



wwPDB NMR Structure Validation Summary Report

Apr 21, 2024 – 09:33 AM EDT


PDB ID : 2LV6
BMRB ID : 18556
Title : The complex between Ca-Calmodulin and skeletal muscle myosin light chain kinase from combination of NMR and aqueous and contrast-matched SAXS data
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Deposited on : 2012-06-29

This is a wwPDB NMR Structure Validation Summary 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:

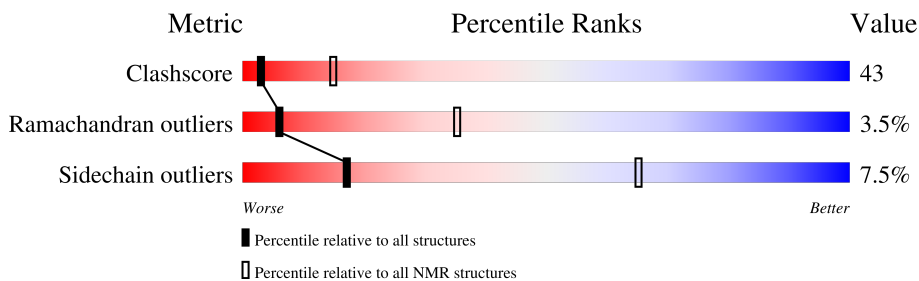
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

1 Overall quality at a glance

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

The overall completeness of chemical shifts assignment is 12%.

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 | 148 | 76% 18% 6% |
| 2 | B | 26 | 12% 54% 35% |

2 Ensemble composition and analysis

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2700 atoms, of which 1323 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 | 148 | 2257 | 713 | 1094 | 187 | 254 | 9 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| A | 99 | PHE | TYR | SEE REMARK 999 | UNP P62158 |
| A | 143 | THR | GLN | SEE REMARK 999 | UNP P62158 |

- Molecule 2 is a protein called Myosin light chain kinase 2, skeletal/cardiac muscle.

| Mol | Chain | Residues | Atoms | | | | | Trace |
|-----|-------|----------|-------|-----|-----|----|----|-------|
| | | | Total | C | H | N | O | |
| 2 | B | 26 | 439 | 134 | 229 | 43 | 33 | 0 |

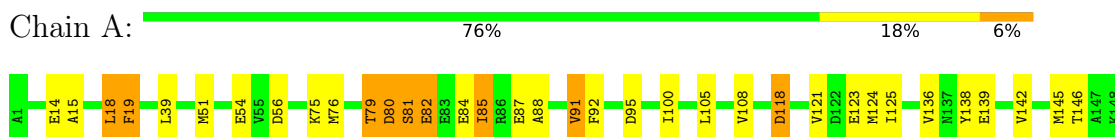
- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

| Mol | Chain | Residues | Atoms | |
|-----|-------|----------|-------|----|
| | | | Total | Ca |
| 3 | A | 4 | 4 | 4 |

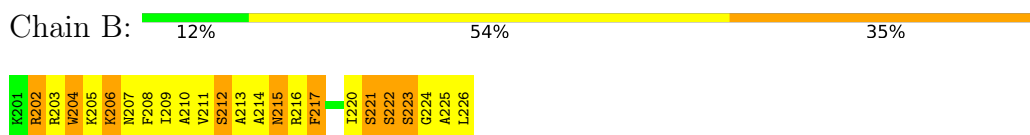
4 Residue-property plots [i](#)

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: Myosin light chain kinase 2, skeletal/cardiac muscle



5 Refinement protocol and experimental data overview

The models were refined using the following method: *rigid-body optimization, simulated annealing*.

Of the 1 calculated structures, 1 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

| Software name | Classification | Version |
|---------------|--------------------|---------|
| Custom | structure solution | |
| CNS | refinement | 1.0 |
| Custom | 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 | 288 |
| Number of shifts mapped to atoms | 288 |
| Number of unparsed shifts | 0 |
| Number of shifts with mapping errors | 0 |
| Number of shifts with mapping warnings | 0 |
| Assignment completeness (well-defined parts) | 12% |

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 | 0.55 | 1/1175 (0.1%) | 0.85 | 3/1576 (0.2%) |
| 2 | B | 0.94 | 0/213 (0.0%) | 0.92 | 0/279 (0.0%) |
| All | All | 0.62 | 1/1388 (0.1%) | 0.86 | 3/1855 (0.2%) |

All bond outliers are listed below.

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 1 | A | 19 | PHE | CB-CG | -5.41 | 1.42 | 1.51 |

All angle outliers are listed below. They are sorted according to the Z-score.

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|------|-------------|----------|
| 1 | A | 118 | ASP | CB-CG-OD1 | 5.55 | 123.30 | 118.30 |
| 1 | A | 56 | ASP | CB-CG-OD1 | 5.46 | 123.21 | 118.30 |
| 1 | A | 95 | ASP | CB-CG-OD1 | 5.25 | 123.02 | 118.30 |

There are no chirality outliers.

There are no planarity outliers.

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 | 1163 | 1094 | 1095 | 99 |
| 2 | B | 210 | 229 | 228 | 95 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes |
|-----|-------|-------|----------|----------|---------|
| All | All | 1377 | 1323 | 1323 | 117 |

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 43.

5 of 117 clashes are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Clash(Å) | Distance(Å) |
|------------------|-----------------|----------|-------------|
| 1:A:18:LEU:HB3 | 2:B:210:ALA:CB | 1.13 | 1.74 |
| 1:A:145:MET:SD | 2:B:205:LYS:HA | 1.04 | 1.93 |
| 1:A:18:LEU:HB3 | 2:B:210:ALA:HB2 | 0.94 | 1.35 |
| 1:A:145:MET:CE | 2:B:208:PHE:CB | 0.88 | 2.51 |
| 1:A:105:LEU:HD22 | 2:B:204:TRP:CH2 | 0.86 | 2.06 |

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 | 146/148 (99%) | 141 (97%) | 2 (1%) | 3 (2%) | 10 | 50 |
| 2 | B | 24/26 (92%) | 17 (71%) | 4 (17%) | 3 (12%) | 1 | 6 |
| All | All | 170/174 (98%) | 158 (93%) | 6 (4%) | 6 (4%) | 6 | 35 |

5 of 6 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 79 | THR |
| 1 | A | 80 | ASP |
| 1 | A | 82 | GLU |
| 2 | B | 221 | SER |
| 2 | B | 222 | SER |

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 | 126/126 (100%) | 121 (96%) | 5 (4%) | 35 83 |
| 2 | B | 21/21 (100%) | 15 (71%) | 6 (29%) | 2 18 |
| All | All | 147/147 (100%) | 136 (93%) | 11 (7%) | 17 65 |

5 of 11 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 18 | LEU |
| 1 | A | 76 | MET |
| 1 | A | 81 | SER |
| 1 | A | 85 | ILE |
| 1 | A | 91 | VAL |

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](#)

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 i

The completeness of assignment taking into account all chemical shift lists is 12% for the well-defined parts and 12% 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 i

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 | 288 |
| Number of shifts mapped to atoms | 288 |
| Number of unparsed shifts | 0 |
| Number of shifts with mapping errors | 0 |
| Number of shifts with mapping warnings | 0 |
| Number of shift outliers (ShiftChecker) | 0 |

7.1.2 Chemical shift referencing i

The following table shows the suggested chemical shift referencing corrections.

| Nucleus | # values | Correction \pm precision, ppm | Suggested action |
|------------------------|----------|---------------------------------|----------------------------|
| $^{13}\text{C}_\alpha$ | 0 | — | None (insufficient data) |
| $^{13}\text{C}_\beta$ | 0 | — | None (insufficient data) |
| $^{13}\text{C}'$ | 0 | — | None (insufficient data) |
| ^{15}N | 144 | 0.12 ± 0.40 | None needed (< 0.5 ppm) |

7.1.3 Completeness of resonance assignments i

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 12%, i.e. 288 atoms were assigned a chemical shift out of a possible 2321. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

| | Total | ^1H | ^{13}C | ^{15}N |
|-----------|---------------|---------------|-----------------|-----------------|
| Backbone | 288/878 (33%) | 144/358 (40%) | 0/348 (0%) | 144/172 (84%) |
| Sidechain | 0/1304 (0%) | 0/835 (0%) | 0/416 (0%) | 0/53 (0%) |

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| | Total | ¹ H | ¹³ C | ¹⁵ N |
|----------|----------------|----------------|-----------------|-----------------|
| Aromatic | 0/139 (0%) | 0/69 (0%) | 0/67 (0%) | 0/3 (0%) |
| Overall | 288/2321 (12%) | 144/1262 (11%) | 0/831 (0%) | 144/228 (63%) |

7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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:

