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mined statistically by noting an increase in the expected incidence rate for that particular cancer. Even when such an increased incidence rate is observed, we cannot distinguish between those cancers that would have normally occurred and those that were due to exposure to the carcinogen.

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Balance in *Science*

I disagree with Daniel E. Koshland, Jr.'s, statement that "the chance of being published in *Science* is approximately the same for all fields of research" (Editorial, 28 July, p. 341).

To favor papers in physics and social sciences over those in biology does help represent the former two disciplines. But a definition of "biology" based on the contents of *Science* excludes many fields of biology. So many of the papers in *Science* are concerned with molecular, cell, and biochemical biology, especially those with human applications, that the journal's name might be changed to "*Biomedical Science*." One has to be in one of those specialized fields to even understand the titles! *Science* publishes so few papers on organismal biology (in such fields as ecology, zoology, or vertebrate morphology—which is the major division of the American Society of Zoologists), that it is no wonder authors from these fields do not bother to submit their papers to *Science*.

I think that *Science* has a long way to go before it "publish[es] the cutting edge of research in every branch of science as well as present[s] research that will interest readers ranging from physicists to social scientists."

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Response: Physicists will find it hard to believe that a biologist feels discriminated against by *Science*, but reader Reilly illustrates the point I was trying to make. Within each major field (physics, biology, and so forth), there are subdivisions (organismal, AIDS, crystallography, cell, and so forth in biology), each of which thinks their own area is underrepresented. What appears in *Science* is to a first approximation a constant fraction of what we receive in each area. That distribution is affected by funding and fashions that control the number of workers in a field, but we do not want it to be further influenced by the preconceptions of authors. We try to judge all papers equally but, if anything, give a slight edge to underrepresented areas—DANIEL E. KOSHLAND, JR.

Correction

We wish to make a correction concerning our 9 September 1988 report "Selection of variable-joining [VJ] region combinations in the α chain of the T cell receptor" (*1*). We have discovered that the $V_{58}J_3$ isolates actually contain part of the 3′ heptamer-spacer sequence from the V_{58} germline (*2*) and thus these do not, in fact, contain a joining segment. Because these isolates exhibit diversity at the coding-signal junction, we incorrectly assumed that they were bona fide VJ transcripts. At this time we do not know whether the junctional bases are nongermline elements introduced at the coding-signal joints, or whether transcripts from such nonrearranged V_α genes might serve some function. Transcripts from nonrearranged gamma genes have recently been reported, and these are inducible by interleukin-3 (*3*).

We would also like to comment on the observation that the $V_{58}J_{58}$ isolates do not contain diversity at the VJ joint. This lack of diversity, in contrast to that of all other VJ isolates from our laboratory, has raised the question of whether these may have been derived, as a polymerase chain reaction contaminant (*4*), from the α chain gene isolated from CTL 2C. At this time we do not have a definitive answer.

Despite the error in our analysis of the $V_{58}J_3$ isolates, the main tenet of our report (that is, the preferential association and expression of particular VJ combinations) holds true. Thus, the J_1 and J_2 isolates (figures 1 and 3) and only a few other J segments (*5*) have been found to be expressed as the predominant V_{58} transcripts.

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