



# Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 11:12 pm BST

PDB ID : 2L51  
Title : Solution structure of calcium bound S100A16  
Authors : Babini, E.; Bertini, I.; Borsi, V.; Calderone, V.; Hu, X.; Luchinat, C.; Parigi, G.  
Deposited on : 2010-10-22

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

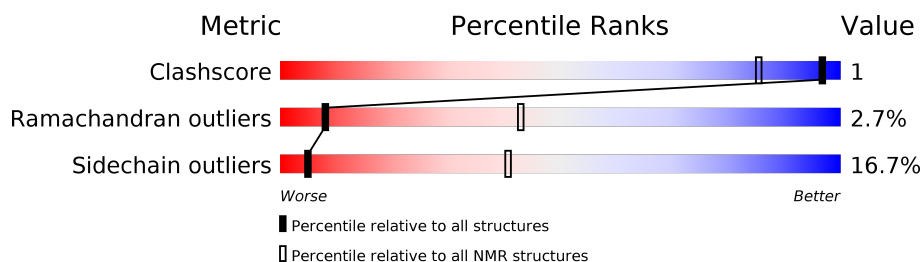
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 74%.

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	102	<div> <div style="width: 71%; background-color: green;"></div> <div style="width: 17%; background-color: yellow;"></div> <div style="width: 13%; background-color: cyan;"></div> </div> <div>71% 17% 13%</div>
1	B	102	<div> <div style="width: 71%; background-color: green;"></div> <div style="width: 17%; background-color: yellow;"></div> <div style="width: 13%; background-color: cyan;"></div> </div> <div>71% 17% 13%</div>

## 2 Ensemble composition and analysis ⓘ

This entry contains 30 models. Model 25 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:5-A:24, A:33-A:101, B:108-B:127, B:136-B:204 (178)	0.54	25

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 2 single-model clusters were found.

Cluster number	Models
1	1, 3, 4, 5, 7, 8, 10, 14, 17, 18, 19, 20, 23, 25, 28
2	2, 6, 9, 11, 12, 13, 16, 21, 22, 24, 26, 29, 30
Single-model clusters	15; 27

### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3282 atoms, of which 1636 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein S100-A16.

Mol	Chain	Residues	Atoms						Trace
1	A	102	Total	C	H	N	O	S	0
			1639	517	818	139	162	3	
1	B	102	Total	C	H	N	O	S	0
			1639	517	818	139	162	3	

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

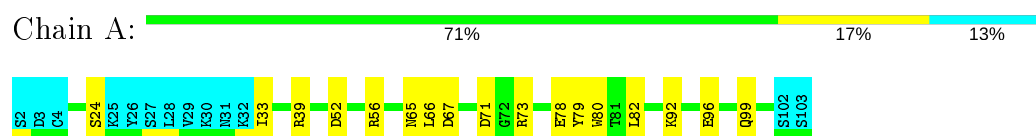
Mol	Chain	Residues	Atoms	
2	B	2	Total	Ca
			2	2
2	A	2	Total	Ca
			2	2

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

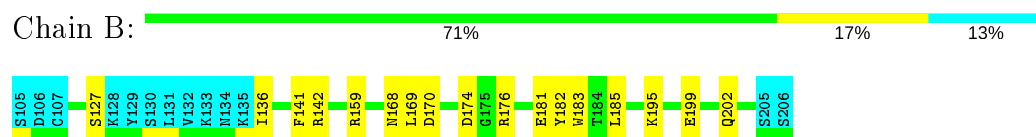
### 4.1 Average score per residue in the NMR ensemble

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-A16



- Molecule 1: Protein S100-A16

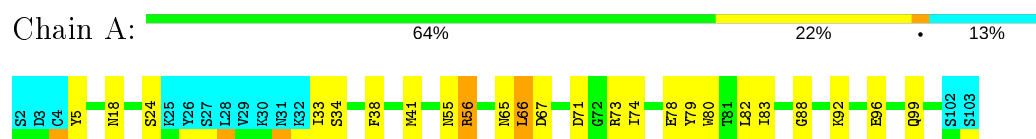


### 4.2 Scores per residue for each member of the ensemble

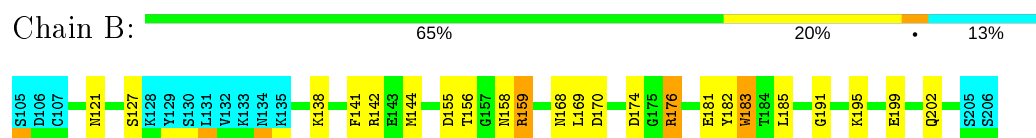
Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

