



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 06:39 PM BST

PDB ID : 1YUS
Title : Solution structure of apo-S100A13
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Structural Proteomics in Europe (SPINE)
Deposited on : 2005-02-14

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

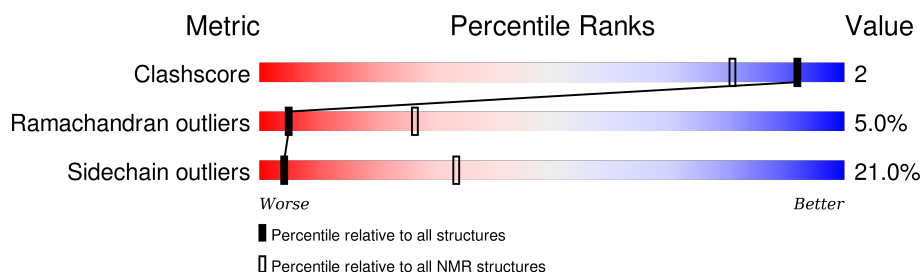
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 73%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	98	
1	B	98	

2 Ensemble composition and analysis

This entry contains 25 models. Model 20 is the overall representative, medoid model (most similar to other models). The authors have identified model 18 as representative, based on the following criterion: *fewest violations*.

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:4-A:22, A:31-A:96, B:4-B:22, B:30-B:96 (171)	0.62	20

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 and 5 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 3280 atoms, of which 1666 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called S100 calcium binding protein A13.

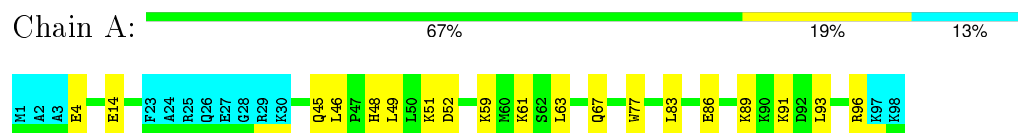
Mol	Chain	Residues	Atoms						Trace
1	A	98	Total	C	H	N	O	S	0
			1640	512	833	136	157	2	
1	B	98	Total	C	H	N	O	S	0
			1640	512	833	136	157	2	

4 Residue-property plots

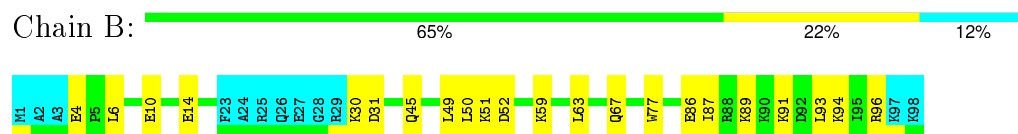
4.1 Average score per residue in the NMR ensemble

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: S100 calcium binding protein A13



- Molecule 1: S100 calcium binding protein A13

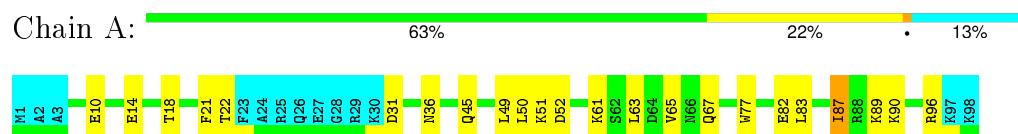


4.2 Scores per residue for each member of the ensemble

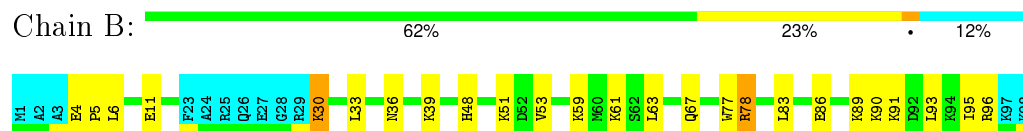
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: S100 calcium binding protein A13

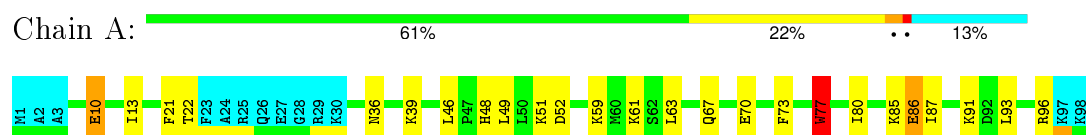


- Molecule 1: S100 calcium binding protein A13

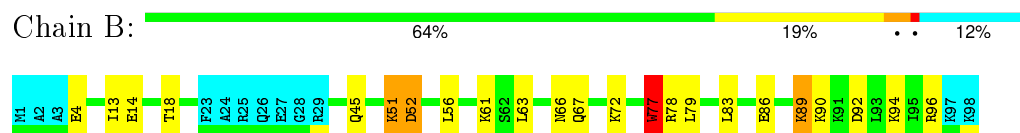


4.2.2 Score per residue for model 2

- Molecule 1: S100 calcium binding protein A13

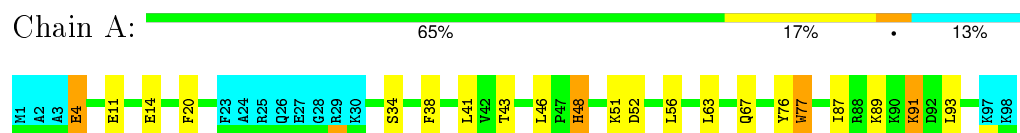


- Molecule 1: S100 calcium binding protein A13

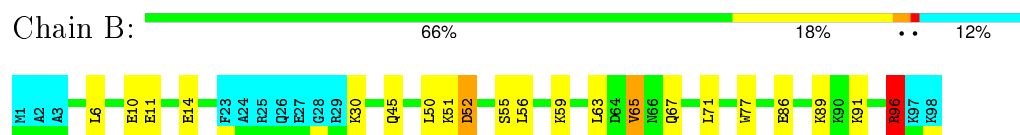


4.2.3 Score per residue for model 3

- Molecule 1: S100 calcium binding protein A13

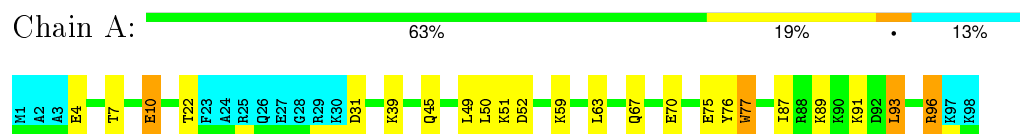


- Molecule 1: S100 calcium binding protein A13

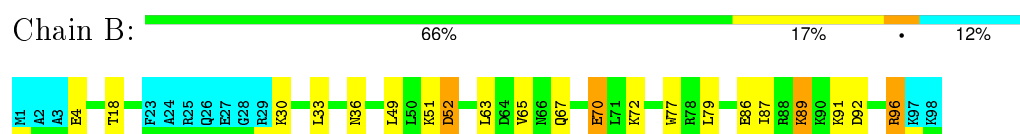


4.2.4 Score per residue for model 4

- Molecule 1: S100 calcium binding protein A13

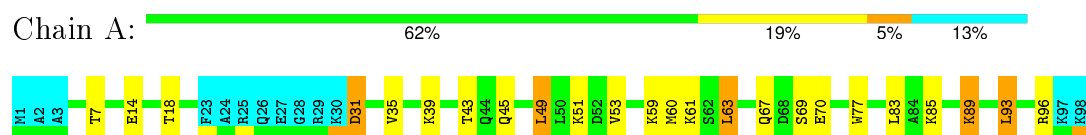


- Molecule 1: S100 calcium binding protein A13

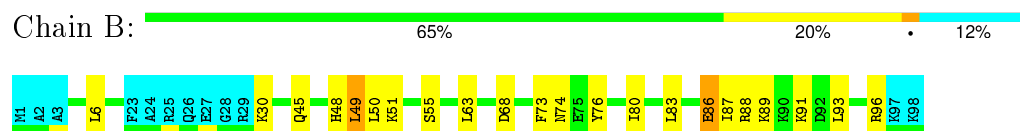


4.2.5 Score per residue for model 5

- Molecule 1: S100 calcium binding protein A13

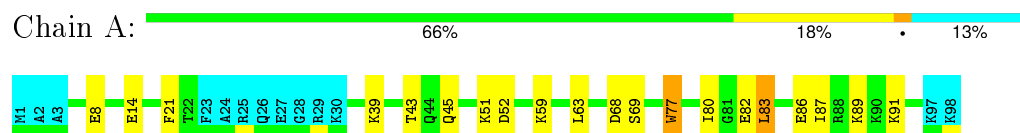


- Molecule 1: S100 calcium binding protein A13

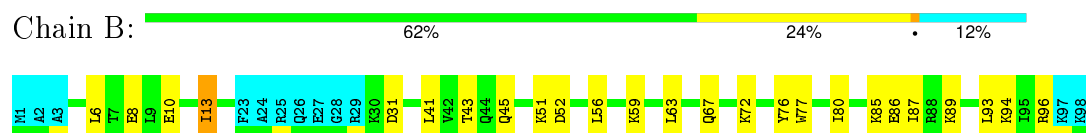


4.2.6 Score per residue for model 6

- Molecule 1: S100 calcium binding protein A13

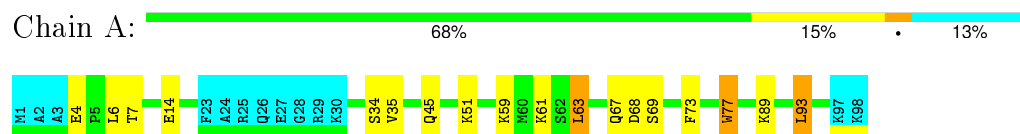


- Molecule 1: S100 calcium binding protein A13

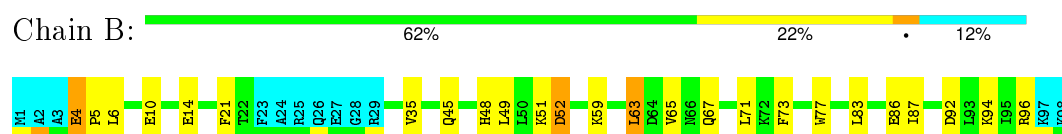


4.2.7 Score per residue for model 7

- Molecule 1: S100 calcium binding protein A13

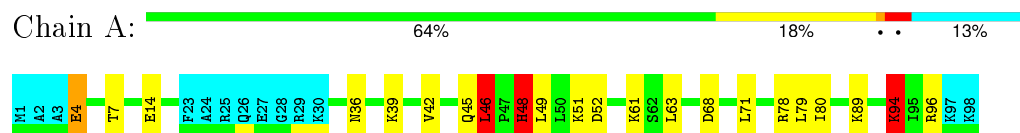


- Molecule 1: S100 calcium binding protein A13

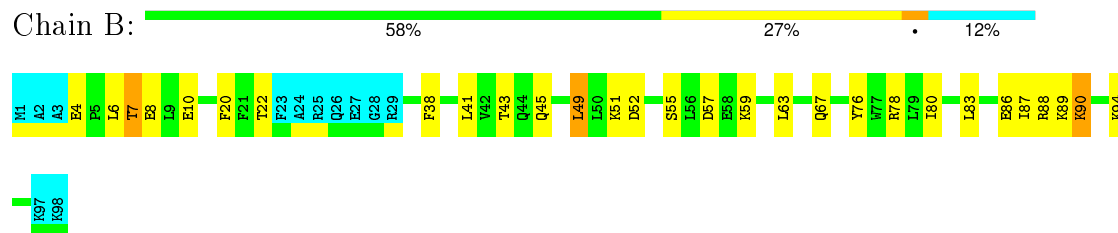


4.2.8 Score per residue for model 8

- Molecule 1: S100 calcium binding protein A13

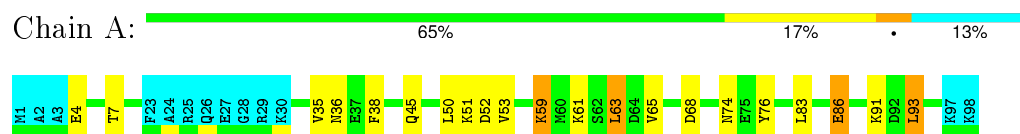


- Molecule 1: S100 calcium binding protein A13

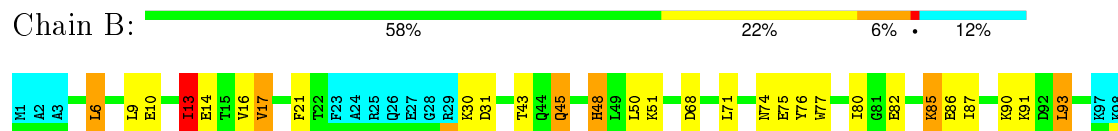


4.2.9 Score per residue for model 9

- Molecule 1: S100 calcium binding protein A13

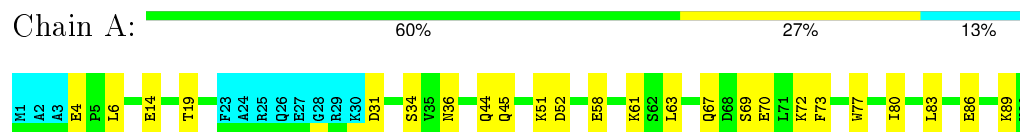


- Molecule 1: S100 calcium binding protein A13



