



## wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Dec 5, 2016 – 03:01 PM EST

PDB ID : 5M5I  
EMDB ID: : EMD-3445  
Title : Pseudo-atomic model of microtubule-bound S.pombe kinesin-5 motor domain in the AMPPNP state (based on cryo-electron microscopy experiment): the N-terminus conformation allows formation of a cover neck bundle.  
Authors : Goulet, A.; Moores, C.A.; Cross, R.A.  
Deposited on : 2016-10-21  
Resolution : 9.30 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20028442

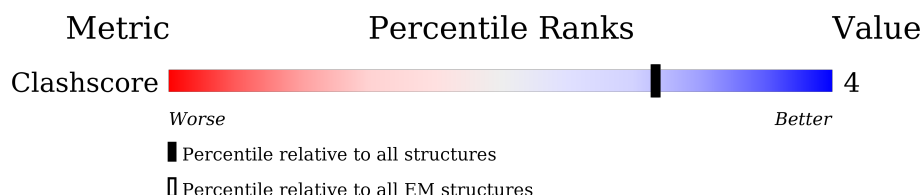
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*


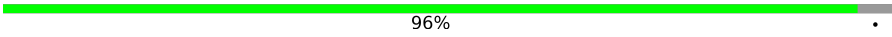
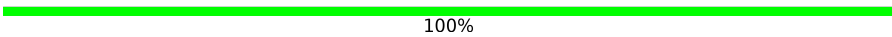
The reported resolution of this entry is 9.30 Å.

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<br>(#Entries) | EM structures<br>(#Entries) |
|------------|-----------------------------|-----------------------------|
| Clashscore | 114402                      | 924                         |

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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     | 451    |  90%                      • 9% |
| 2   | B     | 445    |  96%                      •    |
| 3   | C     | 369    |  100%                      •   |

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 1362 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tubulin alpha-1D chain.

| Mol | Chain | Residues | Atoms |     | AltConf | Trace |
|-----|-------|----------|-------|-----|---------|-------|
| 1   | A     | 412      | Total | C   | 0       | 412   |
|     |       |          | 412   | 412 |         |       |

There are 11 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| A     | 7       | ILE      | VAL    | conflict | UNP Q2HJ86 |
| A     | 114     | ILE      | LEU    | conflict | UNP Q2HJ86 |
| A     | 136     | SER      | LEU    | conflict | UNP Q2HJ86 |
| A     | 137     | VAL      | ILE    | conflict | UNP Q2HJ86 |
| A     | 265     | GLY      | ILE    | conflict | UNP Q2HJ86 |
| A     | 358     | GLU      | GLN    | conflict | UNP Q2HJ86 |
| A     | 437     | VAL      | MET    | conflict | UNP Q2HJ86 |
| A     | 448     | GLY      | GLU    | conflict | UNP Q2HJ86 |
| A     | 449     | GLU      | GLY    | conflict | UNP Q2HJ86 |
| A     | 450     | GLU      | ASP    | conflict | UNP Q2HJ86 |
| A     | 451     | TYR      | GLU    | conflict | UNP Q2HJ86 |

- Molecule 2 is a protein called Tubulin beta-2B chain.

| Mol | Chain | Residues | Atoms |     | AltConf | Trace |
|-----|-------|----------|-------|-----|---------|-------|
| 2   | B     | 426      | Total | C   | 0       | 426   |
|     |       |          | 426   | 426 |         |       |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| B     | 55      | ALA      | THR    | conflict | UNP Q6B856 |
| B     | 170     | VAL      | MET    | conflict | UNP Q6B856 |
| B     | 296     | ALA      | SER    | conflict | UNP Q6B856 |
| B     | 316     | VAL      | ILE    | conflict | UNP Q6B856 |

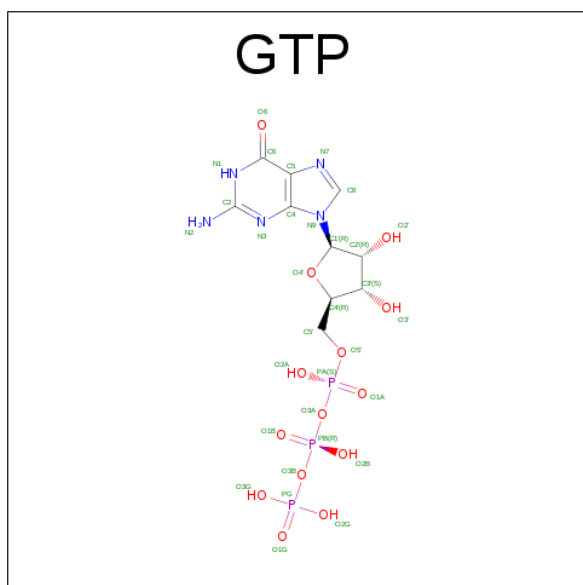
- Molecule 3 is a protein called Kinesin-like protein cut7.

| Mol | Chain | Residues | Atoms              | AltConf | Trace |
|-----|-------|----------|--------------------|---------|-------|
| 3   | C     | 369      | Total C<br>369 369 | 0       | 369   |

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

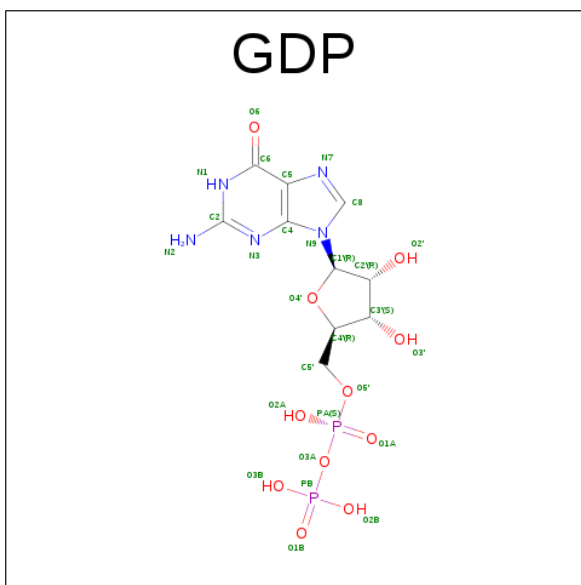
| Mol | Chain | Residues | Atoms           | AltConf |
|-----|-------|----------|-----------------|---------|
| 4   | A     | 1        | Total Mg<br>1 1 | 0       |
| 4   | C     | 1        | Total Mg<br>1 1 | 0       |

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



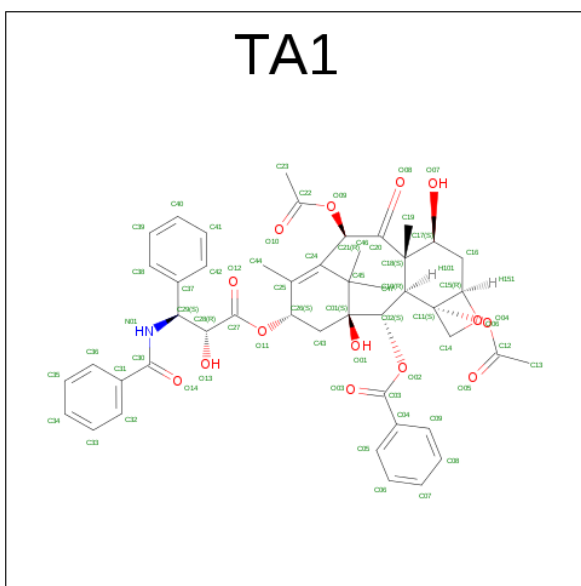
| Mol | Chain | Residues | Atoms                         | AltConf |
|-----|-------|----------|-------------------------------|---------|
| 5   | A     | 1        | Total C N O P<br>32 10 5 14 3 | 0       |

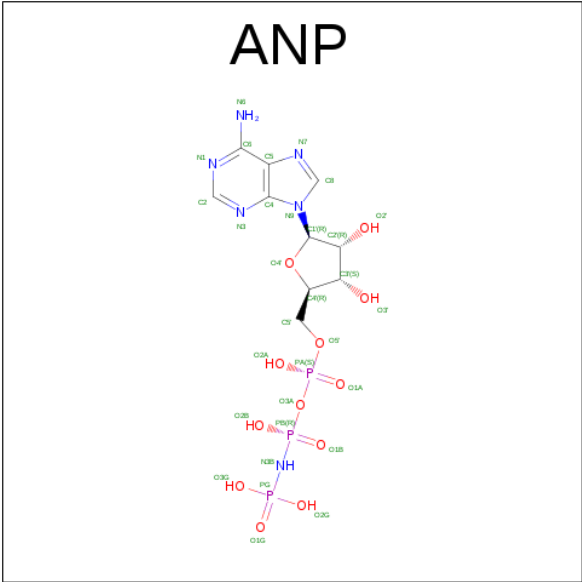
- Molecule 6 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).



| Mol | Chain | Residues | Atoms |    |   |    |   | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| 6   | B     | 1        | Total | C  | N | O  | P | 0       |
|     |       |          | 28    | 10 | 5 | 11 | 2 |         |

- Molecule 7 is TAXOL (three-letter code: TA1) (formula:  $C_{47}H_{51}NO_{14}$ ).



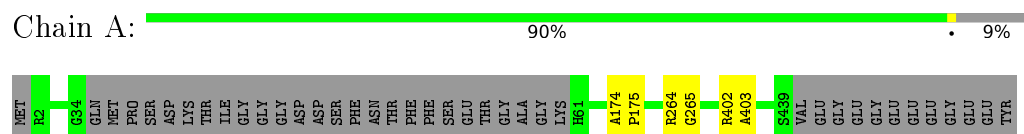


| Mol | Chain | Residues | Atoms |    |   |    |   | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| 8   | C     | 1        | Total | C  | N | O  | P | 0       |
|     |       |          | 31    | 10 | 6 | 12 | 3 |         |

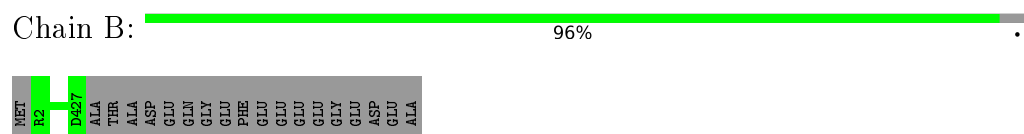
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-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 outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Tubulin alpha-1D chain



- Molecule 2: Tubulin beta-2B chain



- Molecule 3: Kinesin-like protein cut7



There are no outlier residues recorded for this chain.

## 4 Experimental information

| Property                             | Value               | Source    |
|--------------------------------------|---------------------|-----------|
| Reconstruction method                | SINGLE PARTICLE     | Depositor |
| Imposed symmetry                     | POINT, Not provided | Depositor |
| Number of particles used             | 144300              | Depositor |
| Resolution determination method      | FSC 0.5 CUT-OFF     | Depositor |
| CTF correction method                | Not provided        | Depositor |
| Microscope                           | FEI TECNAI F20      | Depositor |
| Voltage (kV)                         | 200                 | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | Not provided        | Depositor |
| Minimum defocus (nm)                 | 700                 | Depositor |
| Maximum defocus (nm)                 | Not provided        | Depositor |
| Magnification                        | 68000               | Depositor |
| Image detector                       | Not provided        | Depositor |



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, GTP, MG, ANP, TA1

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 root-mean-square of all Z scores of the bond lengths (or angles).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | A     | 412   | 0        | 0        | 3       | 0            |
| 2   | B     | 426   | 0        | 0        | 0       | 0            |
| 3   | C     | 369   | 0        | 0        | 0       | 0            |
| 4   | A     | 1     | 0        | 0        | 0       | 0            |
| 4   | C     | 1     | 0        | 0        | 0       | 0            |
| 5   | A     | 32    | 0        | 12       | 0       | 0            |
| 6   | B     | 28    | 0        | 12       | 0       | 0            |
| 7   | B     | 62    | 0        | 51       | 2       | 0            |
| 8   | C     | 31    | 0        | 13       | 1       | 0            |
| All | All   | 1362  | 0        | 88       | 6       | 0            |

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 4.

The worst 5 of 6 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:A:174:ALA:CA   | 1:A:175:PRO:CA   | 2.38                     | 1.01              |
| 7:B:502:TA1:H261 | 7:B:502:TA1:H463 | 1.80                     | 0.64              |
| 1:A:264:ARG:CA   | 1:A:265:GLY:CA   | 2.78                     | 0.61              |
| 1:A:402:ARG:CA   | 1:A:403:ALA:CA   | 2.83                     | 0.56              |
| 7:B:502:TA1:C26  | 7:B:502:TA1:H463 | 2.46                     | 0.46              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths |      |             | Bond angles |      |             |
|-----|------|-------|-----|------|--------------|------|-------------|-------------|------|-------------|
|     |      |       |     |      | Counts       | RMSZ | $\# Z  > 2$ | Counts      | RMSZ | $\# Z  > 2$ |
| 5   | GTP  | A     | 502 | 4    | 26,34,34     | 1.38 | 3 (11%)     | 29,54,54    | 2.33 | 5 (17%)     |
| 6   | GDP  | B     | 501 | -    | 24,30,30     | 2.64 | 8 (33%)     | 26,47,47    | 3.29 | 8 (30%)     |
| 7   | TA1  | B     | 502 | -    | 68,68,68     | 1.92 | 19 (27%)    | 102,105,105 | 1.30 | 8 (7%)      |
| 8   | ANP  | C     | 502 | 4    | 29,33,33     | 1.99 | 7 (24%)     | 26,52,52    | 3.78 | 13 (50%)    |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions     | Rings   |
|-----|------|-------|-----|------|---------|--------------|---------|
| 5   | GTP  | A     | 502 | 4    | -       | 0/18/38/38   | 0/3/3/3 |
| 6   | GDP  | B     | 501 | -    | -       | 0/12/32/32   | 0/3/3/3 |
| 7   | TA1  | B     | 502 | -    | -       | 0/41/127/127 | 0/5/7/7 |
| 8   | ANP  | C     | 502 | 4    | -       | 0/13/38/38   | 0/3/3/3 |

The worst 5 of 37 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms   | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 7   | B     | 502 | TA1  | C08-C07 | -4.84 | 1.26        | 1.38     |
| 6   | B     | 501 | GDP  | PB-O2B  | -4.21 | 1.40        | 1.54     |
| 8   | C     | 502 | ANP  | O5'-C5' | -2.63 | 1.34        | 1.44     |
| 7   | B     | 502 | TA1  | C04-C03 | -2.43 | 1.44        | 1.49     |
| 8   | C     | 502 | ANP  | PB-O3A  | -2.12 | 1.56        | 1.59     |

The worst 5 of 34 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms       | Z      | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-------------|--------|-------------|----------|
| 8   | C     | 502 | ANP  | N3-C2-N1    | -10.38 | 120.72      | 128.87   |
| 6   | B     | 501 | GDP  | C6-C5-C4    | -9.88  | 109.56      | 120.86   |
| 5   | A     | 502 | GTP  | C5-C6-N1    | -7.77  | 113.37      | 123.52   |
| 8   | C     | 502 | ANP  | C5'-C4'-C3' | -6.23  | 91.11       | 115.20   |
| 8   | C     | 502 | ANP  | PA-O3A-PB   | -6.00  | 110.95      | 132.71   |

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 7   | B     | 502 | TA1  | 2       | 0            |
| 8   | C     | 502 | ANP  | 1       | 0            |

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.