	7	1
2:C:96:ILE:HA	2:C:113:TYR:O	0.43	2.13	17	2
2:C:55:THR:CG2	2:C:95:GLY:HA3	0.43	2.43	14	1
1:B:70:PHE:O	1:B:74:VAL:HG23	0.43	2.13	11	5
2:A:94:GLU:OE2	2:A:116:ARG:HD3	0.43	2.13	17	1
2:A:55:THR:HG22	2:A:56:GLY:H	0.43	1.72	19	1
2:C:35:VAL:CG2	2:C:85:PHE:CD1	0.43	3.00	10	8
1:B:56:LEU:O	1:B:60:LEU:HG	0.43	2.14	2	1
2:C:96:ILE:HG23	2:C:113:TYR:O	0.43	2.14	3	3
2:A:33:PRO:HA	2:A:86:LEU:O	0.42	2.14	17	3
2:C:29:ARG:HD2	2:C:32:GLU:OE1	0.42	2.14	13	1
2:C:53:LEU:HD21	2:C:61:TRP:HA	0.42	1.91	3	10
2:C:96:ILE:HG23	2:C:113:TYR:C	0.42	2.35	3	1
2:C:98:ARG:HD2	2:C:112:ASN:OD1	0.42	2.14	14	1
1:B:25:ASP:HB3	1:B:28:THR:OG1	0.42	2.15	3	3
1:B:65:ASP:O	1:B:66:GLN:HB2	0.42	2.15	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:55:THR:HG22	2:C:56:GLY:H	0.42	1.75	19	1
2:A:51:TRP:CZ3	2:A:53:LEU:CD2	0.42	3.03	1	10
2:A:35:VAL:CG2	2:A:85:PHE:CD1	0.42	3.00	9	1
2:A:53:LEU:HD21	2:A:61:TRP:HA	0.42	1.92	3	7
2:A:98:ARG:HD2	2:A:112:ASN:OD1	0.42	2.15	14	1
2:C:51:TRP:O	2:C:61:TRP:CD1	0.41	2.74	5	10
2:C:51:TRP:CZ3	2:C:53:LEU:CD2	0.41	3.03	4	10
2:A:29:ARG:HD2	2:A:32:GLU:OE1	0.41	2.15	13	1
1:B:7:GLN:OE1	1:B:7:GLN:HA	0.41	2.15	18	1
2:A:51:TRP:O	2:A:61:TRP:CD1	0.41	2.74	9	9
2:C:30:ILE:HG23	2:C:117:VAL:HB	0.41	1.91	10	1
1:D:25:ASP:HB3	1:D:28:THR:OG1	0.41	2.15	4	4
2:A:29:ARG:HD3	2:A:32:GLU:OE1	0.41	2.14	11	1
1:B:62:ARG:HB2	2:A:105:ASN:OD1	0.41	2.15	1	1
2:C:52:LYS:O	2:C:98:ARG:HB3	0.41	2.16	8	1
2:A:79:LEU:N	2:A:79:LEU:CD2	0.41	2.84	9	6
1:D:65:ASP:HB3	2:C:44:LYS:NZ	0.41	2.30	18	1
2:C:79:LEU:CD2	2:C:79:LEU:N	0.41	2.84	6	3
2:A:30:ILE:HG23	2:A:117:VAL:HB	0.41	1.93	7	1
2:C:79:LEU:N	2:C:79:LEU:CD2	0.41	2.84	7	4
2:A:79:LEU:CD2	2:A:79:LEU:N	0.41	2.84	8	1
1:B:31:LYS:O	1:B:35:LYS:HB2	0.41	2.16	18	1
2:C:32:GLU:OE2	2:C:33:PRO:HD2	0.41	2.16	19	1
2:A:53:LEU:HD11	2:A:58:THR:HG23	0.40	1.93	12	1
1:D:21:GLY:HA2	1:D:25:ASP:O	0.40	2.16	12	1
1:D:56:LEU:O	1:D:60:LEU:HG	0.40	2.16	2	1
1:D:84:TYR:O	1:D:88:LEU:HG	0.40	2.17	14	1
2:A:96:ILE:HG12	2:A:114:ARG:HG2	0.40	1.94	3	1
1:B:17:HIS:NE2	1:D:85:ASN:ND2	0.40	2.69	8	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	B	87/90 (97%)	83±2 (96±3%)	4±2 (4±3%)	0±0 (0±0%)	54	85

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	87/90 (97%)	84±2 (96±2%)	3±2 (4±2%)	0±0 (0±0%)	54	85
2	A	99/101 (98%)	87±4 (88±4%)	10±3 (10±3%)	2±1 (2±1%)	9	46
2	C	99/101 (98%)	87±4 (88±4%)	10±3 (10±3%)	2±2 (2±2%)	10	49
All	All	7440/7640 (97%)	6818 (92%)	528 (7%)	94 (1%)	16	63

All 18 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	C	118	TYR	10
2	C	94	GLU	10
2	A	118	TYR	10
2	A	58	THR	10
2	C	58	THR	10
2	A	94	GLU	10
2	A	42	PRO	6
2	A	106	GLY	5
2	C	42	PRO	5
2	C	106	GLY	4
2	A	46	PRO	3
2	C	46	PRO	3
1	D	64	LYS	2
2	A	40	GLY	2
2	A	67	GLN	1
1	B	64	LYS	1
2	C	67	GLN	1
2	C	40	GLY	1

### 6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	75/76 (99%)	72±3 (96±4%)	3±3 (4±4%)	37	85
1	D	75/76 (99%)	72±3 (97±4%)	3±3 (3±4%)	40	87
2	A	83/83 (100%)	66±6 (80±7%)	17±6 (20±7%)	3	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	83/83 (100%)	66±6 (80±7%)	17±6 (20±7%)	3	33
All	All	6320/6360 (99%)	5542 (88%)	778 (12%)	8	50

All 99 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	C	27	THR	20
2	A	92	GLN	20
2	A	114	ARG	20
2	C	92	GLN	20
2	A	27	THR	20
2	C	114	ARG	20
2	C	55	THR	17
2	A	51	TRP	17
2	C	51	TRP	17
2	A	55	THR	16
2	A	38	CYS	15
2	C	53	LEU	15
2	A	74	SER	15
2	A	53	LEU	15
2	C	38	CYS	14
2	A	37	LYS	14
2	A	50	GLU	14
2	C	37	LYS	14
2	C	50	GLU	13
2	C	74	SER	13
2	C	111	SER	12
2	A	84	LEU	12
2	A	111	SER	12
2	C	84	LEU	12
2	A	86	LEU	11
2	C	65	SER	11
2	C	29	ARG	11
2	A	29	ARG	11
2	C	86	LEU	11
2	A	48	ARG	10
2	C	91	ILE	10
2	A	116	ARG	10
2	C	30	ILE	10
2	C	116	ARG	10
1	D	46	SER	10

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Mol	Chain	Res	Type	Models (Total)
1	B	46	SER	10
2	C	120	ILE	10
2	A	47	GLN	10
2	C	54	ASN	10
2	A	91	ILE	10
2	A	65	SER	10
2	A	120	ILE	10
2	A	30	ILE	10
2	A	54	ASN	10
2	C	108	GLU	9
2	C	48	ARG	9
1	B	69	ASN	9
2	C	103	ASN	9
2	C	47	GLN	9
1	D	69	ASN	9
1	D	28	THR	8
1	B	28	THR	8
2	A	108	GLU	8
2	A	93	ASP	7
2	A	103	ASN	7
2	A	94	GLU	7
2	C	94	GLU	6
2	C	93	ASP	6
2	C	102	MET	6
2	A	102	MET	5
1	D	5	LEU	4
1	B	61	ASP	4
1	B	71	GLN	4
1	B	5	LEU	4
1	D	61	ASP	4
1	B	63	ASN	3
1	D	71	GLN	3
2	A	98	ARG	3
2	C	98	ARG	3
1	D	11	LEU	3
1	B	11	LEU	3
1	D	63	ASN	3
2	A	43	LYS	3
1	D	17	HIS	2
1	B	59	ASP	2
2	C	43	LYS	2
1	B	17	HIS	2

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Mol	Chain	Res	Type	Models (Total)
1	D	84	TYR	1
2	A	77	ARG	1
2	C	22	MET	1
1	D	58	GLU	1
1	B	22	ARG	1
1	B	75	THR	1
2	C	110	LYS	1
2	C	64	LEU	1
2	C	100	GLN	1
1	B	72	GLU	1
1	D	65	ASP	1
1	B	65	ASP	1
2	C	25	ASN	1
2	A	67	GLN	1
2	C	77	ARG	1
2	A	25	ASN	1
2	A	73	ASP	1
1	D	72	GLU	1
1	B	58	GLU	1
1	B	84	TYR	1
1	D	75	THR	1
2	A	64	LEU	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 8% for the well-defined parts and 8% for the entire structure.

### 7.1 Chemical shift list 1

File name: input\_cs.cif

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

#### 7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	363
Number of shifts mapped to atoms	363
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	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	82	$-0.59 \pm 0.22$	Should be applied
$^{13}\text{C}_\beta$	23	—	None (insufficient data)
$^{13}\text{C}'$	78	$-1.81 \pm 0.39$	Should be applied
$^{15}\text{N}$	84	$0.97 \pm 0.40$	Should be applied

#### 7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 8%, i.e. 361 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	327/1860 (18%)	84/740 (11%)	159/760 (21%)	84/360 (23%)
Sidechain	34/2656 (1%)	0/1562 (0%)	34/954 (4%)	0/140 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)
Overall	361/4790 (8%)	84/2444 (3%)	193/1832 (11%)	84/514 (16%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 8%, i.e. 361 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	327/1860 (18%)	84/740 (11%)	159/760 (21%)	84/360 (23%)
Sidechain	34/2656 (1%)	0/1562 (0%)	34/954 (4%)	0/140 (0%)
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)
Overall	361/4790 (8%)	84/2444 (3%)	193/1832 (11%)	84/514 (16%)

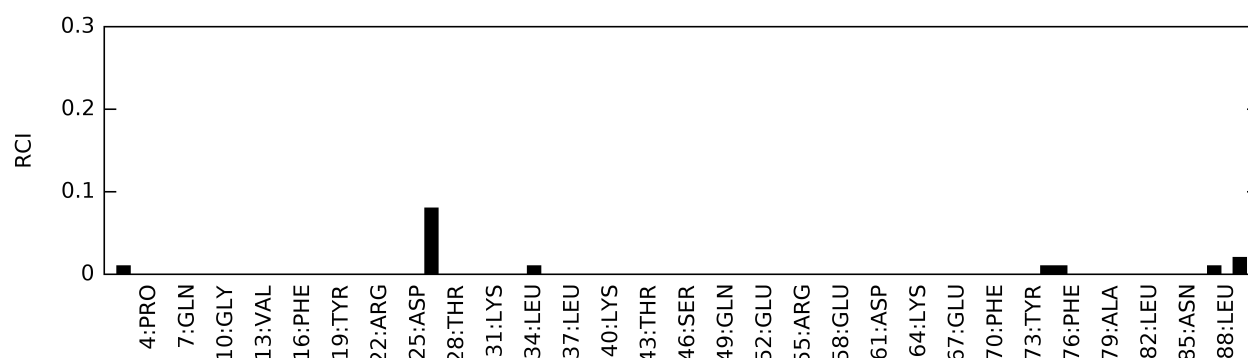
#### 7.1.4 Statistically unusual chemical shifts [i](#)

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 B:



## 7.2 Chemical shift list 2

File name: input\_cs.cif

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

### 7.2.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	32
Number of shifts mapped to atoms	32
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](#)

No chemical shift referencing corrections were calculated (not enough data).

### 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 1%, i.e. 32 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	20/1860 (1%)	7/740 (1%)	6/760 (1%)	7/360 (2%)
Sidechain	12/2656 (0%)	0/1562 (0%)	12/954 (1%)	0/140 (0%)
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)
Overall	32/4790 (1%)	7/2444 (0%)	18/1832 (1%)	7/514 (1%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 1%, i.e. 32 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	20/1860 (1%)	7/740 (1%)	6/760 (1%)	7/360 (2%)
Sidechain	12/2656 (0%)	0/1562 (0%)	12/954 (1%)	0/140 (0%)
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)
Overall	32/4790 (1%)	7/2444 (0%)	18/1832 (1%)	7/514 (1%)



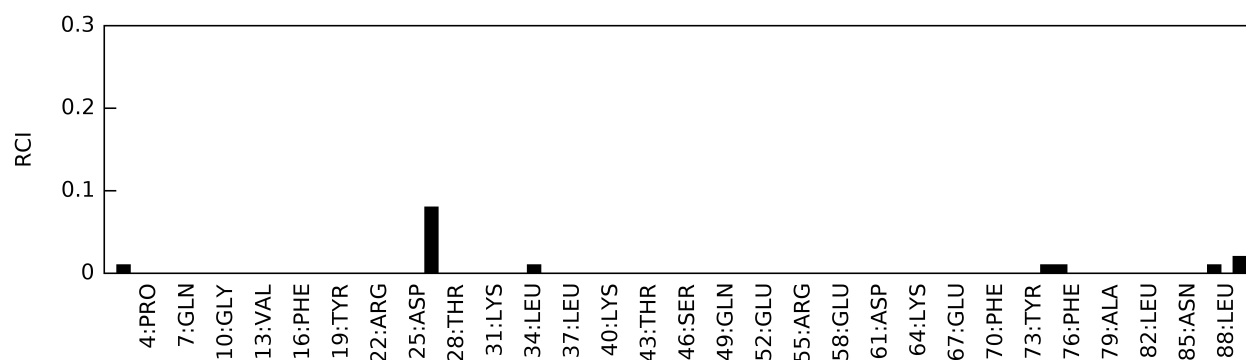
## 7.2.4 Statistically unusual chemical shifts [i](#)

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 B:



## 7.3 Chemical shift list 3

File name: input\_cs.cif

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

### 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	23
Number of shifts mapped to atoms	23
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 [i](#)

No chemical shift referencing corrections were calculated (not enough data).

### 7.3.3 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. 23 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 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	11/1860 (1%)	4/740 (1%)	3/760 (0%)	4/360 (1%)
Sidechain	12/2656 (0%)	0/1562 (0%)	12/954 (1%)	0/140 (0%)
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)
Overall	23/4790 (0%)	4/2444 (0%)	15/1832 (1%)	4/514 (1%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 0%, i.e. 23 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 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	11/1860 (1%)	4/740 (1%)	3/760 (0%)	4/360 (1%)
Sidechain	12/2656 (0%)	0/1562 (0%)	12/954 (1%)	0/140 (0%)
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)
Overall	23/4790 (0%)	4/2444 (0%)	15/1832 (1%)	4/514 (1%)

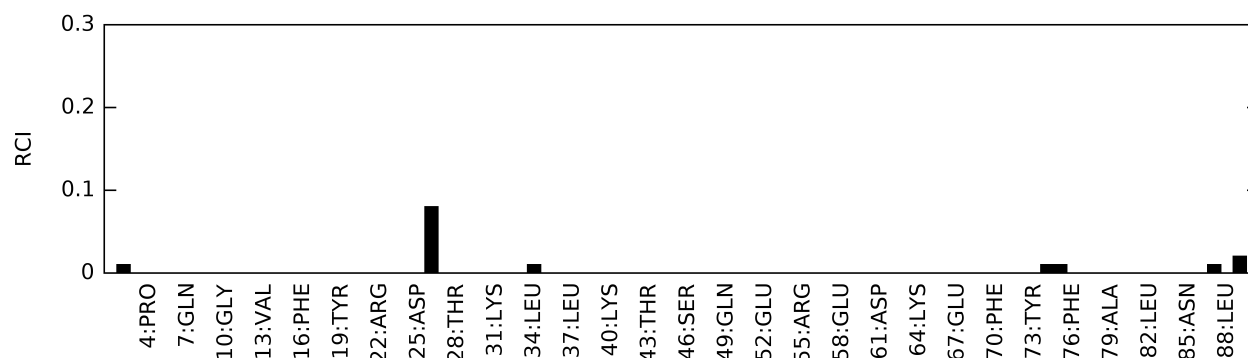
### 7.3.4 Statistically unusual chemical shifts [i](#)

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 B:



## 7.4 Chemical shift list 4

File name: input\_cs.cif

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

### 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	14
Number of shifts mapped to atoms	14
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](#)

No chemical shift referencing corrections were calculated (not enough data).

### 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. 14 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	2/1860 (0%)	1/740 (0%)	0/760 (0%)	1/360 (0%)
Sidechain	12/2656 (0%)	0/1562 (0%)	12/954 (1%)	0/140 (0%)
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Overall	14/4790 (0%)	1/2444 (0%)	12/1832 (1%)	1/514 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 0%, i.e. 14 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 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	2/1860 (0%)	1/740 (0%)	0/760 (0%)	1/360 (0%)
Sidechain	12/2656 (0%)	0/1562 (0%)	12/954 (1%)	0/140 (0%)
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)
Overall	14/4790 (0%)	1/2444 (0%)	12/1832 (1%)	1/514 (0%)

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

There are no statistically unusual chemical shifts.

#### 7.4.5 Random Coil Index (RCI) plots [i](#)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned\_chem\_shift\_list\_4). RCI is only applicable to proteins.

### 7.5 Chemical shift list 5

File name: input\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list\_5*

#### 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	9
Number of shifts mapped to atoms	9
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](#)

No chemical shift referencing corrections were calculated (not enough data).

### 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 0%, i.e. 9 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/1860 (0%)	0/740 (0%)	0/760 (0%)	0/360 (0%)
Sidechain	9/2656 (0%)	0/1562 (0%)	9/954 (1%)	0/140 (0%)
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)
Overall	9/4790 (0%)	0/2444 (0%)	9/1832 (0%)	0/514 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 0%, i.e. 9 atoms were assigned a chemical shift out of a possible 4790. 0 out of 64 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	0/1860 (0%)	0/740 (0%)	0/760 (0%)	0/360 (0%)
Sidechain	9/2656 (0%)	0/1562 (0%)	9/954 (1%)	0/140 (0%)
Aromatic	0/274 (0%)	0/142 (0%)	0/118 (0%)	0/14 (0%)
Overall	9/4790 (0%)	0/2444 (0%)	9/1832 (0%)	0/514 (0%)

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

There are no statistically unusual chemical shifts.

### 7.5.5 Random Coil Index (RCI) plots [i](#)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned\_chem\_shift\_list\_5). RCI is only applicable to proteins.