



Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 10:49 pm BST

PDB ID : 2KXW
Title : Structure of the C-domain Fragment of apo Calmodulin Bound to the IQ motif of Nav1.2
Authors : Feldkamp, M.D.; Yu, L.; Shea, M.A.
Deposited on : 2010-05-13

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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

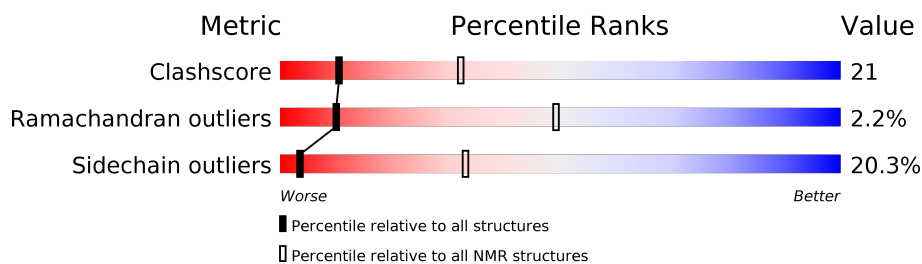
1 Overall quality at a glance i

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	73	
2	B	27	

2 Ensemble composition and analysis i

This entry contains 21 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *energy minimized average structure*.

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:81-A:92, A:98-A:129, A:136-A:146, B:1905- B:1920 (71)	0.15	6

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 4 clusters and 3 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1651 atoms, of which 828 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	73	1142	358	556	97	126	5	0

- Molecule 2 is a protein called Sodium channel protein type 2 subunit alpha.

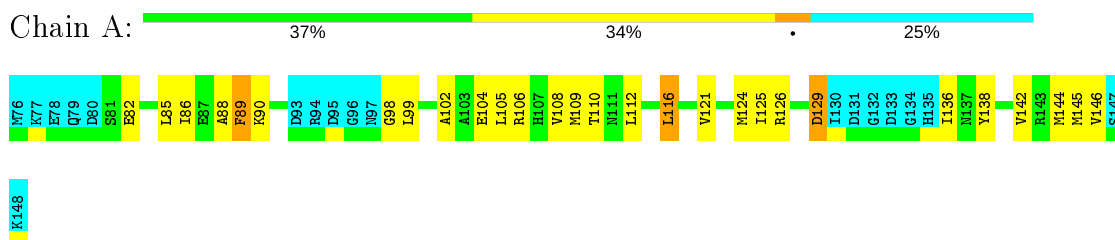
Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
2	B	27	509	151	272	48	38	0

4 Residue-property plots [i](#)

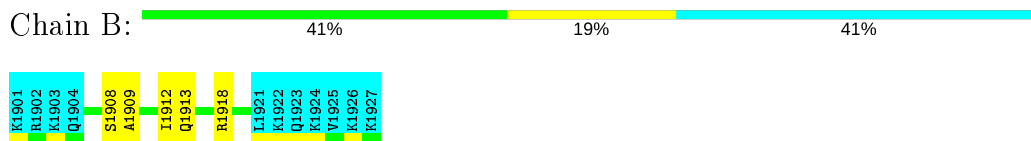
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Calmodulin



- Molecule 2: Sodium channel protein type 2 subunit alpha

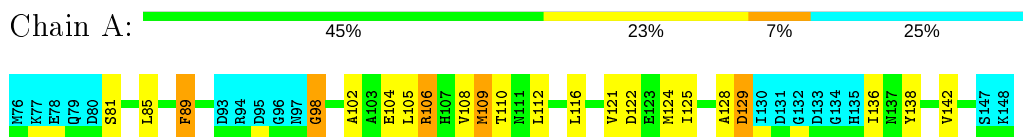


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

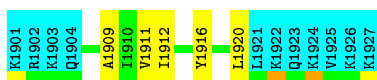
4.2.1 Score per residue for model 1

- Molecule 1: Calmodulin



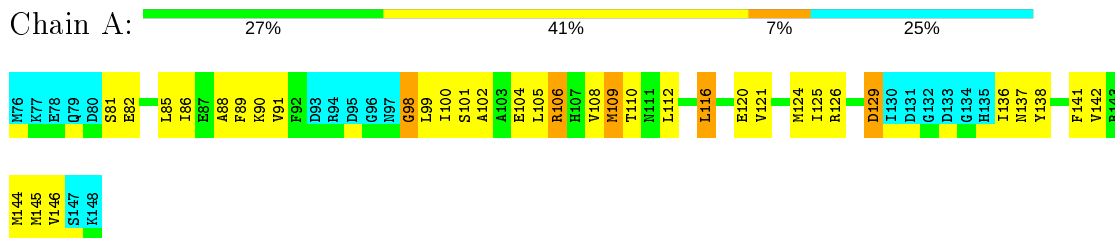
- Molecule 2: Sodium channel protein type 2 subunit alpha



