



Full wwPDB NMR Structure Validation Report ⓘ

Feb 16, 2022 – 10:48 AM EST

PDB ID : 1MPH
Title : PLECKSTRIN HOMOLOGY DOMAIN FROM MOUSE BETA-SPECTRIN,
NMR, 50 STRUCTURES
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Deposited on : 1997-04-23

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

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 : 2.26
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.26

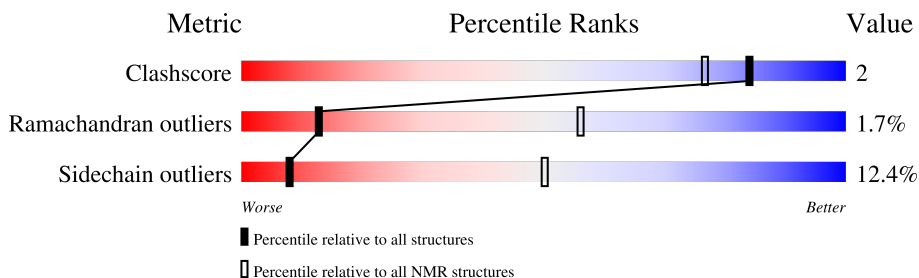
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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 ≥ 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	106	 73% 13% 14%

2 Ensemble composition and analysis i

This entry contains 50 models. Model 39 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:2-A:11, A:22-A:69, A:74-A:106 (91)	0.42	39

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, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 19, 20, 22, 24, 25, 26, 27, 28, 29, 31, 32, 33, 34, 35, 36, 37, 39, 40, 41, 42, 44, 45, 46, 48, 49, 50
2	4, 18, 43
3	23, 47
Single-model clusters	3; 17; 21; 30; 38

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1698 atoms, of which 834 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called BETA SPECTRIN.

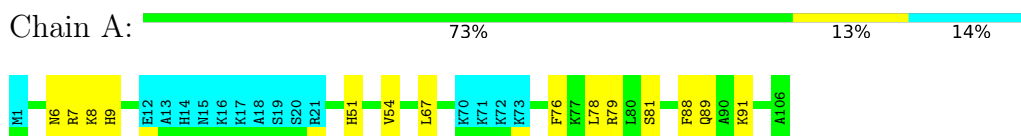
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	106	1698	546	834	150	163	5	0

