Microtubule structure

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Over the past year or so, there have been a number of advances regarding the structure and assembly of microtubules. Examples are kinesin-decorated microtubules (akin to decorated actomyosin), the direct visualization of GTP at microtubule ends, the expression of tubulins via chaperones, further effects of microtubule-associated proteins, drugs, and nucleotides on dynamic instability, and the beginning of a high resolution structure analysis by electron diffraction.

Introduction

Microtubules are filamentous structures involved in many aspects of cell structure, motility, and transport. A microtubule consists of a hollow cylinder of tubulin subunits (α, β, and their isoforms) to which a variety of proteins may be attached, notably the microtubule-based motor proteins (dynein, kinesin, and related motors) and the microtubule-associated proteins (MAPs) that play a more structural role (MAP1, MAP2, tau, etc.). Thus, a comprehensive review of microtubule structure should consider the tubulin, motor proteins, MAPs, and their effects on microtubule functions (dynamics of assembly, transport mechanisms, interactions with other cell components). Each of these areas has diversified enormously in recent years. Here, we will mainly restrict ourselves to novel aspects of microtubule structure, and mention other proteins only in this context. For other aspects, we refer the reader to recent reviews on non-motor MAPs [1,2], motor proteins [3,4], tubulin isoforms [5], and microtubule assembly and dynamics [6,7]. A collection of reviews on microtubule-related proteins can be found in [8], a recent review of structural aspects in [9], and a useful map of antibody epitopes of tubulin in [10].

GTP and microtubule ends

During the past year, several long-standing open questions about microtubule structure have been addressed by new methods. The building blocks of microtubules are the α-β-heterodimers of tubulins, arranged in a polar fashion along the 13 protofilaments (Fig. 1). This means that microtubules as a whole are polar; the plus end is usually distal to nucleating centers (such as centrosomes, or basal bodies) and is more dynamic than the minus end, which is attached to nucleation centers and is less dynamic when free in solution. One question was: Which end terminates with α-tubulin and which with β-tubulin?

Another well established property of tubulin is that each subunit can bind GTP. The GTP bound to α-tubulin appears to have a structural role and cannot be exchanged. In contrast, the GTP on β-tubulin can be exchanged against GTP from the solution. It is the α-tubulin associated GTP that is hydrolyzed to GDP during microtubule assembly, so that the β-tubulin subunits in the interior of a microtubule contain GDP — this hydrolysis provides the driving force for microtubule dynamics (Fig. 2). This raises two questions about the nature of GTP in the microtubule. First, does β-tubulin-GTP exist at all in a microtubule? A 'GTP-cap' at microtubule ends had been postulated on theoretical grounds, but experimentally it has remained elusive and in any case is very small, perhaps no more than one layer of subunits deep (reviewed in [6,7]). Second, if a microtubule indeed contains GTP, is it on the plus or minus end?

To answer these questions, Mitchison [11°] constructed GTP analogues that could be coupled to beads that are visible by light microscopy. The beads were found on the plus end of microtubules, showing that this is the end where β-tubulin-GTP is incorporated. Regarding polarity, a natural interpretation was that the terminal subunits on the plus end are β-tubulin in association with bound GTP (Fig. 2a). However, another possibility is the inverted arrangement (Fig. 2b) where the terminal layer is α-tubulin, with β-tubulin buried inside but still retaining its bound GTP. This latter model would be consistent with the proposal of Oakley [12]: He demonstrated that there is a third variant, γ-tubulin, which is located in nucleating centers at, or near, the minus ends, and that there is a genetic linkage between γ- and β-tubulin. This would imply that the terminal crown at the minus end is β-tubulin (Fig. 2b). Image reconstruction of microtubules decorated with kinesin

Abbreviation

MAP—microtubule associated protein.

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Fig. 1. Model illustrating some new structural features of microtubules. The hollow cylinder consists of 13 protofilaments, each consisting of a string of alternating tubulin subunits, α (dark shade) and β (light shade). The stagger between protofilaments is 0.92 nm, generating a left-handed three-start helix (direction indicated on left, 3) as well as other families of helices. A microtubule is polar, the plus end (top) is usually distal, the minus end (bottom) proximal to a microtubule nucleating center. The exchangeable GTP site is on α-tubulin; this GTP becomes hydrolyzed to GDP upon incorporation of the subunit into a microtubule. This figure emphasizes two points: first, that the plus end terminates with a crown of α-subunits (dark shade, top), which implies that the minus end would end with β-subunits (compare with Fig. 2b); second, microtubules can be decorated with one kinesin head per tubulin dimer, bound to β-tubulin (light shade, see Fig. 3). The axial distance between kinesin heads is 8 nm, consistent with the length of a dimer. The dimers are aligned along the three-start helix, consistent with a ‘B-lattice’ of microtubules but not with the ‘A-lattice’ [16**]. Since a 13-protofilament microtubule with a B-lattice cannot be symmetrical there must be a discontinuity (arrow); however, its position and course along the microtubule is currently unknown.

now suggests that the polarity of Fig. 2b is the correct one, that is, α-tubulin at the plus end and β-tubulin at the minus end (as shown in Fig. 1; Y-H Song and E Mandelkow, unpublished data). This may seem counterintuitive since a higher dynamic activity is observed at the plus end (for a detailed analysis of rates and their variability see [13,14]), but it could presumably be explained if a high resolution structure of tubulin were available.

Fig. 2. Alternative models of protofilament polarity. The light shade represents β, and the dark shade represents α-tubulin. In both cases the microtubule-bound GTP is on the plus end, whereas the interior subunits contain GDP [11**]. On the minus end we show a subunit of γ-tubulin as this is involved in nucleating microtubules off the microtubule organizing centers [12,28]. (a) In the left model, the plus end has a terminal β-subunit carrying GTP; the minus end has a terminal α-subunit. This model would naturally explain the observations of Mitchison [11**] but would contradict those of Oakley [12] (unless the linkage between γ- and β-tubulin is more indirect). (b) The model on the right shows the opposite polarity (α on plus, β on minus end, as in Fig. 1). This would fit the assumptions of Oakley that α-subunits lie at the plus end, but not those of Mitchison, except if one assumes that the terminal GTP may be partially buried inside a protofilament.

Decoration of microtubules by kinesin and the microtubule surface lattice

A second issue is that of the tubulin lattice within microtubules. Amos and Klug [15] had originally proposed the ‘A’ lattice for the A-microtubules of flagellar outer doublets and the ‘B’ lattice for B-tubules (for a review of flagellar structure see Murray, this issue pp 180–186). Both lattices have the same polar arrangement of protofilaments, but they differ in the stagger between protofilaments; the A-lattice has a stagger of about 3.1 nm, the B-lattice has about 0.9 nm (as in Fig. 1). With 13 protofilaments, only the A-lattice can form a helically symmetric microtubule, and this was therefore the favored model. By contrast, the B-lattice requires some kind of discontinuity which
seems somewhat awkward and difficult to rationalize (one possibility is drawn in Fig. 1). Over the years, several authors had argued that the B-lattice was really the predominant one, but the evidence on which this argument was based was derived from the contrast between α- and β-tubulin which is very weak and therefore not entirely satisfactory.

This situation has now changed because the contrast between α- and β-tubulin can be dramatically enhanced by labeling β-tubulin with the head domain of the motor protein, kinesin, expressed in recombinant form in Escherichia coli (this is equivalent to the distinguishing of α- and β-tubulin in Fig. 1 by different shades). Chemical crosslinking has demonstrated that the kinesin head binds to β-tubulin, implying a stoichiometry of one head per tubulin dimer. In a manner consistent with this, the axial spacing of kinesin head along microtubules is 8 nm (the dimer spacing). Diffraction analysis has also shown that the lattice of dimers is of the B-type [16**]. In cryoelectron microscopy, the head appears to form an angle with the microtubule wall and has an 8 nm axial spacing as well [17]. We have now extended these studies by decorating flagellar doublet microtubules, both types of central pair microtubules, and extensions of brain tubulin polymerized onto axonemal microtubules; in each case the results show the B-lattice architecture (Y-H Song and E Mandelkow, unpublished data).

The consequences of microtubules adopting B-lattice structure are threefold. First, microtubules have a discontinuity somewhere in their wall; the exact nature of the discontinuity and its function — if any — is not yet known. This holds even for microtubules whose protofilament number differs from 13, and even in cases where protofilaments have a supertwist (see below). Second, the ends of microtubules can be almost even (as in Fig. 1), rather than ragged, as would be required for the A-lattice. Third, models of the motile machinery of a flagellum need to be adapted to the B-lattice, since this affects the way in which the associated proteins and motors can be arranged on the microtubules.

Microtubule structure and kinesin-induced motility

The microtubule surface can be viewed in terms of tubulin monomers, dimers, protofilaments, or helices. As kinesin or dynein move along microtubules, the question is, which of these structural units are important for motility? For example, does the path of kinesin follow the protofilaments or some other helix, or are these constraints of no importance? This problem was recently addressed by two studies, which both show...
that the path of kinesin is parallel to the protofilaments. In our study [18], different polymorphic assembly forms of tubulin were tested for their ability to support movement (microtubules, open microtubule walls, zinc-induced sheets, duplex tubules). We concluded that the interaction with kinesin occurred only with the outside surface of a protofilament, and not between antiparallel protofilaments (which is the predominant arrangement in zinc-induced sheets) suggesting that a protofilament represented the minimal track. Ray et al. [19] reached a similar conclusion by observing microtubules with 14 or more protofilaments which have a super-twist; consequently these microtubules rotated during their advance, emphasizing a path along protofilaments.

The spacing of structural units along the protofilaments is 4 nm (tubulin monomers) or 8 nm (dimers). As before, the question is whether one of these spacings represents the step size, or whether the subunit structure is only of secondary importance (this latter possibility is being debated for the analogous case of actomyosin motility, e.g. [20]; that is, is the movement quantized or not? The decoration of the protofilaments by kinesin heads at 8 nm intervals points to a basic role for the tubulin dimer, but this need not be the case during actual motion. To answer this question, sophisticated methods of light microscopy with nm resolution had to be developed; these have been used to track the motion of beads covered with motor proteins along microtubules. Some time ago, Gelles et al. [21] presented evidence for a 4 nm step size for kinesin driven movement. More recently, Svoboda et al. [22**] used a laser-trap technique to show a predominant step size of 8 nm; this would be consistent both with the dimer spacing and with the decoration with kinesin heads. Intermediate results were presented by Kamimura and Kamiya [23**] who observed both 4 nm and 8 nm components for the case of dynein. The common aspect of these data is that microtubule motors are quantized, with steps in the tubulin dimer (and perhaps monomer) range.

Reactions inside a microtubule

When discussing microtubule structure and assembly, one usually pays attention to the ends, without much regard for the interior. Some years ago there had been a debate on whether assembly could take place by addition of subunits to the sides, but this view fell into disgrace when microscopic techniques improved, and it was shown that dynamic instability took place only at the ends. However, new evidence shows that the interior can be more dynamic than previously thought. Intriguing new proteins, or protein complexes, that are capable of severing microtubules have been described [30,31*,32]. This would provide a direct route for the redistribution of microtubule lengths during restructuring of the cell, such as occurs during mitosis, rather than relying just on the higher degree of dynamic instability that also accompanies this process [33].

A second advantage of internal breakage is that it greatly speeds up microtubule disassembly (down to the millisecond range). In some marine organisms this takes place in preformed regions and in a Ca2+-dependent fashion [34].

Weak points inside a microtubule can also be observed directly in vitro. In one case, Chretien et al. [35] used cryoelectron microscopy (which allows the counting of protofilaments) to demonstrate lattice defects where the protofilament number changed abruptly within microtubules (say, from 13 to 14), presumably reflecting a 'construction error' made during assembly. A second example is that described by Dye et al. [36], who capped microtubules at both ends by flagellar axonemes, then washed the remaining tubulin out and found that these microtubules were very stable, except for the cases where a break point developed inside; this internal loss of subunits could be reversed by adding tubulin back again. In the same context it should be recalled that protofilaments of disassembling microtubules can coil and fray apart from the end to points deep inside the microtubule, and even at bends inside a microtubule [37]. All of this argues that bending, breaking, or severing occurs both in vitro and in vivo, and probably starts by nicking the wall between two protofilaments and then exploiting their inherent tendency to coil apart.
Higher order structure

Since microtubules are thought to function as "stays", stabilizing the shapes of cells, their flexibility or stiffness is of particular interest. Dye et al. [38] studied this by video microscopy and concluded, for example, that MAPs make microtubules stiffer (as one might expect) but that the drug taxol makes microtubules more flexible (which is somewhat surprising, considering that taxol is a strong microtubule stabilizer). On the other hand, Gittes et al. [39] observed the opposite effect with taxol (i.e. microtubules became stiffer). Whether or not these discrepancies can be explained by the different experimental protocols remains to be seen.

Another way to stiffen microtubules is to pack them into bundles. This process can be enhanced by transfecting cells with cDNAs for MAPs such as MAP2, MAP2c, or tau. These MAP proteins have homologous microtubule-binding domains (near the carboxyl terminus) but differ greatly in the size of the amino-terminal 'projection' domain. The dominant effect on the spacing between microtubules in a bundle appears to be the size of the projection domain; for example, MAP2 keeps microtubules further apart than tau [40**,41]. Whether or not these MAPs actually cross link microtubules at a given spacing is another issue. Weisshaar et al. [42] argue that bundles are induced when microtubule nucleation in the cytoplasm becomes highly efficient, leading to a parallel liquid crystal like arrangement. This depends possibly on the nucleation activity of MAPs, but not necessarily on their cross-linking activity. The liquid crystal view of a microtubule bundle is supported by the experiments of Miyata and Hotani [43] who succeeded in polymerizing microtubules from pure tubulin inside a liposome which produced 'neurite-like' protrusions on the surface.

Ordered structures on a much larger scale, extending even into the visible range were reported by Tabony and Job [44] who showed that domains within a reaction vessel spontaneously acquire alternating microtubule orientations under the influence of a weak field, which could explain the role of microtubules in biological gravitropism.

Tubulin, nucleotides, and post-translational modifications

Tubulin binds GTP, but when its sequence is compared to the consensus sequences of other G-proteins there is a discrepancy — the glycine-rich loop region favored so far for binding the phosphate moiety (Gly-Gly-Gly-Thr-Gly-Ser-Gly; residues 140-146 of β-tubulin) is one residue too long and is on the 'wrong' side of the region thought to bind the base (around residue 70), as judged by chemical cross-linking and homology with other G-proteins; for details see Linse and Mandelkow, [45]. Shivanna et al. [46] have now found that GTP can also be crosslinked to Cys12 of β-tubulin. This confirms that the exchangeable GTP is indeed bound to β-tubulin and suggests that the tubulin chain between residues 12 and 70 loops around the guanine-binding pocket. Unexpected support for the GTP-binding function of the glycine-rich loop of tubulin comes from the observation that it matches very well with a sequence in the bacterial FtsZ protein. This protein is also a GTPase, self-assembles, and has a function in bacterial cell division [47]. It may therefore turn out that tubulin, FtsZ, and perhaps other proteins fall into one class of GTP-binding proteins which is distinct from the better known G-protein class. These considerations may eventually help in building computer models of tubulin based on other known structures.

There has been a long-standing debate on whether, and how well, tubulin-GDP (Tu-GDP) can assemble into microtubules. GTP clearly drives assembly much more efficiently than GDP, but several authors have shown that growing microtubules can accommodate a fraction of Tu-GDP subunits. Diaz and Andreu [48] have now succeeded in growing microtubules entirely from Tu-GDP, making use of the stabilizing function of taxotere, a derivative of the anti-cancer drug taxol (which inhibits cell division by blocking microtubule dynamics). They also found a stoichiometry of one taxotere binding to every tubulin dimer, indicating that α- and β-tubulin do not both bind the drug. In this context it is notable that the binding site of colchicine, another well-known antimotic drug, has been localized to near the amino terminus of β-tubulin [49].

Given that nucleotides affect the stability of microtubules, one would expect that they also affect the conformation of tubulin. This conformation is not visible at the level of single tubulin molecules, but it can be deduced from the extent to which tubulin protofilaments coil. Thus, assembly-competent tubulin tends to be in the 'straight' conformation as the protofilaments of growing microtubules are straight, whereas non-competent subunits would be in the 'coiled' conformation as shrinking microtubules have coiled protofilaments at their ends (see Mandelkow et al. [37]). Furthermore, since protofilaments grow by addition of Tu-GTP and shrink by release of Tu-GDP, it was anticipated that the conformation was related to the nucleotide status. This was demonstrated by Hyman et al. [50], who used the GTP analogue α-β-methylene-GTP (GMP CPP) which is hydrolyzed only slowly so that most microtubules are in the 'triphasate' state. These microtubules were very stable, and in addition had straight ends, emphasizing that conformation, nucleotide status, and assembly competence of tubulin were linked to one another.

The diversity of post-translational modifications of tubulin continue to be a source of surprise, but also of frustration since their influence on microtubule behavior remains elusive. Phosphorylation of β-tubulin, acetylation of α-tubulin, detyrosination and re-tyrosination of α-tubulin, or glutamylation of α- and β-tubu-
lin have all been described; many aspects of modification have been reviewed by Guenette and Solomon [5]. In particular, the addition of Glu residues to an already highly acidic carboxy-terminal region is quite unique, as is the removal and attachment of the carboxy-terminal Tyr by a tubulin carboxypeptidase and a tubulin tyrosine ligase, respectively. The latter enzyme has now been described in detail [51]. Since the modifications on α-tubulin are only a few residues apart (at Glu445 and Tyr451, respectively), one might suspect that there is a cross-talk between them. This, however, is not the case, as both modifications occur independently of one another [52]. There is increasing evidence that the diversity of tubulins, both on the level of expressed isoforms and their posttranslational modifications, is related to the differentiation of brain cells. For example, neurons contain six α- and six β-tubulin isoforms; they can receive sidechains of up to six Glu residues, the longer ones being found preferentially in assembled microtubules [53]. By contrast, the marginal band of avian erythrocytes contains only one α- and one β-tubulin unit each (α1 and β6), with no acetylation at Lys40(α) or glutamylation at either α- or β-tubulin, making this an unusually homogeneous source of tubulin [54]. As mentioned later, this tubulin also shows very little dynamic instability, suggesting that such behavior depends on tubulin isoforms and their modifications more than on the MAPs [55].

**Effects of microtubule-associated proteins on microtubules**

MAPs affect the structure and behavior of microtubules in a variety of ways. The best known effect is that they bind to microtubules and stimulate their overall assembly (hence their name). On the level of single microtubules observed by video microscopy, MAPs enhance those parameters leading to more stable microtubules (e.g., growth rate, rescue frequency) and decrease the opposite parameters, such as catastrophe [56–58]. Since phosphorylation reduces the binding of MAPs to microtubules its effect tends to be similar to the withdrawal of MAPs [56,59]. One caveat is that these global explanations may not be applicable in detail: certain tubulin isoforms can strongly reduce dynamic instability so that MAPs may not always be required to explain microtubule stability, as in the case of avian erythrocyte [55] or sea urchin egg [60] microtubules; and phosphorylation sites and the corresponding kinases may differ greatly in how they affect the binding of MAPs to microtubules [61].

The mode of MAP binding to microtubules is quite variable, depending both on the type of MAP used and on its subdomains. Binding appears to be cooperative in the case of MAP2 [62] but not in the case of tau [63,61]; this is somewhat surprising, considering that there are repetitive microtubule binding sequences in tau.

As mentioned above, the size of the amino-terminal projection domain of MAPs determines the spacing between microtubules in a bundle [40**,41]. The generation of many microtubules in a small volume is related to the nucleation activity of MAPs, in particular of certain domains such as the microtubule-binding repeats and the adjacent proline-rich basic domain (see [64,65] for the case of tau, and [66] for the case of MAP4). In the context of the spacing between microtubules, it is interesting to note that MAPs can also interact with one another. In particular, MAP2, MAP2c, or tau can form antiparallel dimers [67], and the repeat domain of tau can even self-assemble into paired helical filaments similar to those occurring in the tangles seen in Alzheimer's disease [68**]. Whether or not this MAP–MAP interaction plays a role in the stabilization of microtubule bundles is not clear at present.

Despite the many effects of MAPs it is worth noting that they faithfully preserve the cylindrical structure of microtubules. To appreciate this one should recall that tubulin can assemble into an unusually large variety of polymorphic structures, which are often not cylindrical at all, depending on the presence of various cofactors or drugs (the example of zinc-induced sheets is described below). One subtle variable which changes with MAP concentration is the number of protofilaments; microtubules assembled from pure tubulin tend to have 14 or more protofilaments, while MAPs favor 13; with taxol the number becomes even less. These variations can be observed in solution by cryoelectron microscopy and X-ray scattering [69].

One should also mention that there are other types of microtubule-associated proteins which perform more specialized and localized functions. One example is the high molecular weight complex which plugs the ends of ciliary microtubules, a component of which (97 kDa) has now been identified [70].

**Theory and computer modelling of microtubule structure and dynamics**

For most self-assembling biopolymers one of the main challenges is to understand how the correct structure is initiated (nucleation) and how it then grows by addition of subunits (elongation). Microtubules present an additional problem because they are not stable, even after assembly has reached an overall 'steady state'. This behavior is called dynamic instability, while the transitions between growth and shrinkage are 'catastrophe' and 'rescue', respectively (for reviews see [67,71,72]). There is general agreement that this instability is related to GTP hydrolysis, whereby an irreversible chemical reaction is coupled to microtubule assembly, but this in itself does not suffice to explain the phenomenon. Several recent papers have addressed different aspects; these are discussed below.

Martin et al. [73] elaborated the lateral cap model, which assumes that microtubule dynamics is determined by the terminal subunits and their immediate environment. While the previous formulation of the
model was based on the A-lattice (as described above), the new treatment is lattice-independent and thus more general. Dogterom and Leibler [74] consider the problem of how growing and shrinking microtubules can coexist in solution, special attention being given to the diffusion of subunits by which microtubule ends can potentially 'communicate' with one another. There is, however, a debate on whether diffusion can play a crucial role in microtubule dynamics, as it is a very fast process, especially when compared to the rates of dynamics at microtubule ends (see commentary by Bayley [75]). Glikson et al. [33] consider why interphase and mitotic microtubules differ in terms of dynamics, growth rates, and length distribution, and account for this by altered rates of catastrophe, rescue, and nucleation. Finally, we have [76] addressed the question of microtubule oscillations, where microtubules grow and shrink in synchrony (this is still the only example of a biological oscillator based on a self-assembling polymer). The maintenance of synchrony throughout a solution can be explained by cooperativity between subunits at microtubule ends and signalling between microtubules via their disassembly products.

Prospects for a high resolution structure of tubulin

Statements such as "Tubulin crystals suitable for a high resolution X-ray analysis are not yet available..." belong to the inventory of review articles on tubulin and, unfortunately, this is still true today. However, there now appears to be an alternative route: Downing and Jones [77] have succeeded in growing extremely well-ordered zinc-induced tubulin sheets. These are polymorphic forms of tubulin assembling in two-dimensional crystals where protofilaments have alternating polarities (unlike a microtubule where the polarities are the same, see [78]). Their electron diffraction patterns extend into the 0.4 nm region. They show, for example, that there must be β-pleated sheets running across a protofilament. Such specimens have the promise of leading to a high resolution structure, by combining tilt series in the electron microscope, low dose imaging, and cryotechniques.

Conclusion

Microtubule research continues to be an exciting area at the interface between cell biology, molecular biology, and biochemistry. Microtubules are small enough to be 'molecular', yet large enough to be seen in a light microscope. It is fascinating to watch them crawling under the influence of some motor protein, growing or shrinking at their own restless pace, or being severed by molecular scissors. Microtubules interact with a host of other cell components which often become observable only because of that. Due to their complexity, microtubules have been difficult to deal with (to quote one famous biochemist, "if you deal with dirty proteins you get dirty results"). Added to this is their notorious lability, which explains why many structural questions had existed for so long, but just haven't been solved. Now there seems light at the end of the tunnel: high resolution structures are coming up, and the folding problem is on the way to a solution. Finally, one should remember that microtubules are important for biomedical research: cancer drugs like taxol were discovered through their action on microtubules, and proteins involved in Alzheimer's disease were identified as microtubule-associated proteins — reason enough to continue.

Acknowledgements

We are grateful to YH Song and A Marx for the diagrams.

References and recommended reading

Papers of particular interest published within the annual period of review have been highlighted as:
• of special interest
• of outstanding interest
The exchangeable GTP is made visible by coupling it to beads, showing that it is located at the plus end of microtubules (see Fig. 2).
178 Macromolecular assemblages


Demonstration that kinesin binds to β-tubulin; labeling of microtubules with kinesin head at a ratio of 1 kinesin per tubulin dimer; analysis of microtubule surface lattice as a B-Surface (see Fig. 1).


The step size of kinesin-dependent motion along microtubules is 8 nm.


High resolution analysis of the dynein-dependent motion of flagellar microtubules, showing step sizes with components of 4nm and 8 nm.


High resolution analysis of the dynein-dependent motion of flagellar microtubules, showing step sizes with components of 4nm and 8 nm.


The sizes of the N-terminal projection domains of MAPs determine spacings between microtubules.


A new severing protein capable of cutting a microtubule.


The sizes of the N-terminal projection domains of MAPs determine how far microtubules are spaced.


75. Highly ordered two-dimensional arrays of tubulin analyzed by electron microscopy show near-atomic structural resolution.