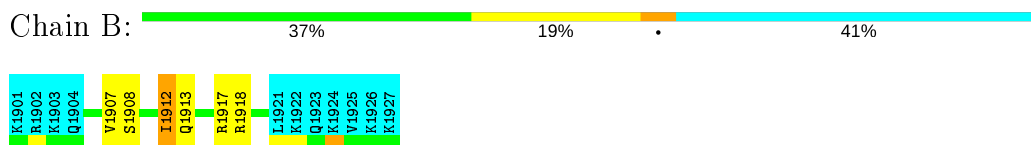


4.2.2 Score per residue for model 2

- Molecule 1: Calmodulin

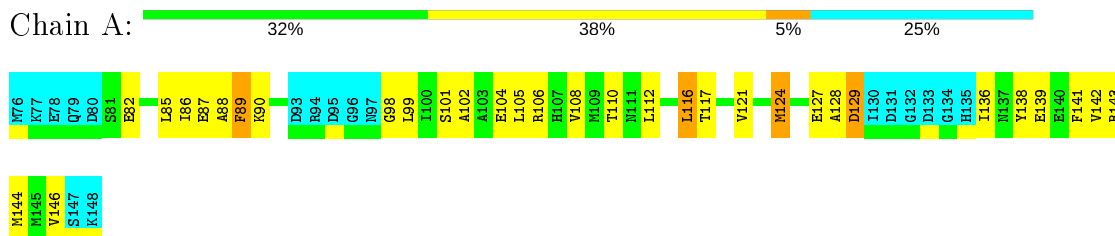


- Molecule 2: Sodium channel protein type 2 subunit alpha

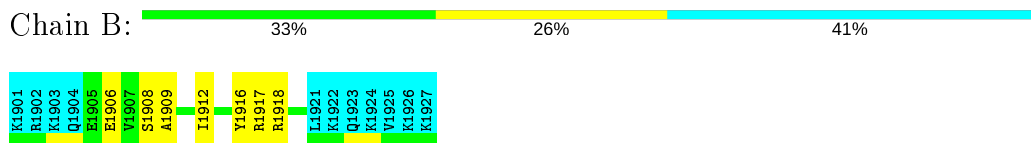


4.2.3 Score per residue for model 3

- Molecule 1: Calmodulin

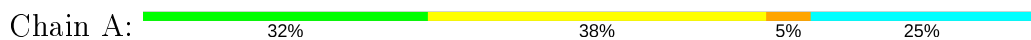


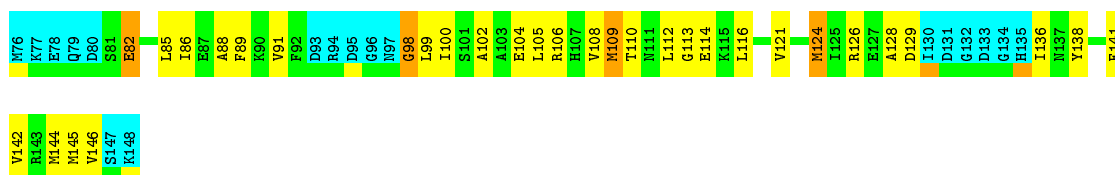
- Molecule 2: Sodium channel protein type 2 subunit alpha



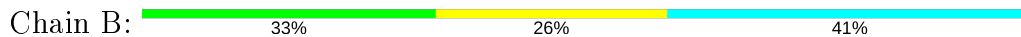
4.2.4 Score per residue for model 4

- Molecule 1: Calmodulin



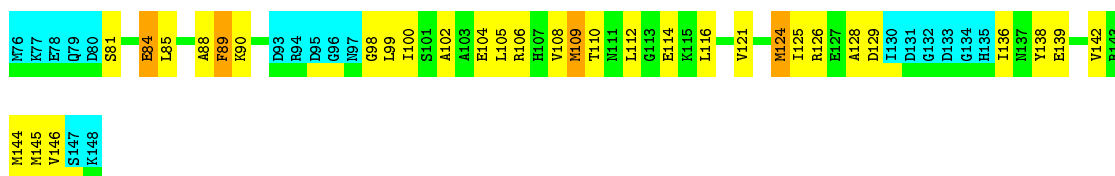


- Molecule 2: Sodium channel protein type 2 subunit alpha

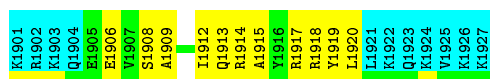
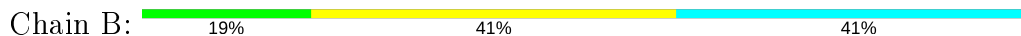


4.2.5 Score per residue for model 5

- Molecule 1: Calmodulin

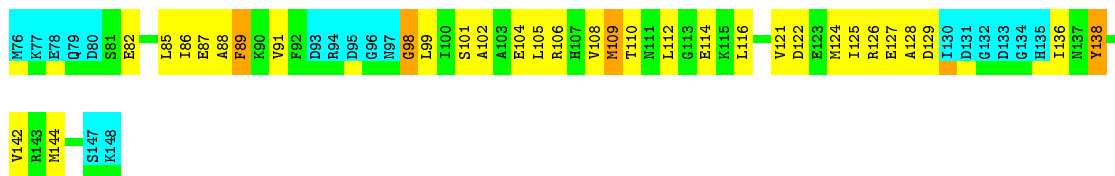
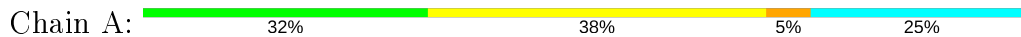


- Molecule 2: Sodium channel protein type 2 subunit alpha



4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Calmodulin



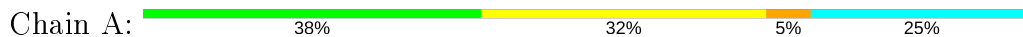
- Molecule 2: Sodium channel protein type 2 subunit alpha



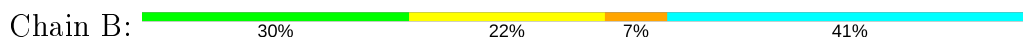


4.2.7 Score per residue for model 7

- Molecule 1: Calmodulin



- Molecule 2: Sodium channel protein type 2 subunit alpha

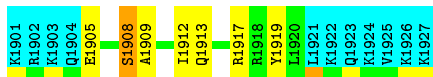
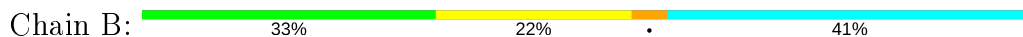


4.2.8 Score per residue for model 8

- Molecule 1: Calmodulin

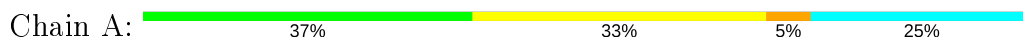


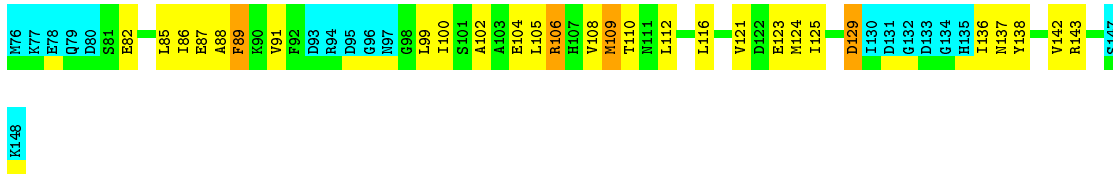
- Molecule 2: Sodium channel protein type 2 subunit alpha



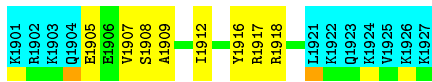
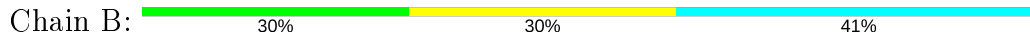
4.2.9 Score per residue for model 9

- Molecule 1: Calmodulin



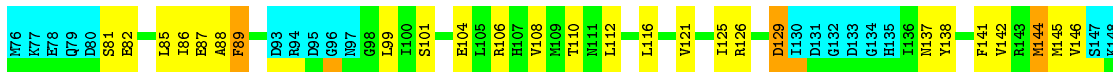


- Molecule 2: Sodium channel protein type 2 subunit alpha

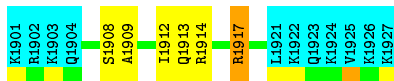
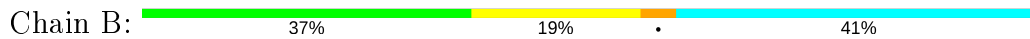


4.2.10 Score per residue for model 10

- Molecule 1: Calmodulin

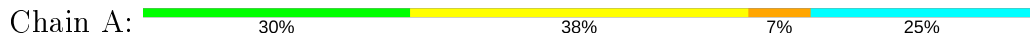


- Molecule 2: Sodium channel protein type 2 subunit alpha

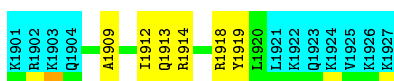


4.2.11 Score per residue for model 11

- Molecule 1: Calmodulin

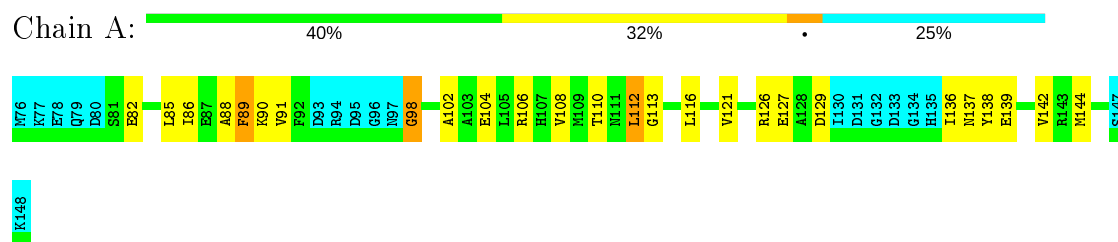


- Molecule 2: Sodium channel protein type 2 subunit alpha

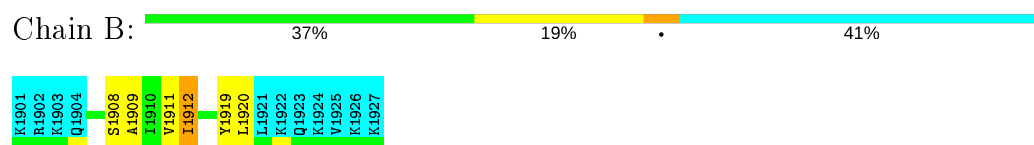


4.2.12 Score per residue for model 12

- Molecule 1: Calmodulin

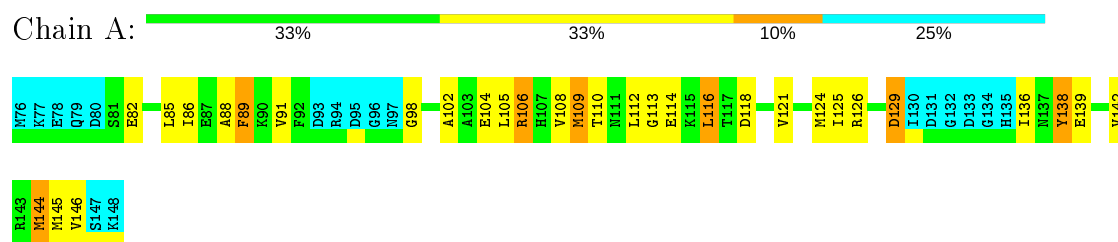


- Molecule 2: Sodium channel protein type 2 subunit alpha

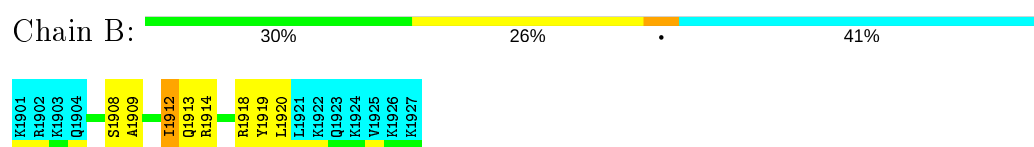


4.2.13 Score per residue for model 13

- Molecule 1: Calmodulin

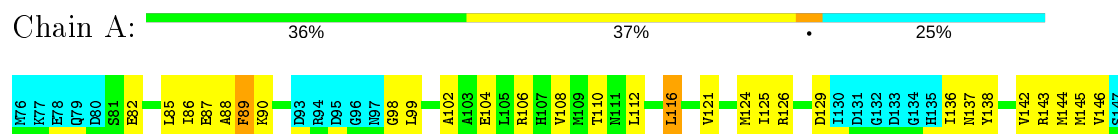


- Molecule 2: Sodium channel protein type 2 subunit alpha



4.2.14 Score per residue for model 14

- Molecule 1: Calmodulin



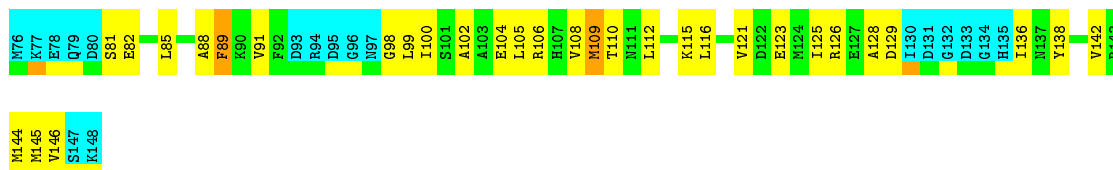
K148

- Molecule 2: Sodium channel protein type 2 subunit alpha

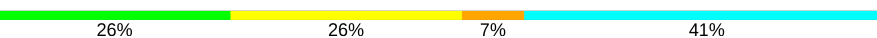
Chain B:  44% 11% 0% 41%


4.2.15 Score per residue for model 15

- Molecule 1: Calmodulin

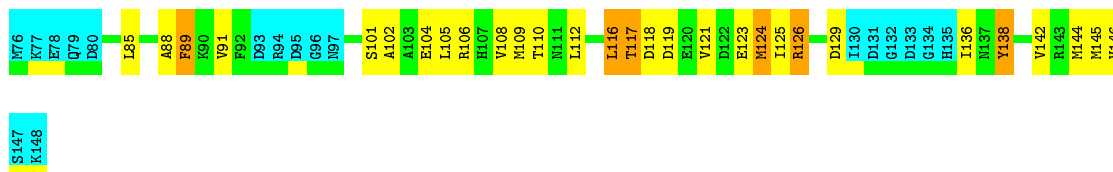
Chain A:  33% 40% 0% 25%


- Molecule 2: Sodium channel protein type 2 subunit alpha


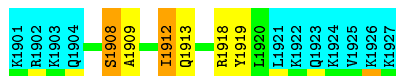
Chain B:  26% 26% 7% 41%


4.2.16 Score per residue for model 16

- Molecule 1: Calmodulin

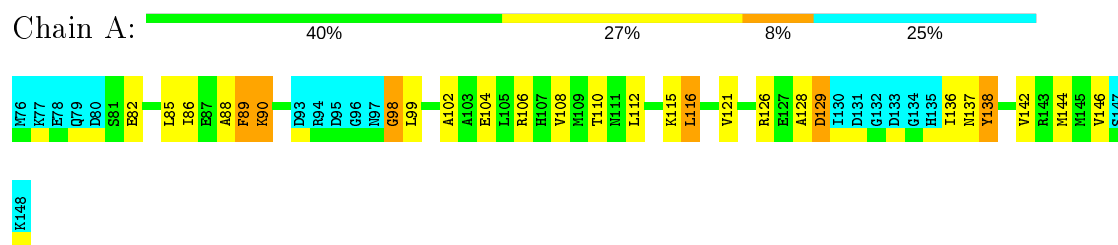
Chain A:  36% 32% 8% 25%


- Molecule 2: Sodium channel protein type 2 subunit alpha

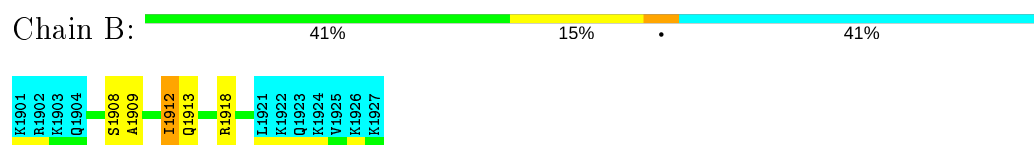
Chain B:  37% 15% 7% 41%


4.2.17 Score per residue for model 17

- Molecule 1: Calmodulin

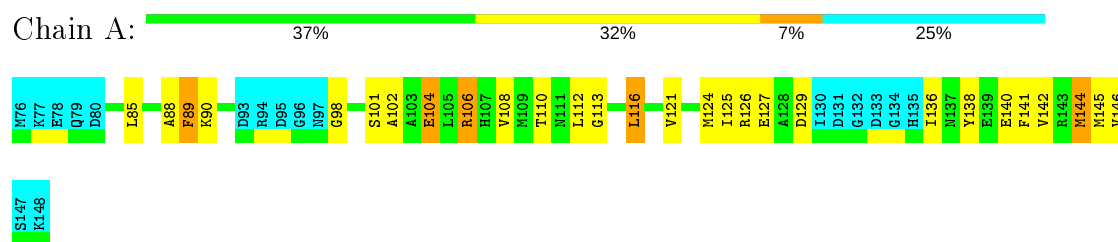


- Molecule 2: Sodium channel protein type 2 subunit alpha

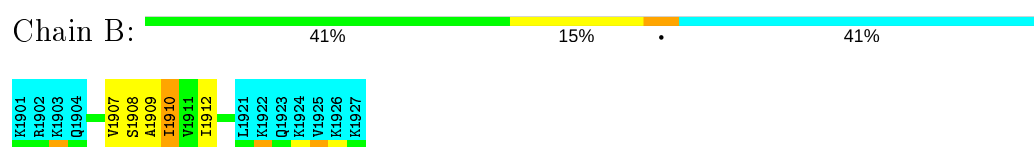


4.2.18 Score per residue for model 18

