



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 10:26 AM UTC

PDB ID : 2M0J / pdb_00002m0j
BMRB ID : 17771
Title : 3D Structure of Calmodulin and Calmodulin binding domain of Olfactory cyclic nucleotide-gated ion channel complex
Authors : Deli, I.; Chyan, C.
Deposited on : 2012-10-29

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

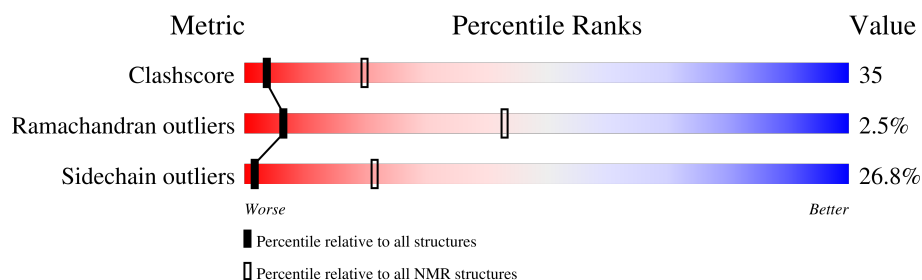
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 86%.

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	148	
2	B	28	

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:148, B:60-B:83 (171)	0.41	7

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2744 atoms, of which 1340 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms						Trace
1	A	148	Total	C	H	N	O	S	0
			2259	714	1094	188	254	9	

- Molecule 2 is a protein called Peptide from Cyclic nucleotide-gated olfactory channel.

Mol	Chain	Residues	Atoms					Trace
2	B	28	Total	C	H	N	O	0
			481	147	246	54	34	

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

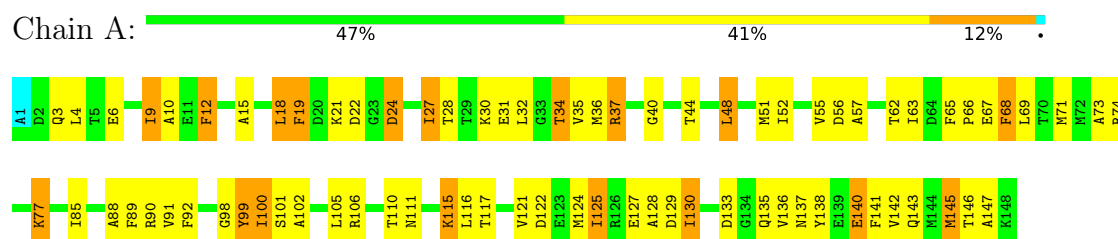
Mol	Chain	Residues	Atoms	
3	A	4	Total	Ca
			4	4

4 Residue-property plots [i](#)

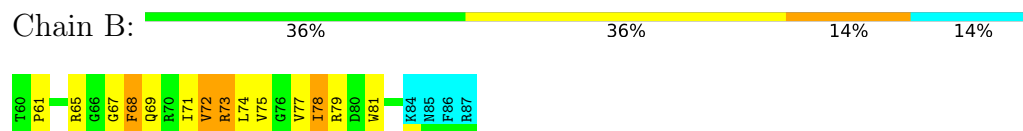
4.1 Average score per residue in the NMR ensemble

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



- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

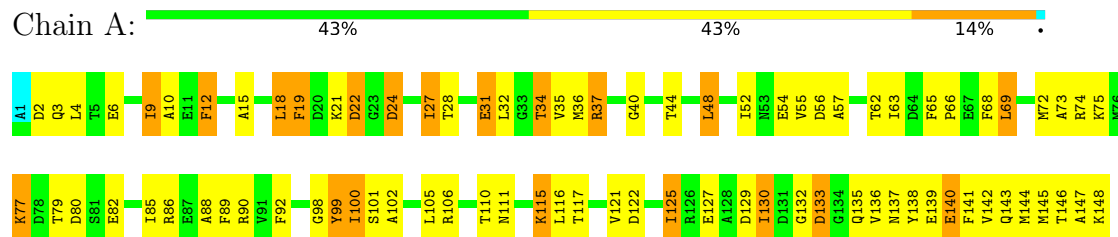


4.2 Scores per residue for each member of the ensemble

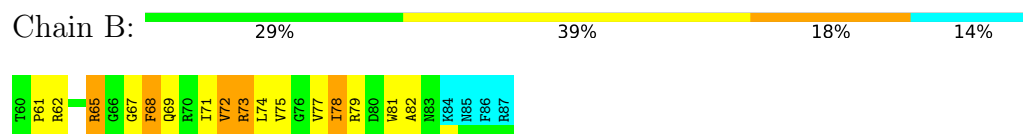
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Calmodulin