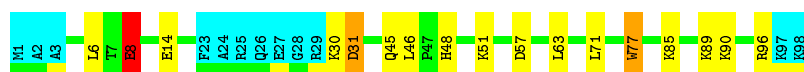
4.2.10 Score per residue for model 10

- Molecule 1: S100 calcium binding protein A13



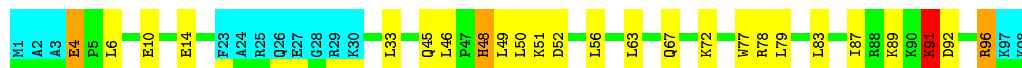
- Molecule 1: S100 calcium binding protein A13



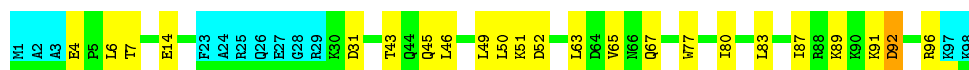


4.2.11 Score per residue for model 11

- Molecule 1: S100 calcium binding protein A13

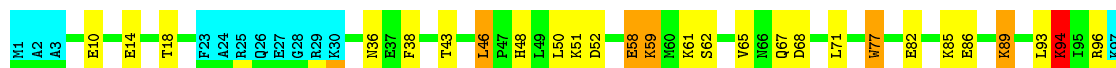


- Molecule 1: S100 calcium binding protein A13



4.2.12 Score per residue for model 12

- Molecule 1: S100 calcium binding protein A13

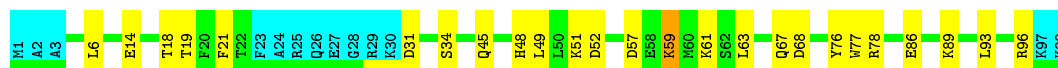


- Molecule 1: S100 calcium binding protein A13



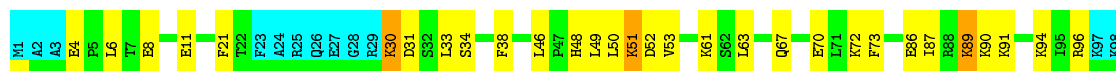
4.2.13 Score per residue for model 13

- Molecule 1: S100 calcium binding protein A13



- Molecule 1: S100 calcium binding protein A13

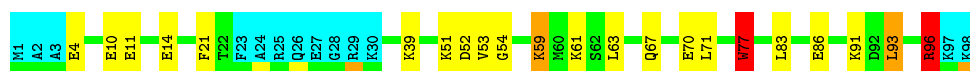
Chain B: 



4.2.14 Score per residue for model 14

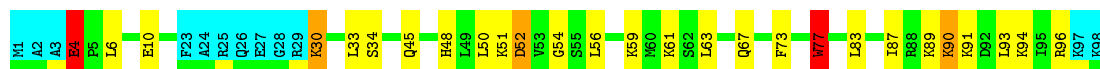
- Molecule 1: S100 calcium binding protein A13

Chain A: 



- Molecule 1: S100 calcium binding protein A13

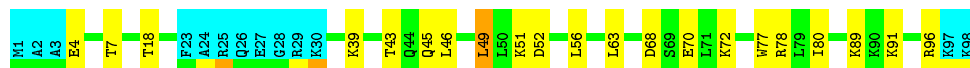
Chain B: 



4.2.15 Score per residue for model 15

- Molecule 1: S100 calcium binding protein A13

Chain A: 



- Molecule 1: S100 calcium binding protein A13

Chain B: 



4.2.16 Score per residue for model 16

- Molecule 1: S100 calcium binding protein A13

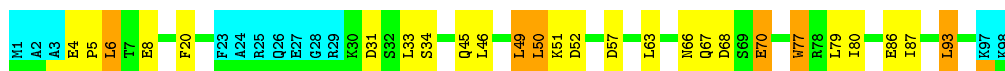
Chain A: 





- Molecule 1: S100 calcium binding protein A13

Chain B: 61% 20% 6% 12%



4.2.17 Score per residue for model 17

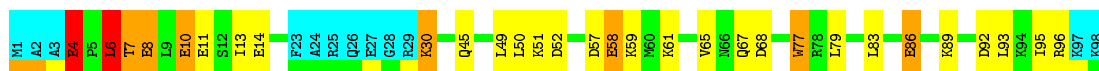
- Molecule 1: S100 calcium binding protein A13

Chain A: 59% 24% 13%



- Molecule 1: S100 calcium binding protein A13

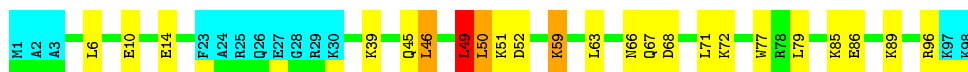
Chain B: 57% 21% 7% 12%



4.2.18 Score per residue for model 18

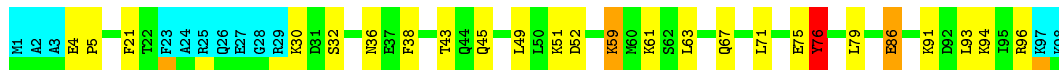
- Molecule 1: S100 calcium binding protein A13

Chain A: 63% 19% 13%



- Molecule 1: S100 calcium binding protein A13

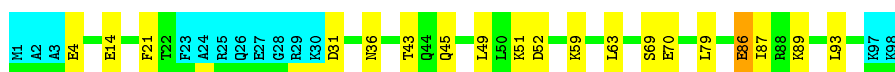
Chain B: 62% 22% 12%



4.2.19 Score per residue for model 19

- Molecule 1: S100 calcium binding protein A13

Chain A: 67% 18% 13%



- Molecule 1: S100 calcium binding protein A13

Chain B: 



4.2.20 Score per residue for model 20 (medoid)

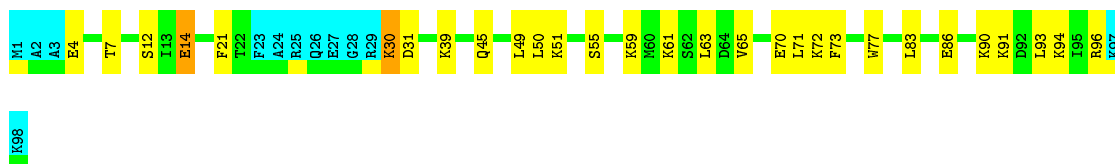
- Molecule 1: S100 calcium binding protein A13

Chain A: 



- Molecule 1: S100 calcium binding protein A13

Chain B: 



4.2.21 Score per residue for model 21

- Molecule 1: S100 calcium binding protein A13

Chain A: 



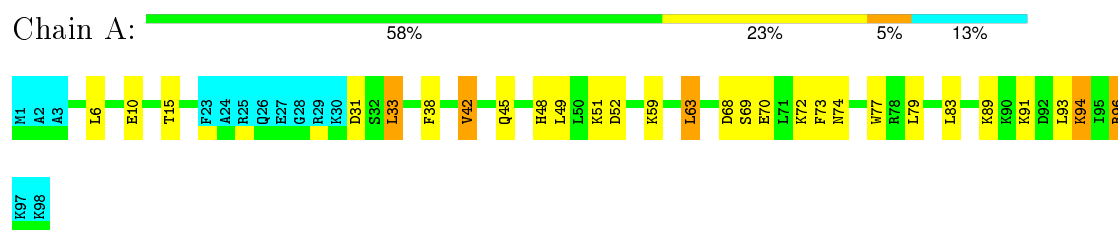
- Molecule 1: S100 calcium binding protein A13

Chain B: 

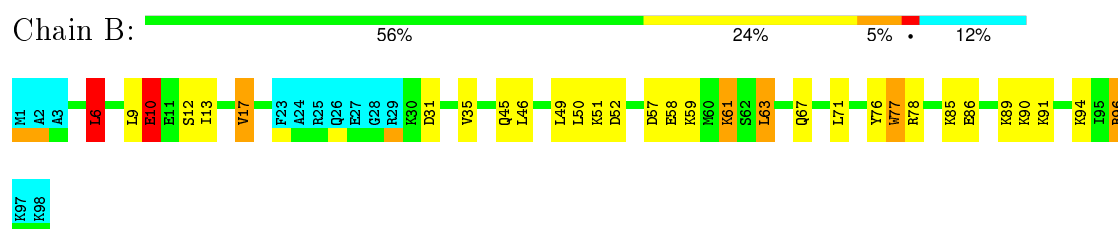


4.2.22 Score per residue for model 22

- Molecule 1: S100 calcium binding protein A13

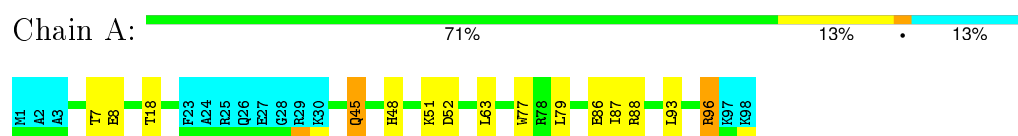


- Molecule 1: S100 calcium binding protein A13

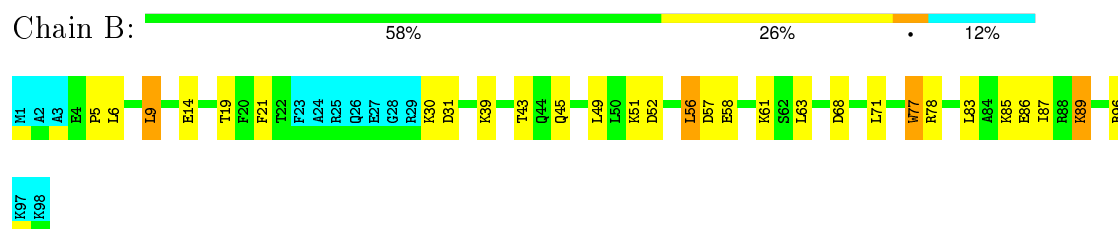


4.2.23 Score per residue for model 23

- Molecule 1: S100 calcium binding protein A13

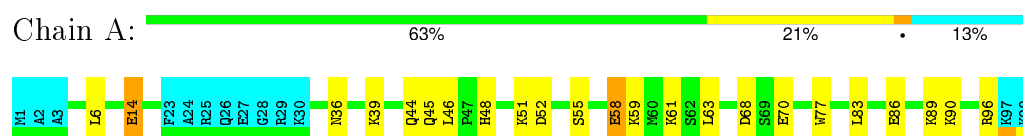


- Molecule 1: S100 calcium binding protein A13

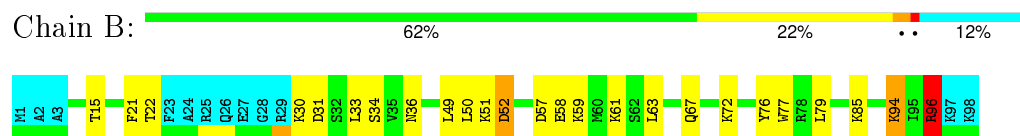


4.2.24 Score per residue for model 24

- Molecule 1: S100 calcium binding protein A13

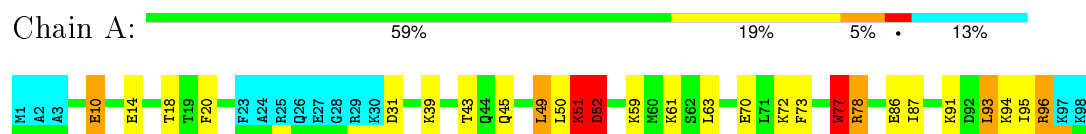


- Molecule 1: S100 calcium binding protein A13

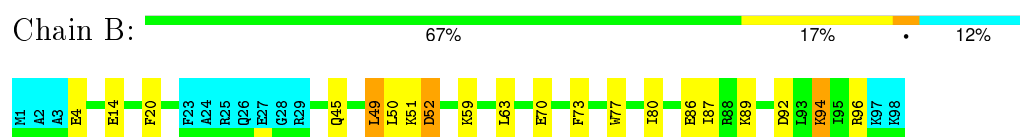


4.2.25 Score per residue for model 25

- Molecule 1: S100 calcium binding protein A13



- Molecule 1: S100 calcium binding protein A13



5 Refinement protocol and experimental data overview

The models were refined using the following method: *Restrained energy minimization*.

