



Full wwPDB NMR Structure Validation Report ⓘ

Apr 15, 2026 – 11:19 AM UTC

PDB ID : 7UI5 / pdb_00007ui5
BMRB ID : 31007
Title : Evolution avoids a pathological stabilizing interaction in the immune protein S100A9
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Deposited on : 2022-03-28

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 41%.

There are no overall percentile quality scores available for this entry.

The sequence quality summary graphics cannot be shown.

2 Ensemble composition and analysis

This entry contains 10 models. Model 5 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:87, B:4-B:87 (167)	1.25	5

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	2, 3, 4, 5, 6, 7
2	8, 10
Single-model clusters	1; 9

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3672 atoms, of which 1806 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein S100-A9.

Mol	Chain	Residues	Atoms						Trace
1	A	114	Total	C	H	N	O	S	0
			1834	583	903	163	180	5	
1	B	114	Total	C	H	N	O	S	0
			1834	583	903	163	180	5	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	SER	CYS	engineered mutation	UNP P06702
A	63	PHE	MET	engineered mutation	UNP P06702
B	3	SER	CYS	engineered mutation	UNP P06702
B	63	PHE	MET	engineered mutation	UNP P06702

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

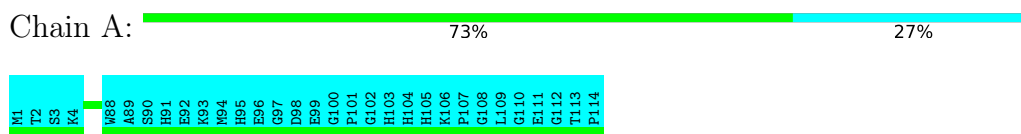
Mol	Chain	Residues	Atoms	
2	A	2	Total	Ca
			2	2
2	B	2	Total	Ca
			2	2

4 Residue-property plots [i](#)

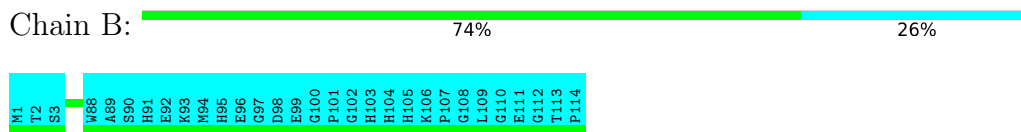
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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-A9



- Molecule 1: Protein S100-A9

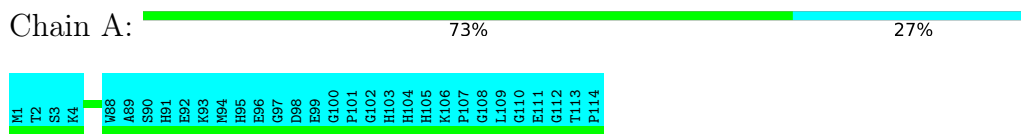


4.2 Scores per residue for each member of the ensemble

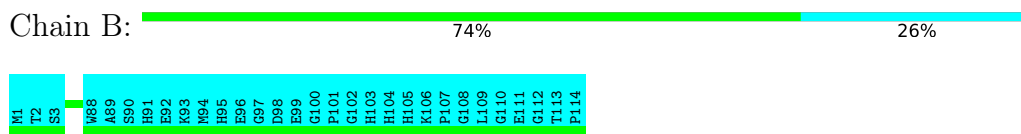
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Protein S100-A9



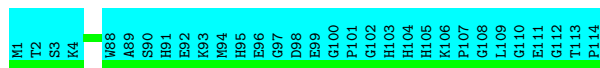
- Molecule 1: Protein S100-A9



4.2.2 Score per residue for model 2

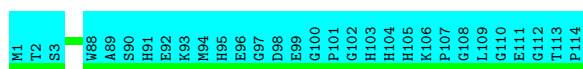
- Molecule 1: Protein S100-A9

Chain A:  73% 27%



- Molecule 1: Protein S100-A9

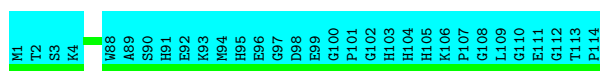
Chain B:  74% 26%



4.2.3 Score per residue for model 3

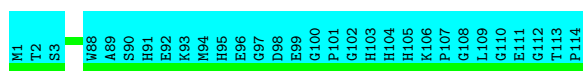
- Molecule 1: Protein S100-A9

Chain A:  73% 27%



- Molecule 1: Protein S100-A9

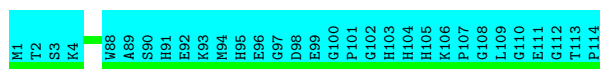
Chain B:  74% 26%



4.2.4 Score per residue for model 4

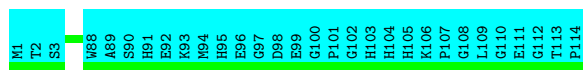
- Molecule 1: Protein S100-A9

Chain A:  73% 27%



- Molecule 1: Protein S100-A9

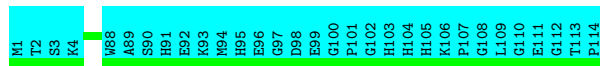
Chain B:  74% 26%



4.2.5 Score per residue for model 5 (medoid)

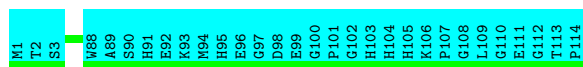
- Molecule 1: Protein S100-A9

Chain A:  73% 27%



- Molecule 1: Protein S100-A9

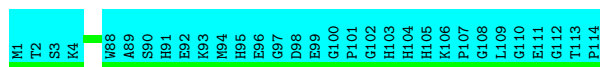
Chain B:  74% 26%



4.2.6 Score per residue for model 6

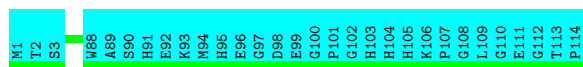
- Molecule 1: Protein S100-A9

Chain A:  73% 27%



- Molecule 1: Protein S100-A9

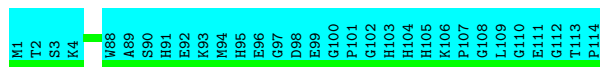
Chain B:  74% 26%



4.2.7 Score per residue for model 7

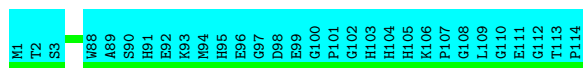
- Molecule 1: Protein S100-A9

Chain A:  73% 27%



- Molecule 1: Protein S100-A9

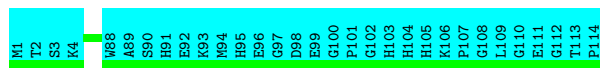
Chain B:  74% 26%



4.2.8 Score per residue for model 8

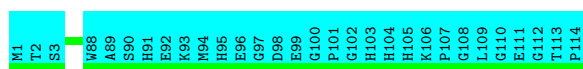
- Molecule 1: Protein S100-A9

Chain A:  73% 27%



- Molecule 1: Protein S100-A9

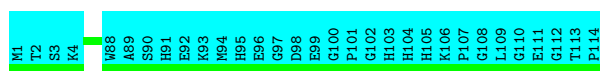
Chain B:  74% 26%



4.2.9 Score per residue for model 9

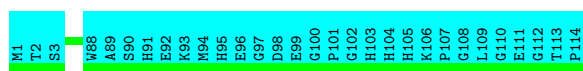
- Molecule 1: Protein S100-A9

Chain A:  73% 27%



- Molecule 1: Protein S100-A9

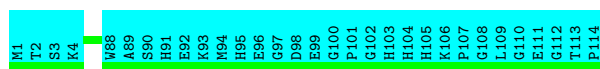
Chain B:  74% 26%



4.2.10 Score per residue for model 10

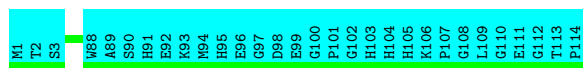
- Molecule 1: Protein S100-A9

Chain A:  73% 27%



- Molecule 1: Protein S100-A9

Chain B:  74% 26%



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

The authors did not provide any information on software used for structure solution, optimization or 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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1038
Number of shifts mapped to atoms	1038
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	41%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.3.3 RNA [i](#)

MolProbity failed to run properly - this section will have to be empty.

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

MolProbity failed to run properly - this section will have to be empty.

6.5 Carbohydrates [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.6 Ligand geometry [i](#)

MolProbity failed to run properly - this section will have to be empty.

6.7 Other polymers [i](#)

MolProbity failed to run properly - this section will have to be empty.

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 41% for the well-defined parts and 33% for the entire structure.

7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: *starch_output*

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	1038
Number of shifts mapped to atoms	1038
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	85	-0.74 ± 0.28	Should be checked
$^{13}\text{C}_\beta$	82	0.45 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}'$	72	1.65 ± 0.54	Should be applied
^{15}N	85	1.53 ± 0.28	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 41%, i.e. 997 atoms were assigned a chemical shift out of a possible 2430. 0 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	388/835 (46%)	160/336 (48%)	149/334 (45%)	79/165 (48%)
Sidechain	577/1415 (41%)	395/906 (44%)	182/450 (40%)	0/59 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	32/180 (18%)	32/92 (35%)	0/82 (0%)	0/6 (0%)
Overall	997/2430 (41%)	587/1334 (44%)	331/866 (38%)	79/230 (34%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 33%, i.e. 1038 atoms were assigned a chemical shift out of a possible 3158. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	416/1140 (36%)	174/464 (38%)	157/456 (34%)	85/220 (39%)
Sidechain	586/1744 (34%)	400/1118 (36%)	186/562 (33%)	0/64 (0%)
Aromatic	36/274 (13%)	35/144 (24%)	0/112 (0%)	1/18 (6%)
Overall	1038/3158 (33%)	609/1726 (35%)	343/1130 (30%)	86/302 (28%)

7.1.4 Statistically unusual chemical shifts [i](#)

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.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	113	THR	CG2	29.47	16.06 – 27.03	7.2
1	A	54	LYS	CE	36.05	37.57 – 46.21	-6.8
1	A	29	PRO	HD2	1.69	1.93 – 5.38	-5.7
1	A	29	PRO	HD3	1.69	1.76 – 5.48	-5.2
1	A	23	SER	HB2	2.58	2.61 – 5.13	-5.1

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

