Lis1 Acts as a “Clutch” between the ATPase and Microtubule-Binding Domains of the Dynein Motor

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SUMMARY

The lissencephaly protein Lis1 has been reported to regulate the mechanical behavior of cytoplasmic dynein, the primary minus-end-directed microtubule motor. However, the regulatory mechanism remains poorly understood. Here, we address this issue using purified proteins from Saccharomyces cerevisiae and a combination of techniques, including single-molecule imaging and single-particle electron microscopy. We show that rather than binding to the main ATPase site within dynein’s AAA+ ring or its microtubule-binding stalk directly, Lis1 engages the interface between these elements. Lis1 causes individual dynein motors to remain attached to microtubules for extended periods, even during cycles of ATP hydrolysis that would canonically induce detachment. Thus, Lis1 operates like a “clutch” that prevents dynein’s ATPase domain from transmitting a detachment signal to its track-binding domain. We discuss how these findings provide a conserved mechanism for dynein functions in living cells that require prolonged microtubule attachments.

INTRODUCTION

To help create the complex internal organization within eukaryotic cells, the myosin and kinesin motor protein families have undergone widespread gene duplication and evolution, presumably so they can fulfill particular functional niches (e.g., transporting cargos, bearing tension, and sliding filaments; Vale, 2003). Accordingly, their members show a spectrum of properties, with different catalytic rates and structural adaptations. A striking departure from this pattern is one of the least understood cytoskeletal motors, cytoplasmic dynein (Figure 1A). This one motor powers nearly all movement toward the microtubule minus end in most eukaryotic cells. Its many functions include transporting and positioning diverse cargos (e.g., mRNAs, proteins, and organelles) during interphase, exerting tension between the microtubule network and cell cortex during cell migration, and helping to construct the spindle during mitosis and meiosis (Karki and Holzbaur, 1999; Vale, 2003). Regulation of dynein is therefore critical, and human diseases arise from its dysfunction (Gerdes and Katsanis, 2005). In addition to task-specific regulators, cytoplasmic dynein has three ubiquitous cofactors that are required for most, if not all, of its functions across eukaryotes (Kardon and Vale, 2009; Vallee et al., 2012): the dynactin complex and two proteins analyzed in this study, Lis1 and Nudel.

Dynein’s ATP-hydrolyzing and track-binding elements are key potential targets for regulation and differ in three significant ways from those of myosin and kinesin. First, rather than a compact fold, dynein’s ATPase domain is ring shaped, containing six covalently linked AAA+ modules (Neuwald et al., 1999; Roberts et al., 2009). Second, rather than a single site of ATP binding/hydrolysis, four of dynein’s AAA+ modules (AAA1–AAA4) can bind nucleotide, with AAA1 being the main site of ATP hydrolysis (Cho et al., 2008; Gibbons et al., 1991; Kon et al., 2004, 2012; Schmidt et al., 2012). Finally, instead of close integration of the track-binding and hydrolysis sites, these domains in dynein are spatially separated by a 10 nm intramolecular coiled-coil stalk, which protrudes from AAA4 (Cho and Vale, 2012).

Together, dynein’s architectural features make interdomain communication a central part of its mechanism and an additional potential target for regulation. For example, structural changes within dynein’s AAA+ ring, driven by ATP binding and hydrolysis at AAA1, produce cyclic changes in the affinity of the microtubule-binding domain at the stalk’s tip (Imamura et al., 2007; Kon et al., 2004, 2009). In some distantly related AAA+ ATPases, pulses of structural changes are transmitted around the ATPase ring with the assistance of arginine finger motifs that reach from one subunit into the active site of the neighboring subunit (Erzberger and Berger, 2006). However, the extent to which dynein uses similar mechanisms is unknown.

A strong candidate for altering the structural changes within dynein is the evolutionarily conserved protein Lis1. Mutations in the human LIS1 gene cause classical lissencephaly, a severe brain development disorder (Reiner et al., 1993). In brain slices
and cultured cells, perturbing Lis1 levels causes defects in dynein-mediated processes such as nuclear migration, mitosis, and cargo transport (Ding et al., 2009; Faulkner et al., 2000; Pandey and Smith, 2011; Smith et al., 2000; Tai et al., 2002; Tanaka et al., 2004; Tsai et al., 2007; Yi et al., 2011). Like cytoplasmic dynein’s force-generating subunit, Lis1 is dimeric. Each Lis1 protomer contains an N-terminal dimerization domain and a C-terminal β-propeller domain that binds to the dynein motor domain (Figure 1A; Sasaki et al., 2000; Tai et al., 2002; Tarricone et al., 2004). A coiled-coil protein, Nudel (or its parologue, NudE), is thought to further tether Lis1 to dynein (McKenney et al., 2010), allowing Lis1 to function at lower concentrations in vivo (Efimov, 2003; Li et al., 2005; Wang and Zheng, 2011; Żytkiewicz et al., 2011). In Saccharomyces cerevisiae, the Lis1 and Nudel orthologs (Pac1 and Ndl1, respectively) serve to concentrate dynein at the plus ends of microtubules (Lee et al., 2003; Li et al., 2005; Sheeman et al., 2003). This is a critical step in targeting dynein to the cell membrane, where it positions the nucleus during cell division.

A range of properties has been ascribed to Lis1, including slowing dynein-driven microtubule sliding in multiple motor assays, prolonging dynein stall events under load, and enhancing the microtubule affinity of dynein when ADP and V1 (a phosphate analog) are bound (McKenney et al., 2010; Torsisawa et al., 2011; Yamada et al., 2008). However, Lis1’s mechanism of action remains largely mysterious, in part because of the lack of a recombinant system in which both Lis1 and dynein can be manipulated and studied at the single-molecule level. Although reports have suggested that Lis1 binds the AAA1 module of dynein (Sasaki et al., 2000; Tai et al., 2002), this has not been tested with functional proteins, and structural information on the dynein/Lis1 complex is not yet available. Moreover, reconciling the reported in vitro effects of Lis1 and Nudel with specific dynein activities in vivo has been controversial (Allan, 2011).

Here, using functional, recombinant proteins from S. cerevisiae, we show that Lis1 engages dynein at AAA3/AAA4. From this site, Lis1 acts like a “clutch” to regulate communication between dynein’s catalytic ring and microtubule-binding stalk, promoting a microtubule-bound state. Supporting these results, we identify mutations at the AAA3/4 junction that drastically impair Lis1 binding and motility regulation in vitro and dynein function in vivo. In addition, we identify an arginine finger motif within AAA4 and find that its mutation mimics aspects of Lis1’s effect in vitro. Previous genetic studies in an evolutionarily distant filamentous fungus showed that the same mutation can partially rescue Lis1 loss in vivo (Zhuang et al., 2007). These results allow us to propose how Lis1 biases dynein to a microtubule attached-state and assists in a variety of cellular functions across eukaryotes.

RESULTS

Lis1 Promotes a Microtubule-Attached State in Single Dynein Molecules

To dissect how Lis1 and Nudel regulate dynein’s motility, we wanted a system in which all three components could be manipulated and studied at the single-molecule level (Figure 1A). We previously developed methods to purify native cytoplasmic dynein complexes from S. cerevisiae, fluorescently label them with tetramethylrhodamine (TMR; via a C-terminal HaloTag), and visualize their movement along immobilized microtubules (Reck-Peterson et al., 2006). Here, we purified Lis1 and Nudel (Figure 1B), which were expressed from their genomic loci in S. cerevisiae. We inserted cleavable tags for affinity purification and a C-terminal SNAP-tag (giving the option of covalent labeling). The 20-kDa SNAP-tag did not interfere with the function of either protein, as revealed in nuclear segregation assays (Figure 1C). We eliminated the risk of endogenous regulators (Lis1, Nudel, and dynactin) from copurifying with dynein via genomic deletions (Table S1 available online).

We began by observing dynein motility at the single-molecule level over a range of Lis1 concentrations. In the absence of Lis1, dynein bound to and traveled along microtubules with a mean velocity of ~100 nm/s (Figure 1D), similar to previous reports (Reck-Peterson et al., 2006). As the Lis1 concentration increased, two trends were apparent. First, dynein velocity became progressively slower, reaching ~7 nm/s at the highest Lis1 concentration tested (1,200 nM). This can be appreciated in the kymographs in Figure 1D, in which steeper lines indicate slower movement. Second, Lis1 increased the length of time that dynein remained attached to the microtubule. For example, at 1,200 nM Lis1, many dynein molecules were attached for the entire duration of a 10 min movie (seen in Figure 1D as lines that span the kymograph’s y axis; see Figures S1A–S1D for quantification). Control assays with kinesin showed that the effect of Lis1 is specific to dynein (Figures S1E and S1F). Thus we conclude that Lis1 can convert dynein to a mechanochemical state in which its velocity is slowed and its microtubule attachments are prolonged.

Notably, at a given Lis1 concentration, the population of dynein molecules responded similarly: velocity histograms remained unimodal as the mean decreased (Figure 1F). We plotted dynein’s velocity as a function of Lis1 concentration. The plot is well fitted by a hyperbolic curve with a maximal velocity reduction of 95.7 ± 3.1% (Figure 1G; Table S2A). These data show that saturating concentrations of Lis1 can almost entirely arrest dynein on the microtubule. The Lis1 concentration giving half-maximal velocity reduction (K1/2) in this assay is 60.1 ± 10.0 nM. Hereafter, we refer to dynein in the presence of near-saturating Lis1 concentrations (>5-fold higher than the K1/2) as dynein/Lis1.

We next tested whether Nudel, Lis1 and dynein’s binding partner, affects the behavior of single dynein molecules in vitro. At 37.5 nM, Nudel alone had little effect on dynein motility (Figures S1G and S1H). By contrast, a mixture of 37.5 nM Nudel and 37.5 nM Lis1 elicted a change in dynein behavior akin to that induced by a ~5-fold higher Lis1 concentration. The mean velocity was slowed to ~29 nm/s, and microtubule encounters were markedly prolonged (Figures 1E and S1H). These results show interesting similarities and differences compared with earlier work. In previous in vitro experiments, mammalian Nudel was found to dissociate dynein from microtubules and suppress Lis1’s effect on the velocity of unloaded dynein (McKenney et al., 2010; Yamada et al., 2008). In contrast, we find that Nudel from S. cerevisiae allows Lis1 to exert its effect on dynein at lower
The Lis1 β Propeller Domain Contains Regulatory Elements that Act on Dynein’s Motor

To test which structural domains are required for Lis1 to regulate dynein motility, we analyzed the motility of a well-characterized dimeric motor domain construct (GST-dynein331 kDa; Reck-Peterson et al., 2006). GST-dynein331 kDa, which lacks the N-terminal tail, endogenous dimerization motif, and binding sites for associated dynein subunits, contains two motor domains dimerized by GST (Figure 2A) and displays processive motility similar to that of native dynein. In the presence of increasing concentrations of Lis1, the Lis1 concentration, Lis1/[Lis1], required for half maximal velocity reduction. The best-fit values (± error of the fit) are V0 = 100.0 ± 3.506 nm/s, Fmax = 0.957 ± 0.031, and K1/2 = 60.1 ± 10.0 nM. The R² value is 0.9797. See also Table S2A.
monomeric Lis1ΔN (green) from a size-exclusion column. Elution volumes of standards with known Stokes radii (R_s) are shown above. The calculated Stokes radii of dimeric Lis1 and Lis1ΔN are 5.3 nm and 3.3 nm, respectively. See also Figure S2E.

We next tested whether dimerization of either Lis1 or dynein is an essential part of the regulatory mechanism, using purified monomeric dynein331 kDa, whose motor activity can be analyzed in living cells. Yeast expressing brain-purified dynein in the presence of Lis1 have varied corresponding to strong microtubule affinity (e.g., with ADP or no nucleotide bound). Previous ATPase results obtained with preparations. To test for Lis1-induced catalytic arrest in our system, we measured the ATPase activity of dynein with different concentrations of Lis1 and microtubules. The basal ATPase rate of GST-dynein331 kDa alone was activated by microtubules to an essential part of the regulatory mechanism, using purified dynein motility by acting on elements within the motor domain.

We next tested whether dimerization of either Lis1 or dynein is an essential part of the regulatory mechanism, using purified monomeric dynein331 kDa, whose motor activity can be analyzed using a microtubule gliding assay (Figure 2D). To produce monomeric Lis1 (Lis1ΔN), we removed Lis1's N-terminal dimerization domain. The monomeric state of Lis1ΔN was verified by size-exclusion chromatography (Figure 2E) and crosslinking (Figure S2E). Monomeric dynein331 kDa drove microtubule gliding at a velocity of 55.5 nm/s (Figure 2F). Significantly, in the presence of 800 nM Lis1ΔN, gliding velocity slowed by ~60% (to 21.5 nm/s) and decreased by ~70% (to 16.2 nm/s) when the Lis1ΔN concentration was increased to 1,600 nM. These data indicate that a single β-propeller domain of Lis1 can regulate the activity of a single dynein motor domain, provided it is supplied at an elevated concentration (perhaps explaining why similar effects were not observed in a previous study; Torisawa et al., 2011).

We next tested these findings in living cells. Yeast expressing monomeric Lis1ΔN as the sole source of Lis1 exhibited a strong nuclear segregation defect (~22%; Figure 2G), consistent with malfunction of the dynein pathway. However, when the cellular concentration of Lis1ΔN was increased >10-fold with the use of a strong, galactose-inducible promoter (Figure S2G), the percentage of cells with a nuclear segregation defect was rescued to ~10% (Figure 2G). This suggests that a monomeric Lis1 construct comprising the β-propeller domain can regulate dynein both in vitro and in vivo, provided its concentration is sufficiently high. Thus, dimerization serves to enhance the apparent affinity between dynein and Lis1.

Lis1 Alters Allosteric Communication between Dynein’s ATPase and Microtubule-Binding Domains

In principle, dynein could be converted to a microtubule-attached state by arresting its ATPase cycle at a stage corresponding to strong microtubule affinity (e.g., with ADP or no nucleotide bound). Previous ATPase results obtained with brain-purified dynein in the presence of Lis1 have varied (McKenney et al., 2010; Mesngon et al., 2006; Yamada et al., 2008), perhaps due to heterogeneity between and within dynein preparations. To test for Lis1-induced catalytic arrest in our system, we measured the ATPase activity of dynein with different concentrations of Lis1 and microtubules. The basal ATPase rate of GST-dynein331 kDa alone was activated by microtubules to
dynein331 kDa molecules were bound to surface-immobilized microtubules (Figure 3B). This was the case even in extremely high Lis1 concentrations (2 μM; data not shown). Thus, in the presence of microtubules, dynein/Lis1 can continue to hydrolyze ATP, indicating that Lis1-mediated motility regulation is more complex than a simple arrest of the ATPase cycle.

In a canonical mechanochemical cycle, dynein’s motor domain dissociates from the microtubule after ATP binding. In a dynein dimer, this allows one motor to detach and undergo a forward excursion along the microtubule while the partnering motor remains bound. To test whether Lis1 alters this mechanochemical coupling, we developed an assay to visualize the motor remains bound. To test whether Lis1 alters this mechanochemical cycle, dynein’s motor domain dissociates from the microtubule (Figure 3E, arrow). Dissociation was not due to laminar flow or dilution, as the molecules remained attached after perfusion with buffer (Figure 3D, arrow). After ATP-induced dissociation, monomeric dynein331 kDa was free to diffuse away from the microtubule. Subsequent rebinding events were short and probably correspond to single turnovers of ATP (Figure 3E). The presence of Lis1 caused two main differences in these behaviors. First, instead of dissociating rapidly after ATP addition, dynein331 kDa remained bound to the microtubule for extended periods (average duration of ~6 s) before detaching (Figures 3F and S3A). Second, the duration of rebinding events was similarly prolonged (Figure S3B). Thus, Lis1 slows the microtubule off-rate of dynein in ATP conditions. Multiple ATP hydrolysis cycles are likely to occur during these extended periods of microtubule attachment (see Figure 3B and data below). These results suggest a model in which Lis1 alters communication between dynein’s catalytic AAA+ modules and microtubule-binding stalk, allowing the motor domain to remain tightly bound to the microtubule even in high ATP concentrations.

**Impact of Lis1 on Dynein Stepping Behavior**

A prediction of this model is that Lis1 will cause the motor domains in a dynein dimer to remain attached to the microtubule for longer periods between steps, giving rise to slower motion. If this prediction is correct, then it might be possible to observe individual steps even at a physiological ATP concentration (~1 mM) without hindering load, conditions under which dynein’s steps have previously been too rapid to detect. To test this, we...
Lis1 traces may correspond to “bursts” of multiple rapid steps at the rate observed for free dynein in 1 mM ATP (Figure 4B, green trace) and could reflect Lis1 dissociation events. In summary, we conclude that the slow movement of dynein/Lis1 is not due to smaller forward steps or more frequent back steps (Figure S3C); rather, it is accounted for by longer dwells between steps.

Most frequently, dynein/Lis1 paused for ~1 s between steps (Figure 4C), and longer dwells lasting up to 15 s can be seen in the traces (Figure 4B, asterisk). For comparison, the average duration of an ATP turnover in steady-state assays was ~0.1 s (Figure 3B). The dwells we observe between individual steps in the presence of Lis1 may be related to the pauses previously seen between longer movements in mammalian dynein (see Figure S3 of McKenney et al., 2010). During Lis1-induced pauses, the displacement fluctuations of the Qdot were equivalent to those seen for dynein alone while tightly bound to the microtubule waiting for ATP to bind (in each case, SD = ±4 nm). Together, these results show that Lis1 causes dynein to remain tightly attached to the microtubule for typically more than a second in high concentrations of ATP. This is a pronounced change from dynein’s canonical stepping pattern.

**Lis1 Binds Between Dynein’s Microtubule-Binding and ATPase Domains at AAA3/4**

We next explored the structural basis for the striking effects of Lis1 on dynein’s mechanochemistry. Using size-exclusion chromatography, we were able to purify the complex of GST-dynein331 kDa and Lis1 in buffer supplemented with ATP + V_{i}, ATP, or no added nucleotide (Figures 5A and 5B). Complex formation was evident from the coelution of dynein and Lis1 (Figures 5A, blue arrow, and 5B) and depletion of free Lis1 (Figure 5A, gray arrow). This differs from a previous report in which interactions were detected in the presence of ATP + V_{i} (thought to trap the prepowerstroke state of dynein) but not in nucleotide-free conditions (McKenney et al., 2010). It may be that Lis1 affinity in the no-nucleotide state is stronger with dimeric, yeast dynein compared with the monomeric, mammalian dynein construct used in earlier work. We used electron microscopy (EM) to investigate structural differences between the free dynein and dynein/Lis1 fractions in the absence of nucleotide, allowing direct comparison with the yeast motor domain crystal structure (Schmidt et al., 2012) obtained in the same state.

Figure 5C shows negative-stain EM images of GST-dynein331 kDa both alone and bound to Lis1. Molecules from the two samples have the same general form, with the paired motor domains adopting a range of relative orientations about the GST moiety. However, the two motor domains are slightly closer and less variably spaced in the presence of Lis1 (Figure 5D), suggesting that Lis1 might bind between them (see Figure S4A).

We next mapped the Lis1 binding site on dynein using single-particle image processing. Images of individual motor domains were extracted from the dimer micrographs, aligned, classified into similar groups, and averaged, revealing a range of molecular views in the data sets. The two main views of the motor domain are close to those previously seen in other dyneins (Figures 5E
and 5F; Burgess et al., 2003; Roberts et al., 2009). Detail was sufficient to match these views unambiguously to orientations of the yeast dynein crystal structure (Figures S4B and S4C). Both the coiled-coil stalk and the microtubule-binding domain at its tip are also resolved in class averages (Figures 5E and 5F, insets), further aiding interpretation of the images.

In the presence of Lis1, there is a pronounced extra density on the margin of dynein’s motor domain, near the emergence of the stalk (Figure 5E, arrowhead). This observation is quantified in a difference map, where the additional density gives rise to a strong difference peak (Figure 5E, right panel). Analysis of the second main view (Figure 5F) yields a difference peak in the same position. This extra Lis1 density in both views overlaps with AAA3/4 (Figures 5E and 5F, lower; Figures S4B–S4E). We detect no significant density changes near AAA1 in the presence of Lis1, contrary to earlier reports that Lis1 binds AAA1 (Sasaki et al., 2000; Tai et al., 2002).

To determine whether Lis1 binding at AAA3/4 is responsible for regulating dynein motility, we mutated a series of highly conserved, charged amino acids in dynein at this putative interface (Figures 6A and S5A). Whereas these mutations had little or no effect on dynein’s intrinsic motility, Lis1-induced velocity reduction was impaired by a single point mutation (K2721E) and nearly abolished by a quadruple substitution (K2721A, D2725G, E2726S, and E2727G) near the AAA3/4 junction (Figure 6B). These four mutations also virtually abolished Lis1 binding in a gel filtration experiment (Figures S5B and S5C). Furthermore, in living yeast cells, the quadruple substitution produced a nuclear segregation phenotype indistinguishable from that caused by Lis1 deletion (Figure 6C). Thus, we conclude

Figure 5. Purification and Structure of the Dynein/Lis1 Complex

(A) Purification of the dynein/Lis1 complex by size-exclusion chromatography. Traces show the elution profiles of Lis1 (green), GST-dynein331 kDa (red), and a mixture of both proteins (blue) in ATP + V_i buffer conditions. Complex formation is indicated by the coelution of dynein and Lis1 (blue arrow) and depletion of free Lis1 (gray arrow). Elution volumes of standards with known Stokes radii (R_s) and the void volume (V_0) are shown above.

(B) SDS-PAGE of size-exclusion chromatography fractions, colored as in (A). GST-dynein331 kDa and Lis1 coelute in a complex (blue bands) in ATP + V_i buffer conditions (main panel) as well as in ATP and no-nucleotide conditions (lower right: peak fractions).

(C) Negative-stain EM images of GST-dynein331 kDa alone (− Lis1) and bound to Lis1 (+ Lis1). Examples of paired motor domains are outlined in white. The scale bar represents 50 nm.

(D) Histogram showing motor-motor separation distances for dynein dimers alone (dark gray) or bound to Lis1 (light gray). Each distribution is fit with a Gaussian (R^2 values of 0.9443 and 0.9830, respectively). Motor-motor separation of dynein alone is 21.0 ± 0.2 nm (± error of the fit) and the SD is 3.1 ± 0.2 nm (n = 854). In the presence of Lis1, the motor-motor separation is 19.3 ± 0.1 nm and the SD is 2.1 ± 0.1 nm (n = 1067). The motor-motor separation is significantly reduced in the presence of Lis1 (p < 0.0001, Welch t test), and the variation in motor-motor spacing is significantly smaller (p < 0.0001, f test).

(E and F) Analysis of the Lis1 binding site on dynein. The two main views of the dynein motor domain following single-particle analysis are shown (top view [E] and right view [F]). In each case, the upper row shows an average of the dynein/Lis1 complex (left panel), dynein alone (middle panel), and the difference map between these images overlaid on the dynein average (right panel). Differences are shown at 4σ above the mean and colored according to the chart. Prominent extra density in the dynein/Lis1 complex is indicated (arrowhead in E). The window width corresponds to 26.4 nm. Lower: the difference peak overlaid on the corresponding view of the yeast dynein motor domain crystal structure (PDB 4AKI; Schmidt et al., 2012), as determined by projection matching (see Figures S4B and S4C). The stalk, linker, AAA+ modules (1–6), and C-terminal region (C) are indicated. Insets show class averages revealing the full length of the stalk and microtubule-binding domain at its tip, which are truncated in the crystal structure.
that Lis1 engages dynein at AAA3/4, near the interface between its catalytic ring and microtubule-binding stalk.

**Mutation of Dynein’s AAA4 “Arginine Finger” Mimics the Lis1 Effect at the Single-Molecule Level**

A pre-existing clue to the involvement of AAA3/4 in Lis1’s mechanism comes from genetic studies in *Aspergillus nidulans*. In this filamentous fungus, a single Arg→Cys mutation within AAA4 can partially suppress the phenotype associated with deletion or mutation of the Lis1 gene (*nudF*) (Zhuang et al., 2007). On close inspection, this residue is a strong candidate to form the “arginine finger” motif of AAA4. By analogy to related ring-shaped AAA+ ATPases, this motif is expected to reach from AAA4 into the adjacent nucleotide-binding pocket of AAA3 and help transmit structural changes around the ring (Figure 6D; Erzberger and Berger, 2006; Kon et al., 2012; Schmidt et al., 2012). To investigate the role of AAA4’s arginine finger and the consequences of the suppressor mutation, we engineered the equivalent mutation (R2911C) in *S. cerevisiae* dynein. In single-molecule assays, GST-dynein<sup>331 kDa</sup> and GST-dynein<sup>R2911C</sup> retained the ability to bind to and move along microtubules. However, its mean velocity was slowed to ~5 nm/s, and its microtubule encounters were extended in time compared with the parental construct with an intact AAA4 arginine finger (Figure 6E). Strikingly, these properties of the mutant closely resemble dynein behavior in saturating Lis1 concentrations (Figure 6E). As expected, the Lis1<sup>Δ</sup> phenotype in *S. cerevisiae* is not rescued by the arginine finger mutation (Figure SSD), because here Lis1 is also required for proper dynein localization (Lee et al., 2003; Markus et al., 2009; Sheehan et al., 2003). By contrast, in *A. nidulans*, this mutation partially bypasses the need for Lis1, likely because dynein localization is less dependent on Lis1 in these cells (Zhang et al., 2002). In summary, mutating the arginine finger motif of AAA4 confers motile properties similar to those produced by Lis1; moreover, the same mutation can in part circumvent the requirement for Lis1 in *A. nidulans* (Zhuang et al., 2007).

**DISCUSSION**

Our single-molecule and ensemble data illuminate the mechanism by which Lis1 alters cytoplasmic dynein’s mechanical behavior and assists in its wealth of cellular functions. Based on these findings, models for Lis1’s mechanism must take the following observations into account. First, Lis1 converts single dynein molecules to a microtubule-attached state in a dose-dependent fashion, bringing dynein to a virtual standstill at
**S. cerevisiae.**

A ''Clutch'' Model for Lis1’s Mechanism of Action (Figure 7). We first bring these observations and previous results together into these elements, at AAA3/4.

Fourth, Lis1 engages dynein close to the interface between dynein's ATP hydrolyzing ring and its microtubule-binding stalk. This indicates that Lis1 can alter communication between charged amino acids are highly conserved in available cytoplasmic dynein sequences (Figure S5A), suggesting that binding pocket of AAA3, contributes to the normal function of cytoplasmic dynein. Our functional studies also support a role for AAA3/4 being the site of Lis1 interaction; mutation of four charged amino acids in AAA4's N-terminal helix severely impairs Lis1 binding, renders dynein nearly completely insensitive to Lis1 in motility assays, and necropoies a Lis1 null allele in living cells. Furthermore, these charged amino acids are highly conserved in available cytoplasmic dynein sequences (Figure S5A), suggesting that binding at AAA3/4 is likely to be a common feature of Lis1-dynein interactions. A notable exception to this pattern of conservation is found in *Schizosaccharomyces pombe*, which lacks an obvious Lis1 ortholog. The AAA3/4 binding site also provides a simple explanation for why the Lis1-dynein affinity is sensitive to the "neck" region of dynein's tail (Markus and Lee, 2011; Markus et al., 2009), as these domains are closely apposed (Burgess et al., 2003; Roberts et al., 2012).

Although the ATP-driven domain motions within dynein's ring have not yet been delineated, our data and recent structural studies (Kon et al., 2012; Schmidt et al., 2012) suggest that an "arginine finger" motif, reaching from AAA4 into the catalytic pocket of AAA3, contributes to the normal function of cytoplasmic dynein's ring. Our functional studies also show that mutation of this AAA4 arginine finger mimics aspects of Lis1's impact on dynein motility. Based on comparisons with related ring-shaped AAA+ machines, this motif is expected to be important for the hydrolysis of ATP at AAA3 and/or the transmission of structural changes from AAA3 to AAA4 (Erzberger and Berger, 2006). Consistent with this, the motile properties that we observe in the AAA4 arginine finger mutant closely resemble those of...
mutants with disrupted ATP binding/hydrolysis motifs in AAA3 (Cho et al., 2008; Kon et al., 2004). An important mechanistic distinction between the AAA4 arginine finger mutant and Lis1 is that the mutation appears to substantially reduce ATPase turnover (Zhuang et al., 2007), whereas Lis1 does not. A possible role of ATP hydrolysis in the dynein-Lis1 complex is to keep the system dynamic and therefore adaptable (see below). Because AAA1 is the principal ATPase site in dynein’s ring, AAA3 and AAA4 have previously been referred to as “regulatory” AAA+ modules. Here we show that not only do AAA3 and AAA4 regulate the motions within dynein’s ring, but they also form the binding site for Lis1, a ubiquitous cytoplasmic dynein regulator.

The Functional Role of Nudel
We found that Nudel allowed Lis1 to act on dynein at lower concentrations in our single-molecule experiments. This supports a tethering role for Nudel, in which it attaches to dynein’s tail (via the intermediate chain of dynein) with one end of its coiled coil and binds to Lis1 with the other (Feng et al., 2000; McKenney et al., 2010; Niethammer et al., 2000; Sasaki et al., 2000; Tarricone et al., 2004; Wang and Zheng, 2011; Żylikiewicz et al., 2011), thus increasing Lis1’s effective concentration. However, evidence suggests that within Nudel’s tethering role exist additional regulatory layers. For example, an intriguing property of purified mammalian NudE/Nudel proteins is to suppress Lis1’s effects on unloaded dynein (Torigawa et al., 2011; Yamada et al., 2008) while still enabling Lis1 to prolong dynein’s microtubule attachments under force (McKenney et al., 2010). One possibility here is that Nudel positions Lis1 such that it engages AAA3/4 when dynein is strained. This would allow dynein/Lis1/Nudel to move rapidly until a high load is encountered, at which point Lis1 would engage and resist microtubule detachment. This differs from our results from S. cerevisiae, in which Nudel enhanced Lis1’s effects on dynein even in unloaded conditions. Therefore, the load-dependent behavior of dynein, Lis1, and Nudel may vary among species or as a function of posttranslational modification.

Biological Implications
Lis1 has been proposed to facilitate two general steps in the cytoplasmic dynein pathway: preparing dynein for transport and allowing dynein to move large, high-load cargos. Our model (Figure 7) provides a plausible mechanism for both types of Lis1 function and also identifies additional possible roles for dynein/Lis1 in living cells. A common theme in these functions is that by acting as a molecular clutch, Lis1 prolongs dynein’s attachments to microtubules.

An initial step in many dynein-mediated transport events is the targeting of dynein to the plus ends of microtubules, which grow and shrink near the cell periphery (Kardon and Vale, 2009). Here, dynein is thought to be loaded with cargo before transporting these cargo molecules toward the microtubule minus end. In cells, Lis1 is also concentrated at microtubule plus ends and can be targeted there either in complex with dynein (as in S. cerevisiae and possibly mammalian cells) or separately (as in A. nidulans and Ustilago maydis; Lee et al., 2003; Lenz et al., 2006; Sheeman et al., 2003; Yamada et al., 2008; Zhang et al., 2002). In either scenario, our data indicate that binding of Lis1 to dynein at the microtubule plus end will bias dynein toward a microtubule-attached state. This could increase dynein’s residence time at the microtubule plus end, assist in the kinetics of cargo loading, and/or form the starting configuration for motility toward the minus end. By binding near the neck region of dynein’s tail, Lis1 may also be involved in “unmasking” the tail to promote interactions with cargo (Egan et al., 2012; Lenz et al., 2006; Markus and Lee, 2011; Markus et al., 2009).

In S. cerevisiae, the cue for transferring dynein onto its cargo protein could also involve the controlled assembly of dynein with the dynactin complex (Markus and Lee, 2011; Markus et al., 2009; Woodruff et al., 2009). Formation of the dynein/dynactin complex may help displace Lis1 and Nudel (McKenney et al., 2011) and convert dynein from a strongly microtubule-attached state (with Lis1 bound) to a rapidly moving progressive state (with dynactin bound).

A second, more recently proposed role of Lis1 is to adapt dynein for tasks involving high loads, such as transporting and exerting tension on large organelles and cellular structures (McKenney et al., 2010). By binding near the base of dynein’s microtubule-binding stalk and causing it to resist detachment, Lis1 appears ideally suited to facilitate dynein’s tension-bearing roles. It remains to be seen whether the ATP-driven movements of dynein’s mechanical element (the “linker”) persist with Lis1 bound (Burgess et al., 2003; Kon et al., 2005; Roberts et al., 2009, 2012). If so, this might allow dynein/Lis1 to perform repeated “tugs” on cargo while attached to the microtubule, thereby maintaining tension. Alternatively, Lis1 might regulate the linker domain’s motions, as the distal end of the linker lies in close proximity to the Lis1 binding site at AAA3/4 (Figure S4E). The impressive duration of dynein’s microtubule attachments in the presence of Lis1 also provides clues to additional possible functions in vivo. A subset of macromolecules and organelles, including mRNAs and the Golgi apparatus, appears to require dynein for retention at specific sites in the cytoplasm (Delanoue and Davis, 2005; Ding et al., 2009; Lam et al., 2010). An idea compatible with our data is that tension-bearing dynein/Lis1 complexes are responsible for anchoring these cargos in place.

An important question is how Lis1 might assist in the rapid, dynein-driven transport of large organelles, as was recently reported in neuronal cells (Pandey and Smith, 2011; Yi et al., 2011). Given that the velocity of these movements (~300 nm/s) exceeds those expected from dynein in saturating Lis1 concentrations (Yamada et al., 2008), one possibility is that Lis1 is substoichiometrically associated with dynein on such cargos. Alternatives include Lis1 allowing the summation of multiple individual dynein forces (McKenney et al., 2010), and Nudel modulating the dynein-Lis1 interaction in a load-sensitive manner. Quantifying the endogenous copy number of dynein, Lis1, and Nudel on these cargos by live-cell imaging would help distinguish among these possibilities.

In the other classes of cytoskeletal motors, different motile properties have been achieved by gene duplication and divergent evolution. In the case of cytoplasmic dynein, our results reveal that Lis1 can generate mechanical diversity by regulating the structural changes that propagate through dynein’s large motor domain.
EXPERIMENTAL PROCEDURES

Protein Expression, Purification, and Labeling
The S. cerevisiae strains used in this study are listed in Table S1. Dynein constructs were purified and labeled essentially as described previously (Reck-Peterson et al., 2006). For modifications and details of the Lis1 and Nudel purifications, see Extended Experimental Procedures. Protein concentrations were determined by comparisons with standards using Bradford protein assays or SDS-PAGE with SYPRO Red (Invitrogen) staining. All protein concentrations (dynein, Lis1, Nudel, and α/β-tubulin) are expressed for the dimer, with the exception of Lis1 ∆N, for which the monomer concentration is given.

Single-Molecule Microscopy and ATPase Assays
Assays are described in detail in the Extended Experimental Procedures. Briefly, motility assays were assembled using flow chambers, and fluorescently labeled dynein molecules and microtubules were visualized by TIRF microscopy (Qiu et al., 2012; Reck-Peterson et al., 2006). Microtubule-activated ATPase assays were performed using the EnzChek phosphatase kit (Molecular Probes; Cho et al., 2008; Reck-Peterson et al., 2006).

Size-Exclusion Chromatography and EM
GST-dynein331 kDa (350–400 nM), Lis1 (700–800 nM), or a mixture of both proteins was preincubated for 10 min at 4°C under the indicated nucleotide conditions (200 μM Mg-ATP + 200 μM sodium vanadate, 200 μM Mg-ATP alone, or no added nucleotide). Samples were fractionated on a Superose 6 PC 3.2/30 column equilibrated with buffer and nucleotide as required. For negative-stain EM, peak fractions were stained with 1% uranyl formate and imaged using a Tecnai G2 Spirit microscope, as detailed in the Extended Experimental Procedures.

SUPPLEMENTAL INFORMATION
Supplemental Information includes Extended Experimental Procedures, five figures, and two tables and can be found with this article online at http://dx.doi.org/10.1016/j.cell.2012.07.022.

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REFERENCES


