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An introduction to kinesin nomenclature problems

Kinesins constitute a superfamily of microtubule-based motor proteins with a diversity of functions including the transport of vesicles, organelles, and chromosomes and the regulation of microtubule dynamics (reviewed in 1). Individual kinesins are often named based upon their functional characteristics (2). However, kinesins are sometimes named based upon the position of the motor core within the protein (3), or by their evolutionary relatedness to other kinesins (e.g., many of the KHC family members reviewed in 4). It was possible to name and categorize all the known kinesins in 1994 (5), but today there are literally hundreds being named based upon differing criteria, and inconsistencies are emerging that can cause genuine confusion.

Kinesins with internal motor cores (KinI) are a good case in point. The MCAK family is often called the KinI family to emphasize the internal position of its members' motor cores. MCAK/KinI family members are thought to depolymerize microtubules (6), but not all kinesins that depolymerize microtubules belong to the MCAK/KinI family. Klp67A and Kar3 family members also have been shown to depolymerize microtubules (7, 8). *Saccharomyces cerevisiae* Kip3 and *Schizosaccharomyces pombe* Klp5 and Klp6 are three Klp67A family members which are thought to depolymerize microtubules (9, 10). Despite their phylogeny and the fact that members of the Kip3 family have N-terminal motor cores (Figure 1), Klp5 and Klp6 were recently called KinI family proteins to emphasize their function as microtubule depolymerizers (10). There also are kinesin sequences with internal motor cores that fall into families other than MCAK. Examples are KIF4 family members *Arabidopsis* AL049655_15 and *C. elegans* Z92811, Unc-104 family member human CMKRP, and CENP-E family member *Ustilago maydis* KIN1. Similarly, some KIFC2 sequences have C-terminal motor cores (e.g., mouse KIFC2, *C. elegans* KLP3, and *Morone saxatilis* FKIF2), but the motor position for the KIFC2 family is internal on average (Figure 1).

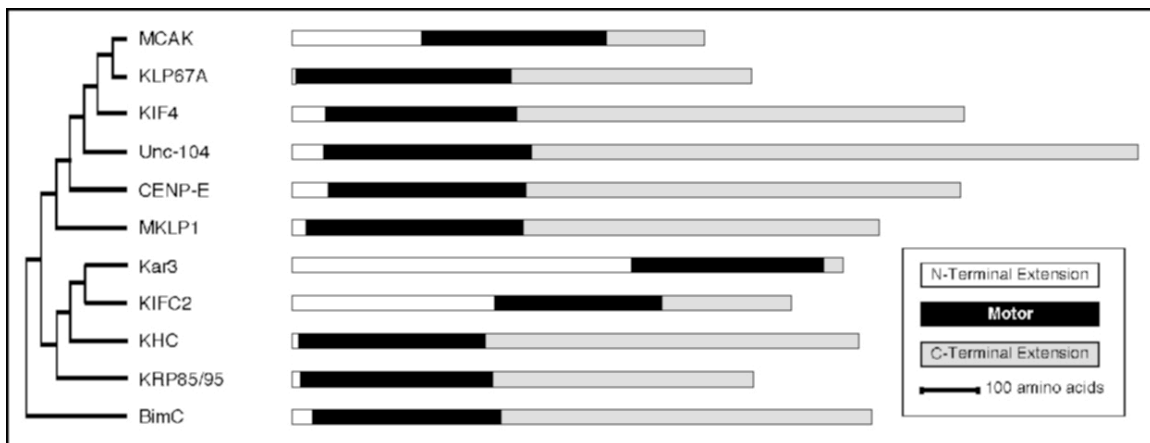


Figure 1. Average motor position for each kinesin family. (See also the table on page 10.) To the left of each family name is a cladogram depicting the relatedness of kinesin families to one another (11). To the right is a scaled diagram representing the family's average motor core location relative to the amino- and carboxy-termini of the protein. These average locations were determined by calculating the mean lengths of the amino-terminal extension, motor, and carboxy-terminal extension for all full-length sequences from the Lawrence et al. dataset (11).

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