Of the 300 calculated structures, 25 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
DYANA	structure solution	5.1
AMBER	refinement	6

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)	BMRB entry 6532
Number of chemical shift lists	1
Total number of shifts	1940
Number of shifts mapped to atoms	1940
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	73%

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

6 Model quality

6.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.54±0.01	0±0/711 (0.0±0.0%)	1.03±0.12	1±1/957 (0.1±0.1%)
1	B	0.55±0.01	0±0/720 (0.0±0.0%)	1.02±0.05	1±1/968 (0.1±0.1%)
All	All	0.54	0/35775 (0.0%)	1.03	37/48125 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.7±1.1	1.4±1.1
1	B	0.7±1.0	1.2±1.1
All	All	35	66

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	19	THR	O-C-N	30.30	171.18	122.70	13	1
1	A	19	THR	CA-C-O	-16.86	84.69	120.10	13	1
1	A	19	THR	CA-C-N	-13.94	86.53	117.20	13	1
1	B	8	GLU	CA-CB-CG	12.88	141.74	113.40	10	1
1	B	10	GLU	CB-CA-C	11.46	133.31	110.40	22	1
1	B	86	GLU	CA-CB-CG	8.00	131.00	113.40	9	1
1	A	88	ARG	CB-CG-CD	7.98	132.34	111.60	21	1
1	B	17	VAL	CB-CA-C	7.91	126.43	111.40	22	1
1	A	96	ARG	NE-CZ-NH2	-7.49	116.56	120.30	4	3
1	B	6	LEU	CB-CG-CD2	7.00	122.90	111.00	17	1
1	B	4	GLU	CB-CA-C	6.95	124.29	110.40	12	3
1	B	78	ARG	NE-CZ-NH2	-6.66	116.97	120.30	2	1
1	A	89	LYS	CB-CG-CD	6.14	127.56	111.60	12	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	96	ARG	NE-CZ-NH2	-5.83	117.38	120.30	24	2
1	B	12	SER	N-CA-CB	5.76	119.14	110.50	20	1
1	B	78	ARG	NE-CZ-NH1	5.55	123.08	120.30	22	1
1	A	94	LYS	CB-CA-C	5.51	121.42	110.40	22	1
1	B	48	HIS	CA-CB-CG	5.46	122.88	113.60	19	1
1	B	13	ILE	CA-CB-CG1	5.43	121.33	111.00	6	1
1	A	96	ARG	CA-CB-CG	5.34	125.16	113.40	14	1
1	B	7	THR	C-N-CA	5.34	135.04	121.70	17	1
1	A	22	THR	C-N-CA	5.32	135.01	121.70	17	1
1	A	94	LYS	N-CA-CB	5.29	120.11	110.60	12	2
1	B	7	THR	CA-CB-CG2	5.27	119.77	112.40	17	1
1	A	78	ARG	NE-CZ-NH1	5.23	122.92	120.30	21	2
1	B	14	GLU	CB-CA-C	5.23	120.85	110.40	20	1
1	B	9	LEU	CB-CG-CD1	5.15	119.76	111.00	23	1
1	B	96	ARG	NE-CZ-NH1	5.07	122.83	120.30	19	1
1	B	6	LEU	C-N-CA	5.01	134.23	121.70	22	1
1	B	16	VAL	CA-CB-CG1	5.01	118.41	110.90	9	1

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

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	19	THR	CB,CA	3
1	B	7	THR	CB,CA	3
1	A	22	THR	CB	2
1	A	11	GLU	CA	2
1	B	10	GLU	CA	2
1	A	46	LEU	CA	2
1	A	94	LYS	CA	2
1	B	11	GLU	CA	2
1	A	31	ASP	CA	1
1	B	6	LEU	CA	1
1	B	13	ILE	CA	1
1	B	9	LEU	CA	1
1	B	4	GLU	CA	1
1	B	5	PRO	CA	1
1	A	6	LEU	CA	1
1	A	95	ILE	CB	1
1	A	96	ARG	CA	1
1	A	18	THR	CA	1
1	B	15	THR	CB	1
1	B	12	SER	CA	1

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Mol	Chain	Res	Type	Atoms	Models (Total)
1	B	14	GLU	CA	1
1	A	33	LEU	CA	1
1	B	17	VAL	CA	1
1	A	92	ASP	CA	1

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	73	PHE	Sidechain	8
1	A	96	ARG	Sidechain	6
1	B	96	ARG	Sidechain	5
1	B	73	PHE	Sidechain	5
1	B	76	TYR	Sidechain	5
1	A	76	TYR	Sidechain	4
1	B	20	PHE	Sidechain	3
1	B	21	PHE	Sidechain	3
1	B	4	GLU	Peptide	3
1	B	78	ARG	Sidechain	3
1	A	78	ARG	Sidechain	3
1	A	22	THR	Peptide	2
1	A	70	GLU	Peptide	2
1	A	20	PHE	Sidechain	2
1	A	38	PHE	Sidechain	2
1	A	48	HIS	Sidechain	2
1	A	51	LYS	Peptide	1
1	A	33	LEU	Peptide	1
1	A	91	LYS	Peptide	1
1	B	88	ARG	Sidechain	1
1	B	38	PHE	Sidechain	1
1	B	48	HIS	Sidechain	1
1	A	21	PHE	Peptide	1
1	A	34	SER	Peptide	1

6.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	701	716	716	3±2
1	B	710	729	729	3±2
All	All	35275	36125	36125	135

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 2.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:THR:HG23	1:B:8:GLU:HB2	0.68	1.64	10	1
1:A:93:LEU:HD23	1:A:93:LEU:H	0.66	1.51	17	3
1:A:93:LEU:H	1:A:93:LEU:HD23	0.64	1.52	7	1
1:B:6:LEU:O	1:B:6:LEU:HD23	0.63	1.93	16	1
1:A:93:LEU:HD13	1:A:93:LEU:H	0.61	1.56	9	2
1:A:7:THR:HG21	1:B:45:GLN:HG3	0.57	1.76	9	1
1:A:19:THR:CG2	1:B:8:GLU:HB2	0.56	2.31	10	1
1:B:56:LEU:HD13	1:B:57:ASP:N	0.55	2.15	23	1
1:B:30:LYS:NZ	1:B:70:GLU:OE2	0.54	2.40	20	4
1:A:94:LYS:HB3	1:B:4:GLU:HB3	0.54	1.79	12	1
1:B:6:LEU:HD12	1:B:10:GLU:HG3	0.54	1.80	9	1
1:B:10:GLU:HA	1:B:13:ILE:HD12	0.52	1.80	17	1
1:B:93:LEU:HD13	1:B:93:LEU:H	0.52	1.65	9	1
1:A:94:LYS:HG2	1:B:6:LEU:HD22	0.51	1.82	16	1
1:A:45:GLN:HG3	1:B:7:THR:HG22	0.50	1.84	20	2
1:A:51:LYS:HD3	1:A:52:ASP:N	0.50	2.22	16	1
1:A:39:LYS:CB	1:A:63:LEU:HD21	0.49	2.36	8	3
1:B:7:THR:HG23	1:B:8:GLU:H	0.49	1.67	8	1
1:A:35:VAL:CG1	1:A:63:LEU:HD12	0.48	2.39	7	3
1:A:51:LYS:HD3	1:A:52:ASP:H	0.48	1.68	25	1
1:B:4:GLU:CG	1:B:6:LEU:HD22	0.48	2.39	17	1
1:B:4:GLU:HG2	1:B:6:LEU:HD22	0.48	1.85	17	1
1:B:83:LEU:O	1:B:87:ILE:HG22	0.48	2.09	19	1
1:B:35:VAL:CG1	1:B:63:LEU:HD12	0.47	2.39	7	1
1:A:7:THR:HG21	1:B:45:GLN:CG	0.47	2.39	9	1
1:A:33:LEU:N	1:A:33:LEU:HD22	0.47	2.23	17	1
1:B:39:LYS:CB	1:B:63:LEU:HD21	0.47	2.40	21	1
1:B:6:LEU:HD22	1:B:10:GLU:OE1	0.46	2.11	6	1
1:A:33:LEU:HD23	1:A:38:PHE:CD1	0.46	2.45	17	1
1:A:59:LYS:NZ	1:A:86:GLU:OE1	0.46	2.48	12	6
1:A:48:HIS:NE2	1:A:93:LEU:HD12	0.46	2.26	3	1
1:A:93:LEU:H	1:A:93:LEU:HD13	0.46	1.71	25	1
1:B:13:ILE:O	1:B:17:VAL:HG13	0.45	2.11	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:GLU:OE2	1:B:89:LYS:NZ	0.45	2.48	12	2
1:A:93:LEU:HD21	1:B:14:GLU:OE1	0.45	2.11	7	1
1:A:45:GLN:CG	1:B:9:LEU:HD13	0.45	2.42	23	1
1:A:63:LEU:HD11	1:A:79:LEU:HD21	0.44	1.89	22	1
1:A:89:LYS:HG2	1:A:93:LEU:HD22	0.44	1.88	7	3
1:B:4:GLU:HG3	1:B:6:LEU:HD22	0.44	1.89	15	1
1:A:35:VAL:HG23	1:A:69:SER:O	0.44	2.11	7	1
1:A:89:LYS:HG2	1:A:93:LEU:HD13	0.44	1.89	17	3
1:A:89:LYS:CG	1:A:93:LEU:HD13	0.44	2.41	3	1
1:B:82:GLU:OE1	1:B:85:LYS:NZ	0.44	2.50	9	1
1:A:83:LEU:HD12	1:A:83:LEU:C	0.44	2.33	6	1
1:A:80:ILE:CD1	1:B:77:TRP:HE1	0.43	2.26	16	1
1:A:10:GLU:OE1	1:B:89:LYS:NZ	0.43	2.51	25	3
1:B:51:LYS:HD3	1:B:52:ASP:N	0.43	2.28	13	2
1:B:58:GLU:OE1	1:B:85:LYS:NZ	0.43	2.51	22	1
1:B:89:LYS:HG3	1:B:93:LEU:HD13	0.43	1.91	1	1
1:B:33:LEU:HD22	1:B:33:LEU:N	0.43	2.29	13	2
1:A:56:LEU:HD23	1:A:57:ASP:H	0.43	1.74	20	1
1:A:77:TRP:HE1	1:B:80:ILE:CD1	0.43	2.27	25	1
1:B:59:LYS:NZ	1:B:86:GLU:OE1	0.43	2.52	8	3
1:A:14:GLU:CB	1:B:93:LEU:HD11	0.42	2.44	5	1
1:A:58:GLU:OE1	1:A:61:LYS:NZ	0.42	2.52	12	1
1:A:4:GLU:CD	1:A:4:GLU:N	0.42	2.72	11	3
1:A:45:GLN:CG	1:B:7:THR:HG22	0.42	2.44	8	1
1:B:59:LYS:NZ	1:B:86:GLU:OE2	0.42	2.52	17	2
1:A:42:VAL:O	1:A:46:LEU:HD12	0.42	2.15	8	1
1:A:77:TRP:CD1	1:B:77:TRP:CD1	0.42	3.07	14	1
1:A:91:LYS:NZ	1:A:92:ASP:OD2	0.42	2.52	11	1
1:A:93:LEU:H	1:A:93:LEU:HD22	0.42	1.75	4	1
1:B:38:PHE:CE1	1:B:76:TYR:CD1	0.42	3.07	18	1
1:B:38:PHE:CZ	1:B:76:TYR:CD2	0.42	3.07	8	1
1:B:70:GLU:OE1	1:B:72:LYS:NZ	0.42	2.52	19	1
1:A:14:GLU:OE2	1:B:94:LYS:NZ	0.41	2.52	24	1
1:B:7:THR:H	1:B:10:GLU:CD	0.41	2.18	17	1
1:B:58:GLU:OE1	1:B:61:LYS:NZ	0.41	2.52	17	1
1:A:59:LYS:NZ	1:A:86:GLU:OE2	0.41	2.53	13	3
1:B:92:ASP:O	1:B:95:ILE:CG1	0.41	2.68	17	1
1:B:6:LEU:CD1	1:B:10:GLU:HB2	0.41	2.45	22	1
1:B:49:LEU:C	1:B:50:LEU:HD13	0.41	2.36	16	1
1:B:56:LEU:HD13	1:B:56:LEU:C	0.41	2.36	14	2
1:A:61:LYS:CG	1:A:62:SER:N	0.41	2.83	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:82:GLU:OE1	1:A:85:LYS:NZ	0.41	2.53	12	1
1:A:38:PHE:CD1	1:A:76:TYR:CE2	0.41	3.09	3	1
1:A:67:GLN:NE2	1:A:67:GLN:H	0.41	2.13	21	1
1:A:87:ILE:O	1:A:87:ILE:HG23	0.41	2.16	1	1
1:B:35:VAL:HG12	1:B:63:LEU:HG	0.41	1.93	22	1
1:A:93:LEU:CD2	1:A:93:LEU:H	0.41	2.23	17	1
1:A:13:ILE:HG23	1:A:77:TRP:CH2	0.41	2.51	2	1
1:B:13:ILE:HG23	1:B:77:TRP:CH2	0.41	2.50	2	1
1:A:39:LYS:HB3	1:A:63:LEU:HD21	0.41	1.92	8	1
1:A:38:PHE:O	1:A:42:VAL:HG13	0.41	2.16	22	1
1:B:9:LEU:H	1:B:9:LEU:HD22	0.41	1.75	9	1
1:B:58:GLU:OE2	1:B:61:LYS:NZ	0.41	2.52	24	1
1:A:49:LEU:C	1:A:50:LEU:HD13	0.41	2.36	18	1
1:A:14:GLU:OE2	1:B:89:LYS:NZ	0.41	2.53	11	2
1:A:96:ARG:HB3	1:B:4:GLU:CB	0.41	2.46	14	1
1:B:7:THR:HG23	1:B:8:GLU:N	0.40	2.31	8	1
1:B:58:GLU:OE2	1:B:85:LYS:NZ	0.40	2.54	23	1
1:A:58:GLU:OE2	1:A:61:LYS:NZ	0.40	2.52	24	1
1:A:14:GLU:OE1	1:B:94:LYS:NZ	0.40	2.53	6	2
1:B:91:LYS:NZ	1:B:92:ASP:OD2	0.40	2.55	11	1
1:B:48:HIS:CE1	1:B:93:LEU:HD11	0.40	2.51	1	1
1:B:32:SER:OG	1:B:71:LEU:HD11	0.40	2.15	18	1
1:B:7:THR:C	1:B:10:GLU:OE1	0.40	2.59	17	1
1:B:57:ASP:OD1	1:B:61:LYS:NZ	0.40	2.54	22	1
1:A:89:LYS:NZ	1:B:10:GLU:OE2	0.40	2.55	21	1
1:A:52:ASP:N	1:A:52:ASP:OD1	0.40	2.55	21	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	85/98 (87%)	66±2 (78±3%)	15±2 (18±3%)	4±1 (5±1%)	5	29
1	B	86/98 (88%)	64±3 (74±3%)	18±3 (20±4%)	5±2 (5±2%)	4	24
All	All	4275/4900 (87%)	3246 (76%)	815 (19%)	214 (5%)	5	26

All 40 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	52	ASP	22
1	B	52	ASP	18
1	B	91	LYS	12
1	A	77	TRP	11
1	B	86	GLU	10
1	B	31	ASP	9
1	A	91	LYS	9
1	B	30	LYS	8
1	B	77	TRP	8
1	B	90	LYS	8
1	B	65	VAL	7
1	A	46	LEU	7
1	A	31	ASP	7
1	A	49	LEU	6
1	A	48	HIS	6
1	B	49	LEU	6
1	B	5	PRO	6
1	A	69	SER	5
1	B	96	ARG	5
1	A	70	GLU	5
1	A	86	GLU	5
1	A	96	ARG	4
1	B	46	LEU	4
1	A	65	VAL	3
1	B	70	GLU	3
1	A	50	LEU	2
1	B	48	HIS	2
1	B	54	GLY	2
1	A	89	LYS	2
1	B	4	GLU	2
1	A	90	LYS	1
1	B	93	LEU	1
1	B	50	LEU	1
1	B	13	ILE	1
1	A	54	GLY	1
1	B	69	SER	1
1	A	53	VAL	1
1	A	94	LYS	1
1	B	8	GLU	1
1	B	89	LYS	1

6.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	82/91 (90%)	65±3 (80±3%)	17±3 (20±3%)	4	35
1	B	83/91 (91%)	65±2 (78±3%)	18±2 (22±3%)	4	32
All	All	4125/4550 (91%)	3258 (79%)	867 (21%)	4	33

All 131 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	A	51	LYS	25
1	B	51	LYS	25
1	B	63	LEU	22
1	A	45	GLN	20
1	A	77	TRP	20
1	B	45	GLN	20
1	A	63	LEU	19
1	B	6	LEU	18
1	B	77	TRP	18
1	B	67	GLN	17
1	B	96	ARG	15
1	B	87	ILE	15
1	B	89	LYS	14
1	A	96	ARG	14
1	B	49	LEU	14
1	A	67	GLN	14
1	A	59	LYS	13
1	A	89	LYS	13
1	A	93	LEU	13
1	A	61	LYS	12
1	A	83	LEU	12
1	A	4	GLU	12
1	B	59	LYS	11
1	B	30	LYS	11
1	A	68	ASP	11
1	A	14	GLU	11
1	B	4	GLU	11
1	B	94	LYS	11

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Mol	Chain	Res	Type	Models (Total)
1	B	14	GLU	11
1	A	49	LEU	11
1	B	83	LEU	11
1	B	50	LEU	11
1	A	43	THR	10
1	A	36	ASN	10
1	A	18	THR	9
1	A	87	ILE	9
1	B	61	LYS	9
1	B	93	LEU	9
1	A	46	LEU	8
1	A	6	LEU	8
1	A	39	LYS	8
1	B	68	ASP	8
1	B	52	ASP	7
1	B	72	LYS	7
1	A	7	THR	7
1	B	71	LEU	7
1	A	10	GLU	7
1	A	79	LEU	7
1	B	10	GLU	7
1	A	21	PHE	6
1	B	21	PHE	6
1	B	79	LEU	6
1	B	80	ILE	6
1	B	34	SER	6
1	A	72	LYS	6
1	B	43	THR	6
1	B	86	GLU	6
1	B	36	ASN	6
1	A	48	HIS	6
1	A	91	LYS	6
1	A	80	ILE	6
1	B	48	HIS	6
1	B	55	SER	5
1	B	57	ASP	5
1	A	50	LEU	5
1	A	71	LEU	5
1	B	92	ASP	5
1	A	56	LEU	5
1	B	56	LEU	4
1	B	18	THR	4

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Mol	Chain	Res	Type	Models (Total)
1	B	39	LYS	4
1	A	44	GLN	4
1	A	94	LYS	4
1	A	70	GLU	4
1	B	31	ASP	4
1	B	11	GLU	4
1	A	34	SER	4
1	A	33	LEU	4
1	B	33	LEU	4
1	B	85	LYS	4
1	B	8	GLU	4
1	A	82	GLU	3
1	B	90	LYS	3
1	A	58	GLU	3
1	B	66	ASN	3
1	A	53	VAL	3
1	A	11	GLU	3
1	B	88	ARG	3
1	A	85	LYS	3
1	A	66	ASN	3
1	B	7	THR	3
1	A	74	ASN	3
1	B	74	ASN	3
1	A	86	GLU	3
1	A	8	GLU	2
1	B	22	THR	2
1	B	13	ILE	2
1	B	41	LEU	2
1	A	52	ASP	2
1	A	88	ARG	2
1	A	31	ASP	2
1	B	17	VAL	2
1	A	78	ARG	2
1	B	95	ILE	2
1	B	76	TYR	2
1	A	60	MET	2
1	A	57	ASP	2
1	A	75	GLU	2
1	B	91	LYS	2
1	B	53	VAL	2
1	B	46	LEU	2
1	B	70	GLU	2

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Mol	Chain	Res	Type	Models (Total)
1	B	75	GLU	2
1	A	42	VAL	1
1	A	90	LYS	1
1	B	73	PHE	1
1	A	76	TYR	1
1	A	55	SER	1
1	B	19	THR	1
1	B	58	GLU	1
1	B	12	SER	1
1	A	41	LEU	1
1	B	60	MET	1
1	A	69	SER	1
1	B	9	LEU	1
1	A	22	THR	1
1	A	9	LEU	1
1	A	15	THR	1
1	B	15	THR	1
1	B	78	ARG	1
1	B	65	VAL	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 73% for the well-defined parts and 67% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 6532

Chemical shift list name: *assigned_chem_shift_list_1*

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	1940
Number of shifts mapped to atoms	1940
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	170	2.11 ± 0.16	Should be applied
$^{13}\text{C}_\beta$	164	3.15 ± 0.09	Should be applied
$^{13}\text{C}'$	0	—	—
^{15}N	168	0.59 ± 0.30	None needed (imprecise)

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 73%, i.e. 1638 atoms were assigned a chemical shift out of a possible 2232. 28 out of 38 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	634/847 (75%)	318/338 (94%)	159/342 (46%)	157/167 (94%)
Sidechain	970/1259 (77%)	604/732 (83%)	356/476 (75%)	10/51 (20%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	34/126 (27%)	32/68 (47%)	0/54 (0%)	2/4 (50%)
Overall	1638/2232 (73%)	954/1138 (84%)	515/872 (59%)	169/222 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 67%, i.e. 1720 atoms were assigned a chemical shift out of a possible 2580. 28 out of 38 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	678/972 (70%)	340/388 (88%)	170/392 (43%)	168/192 (88%)
Sidechain	1008/1464 (69%)	628/856 (73%)	370/538 (69%)	10/70 (14%)
Aromatic	34/144 (24%)	32/78 (41%)	0/62 (0%)	2/4 (50%)
Overall	1720/2580 (67%)	1000/1322 (76%)	540/992 (54%)	180/266 (68%)

7.1.4 Statistically unusual chemical shifts ⓘ

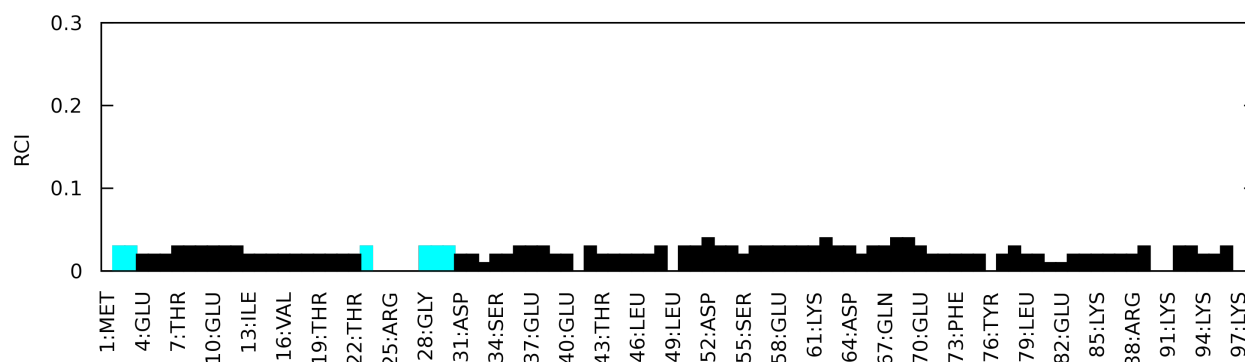
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	81	GLY	HA2	1.76	5.87 – 2.07	-5.8
1	B	81	GLY	HA2	1.76	5.87 – 2.07	-5.8
1	B	88	ARG	CD	38.52	47.57 – 38.77	-5.3
1	A	88	ARG	CD	38.52	47.57 – 38.77	-5.3

7.1.5 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:

