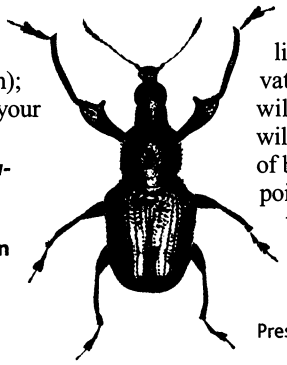
jects in the countries of origin. The message conveyed by this rigorous process is unmistakable: By giving a certain sum, you can both promote the discovery and description of new species (taxonomy) and support research into, and the protection of, biodiversity in natural habitats (conservation); and in recognition of your support, you will be honored with a dedicatory name.



What's in the name *Euops doertheae*? Sponsorship for taxonomy and for conservation in this bug's native land, Papua, New Guinea. (Length, ~2 to 3 cm.)

Anyone can sell names; there is nothing in the international codes to prevent this. In our experience, however, sponsors are interested in high-quality work resulting in reliable, enduring nomenclature; they are wary of dubious amateur publications that are likely, sooner or later, to result in duplication. BIOPAT is unique in this respect, and we do not accept that the risk referred to by Minelli *et al.* that "vendors could 'discover' species and invent genera for profit" will be increased as a result of serious scientific activity that is subject to rigorous review. Thus, while agreeing that "name selling" is not an acceptable approach, we dispute the notion that BIOPAT engages in this. We believe, on the contrary, that the kind of private sponsorship encouraged by BIOPAT will promote serious taxonomic work and will foster the description and conservation of biodiversity. Finally, we should also like to point out that BIOPAT is a transnational initiative to which any reputable museum, collection, or research institution may apply for membership.

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Metabolic Analysis in Drug Discovery

The special issue on drug discovery (17 Mar., pp. 1951–1981) focuses on the revolution being brought about by the Human Genome Project, making almost no direct mention of metabolism.

Numerable illnesses are disturbances of metabolism, and many drugs act by altering metabolism. The implied assumption is that once an enzyme inhibitor has been identified and a means found for delivering it to its target, the metabolic consequences are so obvious that they do not need to be thought about in advance. However, partial inhibition of a typical enzyme has little or no effect in vivo (*1*). Coping economically with huge increases in the number of potential drug targets that genomic science is uncovering—from about 500 molecular targets in current drug therapy to as many as 100,000 human gene products—will require procedures for eliminating the useless ones in advance. Such a screening process will require metabolic simulation (*2*) supported by mathematical methods for converting lists of gene products into metabolic pathways (*1*). Of the current molecular targets, about 30% are enzymes and 45% are receptors, and few

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if any are genes, so referring to 100,000 human genes as potential drug targets, as Bruce Agnew does in his News article ("When Pharma merges, R&D is the dowry," 17 Mar., p. 1952), is to focus attention in the wrong place.

With little attention being paid to metabolism with regard to drug discovery, it is not surprising that, as J. Drews points out in his Review ("Drug discovery: A historical perspective," 17 Mar., p. 1960), few leads and development compounds, if any, can be credited to the new drug discovery paradigm, which relies on the economy of numbers afforded by the advances in genomic science and related technologies. Nor is it surprising that genetic validation of targets can be misleading, as J. Rosamond and A. Allsop mention in their Review ("Harnessing the power of the genome in the search for new antibiotics," 17 Mar., p. 1973). An uncritical assault on the thousands of new targets revealed by the Human Genome Project might prove to be just trial and error in new clothes.

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Response

Metabolic analysis is by no means forgotten, as implied by Cárdenas and Cornish-Bowden. What is often called target validation must eventually include this type of analysis. As I discussed in my Review, the functional role of a particular target must be understood. Structural genomics, the systematic study of the three-dimensional structure of all proteins, will be helpful in this regard (*1*, *2*), as will traditional biochemistry and pathophysiology. Contrary to Agnew's reference in his News article to 100,000 genes in the human genome as potential drug targets, my colleagues and I have estimated, using genetic and biochemical data, the number of potential drug targets to be in the range of 5000 to 10,000 proteins, a figure that has since been broadly cited in the literature related to drug discovery (*3*).

Many drugs, such as antibiotics, have been around for several decades, and many were found empirically. This, however, does not invalidate approaches that target the molecular mechanism of action of new drugs. Without exception, antibiotics elicit their effects by modifying a single molecular target in a highly specific way. Finally, there are many ways to select potential drug targets from the ~100,000 human gene products. Genetic and biochemical tools as well as the methods of developmental biology are at our disposal. There does not have to be an "uncritical assault" on thousands of new drug targets, as Cárdenas and Cornish-Bowden imply.

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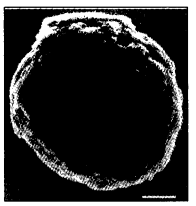
Planetary Solids Older than Earth



A presolar grain of graphite (~4 μm across).

CREDIT: T. BERNATOWICZ AND S. AMARI, WASHINGTON UNIVERSITY

David Stevenson in his Pathways of Discovery Essay "Planetary science: A space odyssey" (11 Feb., p. 997) surveys the role that planetary science has played and is playing in the evolution of the world views held by modern humankind, but he does not include one new window of wide philosophic interest that is so stunning as to contribute to the immense sweep of his canvas.

Pieces of small planets fall to the ground (meteorites) containing within them small, solid particles that are themselves older than Earth and older than our entire planetary system. These presolar solids (mostly SiC and graphite) floated amid the interstellar dust and gas that collapsed with the solar cloud in the event that gave birth to our solar system, and they were incorporated intact into the surface debris of the small planets from which meteorites arise (*1*). They are recognized by laboratory experiments to contain bulk isotopic compositions (*2*) of C, Si, Mg, Ti, N, and O and heavy trace elements that are wildly different from the mean composition shared by all of our planetary bodies.

Presolar solids came from long ago and far away, and they contain precise new information on the origin of the elements of which our solar system would later be born. Humankind thereby holds in its hands and studies in its laboratories solid samples that substantially predate the birth of our planetary system, but it is, ironically, our planetary system that delivers them to Earth. Stones from a time before there was an Earth, they speak not only of other systems in our universe but of times before our world existed. Their very existence shattered the belief that