logical monitoring could include surveillance for pests and their impacts on agriculture, nutrition, and health.

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In our sometimes desperate struggle to minimize the ongoing massive extinction event, scientists and conservationists have resorted to arguments about the value of biodiversity. Arguments with direct or indirect economic components are often front and center, and moderate support for them is abundant (*1*). However, such arguments run the risk of becoming the primary reason for the conservation of biodiversity, a result likely to doom many species (*2*). Evidence for the economic necessity of high species richness is hard to produce, as evidenced in the article by Baskin in which she reports the difficulty in demonstrating clearly the practical value of many species in maintaining ecosystem function.

The "wildlife must pay its way" approach to conservation must be only a part of an overall strategy that also relies on noneconomic values. Increasingly, the public worldwide is aware of and sympathetic to the conservation of biodiversity in its own right, independent of direct or indirect economic benefits (*3*). This is only hinted at in the single disclaimer in Baskin's article (p. 203) that "[c]onversely, participants emphasized even a species that seems to be a fifth wheel in the working of an ecosystem might be worth saving for economic, moral, or aesthetic reasons." We as a species are in the process of deciding that all species are worth saving and that our devastating assault on the world's biodiversity can no longer be justified on any grounds.

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Protein Configurations

The Research Article "Protein design by binary patterning of polar and nonpolar amino acids" by Satwik Kamtekar *et al.* (10 Dec. 1993, p. 1680) describes a strategy to test and validate the idea that only the sequence location, not the identity of the polar and nonpolar amino acid residues, must be specified explicitly in order for a stably folded protein structure to form. We previously published a related approach, based on a symmetrical characteristic of genetic information (*1*), which we believe should have been cited. Specifically, our work was based on the fact that the first two bases of a codon specify a particular amino acid, whereas the second base of the triplet encodes the amino acid's hydropathic character; therefore in-frame amino acid assignment to messenger RNA in the nonconventional 3' to 5' direction changes the primary sequence, but maintains the polar and nonpolar (binary) pattern for any peptide or protein (*1*, *2*). My colleagues and I exploited the symmetrical characteristic to ascertain whether the linear array of hydropathy (or binary code) patterned by a specific nucleotide sequence could determine structure (*1*, *3*) and function (*3*). By preparing peptides decoded from a 3' to 5' reading of the mRNA for both ACTH and GHRH, we showed antigenic cross reactivity, receptor binding, signal transduction, and hormonal activity (*1*, *3*). The elegant studies of Kamtekar *et al.* strongly confirm our previous findings on the role of the linear pattern of hydropathy (or binary code) in protein structure and clearly establish its degenerate nature.

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Corrections and Clarifications

The 1994 meeting of the American Institute of Biological Sciences, held concurrently with the meeting of the Ecological Society of America covered in the Meeting Briefs of 26 August (Research News, p. 1178), took place in Knoxville, Tennessee, not Nashville, as the title indicated.