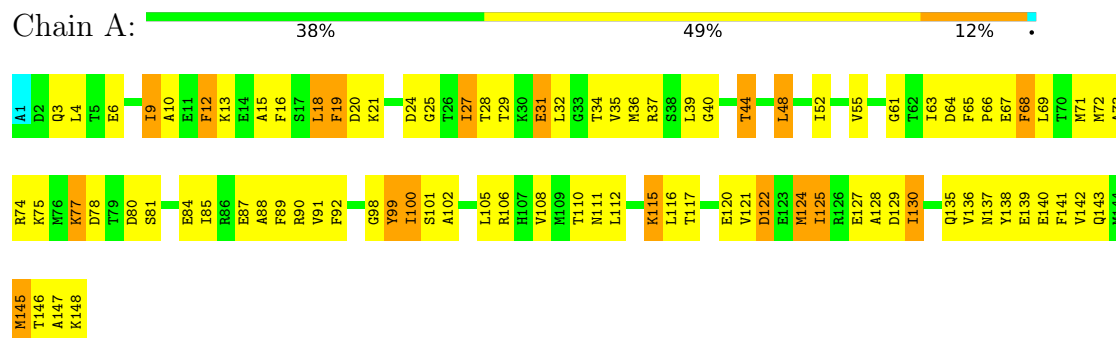


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

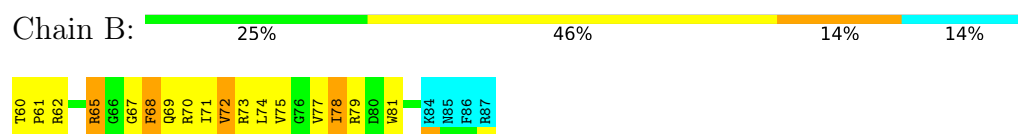


4.2.2 Score per residue for model 2

- Molecule 1: Calmodulin

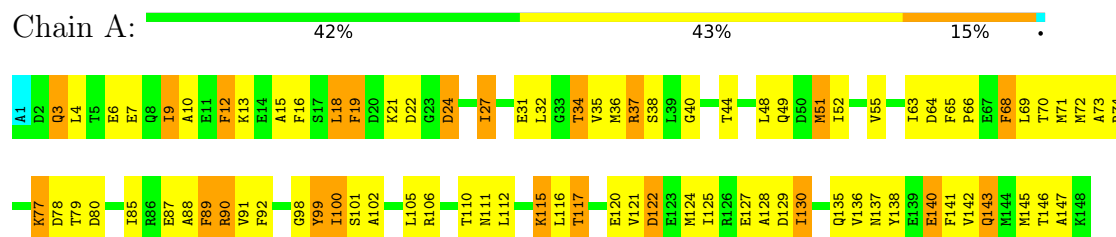


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

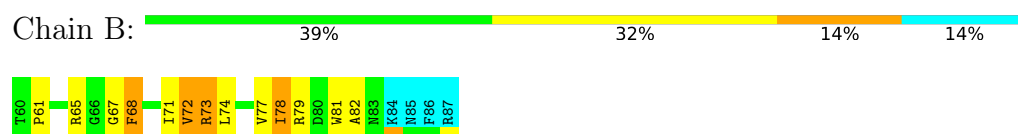


4.2.3 Score per residue for model 3

- Molecule 1: Calmodulin

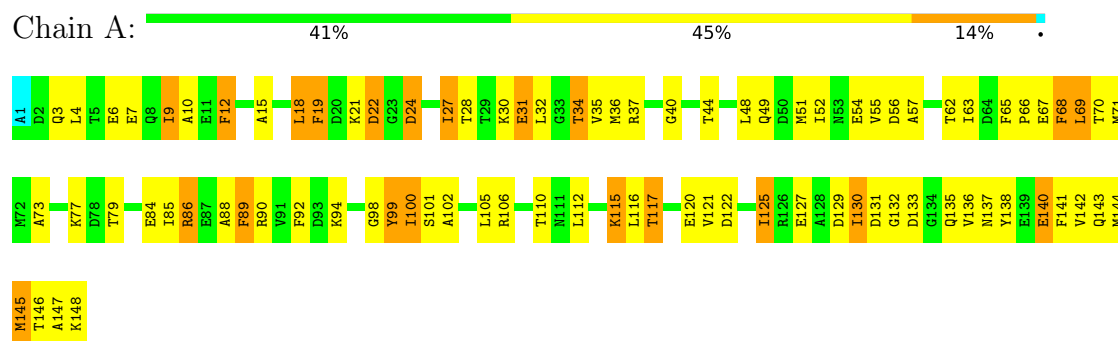


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

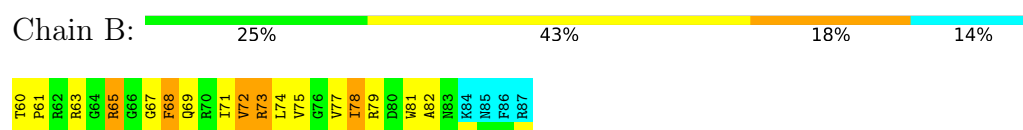


4.2.4 Score per residue for model 4

- Molecule 1: Calmodulin

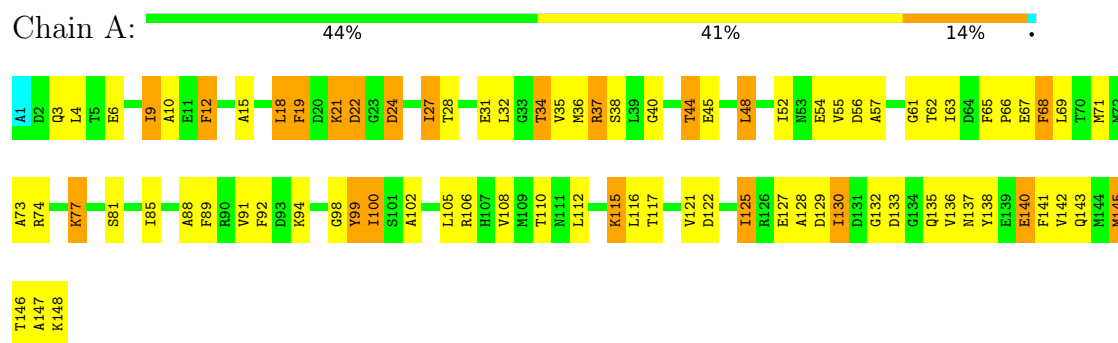


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

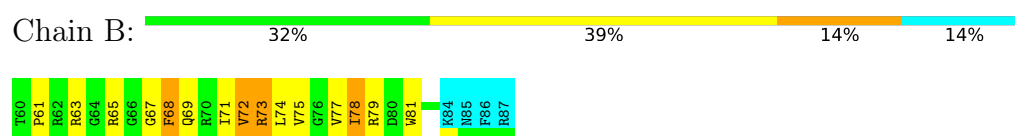


4.2.5 Score per residue for model 5

- Molecule 1: Calmodulin



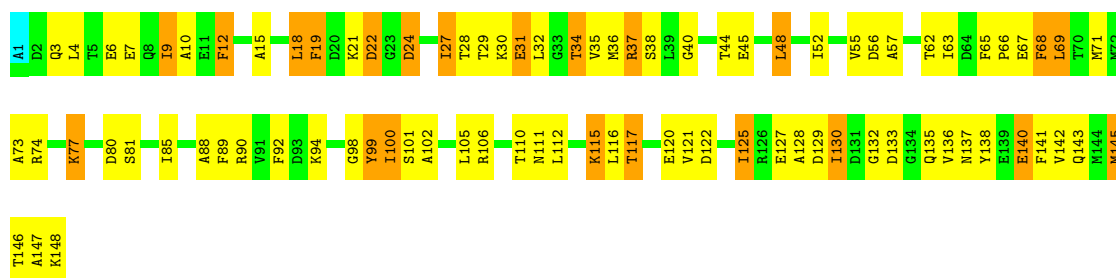
- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel



4.2.6 Score per residue for model 6

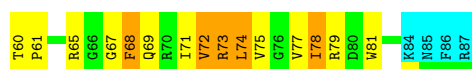
- Molecule 1: Calmodulin





- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

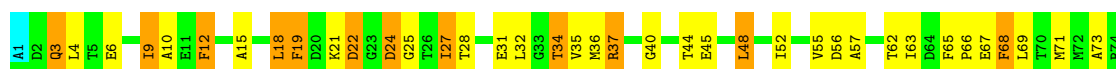
Chain B: 32% 36% 18% 14%



4.2.7 Score per residue for model 7 (medoid)

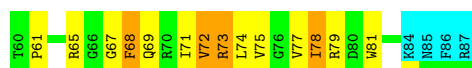
- Molecule 1: Calmodulin

Chain A: 45% 41% 14% 14%



- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

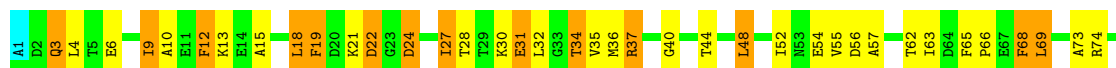
Chain B: 36% 36% 14% 14%



4.2.8 Score per residue for model 8

- Molecule 1: Calmodulin

Chain A: 47% 38% 15% 14%

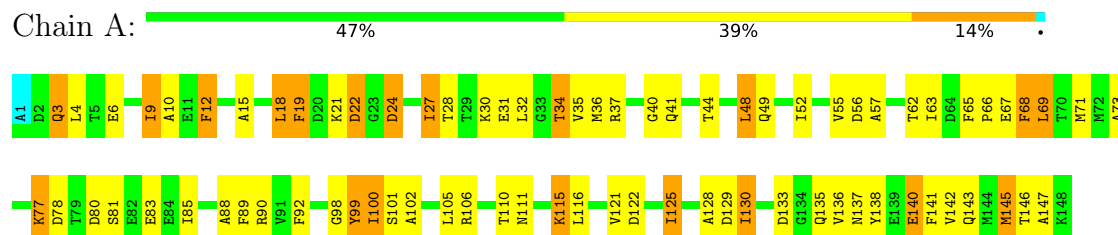


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

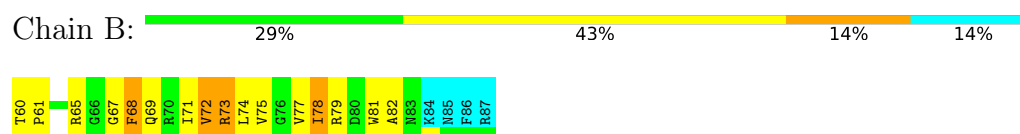


4.2.9 Score per residue for model 9

- Molecule 1: Calmodulin

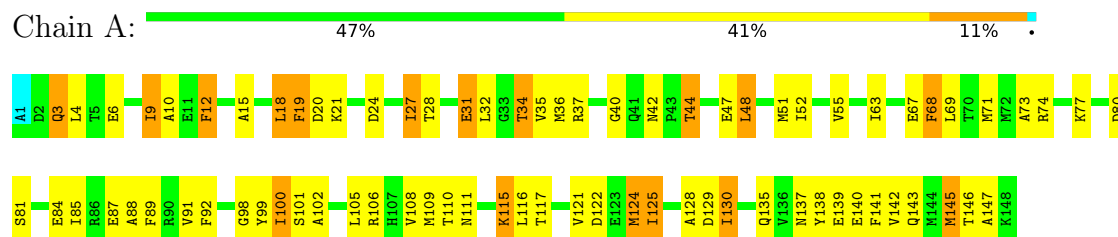


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel



4.2.10 Score per residue for model 10

- Molecule 1: Calmodulin

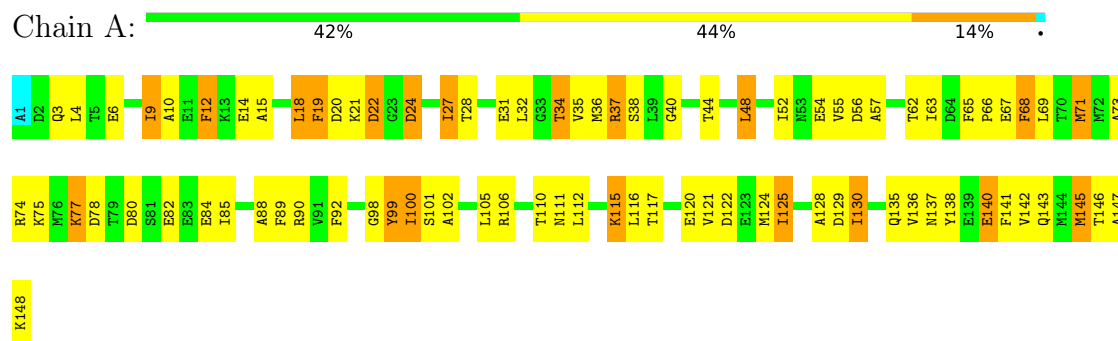


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

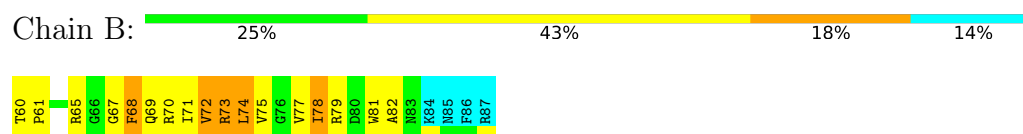


4.2.11 Score per residue for model 11

- Molecule 1: Calmodulin

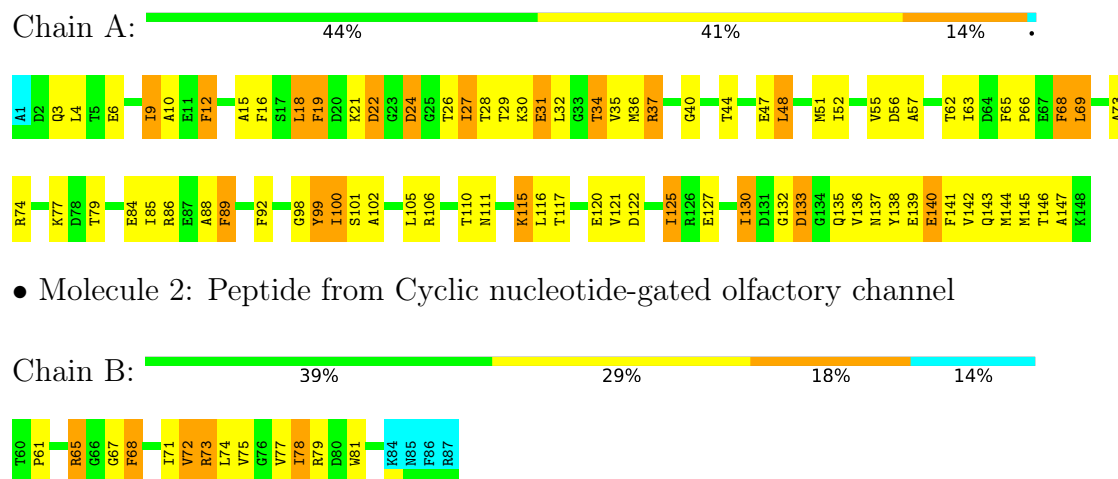


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

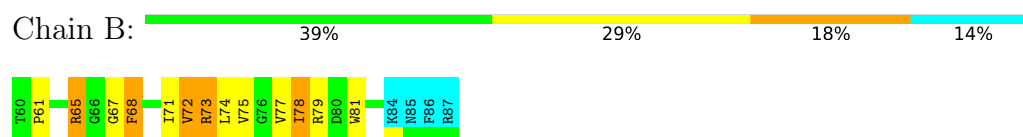


4.2.12 Score per residue for model 12

- Molecule 1: Calmodulin

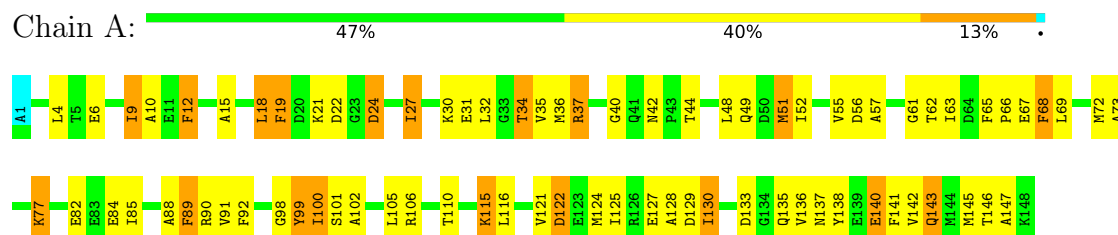


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

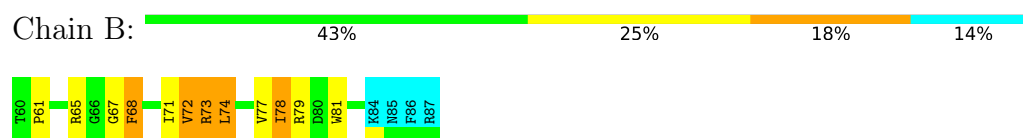


4.2.13 Score per residue for model 13

- Molecule 1: Calmodulin

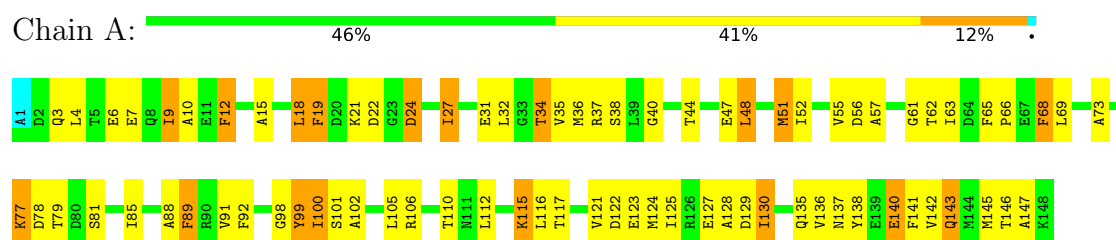


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

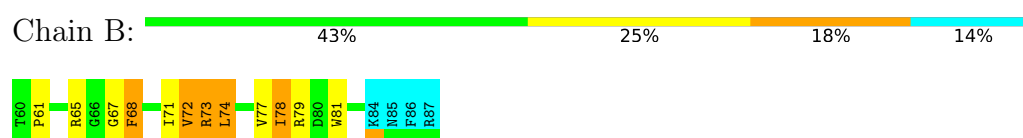


4.2.14 Score per residue for model 14

- Molecule 1: Calmodulin

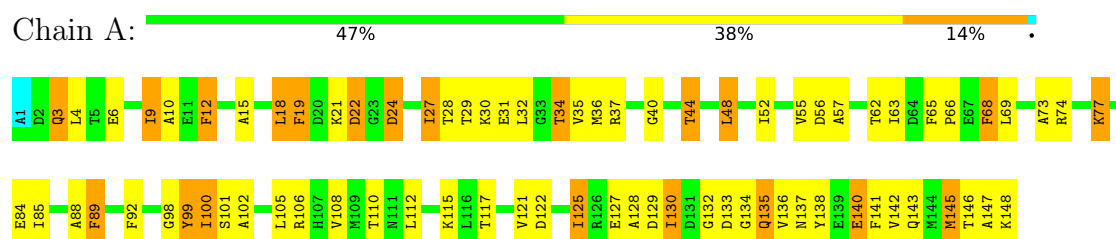


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel



4.2.15 Score per residue for model 15

- Molecule 1: Calmodulin

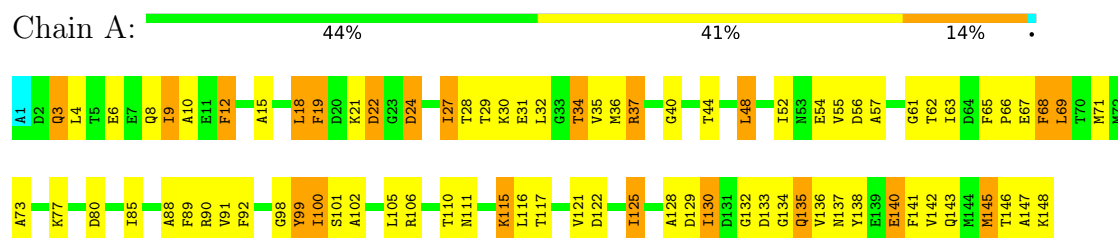


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

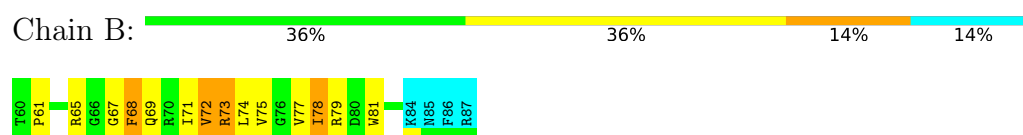


4.2.16 Score per residue for model 16

- Molecule 1: Calmodulin

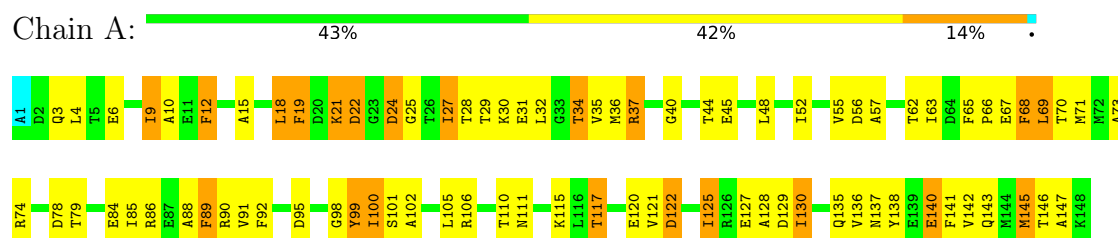


- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel



4.2.17 Score per residue for model 17

- Molecule 1: Calmodulin



- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

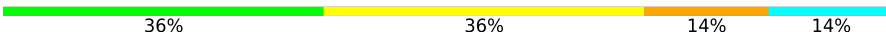


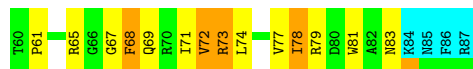
4.2.18 Score per residue for model 18

- Molecule 1: Calmodulin



- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

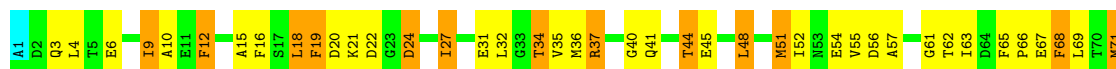
Chain B: 



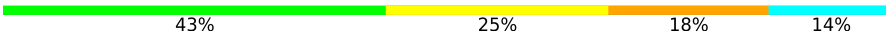
4.2.19 Score per residue for model 19

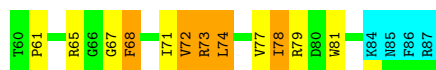
- Molecule 1: Calmodulin

Chain A: 



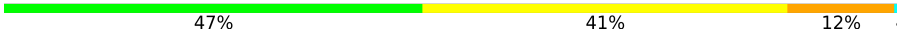
- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

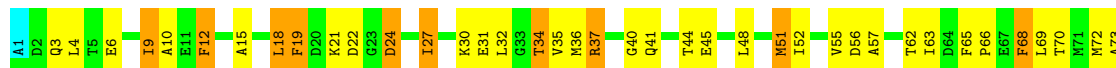
Chain B: 



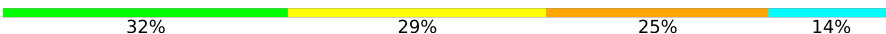
4.2.20 Score per residue for model 20

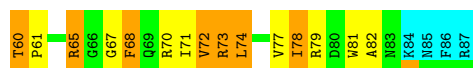
- Molecule 1: Calmodulin

Chain A: 



- Molecule 2: Peptide from Cyclic nucleotide-gated olfactory channel

Chain B: 



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	refinement	

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	2025
Number of shifts mapped to atoms	2025
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	86%

6 Model quality ⓘ

6.1 Standard geometry ⓘ

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

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	1160	1090	1089	84±6
2	B	196	205	205	20±2
All	All	27200	25900	25880	1855

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 35.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:55:VAL:HG23	1:A:63:ILE:HD12	0.91	1.42	8	20
1:A:52:ILE:HG23	1:A:63:ILE:CD1	0.82	2.05	1	18
1:A:51:MET:HE1	2:B:81:TRP:CD1	0.80	2.11	13	5
2:B:71:ILE:O	2:B:75:VAL:HG23	0.76	1.81	2	14
1:A:145:MET:HE3	1:A:146:THR:HG22	0.74	1.60	5	12
1:A:3:GLN:HG2	1:A:69:LEU:HD23	0.73	1.60	4	6
1:A:144:MET:HE3	2:B:65:ARG:HA	0.73	1.59	12	3
1:A:67:GLU:O	1:A:71:MET:HE3	0.73	1.83	11	2
1:A:15:ALA:HA	2:B:74:LEU:HD21	0.72	1.59	13	20
1:A:87:GLU:O	1:A:91:VAL:HG13	0.72	1.85	2	2
1:A:106:ARG:O	1:A:110:THR:HG22	0.71	1.84	3	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:73:ARG:O	2:B:77:VAL:HG23	0.71	1.85	19	20
1:A:51:MET:HE1	1:A:55:VAL:HG11	0.70	1.64	18	1
1:A:52:ILE:HG23	1:A:63:ILE:HD11	0.70	1.62	8	15
1:A:85:ILE:HD11	1:A:145:MET:HE1	0.70	1.64	12	20
1:A:9:ILE:HD11	1:A:69:LEU:HD21	0.69	1.63	10	4
1:A:12:PHE:CE2	1:A:69:LEU:HD13	0.69	2.23	2	8
1:A:130:ILE:HG23	2:B:61:PRO:CB	0.68	2.19	2	15
1:A:51:MET:HE2	2:B:81:TRP:O	0.68	1.88	18	2
1:A:138:TYR:CE1	1:A:142:VAL:HG11	0.68	2.23	1	20
1:A:85:ILE:CD1	1:A:145:MET:HE1	0.67	2.20	15	14
1:A:142:VAL:HG23	1:A:143:GLN:N	0.67	2.05	4	20
1:A:32:LEU:HD22	2:B:81:TRP:CZ3	0.67	2.25	7	19
1:A:3:GLN:OE1	1:A:69:LEU:HD23	0.66	1.90	9	1
1:A:31:GLU:O	1:A:35:VAL:HG12	0.66	1.90	20	20
1:A:55:VAL:O	1:A:71:MET:HE3	0.66	1.90	10	3
2:B:78:ILE:HD13	2:B:78:ILE:O	0.66	1.90	17	19
1:A:55:VAL:HG23	1:A:63:ILE:CD1	0.66	2.20	10	20
1:A:4:LEU:HD21	1:A:73:ALA:HA	0.65	1.69	6	20
1:A:102:ALA:HA	1:A:125:ILE:HD12	0.65	1.68	12	20
1:A:3:GLN:CG	1:A:69:LEU:HD23	0.65	2.22	18	6
1:A:35:VAL:HG23	1:A:112:LEU:HD22	0.64	1.69	18	3
1:A:100:ILE:N	1:A:100:ILE:HD12	0.64	2.08	2	20
1:A:67:GLU:O	1:A:71:MET:HE2	0.64	1.93	9	7
1:A:115:LYS:C	1:A:116:LEU:HD22	0.63	2.18	2	18
2:B:60:THR:HG21	2:B:65:ARG:HD2	0.63	1.70	20	2
1:A:130:ILE:HG23	2:B:61:PRO:HB2	0.63	1.69	12	15
1:A:36:MET:HE1	2:B:83:ASN:HD21	0.63	1.53	18	1
1:A:143:GLN:HA	1:A:147:ALA:HB3	0.63	1.71	1	15
1:A:51:MET:HE1	2:B:81:TRP:NE1	0.63	2.08	19	5
1:A:6:GLU:O	1:A:10:ALA:HB2	0.62	1.95	1	20
1:A:15:ALA:CB	2:B:74:LEU:HD21	0.62	2.25	11	9
1:A:130:ILE:HG23	2:B:61:PRO:HB3	0.61	1.73	18	9
1:A:92:PHE:CZ	2:B:71:ILE:HG22	0.60	2.31	18	7
1:A:117:THR:HG22	1:A:120:GLU:CD	0.60	2.21	12	6
1:A:124:MET:O	1:A:128:ALA:HB2	0.60	1.96	19	6
1:A:124:MET:HE2	1:A:128:ALA:HB2	0.59	1.73	10	8
1:A:67:GLU:OE2	1:A:71:MET:HE1	0.59	1.98	19	2
1:A:63:ILE:HG21	1:A:68:PHE:HB2	0.59	1.75	18	1
1:A:142:VAL:HG23	1:A:143:GLN:H	0.58	1.58	2	20
1:A:133:ASP:N	1:A:133:ASP:OD1	0.57	2.37	8	3
1:A:9:ILE:CG2	1:A:10:ALA:N	0.57	2.68	7	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:105:LEU:HD13	2:B:68:PHE:CZ	0.57	2.34	7	17
1:A:117:THR:HG22	1:A:120:GLU:OE1	0.57	1.99	19	2
1:A:138:TYR:C	1:A:138:TYR:CD1	0.57	2.83	5	20
1:A:52:ILE:HG23	1:A:63:ILE:HD13	0.56	1.76	1	13
1:A:32:LEU:O	1:A:36:MET:HG3	0.56	2.00	20	20
1:A:44:THR:O	1:A:48:LEU:HG	0.56	2.00	5	20
1:A:3:GLN:CD	1:A:69:LEU:HD23	0.56	2.25	3	4
2:B:78:ILE:HD13	2:B:78:ILE:C	0.56	2.26	10	19
1:A:69:LEU:O	1:A:73:ALA:CB	0.55	2.54	13	20
1:A:32:LEU:HD22	2:B:81:TRP:CH2	0.55	2.36	15	19
1:A:102:ALA:HA	1:A:125:ILE:CD1	0.55	2.32	1	20
1:A:29:THR:O	1:A:48:LEU:HD13	0.55	2.01	2	7
1:A:102:ALA:CA	1:A:125:ILE:HD12	0.55	2.30	17	20
1:A:12:PHE:CZ	1:A:69:LEU:HD13	0.55	2.36	2	6
1:A:15:ALA:HB2	2:B:74:LEU:HD21	0.55	1.77	11	5
1:A:65:PHE:N	1:A:66:PRO:HD2	0.55	2.17	16	18
2:B:60:THR:HG22	2:B:61:PRO:HD2	0.55	1.78	20	1
1:A:68:PHE:CD1	1:A:68:PHE:C	0.55	2.85	15	20
1:A:146:THR:HG23	1:A:146:THR:O	0.54	2.02	5	12
1:A:55:VAL:HG12	1:A:71:MET:HG2	0.54	1.79	3	4
1:A:9:ILE:CD1	1:A:69:LEU:HD21	0.54	2.32	10	2
1:A:100:ILE:N	1:A:100:ILE:CD1	0.54	2.70	18	18
1:A:124:MET:HE2	1:A:124:MET:O	0.54	2.02	10	2
1:A:15:ALA:CA	2:B:74:LEU:HD21	0.54	2.33	20	20
1:A:142:VAL:O	1:A:146:THR:N	0.53	2.42	18	14
1:A:52:ILE:HG21	1:A:61:GLY:C	0.53	2.28	13	7
1:A:12:PHE:CD1	1:A:68:PHE:CE1	0.53	2.97	20	18
1:A:100:ILE:CD1	1:A:100:ILE:N	0.53	2.72	4	2
1:A:99:TYR:CE1	1:A:137:ASN:HB3	0.52	2.39	18	13
1:A:89:PHE:CE2	1:A:138:TYR:HA	0.52	2.40	10	20
1:A:140:GLU:HA	1:A:140:GLU:OE1	0.52	2.05	7	13
1:A:22:ASP:N	1:A:22:ASP:OD1	0.52	2.43	6	6
1:A:142:VAL:CG2	1:A:143:GLN:N	0.51	2.73	3	20
1:A:99:TYR:HA	1:A:136:VAL:O	0.51	2.05	12	16
1:A:39:LEU:HD21	1:A:112:LEU:HD11	0.51	1.80	18	1
1:A:89:PHE:CZ	1:A:138:TYR:HA	0.51	2.40	3	17
1:A:24:ASP:OD1	1:A:24:ASP:N	0.50	2.44	17	17
1:A:9:ILE:HG13	1:A:69:LEU:HD11	0.50	1.83	18	2
1:A:36:MET:HE1	2:B:83:ASN:ND2	0.50	2.18	18	1
1:A:19:PHE:CB	1:A:27:ILE:HD12	0.50	2.37	16	19
1:A:138:TYR:CZ	1:A:142:VAL:HG11	0.50	2.42	12	17

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:105:LEU:HD22	1:A:125:ILE:HG13	0.50	1.83	7	12
1:A:88:ALA:O	1:A:92:PHE:CD2	0.50	2.64	18	20
1:A:121:VAL:HG13	1:A:122:ASP:N	0.50	2.22	10	20
1:A:39:LEU:HD23	1:A:112:LEU:HD21	0.50	1.83	2	1
1:A:92:PHE:CZ	2:B:75:VAL:HG21	0.50	2.41	10	1
1:A:144:MET:HE3	2:B:65:ARG:CA	0.49	2.33	1	2
2:B:60:THR:O	2:B:60:THR:HG23	0.49	2.06	4	5
1:A:4:LEU:HG	1:A:73:ALA:HB2	0.49	1.83	10	10
1:A:12:PHE:CD1	1:A:68:PHE:CD1	0.49	3.01	3	4
1:A:143:GLN:CA	1:A:147:ALA:HB3	0.49	2.38	6	12
1:A:18:LEU:HD23	1:A:18:LEU:N	0.49	2.23	10	20
1:A:143:GLN:N	1:A:147:ALA:HB3	0.49	2.23	4	12
1:A:85:ILE:HD11	1:A:145:MET:CE	0.49	2.36	12	1
1:A:32:LEU:HD11	2:B:82:ALA:HB2	0.49	1.84	10	8
1:A:89:PHE:CE1	1:A:100:ILE:HD13	0.49	2.42	17	17
1:A:102:ALA:CB	1:A:121:VAL:HG22	0.49	2.37	18	20
2:B:68:PHE:O	2:B:72:VAL:HG13	0.49	2.08	15	20
2:B:78:ILE:HG23	2:B:79:ARG:N	0.49	2.22	7	20
1:A:88:ALA:O	1:A:91:VAL:HG22	0.49	2.07	18	4
1:A:3:GLN:NE2	1:A:69:LEU:HD23	0.49	2.22	8	1
1:A:98:GLY:O	1:A:137:ASN:HA	0.49	2.08	17	17
1:A:51:MET:HE1	1:A:55:VAL:CG1	0.49	2.36	18	1
1:A:85:ILE:HG23	1:A:141:PHE:HD2	0.48	1.68	1	14
1:A:92:PHE:HZ	2:B:71:ILE:HG22	0.48	1.67	19	6
2:B:74:LEU:O	2:B:78:ILE:HG22	0.48	2.09	10	18
1:A:56:ASP:CG	1:A:62:THR:O	0.48	2.56	13	9
1:A:21:LYS:HG2	1:A:31:GLU:CD	0.48	2.34	16	13
1:A:76:MET:HE3	2:B:73:ARG:NH2	0.48	2.24	7	1
1:A:32:LEU:HD13	2:B:81:TRP:CZ3	0.47	2.44	10	5
1:A:69:LEU:O	1:A:73:ALA:HB3	0.47	2.08	13	16
1:A:36:MET:HE2	1:A:41:GLN:OE1	0.47	2.09	9	1
1:A:129:ASP:HA	1:A:140:GLU:HG3	0.47	1.87	1	1
1:A:85:ILE:HD13	1:A:145:MET:HE1	0.47	1.86	5	1
2:B:78:ILE:CG2	2:B:79:ARG:N	0.47	2.78	18	20
1:A:129:ASP:OD1	1:A:130:ILE:N	0.47	2.47	17	9
1:A:130:ILE:CG1	1:A:140:GLU:CD	0.47	2.88	13	13
1:A:12:PHE:CE2	1:A:69:LEU:CD1	0.47	2.98	3	7
1:A:102:ALA:CA	1:A:125:ILE:CD1	0.47	2.93	18	20
1:A:129:ASP:HA	1:A:140:GLU:OE2	0.47	2.09	8	12
1:A:22:ASP:OD1	1:A:22:ASP:N	0.47	2.48	5	6
1:A:21:LYS:NZ	1:A:34:THR:HG21	0.47	2.25	4	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:102:ALA:HB1	1:A:121:VAL:CG2	0.46	2.40	17	17
1:A:138:TYR:CE1	1:A:142:VAL:CG1	0.46	2.97	1	18
1:A:89:PHE:CE1	1:A:98:GLY:O	0.46	2.68	2	2
1:A:56:ASP:OD1	1:A:57:ALA:N	0.46	2.49	16	16
1:A:67:GLU:OE1	1:A:71:MET:HE1	0.46	2.11	5	2
1:A:26:THR:HG22	1:A:64:ASP:HA	0.46	1.88	18	1
1:A:72:MET:HG3	1:A:76:MET:HE2	0.46	1.88	18	1
1:A:102:ALA:N	1:A:125:ILE:CD1	0.45	2.79	10	20
1:A:136:VAL:HG13	1:A:140:GLU:OE1	0.45	2.11	1	1
1:A:130:ILE:N	1:A:140:GLU:OE2	0.45	2.50	3	2
1:A:20:ASP:CG	1:A:24:ASP:OD1	0.45	2.60	10	3
2:B:60:THR:HG22	2:B:62:ARG:O	0.45	2.12	2	1
1:A:72:MET:SD	2:B:77:VAL:HG11	0.45	2.51	1	1
1:A:16:PHE:CG	1:A:65:PHE:CE1	0.45	3.04	19	1
1:A:142:VAL:CG2	1:A:143:GLN:H	0.44	2.24	19	20
1:A:105:LEU:O	1:A:108:VAL:HG12	0.44	2.12	15	5
1:A:141:PHE:CZ	2:B:69:GLN:OE1	0.44	2.70	2	12
1:A:35:VAL:HG23	1:A:112:LEU:CD2	0.44	2.42	15	1
1:A:27:ILE:O	1:A:62:THR:HA	0.44	2.12	14	15
1:A:139:GLU:O	1:A:143:GLN:HB2	0.44	2.13	12	6
1:A:129:ASP:OD2	1:A:132:GLY:N	0.44	2.50	4	5
1:A:55:VAL:CG2	1:A:63:ILE:CD1	0.44	2.94	10	1
1:A:140:GLU:OE1	1:A:140:GLU:CA	0.44	2.66	3	3
2:B:60:THR:HG21	2:B:65:ARG:CD	0.44	2.42	20	1
1:A:102:ALA:HB1	1:A:121:VAL:CG1	0.44	2.42	12	19
1:A:85:ILE:HG23	1:A:141:PHE:CD2	0.43	2.48	7	9
1:A:137:ASN:OD1	1:A:137:ASN:N	0.43	2.51	2	2
1:A:6:GLU:O	1:A:10:ALA:CB	0.43	2.66	6	7
1:A:16:PHE:CD1	1:A:25:GLY:O	0.43	2.71	18	2
1:A:27:ILE:HD13	1:A:27:ILE:N	0.43	2.29	13	8
1:A:39:LEU:CD2	1:A:112:LEU:HD21	0.43	2.44	18	1
1:A:137:ASN:OD1	1:A:140:GLU:N	0.43	2.50	18	1
1:A:134:GLY:C	1:A:135:GLN:HG2	0.43	2.38	16	2
1:A:117:THR:HG23	1:A:120:GLU:H	0.43	1.74	8	4
1:A:129:ASP:OD2	1:A:133:ASP:N	0.43	2.52	7	8
2:B:73:ARG:HD3	2:B:77:VAL:HG23	0.43	1.90	8	3
1:A:55:VAL:HG11	2:B:81:TRP:HE1	0.42	1.75	2	1
1:A:102:ALA:N	1:A:125:ILE:HD13	0.42	2.29	2	2
2:B:78:ILE:C	2:B:78:ILE:CD1	0.42	2.92	10	13
1:A:128:ALA:O	1:A:140:GLU:OE2	0.42	2.37	17	11
1:A:20:ASP:OD1	1:A:21:LYS:N	0.42	2.52	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:89:PHE:CE1	1:A:100:ILE:CD1	0.42	3.02	15	14
1:A:124:MET:HE3	1:A:128:ALA:HB2	0.42	1.92	11	2
1:A:130:ILE:HD11	1:A:140:GLU:OE1	0.42	2.13	18	1
1:A:38:SER:HB3	1:A:112:LEU:HD23	0.42	1.89	14	2
1:A:38:SER:CB	1:A:112:LEU:HD21	0.42	2.44	5	2
1:A:34:THR:O	1:A:37:ARG:HG3	0.42	2.14	3	18
1:A:19:PHE:HB3	1:A:27:ILE:HD12	0.42	1.90	18	2
1:A:130:ILE:HG13	1:A:140:GLU:CD	0.42	2.40	17	10
1:A:146:THR:OG1	1:A:147:ALA:N	0.42	2.52	1	2
1:A:99:TYR:CE1	1:A:137:ASN:CG	0.42	2.97	10	2
1:A:65:PHE:N	1:A:66:PRO:CD	0.42	2.82	14	6
1:A:52:ILE:HG21	1:A:61:GLY:O	0.42	2.14	18	1
1:A:99:TYR:CE1	1:A:137:ASN:CB	0.42	3.02	10	2
1:A:109:MET:HE1	2:B:71:ILE:HD12	0.42	1.92	18	2
1:A:12:PHE:CD2	1:A:69:LEU:CD1	0.42	3.02	18	2
1:A:124:MET:HE1	2:B:68:PHE:HD2	0.42	1.74	18	2
1:A:67:GLU:HA	1:A:67:GLU:OE1	0.41	2.15	2	1
1:A:36:MET:HG2	2:B:78:ILE:HD11	0.41	1.92	12	1
1:A:141:PHE:O	1:A:145:MET:HG2	0.41	2.14	10	3
1:A:141:PHE:CE1	2:B:69:GLN:NE2	0.41	2.88	1	1
1:A:123:GLU:O	1:A:127:GLU:CG	0.41	2.69	19	3
1:A:32:LEU:HD11	2:B:82:ALA:CB	0.41	2.45	10	1
1:A:4:LEU:HD23	1:A:77:LYS:HG2	0.41	1.91	12	1
1:A:19:PHE:CZ	2:B:78:ILE:HG12	0.41	2.50	18	1
1:A:16:PHE:HA	1:A:27:ILE:HD11	0.41	1.93	3	1
1:A:14:GLU:O	1:A:18:LEU:HG	0.41	2.16	11	1
1:A:86:ARG:CD	1:A:90:ARG:NE	0.41	2.84	4	1
1:A:25:GLY:O	1:A:65:PHE:CE1	0.41	2.74	7	2
1:A:136:VAL:HG22	1:A:140:GLU:OE1	0.40	2.16	12	1
1:A:131:ASP:OD1	1:A:131:ASP:C	0.40	2.63	4	1
1:A:88:ALA:O	1:A:92:PHE:CG	0.40	2.74	9	2
1:A:20:ASP:OD1	1:A:31:GLU:OE2	0.40	2.40	19	1
1:A:87:GLU:O	1:A:90:ARG:HG2	0.40	2.16	3	2
1:A:27:ILE:N	1:A:27:ILE:HD13	0.40	2.32	4	3
1:A:140:GLU:OE1	1:A:140:GLU:HA	0.40	2.16	4	1
1:A:38:SER:CB	1:A:112:LEU:CD2	0.40	3.00	11	1
1:A:16:PHE:CD1	1:A:26:THR:HA	0.40	2.52	12	1
1:A:51:MET:CE	2:B:81:TRP:NE1	0.40	2.85	4	1
1:A:45:GLU:HA	1:A:48:LEU:HD12	0.40	1.91	7	1
1:A:141:PHE:CE1	2:B:69:GLN:OE1	0.40	2.74	16	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	146/148 (99%)	131±1 (90±1%)	12±1 (8±1%)	3±1 (2±1%)	8	48
2	B	23/28 (82%)	18±1 (80±2%)	3±1 (15±3%)	1±1 (6±2%)	2	21
All	All	3380/3520 (96%)	2990 (88%)	304 (9%)	86 (3%)	6	43

All 9 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	40	GLY	20
2	B	67	GLY	20
1	A	77	LYS	15
1	A	80	ASP	10
1	A	79	THR	6
1	A	147	ALA	6
2	B	61	PRO	5
1	A	132	GLY	3
2	B	83	ASN	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	126/126 (100%)	93±3 (74±3%)	33±3 (26±3%)	2	22
2	B	19/23 (83%)	13±1 (70±4%)	6±1 (30±4%)	1	17
All	All	2900/2980 (97%)	2122 (73%)	778 (27%)	2	21

All 77 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	20
1	A	12	PHE	20
1	A	18	LEU	20
1	A	27	ILE	20
1	A	34	THR	20
1	A	100	ILE	20
1	A	115	LYS	20
1	A	130	ILE	20
1	A	135	GLN	20
1	A	140	GLU	20
2	B	65	ARG	20
2	B	68	PHE	20
2	B	72	VAL	20
2	B	78	ILE	20
1	A	19	PHE	19
1	A	99	TYR	19
2	B	73	ARG	19
1	A	68	PHE	19
1	A	3	GLN	17
1	A	22	ASP	17
1	A	24	ASP	17
1	A	77	LYS	17
1	A	101	SER	17
1	A	28	THR	15
1	A	48	LEU	15
1	A	125	ILE	15
1	A	37	ARG	14
1	A	74	ARG	14
1	A	111	ASN	13
1	A	117	THR	13
1	A	145	MET	13
1	A	90	ARG	12
1	A	127	GLU	12
1	A	30	LYS	11
1	A	84	GLU	9
1	A	89	PHE	9
1	A	31	GLU	8
1	A	54	GLU	8
1	A	69	LEU	8
1	A	148	LYS	8
1	A	78	ASP	8
1	A	81	SER	8
1	A	21	LYS	7

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Mol	Chain	Res	Type	Models (Total)
1	A	44	THR	6
1	A	51	MET	6
1	A	146	THR	6
2	B	74	LEU	6
1	A	75	LYS	5
1	A	72	MET	5
2	B	70	ARG	5
1	A	91	VAL	5
1	A	143	GLN	5
1	A	45	GLU	5
1	A	82	GLU	4
1	A	86	ARG	4
1	A	122	ASP	4
1	A	7	GLU	4
1	A	49	GLN	4
1	A	70	THR	4
1	A	83	GLU	4
1	A	47	GLU	4
1	A	133	ASP	3
1	A	13	LYS	3
1	A	94	LYS	3
1	A	67	GLU	3
1	A	71	MET	3
1	A	64	ASP	2
1	A	124	MET	2
2	B	63	ARG	2
1	A	42	ASN	2
1	A	41	GLN	2
1	A	2	ASP	1
2	B	62	ARG	1
1	A	136	VAL	1
1	A	8	GLN	1
1	A	95	ASP	1
2	B	60	THR	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 [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 86% for the well-defined parts and 85% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

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	2025
Number of shifts mapped to atoms	2025
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	174	-0.37 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	159	0.37 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}'$	171	-0.52 ± 0.09	Should be applied
^{15}N	169	0.10 ± 0.20	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 86%, i.e. 1967 atoms were assigned a chemical shift out of a possible 2300. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	853/864 (99%)	350/354 (99%)	338/342 (99%)	165/168 (98%)
Sidechain	1060/1308 (81%)	719/836 (86%)	336/414 (81%)	5/58 (9%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	54/128 (42%)	53/63 (84%)	0/62 (0%)	1/3 (33%)
Overall	1967/2300 (86%)	1122/1253 (90%)	674/818 (82%)	171/229 (75%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 85%, i.e. 2012 atoms were assigned a chemical shift out of a possible 2380. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	872/889 (98%)	358/364 (98%)	345/352 (98%)	169/173 (98%)
Sidechain	1086/1353 (80%)	737/864 (85%)	343/426 (81%)	6/63 (10%)
Aromatic	54/138 (39%)	53/68 (78%)	0/67 (0%)	1/3 (33%)
Overall	2012/2380 (85%)	1148/1296 (89%)	688/845 (81%)	176/239 (74%)

7.1.4 Statistically unusual chemical shifts ⓘ

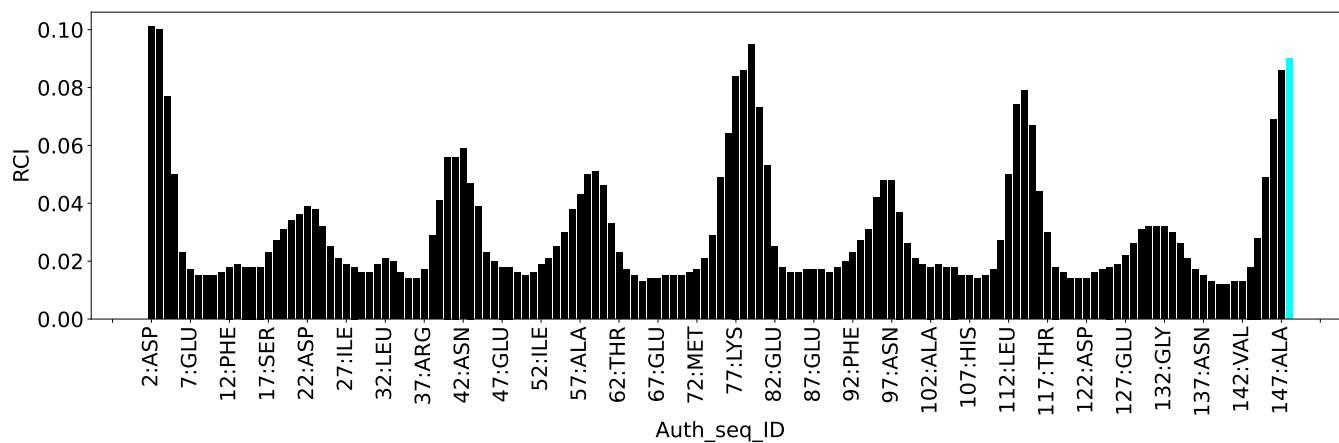
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	B	73	ARG	NE	110.85	76.53 – 92.65	16.3
1	B	79	ARG	NE	110.68	76.53 – 92.65	16.2
1	B	70	ARG	NE	110.03	76.53 – 92.65	15.8
1	A	93	ASP	HB2	1.39	1.41 – 4.01	-5.1

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. 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 B:

