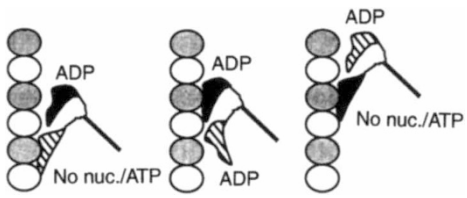

FIG. 4 A model, based on the observed change in angle, of how a pair of kinesin heads could move 8 nm along a tubulin protofilament. Although the spikes that project from the heads in our reconstructed images appear short, the extra protein sequence required to form dimers[25] presumably increases the leverage of the spikes. The simplest way that heads might act alternately over a long distance is for flexible connections to allow them to rotate freely around each other; the direction of movement is determined if, after the attached head changes conformation during ADP release, only the next binding site along the protofilament in the plus direction is within reach of the second head. This model is similar to model A proposed by Hackney[15], except that the angle change accompanies ADP release instead of ATP binding. The kinesin-like protein ncd moves towards microtubule minus ends. If ncd has a similar projecting spike which is tilted in the opposite direction in the strongly bound no-nucleotide and AMP–PNP states, then motility in the opposite direction could be explained by a similar model.

plus end, and thus produce the 8-nm step (Fig. 4). Therefore our results are consistent with a mechanism in which structural changes in the heads result in directional movement. □

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CORRECTIONS

Structure of a new nucleic-acid-binding motif in eukaryotic transcriptional elongation factor TFIIS

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WE previously reported binding of TFIIS residues 231–280 to single-stranded DNA by gel mobility-shift assay (Fig. 1 of this Letter). We have since discovered that the extended form (residues 175–280), rather than the shorter form (residues 231–280), of the protein was inadvertently used in this assay by one of our laboratories (K.A.). The binding of the shorter polypeptide to single-stranded DNA is not reproducible: we therefore retract Fig. 1. Although there is no published spectrofluorometric evidence of interaction between isolated zinc ribbon and nucleic acid, when site-directed mutations in the zinc ribbon domain of the intact protein are used in a stalled transcription assay this domain appears to interact with nucleic acids, as indicated by decrease or elimination of antitermination and RNA cleavage activities[1]. □

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Primary production required to sustain global fisheries

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THERE were several numerical errors published in this Letter, some kindly brought to our attention by M. Baumann and T. R. Parsons (personal communication).

- In Fig. 1, the catch of Nile perch should be 0.01 t km^{-2} yr^{-1} (not 0.1 t km^{-2} yr^{-1}).
- In Table 1, the primary production required (PPR) for squid in the upwelling system should be 4.1, that for shrimps on tropical shelves should be 3.5, and the k value of miscellaneous teleosteans should be 155.
- In Fig. 2, the abscissa should change in steps of 4%.

None of these errors affects the results of our study. □