- Molecule 1: Calmodulin

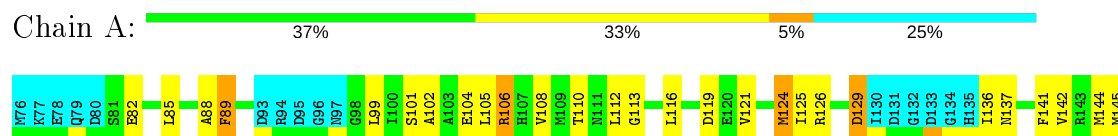


- Molecule 2: Sodium channel protein type 2 subunit alpha



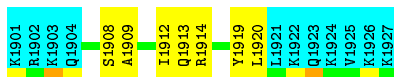
4.2.19 Score per residue for model 19

- Molecule 1: Calmodulin





- Molecule 2: Sodium channel protein type 2 subunit alpha

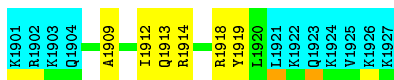
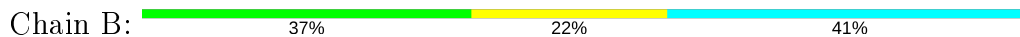


4.2.20 Score per residue for model 20

- Molecule 1: Calmodulin



- Molecule 2: Sodium channel protein type 2 subunit alpha

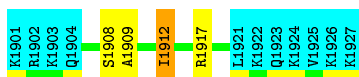


4.2.21 Score per residue for model 21

- Molecule 1: Calmodulin



- Molecule 2: Sodium channel protein type 2 subunit alpha



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 300 calculated structures, 21 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	structure solution	1.2
CNS	refinement	1.2

No chemical shift data was provided. 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.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	446	433	432	24±5
2	B	138	143	143	8±2
All	All	12264	12096	12075	513

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 21.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:LEU:HD23	1:A:142:VAL:HG23	1.02	1.30	11	12
1:A:102:ALA:HB2	1:A:136:ILE:HD11	0.86	1.44	16	20
1:A:104:GLU:O	1:A:108:VAL:HG23	0.78	1.78	4	21
1:A:142:VAL:O	1:A:146:VAL:HG22	0.77	1.78	2	12
2:B:1910:ILE:O	2:B:1910:ILE:HD13	0.74	1.83	18	2
1:A:91:VAL:HG21	2:B:1908:SER:OG	0.71	1.85	2	8
1:A:112:LEU:HD21	2:B:1909:ALA:CB	0.71	2.16	4	4
1:A:89:PHE:CD2	2:B:1912:ILE:HD11	0.70	2.21	9	12
1:A:85:LEU:HD23	1:A:142:VAL:CG2	0.69	2.14	11	10
1:A:142:VAL:O	1:A:146:VAL:HG12	0.69	1.88	15	4
1:A:89:PHE:CG	2:B:1912:ILE:HD11	0.68	2.23	3	20
1:A:138:TYR:O	1:A:142:VAL:HG12	0.68	1.89	3	19
1:A:85:LEU:HD11	1:A:89:PHE:CE2	0.68	2.24	15	11

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:LEU:HD12	2:B:1912:ILE:CG1	0.66	2.20	5	9
1:A:106:ARG:HA	1:A:121:VAL:HG21	0.66	1.67	3	19
1:A:99:LEU:HD11	1:A:137:ASN:ND2	0.66	2.05	17	1
1:A:121:VAL:O	1:A:125:ILE:HG23	0.66	1.91	5	15
1:A:116:LEU:HD13	1:A:121:VAL:HG22	0.64	1.69	14	1
2:B:1910:ILE:HD13	2:B:1910:ILE:O	0.64	1.93	7	1
1:A:116:LEU:HD22	1:A:121:VAL:HG23	0.63	1.71	14	1
1:A:91:VAL:HG21	2:B:1908:SER:CB	0.63	2.23	16	1
1:A:102:ALA:HB2	1:A:136:ILE:CD1	0.63	2.22	1	8
2:B:1907:VAL:O	2:B:1910:ILE:HG22	0.62	1.94	18	3
1:A:121:VAL:HG23	1:A:124:MET:HE3	0.62	1.72	3	2
1:A:112:LEU:HD11	2:B:1909:ALA:HB3	0.62	1.71	4	4
1:A:102:ALA:HB1	1:A:125:ILE:HD12	0.61	1.73	2	1
1:A:108:VAL:O	1:A:112:LEU:HD23	0.61	1.96	12	6
1:A:100:ILE:HD11	1:A:105:LEU:HD13	0.61	1.71	5	4
1:A:98:GLY:C	1:A:99:LEU:HD12	0.60	2.17	6	2
1:A:88:ALA:CB	2:B:1912:ILE:HD12	0.59	2.26	17	7
1:A:112:LEU:HD12	1:A:113:GLY:N	0.59	2.13	12	7
1:A:88:ALA:HB1	2:B:1908:SER:O	0.59	1.98	15	18
1:A:105:LEU:HD11	1:A:109:MET:SD	0.57	2.40	5	12
1:A:85:LEU:HD12	2:B:1912:ILE:HG13	0.57	1.76	5	8
1:A:116:LEU:HD22	1:A:121:VAL:CG2	0.56	2.30	14	1
1:A:99:LEU:HD23	1:A:137:ASN:OD1	0.55	2.01	19	1
1:A:84:GLU:OE2	2:B:1915:ALA:HB2	0.55	2.01	5	1
1:A:99:LEU:HD23	1:A:137:ASN:N	0.54	2.18	9	3
1:A:82:GLU:CG	1:A:86:ILE:HD11	0.53	2.32	11	2
1:A:85:LEU:HD21	1:A:89:PHE:CE2	0.53	2.39	13	9
1:A:89:PHE:CE2	2:B:1912:ILE:HD11	0.53	2.39	1	1
1:A:112:LEU:HD11	2:B:1909:ALA:CB	0.53	2.33	4	4
1:A:105:LEU:HD21	1:A:124:MET:HE1	0.53	1.79	16	4
1:A:82:GLU:HG3	1:A:86:ILE:HD11	0.52	1.81	3	2
1:A:86:ILE:HG22	1:A:90:LYS:HE2	0.52	1.80	17	1
1:A:106:ARG:O	1:A:110:THR:HG23	0.52	2.05	21	21
1:A:88:ALA:HB3	2:B:1912:ILE:HD12	0.52	1.81	17	5
1:A:85:LEU:HD13	1:A:85:LEU:C	0.52	2.25	16	6
1:A:112:LEU:CD1	2:B:1909:ALA:HB3	0.51	2.35	13	4
1:A:85:LEU:HD21	1:A:89:PHE:CD2	0.51	2.40	19	4
1:A:85:LEU:C	1:A:85:LEU:HD13	0.50	2.27	17	3
1:A:106:ARG:HG3	1:A:121:VAL:HG11	0.50	1.84	7	3
1:A:106:ARG:HA	1:A:121:VAL:HG11	0.49	1.83	14	1
2:B:1909:ALA:O	2:B:1912:ILE:HG22	0.48	2.08	5	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:124:MET:HE2	2:B:1916:TYR:CZ	0.47	2.44	4	1
1:A:110:THR:HG22	1:A:116:LEU:O	0.47	2.09	20	9
1:A:112:LEU:C	1:A:112:LEU:HD12	0.47	2.29	11	2
1:A:100:ILE:CD1	1:A:105:LEU:HD13	0.47	2.40	9	5
1:A:144:MET:HE2	2:B:1919:TYR:CZ	0.47	2.45	13	1
1:A:121:VAL:HG23	1:A:124:MET:HE2	0.47	1.86	21	2
1:A:128:ALA:HB1	1:A:136:ILE:CG2	0.47	2.40	3	5
1:A:116:LEU:HD21	1:A:120:GLU:OE2	0.47	2.09	11	1
1:A:105:LEU:HD21	1:A:124:MET:SD	0.46	2.51	3	1
1:A:124:MET:CG	1:A:141:PHE:CZ	0.46	2.98	4	2
1:A:141:PHE:CE2	1:A:145:MET:CE	0.46	2.99	11	4
1:A:98:GLY:CA	1:A:138:TYR:CZ	0.46	2.99	3	11
1:A:85:LEU:HD11	1:A:89:PHE:CD2	0.46	2.46	3	2
1:A:82:GLU:OE1	1:A:146:VAL:HG21	0.46	2.10	13	1
1:A:144:MET:HE3	1:A:145:MET:HA	0.45	1.89	10	2
1:A:144:MET:CE	2:B:1919:TYR:CE1	0.45	3.00	19	5
1:A:82:GLU:HG3	1:A:146:VAL:HG11	0.45	1.88	14	1
1:A:124:MET:CE	2:B:1916:TYR:CZ	0.45	2.99	3	4
1:A:99:LEU:N	1:A:99:LEU:HD12	0.45	2.27	6	1
1:A:141:PHE:CZ	1:A:145:MET:CE	0.45	3.00	2	3
1:A:85:LEU:HD23	1:A:142:VAL:CB	0.45	2.42	20	2
1:A:107:HIS:CD2	1:A:111:ASN:ND2	0.45	2.85	11	1
1:A:112:LEU:HD11	2:B:1909:ALA:HB1	0.45	1.88	1	1
1:A:98:GLY:CA	1:A:138:TYR:CE2	0.45	3.00	15	4
1:A:116:LEU:HD23	1:A:117:THR:N	0.45	2.27	16	2
1:A:112:LEU:CD1	2:B:1909:ALA:HB1	0.45	2.42	16	1
1:A:82:GLU:O	1:A:86:ILE:HD12	0.44	2.12	7	11
1:A:129:ASP:HB2	1:A:136:ILE:HG23	0.44	1.89	8	1
1:A:99:LEU:HD23	1:A:137:ASN:CA	0.44	2.43	9	1
1:A:145:MET:CG	2:B:1919:TYR:CD1	0.44	3.01	11	2
1:A:99:LEU:HD11	1:A:137:ASN:CG	0.44	2.33	17	1
1:A:124:MET:HG2	1:A:141:PHE:CZ	0.43	2.48	3	2
1:A:112:LEU:HD21	2:B:1909:ALA:HB1	0.43	1.90	18	1
1:A:85:LEU:HD22	1:A:145:MET:HE3	0.43	1.91	2	1
1:A:121:VAL:HG23	1:A:124:MET:CE	0.42	2.44	11	1
1:A:116:LEU:HD21	1:A:120:GLU:OE1	0.42	2.14	21	1
2:B:1907:VAL:HG13	2:B:1908:SER:N	0.42	2.29	2	1
1:A:85:LEU:CD2	2:B:1912:ILE:CG1	0.42	2.98	17	8
1:A:89:PHE:CG	2:B:1912:ILE:CD1	0.42	3.02	9	3
1:A:112:LEU:CD2	2:B:1909:ALA:CB	0.42	2.98	3	12
1:A:124:MET:O	1:A:128:ALA:HB2	0.42	2.14	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:109:MET:HB3	1:A:116:LEU:HD13	0.42	1.91	13	1
2:B:1911:VAL:HG13	2:B:1912:ILE:N	0.41	2.29	1	2
1:A:89:PHE:CE1	1:A:100:ILE:HD13	0.41	2.50	5	1
1:A:128:ALA:CB	1:A:136:ILE:HG21	0.41	2.45	3	3
1:A:128:ALA:HB2	1:A:141:PHE:CD1	0.41	2.50	11	1
1:A:102:ALA:CB	1:A:136:ILE:HD11	0.41	2.35	21	1
1:A:85:LEU:CD1	2:B:1912:ILE:CG1	0.41	2.99	10	5
1:A:128:ALA:CB	1:A:136:ILE:CG2	0.41	2.98	15	3
2:B:1906:GLU:O	2:B:1909:ALA:HB3	0.41	2.15	5	1
1:A:85:LEU:HD12	1:A:142:VAL:HB	0.40	1.91	12	1
1:A:112:LEU:HD12	1:A:112:LEU:C	0.40	2.36	10	1
1:A:98:GLY:HA2	1:A:138:TYR:CE2	0.40	2.51	5	2
1:A:92:PHE:CZ	2:B:1908:SER:OG	0.40	2.75	21	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	55/73 (75%)	50±1 (90±1%)	4±1 (7±2%)	2±0 (3±1%)	7	41
2	B	16/27 (59%)	16±1 (97±4%)	0±1 (3±4%)	0±0 (0±0%)	100	100
All	All	1491/2100 (71%)	1368 (92%)	90 (6%)	33 (2%)	10	49

All 2 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	129	ASP	21
1	A	98	GLY	12

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	49/64 (77%)	39±2 (80±4%)	10±2 (20±4%)	4	34
2	B	14/25 (56%)	11±1 (78±10%)	3±1 (22±10%)	3	30
All	All	1323/1869 (71%)	1054 (80%)	269 (20%)	3	33

All 42 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	116	LEU	21
1	A	89	PHE	19
1	A	144	MET	15
1	A	126	ARG	14
2	B	1913	GLN	13
1	A	109	MET	13
1	A	124	MET	12
1	A	129	ASP	12
1	A	90	LYS	11
2	B	1918	ARG	11
1	A	101	SER	10
2	B	1912	ILE	8
2	B	1914	ARG	8
2	B	1920	LEU	7
2	B	1917	ARG	7
1	A	139	GLU	6
1	A	143	ARG	6
1	A	87	GLU	6
1	A	106	ARG	6
1	A	127	GLU	6
1	A	145	MET	5
1	A	81	SER	5
1	A	138	TYR	4
1	A	82	GLU	4
1	A	123	GLU	4
2	B	1908	SER	4
1	A	114	GLU	4
1	A	120	GLU	3
2	B	1910	ILE	3
1	A	119	ASP	3
1	A	118	ASP	2
2	B	1905	GLU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	115	LYS	2
1	A	137	ASN	2
1	A	104	GLU	2
1	A	122	ASP	2
2	B	1906	GLU	2
1	A	112	LEU	1
1	A	117	THR	1
1	A	84	GLU	1
1	A	140	GLU	1
1	A	99	LEU	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 carbohydrates 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