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: BETA SPECTRIN

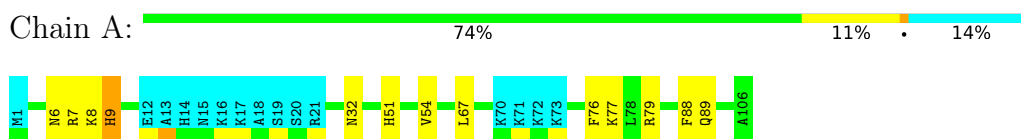


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

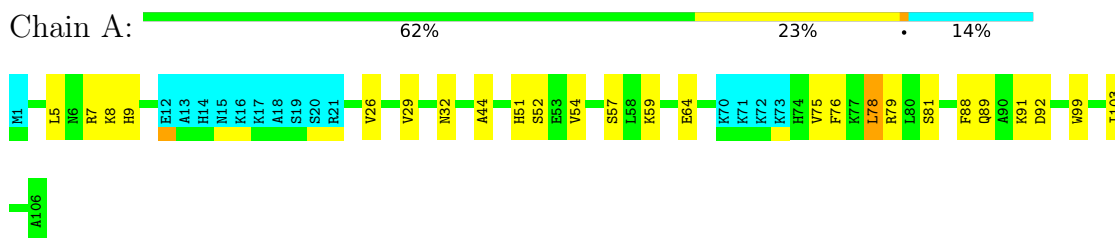
4.2.1 Score per residue for model 1

- Molecule 1: BETA SPECTRIN



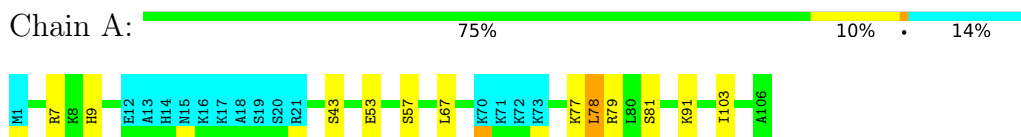
4.2.2 Score per residue for model 2

- Molecule 1: BETA SPECTRIN



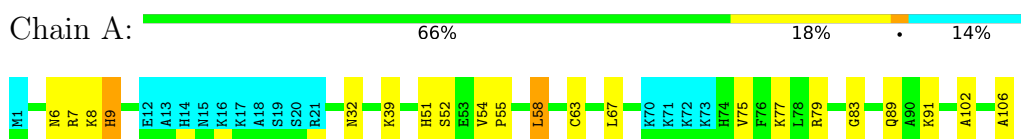
4.2.3 Score per residue for model 3

- Molecule 1: BETA SPECTRIN



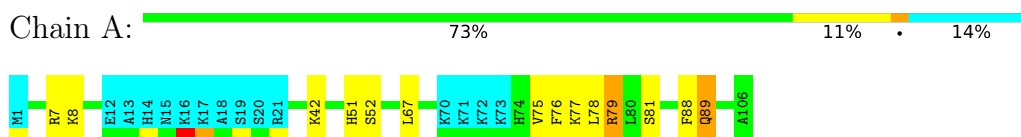
4.2.4 Score per residue for model 4

- Molecule 1: BETA SPECTRIN



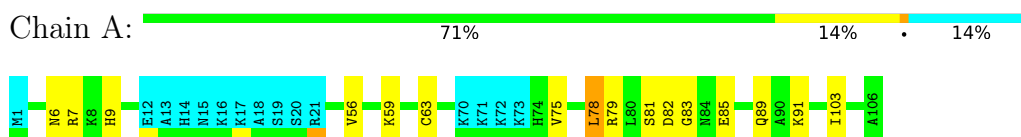
4.2.5 Score per residue for model 5

- Molecule 1: BETA SPECTRIN



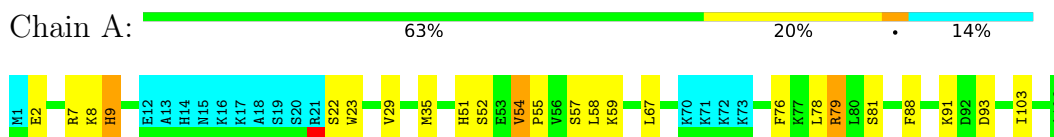
4.2.6 Score per residue for model 6

- Molecule 1: BETA SPECTRIN



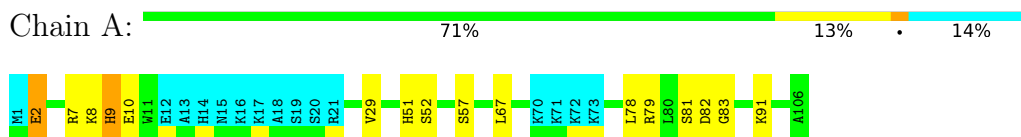
4.2.7 Score per residue for model 7

- Molecule 1: BETA SPECTRIN



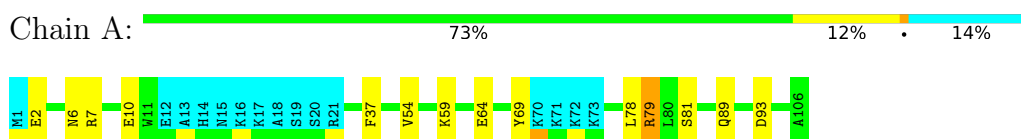
4.2.8 Score per residue for model 8

- Molecule 1: BETA SPECTRIN



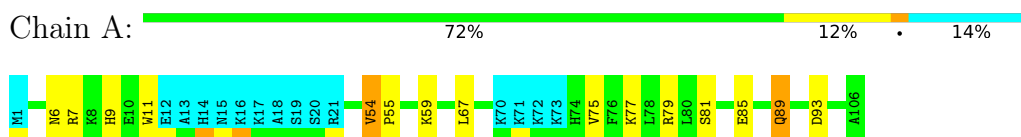
4.2.9 Score per residue for model 9

- Molecule 1: BETA SPECTRIN



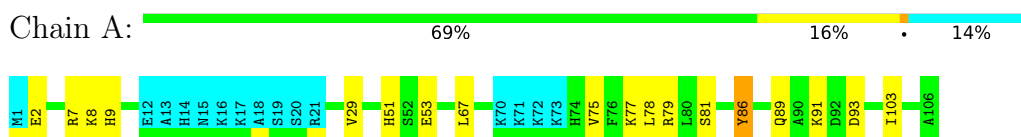
4.2.10 Score per residue for model 10

- Molecule 1: BETA SPECTRIN



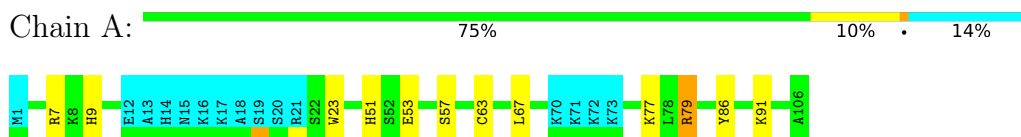
4.2.11 Score per residue for model 11

- Molecule 1: BETA SPECTRIN



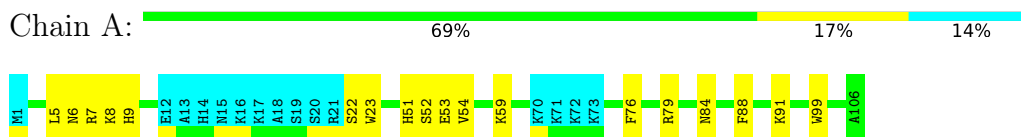
4.2.12 Score per residue for model 12

- Molecule 1: BETA SPECTRIN



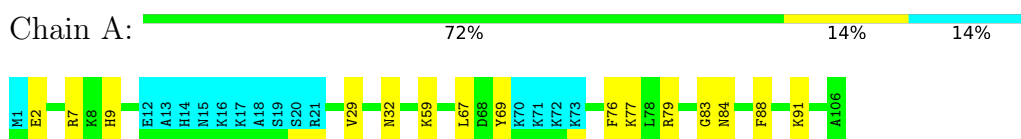
4.2.13 Score per residue for model 13

- Molecule 1: BETA SPECTRIN



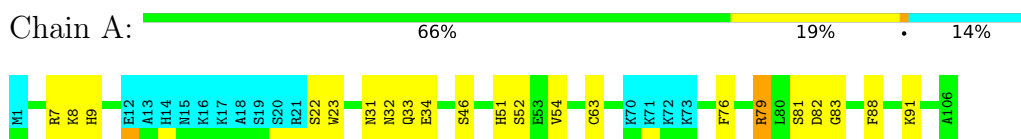
4.2.14 Score per residue for model 14

- Molecule 1: BETA SPECTRIN



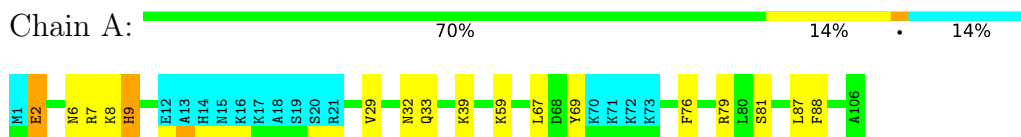
4.2.15 Score per residue for model 15

- Molecule 1: BETA SPECTRIN



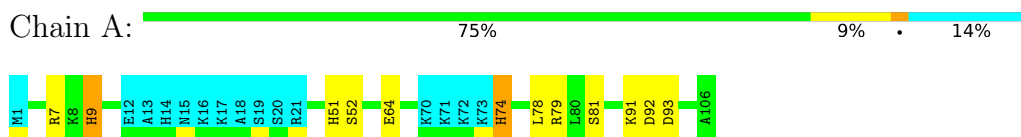
4.2.16 Score per residue for model 16

- Molecule 1: BETA SPECTRIN



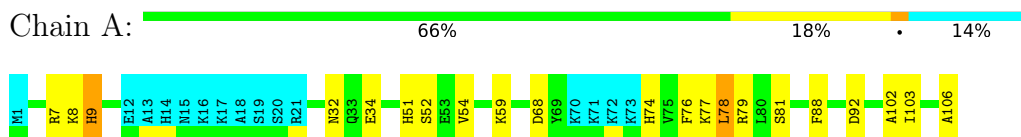
4.2.17 Score per residue for model 17

- Molecule 1: BETA SPECTRIN



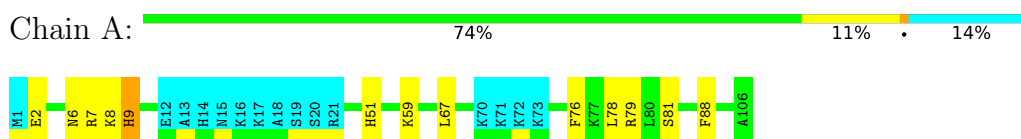
4.2.18 Score per residue for model 18

- Molecule 1: BETA SPECTRIN



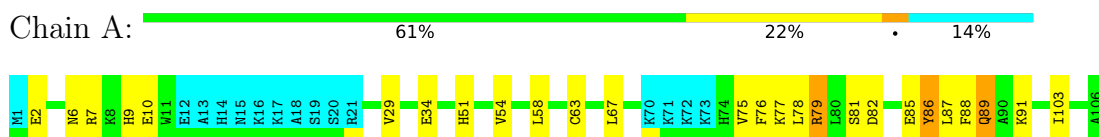
4.2.19 Score per residue for model 19

- Molecule 1: BETA SPECTRIN



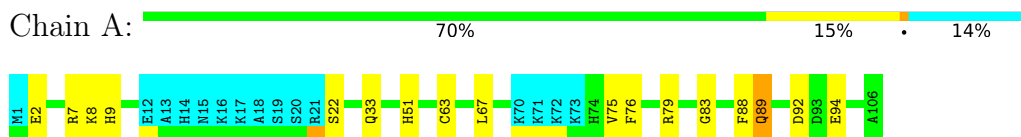
4.2.20 Score per residue for model 20

- Molecule 1: BETA SPECTRIN



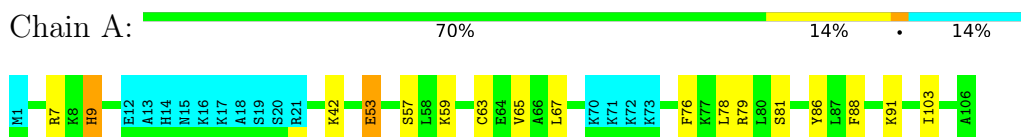
4.2.21 Score per residue for model 21

- Molecule 1: BETA SPECTRIN



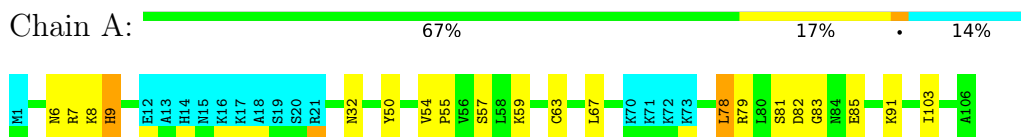
4.2.22 Score per residue for model 22

- Molecule 1: BETA SPECTRIN



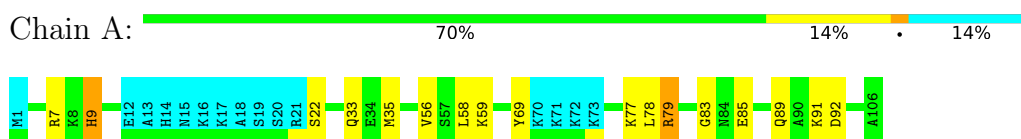
4.2.23 Score per residue for model 23

- Molecule 1: BETA SPECTRIN



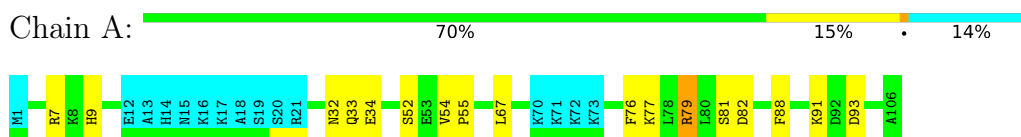
4.2.24 Score per residue for model 24

- Molecule 1: BETA SPECTRIN



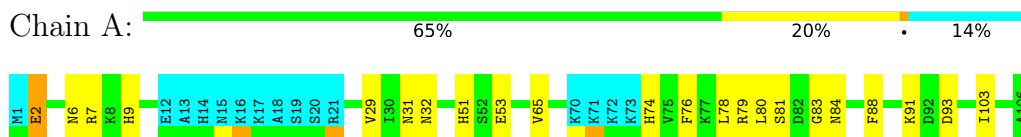
4.2.25 Score per residue for model 25

- Molecule 1: BETA SPECTRIN



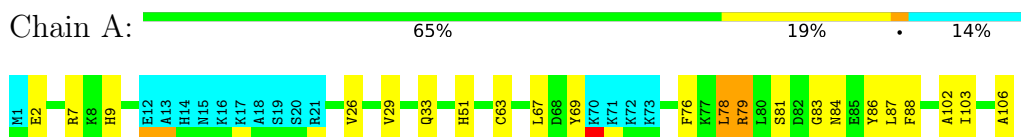
4.2.26 Score per residue for model 26

- Molecule 1: BETA SPECTRIN



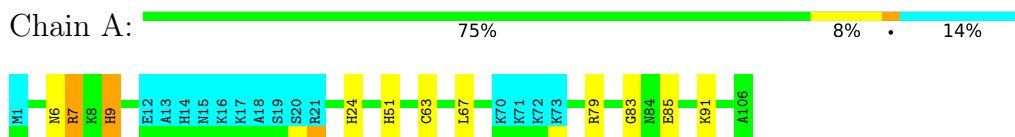
4.2.27 Score per residue for model 27

- Molecule 1: BETA SPECTRIN



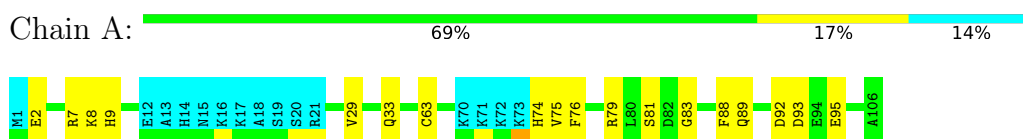
4.2.28 Score per residue for model 28

- Molecule 1: BETA SPECTRIN



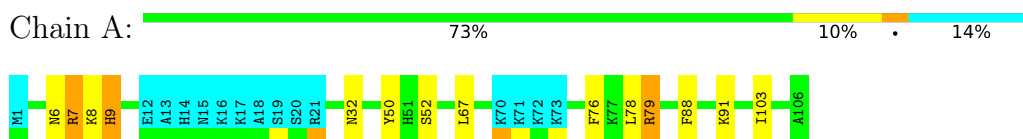
4.2.29 Score per residue for model 29

- Molecule 1: BETA SPECTRIN



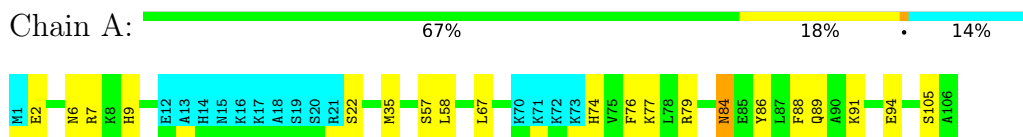
4.2.30 Score per residue for model 30

- Molecule 1: BETA SPECTRIN



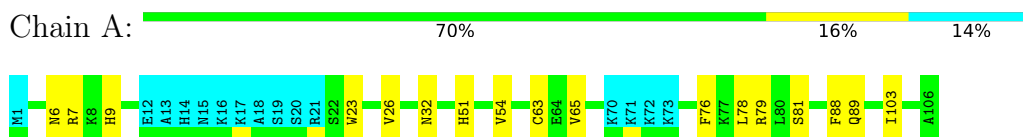
4.2.31 Score per residue for model 31

- Molecule 1: BETA SPECTRIN



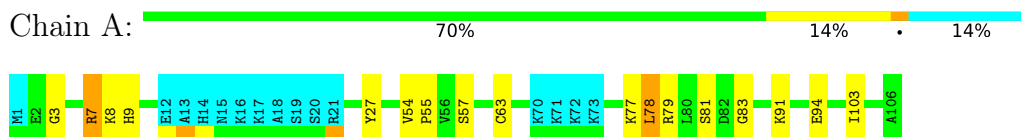
4.2.32 Score per residue for model 32

- Molecule 1: BETA SPECTRIN



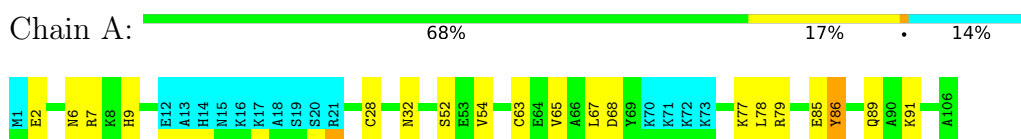
4.2.33 Score per residue for model 33

- Molecule 1: BETA SPECTRIN



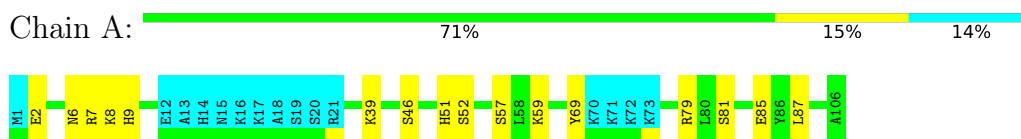
4.2.34 Score per residue for model 34

- Molecule 1: BETA SPECTRIN



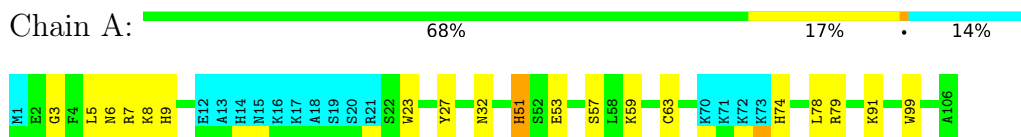
4.2.35 Score per residue for model 35

- Molecule 1: BETA SPECTRIN



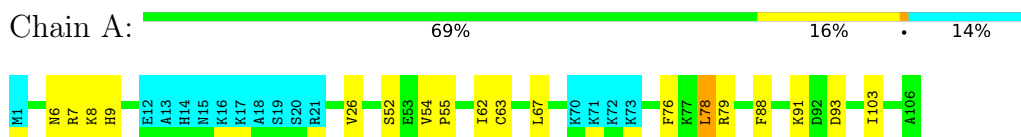
4.2.36 Score per residue for model 36

- Molecule 1: BETA SPECTRIN



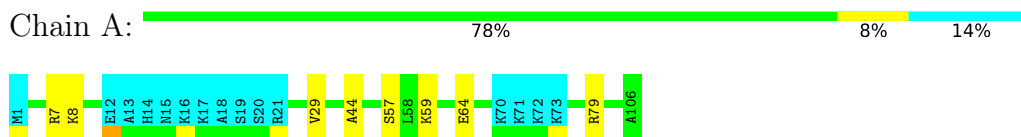
4.2.37 Score per residue for model 37

- Molecule 1: BETA SPECTRIN



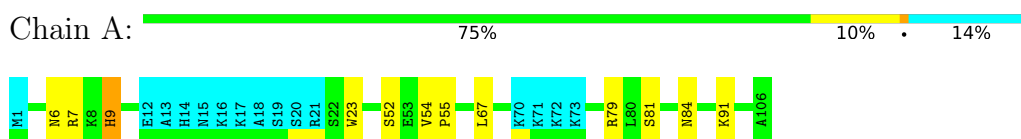
4.2.38 Score per residue for model 38

- Molecule 1: BETA SPECTRIN



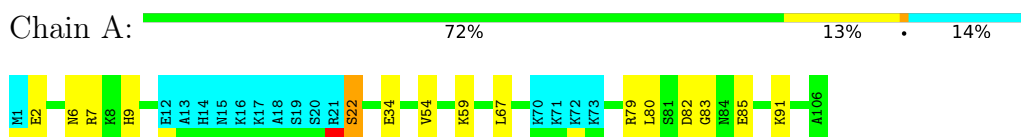
4.2.39 Score per residue for model 39 (medoid)

- Molecule 1: BETA SPECTRIN



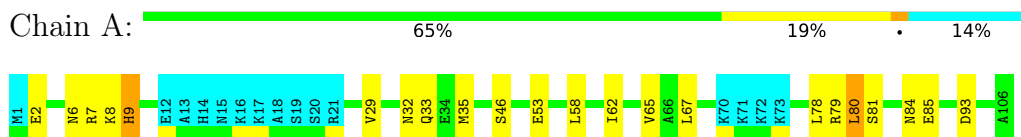
4.2.40 Score per residue for model 40

- Molecule 1: BETA SPECTRIN



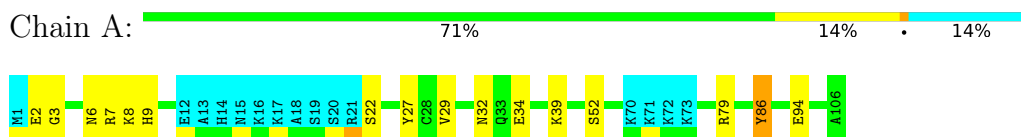
4.2.41 Score per residue for model 41

- Molecule 1: BETA SPECTRIN



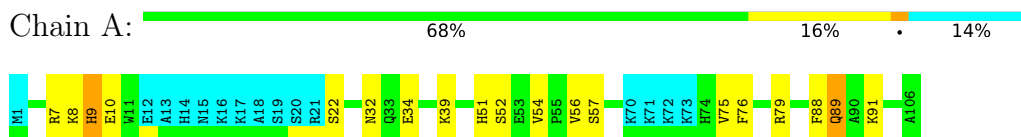
4.2.42 Score per residue for model 42

- Molecule 1: BETA SPECTRIN



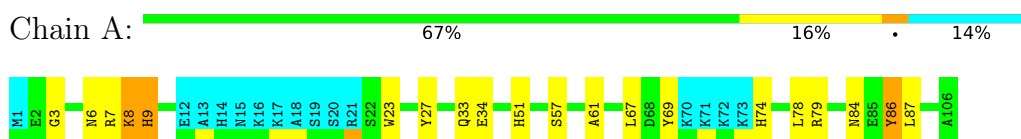
4.2.43 Score per residue for model 43

- Molecule 1: BETA SPECTRIN



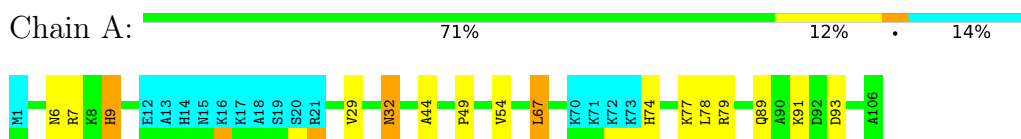
4.2.44 Score per residue for model 44

- Molecule 1: BETA SPECTRIN



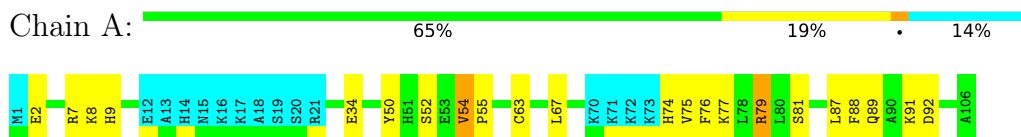
4.2.45 Score per residue for model 45

- Molecule 1: BETA SPECTRIN



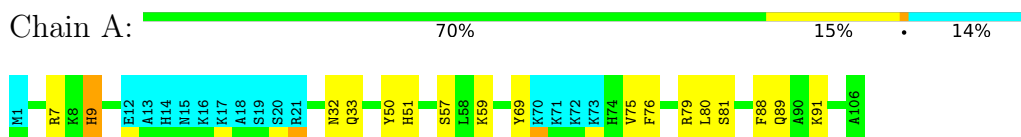
4.2.46 Score per residue for model 46

- Molecule 1: BETA SPECTRIN



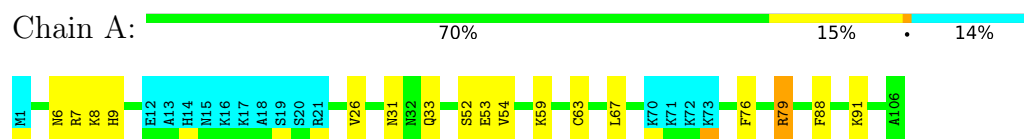
4.2.47 Score per residue for model 47

- Molecule 1: BETA SPECTRIN



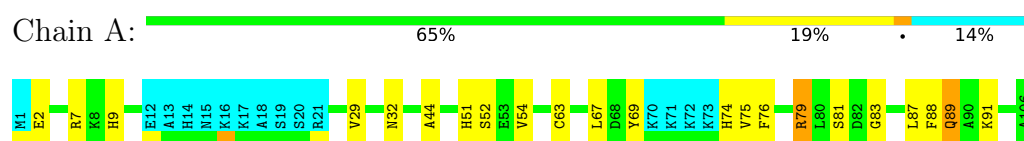
4.2.48 Score per residue for model 48

- Molecule 1: BETA SPECTRIN



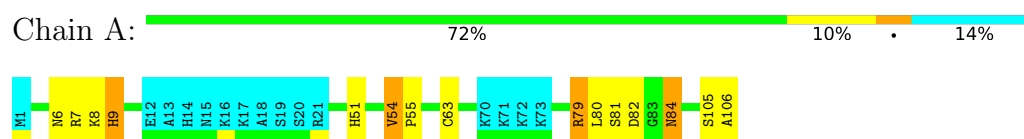
4.2.49 Score per residue for model 49

- Molecule 1: BETA SPECTRIN



4.2.50 Score per residue for model 50

- Molecule 1: BETA SPECTRIN



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 50 were deposited, based on the following criterion: *LOWEST ENERGY*.

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

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

No chemical shift data was provided.

6 Model quality i

6.1 Standard geometry i

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	0.47±0.05	0±0/762 (0.0± 0.1%)	0.59±0.01	0±0/1030 (0.0± 0.0%)
All	All	0.48	6/38100 (0.0%)	0.59	0/51500 (0.0%)

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	2.2±0.4
All	All	0	108

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	50	TYR	CE2-CZ	-12.41	1.22	1.38	46	2
1	A	50	TYR	CE1-CZ	11.96	1.54	1.38	46	2
1	A	86	TYR	CE1-CZ	6.59	1.47	1.38	42	2

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	7	ARG	Sidechain	50
1	A	79	ARG	Sidechain	50
1	A	86	TYR	Sidechain	8

6.2 Too-close contacts [i](#)

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	742	693	693	3±2
All	All	37100	34650	34650	162

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:9:HIS:H	1:A:9:HIS:CD2	0.65	2.09	24	17
1:A:78:LEU:HD21	1:A:103:ILE:HG21	0.61	1.72	7	11
1:A:75:VAL:HG22	1:A:89:GLN:HB2	0.60	1.72	10	7
1:A:75:VAL:HG22	1:A:89:GLN:HG3	0.57	1.76	46	5
1:A:76:PHE:CE1	1:A:88:PHE:HB2	0.57	2.35	18	11
1:A:76:PHE:CE2	1:A:88:PHE:HB2	0.56	2.36	25	11
1:A:62:ILE:H	1:A:62:ILE:HD12	0.55	1.61	41	2
1:A:50:TYR:CG	1:A:51:HIS:N	0.53	2.76	47	1
1:A:75:VAL:HG22	1:A:89:GLN:HG2	0.53	1.79	49	1
1:A:49:PRO:CB	1:A:54:VAL:HG21	0.52	2.34	45	1
1:A:102:ALA:O	1:A:106:ALA:HB2	0.52	2.05	27	3
1:A:69:TYR:CE2	1:A:87:LEU:CD1	0.52	2.92	27	3
1:A:78:LEU:HD22	1:A:103:ILE:HD13	0.52	1.80	18	2
1:A:84:ASN:HB2	1:A:86:TYR:CE2	0.52	2.39	31	1
1:A:58:LEU:HD21	1:A:103:ILE:HG23	0.50	1.81	20	1
1:A:75:VAL:HG22	1:A:89:GLN:CG	0.50	2.36	49	1
1:A:58:LEU:HD13	1:A:58:LEU:O	0.49	2.07	4	1
1:A:78:LEU:HD23	1:A:88:PHE:CE2	0.49	2.43	5	2
1:A:29:VAL:HG21	1:A:44:ALA:HB1	0.49	1.84	2	4
1:A:2:GLU:HB2	1:A:29:VAL:HG22	0.49	1.85	26	1
1:A:67:LEU:HD11	1:A:74:HIS:CD2	0.49	2.43	45	1
1:A:2:GLU:HG2	1:A:29:VAL:HG13	0.49	1.84	7	4
1:A:3:GLY:HA2	1:A:27:TYR:CE1	0.49	2.43	33	4
1:A:54:VAL:N	1:A:55:PRO:CD	0.49	2.76	33	7
1:A:8:LYS:HD3	1:A:87:LEU:HD12	0.49	1.84	44	1
1:A:69:TYR:CE2	1:A:87:LEU:HD13	0.48	2.42	27	1
1:A:80:LEU:HD12	1:A:84:ASN:HB2	0.48	1.86	26	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:35:MET:SD	1:A:58:LEU:HD21	0.47	2.50	7	1
1:A:9:HIS:CD2	1:A:9:HIS:N	0.47	2.82	41	3
1:A:61:ALA:HB1	1:A:78:LEU:HD11	0.47	1.85	44	1
1:A:54:VAL:HB	1:A:55:PRO:CD	0.46	2.40	7	3
1:A:76:PHE:CZ	1:A:88:PHE:CB	0.46	2.98	5	13
1:A:78:LEU:HD21	1:A:103:ILE:CG2	0.45	2.41	23	2
1:A:77:LYS:HD2	1:A:87:LEU:HD11	0.45	1.86	46	1
1:A:54:VAL:HB	1:A:55:PRO:HD3	0.45	1.89	7	2
1:A:2:GLU:CG	1:A:29:VAL:HG13	0.45	2.42	29	2
1:A:69:TYR:CG	1:A:69:TYR:O	0.45	2.70	14	2
1:A:2:GLU:HG3	1:A:29:VAL:HG13	0.45	1.89	49	3
1:A:2:GLU:HB2	1:A:29:VAL:HG13	0.44	1.88	16	1
1:A:84:ASN:ND2	1:A:86:TYR:OH	0.44	2.50	44	1
1:A:69:TYR:CE2	1:A:87:LEU:CD2	0.44	3.00	49	1
1:A:78:LEU:HD11	1:A:103:ILE:HD13	0.44	1.89	22	1
1:A:2:GLU:HG3	1:A:29:VAL:HG22	0.44	1.89	42	2
1:A:80:LEU:N	1:A:80:LEU:HD12	0.44	2.28	47	1
1:A:78:LEU:HD11	1:A:103:ILE:HG21	0.44	1.90	20	1
1:A:35:MET:SD	1:A:58:LEU:HD13	0.43	2.54	41	3
1:A:80:LEU:HD12	1:A:84:ASN:CB	0.43	2.43	50	1
1:A:105:SER:O	1:A:106:ALA:HB2	0.43	2.13	50	1
1:A:37:PHE:O	1:A:54:VAL:HG13	0.43	2.13	9	1
1:A:5:LEU:HD11	1:A:99:TRP:CD2	0.42	2.49	36	3
1:A:54:VAL:CG1	1:A:55:PRO:HD3	0.42	2.45	4	1
1:A:62:ILE:HD12	1:A:62:ILE:N	0.42	2.26	41	1
1:A:86:TYR:CD1	1:A:86:TYR:N	0.41	2.89	34	1
1:A:80:LEU:HD12	1:A:84:ASN:O	0.41	2.14	41	1
1:A:3:GLY:CA	1:A:27:TYR:CE1	0.41	3.04	42	1
1:A:10:GLU:HG3	1:A:87:LEU:HD21	0.40	1.94	20	1
1:A:80:LEU:HD12	1:A:80:LEU:N	0.40	2.31	40	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	90/106 (85%)	78±2 (87±3%)	10±2 (11±3%)	2±1 (2±1%)	13	56
All	All	4500/5300 (85%)	3910 (87%)	513 (11%)	77 (2%)	13	56

All 13 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	32	ASN	20
1	A	83	GLY	15
1	A	23	TRP	8
1	A	82	ASP	7
1	A	53	GLU	5
1	A	22	SER	4
1	A	54	VAL	4
1	A	51	HIS	4
1	A	52	SER	3
1	A	59	LYS	2
1	A	74	HIS	2
1	A	93	ASP	2
1	A	50	TYR	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	79/92 (86%)	69±2 (88±3%)	10±2 (12±3%)	8	50
All	All	3950/4600 (86%)	3459 (88%)	491 (12%)	8	50

All 50 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	9	HIS	45
1	A	91	LYS	33
1	A	67	LEU	31
1	A	81	SER	30
1	A	8	LYS	28

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Mol	Chain	Res	Type	Models (Total)
1	A	6	ASN	27
1	A	51	HIS	22
1	A	63	CYS	20
1	A	52	SER	17
1	A	59	LYS	17
1	A	77	LYS	16
1	A	78	LEU	16
1	A	57	SER	15
1	A	79	ARG	14
1	A	89	GLN	13
1	A	54	VAL	12
1	A	2	GLU	11
1	A	33	GLN	11
1	A	85	GLU	10
1	A	93	ASP	9
1	A	34	GLU	9
1	A	92	ASP	7
1	A	74	HIS	7
1	A	22	SER	6
1	A	84	ASN	6
1	A	26	VAL	5
1	A	39	LYS	5
1	A	53	GLU	5
1	A	65	VAL	5
1	A	64	GLU	4
1	A	94	GLU	4
1	A	56	VAL	3
1	A	10	GLU	3
1	A	31	ASN	3
1	A	46	SER	3
1	A	7	ARG	3
1	A	42	LYS	2
1	A	68	ASP	2
1	A	43	SER	1
1	A	58	LEU	1
1	A	11	TRP	1
1	A	86	TYR	1
1	A	69	TYR	1
1	A	24	HIS	1
1	A	95	GLU	1
1	A	105	SER	1
1	A	28	CYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	82	ASP	1
1	A	80	LEU	1
1	A	32	ASN	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided