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I think the most effective solution would be to follow the myosin model and continue the numbering system: Kinesin I, Kinesin II, Kinesin III, etc.. Yes, it would be hard to remember which group is which, but not as hard as now. I can't even remember the names in my own systems, flies and worms, from one day to the next. The advantages of the admittedly non-creative numbering are evident:

- 1) It allows groupings based on absolute qualities (sequence).
- 2) We avoid trying to give functional designations to groups of proteins whose functions aren't clear.
- 3) We avoid polarizing the community by choosing a nomenclature that favors any one of our strong past contributors over another.

The last one (#3) worries me the most. A uniform nomenclature is doomed unless most of the major labs cooperate.