



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 05:56 PM UTC

PDB ID : 5OEO / pdb_00005oeo
BMRB ID : 34161
Title : Solution structure of the complex of TRPV5(655-725) with a Calmodulin E32Q/E68Q double mutant
Authors : Vuister, G.W.; Bokhovchuk, F.M.; Bate, N.; Kovalevskaya, N.; Goult, B.T.; Spronk, C.A.E.M.
Deposited on : 2017-07-09

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

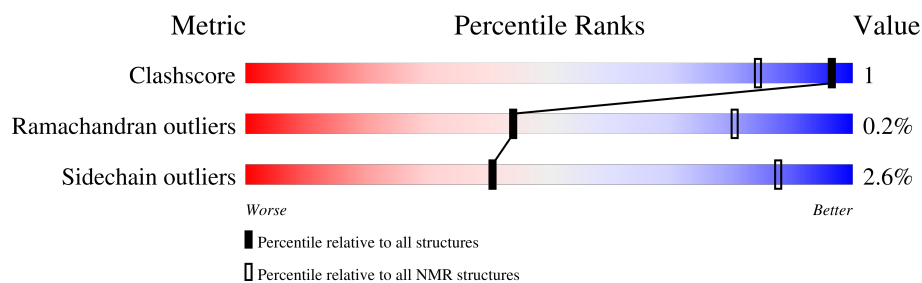
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 77%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	150	
2	C	73	

2 Ensemble composition and analysis

This entry contains 20 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:7-A:73 (67)	1.24	7
2	A:84-A:146, C:698-C:710 (76)	0.98	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 and 2 single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3347 atoms, of which 1623 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms						Trace
1	A	150	Total	C	H	N	O	S	0
			2294	722	1114	192	256	10	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP P0DP23
A	31	GLN	GLU	engineered mutation	UNP P0DP23
A	67	GLN	GLU	engineered mutation	UNP P0DP23

- Molecule 2 is a protein called Transient receptor potential cation channel subfamily V member 5.

Mol	Chain	Residues	Atoms					Trace
2	C	73	Total	C	H	N	O	0
			1051	320	509	101	121	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	653	GLY	-	expression tag	UNP Q9NQA5
C	654	ALA	-	expression tag	UNP Q9NQA5

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

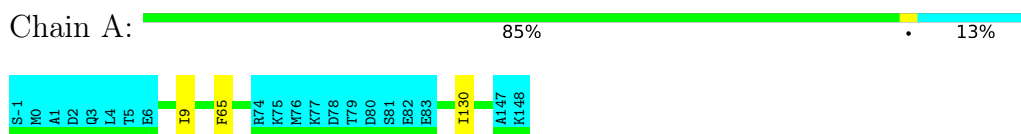
Mol	Chain	Residues	Atoms	
3	A	2	Total	Ca
			2	2

4 Residue-property plots [i](#)

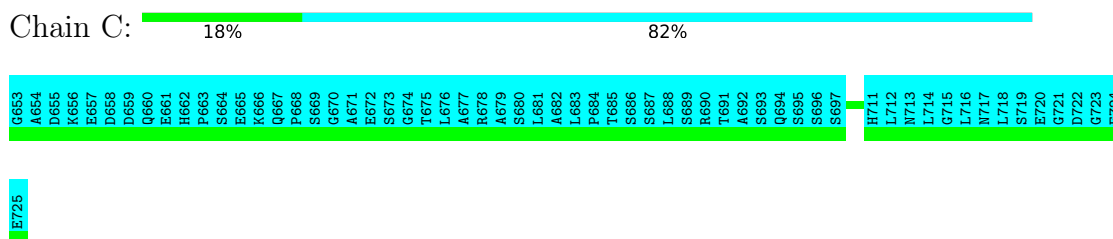
4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Calmodulin-1



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

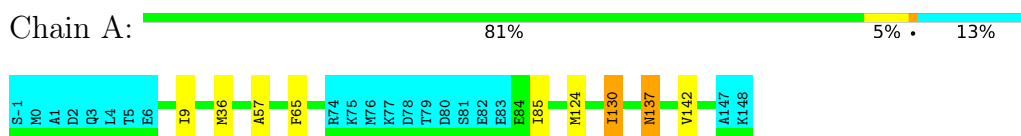


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

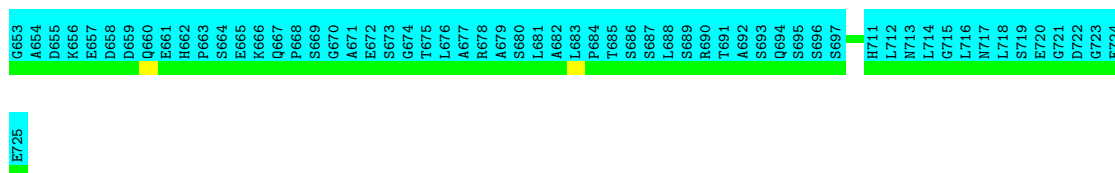
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Calmodulin-1



- Molecule 2: Transient receptor potential cation channel subfamily V member 5





4.2.2 Score per residue for model 2

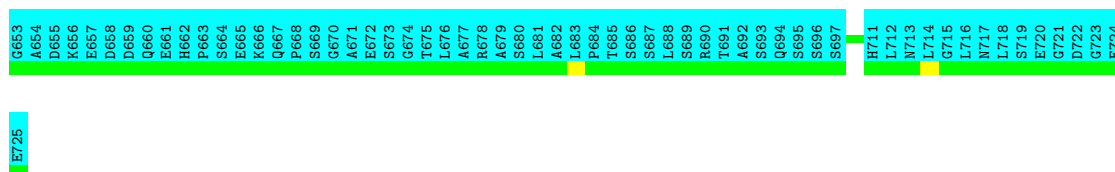
- Molecule 1: Calmodulin-1

Chain A: 84% 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

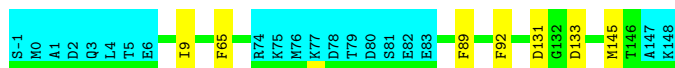
Chain C: 18% 82%



4.2.3 Score per residue for model 3

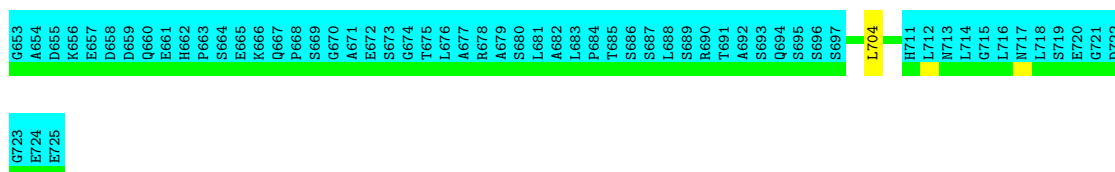
- Molecule 1: Calmodulin-1

Chain A: 82% 5% 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

Chain C: 16% 82%



4.2.4 Score per residue for model 4

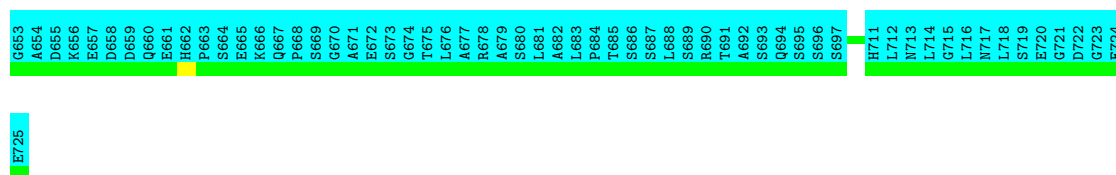
- Molecule 1: Calmodulin-1

Chain A:  83% • • 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

Chain C:  18% 82%



4.2.5 Score per residue for model 5