- Molecule 1: Protein S100-A16

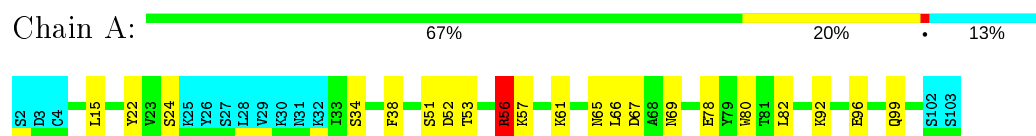


- Molecule 1: Protein S100-A16

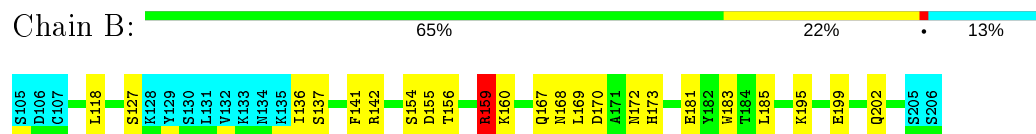


### 4.2.2 Score per residue for model 2

- Molecule 1: Protein S100-A16

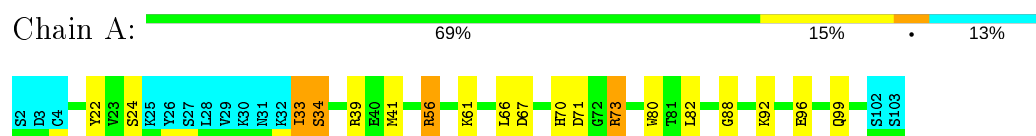


- Molecule 1: Protein S100-A16

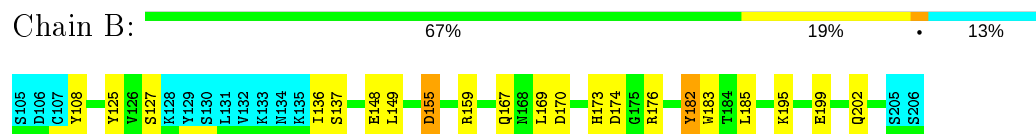


### 4.2.3 Score per residue for model 3

- Molecule 1: Protein S100-A16

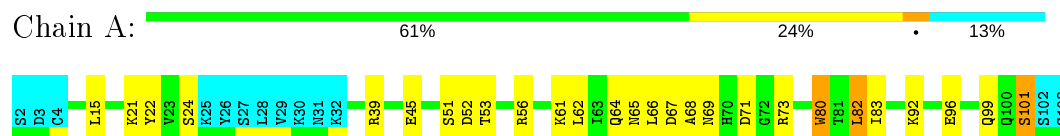


- Molecule 1: Protein S100-A16

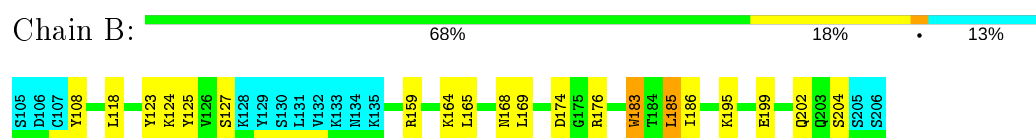


### 4.2.4 Score per residue for model 4

- Molecule 1: Protein S100-A16

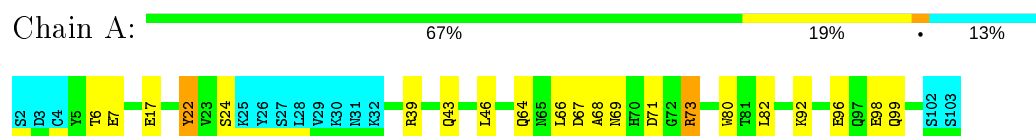


- Molecule 1: Protein S100-A16

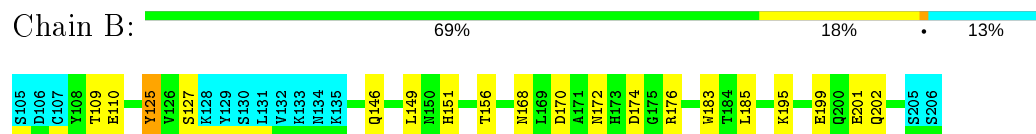


### 4.2.5 Score per residue for model 5

- Molecule 1: Protein S100-A16

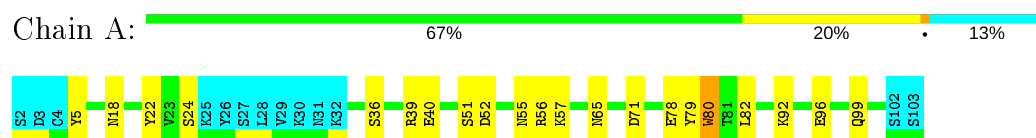


- Molecule 1: Protein S100-A16

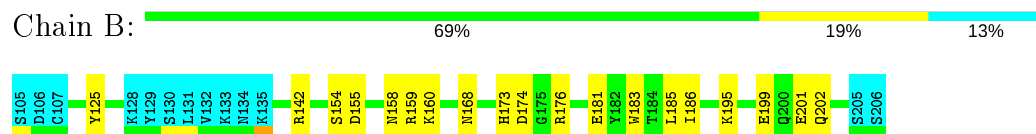


### 4.2.6 Score per residue for model 6

- Molecule 1: Protein S100-A16

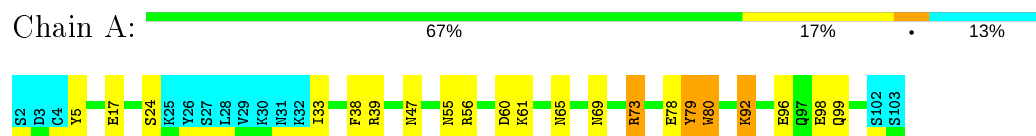


- Molecule 1: Protein S100-A16

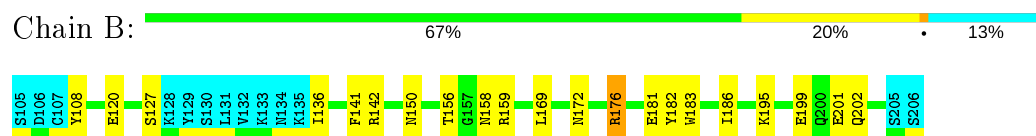


### 4.2.7 Score per residue for model 7

- Molecule 1: Protein S100-A16

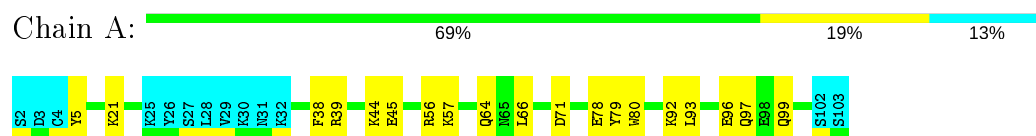


- Molecule 1: Protein S100-A16

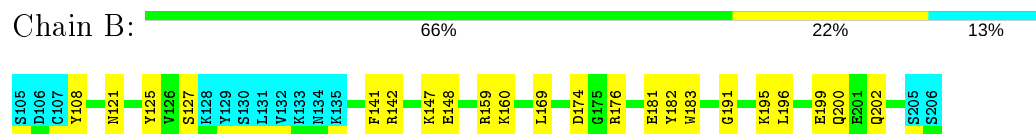


### 4.2.8 Score per residue for model 8

- Molecule 1: Protein S100-A16

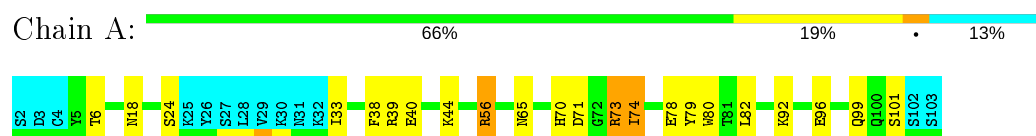


- Molecule 1: Protein S100-A16

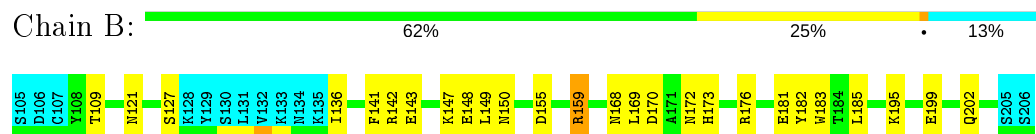


### 4.2.9 Score per residue for model 9

- Molecule 1: Protein S100-A16

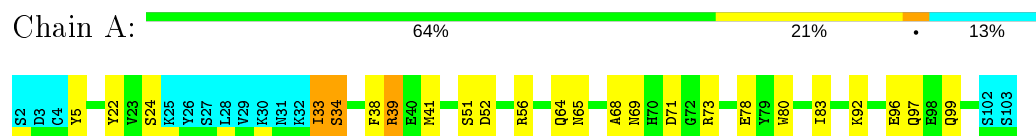


- Molecule 1: Protein S100-A16

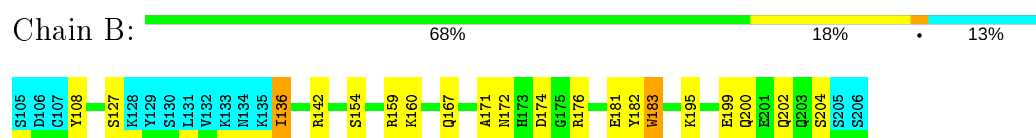


### 4.2.10 Score per residue for model 10

- Molecule 1: Protein S100-A16



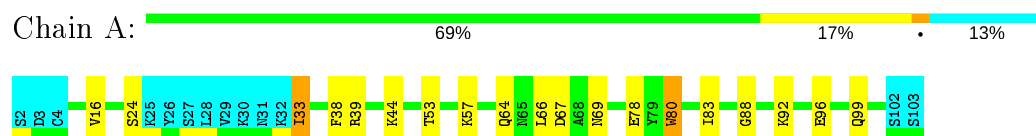
- Molecule 1: Protein S100-A16



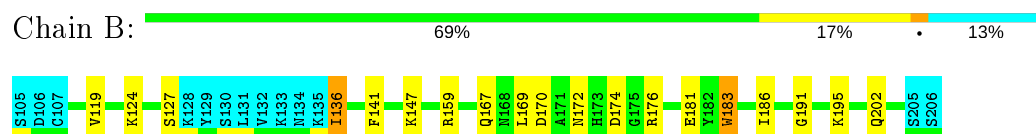


### 4.2.11 Score per residue for model 11

- Molecule 1: Protein S100-A16

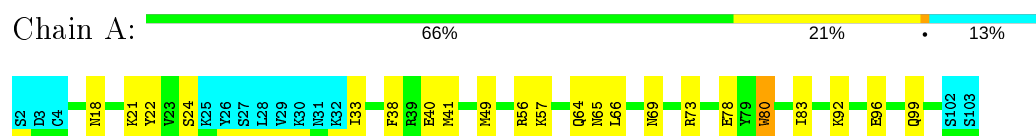


- Molecule 1: Protein S100-A16

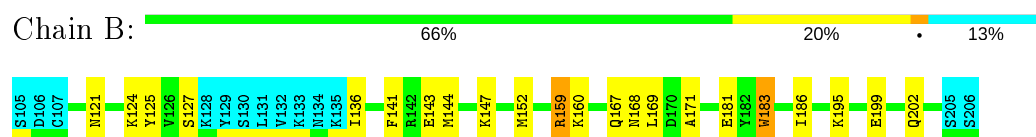


### 4.2.12 Score per residue for model 12

- Molecule 1: Protein S100-A16

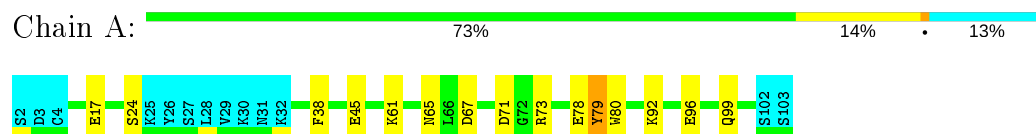


- Molecule 1: Protein S100-A16

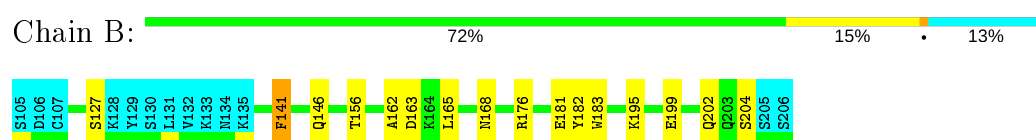


### 4.2.13 Score per residue for model 13

- Molecule 1: Protein S100-A16

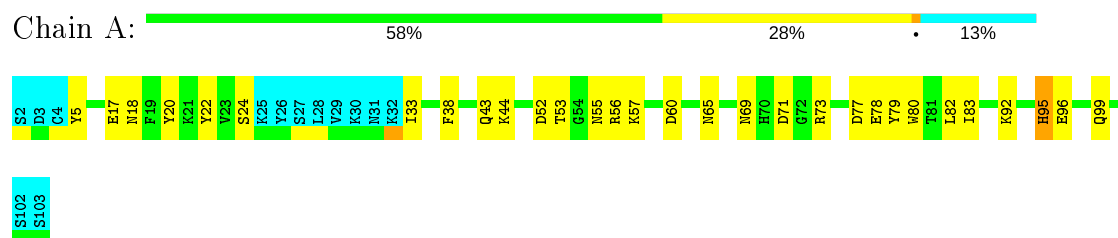


- Molecule 1: Protein S100-A16

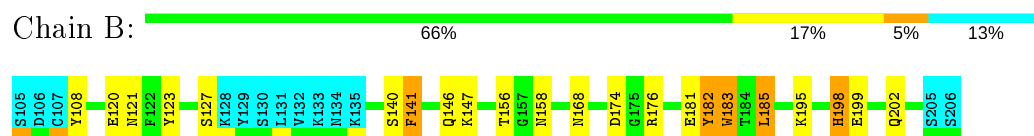


### 4.2.14 Score per residue for model 14

- Molecule 1: Protein S100-A16

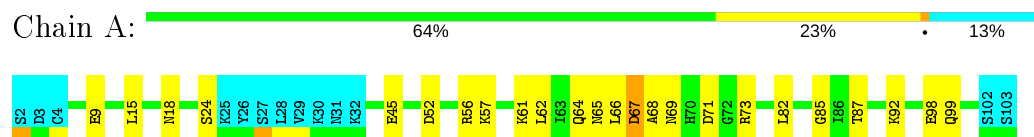


- Molecule 1: Protein S100-A16

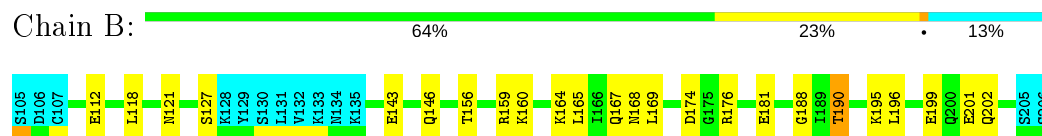


### 4.2.15 Score per residue for model 15

- Molecule 1: Protein S100-A16

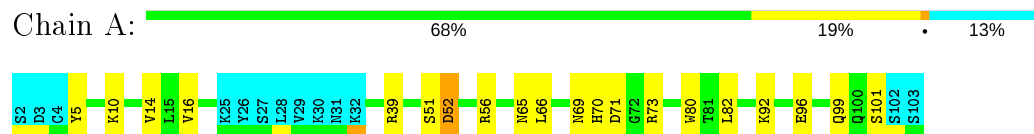


- Molecule 1: Protein S100-A16



### 4.2.16 Score per residue for model 16

- Molecule 1: Protein S100-A16



- Molecule 1: Protein S100-A16





#### 4.2.17 Score per residue for model 17

- Molecule 1: Protein S100-A16

Chain A: 66% 20% 13%



- Molecule 1: Protein S100-A16

Chain B: 69% 18% 13%



#### 4.2.18 Score per residue for model 18

- Molecule 1: Protein S100-A16

Chain A: 65% 19% 13%



- Molecule 1: Protein S100-A16

Chain B: 68% 17% 13%



#### 4.2.19 Score per residue for model 19

- Molecule 1: Protein S100-A16

Chain A: 70% 16% 13%



- Molecule 1: Protein S100-A16

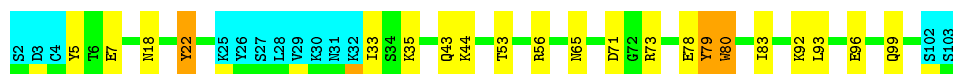
Chain B: 65% 19% 13%



#### 4.2.20 Score per residue for model 20

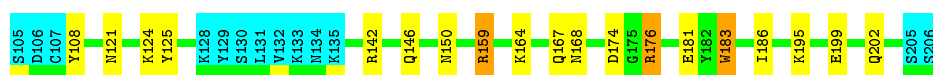
- Molecule 1: Protein S100-A16

Chain A: 67% 18% 13%



- Molecule 1: Protein S100-A16

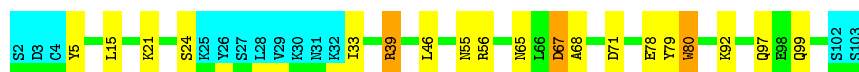
Chain B: 69% 16% 13%



#### 4.2.21 Score per residue for model 21

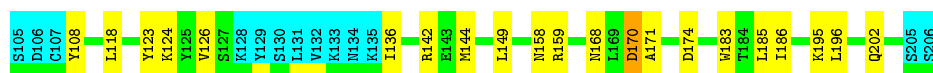
- Molecule 1: Protein S100-A16

Chain A: 69% 16% 13%



- Molecule 1: Protein S100-A16

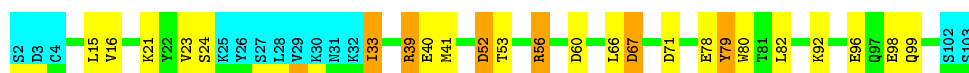
Chain B: 67% 20% 13%



#### 4.2.22 Score per residue for model 22

- Molecule 1: Protein S100-A16

Chain A: 64% 18% 6% 13%



- Molecule 1: Protein S100-A16

Chain B: 63% 21% 13%



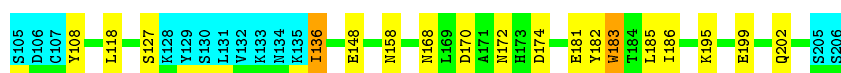


#### 4.2.23 Score per residue for model 23

- Molecule 1: Protein S100-A16



- Molecule 1: Protein S100-A16



#### 4.2.24 Score per residue for model 24

- Molecule 1: Protein S100-A16



- Molecule 1: Protein S100-A16



#### 4.2.25 Score per residue for model 25 (medoid)

- Molecule 1: Protein S100-A16



- Molecule 1: Protein S100-A16





#### 4.2.26 Score per residue for model 26

- Molecule 1: Protein S100-A16

Chain A: 74% 13% • 13%



- Molecule 1: Protein S100-A16

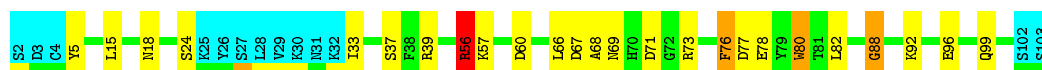
Chain B: 75% 10% •• 13%



#### 4.2.27 Score per residue for model 27

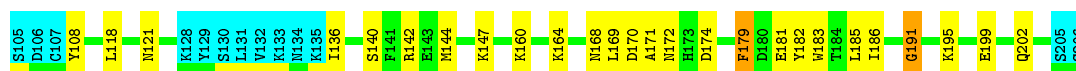
- Molecule 1: Protein S100-A16

Chain A: 63% 21% •• 13%



- Molecule 1: Protein S100-A16

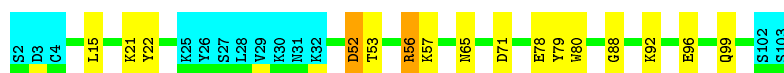
Chain B: 62% 24% • 13%



#### 4.2.28 Score per residue for model 28

- Molecule 1: Protein S100-A16

Chain A: 72% 14% • 13%



- Molecule 1: Protein S100-A16

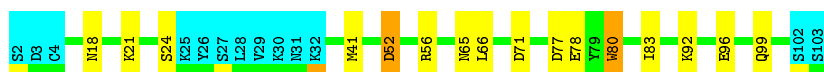
Chain B: 69% 18% • 13%



#### 4.2.29 Score per residue for model 29

- Molecule 1: Protein S100-A16

Chain A: 72% 14% 13%



- Molecule 1: Protein S100-A16

Chain B: 74% 12% 13%



#### 4.2.30 Score per residue for model 30

- Molecule 1: Protein S100-A16

Chain A: 67% 20% 13%



- Molecule 1: Protein S100-A16

Chain B: 69% 18% 13%



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 350 calculated structures, 30 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
Amber	structure solution	10.0
CYANA	structure solution	2.1
ProcheckNMR	structure solution	
TALOS	structure solution	
WHAT IF	structure solution	
WHAT IF	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1932
Number of shifts mapped to atoms	1932
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	74%

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

COVALENT-GEOMETRY INFOmissingINFO

### 5.1 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	720	713	713	2±1
1	B	720	713	713	2±1
All	All	43320	42780	42779	58



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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:33:ILE:HG23	1:A:34:SER:H	0.65	1.49	10	1
1:A:11:ALA:HB1	1:B:114:ALA:HB1	0.53	1.79	19	1
1:A:83:ILE:HG23	1:B:183:TRP:CZ3	0.47	2.45	18	14
1:B:141:PHE:CE1	1:B:182:TYR:CE1	0.47	3.02	14	1
1:A:80:TRP:CZ3	1:B:186:ILE:HG23	0.46	2.45	18	13
1:B:165:LEU:HD13	1:B:185:LEU:O	0.46	2.11	4	1
1:A:18:ASN:HA	1:A:21:LYS:HE2	0.46	1.88	12	1
1:A:20:TYR:CD2	1:B:198:HIS:CG	0.45	3.05	14	1
1:B:146:GLN:HE22	1:B:159:ARG:NH1	0.45	2.10	16	1
1:A:10:LYS:O	1:A:14:VAL:HG23	0.45	2.12	23	2
1:A:38:PHE:CE1	1:A:79:TYR:CE1	0.44	3.06	24	1
1:A:62:LEU:HD13	1:A:82:LEU:O	0.44	2.13	4	1
1:B:121:ASN:HA	1:B:124:LYS:HE2	0.44	1.88	12	1
1:B:162:ALA:HA	1:B:165:LEU:HD12	0.44	1.89	13	1
1:B:113:LYS:O	1:B:117:VAL:HG23	0.43	2.13	16	1
1:B:149:LEU:HD11	1:B:186:ILE:CD1	0.43	2.42	25	1
1:A:76:PHE:CD2	1:B:191:GLY:HA2	0.43	2.48	27	2
1:A:83:ILE:HG23	1:B:183:TRP:HZ3	0.43	1.74	4	1
1:A:95:HIS:CG	1:B:123:TYR:CD2	0.43	3.06	14	1
1:B:142:ARG:HE	1:B:166:ILE:CD1	0.43	2.27	17	1
1:A:73:ARG:C	1:A:74:ILE:HD12	0.42	2.35	9	1
1:A:22:TYR:CZ	1:A:33:ILE:HD12	0.42	2.49	12	1
1:A:88:GLY:HA2	1:B:179:PHE:CD2	0.42	2.49	27	1
1:A:62:LEU:HD11	1:A:85:GLY:C	0.42	2.35	15	1
1:B:125:TYR:CZ	1:B:136:ILE:HD12	0.42	2.50	12	1
1:B:126:VAL:HG23	1:B:136:ILE:HG23	0.41	1.90	22	1
1:A:80:TRP:HZ3	1:B:186:ILE:HG23	0.41	1.75	4	1
1:B:165:LEU:HD11	1:B:188:GLY:C	0.41	2.36	15	1
1:A:22:TYR:C	1:A:22:TYR:CD1	0.41	2.94	20	1
1:A:92:LYS:HA	1:A:92:LYS:HE2	0.40	1.93	7	1
1:B:141:PHE:CE1	1:B:182:TYR:CE2	0.40	3.10	13	1

## 5.2 Torsion angles ⓘ

### 5.2.1 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	89/102 (87%)	77±2 (87±2%)	9±2 (10±2%)	2±1 (3±1%)	8	42
1	B	89/102 (87%)	78±3 (88±3%)	8±2 (9±3%)	2±1 (3±1%)	8	43
All	All	5340/6120 (87%)	4673 (88%)	521 (10%)	146 (3%)	8	43

All 33 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	24	SER	20
1	B	127	SER	20
1	B	136	ILE	13
1	A	33	ILE	12
1	B	191	GLY	9
1	A	52	ASP	8
1	A	88	GLY	7
1	A	69	ASN	6
1	B	155	ASP	6
1	B	172	ASN	5
1	A	34	SER	4
1	B	156	THR	4
1	A	66	LEU	3
1	B	169	LEU	3
1	A	5	TYR	2
1	A	101	SER	2
1	A	51	SER	2
1	B	108	TYR	2
1	B	137	SER	2
1	B	204	SER	2
1	A	67	ASP	2
1	B	171	ALA	1
1	A	77	ASP	1
1	B	190	THR	1
1	A	68	ALA	1
1	B	173	HIS	1
1	A	70	HIS	1
1	B	185	LEU	1
1	A	53	THR	1
1	B	150	ASN	1
1	B	124	LYS	1
1	A	45	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	87	THR	1

### 5.2.2 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	79/92 (86%)	66±3 (83±3%)	14±3 (17±3%)	5	40
1	B	79/92 (86%)	66±3 (84±3%)	13±3 (16±3%)	5	41
All	All	4740/5520 (86%)	3947 (83%)	793 (17%)	5	41

All 112 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	B	202	GLN	30
1	A	99	GLN	30
1	B	195	LYS	29
1	B	183	TRP	29
1	A	92	LYS	29
1	A	80	TRP	28
1	A	96	GLU	27
1	B	199	GLU	27
1	A	65	ASN	22
1	B	168	ASN	21
1	A	82	LEU	16
1	B	185	LEU	15
1	B	176	ARG	15
1	A	66	LEU	15
1	B	141	PHE	15
1	A	38	PHE	14
1	A	79	TYR	14
1	A	73	ARG	14
1	B	182	TYR	13
1	B	169	LEU	13
1	A	57	LYS	11
1	A	15	LEU	11
1	B	160	LYS	11

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Mol	Chain	Res	Type	Models (Total)
1	B	144	MET	10
1	B	118	LEU	10
1	B	121	ASN	10
1	A	64	GLN	9
1	B	158	ASN	9
1	A	41	MET	9
1	B	167	GLN	9
1	A	18	ASN	8
1	A	61	LYS	8
1	A	69	ASN	8
1	A	55	ASN	8
1	B	147	LYS	8
1	A	44	LYS	8
1	B	159	ARG	7
1	A	56	ARG	7
1	A	21	LYS	7
1	A	53	THR	7
1	B	201	GLU	7
1	B	172	ASN	6
1	A	17	GLU	6
1	B	146	GLN	6
1	A	45	GLU	6
1	A	40	GLU	6
1	B	124	LYS	6
1	B	143	GLU	6
1	A	74	ILE	5
1	A	101	SER	5
1	B	164	LYS	5
1	A	60	ASP	5
1	B	156	THR	5
1	B	173	HIS	4
1	A	33	ILE	4
1	B	163	ASP	4
1	B	149	LEU	4
1	B	142	ARG	4
1	A	98	GLU	4
1	B	196	LEU	4
1	A	16	VAL	4
1	A	77	ASP	4
1	B	200	GLN	4
1	A	52	ASP	3
1	A	70	HIS	3

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Mol	Chain	Res	Type	Models (Total)
1	A	93	LEU	3
1	B	204	SER	3
1	B	120	GLU	3
1	B	177	ILE	3
1	B	140	SER	3
1	A	43	GLN	3
1	A	97	GLN	3
1	A	51	SER	3
1	B	148	GLU	3
1	B	155	ASP	3
1	A	46	LEU	3
1	B	136	ILE	2
1	B	151	HIS	2
1	A	39	ARG	2
1	B	109	THR	2
1	A	24	SER	2
1	B	119	VAL	2
1	A	7	GLU	2
1	B	170	ASP	2
1	B	150	ASN	2
1	A	67	ASP	2
1	A	49	MET	2
1	A	6	THR	2
1	B	154	SER	2
1	A	48	HIS	1
1	B	190	THR	1
1	A	36	SER	1
1	A	95	HIS	1
1	A	34	SER	1
1	B	180	ASP	1
1	B	152	MET	1
1	A	76	PHE	1
1	B	179	PHE	1
1	A	47	ASN	1
1	A	81	THR	1
1	A	23	VAL	1
1	B	112	GLU	1
1	A	5	TYR	1
1	B	127	SER	1
1	A	37	SER	1
1	B	198	HIS	1
1	A	9	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	B	138	LYS	1
1	A	35	LYS	1
1	B	110	GLU	1
1	B	108	TYR	1
1	A	22	TYR	1

### 5.2.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.3 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.4 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.5 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

### 5.6 Other polymers [i](#)

There are no such molecules in this entry.

### 5.7 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 74% for the well-defined parts and 74% for the entire structure.

### 6.1 Chemical shift list 1

File name: input\_cs.cif

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

#### 6.1.1 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	1932
Number of shifts mapped to atoms	1932
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	10

#### 6.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	202	$2.04 \pm 0.29$	Should be applied
$^{13}\text{C}_\beta$	192	$2.95 \pm 0.16$	Should be applied
$^{13}\text{C}'$	188	$2.34 \pm 0.19$	Should be applied
$^{15}\text{N}$	196	$0.26 \pm 0.19$	None needed ( $< 0.5$ ppm)

#### 6.1.3 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 74%, i.e. 1662 atoms were assigned a chemical shift out of a possible 2246. 26 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	862/886 (97%)	348/354 (98%)	342/356 (96%)	172/176 (98%)
Sidechain	800/1176 (68%)	408/686 (59%)	366/438 (84%)	26/52 (50%)

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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>
Aromatic	0/184 (0%)	0/98 (0%)	0/78 (0%)	0/8 (0%)
Overall	1662/2246 (74%)	756/1138 (66%)	708/872 (81%)	198/236 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 74%, i.e. 1882 atoms were assigned a chemical shift out of a possible 2558. 30 out of 30 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	984/1016 (97%)	398/406 (98%)	390/408 (96%)	196/202 (97%)
Sidechain	898/1342 (67%)	452/786 (58%)	418/496 (84%)	28/60 (47%)
Aromatic	0/200 (0%)	0/106 (0%)	0/86 (0%)	0/8 (0%)
Overall	1882/2558 (74%)	850/1298 (65%)	808/990 (82%)	224/270 (83%)

#### 6.1.4 Statistically unusual chemical shifts ⓘ

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

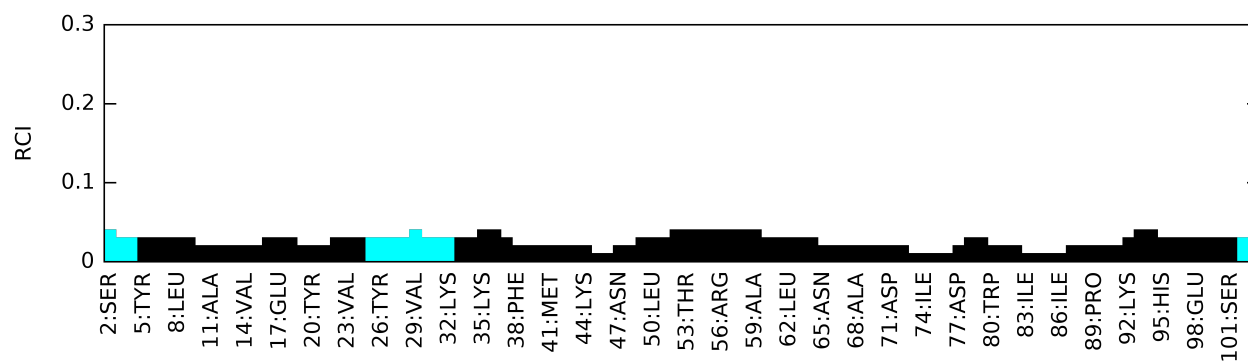
Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	73	ARG	NE	125.00	92.63 – 76.73	25.4
1	B	176	ARG	NE	125.00	92.63 – 76.73	25.4
1	B	159	ARG	NE	124.90	92.63 – 76.73	25.3
1	A	56	ARG	NE	124.90	92.63 – 76.73	25.3
1	B	142	ARG	NE	124.80	92.63 – 76.73	25.2
1	A	39	ARG	NE	124.80	92.63 – 76.73	25.2
1	A	32	LYS	CD	39.20	34.86 – 23.06	8.7
1	B	135	LYS	CD	39.20	34.86 – 23.06	8.7
1	A	84	GLY	HA3	1.77	5.80 – 2.00	-5.6
1	B	187	GLY	HA3	1.77	5.80 – 2.00	-5.6

#### 6.1.5 Random Coil Index (RCI) plots ⓘ

The images below report *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:





Random coil index (RCI) for chain B:

