P. falciparum parasites cause malaria and are responsible annually for hundreds of thousands of deaths. Kinesins are a superfamily of microtubule-dependent ATPases that play important roles in the parasite replicative machinery, which is a potential target for antiparasite drugs. Kinesin-5, a molecular motor that cross-links microtubules, is an established antimitotic target in other disease contexts, but its mechanism in Plasmodium falciparum is unclear. Here, we characterized P. falciparum kinesin-5 (PfK5) using cryo-EM to determine the motor’s nucleotide-dependent microtubule-bound structure and introduced 3D classification of individual motors into our microtubule image processing pipeline to maximize our structural insights. Despite sequence divergence in PfK5, the motor exhibits classical kinesin mechanochemistry, including ATP-induced subdomain rearrangement and cover neck bundle formation, consistent with its plus-ended directed motility. We also observed that an insertion in loop5 of the PfK5 motor domain creates a different environment in the well-characterized human kinesin-5 drug-binding site. Our data reveal the possibility for selective inhibition of PfK5 and can be used to inform future exploration of Plasmodium kinesins as antiparasite targets.

Cryo-EM structure of a microtubule-bound parasite kinesin motor and implications for its mechanism and inhibition

Plasmodium parasites cause malaria and are responsible annually for hundreds of thousands of deaths. Kinesins are a superfamily of microtubule-dependent ATPases that play important roles in the parasite replicative machinery, which is a potential target for antiparasite drugs. Kinesin-5, a molecular motor that cross-links microtubules, is an established antimitotic target in other disease contexts, but its mechanism in Plasmodium falciparum is unclear. Here, we characterized P. falciparum kinesin-5 (PfK5) using cryo-EM to determine the motor’s nucleotide-dependent microtubule-bound structure and introduced 3D classification of individual motors into our microtubule image processing pipeline to maximize our structural insights. Despite sequence divergence in PfK5, the motor exhibits classical kinesin mechanochemistry, including ATP-induced subdomain rearrangement and cover neck bundle formation, consistent with its plus-ended directed motility. We also observed that an insertion in loop5 of the PfK5 motor domain creates a different environment in the well-characterized human kinesin-5 drug-binding site. Our data reveal the possibility for selective inhibition of PfK5 and can be used to inform future exploration of Plasmodium kinesins as antiparasite targets.

Malaria is a massive disease burden worldwide, with an estimated 219 million cases in 2017, a year that also saw the first increase in cases for nearly two decades (https://www.who.int/publications/i/item/9789241566563). With resistance to current frontline therapeutics rapidly rising (https://apps.who.int/iris/handle/10665/274362) (1, 2), new drug targets are urgently needed. Malaria is caused by Plasmodium parasites, which are unicellular eukaryotes belonging to the Apicomplexa phylum. Malaria parasites have a complex life cycle involving distinct stages that are transmitted between, and reproduce in, human and mosquito hosts (3). The cytoskeleton plays an important role throughout the parasite life cycle, and the microtubule (MT)-based spindle machinery is involved in the many rounds of mitotic and meiotic replication required for parasite proliferation. Antimitotics are well established as drugs in a variety of settings, notably human cancer (4)—thus, components of the malaria replicative machinery are attractive antiparasite targets. However, given the obligate intracellular nature of malaria parasites, any therapeutic target must be sufficiently divergent to be selectively disrupted compared with host homologues.

Members of the kinesin superfamily are such potential targets. Kinesins are motor proteins that bind to MTs and convert the energy of ATP binding and hydrolysis into MT-based mechanical work. Different kinesin families have specialized functions, such as translocation of cargo along MTs, regulation of MT polymer dynamics, and organization of higher-order MT structures such as mitotic and meiotic spindles (5, 6). MTs are built from heterodimers of the highly conserved α- and β-tubulin, whereas there is approximately 95% sequence conservation of tubulins between Plasmodium sp. and Homo sapiens, sequence conservation within kinesin families is much lower, typically 40–50%. This raises two important questions: do distantly related members of kinesin families diverge in their molecular properties, and could such sequence divergence allow selective inhibitors to be developed?

The kinesin-5 family is involved in cell division in many organisms, has long been investigated as an antimitotic therapeutic target for human cancer (7), and has also been considered as a target for antifungals (8). Kinesin-5 family members are found in most eukaryotes, including Plasmodium sp., and the family is predicted to have been established in the last eukaryotic common ancestor (9). Kinesin-5s form a tetrameric bipolar structure, with two opposing pairs of motor domains that can organize MT arrays such as those found in spindles (10–12). Several classes of selective H. sapiens kinesin-5 (HsK5) inhibitors have been characterized that block motor ATPase activity and bind to allosteric sites in the motor domain. The best studied of these allosteric binding pockets is defined by kinesin-5-specific sequences in a key structural region of the motor domain, loop5 (13). Loop5 is critical for the correct operation of human kinesin-5, since its deletion or mutation disrupts the motor’s mechanochemical cycle (14–16). Furthermore, Drosophila kinesin-5 is resistant to the
Molecular mechanism of a parasite kinesin

HsK5 inhibitor STLC, but can be sensitized by replacement of loop5 with the cognate HsK5 sequence (17). The loop5-defined allosteric site thus has proven promise in mediating selective inhibition of kinesin-5 family members from different species.

To investigate the idea that kinesin-5 from Plasmodium falciparum (PfK5)—the deadliest form of human malaria—could be a selective antimalarial therapeutic target, we characterized the biochemical properties and MT-bound structure of the PfK5 motor domain. We show that the PfK5 motor domain is an ATPase with MT plus-end directed motility, as demonstrated in MT gliding experiments. MT-bound structures of the PfK5 motor domain were determined using cryo-electron microscopy (cryo-EM), and processed in our RELION-based MT image processing pipeline (18). These structures reveal classical kinesin mechanochemistry despite the significant sequence divergence of this motor. This includes ATP-induced subdomain rearrangements that support neck-linker docking to the motor domain and cover neck bundle (CNB) formation, which together are consistent with PfK5 motor domain plus-ended directed motility. Finally, we show that a large insertion in loop5 of the PfK5 motor domain creates a different environment in the well characterized loop5 drug-binding site, revealing the possibility for selective inhibition of PfK5.

Results

PfK5ΔL6-MD is a slow ATPase

To characterize PfK5 mechanochemistry, we first wanted to measure its MT-stimulated ATPase activity. The PfK5 motor domain (PfK5MD, amino acids 1–493) contains a 105 amino acid asparagine and lysine-rich insertion in loop6 that is characteristically poor conservation (16%) among Plasmodium kinesins-5. We engineered loop6 out of our construct, an approach previously taken by another group (20); this prevented further show that the PfK5 motor domain creates a different environment in the well characterized loop5 drug-binding site, revealing the possibility for selective inhibition of PfK5.

PfK5ΔL6-MD generates slow MT gliding

To determine the motile properties of PfK5ΔL6-MD, we used an MT gliding assay. PfK5ΔL6-MD was expressed with a C-terminal SNAP-tag (PfK5ΔL6-MD-SNAP), purified to 92% purity (Fig. 2A), covalently labeled with biotin, and attached to a neutravidin-coated surface. The velocity of fluorescently labeled MTs driven by PfK5ΔL6-MD-SNAP activity was measured. PfK5ΔL6-MD-driven MTs moved at an average velocity of 5.4 nm/s (95% confidence interval = 5–5.9) (Figs. 2B and 2C). This is slow compared with 23–92 nm/s reported for HsK5-MD (21, 24, 25). However, this slow MT gliding corresponds with the slow rate of ATP hydrolysis observed in the ATPase assay. Inclusion of polarity-marked MTs in the assay further showed that PfK5ΔL6-MD is a plus-end directed motor (Fig. 2B).

Figure 1. PfK5ΔL6-MD is a slow MT-stimulated ATPase. A, left, domains of full-length PKS and PfK5ΔL6-MD, displaying the N-terminus (Nt), motor domain (MD), neck linker (NL), stalk (S), C-terminus (Ct) aa = amino acids; right, Coomassie-stained SDS-PAGE of PfK5ΔL6-MD after purification. B, PfK5ΔL6-MD ATPase rate in the absence of MTs. Technical replicates = 12 (circles), experimental replicates = 4 (triangles), biological replicates (i.e., number of different protein purifications used in the experiments) = 2. The mean of experimental replicates (0.039 ATP s⁻¹) and 95% confidence interval are plotted. C, PfK5ΔL6-MD MT stimulated ATPase activity. The mean and standard deviation of three experimental replicates (no technical replicates are plotted). Biological replicates = 2. The fit is plotted as a blue line, with corresponding 95% confidence interval plotted as black lines. Inset displays an example of raw data (L = ATP, P = PfK5ΔL6-MD, and M = MTs). D, PfK5ΔL6-MD MT stimulated ATPase activity as in (C), except with ATP as the substrate variable, and using a constant of 1 μM MT.

In the absence of MTs, PfK5ΔL6-MD exhibited a low ATP hydrolysis rate (Fig. 1B), but addition of MTs stimulated PfK5ΔL6-MD ATPase activity (Fig. 1C). Changes in pH or ionic strength showed no or minimal impact respectively on PfK5ΔL6-MD ATPase rate (Fig. S1, A and B). From these data, the motor kcat and km of MTs (kMT) for PfK5ΔL6-MD were calculated. The km of ATP (KATP) was also determined (Fig. 1D). PfK5ΔL6-MD has a MT-stimulated ATP hydrolysis rate of 0.13 ATP s⁻¹, which is slow compared with kinesin-5 from Sus pombe (21), Sus cerevisiae (22), and H. sapiens (23) (with rates of 1.2, 0.5, and 2.9 ATP s⁻¹ respectively). However, PfK5ΔL6-MD has similar KMT (5.4 μM) and KATP (9.5 μM) values compared with previously characterized kinesin-5s (22, 23). Thus, despite substantial sequence divergence, and although it has the lowest ATPase rate observed to date for the family, PfK5ΔL6-MD exhibits overall similar ATPase properties compared with other kinesin-5s.
PfK5ΔL6-MD single-molecule interactions with MTs

To provide some context for the slow ATPase and MT gliding activity we observed for PfK5ΔL6-MD, we analyzed the interactions of single molecules of fluorescently labeled PfK5ΔL6-MD-SNAP with MTs. We made single-molecule measurements in different nucleotide conditions, to investigate how MT affinity changes with nucleotide state (Figs. 2C and S1D), using the nonhydrolyzable ATP analogue AMPPNP to mimic the ATP bound state. From these data, we calculated the MT association rate, or $k_{MTlanding}$ (Fig. 2D), and MT dissociation rate, or $k_{off}$ of PfK5ΔL6-MD (Fig. 2E). This demonstrated that in saturating ADP conditions, PfK5ΔL6-MD-SNAP had a comparatively low $k_{MTlanding}$ and a high $k_{off}$, indicating that PfK5ΔL6-MD-SNAP has low MT affinity when bound to ADP (Fig. 2F). In the absence of nucleotide or in saturating AMPPNP conditions, PfK5ΔL6-MD-SNAP had a comparatively high $k_{MTlanding}$ and a low $k_{off}$, showing that when no nucleotide is present, or in its ATP-bound state, PfK5ΔL6-MD-SNAP has high MT affinity.

In saturating ATP conditions, $k_{MTlanding}$ was higher compared with the ADP state; however, $k_{off}$ was similar, suggesting that PfK5ΔL6-MD-SNAP also has relatively low MT affinity in the presence of ATP. Overall, we observe that PfK5ΔL6-MD-SNAP has high MT affinity in the no nucleotide and AMPPNP states compared with ADP and ATP saturating conditions, which is comparable to HsK5 (26). The identification of two high-affinity states provided an opportunity to study the structure of the motor.

**MT-bound PfK5ΔL6-MD structure determination using cryo-EM**

To gain molecular insight into the behavior of PfK5ΔL6-MD, its interaction with MTs, and its sensitivity to nucleotide binding, we visualized MT-bound PfK5ΔL6-MD in
Molecular mechanism of a parasite kinesin

different nucleotide states using cryo-EM. We calculated 3D reconstructions of PfK5ΔL6-MD bound to MTs in the absence of nucleotide and in an ATP-like state, using AMPPNP (Table 1). To do this we used MiRP (Fig. S2, A and B), our previously developed pipeline for image processing of MTs with RELION (18, 27). As part of the current study, we have updated MiRP to operate with RELION v3.1 and improved usability of the procedure such that it can be run from the RELION GUI, among other updates (see Experimental procedures and https://github.com/moores-lab/MiRPv2).

PfK5ΔL6-MD binds MTs every 8 nm (one PfK5ΔL6-MD per αβ-tubulin) on the ridge of MT protofilaments (Fig. 3A), a binding site shared by all other kinesins characterized to date (28, 29). MiRP initially produced reconstructions for the no nucleotide (Figs. 3B and S2C) and AMPPNP states (Figs. 3C and S2D) at overall resolutions of 4.8 Å and 4.5 Å, respectively. The resolution in the MT region of both reconstructions is approximately 4.5–5.5 Å—in contrast, the resolution of PfK5ΔL6-MD exhibits a marked falloff as a function of distance from the MT surface (Fig. S2C). This is typical of kinesin-MT reconstructions (30, 31) and is attributable to a number of factors, including incomplete occupancy of the MT lattice by the motor that is not immediately apparent in the micrographs, as well as flexibility in the PfK5ΔL6-MD protein itself. We therefore used symmetry expansion and 3D classification focused on PfK5ΔL6-MD from one PfK5ΔL6-MDαβ-tubulin dimer asymmetric unit to select data with the best PfK5ΔL6-MD occupancy (Fig. S2A). We rejected classes that had a clear absence of PfK5ΔL6-MD density, as well as classes that did not contain continuous motor density (Fig. S2C). This is typical of kinesin-MT reconstructions (30, 31) and is attributable to a number of factors, including incomplete occupancy of the MT lattice by the motor that is not immediately apparent in the micrographs, as well as flexibility in the PfK5ΔL6-MD protein itself. We therefore used symmetry expansion and 3D classification focused on PfK5ΔL6-MD from one PfK5ΔL6-MDαβ-tubulin dimer asymmetric unit to select data with the best PfK5ΔL6-MD occupancy (Fig. S2A). We rejected classes that had a clear absence of PfK5ΔL6-MD density, as well as classes that did not contain continuous motor density (Fig. S2C). The resulting 3D structures (no nucleotide—Fig. 3D, AMPPNP—Fig. 3E) were substantially improved, as shown by reduced resolution decay in the motor domain density (Fig. S2, C and D). The average resolution of these reconstructions was 4.4 and 4 Å for the no nucleotide and AMPPNP states, respectively, with PfK5ΔL6-MD having a resolution range of 4.5–7 Å.

Alignment and superposition of our reconstructions directly reveal nucleotide-dependent differences in these structures (Fig. S3A). However, to facilitate interpretation of the differences, we also calculated a PfK5ΔL6-MD homology model and performed flexible fitting of this model within the cryo-EM density, in which individual secondary structure elements were well resolved (Fig. S3B). Local cross-correlation scoring showed overall improvement of model fit to density as a result of flexible fitting (Fig. S3C) and produced molecular models of each of the PfK5ΔL6-MDαβ-tubulin dimer complexes (Table 1). These provide a detailed picture of how PfK5ΔL6-MD interacts with both α- and β-tubulin. They also show that this divergent parasite motor has a canonical kinesin fold: it is built from a central β-sheet, sandwiched between three α-helices on each side, and flanked by a small β-sheet (β-lobe1) and a β-hairpin (β-lobe2) (Fig. 3, F and G). Using these models, we analyzed conformational differences between the no nucleotide and AMPPNP states.

**AMPPNP binding causes PfK5ΔL6-MD nucleotide-binding site closure**

The PfK5ΔL6-MD nucleotide-binding site (NBS) is located away from the MT surface, and despite the overall low sequence conservation of PfK5ΔL6-MD compared with HsK5 (Fig. S4), it is composed of three loops containing conserved sequence motifs. These are the P-loop—which interacts with the α- and β-phosphates of bound nucleotide—loop9 and loop11, which contain the switch-I and switch-II motifs, respectively (32).

In the absence of bound nucleotide, density for all three NBS loops is visible in PfK5ΔL6-MD, although density for the P-loop in the no nucleotide state is poorly defined (Fig. 4A). In addition, density corresponding to the C-terminal end of loop11, which is approximately 19 Å from the NBS, and contains a two residue Plasmodium-conserved insertion, is not visible. In the no nucleotide state, density corresponding to loop9 and the P-loop is well separated, while density is observed connecting loop9 and 11 (Fig. 4A). These configurations create an “open” NBS primed for ATP binding formed by a cavity between these three loops. Docking of a model of no nucleotide MT-bound kinesin-1 (33) into PfK5ΔL6-MD density reveals that the kinesin-1 switch loops fit poorly compared with the PfK5ΔL6-MD model, highlighting variations in the “open” NBS conformation between kinesins (Fig. S5A). In contrast to the no nucleotide state, in the AMPPNP state, there is clear density corresponding to the bound nucleotide in the PfK5ΔL6-MD NBS (Figs. 4A and S5B). In addition, the nucleotide is surrounded by loop9 and 11, which have closed around the bound nucleotide to form a cavity that supports ATP hydrolysis (Fig. 4A) (34).

Superimposing the PfK5ΔL6-MD no nucleotide and AMPPNP state models by alignment on αβ-tubulin allows visualization of the structural response of the PfK5ΔL6-MD

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**Table 1**

Cryo-EM data collection, 3D image processing and model refinement statistics

| Data collection parameter                  | PfK5ΔL6-MD nucleotide state | No nucleotide | AMPPNP |
|-------------------------------------------|-----------------------------|---------------|--------|
| Data Collection and 3D Image Processing   |                             | 160,000       | 160,000|
| Magnification                             |                             | .300          | .300   |
| Voltage (kV)                              |                             | .58           | .58    |
| Electron dose (e-/Å²)                      |                             | 1.39          | 1.39   |
| Pixel size (Å)                            |                             | 1320          | 335    |
| Number of Images                          |                             | 73,684        | 206,666|
| Data Collection Strategy                  | Manual                      |               |        |
|                                          | and automated               |               |        |
| Starting number of particles              |                             | 48,165        | 37,843 |
| Final particle number                     |                             | 73,684        | 206,666|
| (after particle symmetry expansion)       |                             |               |        |
| Box size (pixels)                         |                             | 432           | 432    |
| C1 reconstruction resolution (Å)           |                             | 4.5           | 4.8    |
| Asymmetric unit refine resolution (Å)      |                             | 4             | 4      |
| Model Refinement                          |                             |               |        |
| Global Cross-correlation                  |                             |               |        |
| Homology model                            |                             | 0.88          | 0.86   |
| Final model                               |                             | 0.89          | 0.89   |
| MolProbity                                |                             | 3.46          | 3.46   |
| Homology model                            |                             | 1.13          | 0.98   |
| Final model                               |                             |               |        |
| QMEAN                                     |                             |               |        |
| Homology model                            |                             | -2.21         | -2.21  |
| Final model                               |                             | -0.36         | 0.16   |
AMPPNP binding causes PfK5ΔL6-MD subdomain rearrangement

What are the consequences of these NBS rearrangements on the structure of PfK5ΔL6-MD? The structure of PfK5ΔL6-MD can be subdivided into three distinct subdomains (35), which are predicted to move with respect to each other during the motor’s MT-based ATPase cycle (Fig. 4C). The tubulin-binding subdomain (Fig. 4C, purple hues) consists of MT-binding elements in which helixα8 binds a shallow cavity at the intratubulin dimer interface. In addition, helixα5 and β-
lobe2 contact β-tubulin. The remaining two subdomains, the P-loop subdomain (Fig. 4C, blue hues) and switch-I/II subdomain (Fig. 4C, green hues), contain approximately half of the central β-sheet each, along with adjacent secondary structure elements. The NBS is located at the junction of these subdomains (Fig. 4C).

We measured the relative rotation of each helix (Table S1) in the transition from no nucleotide to AMPPNP states. This reveals the rearrangement of the P-loop and switch-I/II subdomains around a static MT-binding domain (Fig. 4D). The P-loop subdomain pivots such that helixα0 moves toward the MT surface, while helixα6 and the majority of the subdomain

Figure 4. AMPNPP binding causes PKSΔL6-MD subdomain rearrangement and switch loop closure. A, rearrangements of PKSΔL6-MD switch loops upon AMPPNP binding, with a schematic showing connectivity of the switch loops to motor domain secondary structure elements on the left. Models and corresponding density are displayed on the right, with nucleotide-binding loops colored according to the schematic. The brown arrow indicates where there is missing density for loop11, and the gray arrow indicates connecting density between loop9 and 11. B, comparison of PKSΔL6-MD no nucleotide and AMPPNP nucleotide binding loops, demonstrating AMPPNP induced conformational changes. C, the PKSΔL6-MD no nucleotide state model, colored according to kinesin subdomain, with α and β-tubulin depicted in light and dark gray surface rendering, respectively. D, PKSΔL6-MD subdomain rearrangement, showing no overall movement in the tubulin-binding subdomain, with rotations in the P-loop subdomain shown on the left, and the switch-I/II subdomain on the right.
move away from the MT surface. The switch-I/II subdomain rotates such that its constituent secondary structure elements move toward β-tubulin.

AMPPNP binding supports PfK5ΔL6-MD neck linker docking and cover neck bundle formation

What are the consequences for these subdomain rearrangements for the functional output of PfK5ΔL6-MD? Approximately 18 Å away from the MT surface, and 27 Å away from the NBS, is the neck linker. The neck linker is a C-terminal peptide extending from helixα6, which links the motor domain to the kinesin stalk, and which is relatively conserved in the kinesin superfamily (Fig. S6A). In the PfK5ΔL6-MD no nucleotide reconstruction, no density is observed extending from helixα6, indicating that the neck linker is disordered in this nucleotide state (Fig. 5A and S6B). At equivalent thresholds in the AMPPNP state, however, there is clear density corresponding to the neck linker at the C-terminus of helixα6 that extends along the motor domain in the direction of the MT plus-end (Fig. 5B). Docking of the AMPPNP state model into no nucleotide density confirms a lack of density to accommodate the neck linker, while density is unaccounted for when the no nucleotide model is docked in AMPPNP density (Fig. S6C). In addition, density corresponding to the PfK5ΔL6-MD N-terminus is also visualized in the AMPPNP state; this is consistent with formation of backbone interactions between this region and the neck linker, to form short β-strands known as the CNB, which is characteristic of plus-end directed kinesins (36) (Fig. 5B, dotted black oval; S6B). No such CNB density is observed in the no nucleotide reconstruction (Fig. S6B). Neck linker docking is enabled by the above-described rotation of the P-loop subdomain, which moves the N-terminus and the central β-sheet away from helixα5/loop13 in the static MT-binding subdomain (Fig. 4D) (37–40). This creates a cavity between loop13 and the N-terminus, known as the docking cleft, which enables neck linker docking. Thus, PfK5ΔL6-MD subdomain rearrangement causes opening of the docking cleft upon AMPPNP binding, a structural transition that is consistent with the ability of PfK5ΔL6-MD to drive ATP-dependent plus-end directed gliding motility (35).

MT-binding interface

PfK5ΔL6-MD binds to one αβ-tubulin dimer, with helixα4 centered at the intradimer interface (Fig. 6, A and B). At the PfK5ΔL6-MD-binding site, the sequence of the Sus scrofa αβ-tubulin used in our reconstruction is identical to that of P. falciparum αβ-tubulin (Fig. S7), facilitating a more detailed

Figure 5. AMPNPP binding supports PfK5ΔL6-MD cover neck bundle formation. A, no nucleotide PfK5ΔL6-MD model and corresponding cryo-EM density of the cover neck bundle region. Helixα6/neck linker, the N-terminus, and loop13 are colored according to the schematic. Note the lack of density for the neck linker at the terminus of helixα6. +/- symbols denote the MT polarity. Pink arrow indicates the lack of density for an ordered neck linker. B, as in (A) for the AMPPNP state (at equivalent density thresholds), showing density corresponding to the neck linker docked along the motor domain and cover neck bundle formation (CNB), which is highlighted by the dotted black circle.
investigation of this interface. To analyze which Pf\(K5\)Δ\(L6\)-MD secondary structure elements interact with \(\alpha\beta\)-tubulin in the no nucleotide state, we colored an \(\alpha\beta\)-tubulin surface representation according to different Pf\(K5\)Δ\(L6\)-MD secondary structure elements; we also colored Pf\(K5\)Δ\(L6\)-MD according to proximity to \(\alpha\) or \(\beta\)-tubulin (Fig. 6C). This analysis shows that helix\(\alpha4\) interacts with both \(\alpha\)- and \(\beta\)-tubulin, while \(\beta\)lobe1, loop11, and helix\(\alpha6\) interact with helices 4, 5, and 12 of \(\alpha\)-tubulin, and loop7, \(\beta\)lobe2, and helix\(\alpha5\) interact with similar secondary structure elements in \(\beta\)-tubulin.

Much of this Pf\(K5\)Δ\(L6\)-MD-MT interface is similar between the no nucleotide and AMPPNP states (Fig. 6D, Table S2). However, subdomain rearrangement and NBS closure in the AMPPNP state result in some changes. The largest of these occurs at the \(\alpha\)-tubulin interface, where rotation of the P-loop subdomain decreases the interaction of helix\(\alpha6\) with \(\alpha\)-tubulin, and positions \(\beta\)lobe1 closer to \(\alpha\)-tubulin, increasing its interface area. The interface area of loop11 also increases in the AMPPNP state. Interestingly, \(\beta\)lobe1/loop2 forms an interface area with \(\alpha\)-tubulin of 181 and 145 Å\(^2\) in the no nucleotide and AMPPNP states, respectively. Taken together, this shows that the Pf\(K5\)Δ\(L6\)-MD-MT interface is similar to that observed for other kinesin-5s, although the extent to which \(\beta\)lobe1/loop2 interacts with \(\alpha\)-tubulin differs between different family members (8, 21, 41).

Pf\(K5\)Δ\(L6\)-MD **loop5 forms a unique putative drug-binding site**

Loop5 plays an important role in the mechanochemistry of HsK5 (14, 16), and forms the drug-binding pocket of HsK5-specific inhibitors (17). It is a solvent exposed loop that creates a break in helix\(\alpha2\) and protrudes from the surface of the motor domain away from the MT. The loop5 sequence is well conserved between Plasmodium species (76–91% sequence identity) and is longer compared with HsK5 (Fig. 7A). In the no nucleotide state of Pf\(K5\)Δ\(L6\)-MD, some very poorly defined density corresponding to loop5 can be seen at a low threshold (Fig. 7B), suggesting that this region is largely disordered in this state.

In the AMPPNP state, however, clear density corresponding to loop5 can be seen, which forms two distinct regions. This density extends at an angle from helix\(\alpha2\), forming elongated density projecting from the motor domain between helixa1 and helixa3 (Fig. 7C). This region is at lower resolution than
other parts of the reconstruction, possibly owing to intrinsic flexibility, but also possibly because of the residual resolution gradient toward the outer surface of PfK5ΔL6-MD (Fig. S2C). There is no secondary structure-like density in this region of the motor, consistent with sequence-based predictions (Fig. S4) and, therefore, a model for PfK5ΔL6-MD loop5 was not calculated.

Strikingly, however, the density corresponding to loop5 in the AMPPNP state does not protrude away from the surface of the motor but appears to cover the site between helices α2 and 3, equivalent to the well-described inhibitor-binding site in HsK5. Docking of a crystal structure of HsK5 bound to the well-characterized inhibitor STLC in the PfK5ΔL6-MD density reveals the poor match between HsK5 loop5 and the PfK5ΔL6-MD loop5 cryo-EM density is depicted in gray. E, conservation of residues partaking in STLC binding between PfK5ΔL6-MD and HsK5, based on primary sequence alignment in (A). Using PDB ID: 2WOG, HsK5 residues contacting STLC were found using Chimera, and are displayed, with loop5 residues colored blue, and residues from helicesα2-3 colored green. Equivalent PfK5 residues are shown in gray with HsK5 residue labels. Nonconserved residues are displayed in red boxes, with conserved ones shown in black boxes. F, ATPase rates of PfK5ΔL6-MD and HsK5 rate in the absence of MTs, with either no treatment, + 20 μM STLC, or DMSO (with the same % v/v as the % v/v of STLC). Statistical relationships were tested using a one-way ANOVA, followed by a post-hoc Tukey’s multiple comparison test.

Figure 7. PfK5ΔL6-MD loop5 alters the environment of the kinesin-5 drug-binding site. A, primary sequence alignment of loop5 from HsK5 (UniProt ID: P52732), PK5 (O77382) and various other Plasmodium species (Py = vivax (A0A564ZV10), Pk = knowlesi (A0A1Y3DT2), Ph = berghei (A0A12214M3)). Conserved positions are colored according to the ClustalX scheme, and a conservation score as calculated in Jalview is given below. B, Loop5 density (gray) in the no nucleotide state, compared with other PfK5ΔL6-MD density (blue). C, Loop5 density (gray) in the AMPPNP state, compared with other PfK5ΔL6-MD density (left), and the PfK5ΔL6-MD model (right). D, the STLC bound HsK5 crystal structure in lime (PDB ID: 2WOG (89)), which was rigid body fitted into the PfK5ΔL6-MD AMPPNP state map. STLC is colored purple, and HsK5 loop5 is colored blue. PfK5ΔL6-MD loop5 cryo-EM density is depicted in gray.

Molecular mechanism of a parasite kinesin
**Molecular mechanism of a parasite kinesin**

by STLC (42). Consistent with our structural prediction, while STLC inhibits HsK5 ATPase activity, it does not inhibit PfK5ΔL6-MD (Fig. 7F). Thus, despite the conserved aspects of PfK5ΔL6-MD mechanochemistry uncovered by our data, evolutionary divergence between PfK5ΔL6-MD and HsK5 mediates differential inhibition of these kinesin-5 motors.

**Discussion**

We have determined the biochemical properties and MT-bound cryo-EM structures of a spindle-associated kinesin-5 motor from the malaria parasite. Despite considerable divergence from the human host kinesin-5 sequence, our *P. falciparum* kinesin-5 PfK5ΔL6-MD construct shares with HsK5 a comparatively slow MT-stimulated ATPase, plus-end directed MT gliding activity, and nucleotide-dependent conformational changes that support plus-end directed motility. Significantly, however, our structures revealed a different configuration of the well-characterized loop5-defined drug-binding pocket. Further, we also showed that PfK5ΔL6-MD exhibits no sensitivity to the classical HsK5 loop5-binding drug STLC.

The steady-state ATPase activity of PfK5ΔL6-MD is ~340 times slower than *H. sapiens* kinesin-1 (40), 3–25 times slower than other members of the kinesin-5 family (22, 23, 41), and its MT gliding activity is similarly and proportionally slow. Our use of mammalian brain tubulin rather than native *P. falciparum* tubulin might, in principal, contribute to this—however, αβ-tubulin is well conserved between *S. scrofa* and *P. falciparum*, and the two species have identical residues at the kinesin-binding site (Fig. S7), suggesting that tubulin source is unlikely to influence PfK5ΔL6-MD activity. In further support of this, experiments comparing ATPase rates of a yeast kinesin-5 motor domain interacting with mammalian and yeast tubulin showed no difference (41). A previous study of *P. falciparum* and *vivax* kinesin-5s also observed slow ATPase rates for these motors (20). These findings are reminiscent of the properties of other kinesin-5s and indeed, this may be critical for their function—substitution of the slow motor activity of vertebrate kinesin-5 with faster kinesin-1 was functionally disruptive in the complex context of the spindle (43). This suggests that PfK5—like other kinesin-5s—operates in motor ensembles, where slow-moving teams of PfK5 collaborate to drive MT organization (11).

The malaria kinesin-5 protein we studied was engineered to remove a low-complexity region in loop6, a strategy that had previously been adopted both in characterizing malaria kinesin-5 (20) and other malaria proteins (44). The insertion point of loop6 lies approximately 40 Å from the NBS and, although we cannot exclude that removal of this region influences PfK5ΔL6-MD’s behavior, our structures clearly demonstrate that the engineered protein adopts a canonical kinesin fold and undergoes a structural response to AMPPNP binding. Loop6 residues are therefore not required for protein folding and fundamental kinesin mechanochemistry. Low-complexity regions such as PfK5 loop6 are very common in malaria proteins and are often found inserted in otherwise well-conserved three-dimensional folds (19). While the role of such low-complexity regions in immune evasion is logical for extracellular parasite proteins (45), it remains unclear if and how such regions modulate intracellular protein function.

Improvements of our MiRP image analysis procedures allowed us to efficiently handle the incomplete binding of PfK5ΔL6-MD along the MTs in our cryo-EM data (Fig. S2) and to clearly visualize MT-bound PfK5ΔL6-MD at 5–6 Å resolution. Our structures showed that PfK5ΔL6-MD exhibits an open-to-closed conformational change in the NBS, kinesin motor subdomain rearrangements, and CNB formation on ATP analogue binding, typical of a classical plus-end kinesin (33, 40, 46). The lowest resolution region of our PfK5ΔL6-MD is its MT-distal surface, which encompasses the potential drug-binding loop5 region. Because we used GMPCPP-stabilized MTs, we do not think that MT lattice discontinuities—that can occur on paclitaxel-stabilized MTs (31, 47)—cause this resolution loss. Rather, loop5 of PfK5ΔL6-MD, which is 21 residues longer than in HsK5 and composed mainly of hydrophilic residues, appears to be intrinsically flexible and thus its conformation is more challenging to capture structurally. Density for loop5 is only well defined in the AMPPNP state and not the no nucleotide state, suggesting it is conformationally sensitive to bound nucleotide, as also observed with HsK5 loop5 (48). Strikingly, density attributable to loop5 impinges on the pocket corresponding to the well-characterized drug-binding site in HsK5 (49) and provides a possible explanation for the lack of sensitivity of PfK5ΔL6-MD to inhibition by the small-molecule STLC. Given the strong sequence conservation in loop5 between different *Plasmodium* species, this encouraging finding raises the possibility of selective inhibition of parasite motors. Indeed, a small-molecule screen identified a compound able to inhibit *Plasmodium* kinesin-5 ATPase activity, but not that of HsK5 (20).

*Plasmodium berghei* kinesin-5 localizes to mitotic and meiotic spindles in blood and mosquito stages of the parasite life cycle (50), consistent with a conserved role for this motor in the parasite cell division machinery. Although we know very little else about the function of this motor, we infer from our biochemical and structural data that *Plasmodium* kinesin-5 is likely to play an MT-organizing role within parasite spindles. Kinesin-5 is not essential during the blood stages of the *Plasmodium* life cycle (50, 51). However, knockout of *P. berghei* kinesin-5 substantially reduces the number of sporozoites in oocysts and mosquito salivary glands. This highlights the operational diversity of replication at different parasite life cycle stages in general and specifically suggests a key role for kinesin-5 in the multiple rounds of mitosis that occur during sporozoite production in the mosquito host (50).

There is increasing focus on tackling malaria not only during the symptomatic blood stages of the parasite life cycle but also by perturbing *Plasmodium* transmission between vector and host to facilitate malaria control at the population level (52). Intriguingly, despite the reduction of sporozoite numbers in kinesin-5 knockout parasites, the residual sporozoites achieved normal infectivity. Nevertheless, the role of kinesin-5 in this life cycle stage sheds light on parasite...
transmission vulnerabilities. Particularly given the distinct parasite number threshold that supports onward transmission between vector and host (53), combinations of perturbations that reduce overall sporozoite production could enable transmission control. Moreover, the diverse mechanisms by which small molecules can inhibit HsK5 function have demonstrated that some modes of motor inhibition can be more functionally disruptive than preventing MT binding or than removing motor function completely, for example, by trapping it in a tightly bound MT state (21). In fact, tight MT binding is the proposed mechanism for the antifungal small molecules that target Candida albicans kinesin-5, despite that motor being nonessential (54). In the context of these promising findings, our data provide a structural basis for future investigations into parasite-specific kinesin inhibitors.

**Experimental procedures**

**Protein expression and purification**

The PfK5 motor domain (PfK5MD, residues 1–493) was expressed and purified, but with low yield due to precipitation during purification. Therefore, PfK5MD was engineered such that 105 amino acids of the asparagine/lysine-rich insertion in loop6 (residues 175–269) were removed. The resulting construct, which we refer to as PfK5ΔL6-ΔMD, was cloned in a pET-15D-TOPO vector (Invitrogen) with an N-terminal His6-tag and TEV protease cleavage site, and each preparation was expressed in 12 L BL21 Star DE3 Escherichia coli cells (Invitrogen) grown in LB media. Cells were grown at 37 °C until they reached an optical density of 0.8–1.0 and were then induced with 0.1 mM IPTG for 3 h at 26 °C. Cells were harvested (6300g, 15 min, 4 °C) and stored at −80 °C.

Cells were lysed with three passages through a C3 homogenerizer (Avestin) in 100 ml IMAC W buffer (50 mM Tris-HCl pH 8, 400 mM NaCl, 2 mM MgCl2, 2 mM DTT, 1 mM ATP, 10 mM imidazole pH 8), which was supplemented with 2× Complete EDTA-free protease inhibitor tablets (Roche), 15 μg/ml DNase I (Roche), 0.5 mg/ml Lysozyme, 10% v/v glycerol. The lysate was then clarified by centrifugation (48,000g, 45 min, 4 °C). PfK5ΔL6-MD was purified from the clarified lysate at 4 °C using an AKTA Pure (GE Healthcare) in 1 day, which reduced loss of protein due to aggregation. First, nickel affinity chromatography was performed where the lysate was loaded onto a 5 ml HisTrap Excel column (GE Healthcare), followed by a wash with 20 column volumes (CV) of IMAC W, then reverse elution with 10 CV of IMAC E buffer (same composition as IMAC W, but with 300 mM imidazole). The eluate from this step was concentrated to 10–15 ml with a Vivaspin concentrator (Sartorius). Concentrated sample was then exchanged into IEX W buffer (same as IMAC W, except containing 80 mM NaCl and no imidazole) using a HiPrep 26/10 desalting column (GE Healthcare). Next, anion exchange chromatography (1 ml HiTrap Q HP) was performed, where the flow-through and wash fractions containing PfK5ΔL6-MD were pooled. The His6-tag was then cleaved by incubation with 100 μg/ml TEV protease for 2–4 h at 4 °C. TEV-protease and any remaining contaminants were removed using nickel affinity chromatography (1 ml HisTrap HP), where flow-through and wash fractions containing PfK5ΔL6-MD were pooled. PfK5ΔL6-MD was concentrated to 100–150 μl then, using 0.5 ml Zeba 7K MWCO spin columns, was exchanged into T50K20 buffer (50 mM Tris-HCl pH 8, 20 mM KCl, 2 mM MgCl2, 2 mM DTT). This purified PfK5ΔL6-MD was snap frozen in liquid nitrogen and stored at −80 °C. PfK5ΔL6-MD purity was measured using Coomassie-stained SDS-PAGE band intensity measurement in Fiji (55).

**Protein labeling**

Gibson assembly (56) was used to clone in-frame a C-terminal SNAP-tag on PfK5ΔL6-MD (PfK5ΔL6-MD-SNAP) for use in total internal reflection microscopy (TIRFM) experiments. Expression and purification of PfK5ΔL6-MD-SNAP were performed as for PfK5ΔL6-MD, except the anion exchange chromatography step was altered as follows: concentrated and desalted sample was added to a 1 ml HiTrap Q HP column, washed with 10 CV IEX W buffer, and eluted with a 20 CV gradient elution to 500 mM NaCl. Eluted fractions containing PfK5ΔL6-MD-SNAP were pooled. PfK5ΔL6-MD-SNAP was biotinylated or fluorescently labeled by overnight incubation at 4 °C with SNAP-Biotin or SNAP-Surface Alex Fluor 647 (New England BioLabs) with at least a 3:1 M excess of these labels to PfK5ΔL6-MD-SNAP. Free SNAP-ligand was removed by two repeats of buffer exchange in T50K20 buffer (0.5 ml Zeba 7K MWCO spin columns).

**MT preparation**

Purified and lyophilized unlabeled, X-rhodamine labeled, or biotin labeled S. scrofa brain tubulin—except X-rhodamine, which was from Bos taurus—(catalogue numbers T240C, TL620M T333P, respectively, all >99% pure, Cytoskeleton Inc) was reconstituted to 10 mg/ml in BRB80 (80 mM PIPES pH 6.8, 2 mM MgCl2, 1 mM EGTA pH 6.8), centrifuged at 611,453g for 10 min at 4 °C, and the supernatant snap frozen in liquid nitrogen and stored at −80 °C. Double cycle GMPcPP polymerization was performed as follows: reconstituted tubulin was supplemented with 1 mM GMPcPP (Jena Biosciences) and incubated for 5 min on ice. Tubulin was then polymerized at 4–5 mg/ml for 20 min at 37 °C. MTs were then pelleted at 611,453g for 10 min at 23 °C, washed twice, then resuspended, both with BRB80. MTs were then depolymerized on ice for 15 min, and a second round of polymerization performed as above. MTs for the ATPase assay were pelleted on a 50% v/v sucrose/BRB80 cushion after the second polymerization, to aid separation of MTs from unpolymerized tubulin.

For labeled MTs, X-rhodamine and unlabeled tubulin were mixed in a 1:9 ratio, or X-rhodamine, biotinylated, and unlabeled tubulin were mixed in a 1:1:8 ratio and polymerized at approximately 4 mg/ml total tubulin with 1 mM GTP at 37 °C for 20 min 40 μM Paclitaxel (Merck) dissolved in DMSO was then added, followed by a further incubation at 37 °C for 15 min, and then incubation at room temperature for at least 1 day before use. To prepare polarity marked MTs (57), long,
Molecular mechanism of a parasite kinesin

dimly labeled MTs (1:9 ratio of X-rhodamine to unlabeled tubulin) were polymerized at 2 mg/ml total tubulin for 2 h with 1 mM GMPCPP. To prepare NEM-tubulin, by which minus-end MT growth is blocked, 8 mg/ml unlabeled tubulin was incubated with 1 mM N-ethyl maleimide (Sigma) on ice for 10 min, then with 100 mM β-mercaptoethanol (Sigma) for 10 min. To polymerize the bright plus-end MT cap, NEM-tubulin was mixed 1:1 with X-rhodamine tubulin and incubated at 37 °C for 15 min. Finally, long, dim MTs were pelleted (15 min, 17,000 rpm, room temperature), the pellet resuspended with bright MT caps, incubated 37 °C for 15 min, then 40 μM paclitaxel added.

Steady-state ATPase activity

An NADH-coupled ATPase assay (58) containing 1.5 mM Phosphoenolpyruvate (Sigma), 9–15 U/ml pyruvate dehydrogenase (Sigma), 13.5–21 U/ml lactate dehydrogenase (Sigma), and 0.25 mM NADH (Roche) was used to measure PfK5ΔL6-MD ATPase rates. Reactions were performed in T50K40 buffer (50 mM Tris–HCl pH 8, 400 mM KCl, 2 mM MgCl2, 2 mM DTT) with 100–200 nM PfK5ΔL6-MD. A340 readings were taken on a SpectraMax 384 (Molecular Devices) from 100 μl reactions at 26 °C, with automatic path length correction to 1 cm, taking readings every 10 s for 30 min. Background readings containing no PfK5ΔL6-MD were subtracted from all readings. ATP hydrolysis per second per site was derived with the Beer–Lambert equation, and kcat calculated using the Michaelis–Menten equation with the term Km (rate at substrate concentration of 0).

\[
ATP \text{ s}^{-1} \text{ site}^{-1} = \frac{(k_{cat} - K_m)[S]}{K_m + [S]} + K_0
\]

MT gliding and single-molecule TIRFM assays

TIRFM assays with fluorescently labeled protein were performed in a flow-chamber, created by adhering biotin-PEG coverslips (MicroSurfaces Inc) to glass slides with double-sided tape. To prepare flow chambers for the MT gliding assay, the following treatments were made. (1) 0.75% Pluronic acid +5 mg/ml casein was added for 5 min, and the chamber was washed with T50K20 buffer + 20 μM paclitaxel (T50T). (2) 0.5 mg/ml neutravidin was added for 2 min, then the chamber was washed twice with T50T + 1 mg/ml casein (T50TC). (3) 1–2.5 μM PfK5ΔL6-MD-SNAP was added for 2 min, then washed twice with T50TC. (4) Finally, T50TC supplemented with 20 mM glucose, 300 μM glucose oxidase, 60 μg/ml catalase, 71 mM β-mercaptoethanol, and 0.5 μM X-rhodamine MTs was added. For single-molecule experiments, the same preparations were performed with the following exceptions. (3) 0.5 μM X-rhodamine/biotin MTs was added for 2 min, then washed twice with T50TC. (4) As above, except 1–100 nM PfK5ΔL6-MD-SNAP-alexa647 was added instead of MTs.

Fluorescent molecules were visualized on an Eclipse Ti-E inverted microscope with H-TIRF illuminator, LU-N4 laser unit, and CFI Apo TIRF 1.49 NA oil objective lens 100× (Nikon) (59). Images were recorded on an iXon DU888 Ultra EMCCD camera (Andor) with 60–100 ms exposures. MT velocity and parameters of PfK5ΔL6-MD MT binding were calculated from kymographs generated in FIJI (55). For MT binding, only events ≥3 frames were considered. Mean dwell time/kcat was calculated by fitting a one-phase exponential decay model to the data. Background kcat rates were measured by randomly sampling areas without MTs in the ADP and ATP states, because these states had high background binding, owing to the high concentrations needed to observe PfK5ΔL6-MD-SNAP-binding events.

Cryo-EM sample preparation, imaging, and data processing

Nucleotide-free PfK5ΔL6-MD was prepared by incubation with 10 U/ml apryrase (Sigma) for at least 15 min at 4 °C, to remove any nucleotides still present following purification. UltraAufoil 1.2/1.3 gold (Quantifoil) electron microscopy grids were glow discharged in air for 1 min at 0.3 mpa using a PELCO easyGlow (Ted Pella, Inc.). Using a Vitrobot Mark IV (ThermoFisher), with the chamber set to 23 °C and 95% humidity, 4 μl of 3.5 μM GMPCPP MTs was added to grids and incubated for 30 s, then blotted. Four microliter of 50 μM no nucleotide PfK5ΔL6-MD was then immediately added, incubated for 30 s, then blotted. A second round of PfK5ΔL6-MD was added before blotting and plunge freezing into an ethane slush. AMPPNP PfK5ΔL6-MD was prepared by incubation with 5 mM AMPPNP (R&D Systems) for at least 5 min at 4 °C. Vitrifition was performed as above, except using C-flat 2/2 carbon (Protochips) holey grids with 5 μM GMPCPP MTs.

Imaging was manually or automatically performed on a G2 Polara (FEI/ThermoFisher) operating at 300 kV using SerialEM (60). Images were collected on a K2 summit detector in counting mode, with a GIF Quantum LS Imaging Filter (Gatan). The sample was exposed with 58 e−/Å2 for 18 s and 60 frames collected with a pixel size at the sample of 1.39 Å.

All image processing steps were performed with RELION v3.0.0 and 3.1 (27, 61) except where otherwise noted. Beam-induced motion in micrographs was corrected using RELION’s implementation of MotionCor2, and the CTF was determined for each micrograph using Gctf (62). The start/end coordinates of each MT were manually assigned, and MT particles with a box size of 432 pixels were extracted every 82 Å and normalized. Alignment and asymmetric reconstruction of 14 protofilament (PF) MTs (which are the dominant MT type in GMPCPP preparations (63)) was performed using MiRP (18), as follows, with new MiRP updates noted (Fig. S2). RELION parameters used for MiRP PF sorting, initial seam alignment, and seam checking steps are listed in Table S3. Briefly, PF number assignment for each MT was performed with supervised 3D classification. As part of the MiRP update undertaken during this work, after 3D classification, PF number class assignments for each MT were smoothened by calculating the mode of class assignment over a seven-particle window. Where changes in class assignment occurred within a single MT—due to, for example, changes in...
PF number or major defects within a single MT—MT regions were subsequently treated as distinct MTs. This improved the homogeneity of each MT, increasing confidence in protofilament number assignment and seam location determination. Initial seam alignment was then performed with several iterations of 3D alignment. This was followed, as previously, by Rot angle and X/Y coordinate fitting—however, a local search step was added to improve Rot angle and X/Y shift assignment. Seam checking via supervised 3D classification was then performed, and MTs with less than 50% confidence in seam class assignment were removed. C1 reconstructions were obtained with a 3D auto-refine run (using the parameters for X/Y refine in Table S3, with a solvent mask obtained from a 3D reconstruction of seam checking results), followed by per-particle CTF refinement, Bayesian polishing, and beam-tilt estimation, then a second 3D auto-refine with these new corrections. MiRP was also updated to improve usability, by creating three programs for each MiRP step that can be operated from the RELION v3.1 GUI (https://github.com/moores-lab/MiRPv2).

Symmetrized maps were obtained by first performing 2D classification without alignment (200 classes, T = 8) and selecting well-aligned classes with many particles and an estimated resolution better than 6 Å. A 3D auto-refine run was then performed where 14-fold local symmetry was applied, as previously described (64). To address Pfk5ΔL6-MD heterogeneity, 3D classification was performed at the level of a Pfk5ΔL6-MD:αβ-tubulin asymmetric unit. For this, symmetry expansion was applied to all particles, then 3D classification (4 classes, T = 256) without alignment and a mask around one Pfk5ΔL6-MD site opposite the seam was applied. This resulted in one class with clear Pfk5ΔL6-MD decoration, which was selected and subjected to a 3D auto-refine procedure. The MT-bound nucleotide-free and AMPPNP-bound Pfk5ΔL6-MD reconstructions are deposited with the Electron Microscopy Data Bank, deposition number 12257 and 12258, respectively.

Sequence analysis, comparative modeling, and flexible fitting

To obtain a kinesin-5 family sequence alignment, the motor domains of all kinesin-5 family members in the Swiss-Prot database were aligned with MAFFT (65). A hidden Markov model of this alignment was created and queried against the UniProt Reference Proteomes database using HMMER (66). Sequences obtained were then compared with a kinesin profile from the Pfam database (67), and those with less than 400 identities were removed. Finally, the sequences were aligned with MAFFT, using the L-INS-i method (File S1). Secondary structure prediction was performed using Quick2D (68), using various prediction algorithms (69–73). A residue was assigned helical or beta-sheet identity if three or more prediction algorithms agreed.

The above sequence alignment was used in homology modeling of Pfk5ΔL6-MD, using the human kinesin-5 AMPPNP-bound crystal structure (PDB ID: 3HQD (34)) as a template. For this, 100 homology models were produced with Modeler v9.2 (74), then scored using QMEAN (75) and the top model selected. Restrictions used to model the extended helixα2 and for highly conserved positions in the nucleotide binding site are listed in Table S4. Flexible fitting of Pkf5ΔL6-MD secondary structure elements into no nucleotide and AMPPNP cryo-EM reconstructions was performed using FlexEM (76) (cap shift = 0.15) after rigid body docking of the top homology model using the Fit in Map tool in Chimera (77). During this procedure, the NBS (AMPPNP, Mg2+, switch-I/II loops, and the P-loop) was defined as a rigid body, while loop regions were treated as “all atoms.” Models of the N-terminus, loops 2, 8, 9, 10, 11, and 12, and the neck linker were predicted using Rosetta, firstly using a coarse method (500 models using cyclic coordinate descent with fragment insertion in the centroid modeling step (78)), then the model with highest cross-correlation was selected for a second prediction (500 models using kinematic closure with a fit to density term in the centroid modeling step (79)). A local all-atom fit to density step was then performed using the Rosetta Relax procedure including a fit to density term (80). Finally, the interface between Pfk5ΔL6-MD and αβ-tubulin was refined with protein–protein docking restrained by cryo-EM density in HADDOCK (81) as described previously (30), using the PDB ID 3JAT (82) as αβ-tubulin atomic model. SMOC scores were calculated using the TEMPy software package (83, 84). The molecular models of MT-bound nucleotide-free and AMPPNP-bound Pfk5ΔL6-MD are deposited with the Worldwide Protein Data Bank, deposition numbers 7NB8 and 7NBA, respectively.

Visualization and analysis

Plotting was performed with GraphPad Prism 8. Cryo-EM density and model analysis was done in Chimera (85) and ChimeraX (86). Protein sequence analysis was done in Jalview (87). Protein interface areas were calculated with PDBe PISA (88). Updated MiRP scripts and instructions are available on GitHub: https://github.com/moores-lab/MiRPv2. The MT-bound nucleotide-free and AMPPNP-bound Pfk5ΔL6-MD reconstructions are deposited with the Electron Microscopy Data Bank, deposition number 12257 and 12258, respectively. The molecular models of MT-bound nucleotide-free and AMPPNP-bound Pfk5ΔL6-MD are deposited with the Worldwide Protein Data Bank, deposition numbers 7NB8 and 7NBA, respectively. The kinesin-5 family motor domain sequence alignment is provided in File S1.

Supporting information—This article contains supporting information.

Acknowledgments—We thank N. Lukoyanova and S. Chen for electron microscopy support, D. Houldershaw for computational support, A. Peña for the gift of HsK5 protein, members of the Moores and Topf groups for helpful discussions, and C. Hoey, Z. Ahmed, and S. Lacey for early work on this project. Cryo-EM data

Molecular mechanism of a parasite kinesin
Molecular mechanism of a parasite kinesin

were collected at the Institute of Structural and Molecular Biology (ISMB), Birkbeck on equipment funded by the Wellcome Trust, UK (079605/Z/06/Z), and the Biotechnology and Biological Sciences Research Council, UK (BB/L014211/1).

Author contributions—A. D. C. and C. A. M. conceptualization; A. D. C. data curation; A. D. C. and A. J. R. formal analysis; M. T. and C. A. M. funding acquisition; A. D. C. investigation; A. J. R., A. J. R., and M. T. methodology; C. A. M. project administration; A. J. R. and R. T. resources; A. J. R., M. T., and C. A. M. supervision; A. J. R. validation; A. D. C. visualization; A. D. C. and C. A. M. writing—original draft; A. D. C., A. J. R., J. R., M. T., and C. A. M. writing—review and editing.

Funding and additional information—A. D. C. was supported by PhD studentships from the Medical Research Council, UK (MR/J003867/1) and funds from the Wellcome Trust (101311-10). This work was also supported by funds from the Wellcome Trust (085945/Z/08/Z) to C. A. M., A. J. R. (104196/Z/14/Z and 217186/Z/19/Z) and M. T. (209250/Z/17/Z and 208398/Z/17/Z) and the Medical Research Council, UK to C. A. M. (MR/R000352/1). R. T. was supported by the Biotechnology and Biological Sciences Research Council, UK (BB/N017609/1).

Conflict of interest—The authors declare that they have no conflicts of interest with the contents of this article.

Abbreviations—The abbreviations used are: CNB, cover neck bundle; cryo-EM, cryo-electron microscopy; HsK5, H. sapiens kinesin-5; MT, microtubule; NBS, nucleotide-binding site; PfK5, P. falciparum kinesin-5.

References

1. Donord, A. M., Nosten, F., Porabuth, Y., Das, D., Phyto, A. P., Tarning, J., Lwin, K. M., Arley, F., Hanphithakpong, W., Lee, S. J., Ringwald, P., Silamut, K., Imwong, M., Chotivanich, K., Lim, P., et al. (2009) Artemisinin resistance in plasmodium falciparum malaria. *N. Engl. J. Med.* 361, 455–467

2. Birnbaum, J., Scharf, S., Schmidt, S., Jonscher, E., Hoeijmakers, W. A. M., Schmidt, A. M., Flemming, S., Toenhake, C. G., Schmitt, M., Sabitzki, R., Bergmann, B., Fröhike, U., Mésén-Ramírez, P., Blancke Soares, A., Herrmann, H., Bärtfi, R., et al. (2020) A Kelch13-defined endocytosis pathway mediates artemisinin resistance in malaria parasites. *Science* 367, 51–59

3. Cowman, A. F., Healer, J., Marapana, D., and Marsh, K. (2016) Malaria: Biology and disease. *Cell* 167, 610–624

4. Van Vuuren, R. J., Visage, M. H., Theron, A. E., and Joubert, A. M. (2015) Antimitotic drugs in the treatment of cancer. *Cancer Chemother. Pharmacol.* 76, 1101–1112

5. Hirokawa, N., Noda, Y., Tanaka, Y., and Niwa, S. (2009) Kinesin superfamly motor proteins and intracellular transport. *Nat. Rev. Mol. Cell Biol.* 10, 682–696

6. Cross, R. A., and McAinsh, A. (2014) Prime movers: The mechanochemistry of mitotic kinesins. *Nat. Rev. Mol. Cell Biol.* 15, 257–271

7. Wojcik, E. J., Buckley, R. S., Richard, J., Liu, L., Huckaba, T. M., and Kim, S. (2013) Kinesin-5: Cross-bridging mechanism to targeted clinical therapy. *Gene* 531, 133–149

8. von Looefelholz, O., and Moores, C. A. (2019) Cryo-EM structure of the Ustilago maydis kinesin-5 motor domain bound to microtubules. *J. Struct. Biol.* 207, 312–316

9. Wickstrad, G., Gull, K., and Richards, T. A. (2010) Patterns of kinesin evolution reveal a complex ancestral eukaryote with a multifunctional cytoskeleton. *BMC Evol. Biol.* 10, 1–12

10. Kapitein, L. C., Kwok, B. H., Weinger, J. S., Schmidt, C. F., Kapoor, T. M., and Peterman, E. J. G. (2008) Microtubule cross-linking triggers the directional motility of kinesin-5. *J. Cell Biol.* 182, 421–428

11. Shimamoto, Y., Forth, S., and Kapoor, T. M. (2015) Measuring pushing and braking forces generated by ensembles of kinesin-5 crosslinking two microtubules. *Dev. Cell.* 34, 669–681

12. Acar, S., Carlson, D. B., Budamagunta, M. S., Yarov-Yarovoy, V., Correia, J. N., Niñonuevo, M. R., Jia, W., Tao, L., Leary, I. A., Voss, J. C., Evans, I. J., and Scholey, J. M. (2013) The bipolar assembly domain of the mitotic motor kinesin-5. *Nat. Commun.* 4, 1343

13. Myers, S. M., and Collins, I. (2016) Recent findings and future directions for interolar mitotic kinesin inhibitors in cancer therapy. *Future Med. Chem.* 8, 463–489

14. Kaseda, K., Crevel, I., Hirose, K., and Cross, R. A. (2008) Single-headed antimitotic drugs in the treatment of cancer. *Nat. Rev. Mol. Cell Biol.* 9, 271–281

15. Liu, L., Parameswaran, S., Liu, J., Kim, S., and Wojcik, E. J. (2011) Loop 5-directed compounds inhibit chimeric Kinesin-5 motors: Implications for conserved allosteric mechanisms. *J. Biol. Chem.* 286, 6201–6210

16. Behnke-Parks, W. M., Vendome, J., Honig, B., Maliga, Z., Moores, C., and Rosenfeld, S. S. (2011) Loop L5 acts as a conformational latch in the mitotic kinesin Eg5. *J. Biol. Chem.* 286, 5242–5253

17. Liu, L., Parameswaran, S., Liu, J., Kim, S., and Wojcik, E. J. (2014) Small molecule screen for candidate antimalarials targeting Plasmodium Kinesin-5. *J. Biol. Chem.* 289, 16160–16164

18. Peña, A., Sweeney, A., Cook, A. D., Topf, M., and Moores, C. A. (2020) Structure of microtubule-trapped human kinesin-5 and its mechanism of inhibition revealed using cryoelectron microscopy. *Structure* 28, 450–457.e5

19. Bell, K. M., Cha, H. K., Sindelar, C. V., and Cochran, J. C. (2017) The yeast kinesin-5 Cin8 interacts with the microtubule in a noncanonical manner. *J. Biol. Chem.* 292, 14680–14694

20. Manka, S. W., and Moores, C. A. (2018) Microtubule structure by cryo-electron microscopy. *J. Struct. Biol.* 209, 107402

21. Izzi, E., and Frontali, C. (2001) Low-complexity regions in plasmid falciparum proteins. *Genome Res.* 11, 218–229

22. Liu, L., Richard, J., Kim, S., and Wojcik, E. J. (2014) Small molecule screen for candidate antimalarials targeting Plasmodium Kinesin-5. *J. Biol. Chem.* 289, 16160–16164

23. Kimanius, D., Hagen, W. J. J. H., Lindahl, E., and Scheres, S. H. W. H. (2018) New tools for automated high-resolution cryo-EM structure determination in RELION-3. *Elife* 7, 1–38

24. Atherton, J., Yu, I.-M., Cook, A., Muretta, J. M., Joseph, A., Major, J., Couriges, Y., Clause, J., Topf, M., Rosenfeld, S. S., Houdusse, A., and Moores, C. A. (2017) The divergent mitotic kinesin MKLP2 exhibits atypical structure and mechanochemistry. *Elife* 6, e27793

25. Debs, G. E., Cha, M., Liu, X., Huen, A. R., and Sindelar, C. V. (2020) Dynamic and asymmetric fluctuations in the microtubule wall captured by high-resolution cryoelectron microscopy. *Proc. Natl. Acad. Sci. U. S. A.* 117, 16976–16984
Molecular mechanism of a parasite kinesin

32. Vale, R. D. (1996) Switches, latches, and amplifiers: Common themes of G proteins and molecular motors. *J. Cell Biol.* 135, 291–302.

33. Shang, Z., Zhou, K., Xu, C., Csencsits, R., Cochran, J. C., and Sindelar, C. V. (2014) High-resolution structures of kinesin on microtubules provide a basis for nucleotide-gated force-generation. *Elife* 3, 1–27.

34. Parke, C. L., Wojciech, E. J., Kim, S., and Worthylake, D. K. (2010) ATP hydrolysis in Eg5 kinesin involves a catalytic two-water mechanism. *J. Biol. Chem.* 285, 5859–5867.

35. Cao, L., Wang, W., Jiang, Q., Wang, C., Knossow, M., and Gigant, B. (2013) From plasmodium falciparum and implications for l-arginine depletion in *P. falciparum* and implications for l-arginine depletion in *P. falciparum*.

36. Vale, R. D. (1996) Switches, latches, and amplifiers: Common themes of G proteins and molecular motors. *J. Cell Biol.* 135, 291–302.

37. Cahu, J., and Surrey, T. (2009) Motile microtubule crosslinkers require distinct dynamic properties for correct functioning during spindle organization. *J. Mol. Biol.* 389, 144–160.

38. Schaber, M., Hartman, G. D., Huber, H. E., and Kuo, L. C. (2004) Inhibition of a mitotic motor protein: Where, how, and conformational consequences. *J. Mol. Biol.* 335, 547–554.

39. Zeeshan, M., Brady, D., Stanway, R. R., Moores, C. A., Holder, A. A., and Tewari, R. (2020) Plasmodium berghei kinesin-5 associates with the spindle apparatus during cell division and is important for efficient production of infectious sporozoites. *Front. Cell. Infect. Microbiol.* 10, 1–14.

40. Zhang, A. M., Wang, C., Otto, T. D., Oberstaller, J., Liao, X., Swamy, R., Udenze, K., Bronner, I. F., Cassandra, D., Mayho, M., Brown, J., Li, S., Swanson, J., Rayner, J. C., Jiang, R. H. Y., et al. (2018) Uncovering the essential genome of the human malaria parasite *Plasmodium falciparum* by saturation mutagenesis. *Science* 360, 1–10.

41. Aleshnicky, M., Ganusov, V. V., Nasir, G., Yenokyan, G., and Sinnis, P. (2020) Experimental determination of the force of malaria infection reveals a non-linear relationship to mosquito sporozoite loads. *PLoS Pathog.* 16, 1–23.

42. Xia, P. R., Root, D. M., Lee, Y., Sakowicz, R., Clarke, D., Pierce, D., Stephens, T., Hamilton, M., Morgan, B., Morgans, D., Nakai, T., Tomasi, A., and Maxon, M. E. (2007) Effective killing of the human pathogen Candida albicans by a specific inhibitor of non-essential mitotic kinesin. *KiPL* *Mol. Microbiol.* 65, 347–362.

43. Schindelin, J., Argandilla-Carreras, I., Frise, E., Kaynig, V., Longair, M., Pietzsch, T., Preibisch, S., Rueden, C., Saalfeld, S., Schmid, B., Tinevez, J. Y., White, D. J., Hartenstein, V., Ellicier, K., Tomancak, P., et al. (2012) Fiji: An open-source platform for biological-image analysis. *Nat. Methods* 9, 67–68.

44. Chua, P. R., Root, D. M., Lee, Y., Sakowicz, R., Clarke, D., Pierce, D., Stephens, T., Hamilton, M., Morgan, B., Morgans, D., Nakai, T., Tomasi, A., and Maxon, M. E. (2007) Effective killing of the human pathogen Candida albicans by a specific inhibitor of non-essential mitotic kinesin. *KiPL* *Mol. Microbiol.* 65, 347–362.

45. Hyman, A. A. (1991) Preparations of marked microtubules for the assay of the polarity of microtubule-based motors by fluorescence. *J. Cell. Sci.* 14, 125–127.

46. Kreuzer, K. N., and Jongeneel, C. V. (1983) Escherichia coli phage T4 topoisomerase. *Methods Enzymol.* 100, 144–160.

47. Lacey, S. E., He, S., Scheres, S. H. W., and Carter, A. P. (2019) Cryo-EM of DNA molecules up to several hundred kilobases. *Nat. Methods* 6, 343–345.
Molecular mechanism of a parasite kinesin

72. Wang, S., Peng, J., Ma, J., and Xu, J. (2015) Protein secondary structure prediction using deep convolutional neural fields. Sci. Rep. 6, 1–11
73. Klausen, M. S., Jespersen, M. C., Nielsen, H., Jensen, K. K., Jurtz, V. L., Sanderby, C. K., Sommer, M. O. A., Winther, O., Nielsen, M., Petersen, B., and Marcet, P. (2019) NetSurfP-2.0: Improved prediction of protein structural features by integrated deep learning. Proteins Struct. Funct. Bioinforma. 87, 520–527
74. Sali, A., and Blundell, T. L. (1993) Comparative protein modelling by satisfaction of spatial restraints. J. Mol. Biol. 234, 779–815
75. Benkert, P., Kunzli, M., and Schwede, T. (2009) QMEAN server for protein model quality estimation. Nucleic Acids Res. 37, 1–5
76. Topf, M., Lasker, K., Webb, B., Wolfson, H., Chiu, W., and Sali, A. (2008) Protein structure fitting and refinement guided by cryo-EM density. Structure 16, 295–307
77. Goddard, T. D., Huang, C. C., and Ferrin, T. E. (2007) Visualizing density maps with UCSF Chimera. J. Struct. Biol. 157, 281–287
78. Wang, C., Bradley, P., and Baker, D. (2007) Protein-protein docking with backbone flexibility. J. Mol. Biol. 373, 503–519
79. Mandell, D. I., Coutsi, A. E., and Kortemme, T. (2009) Sub-angstrom accuracy in protein loop reconstruction by robotics-inspired conformational sampling. Nat. Methods 6, 551–552
80. Wang, R. Y. R., Song, Y., Barad, B. A., Cheng, Y., Fraser, J. S., and DiMaio, F. (2016) Automated structure refinement of macromolecular assemblies from cryo-EM maps using Rosetta. Elife 5, 1–22
81. van Zundert, G. C. P., Rodrigues, J. P. G. I. M., Trellet, M., and Schmitz, C. (2016) The HADDOCK2.2 Web Server: User-friendly integrative modeling of biomolecular complexes. J. Mol. Biol. 428, 720–725
82. Zhang, R., Alushin, G. M., Brown, A., and Nogales, E. (2015) Mechanistic origin of microtubule dynamic instability and its modulation by EB proteins. Cell 162, 849–859
83. Farabella, I., Vasi, S., Joseph, A. P., Pandurangan, A. P., Sahota, H., and Topf, M. (2015) TEMPy: A Python library for assessment of three-dimensional electron microscopy density fits. J. Appl. Crystallogr. 48, 1314–1323
84. Joseph, A. P., Malhotra, S., Burnley, T., Wood, C., Clare, D. K., Winn, M., and Topf, M. (2016) Refinement of atomic models in high resolution EM reconstructions using Flex-EM and local assessment. Methods 100, 42–49
85. Pettersen, E. F., Goddard, T. D., Huang, C. C., Couch, G. S., Greenblatt, D. M., Meng, E. C., and Ferrin, T. E. (2004) UCSF Chimera — a visualization system for exploratory Research and analysis. J. Comput. Chem. 25, 1605–1612
86. Goddard, T. D., Huang, C. C., Meng, E. C., Pettersen, E. F., Couch, G. S., Morris, J. H., and Ferrin, T. E. (2018) UCSF ChimeraX: Meeting modern challenges in visualization and analysis. Protein Sci. 27, 14–25
87. Waterhouse, A. M., Procter, J. B., Martin, D. M. A., Clamp, M., and Barton, G. J. (2009) Jalview Version 2—a multiple sequence alignment editor and analysis workbench. Bioinformatics 25, 1189–1191
88. Krissinel, E., and Henrick, K. (2007) Inference of macromolecular assemblies from crystalline state. J. Mol. Biol. 372, 774–797
89. Kaan, H. Y. K., Ulaganathan, V., Hackney, D. D., and Kozielski, F. (2010) An allosteric transition trapped in an intermediate state of a new kinesin-inhibitor complex. Biochem. J. 425, 55–60