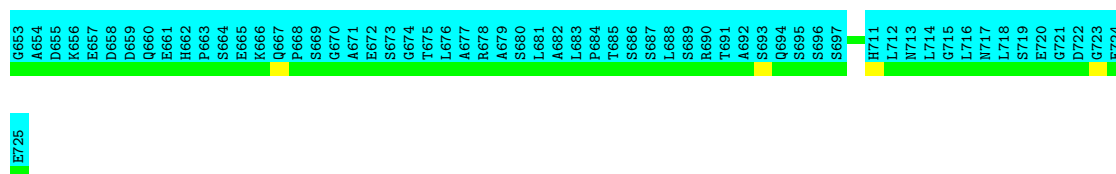
- Molecule 1: Calmodulin-1

Chain A:  83% • 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

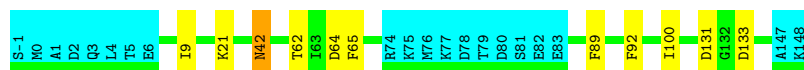
Chain C:  18% 82%



4.2.6 Score per residue for model 6

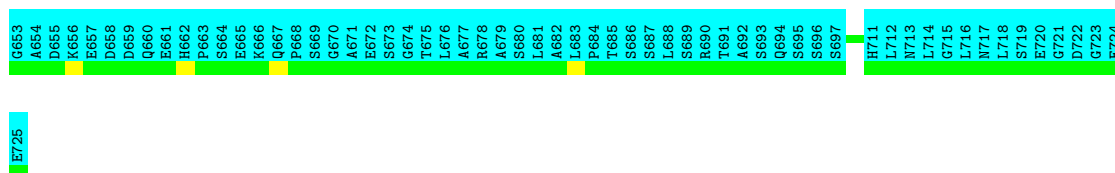
- Molecule 1: Calmodulin-1

Chain A:  79% 7% • 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

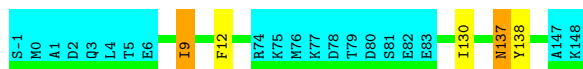
Chain C:  18% 82%



4.2.7 Score per residue for model 7

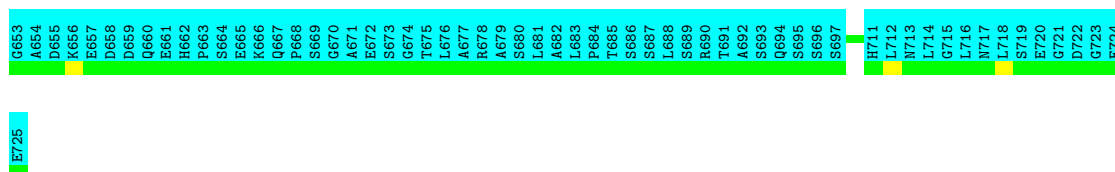
- Molecule 1: Calmodulin-1

Chain A: 83% .. 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

Chain C: 18% 82%



4.2.8 Score per residue for model 8

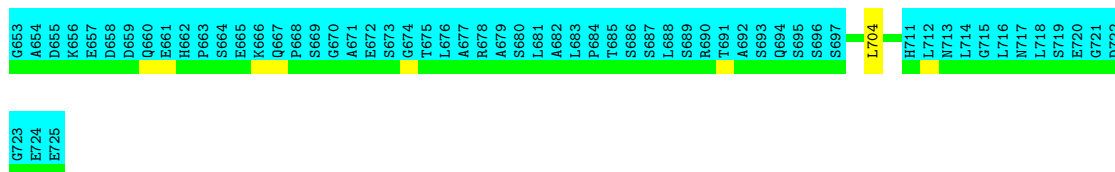
- Molecule 1: Calmodulin-1

Chain A: 80% 6% . 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

Chain C: 16% . 82%



4.2.9 Score per residue for model 9

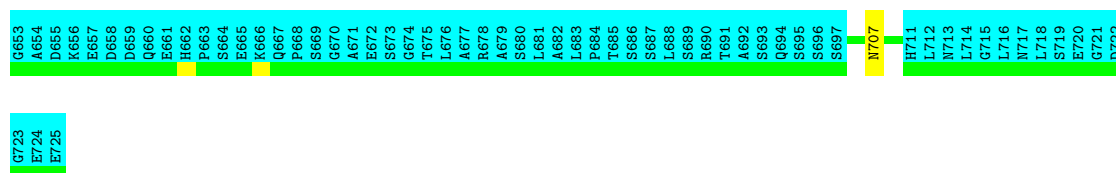
- Molecule 1: Calmodulin-1

Chain A:  83% 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

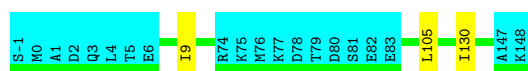
Chain C:  16% 82%



4.2.10 Score per residue for model 10

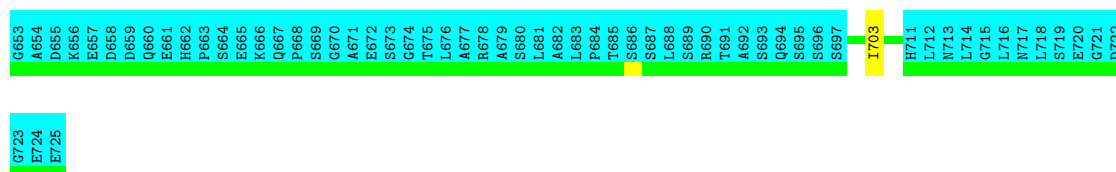
- Molecule 1: Calmodulin-1

Chain A:  85% 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

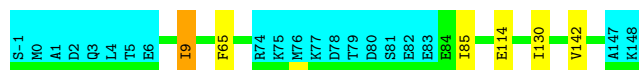
Chain C:  16% 82%



4.2.11 Score per residue for model 11

- Molecule 1: Calmodulin-1

Chain A:  83% 13%

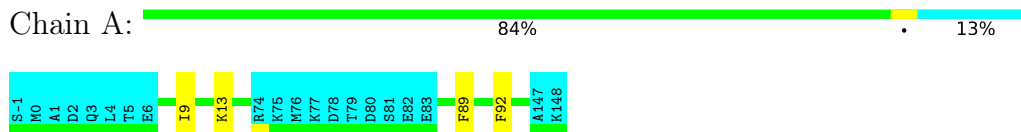


- Molecule 2: Transient receptor potential cation channel subfamily V member 5

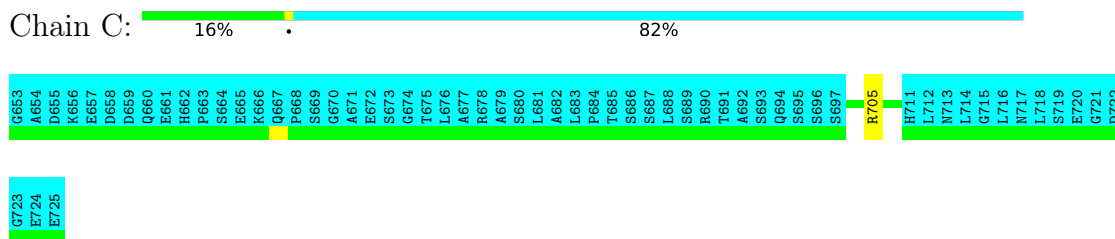
Chain C:  16% 82%

4.2.12 Score per residue for model 12

- Molecule 1: Calmodulin-1

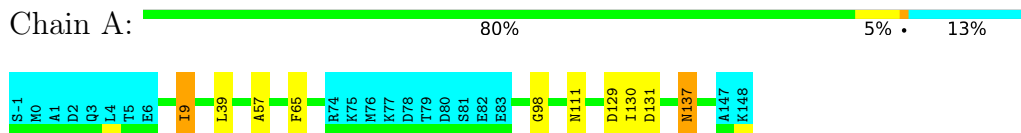


- Molecule 2: Transient receptor potential cation channel subfamily V member 5

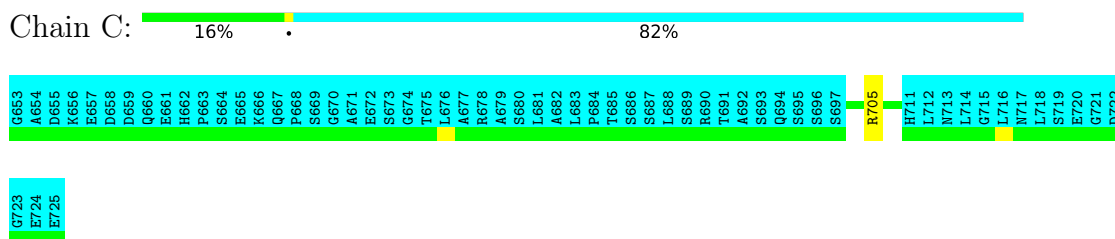


4.2.13 Score per residue for model 13

- Molecule 1: Calmodulin-1



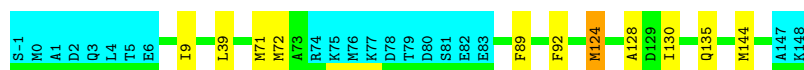
- Molecule 2: Transient receptor potential cation channel subfamily V member 5



4.2.14 Score per residue for model 14

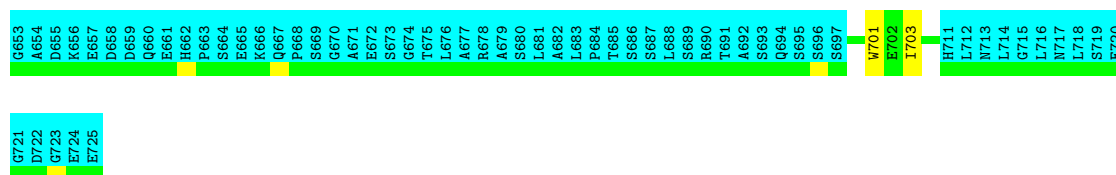
- Molecule 1: Calmodulin-1

Chain A:  79% 7% 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

Chain C:  15% 82%



4.2.15 Score per residue for model 15

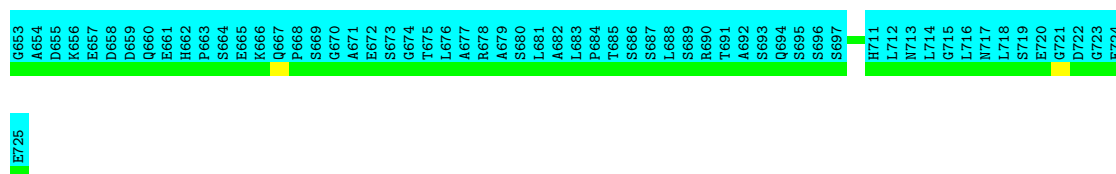
- Molecule 1: Calmodulin-1

Chain A:  83% 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

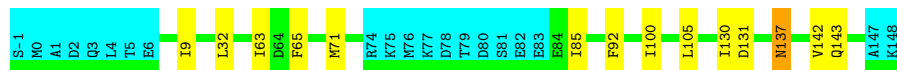
Chain C:  18% 82%



4.2.16 Score per residue for model 16

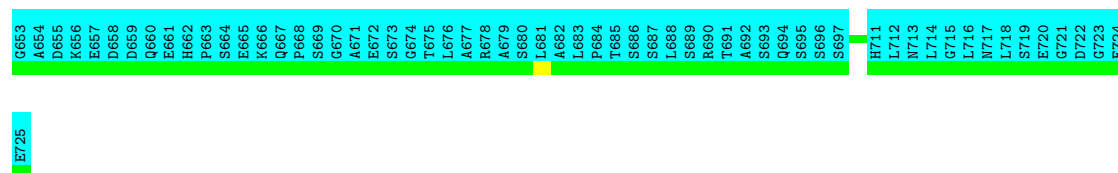
- Molecule 1: Calmodulin-1

Chain A:  77% 9% 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

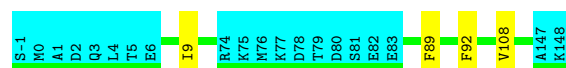
Chain C:  18% 82%



4.2.17 Score per residue for model 17

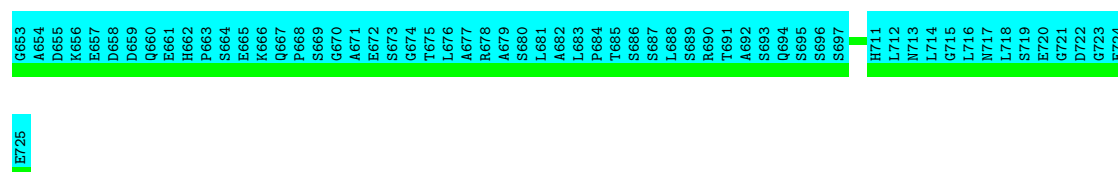
- Molecule 1: Calmodulin-1

Chain A: 84% 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

Chain C: 18% 82%



4.2.18 Score per residue for model 18

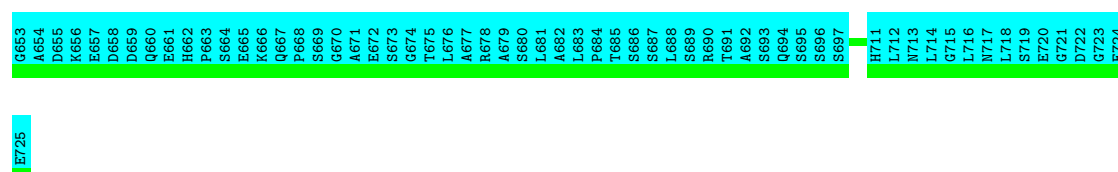
- Molecule 1: Calmodulin-1

Chain A: 79% 7% 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

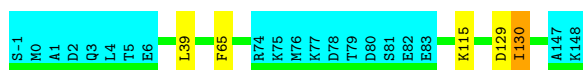
Chain C: 18% 82%



4.2.19 Score per residue for model 19

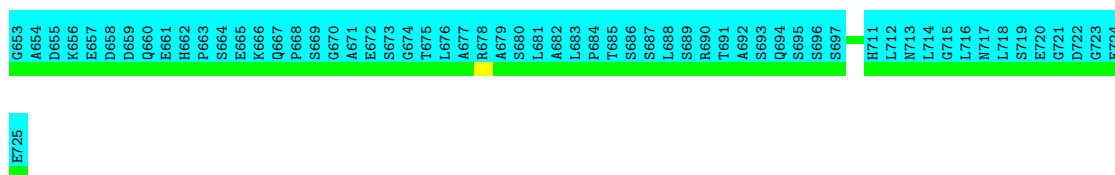
- Molecule 1: Calmodulin-1

Chain A:  83% • • 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

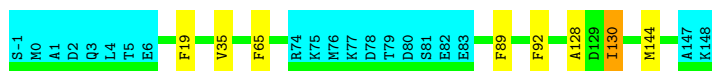
Chain C:  18% 82%



4.2.20 Score per residue for model 20

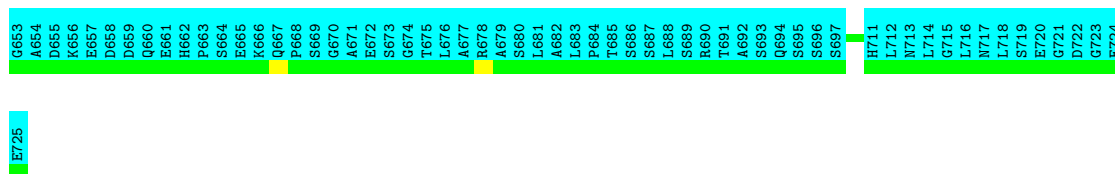
- Molecule 1: Calmodulin-1

Chain A:  81% 5% • 13%



- Molecule 2: Transient receptor potential cation channel subfamily V member 5

Chain C:  18% 82%



5 Refinement protocol and experimental data overview

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

Of the 120 calculated structures, 20 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
CYANA	structure calculation	3.97
YASARA	refinement	15.6

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1766
Number of shifts mapped to atoms	1766
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	77%

6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.98±0.02	0±0/1034 (0.0± 0.0%)	1.04±0.04	2±2/1392 (0.2± 0.1%)
2	C	1.06±0.08	0±0/114 (0.0± 0.2%)	1.18±0.06	0±0/154 (0.0± 0.1%)
All	All	0.99	6/22960 (0.0%)	1.05	48/30920 (0.2%)

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	9	ILE	CA-CB	6.71	1.63	1.54	11	4
1	A	130	ILE	CA-C	5.75	1.60	1.52	19	1
2	C	705	ARG	CZ-NH2	-5.04	1.26	1.33	13	1

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	65	PHE	CA-C-N	-9.53	109.93	119.56	19	11
1	A	65	PHE	C-N-CA	-9.53	109.93	119.56	19	11
1	A	42	ASN	CA-C-N	-8.79	111.33	120.03	9	3
1	A	42	ASN	C-N-CA	-8.79	111.33	120.03	9	3
1	A	130	ILE	N-CA-C	-6.89	106.29	112.90	2	6
1	A	108	VAL	N-CA-C	6.01	117.95	111.58	4	1
1	A	62	THR	N-CA-C	-5.85	99.46	109.24	6	1
1	A	55	VAL	N-CA-C	5.71	118.23	111.09	9	1
1	A	100	ILE	N-CA-C	5.63	116.06	108.17	6	1
1	A	41	GLN	N-CA-C	5.60	118.60	108.69	8	1
1	A	57	ALA	N-CA-C	-5.38	105.50	111.36	1	2
1	A	108	VAL	CB-CA-C	-5.33	105.05	112.02	17	1
1	A	32	LEU	N-CA-C	-5.22	105.59	111.28	4	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	138	TYR	N-CA-C	5.22	116.66	111.07	7	1
1	A	131	ASP	N-CA-C	5.19	119.32	112.89	16	1
1	A	129	ASP	N-CA-C	5.15	116.58	111.07	19	1
2	C	705	ARG	N-CA-C	-5.03	105.88	111.36	12	1
1	A	98	GLY	N-CA-C	-5.01	108.41	115.32	13	1

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	1021	959	959	2±1
2	C	111	109	109	0±0
All	All	22680	21360	21360	36

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:131:ASP:OD2	1:A:133:ASP:OD2	0.73	2.07	6	1
1:A:128:ALA:HB1	1:A:144:MET:HE2	0.64	1.68	20	2
1:A:129:ASP:OD1	1:A:131:ASP:OD2	0.62	2.17	13	1
1:A:85:ILE:HG21	1:A:142:VAL:HG22	0.56	1.78	16	3
1:A:19:PHE:CD1	1:A:35:VAL:HG22	0.54	2.38	20	1
1:A:92:PHE:CE2	1:A:100:ILE:HG23	0.51	2.40	16	1
1:A:137:ASN:C	1:A:137:ASN:HD22	0.50	2.13	16	5
1:A:131:ASP:OD2	1:A:133:ASP:OD1	0.49	2.30	3	1
1:A:92:PHE:CD1	2:C:704:LEU:HD11	0.48	2.43	8	1
1:A:89:PHE:HA	1:A:92:PHE:CE2	0.47	2.45	20	4
1:A:92:PHE:CZ	1:A:100:ILE:HG23	0.46	2.46	16	1
1:A:89:PHE:HA	1:A:92:PHE:CE1	0.46	2.46	3	3
1:A:130:ILE:H	1:A:130:ILE:HD13	0.45	1.72	20	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:143:GLN:HA	1:A:146:THR:HG22	0.43	1.90	8	1
1:A:124:MET:SD	2:C:701:TRP:CD1	0.43	3.12	14	1
1:A:51:MET:SD	1:A:71:MET:HE2	0.43	2.54	5	1
1:A:9:ILE:HD12	1:A:12:PHE:CZ	0.42	2.48	7	1
1:A:9:ILE:HA	1:A:12:PHE:CE1	0.42	2.50	9	1
1:A:32:LEU:HD22	1:A:63:ILE:HD13	0.41	1.91	16	1
1:A:116:LEU:HD13	1:A:124:MET:HE1	0.41	1.91	18	1
1:A:32:LEU:HD12	1:A:63:ILE:HD11	0.40	1.93	18	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	130/150 (87%)	128±1 (99±1%)	1±1 (1±1%)	0±1 (0±1%)	44	80
2	C	13/73 (18%)	13±0 (100±2%)	0±0 (0±2%)	0±0 (0±0%)	100	100
All	All	2860/4460 (64%)	2825 (99%)	29 (1%)	6 (0%)	44	80

All 4 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	42	ASN	2
1	A	65	PHE	2
1	A	64	ASP	1
1	A	130	ILE	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	110/128 (86%)	107±2 (97±1%)	3±2 (3±1%)	41	88
2	C	11/59 (19%)	11±0 (98±4%)	0±0 (2±4%)	44	89
All	All	2420/3740 (65%)	2357 (97%)	63 (3%)	41	88

All 27 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	ILE	16
1	A	130	ILE	6
1	A	137	ASN	5
1	A	71	MET	4
1	A	39	LEU	4
1	A	124	MET	2
1	A	21	LYS	2
2	C	707	ASN	2
1	A	105	LEU	2
2	C	703	ILE	2
1	A	13	LYS	2
1	A	36	MET	1
1	A	145	MET	1
2	C	704	LEU	1
1	A	31	GLN	1
1	A	53	ASN	1
1	A	41	GLN	1
1	A	60	ASN	1
1	A	114	GLU	1
1	A	111	ASN	1
1	A	135	GLN	1
1	A	8	GLN	1
1	A	48	LEU	1
1	A	143	GLN	1
1	A	67	GLN	1
1	A	127	GLU	1
1	A	115	LYS	1

6.3.3 RNA ⓘ

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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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

The completeness of assignment taking into account all chemical shift lists is 77% for the well-defined parts and 62% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *nef_chemical_shift_list_ShiftList_1-final.prot*

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	1766
Number of shifts mapped to atoms	1766
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	153	-1.22 ± 0.11	Should be checked
$^{13}\text{C}_\beta$	152	-0.74 ± 0.08	Should be checked
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	170	0.22 ± 0.24	None needed (< 0.5 ppm)

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 77%, i.e. 1473 atoms were assigned a chemical shift out of a possible 1908. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	544/724 (75%)	281/297 (95%)	126/286 (44%)	137/141 (97%)
Sidechain	864/1060 (82%)	597/680 (88%)	257/339 (76%)	10/41 (24%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	65/124 (52%)	44/62 (71%)	20/59 (34%)	1/3 (33%)
Overall	1473/1908 (77%)	922/1039 (89%)	403/684 (59%)	148/185 (80%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 62%, i.e. 1766 atoms were assigned a chemical shift out of a possible 2867. 0 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	667/1124 (59%)	344/460 (75%)	153/446 (34%)	170/218 (78%)
Sidechain	1034/1605 (64%)	715/1028 (70%)	309/516 (60%)	10/61 (16%)
Aromatic	65/138 (47%)	44/70 (63%)	20/63 (32%)	1/5 (20%)
Overall	1766/2867 (62%)	1103/1558 (71%)	482/1025 (47%)	181/284 (64%)

7.1.4 Statistically unusual chemical shifts [i](#)

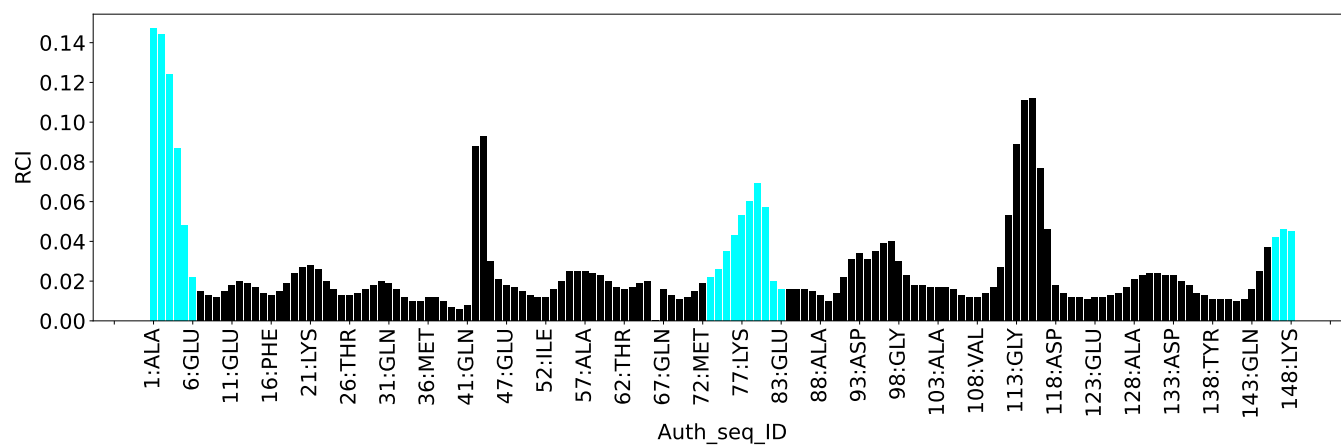
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	39	LEU	HA	1.96	2.04 – 6.55	-5.2

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



Random coil index (RCI) for chain C:

