Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	1LKJ
Title	:	NMR Structure of Apo Calmodulin from Yeast Saccharomyces cerevisiae
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Deposited on	:	2002-04-25

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 (i) symbol.

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

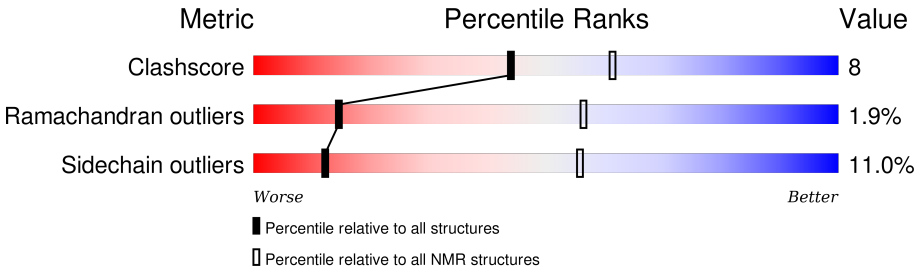
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 17%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	146	64% 20% • 15%

2 Ensemble composition and analysis

This entry contains 31 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:20, A:25-A:56, A:62-A:73 (60)	0.21	16
2	A:82-A:145 (64)	0.46	1

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 6 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 4, 6, 8, 9, 13, 15, 22, 24, 25, 28, 29
2	7, 16, 17, 21, 27, 31
3	5, 12, 18, 20, 30
4	11, 19, 23
5	3, 26
6	10, 14

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2206 atoms, of which 1084 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	146	2206	692	1084	182	244	4	0

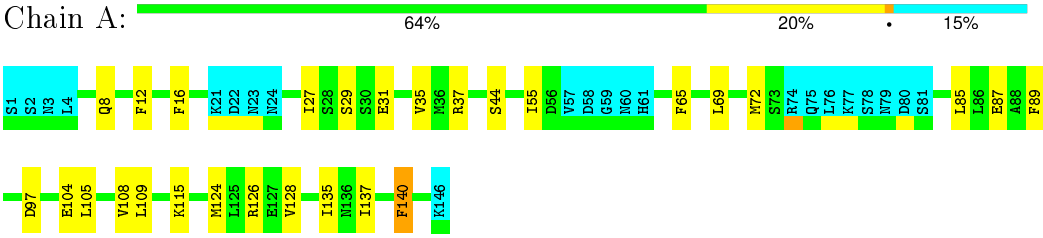
4 Residue-property plots

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: Calmodulin

Chain A:



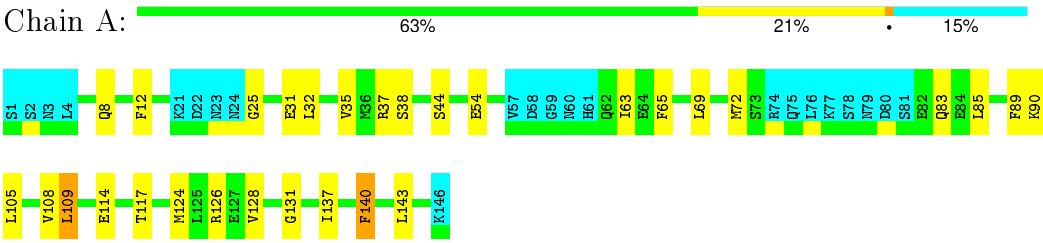
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Calmodulin

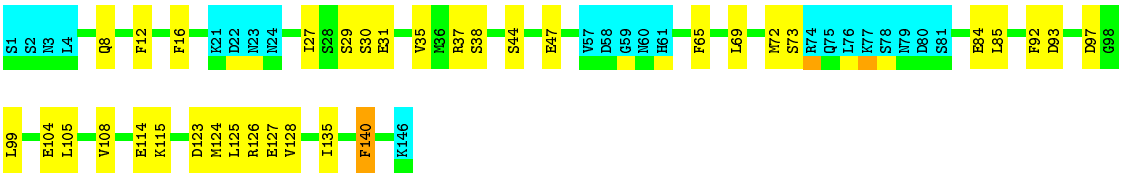
Chain A:



4.2.2 Score per residue for model 2

- Molecule 1: Calmodulin

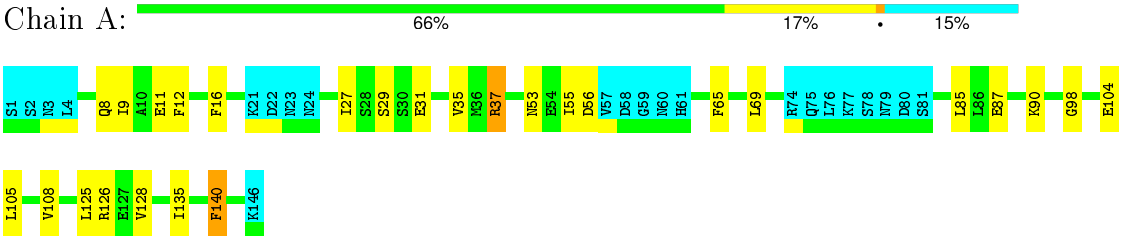
Chain A:



4.2.3 Score per residue for model 3

- Molecule 1: Calmodulin

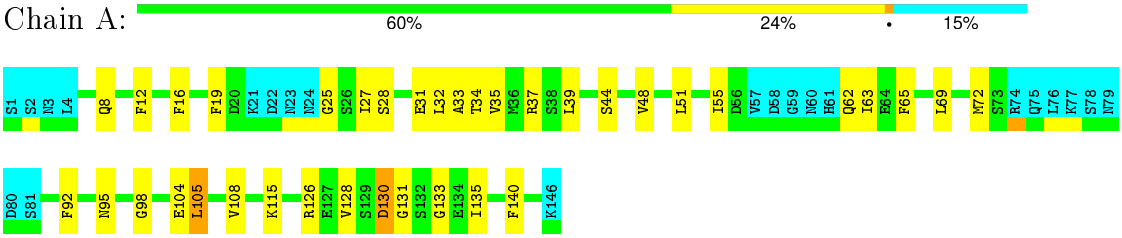
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Calmodulin

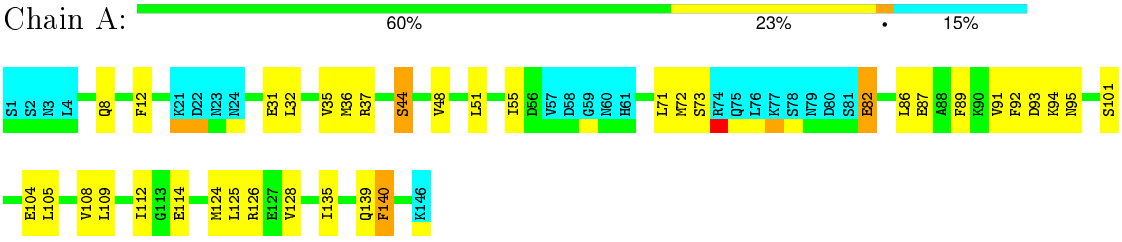
Chain A:



4.2.5 Score per residue for model 5

- Molecule 1: Calmodulin

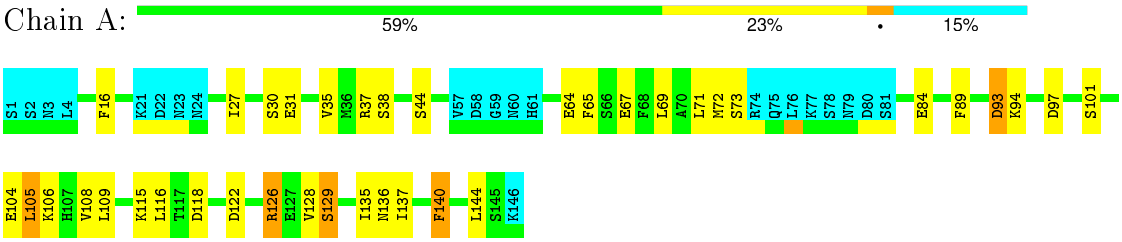
Chain A:



4.2.6 Score per residue for model 6

- Molecule 1: Calmodulin

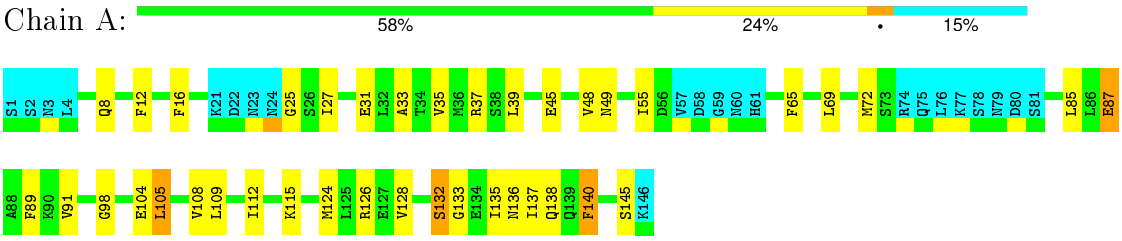
Chain A:



4.2.7 Score per residue for model 7

- Molecule 1: Calmodulin

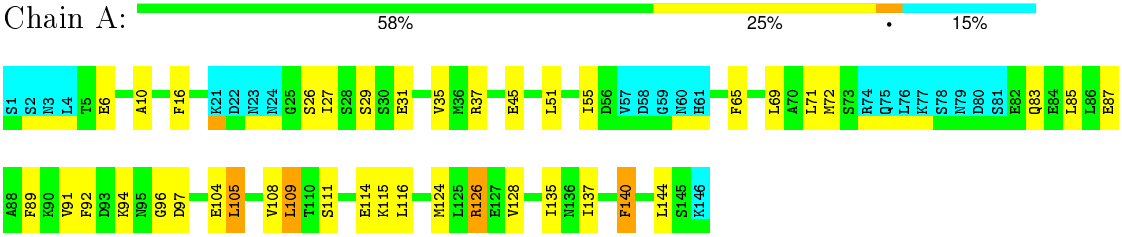
Chain A:



4.2.8 Score per residue for model 8

- Molecule 1: Calmodulin

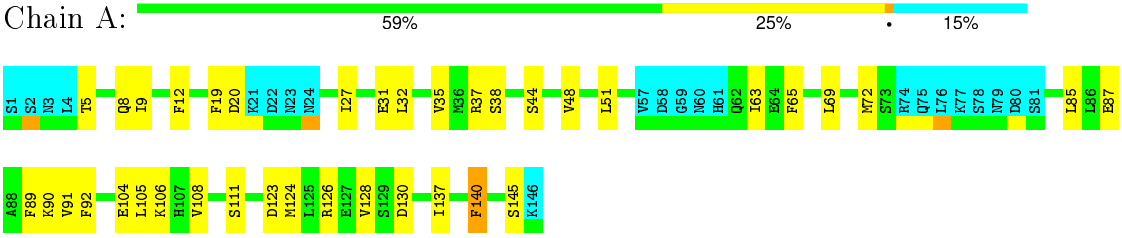
Chain A:



4.2.9 Score per residue for model 9

- Molecule 1: Calmodulin

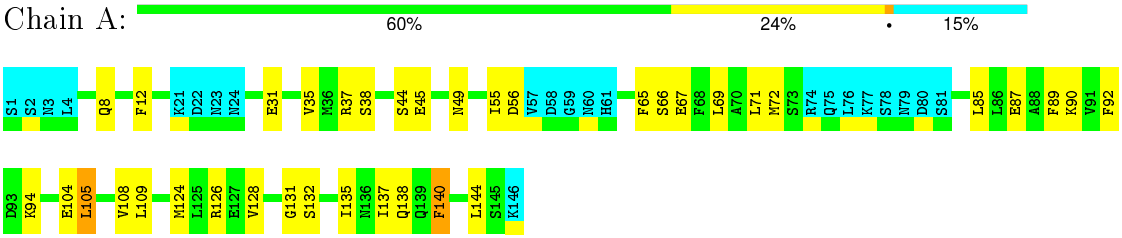
Chain A:



4.2.10 Score per residue for model 10

• Molecule 1: Calmodulin

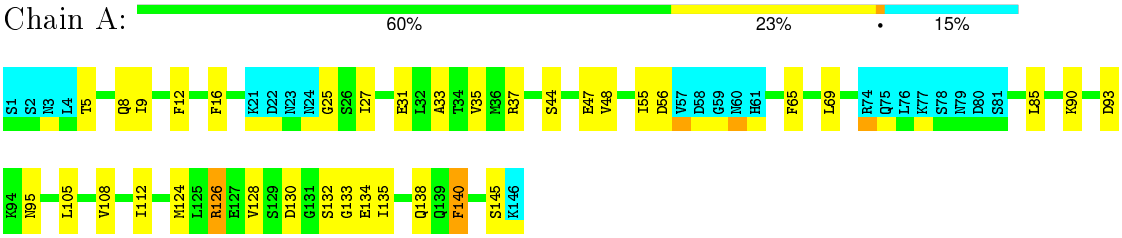
Chain A:



4.2.11 Score per residue for model 11

• Molecule 1: Calmodulin

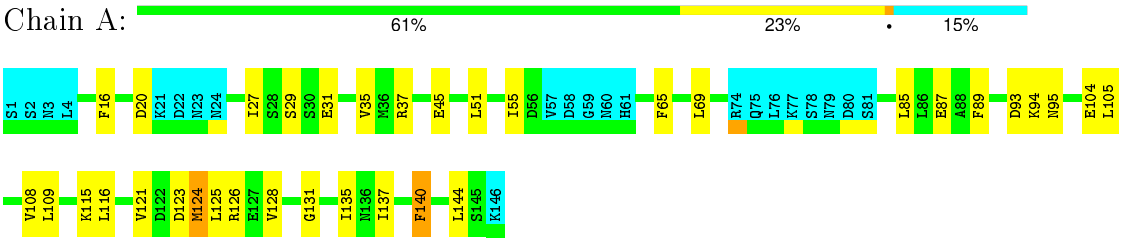
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: Calmodulin

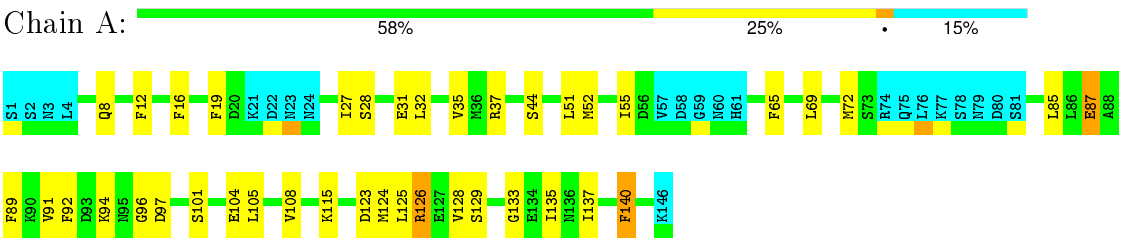
Chain A:



4.2.13 Score per residue for model 13

• Molecule 1: Calmodulin

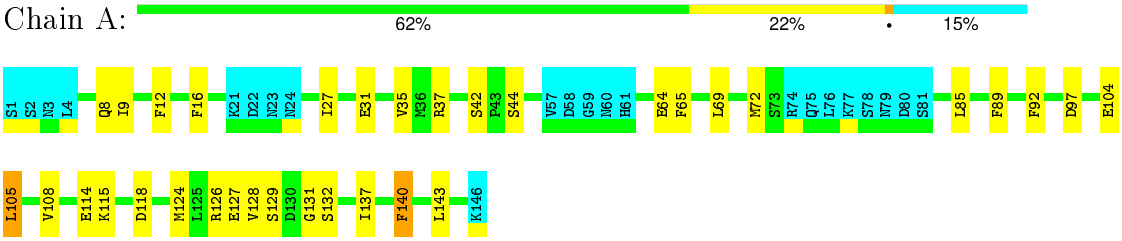
Chain A:



4.2.14 Score per residue for model 14

• Molecule 1: Calmodulin

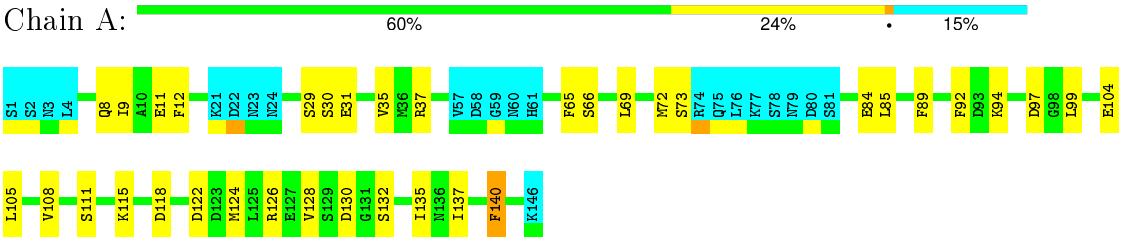
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: Calmodulin

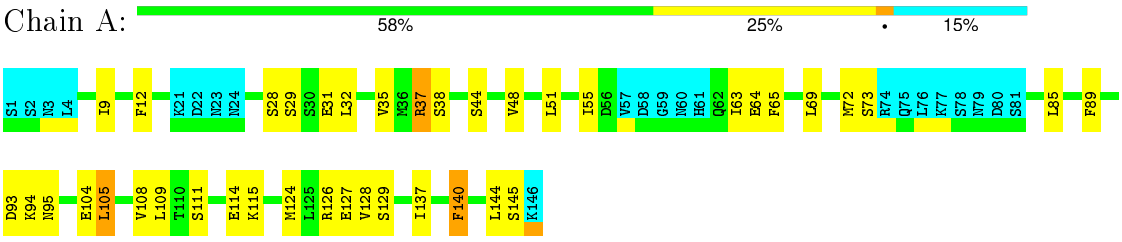
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: Calmodulin

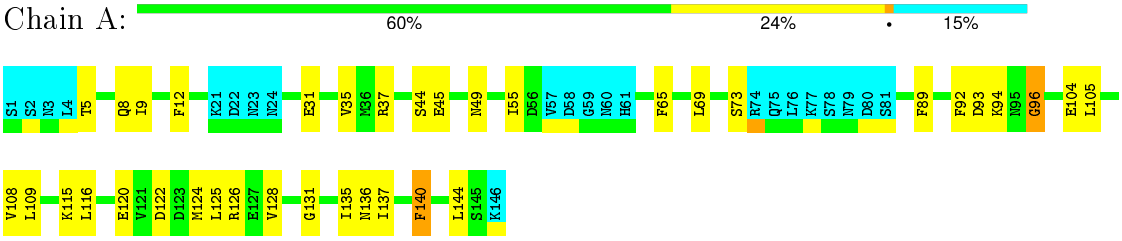
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: Calmodulin

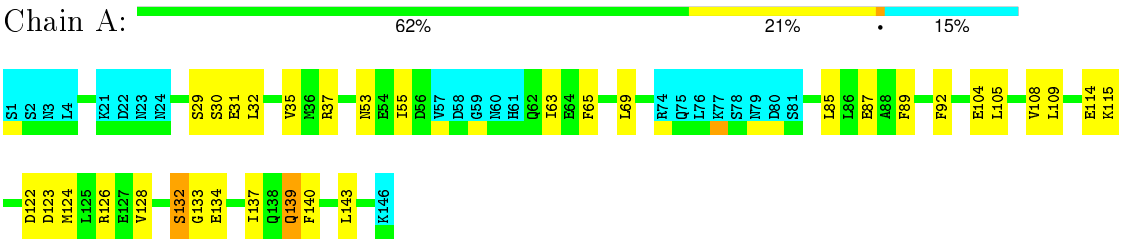
Chain A:



4.2.18 Score per residue for model 18

• Molecule 1: Calmodulin

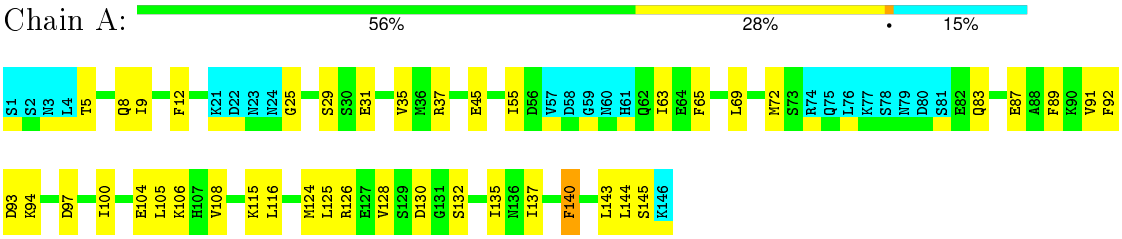
Chain A:



4.2.19 Score per residue for model 19

• Molecule 1: Calmodulin

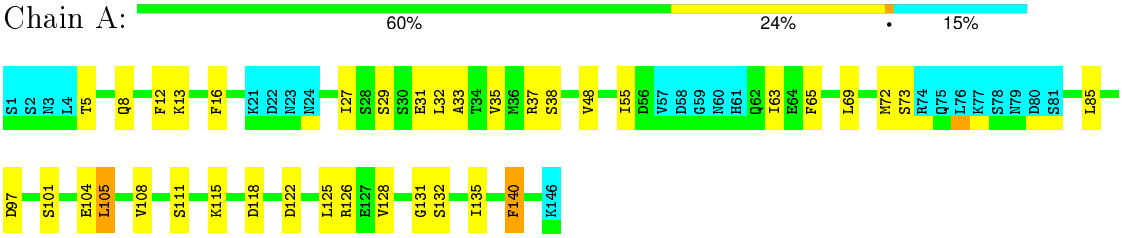
Chain A:



4.2.20 Score per residue for model 20

• Molecule 1: Calmodulin

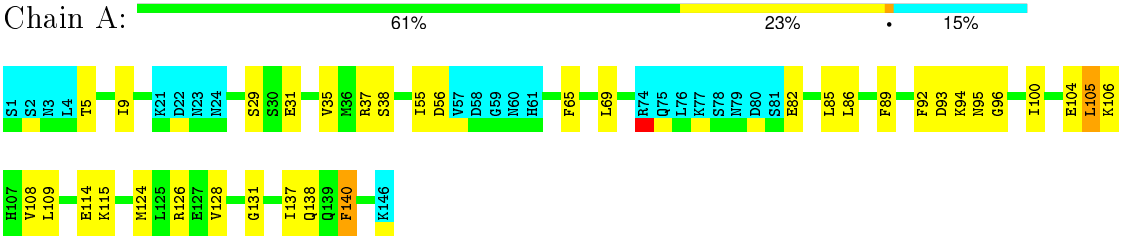
Chain A:



4.2.21 Score per residue for model 21

• Molecule 1: Calmodulin

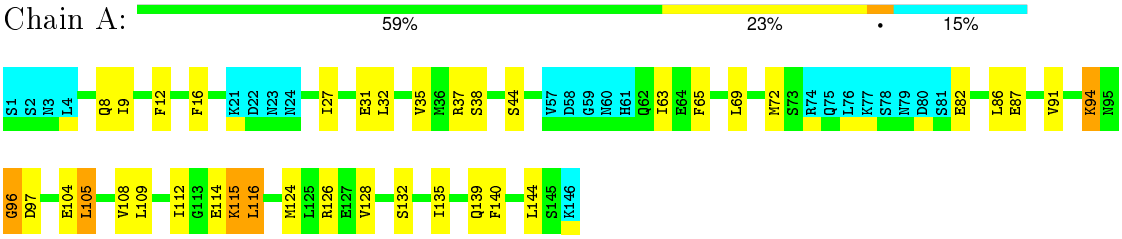
Chain A:



4.2.22 Score per residue for model 22

• Molecule 1: Calmodulin

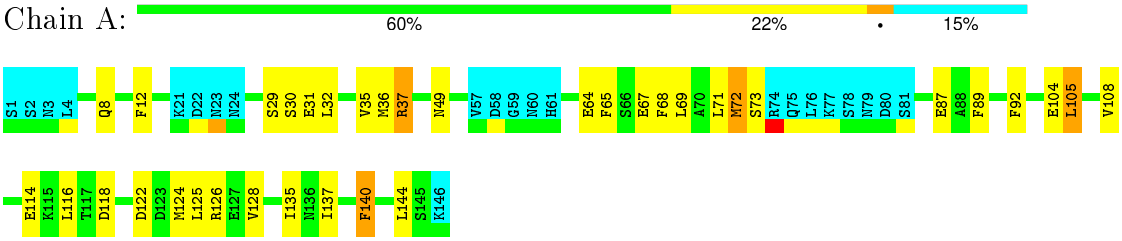
Chain A:



4.2.23 Score per residue for model 23

• Molecule 1: Calmodulin

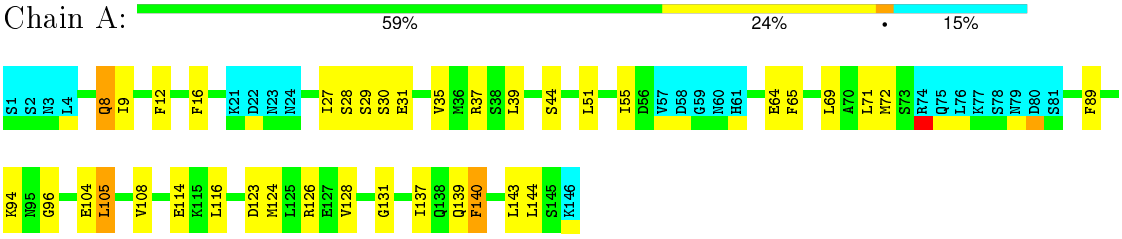
Chain A:



4.2.24 Score per residue for model 24

• Molecule 1: Calmodulin

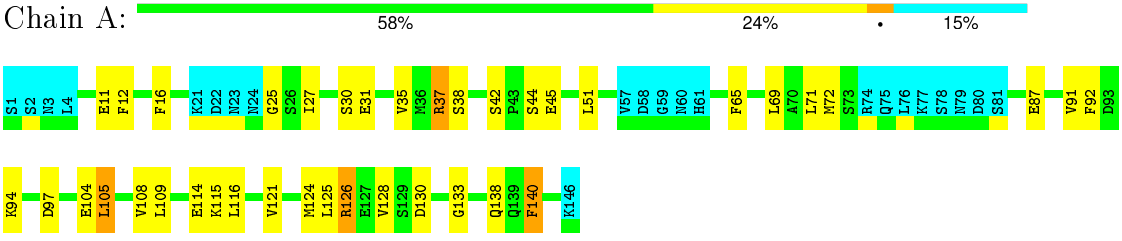
Chain A:



4.2.25 Score per residue for model 25

• Molecule 1: Calmodulin

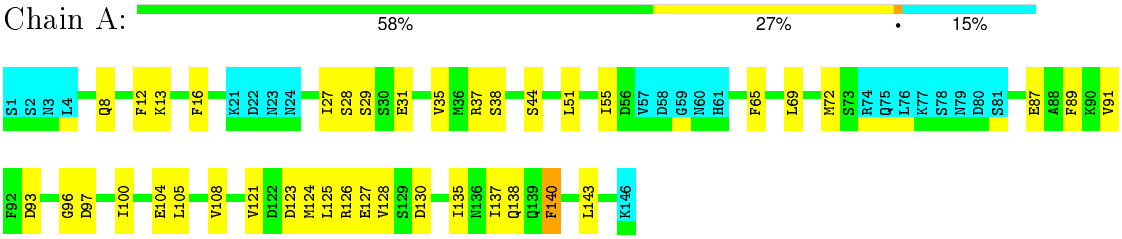
Chain A:



4.2.26 Score per residue for model 26

- Molecule 1: Calmodulin

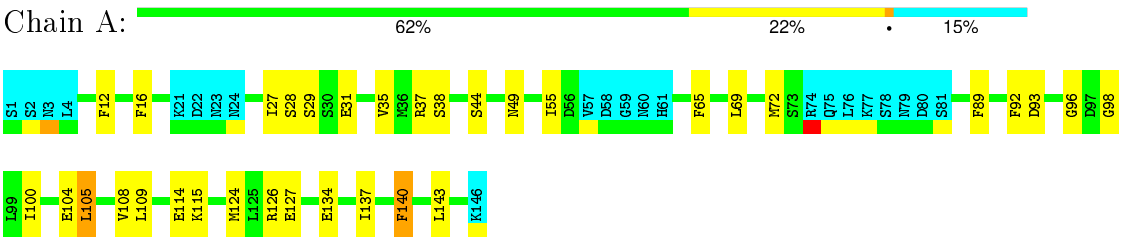
Chain A:



4.2.27 Score per residue for model 27

- Molecule 1: Calmodulin

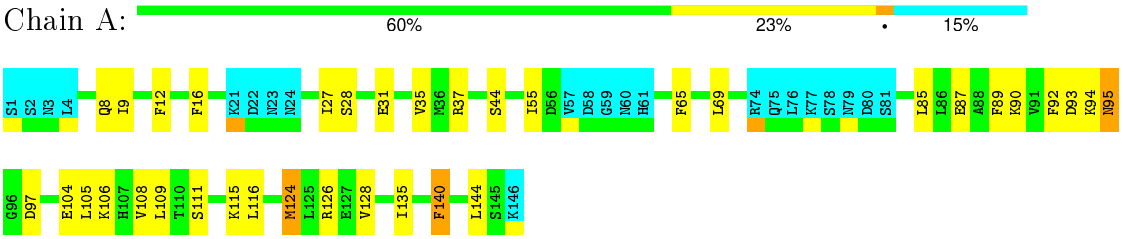
Chain A:



4.2.28 Score per residue for model 28

- Molecule 1: Calmodulin

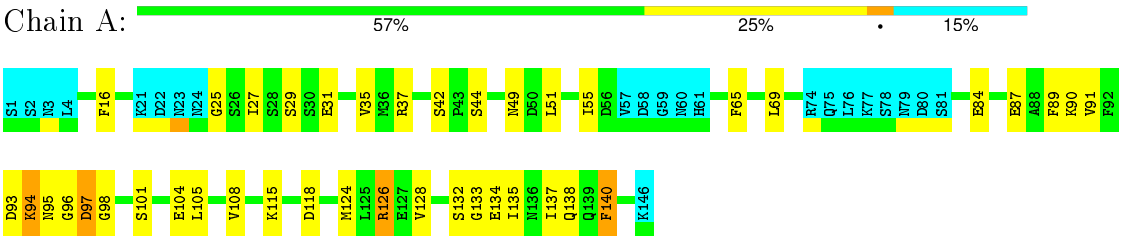
Chain A:



4.2.29 Score per residue for model 29

- Molecule 1: Calmodulin

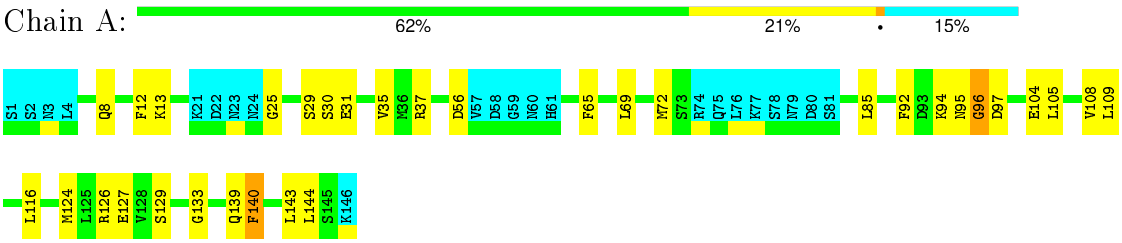
Chain A:



4.2.30 Score per residue for model 30

• Molecule 1: Calmodulin

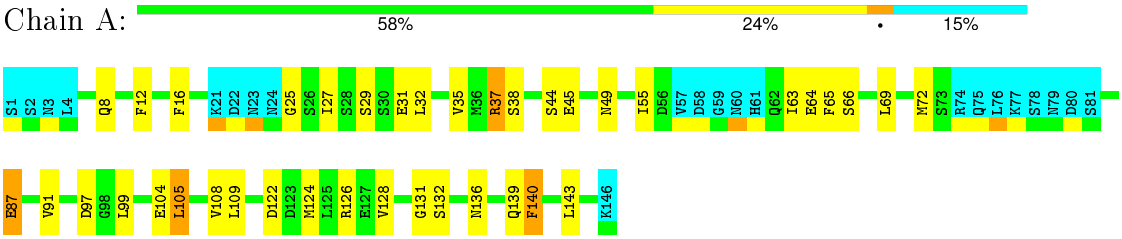
Chain A:



4.2.31 Score per residue for model 31

• Molecule 1: Calmodulin

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 31 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
X-PLOR	structure solution	3.851
X-PLOR	refinement	3.851

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 5353
Number of chemical shift lists	1
Total number of shifts	283
Number of shifts mapped to atoms	283
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	17%

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.

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	0.0±0.0	2.0±0.0
All	All	0	62

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

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	37	ARG	Sidechain	31
1	A	126	ARG	Sidechain	31

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	949	918	918	16±4
All	All	29419	28458	28458	489

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 8.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:105:LEU:HD21	1:A:140:PHE:CE2	0.82	2.10	11	7
1:A:16:PHE:CE1	1:A:27:ILE:HG23	0.78	2.14	6	19
1:A:105:LEU:HD21	1:A:140:PHE:CZ	0.75	2.17	19	29
1:A:31:GLU:O	1:A:35:VAL:HG23	0.74	1.83	3	31
1:A:104:GLU:O	1:A:108:VAL:HG23	0.73	1.84	15	30
1:A:65:PHE:CE2	1:A:69:LEU:HD11	0.72	2.19	2	30
1:A:51:LEU:O	1:A:55:ILE:HD12	0.70	1.86	5	7
1:A:128:VAL:CG1	1:A:135:ILE:HG23	0.69	2.18	17	11
1:A:139:GLN:OE1	1:A:143:LEU:HD12	0.67	1.88	18	1
1:A:105:LEU:HD21	1:A:140:PHE:CE1	0.64	2.27	24	9
1:A:33:ALA:HB2	1:A:48:VAL:HG13	0.64	1.69	4	3
1:A:105:LEU:HD22	1:A:125:LEU:HD21	0.64	1.69	17	3
1:A:116:LEU:HD11	1:A:144:LEU:HD22	0.63	1.69	8	8
1:A:19:PHE:O	1:A:27:ILE:HG22	0.63	1.94	9	2
1:A:87:GLU:O	1:A:91:VAL:HG23	0.62	1.95	22	11
1:A:128:VAL:HG12	1:A:135:ILE:HG23	0.61	1.70	2	17
1:A:55:ILE:HD13	1:A:63:ILE:CD1	0.61	2.25	19	1
1:A:82:GLU:O	1:A:86:LEU:HD12	0.61	1.95	5	2
1:A:32:LEU:HD22	1:A:63:ILE:CD1	0.60	2.27	9	8
1:A:33:ALA:HB2	1:A:48:VAL:CG1	0.60	2.27	7	2
1:A:108:VAL:HG12	1:A:112:ILE:HD11	0.59	1.74	5	3
1:A:124:MET:CG	1:A:143:LEU:HD13	0.59	2.28	31	4
1:A:128:VAL:O	1:A:128:VAL:HG12	0.59	1.97	22	1
1:A:12:PHE:CE1	1:A:72:MET:HE3	0.59	2.32	9	5
1:A:115:LYS:O	1:A:116:LEU:C	0.58	2.41	22	1
1:A:89:PHE:HB3	1:A:137:ILE:HD13	0.58	1.75	1	15
1:A:128:VAL:HG13	1:A:139:GLN:NE2	0.58	2.13	24	1
1:A:89:PHE:CE1	1:A:108:VAL:HG11	0.57	2.33	16	2
1:A:33:ALA:HB2	1:A:48:VAL:HG11	0.57	1.76	7	1
1:A:116:LEU:HD11	1:A:144:LEU:CD2	0.56	2.30	24	2
1:A:116:LEU:CD1	1:A:144:LEU:HD22	0.56	2.30	28	3
1:A:67:GLU:O	1:A:71:LEU:HD12	0.55	2.01	23	3
1:A:89:PHE:HB3	1:A:137:ILE:HG21	0.54	1.79	10	6
1:A:128:VAL:HG22	1:A:139:GLN:OE1	0.54	2.03	18	1
1:A:92:PHE:CD2	1:A:108:VAL:HG22	0.54	2.38	15	3
1:A:105:LEU:O	1:A:109:LEU:HD12	0.53	2.03	8	2
1:A:44:SER:O	1:A:48:VAL:HG23	0.53	2.04	9	3
1:A:97:ASP:HB3	1:A:99:LEU:HD12	0.53	1.81	15	1
1:A:124:MET:O	1:A:128:VAL:HG23	0.53	2.04	14	17
1:A:128:VAL:HG11	1:A:135:ILE:HG23	0.53	1.80	12	2
1:A:116:LEU:HD23	1:A:120:GLU:OE1	0.52	2.05	17	1
1:A:128:VAL:HG11	1:A:140:PHE:CD1	0.52	2.40	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:121:VAL:HG12	1:A:125:LEU:CD1	0.52	2.34	12	3
1:A:105:LEU:CD2	1:A:125:LEU:HD21	0.52	2.35	17	1
1:A:89:PHE:CD1	1:A:137:ILE:HG22	0.52	2.40	17	4
1:A:128:VAL:HG22	1:A:139:GLN:CD	0.52	2.25	18	1
1:A:128:VAL:HG22	1:A:139:GLN:CG	0.52	2.35	18	1
1:A:92:PHE:CE2	1:A:108:VAL:HG22	0.51	2.39	13	6
1:A:105:LEU:O	1:A:109:LEU:HD13	0.51	2.05	7	1
1:A:55:ILE:HD13	1:A:63:ILE:HD11	0.51	1.81	19	2
1:A:32:LEU:HD22	1:A:55:ILE:HD13	0.50	1.83	20	1
1:A:124:MET:HG2	1:A:143:LEU:HD13	0.49	1.84	14	3
1:A:128:VAL:HG13	1:A:139:GLN:CG	0.49	2.37	18	1
1:A:5:THR:O	1:A:9:ILE:HD12	0.49	2.08	9	3
1:A:39:LEU:HD13	1:A:72:MET:CE	0.49	2.38	24	3
1:A:124:MET:HE2	1:A:140:PHE:CE1	0.48	2.44	15	3
1:A:97:ASP:OD2	1:A:99:LEU:HD12	0.48	2.07	2	1
1:A:55:ILE:HD11	1:A:71:LEU:CD1	0.48	2.38	5	1
1:A:128:VAL:HG13	1:A:139:GLN:HE21	0.48	1.68	22	1
1:A:89:PHE:CE1	1:A:105:LEU:HD12	0.48	2.44	5	1
1:A:100:ILE:HD11	1:A:105:LEU:HD12	0.48	1.85	26	3
1:A:85:LEU:HD22	1:A:89:PHE:CE2	0.48	2.43	28	1
1:A:125:LEU:HD23	1:A:135:ILE:CD1	0.47	2.39	5	3
1:A:32:LEU:CD2	1:A:55:ILE:HD13	0.47	2.39	20	2
1:A:121:VAL:HG12	1:A:125:LEU:HD11	0.47	1.86	12	1
1:A:106:LYS:CE	1:A:125:LEU:HD11	0.47	2.40	19	1
1:A:128:VAL:HG11	1:A:140:PHE:HD2	0.47	1.70	22	1
1:A:121:VAL:HG12	1:A:125:LEU:HD12	0.47	1.86	25	2
1:A:89:PHE:CD1	1:A:108:VAL:HG11	0.47	2.45	16	2
1:A:116:LEU:CD2	1:A:116:LEU:N	0.46	2.79	25	1
1:A:106:LYS:HE2	1:A:125:LEU:HD11	0.46	1.87	19	1
1:A:125:LEU:CD2	1:A:135:ILE:HD13	0.46	2.41	17	1
1:A:108:VAL:HG12	1:A:112:ILE:CD1	0.46	2.39	11	2
1:A:124:MET:HE3	1:A:140:PHE:CE1	0.46	2.46	24	1
1:A:96:GLY:O	1:A:98:GLY:N	0.46	2.49	29	1
1:A:124:MET:CE	1:A:140:PHE:CE1	0.46	2.99	22	10
1:A:131:GLY:O	1:A:132:SER:CB	0.46	2.63	20	2
1:A:124:MET:HE1	1:A:144:LEU:HD21	0.45	1.88	10	1
1:A:92:PHE:CD2	1:A:108:VAL:CG2	0.45	3.00	4	12
1:A:93:ASP:O	1:A:95:ASN:N	0.45	2.49	5	6
1:A:32:LEU:HD11	1:A:36:MET:CE	0.45	2.42	5	2
1:A:55:ILE:HD11	1:A:71:LEU:HD13	0.45	1.88	8	1
1:A:92:PHE:CE2	1:A:108:VAL:CG2	0.45	3.00	13	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:PHE:CD1	1:A:72:MET:CE	0.45	2.99	23	1
1:A:12:PHE:CE1	1:A:72:MET:CE	0.45	2.99	2	9
1:A:92:PHE:CZ	1:A:108:VAL:HG22	0.45	2.47	23	2
1:A:128:VAL:HG13	1:A:139:GLN:CD	0.44	2.33	24	1
1:A:114:GLU:O	1:A:116:LEU:N	0.44	2.50	22	1
1:A:94:LYS:O	1:A:96:GLY:N	0.44	2.50	17	3
1:A:89:PHE:CD1	1:A:137:ILE:CG2	0.44	3.00	24	4
1:A:6:GLU:O	1:A:10:ALA:HB2	0.44	2.13	8	1
1:A:8:GLN:O	1:A:12:PHE:CD2	0.43	2.71	23	22
1:A:39:LEU:HD13	1:A:72:MET:HE1	0.43	1.88	7	2
1:A:128:VAL:HG11	1:A:140:PHE:HD1	0.43	1.72	1	1
1:A:69:LEU:HA	1:A:72:MET:CG	0.43	2.43	23	1
1:A:92:PHE:CD1	1:A:108:VAL:HG22	0.43	2.49	14	2
1:A:124:MET:CE	1:A:140:PHE:CE2	0.43	3.01	25	1
1:A:68:PHE:O	1:A:72:MET:HB3	0.43	2.13	23	1
1:A:128:VAL:HG11	1:A:135:ILE:CG2	0.43	2.43	4	1
1:A:92:PHE:CG	1:A:108:VAL:HG22	0.42	2.49	15	1
1:A:93:ASP:CG	1:A:100:ILE:HG23	0.42	2.35	19	1
1:A:51:LEU:HD23	1:A:71:LEU:HD22	0.42	1.89	24	2
1:A:19:PHE:CZ	1:A:34:THR:HG22	0.42	2.49	4	1
1:A:69:LEU:O	1:A:73:SER:CB	0.42	2.68	23	1
1:A:93:ASP:O	1:A:94:LYS:CB	0.42	2.68	6	1
1:A:68:PHE:O	1:A:72:MET:CB	0.42	2.68	23	1
1:A:33:ALA:CB	1:A:48:VAL:HG13	0.42	2.42	4	1
1:A:12:PHE:CE1	1:A:72:MET:HE1	0.41	2.50	23	1
1:A:85:LEU:CD2	1:A:112:ILE:HD13	0.41	2.46	7	1
1:A:128:VAL:HG13	1:A:139:GLN:HG3	0.41	1.91	18	1
1:A:97:ASP:CB	1:A:99:LEU:HD12	0.41	2.44	15	1
1:A:125:LEU:CD2	1:A:135:ILE:CD1	0.41	2.99	13	2
1:A:105:LEU:HD11	1:A:140:PHE:CG	0.41	2.51	16	1
1:A:114:GLU:O	1:A:115:LYS:CB	0.41	2.66	22	1
1:A:20:ASP:OD1	1:A:20:ASP:C	0.41	2.59	9	1
1:A:97:ASP:N	1:A:97:ASP:OD1	0.41	2.54	26	1
1:A:128:VAL:CG1	1:A:135:ILE:CG2	0.41	2.99	28	1
1:A:82:GLU:HG2	1:A:86:LEU:HD11	0.41	1.93	21	1
1:A:116:LEU:CD1	1:A:144:LEU:CD2	0.41	2.99	30	1
1:A:124:MET:SD	1:A:143:LEU:HD13	0.41	2.56	26	1
1:A:124:MET:HE2	1:A:140:PHE:CZ	0.41	2.51	12	1
1:A:32:LEU:HB3	1:A:52:MET:HE3	0.40	1.93	13	1
1:A:128:VAL:HG12	1:A:135:ILE:CG2	0.40	2.45	5	1
1:A:13:LYS:CE	1:A:65:PHE:CE2	0.40	3.04	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:PHE:CE1	1:A:72:MET:SD	0.40	3.15	23	1
1:A:68:PHE:O	1:A:72:MET:N	0.40	2.42	23	1
1:A:99:LEU:HD21	1:A:136:ASN:ND2	0.40	2.32	31	1

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	124/146 (85%)	111±3 (90±2%)	10±2 (8±2%)	2±2 (2±1%)	14	56
All	All	3844/4526 (85%)	3456 (90%)	316 (8%)	72 (2%)	14	56

All 17 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	96	GLY	9
1	A	133	GLY	8
1	A	131	GLY	8
1	A	25	GLY	8
1	A	132	SER	6
1	A	130	ASP	6
1	A	56	ASP	4
1	A	98	GLY	4
1	A	129	SER	4
1	A	145	SER	4
1	A	97	ASP	3
1	A	93	ASP	2
1	A	95	ASN	2
1	A	94	LYS	1
1	A	20	ASP	1
1	A	116	LEU	1
1	A	117	THR	1

6.3.2 Protein sidechains (i)

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	105/126 (83%)	93±3 (89±3%)	12±3 (11±3%)	12	56
All	All	3255/3906 (83%)	2896 (89%)	359 (11%)	12	56

All 54 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	140	PHE	28
1	A	115	LYS	20
1	A	44	SER	18
1	A	29	SER	17
1	A	105	LEU	16
1	A	109	LEU	16
1	A	85	LEU	15
1	A	94	LYS	14
1	A	38	SER	13
1	A	114	GLU	12
1	A	97	ASP	11
1	A	87	GLU	9
1	A	45	GLU	8
1	A	30	SER	8
1	A	49	ASN	7
1	A	73	SER	7
1	A	122	ASP	7
1	A	28	SER	7
1	A	123	ASP	7
1	A	138	GLN	7
1	A	90	LYS	7
1	A	64	GLU	6
1	A	127	GLU	6
1	A	118	ASP	6
1	A	111	SER	6
1	A	126	ARG	6
1	A	37	ARG	5
1	A	132	SER	5
1	A	101	SER	5

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Mol	Chain	Res	Type	Models (Total)
1	A	139	GLN	4
1	A	106	LYS	4
1	A	84	GLU	4
1	A	93	ASP	4
1	A	134	GLU	4
1	A	83	GLN	3
1	A	136	ASN	3
1	A	66	SER	3
1	A	42	SER	3
1	A	11	GLU	3
1	A	5	THR	3
1	A	13	LYS	2
1	A	53	ASN	2
1	A	129	SER	2
1	A	95	ASN	2
1	A	124	MET	2
1	A	47	GLU	2
1	A	143	LEU	2
1	A	130	ASP	2
1	A	54	GLU	1
1	A	62	GLN	1
1	A	82	GLU	1
1	A	26	SER	1
1	A	72	MET	1
1	A	8	GLN	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 17% for the well-defined parts and 17% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5353

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	283
Number of shifts mapped to atoms	283
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	0	—	—
$^{13}C_{\beta}$	0	—	—
$^{13}C'$	0	—	—
^{15}N	141	0.81 ± 0.14	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 17%, i.e. 243 atoms were assigned a chemical shift out of a possible 1440. 0 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	243/618 (39%)	122/247 (49%)	0/248 (0%)	121/123 (98%)
Sidechain	0/743 (0%)	0/428 (0%)	0/295 (0%)	0/20 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	0/79 (0%)	0/44 (0%)	0/34 (0%)	0/1 (0%)
Overall	243/1440 (17%)	122/719 (17%)	0/577 (0%)	121/144 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 17%, i.e. 283 atoms were assigned a chemical shift out of a possible 1711. 0 out of 25 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	283/728 (39%)	142/291 (49%)	0/292 (0%)	141/145 (97%)
Sidechain	0/896 (0%)	0/518 (0%)	0/346 (0%)	0/32 (0%)
Aromatic	0/87 (0%)	0/48 (0%)	0/36 (0%)	0/3 (0%)
Overall	283/1711 (17%)	142/857 (17%)	0/674 (0%)	141/180 (78%)

7.1.4 Statistically unusual chemical shifts

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A: