DNA by Design: An Inference to the Best Explanation for the Origin of Biological Information

Stephen C. Meyer

Introduction

In the second chapter of *Philosophy and Biology*, Elliott Sober warns historians and philosophers of biology against the danger of anachronism. In particular, he notes that many contemporary evolutionary biologists regard the design hypothesis as inherently untestable and, therefore, unscientific in principle, simply because it no longer commands scientific assent. He notes that while logically unbeatable versions of the design hypothesis have been formulated (involving, for example, a "trickster God" who creates a world that appears undesigned), design hypotheses in general need not assume an untestable character. A design hypothesis could, he argues, be formulated as a fully scientific "inference to the best explanation." He notes that scientists often evaluate the explanatory power of a "hypothesis by testing it against one or more competing hypotheses."[1] On these grounds, he notes that William Paley's version of the design hypothesis was manifestly testable, but was rejected precisely because it could not explain the relevant evidence of then contemporary biology as well as the fully naturalistic theory of Charles Darwin. Sober then casts his lot with the neo-Darwinian explanation on evidential rather than methodological grounds. But the possibility remains, he argues,

> that there is some other version of the design hypothesis that both disagrees with the hypothesis of evolution and also is a more likely explanation of what we observe. No one, to my knowledge, has developed such a version of the design hypothesis. But this does not mean that no one ever will.[2]

This paper will develop a design hypothesis, not as an explanation for the origin of species, but as an explanation for the origin of the information required to make a living system in the first place. Whereas Darwinism and neo-Darwinism address

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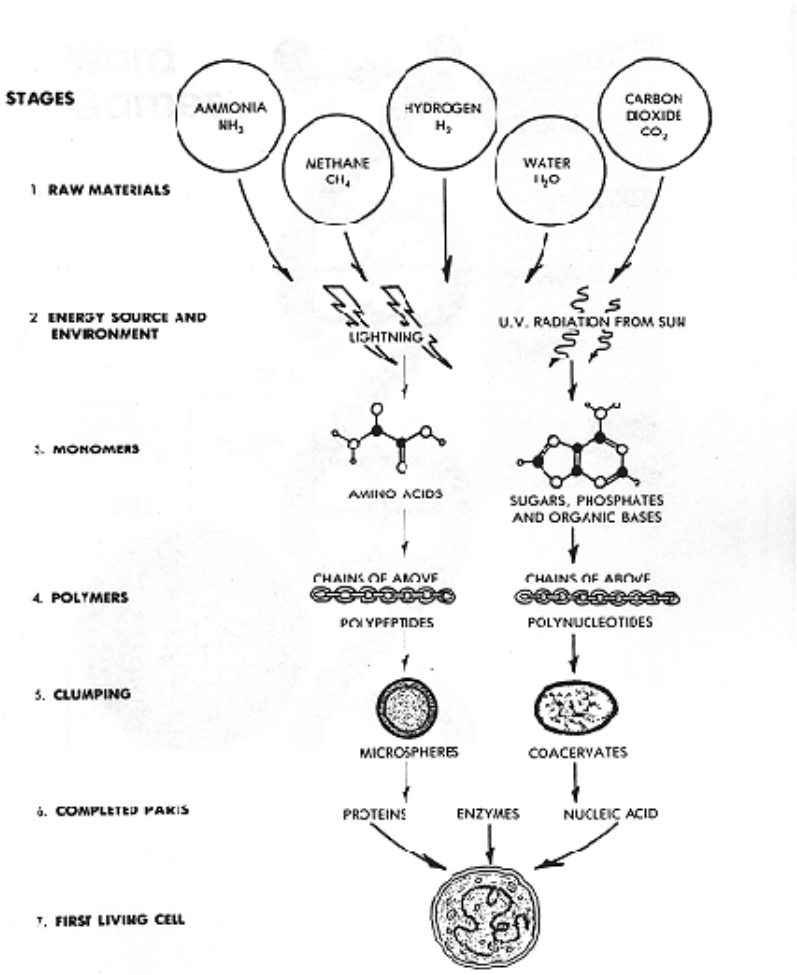
the former question, theories of chemical evolution have addressed the latter question of the ultimate origin of life. This essay will contest the causal adequacy of chemical evolutionary theories based upon "chance," "necessity," and their combination. In the process, it will trace developments in origin-of-life research from the 1920s to the present. As it happens, Jacques Monod's famous categories of "chance and necessity" provide a helpful heuristic for understanding the recent history of this discipline. From the 1920s to the mid-1960s origin-of-life research relied on theories that emphasized the creative role of random events—"chance"—often in tandem with some form of prebiotic natural selection. Since the late 1960s, theorists have instead emphasized deterministic self-organizational laws or properties, i.e., "necessity." This paper will argue that a third type of explanation—intelligent design—provides a better explanation for the origin of the information present in large biomacromolecules such as DNA, RNA, and proteins. To paraphrase Sober, this paper will present a version of the design hypothesis that disagrees with strictly materialistic theories of *chemical* evolution and provides a better explanation for the observed complexity of the simplest living organisms.

CHEMICAL EVOLUTION AND THE PROBLEM OF LIFE'S ORIGIN

After Darwin published *On the Origin of Species* in 1859, many scientists began to think about a problem that Darwin had not addressed, namely, how life had arisen in the first place.[3] While Darwin's theory purported to explain how life could have grown gradually more complex starting from "one or a few simple forms," it did not explain, nor did it attempt to explain, how life had first originated. Yet evolutionary biologists in the 1870s and 1880s such as Ernst Haeckel and Thomas Huxley assumed that devising an explanation for the origin of life would be fairly easy. For one thing, they assumed that life was essentially a rather simple substance called protoplasm that could be easily constructed by combining and recombining simple chemicals such as carbon dioxide, oxygen, and nitrogen. In Haeckel's words, the cell constituted nothing more than a simple "homogeneous globule of plasm."[4]

Though Haeckel and Huxley's own simplistic theories of "abiogenesis"[5] failed to attract much support, a Russian scientist named A. I. Oparin had by the 1930s succeeded in formulating a sophisticated Darwinian-style theory. His so-called chemical evolutionary theory included all the essential Darwinian elements: time, natural selection, and random variation. Like Darwin, Oparin invoked the same presumptively creative interplay of "chance and necessity" to account for the origin of complexity from initial simplicity at the prebiotic level.

Oparin's theory envisioned a series of chemical reactions (see Figure 1) that he thought would enable a complex cell to assemble itself gradually and naturalistically from simple chemical precursors. Oparin, like his nineteenth-century predecessors,



Fiure 1. Chemical evolutionary theorists envision life developing from simple chemicals in a series of steps such as these. Courtesy of John Wiester.

suggested that life could have first evolved as the result of a series of chemical reactions. Unlike his predecessors, however, he envisioned that this process of chemical evolution would involve many more chemical transformations and reactions and many hundreds of millions (or even billions) of years. Oparin believed that simple gases such as ammonia (NH_3), methane (CH_4), water (H_20), carbon dioxide (CO_2), and hydrogen (H_2) would have rained down to the early oceans and combined with metallic compounds extruded from the core of Earth.[6] With the aid of ultraviolet

radiation from the sun, the ensuing reactions would have produced energy-rich hydrocarbon compounds.[7] These in turn would have combined and recombined with various other compounds to make amino acids, sugars, phosphates, and other "building blocks" of the complex molecules (such as proteins) necessary to living cells.[8] These constituents would eventually arrange themselves by chance into simple cell-like enclosures that Oparin called coacervates.[9] Oparin then proposed a kind of Darwinian competition for survival among his coacervates. Those that, by chance, developed increasingly complex molecules and metabolic processes would have survived and grown more complicated. Those that did not would have dissolved.[10]

Thus, cells would have become gradually more and more complex as they competed for survival over billions of years. Like Darwin, Oparin employed time, chance, and natural selection to construct a fully naturalistic account of the origin of complexity from initial simplicity. Nowhere in his scenario did a "mind," "intelligent designer," or "Creator" play any explanatory role. Indeed, for Oparin—a dialectical materialist—such notions were explicitly precluded from scientific consideration on philosophical as well as methodological grounds.[11] Complex cells could be built from simple chemical precursors without any guiding personal or intelligent agency.

THE MILLER-UREY EXPERIMENT

The first experimental support for Oparin's hypothesis came in December 1952. While doing graduate work under Harold Urey at the University of Chicago, Stanley Miller conducted the first experimental test of the Oparin chemical evolutionary model. Miller circulated a gaseous mixture of methane (CH_4), ammonia (NH_3), water vapor (H_20), and hydrogen (H_2) through a glass vessel containing an electrical discharge chamber.[12] Miller sent a high voltage charge of electricity into the chamber via tungsten filaments in an attempt to simulate the effects of ultraviolet light on prebiotic atmospheric gases. After two days, Miller found a small (2 percent) yield of amino acids in the U-shaped water trap he used to collect reaction products at the bottom of the vessel. While Miller's initial experiment yielded only three of the twenty amino acids that occur naturally in proteins, subsequent experiments performed under similar conditions have produced all but one of the others. Other simulation experiments have produced fatty acids and the nucleotide bases found in DNA and RNA, but not the sugar molecules deoxyribose and ribose necessary to build DNA and RNA molecules.[13]

Miller's success in producing biologically relevant "building blocks" under ostensibly prebiotic conditions was heralded as a great breakthrough. His experiment seemed to provide experimental support for Oparin's chemical evolutionary theory by showing that an important step in Oparin's scenario—the production of biological building blocks from simpler atmospheric gases—was possible on early Earth.

Miller's work inspired many similar simulation experiments and an unprecedented optimism about the possibility of developing a compelling naturalistic explanation for the origin of life. Indeed, thanks largely to Miller's experimental work, chemical evolution is now routinely presented in both high school and college biology textbooks as the accepted scientific explanation for the origin of life.[14] Yet as we shall see, chemical evolutionary theory is now known to be riddled with difficulties; and Miller's work is understood by the origin-of-life research community itself to have little, if any, relevance to explaining how amino acids—let alone proteins or living cells—actually arose on the early earth.

PROBLEMS WITH THE OPARIN-MILLER HYPOTHESIS

Despite its status as textbook orthodoxy, the Oparin chemical evolutionary theory has in recent years encountered severe, even fatal, criticisms on many fronts. First, geochemists have failed to find evidence of the nitrogen-rich "prebiotic soup" required by Oparin's model.[15] Second, the remains of single-celled organisms in the very oldest rocks testify that, however life emerged, it did so relatively quickly—i.e., fossil evidence suggests that chemical evolution had little time to work before life emerged on the early Earth.[16] Third, new geological and geochemical evidence suggests that prebiotic atmospheric conditions were hostile, not friendly, to the production of amino acids and other essential building blocks of life. Fourth, molecular biology has revealed such a complexity and specificity of design in even the "simplest" cells and cellular components as to exceed the explanatory resources of current chemical evolutionary theory. Even scientists known for a staunch commitment to the chemical evolutionary approach now concede that no such theory explains the origin of life.[17] As origin-of-life biochemist Klaus Dose has said,

> More than 30 years of experimentation on the origin of life in the fields of chemical and molecular evolution have led to a better perception of the immensity of the problem of the origin of life on Earth rather than to its solution. At present all discussions on principal theories and experiments in the field either end in stalemate or in a confession of ignorance.[18]

To understand the crisis in chemical evolutionary theory, it will be necessary to explain in detail the more severe of these two difficulties, namely, the problem of hostile prebiotic conditions and the problem posed by the complexity of the cell and its biomolecular components.

When Stanley Miller conducted his experiment simulating the production of amino acids on early Earth, he presupposed that the Earth's atmosphere was composed of a mixture of what chemists call reducing gases such as methane (CH_4), ammonia (NH_3), and hydrogen (H_2). He also assumed that the Earth's atmosphere

contained virtually no free oxygen. Miller derived his assumptions about these conditions from Oparin's 1936 book.[19] In the years following Miller's experiment, however, new geochemical evidence made it clear that the assumptions that Oparin and Miller had made about the early atmosphere could not be justified. Instead, evidence strongly suggested that neutral gases such as carbon dioxide, nitrogen, and water vapor—not methane, ammonia, and hydrogen—predominated in the early atmosphere.[20] Moreover, a number of geochemical studies showed that significant amounts of free oxygen were also present even before the advent of plant life, probably as the result of volcanic outgassing and the photodissociation of water vapor.[21]

This new information about the probable composition of the early atmosphere has forced a serious reevaluation of the significance and relevance of Miller-type simulation experiments. As had been well known even before Miller's experiment, amino acids will form readily in an appropriate mixture of reducing gases. In a chemically neutral atmosphere, however, reactions among atmospheric gases will not take place readily and those reactions that do take place will produce extremely low yields of biological building blocks, as simulation experiments under these more realistic conditions have confirmed. Further, even a small amount of atmospheric oxygen will quench the production of biologically significant building blocks and cause any biomolecules otherwise present to degrade rapidly.

Molecular Biology and the Origin of Information

Yet a more fundamental problem remains for all chemical evolutionary scenarios. Even if it could be demonstrated that the building blocks of essential molecules could arise in realistic prebiotic conditions, the problem of assembling those building blocks into functioning proteins or DNA chains would remain. This problem of explaining the specific sequencing and thus, the information, within biopolymers, lies at the heart of the current crisis in chemical evolutionary thinking.

In the early 1950s, molecular biologist Fred Sanger determined the structure of the protein molecule insulin. Sanger's work made clear for the first time that each protein found in the cell comprises a long and definitely arranged sequence of amino acids.[22] The amino acids in protein molecules are linked together to form a chain, rather like individual railroad cars comprising a long train. Moreover, the function of all such proteins (whether as enzymes, signal transducers, or structural components in the cell) depends upon the specific sequencing of the individual amino acids, just as the meaning of an English text depends upon the sequential arrangement of letters.[23] The various chemical interactions between amino acids in any given chain will determine the three-dimensional shape or topography that the amino acid chain adopts. This shape in turn determines what function, if any, the amino acid chain can perform within the cell. For a functioning protein, its three-dimensional shape gives it a "hand-in-glove" fit with other molecules in the cell,

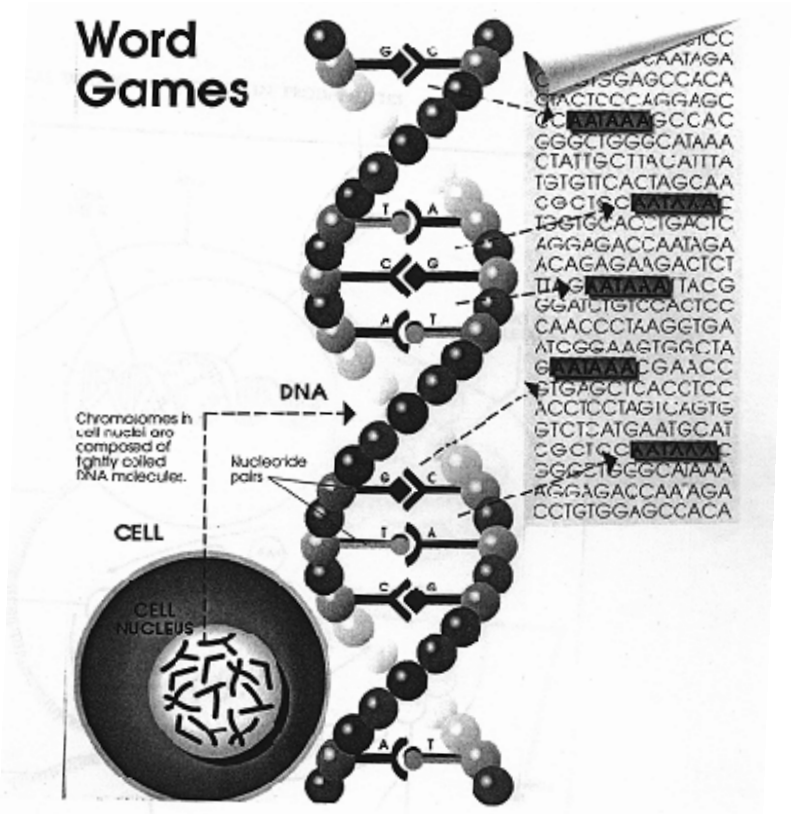


Figure 2. A DNA Molecule and the Genetic Text It Contains. The DNA molecule stores information in the form of many specifically arranged chemicals called nucleotides *(represented by A, T, G, and C). The genetic text (pictured as a scroll on the far right) is read along the spine or long axis of the molecule.* Courtesy of Doug Stevens and *Insight* magazine. Reprinted with permission from *Insight*. Copyright 1994 News World Communications, Inc. All rights reserved.

enabling it to catalyze specific chemical reactions or to build specific structures within the cell. Thus the function of a protein ultimately derives from the precise sequencing of its amino acid building blocks.

The discovery of the complexity and specificity of protein molecules raised serious difficulties for chemical evolutionary theory, even if an abundant supply of amino acids can be granted for the sake of argument. Amino acids alone do not make proteins, any more than letters alone make words, sentences, or poetry. In both cases, the sequence of the constituent parts determines the function (or lack of function) of the whole. In the case of human languages the sequencing of letters

and words is obviously performed by intelligent human agents. In the cell, the sequencing of amino acids is directed by the information—the set of biochemical instructions—encoded on the DNA molecule.

Information Transfer: From DNA to Protein

After James Watson and Francis Crick elucidated the structure of DNA in 1953, molecular biologists soon discovered how DNA directs the process of protein synthesis within the cell.[24] They discovered that the specificity of amino acids in proteins derives from a prior specificity within the DNA molecule—from information on the DNA molecule stored as hundreds of thousands or millions of specifically arranged chemical monomers called nucleotides or bases along the spine of DNA's helical strands (see Figure 2). Chemists represent the four nucleotides with the letters A, T, G, and C (for adenine, thymine, guanine, and cytosine).

Like protein, the DNA molecule has the same property of sequence specificity that human codes and languages have. Indeed, just as the letters in the alphabet of a written language may convey a particular message depending on their sequence, so too do the sequences of nucleotides or bases in the DNA molecule convey precise biochemical instructions that direct protein synthesis within the cell. Whereas the function of the protein molecule derives from the specific arrangement of 20 different amino acids (a 20-letter alphabet), the function of DNA depends upon the arrangement of just four bases. Thus, it takes a group of three nucleotides (or triplets as they are called) on the DNA molecule to specify one amino acid. This process proceeds as long chains of nucleotide triplets (the genetic message) are first copied during a process known as transcription and then transported (by the molecular messenger m-RNA) to a complex organelle called a ribosome.[25] At the ribosome, the genetic message is translated with the aid of an ingenious adaptor molecule called transfer-RNA to produce a growing amino acid chain (see Figure 3).[26] Thus, the sequence specificity in DNA begets sequence specificity in proteins. Or put differently, the sequence specificity of proteins depends upon a prior specificity—upon information—encoded in DNA.

NATURALISTIC EXPLANATIONS FOR THE ORIGIN OF INFORMATION

The explication of this system by molecular biologists in the 1950s and 1960s raised the question of the ultimate origin of the sequence specificity—the information—in both DNA and proteins. Scientists now refer to the information problem as the "Holy Grail" of origin-of-life biology.[27] As Bernd-Olaf Kuppers recently stated, "the problem of the origin of life is clearly basically equivalent to the problem of the origin of biological information."[28] As mentioned previously, the information contained or expressed in natural languages and computer codes

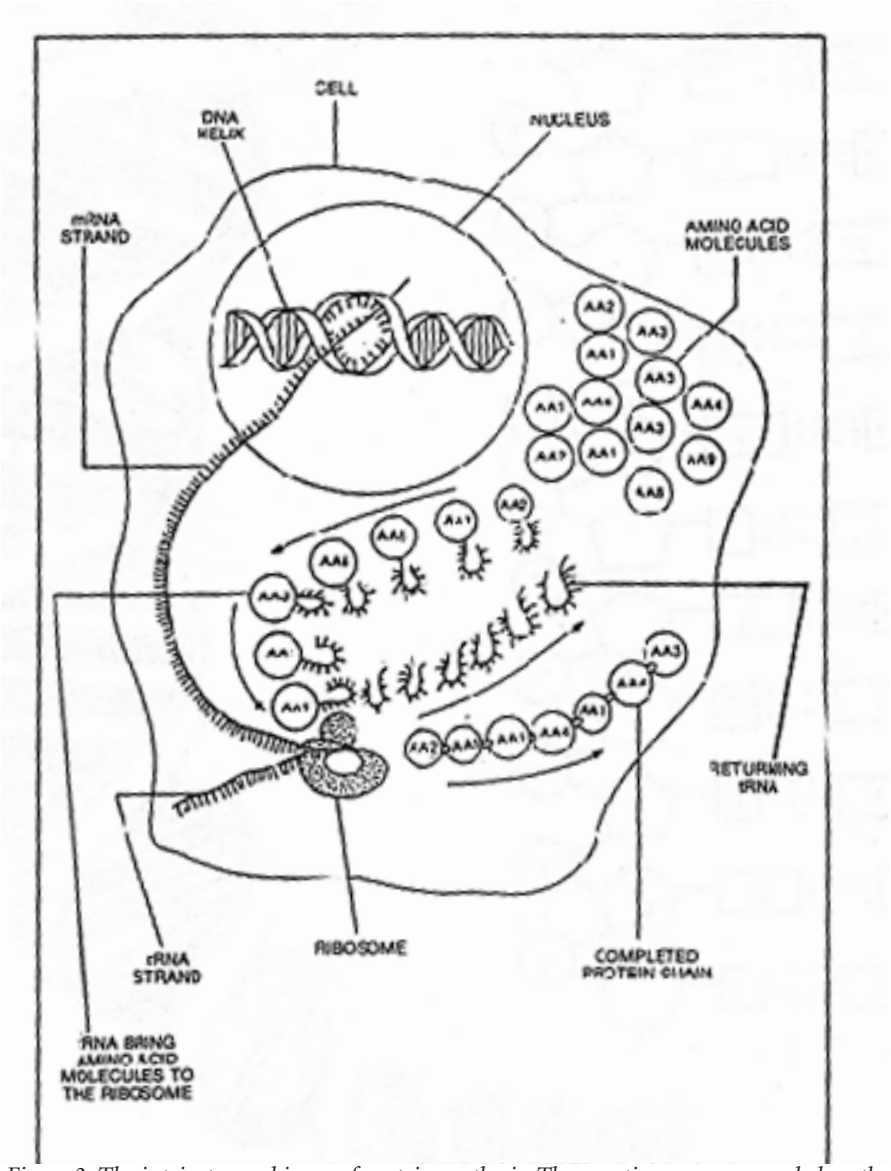


Figure 3. The intricate machinery of protein synthesis. The genetic messages encoded on the DNA molecule are copied and then transported by messenger RNA to the ribosome complex. There the genetic message is "read" and translated with the aid of other large biomolecules (transfer-RNA and specific enzymes) to produce a growing amino acid chain. Courtesy of I. L. Cohen of New Research Publications.

is the product of intelligent minds. Minds frequently create informative arrangements of matter. Yet since the mid-nineteenth century scientists have sought to explain all phenomena by reference to exclusively material causes.[29] Since the 1950s, three broad types of naturalistic explanation have been proposed by scientists to explain the origin of information.

Biological Information: Beyond the Reach of Chance

After the revolutionary developments within molecular biology in the 1950s and early 1960s made clear that Oparin had underestimated the complexity of life, he revised his initial theory. He sought to account for the sequence specificity of the large protein, DNA, and RNA molecules (known collectively as biomacromolecules or biopolymers). In each case, the broad outlines of his theory remained the same, but he invoked the notion of natural selection acting on random variations *within the sequences of the biopolymers* to account for the emergence of their specificity within these molecules.[30] Other theories invoked chance as well. Crick suggested that the origin of the translation system—i.e., the genetic code—might be a "frozen accident."[31] George Wald argued for the causal efficacy of chance by invoking vast expanses of time. As he explained in 1954, "Time is in fact the hero of the plot. . . . Given so much time, the impossible becomes possible, the possible probable, and the probable virtually certain."[32]

While many outside origin-of-life biology may still invoke "chance" as a causal explanation for the origin of biological information, few serious researchers still do.[33] Since molecular biologists began to appreciate the sequence specificity of proteins and nucleic acids in the 1950s and 1960s, many calculations have been made to determine the probability of formulating functional proteins and nucleic acids at random. Various methods of calculating probabilities have been offered by Morowitz, Hoyle, Cairns-Smith, Prigogine, Yockey, and more recently, Robert Sauer.[34] For the sake of argument, these calculations have generally assumed extremely favorable prebiotic conditions (whether realistic or not), much more time than was actually available on early Earth, and theoretically maximal reaction rates among the constituent monomers (i.e., the constituent parts of the proteins, DNA, and RNA). Such calculations have invariably shown that the probability of obtaining functionally sequenced biomacromolecules at random is, in Prigogine's words, "vanishingly small . . . even on the scale of . . . billions of years."[35] As Cairns-Smith wrote in 1971:

> Blind chance . . . is very limited. Low-levels of cooperation he [blind chance] can produce exceedingly easily (the equivalent of letters and small words), but he becomes very quickly incompetent as the amount of organization increases. Very soon indeed long waiting periods and massive material resources become irrelevant.[36]

To illustrate, consider the probabilistic hurdles that must be overcome to construct even one short protein molecule of about 100 amino acids in length. (A typical protein consists of about 300 amino acid residues, and many crucial proteins are very much longer).[37]

First, all amino acids must form a chemical bond known as a peptide bond so as to join with other amino acids in the protein chain. Yet in nature many other types of chemical bonds are possible between amino acids; in fact, peptide and nonpeptide bonds occur with roughly equal probability. Thus, at any given site along a growing amino acid chain the probability of having a peptide bond is roughly 1/2. The probability of attaining four peptide bonds is: (1/2 x 1/2 x 1/2 x 1/2)=1/16 or $(1/2)^4$. The probability of building a chain of 100 amino acids in which all linkages involve peptide linkages is $(1/2)^{100}$ or roughly 1 chance in 10^{30}.

Second, in nature every amino acid has a distinct mirror image of itself, one left-handed version or L-form and one right-handed version or D-form. These mirror-image forms are called optical isomers. Functioning proteins tolerate only left-handed amino acids, yet the right-handed and left-handed isomers occur in nature with roughly equal frequency. Taking this into consideration compounds the improbability of attaining a biologically functioning protein. The probability of attaining at random only L-amino acids in a hypothetical peptide chain 100 amino acids long is again $(1/2)^{100}$ or roughly 1 chance in 10^{30}. The probability of building a 100 amino-acid-length chain at random in which all bonds are peptide bonds and all amino acids are L-form would be $(1/4)^{100}$ or roughly 1 chance in 10^{60} (zero for all practical purposes given the time available on early Earth).

Functioning proteins have a third independent requirement, the most important of all; their amino acids must link up in a specific sequential arrangement just as the letters in a meaningful sentence must. In some cases, even changing one amino acid at a given site can result in a loss of protein function. Moreover, because there are 20 biologically occurring amino acids, the probability of getting a specific amino acid at a given site is small, i.e., 1/20. (Actually the probability is even lower because there are many nonproteineous amino acids in nature). On the assumption that all sites in a protein chain require one particular amino acid, the probability of attaining a particular protein 100 amino acids long would be $(1/20)^{100}$ or roughly 1 chance in 10^{130}.

We know now, however, that some sites along the chain do tolerate several of the 20 proteineous amino acids, while others do not. The biochemist Robert Sauer of M.I.T has used a technique known as "cassette mutagenesis" to determine just how much variance among amino acids can be tolerated at any given site in several proteins. His results have shown that, even taking the possibility of variance into account, the probability of achieving a functional sequence of amino acids[38] in several known proteins at random is still "vanishingly small," roughly 1 chance in 10^{65}—an astronomically large number.[39] (There are 10^{65} atoms in our galaxy).

Moreover, if one also factors in the need for proper bonding and homochirality, the probability of constructing a rather short functional protein at random becomes so small as to be effectively zero (1 chance in 10^{125}), even given our multi-billion-year-old universe.[40] In other words, these (and other) results show that it is extremely unlikely that a random search through the space of combinatorially possible amino acid sequences could generate even a single short functional protein in the time available since the beginning of the universe (let alone the time available on early Earth). Conversely, to have a reasonable chance of finding a short functional protein in a random search of combinatorial space would require vastly more time than either cosmology or geology allows.

More realistic calculations (taking into account the probable presence of non-proteineous amino acids, the need for specific functional proteins of considerable length, and the need for multiple proteins functioning in coordination) only reinforce these results. For example, recent theoretical and experimental work on the so-called "minimal complexity" required to sustain the simplest possible living organism suggests a lower bound of some 250 to 400 genes and their corresponding proteins.[41] The nucleotide sequence space corresponding to such a system of proteins exceeds 4^{300000}. The improbability corresponding to this measure of molecular complexity vastly exceeds the most conservative estimates of the so-called "universal probability bound" of 1 chance in 10^{150}, the point at which appeals to chance become absurd given the "probabilistic resources" of the entire universe.[42] Thus, when one considers the full complement of functional biomolecules required to maintain minimal cell function and vitality, one can see why chance-based theories of the origin of life have been abandoned. What Mora said in 1963 still holds:

> Statistical considerations, probability, complexity, etc., followed to their logical implications suggest that the origin and continuance of life is not controlled by such principles. An admission of this is the use of a period of practically infinite time to obtain the derived result. Using such logic, however, we can prove anything.[43]

Prebiotic Natural Selection: A Contradiction in Terms

Of course, even early theories of chemical evolution did not rely exclusively on chance as a causal mechanism. A. I. Oparin's theory, in particular, invoked prebiotic natural selection as a complement to chance interactions. This approach allegedly helped to overcome the difficulties attending pure chance by providing a mechanism for preserving complexity-increasing events. Yet at the same time that most researchers became disenchanted with a reliance upon "chance" as an explanation, theories of prebiotic natural selection also fell out of favor. Indeed, many scientists quickly recognized that prebiotic natural selection does nothing to overcome the probabilistic hurdles to assembling a minimally complex self-replicating system.

A revised version of Oparin's theory published in 1968 claimed, for example, that natural selection acted upon random polymers as they formed and changed within his coacervate protocells.[44] As more complex molecules accumulated, they presumably survived and reproduced more prolifically. Nevertheless, Oparin's discussion of differential reproduction seemed to presuppose a preexisting mechanism of self-replication. Self-replication in all extant cells depends upon functional (and, therefore, to a high degree sequence-specific) proteins and nucleic acids. Yet the origin of these molecules is precisely what Oparin needed to explain. As Christian de Duve has explained, theories of prebiotic natural selection "need information which implies they have to presuppose what is to be explained in the first place."[45]

Thus, many rejected the postulation of prebiotic natural selection as question-begging.[46] Functioning nucleic acids and proteins (or molecules approaching their complexity) are necessary to self-replication, which in turn is necessary to natural selection. Yet Oparin invoked natural selection to explain the origin of sequence specific proteins and nucleic acids. As the evolutionary biologist Dobzhansky would insist, "prebiological natural selection is a contradiction in terms."[47] Or as Pattee put it:

> . . . there is no evidence that hereditary evolution occurs except in cells which already have the complete complement of hierarchical constraints, the DNA, the replicating and translating enzymes, and all the control systems and structures necessary to reproduce themselves.[48]

In any case, as just discussed, functional sequences of amino acids—i.e., proteins—cannot be counted on to arise via random events, even if some means of selecting them exists after they have been produced. Natural selection can only select what random variation has first produced and chance, at least in a prebiotic setting, seems an implausible agent for producing the information present in even a single functioning protein or DNA molecule. Oparin attempted to circumvent this problem by claiming that the sequences of monomers in the first polymers need not have been highly specific in their arrangement. But this claim raised doubts about whether an accurate mechanism of self-replication (and thus, natural selection) could have functioned at all. In present-day organisms the proteins responsible for DNA replication (such as DNA polymerase) maintain a high degree of specificity and fidelity from generation to generation. Slight alterations in the sequencing of these proteins can diminish the efficiency of replication, which after several generations can produce a so-called "error catastrophe" as the erosion of specificity eventually results in the loss of protein function altogether.

Further, the mathematician Von Neumann,[49] for example, showed that any system capable of self-replication would need to contain subsystems that were functionally equivalent to the information storage, replicating, and processing systems

found in extant cells. His calculations and similar ones by Wigner,[50] Landsberg,[51] and Morowitz,[52] showed that random fluctuations of molecules in all probability (to understate the case) would not produce the minimal complexity needed for even a primitive replication system. Indeed, as noted above, the improbability of developing a replication system vastly exceeds the improbability of developing the protein or DNA components of such system. As P. T. Mora put it:

> To invoke statistical concepts, probability and complexity to account for the origin and the continuance of life is not felicitous or sufficient. As the complexity of a molecular aggregate increases, and indeed very complex arrangements and interrelationships of molecules are necessary for the simplest living unit, the probability of its existence under the disruptive and random influence of physico-chemical forces decreases; the probability that it will continue to function in a certain way, for example, to absorb and to repair, will be even lower; and the probability that it will reproduce, [is] still lower.[53]

For this reason most scientists now dismiss appeals to prebiotic natural selection as essentially indistinguishable from appeals to chance.

Nevertheless, Richard Dawkins[54] and Bernd-Olaf Kuppers[55] have recently attempted to resuscitate prebiotic natural selection as an explanation for the origin of biological information. Both accept the futility of naked appeals to chance and invoke what Kuppers calls a "Darwinian optimization principle." Both use a computer to demonstrate the efficacy of prebiotic natural selection. Each selects a target sequence to represent a desired functional polymer. After creating a crop of randomly constructed sequences, and generating variations among them at random, they then program the computer to select those sequences that match the target sequence most closely. The computer then amplifies the production of those sequences, eliminates the others (thus simulating differential reproduction), and repeats the process. As Kuppers puts it, "Every mutant sequence that agrees one bit better with the meaningful or reference sequence . . . will be allowed to reproduce more rapidly."[56] In Kuppers's case, after a mere 35 generations, his computer succeeds in spelling his target sequence, "NATURAL SELECTION."

Despite superficially impressive results, these "simulations" conceal an obvious flaw: molecules in situ do not have a target sequence "in mind." Nor will they confer any selective advantage on a cell, and thus differentially reproduce, until they combine in a functionally advantageous arrangement. Thus, nothing in nature corresponds to the role that the computer plays in selecting functionally nonadvantageous sequences that happen to agree "one bit better" than others with a target sequence. The sequence "NORMAL ELECTION" may agree more with "NATURAL SELECTION" than does the sequence "MISTRESS DEFECTION," but neither of the two yield any advantage in communication over the other, if, that is, we are trying to communicate something about "NATURAL SELECTION." If so, both are equally ineffectual. Similarly, a com-

pletely nonfunctional polypeptide would confer no selective advantage on a hypothetical protocell, even if its sequence happens to "agree one bit better" with an unrealized target protein than some other nonfunctional polypeptide.

And, indeed, both Kuppers's[57] and Dawkins's[58] published results of their simulations show the early generations of variant phrases awash in nonfunctional gibberish.[59] In Dawkins's simulation, not a single functional English word appears until after the tenth iteration (unlike the more generous example above that starts with actual, albeit incorrect, words). Yet to make distinctions on the basis of function among sequences that have no function whatsoever would seem quite impossible. Such determination can only be made if considerations of proximity to possible future function are allowed, but this requires foresight that molecules do not have. But a computer, programmed by a human being, can perform these functions. To imply that molecules can as well only illicitly personifies nature. Thus, if these computer simulations demonstrate anything, they subtly demonstrate the need for intelligent agents to elect some options and exclude others—that is, to create information.

Self-Organizational Scenarios

Because of the difficulties with chance-based theories, including those that rely upon prebiotic natural selection, most origin-of-life theorists after the mid-1960s attempted to address the problem of the origin of biological information in a completely new way. Christian de Duve explains the logic in a recent *American Scientist* article:

> A single, freak, highly improbable event can conceivably happen. Many highly improbable events—drawing a winning lottery number or the distribution of playing cards in a hand of bridge—happen all the time. But a string of improbable events—drawing the same lottery number twice, or the same bridge hand twice in a row—does not happen naturally. All of which lead me to conclude that life is an obligatory manifestation of matter, bound to arise where conditions are appropriate.[60]

Indeed, from the late 1960s to the present, the perspective that de Duve describes has dominated theoretical work on the origin of life. Researchers have increasingly repudiated chance and prebiotic natural selection, and looked for laws and properties of chemical attraction that might explain the origin of information in DNA and proteins. Thus, most origin-of-life theorists since the late 1960s have advocated self-organizational models for the origin of life. Rather than invoking chance, these theories invoke necessity.

By the late 1960s origin-of-life biologists began to consider the possibility that deterministic forces (stereochemical "necessity") made the origin of life not just

probable, but inevitable. Some suggested that simple chemicals might possess "self-ordering properties" capable of organizing the constituent parts of proteins, DNA, and RNA into the specific arrangements they now possess.[61] Steinman and Cole, for example, suggested that differential bonding affinities or forces of chemical attraction between certain amino acids might account for the origin of the sequence specificity of proteins.[62] Just as electrostatic forces draw sodium (Na+) and chloride ions (Cl-) together into highly ordered patterns within a crystal of salt (NaCl), so too might amino acids with special affinities for each other arrange themselves to form proteins. Kenyon and Steinman developed this idea in a book entitled *Biochemical Predestination* in 1969. They argued that life might have been "biochemically predestined" by the properties of attraction that exist between its constituent chemical parts, particularly between the amino acids in proteins.[63]

In 1977, another self-organizational theory was proposed by Prigogine and Nicolis based on a thermodynamic characterization of living organisms. In *Self Organization in Nonequilibrium Systems*, Prigogine and Nicolis classified living organisms as open, nonequilibrium systems capable of "dissipating" large quantities of energy and matter into the environment.[64] They observed that open systems driven far from equilibrium often display self-ordering tendencies. For example, gravitational energy will produce highly ordered vortices in a draining bathtub; thermal energy flowing through a heat sink will generate distinctive convection currents or "spiral wave activity." Prigogine and Nicolis argued that the organized structures observed in living systems might have similarly "self-originated" with the aid of an energy source. In essence, they conceded the improbability of simple building blocks arranging themselves into highly ordered structures under normal equilibrium conditions. But they suggested that under nonequilibrium conditions where an external source of energy is supplied, biochemical building blocks might arrange themselves into highly ordered patterns.

More recently, Stuart Kauffman[65] and Christian de Duve[66] have proposed self-organizational theories with somewhat less specificity, at least with regard to the problem of the origin of genetic information. Kauffman invokes so-called "autocatalytic properties" that he envisions may emerge from very particular configurations of simple molecules in a rich "chemical minestrone." De Duve envisions the emergence of a protometabolism with genetic information arising later as by-product of simple metabolic activity. He invokes an extraevidential principle, his so-called "Cosmic Imperative," to render the emergence of molecular complexity in his scenario more plausible.

Order vs. Information

For many current origin-of-life scientists self-organizational models now seem to offer the most promising approach to explaining the origin of biological informa-

tion. Nevertheless, critics have called into question both the plausibility and the relevance of self-organizational models. Ironically, perhaps the most prominent early advocate of self-organization, Dean Kenyon, has now explicitly repudiated such theories as both incompatible with empirical findings and theoretically incoherent.[67]

First, empirical studies have shown that some differential affinities do exist between various amino acids (i.e., particular amino acids do form linkages more readily with some amino acids than others).[68] Nevertheless, these differences do not correlate to actual sequencing in large classes of known proteins.[69] In short, differing chemical affinities do not explain the multiplicity of amino acid sequences that exist in naturally occurring proteins or the sequential ordering of any single protein.

In the case of DNA this point can be made more dramatically. Figure 4 shows that the structure of DNA depends upon several chemical bonds. There are bonds, for example, between the sugar and the phosphate molecules that form the two twisting backbones of the DNA molecule. There are bonds fixing individual (nucleotide) bases to the sugar-phosphate backbones on each side of the molecule. There are also hydrogen bonds stretching horizontally across the molecule between nucleotide bases making so-called complementary pairs. These bonds, which hold two complementary copies of the DNA message text together, make replication of the genetic instructions possible. Most importantly, however, notice that there are *no* chemical bonds between the bases along the vertical axis in the center of the helix. Yet it is precisely along this axis of the molecule that the genetic instructions in DNA are encoded.[70]

Further, just as magnetic letters can be combined and recombined in any way to form various sequences on a metal surface, so too can each of the four bases A, T, G, and C attach to any site on the DNA backbone with equal facility, making all sequences equally probable (or improbable). Indeed, there are no differential affinities between any of the four bases and the binding sites along the sugar-phosphate backbone. The same type of (so-called "n-glycosidic") bond occurs between the base and the backbone regardless of which base attaches. All four bases are acceptable, none is preferred. As Kuppers has noted, "the properties of nucleic acids indicate that all the combinatorially possible nucleotide patterns of a DNA are, from a chemical point of view, equivalent." Thus, "self-organizing" bonding affinities cannot explain the sequential ordering of the nucleotide bases in DNA because: (1) there are *no* bonds between bases along the message-bearing axis of the molecule and, (2) there are no *differential* affinities between the backbone and the various bases that could account for variations in sequencing. Because the same holds for RNA molecules, researchers who speculate that life began in an "RNA world" have also failed to solve the sequencing problem[71]—i.e., the problem of explaining how information present in all functioning RNA molecules could have arisen in the first place.

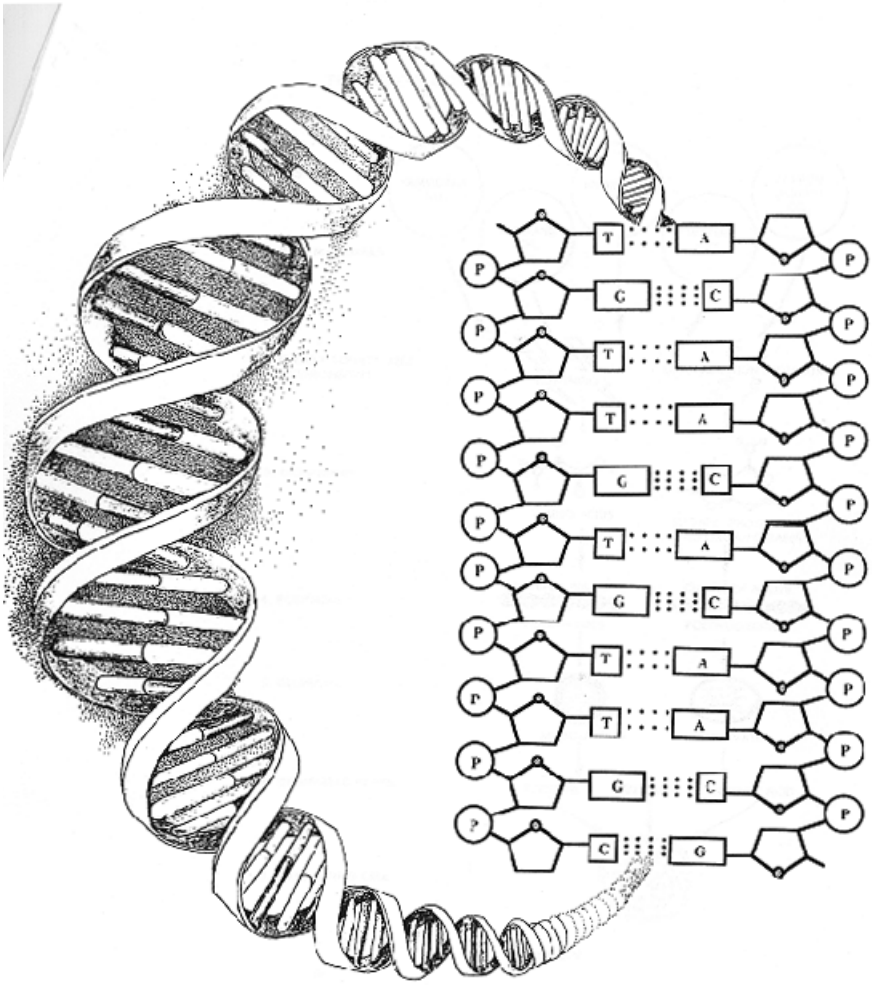


Figure 4. The Bonding Relationships between the Chemical Constituents of the DNA Molecule. Sugars (designated by the pentagons) and phosphates (designated by the circled P's) are linked chemically. Nucleotide bases (A's, T's, G's and C's) are bonded to the sugar-phosphate backbones. Nucleotide bases are linked by hydrogen bonds (designated by dotted double or triple lines) across the double helix. But no chemical bonds exist between the nucleotide bases along the message-bearing spine of the helix. Courtesy of Fred Hereen, Daystar Publications.

For those who want to explain the origin of life as the result of self-organizing properties intrinsic to the material constituents of living systems, these rather elementary facts of molecular biology have devastating implications. The most logical place to look for self-organizing properties to explain the origin of genetic information is in the constituent parts of the molecules carrying that information. But biochemistry and molecular biology make clear that forces of attraction between the constituents in DNA, RNA, and proteins do not explain the sequence specificity of these large information-bearing biomolecules. We know this, in addition to the reasons already specified, because of the multiplicity of variant polypeptides and gene sequences that exist in nature and that can be made in the laboratory. The properties of the monomers constituting nucleic acids and proteins simply do not make a particular gene, let alone life as we know it, inevitable.

Yet if self-organizational scenarios for the origin of biological information are to have any theoretical import, they must claim just the opposite. And, indeed, they often do, albeit without much specificity. As de Duve has put it, "the processes that generated life" were "highly deterministic," making life as we know it "inevitable . . . given the conditions on the prebiotic earth." Yet imagine the most favorable prebiotic conditions. Imagine a pool of all four DNA nucleotides, and all necessary sugars and phosphates; would any particular genetic sequence have to arise? Given all necessary monomers, would any particular functional protein or gene, let alone a specific genetic code, replication system, or signal transduction circuitry, have to arise? Clearly not.

In the parlance of origin-of-life research, monomers are "building blocks." And building blocks can be arranged and rearranged in innumerable ways. The properties of the blocks do not determine the construction of buildings. Similarly, the properties of *biological* building blocks do not determine the construction of functional polymers. Instead, the properties of the monomers allow a vast ensemble of possible configurations, the overwhelming majority of which have no biological function whatsoever. Functional genes or proteins are no more inevitable given the properties of their "building blocks" than the palace of Versailles, for example, was inevitable given the properties of the bricks and stone used to construct it. To anthropomorphize, neither bricks and stone, nor letters in a written text, nor nucleotide bases "care" how they are arranged. In each case, the properties of the constituents remain largely indifferent to the innumerable specific configurations or sequences they can adopt. Conversely, the properties of nucleotide bases and amino acids do not make any specific sequences "inevitable" as self-organizationalists must claim.

Significantly, information theory makes clear that there is a good reason for this. If chemical affinities between the constituents in the DNA message text determined the arrangement of the text, such affinities would dramatically diminish the capacity of DNA to carry information. To illustrate, imagine receiving the following

incomplete message over the wire. The "q-ick brown fox jumped over the lazy dog." Obviously someone who knew the conventions of English could determine which letter had been rubbed out in the transmission. Because "q" and "u" always go together by grammatical necessity, the presence of one indicates the presence of the other in the initial transmission of the message. The "u" in all English communications is an example of what information theorists call "redundancy." Given the grammatical rule "u" must always follow "q," the addition of the "u" adds no new information, when "q" is already present. It is "redundant" or unnecessary to determining the sense of the message (though not to making it grammatically correct).

Now consider what would happen if the individual nucleotide "letters" (A, T, G, C) in a DNA molecule *did* interact by *chemical* necessity with each other. Every time adenine (A) occurred in a growing genetic sequence, it would attract thymine (T) to it.[72] Every time cytosine (C) appeared, guanine would likely follow. As a result, the DNA message text would be peppered with repeating sequences of A's followed by T's and C's followed by G's. Rather than having a genetic molecule capable of unlimited novelty with all the unpredictable and aperiodic sequences that characterize informative texts, we would have a highly repetitive text awash in redundant sequences—much as happens in crystals. Indeed, in a crystal the forces of mutual chemical attraction do completely explain the sequential ordering of the constituent parts and consequently crystals cannot convey novel information. Sequencing in crystals is highly ordered or repetitive, but not informative. Once one has seen "Na" followed by "Cl" in a crystal of salt, for example, one has seen the extent of the sequencing possible. In DNA, however, where any nucleotide can follow any other, innumerable novel sequences are possible, and a countless variety of amino acid sequences can be built.

The forces of chemical necessity, like grammatical necessity in our "q-and-u" example above, produce redundancy or monotonous order, but reduce the capacity to convey information and create novelty. As chemist Michael Polanyi has said:

> Suppose that the actual structure of a DNA molecule were due to the fact that the bindings of its bases were much stronger than the bindings would be for any other distribution of bases, then such a DNA molecule would have no information content. Its code-like character would be effaced by an overwhelming redundancy. . . . Whatever may be the origin of a DNA configuration, it can function as a code only if its order is not due to the forces of potential energy. It *must be* as physically indeterminate as the sequence of words is on a printed page.[73] [emphasis added]

So, if chemists had found that bonding affinities between the nucleotides in DNA produced nucleotide sequencing, they would have also found that they had been mistaken about DNA's information-bearing properties. To put the point quantitatively, to the extent that forces of attraction between constituents in a sequence

determine the arrangement of the sequence, to that extent will the information-carrying capacity of the system be diminished.[74] As Dretske has explained:

> As p(si) [the probability of a condition or state of affairs] approaches 1 the amount of information associated with the occurrence of si goes to 0. In the limiting case when the probability of a condition or state of affairs is unity [p(si) =1], no information is associated with, or generated by, the occurrence of si. This is merely another way to say that no information is generated by the occurrence of events for which there are no possible alternatives.[75]

Bonding affinities, to the extent they exist, militate against the maximization of information.[76] They cannot, therefore, be used to explain the origin of information. Affinities create mantras, not messages.

The tendency to conflate the qualitative distinction between "order" and "information" has characterized self-organizational research efforts and calls into question the relevance of such work to the origin of life. As Yockey has argued, the accumulation of structural or chemical order does not explain the origin of biological complexity (i.e., genetic information).[77] He concedes that energy flowing through a system may produce highly ordered patterns. Strong winds form swirling tornadoes and the "eyes" of hurricanes; Prigogine's thermal baths do develop interesting "convection currents;" and chemical elements do coalesce to form crystals. Self-organizational theorists explain well what does not need explaining. What needs explaining in biology is not the origin of order (in the sense of symmetry or repetition), but the origin of information—the highly improbable, aperiodic, and yet specified sequences that make biological function possible.

To illustrate the distinction between order and information compare the sequence "ABABABABABABAB" to the sequence "Help! The house is on fire!" The first sequence is repetitive and ordered, but not complex or informative. The second sequence is not ordered, in the sense of being repetitious, but it is complex and also informative. The second sequence is complex because its characters do not follow a rigidly repeating or predictable pattern—i.e., it is aperiodic and improbable, and therefore, takes many instructions to specify. It is also informative because, unlike a *merely* complex sequence such as "rfsxdcnct<e%dwqj," the particular arrangement of characters is highly exact or "specified" so as to perform a (communication) function.[78] Systems that are characterized by both specificity and complexity (what William Dembski calls "complex specified information") have "information content." Since such systems have the qualitative feature of complexity (aperiodicity), they are qualitatively distinguishable from systems characterized by simple periodic order. Thus, attempts to explain the origin of order have no relevance to discussions of the origin of information content. Significantly, the nucleotide sequences in the

coding regions of DNA have, by all accounts, a high information content—that is, they are both specified (by independent functional considerations) and highly complex as are meaningful English sentences.[79]

Conflating order and information has led many to attribute properties to brute matter that it does not possess. While energy in a system *can* create patterns of symmetric order such as whirling vortices, there is no evidence that bonding affinities or energy generally can encode functionally specified sequences—whether biochemical or otherwise. As Yockey warns:

> Attempts to relate the idea of order . . . with biological organization or specificity must be regarded as a play on words which cannot stand careful scrutiny. Informational macromolecules can code genetic messages and therefore can carry information because the sequence of bases or residues is affected very little, if at all, by [self-organizing] physico-chemical factors.[80]

The Message and the Medium

The preceding discussion suggests that the properties of the material constituents of DNA—like those of any information-bearing medium—are not responsible for the information conveyed by the molecule. Indeed, in all informational systems, the information content or message does not derive from the properties of the material medium.

To amplify this point consider, first, that many different materials can express the same message. The headline of this morning's *New York Times* was written with ink on paper. Nevertheless, many other materials could have been used. The information in the headline could have been written with chalk on a board, with neon-filled tubes in a sign, or by a skywriter over New York harbor. Clearly, the peculiar chemical properties of ink are not necessary to convey the message. Neither are the physical properties (i.e., the geometric shapes) of the letters necessary to transmit the information. The same message could have been expressed in Hebrew or Greek using entirely different alphabetic characters.

Conversely, the same material medium (and alphabetic characters) can express many different messages—i.e., the medium is not sufficient to determine the message. In November 1996 the *Times* used ink and English characters to tell the reading public that a Democrat, William Jefferson Clinton, won the American presidential election. Yet the properties of the ink and the 26 letters available to the typesetter did not determine the content of the headline. Instead, the ink and English characters permitted the transmission of whatever headline that the typesetter wanted to convey, as well as a vast ensemble of other possible arrangements of text, some meaningful, and many more not. Neither the chemistry of the ink nor the shapes of the letters determined the arrangement of the text.

George Williams illustrates what he calls the "separability of information and matter" with a similar logic:

> You can speak of galaxies and particles of dust in the same terms because they both have mass and charge and length and width. You can't do that with information and matter. Information doesn't have mass or charge or length in millimeters. Likewise matter doesn't have bytes. . . . This dearth of shared descriptors makes matter and information two separate domains.[81]

He notes that computer users routinely transfer "information from one physical medium to another" and then "recover the same information in the original medium."[82] While the physical medium has changed in each transfer, the message has not. A message can be dictated to a secretary, typed into a computer, printed onto paper, faxed across the country, received in another computer and used to light an electronic display. While no single physical substance has traveled from sender to receiver, clearly something—information—has. Yet that information is not coextensive with the physical medium of its transmission. In short, the message transcends the properties of the medium.

The information in DNA transcends the properties of its material medium as well. Williams notes:

> evolutionary biologists have failed to realize that they work with two more or less incommensurable domains: that of information and that of matter. . . . The gene is a package of information, not an object. The pattern of base pairs in a DNA molecule specifies the gene. But the DNA molecule is the medium, it's not the message.[83]

Indeed, because chemical bonds do not determine the arrangement of nucleotide bases, the nucleotides can assume a vast array of possible sequences and thereby express many different messages. Conversely, various materials can express the same messages, as happens in variant versions of the genetic code or when laboratory chemists use English instructions to direct the synthesis of naturally occurring proteins. Thus, the physical and chemical properties of DNA are neither necessary nor sufficient to generate a specific set of genetic instructions.

Thus, again, it follows that the information content of DNA defies explanation by reference to the physical and chemical properties of DNA. The chemistry of ink does not explain the origin of the information in a newspaper headline. The properties of a silicon chip do not give rise to computer software. While the properties of the chip certainly allow a computer to store information, they do not generate (or explain the origin of) the information it contains. In the same way, the properties of DNA allow it to store genetic information, but do not explain the origin of its information. As Michael Polanyi put it: "As the arrangement of a printed page is

extraneous to the chemistry of the printed page, so is the base sequence in a DNA molecule extraneous to the chemical forces at work in the DNA molecule."[84]

THE RETURN OF THE DESIGN HYPOTHESIS

If the properties of matter (i.e., the medium) do not explain the origin of information, including biological information, what does?

Blind chance is, of course, a possibility, but *not*, as we have seen in the case of functional DNA and proteins, where the amount of information (or the improbability of arrangement) gets too immense. The random selection and sequencing of Scrabble pieces out of a grab bag might occasionally produce a few meaningful words such as "cat" or "ran." Nevertheless, undirected selection will inevitably fail as the numbers of letters required to make a specified text increases. Fairly soon, chance becomes clearly inadequate as origin-of-life biologists have almost universally acknowledged.

Some have suggested that the discovery of some new scientific laws might explain the origin of biological information. As Manfred Eigen has argued, "our task is to find an algorithm, a natural law, that leads to the origin of information."[85] But this suggestion betrays a fundamental confusion. Scientific laws describe (almost by definition) highly regular phenomena—i.e., redundant order. Thus, to say that the processes that scientific laws describe can generate informational sequences is essentially a contradiction in terms. The patterns that laws describe are necessarily highly ordered and redundant, not complex. Thus, like crystals, law-like patterns do not generate novel information. One might hope, perhaps, to find a complex set of material conditions capable of generating high information content on a regular basis, but everything we know suggests that the complexity and information content of such conditions would have to equal or exceed that of any system produced, thus again begging the question about the ultimate origin of information.

For example, chemist J. C. Walton has argued (echoing earlier articles by Mora) that even the self-organization produced in Prigogine-style convection currents does not exceed the organization or structural information represented by the experimental apparatus used to create the currents.[86] Similarly, Maynard-Smith,[87] Dyson,[88] and Speigelman[89] have shown that Manfred Eigen's so-called hypercycle model for generating information naturalistically is subject to the same tendency of information to degrade.[90] They show, first, that Eigen's hypercycles presuppose a large initial contribution of information in the form of a long RNA molecule and some 40 specific proteins. More significantly, they show that because hypercycles lack an error-free mechanism of self-replication, they become susceptible to various "error-catastrophes" that ultimately diminish, not increase, the information content of the system over time.

Stuart Kauffman's self-organizational theory also subtly illustrates this same problem. In *The Origins of Order*, Kauffman suggests that large ensembles of

molecules in solution (in a so-called "chemical minestrone") may have "autocatalytic" properties that can explain the origin of the integrated complexity of living cells.[91] He acknowledges, however, that such autocatalysis would not occur unless the molecules in the chemical minestrone achieve very specific spatial-temporal relationships to one another. In other words, for the direct autocatalysis of biological complexity to occur, a system of molecules must first achieve a very specific molecular configuration, or a low configurational entropy state. Yet this claim is isomorphic with the claim that the system must start with a high information content. Thus, to explain the origin of biological complexity at the systems-level, Kauffman must presuppose the existence of a highly specific and complex—i.e., an information-rich—arrangement of matter at the molecular level.[92] Therefore, his work—if it has any relevance to the actual behavior of molecules—assumes rather than explains the ultimate origin of information.

Instead, what Williams calls the "separability of information and matter" suggests an immaterial—indeed, a mental—origin for information. When a computer user traces the information on a screen back to its source, he invariably comes to a mind—a software engineer or a writer. So too with our newspaper example above. Indeed, experience confirms that information-intensive systems (especially codes and languages) always come from an intelligent source—i.e., from mental or personal agents.[93] This generalization about the origin of information holds not only for information present in languages and codes but also for the nongrammatical information (also describable as specified complexity) inherent in machines or expressed in works of art. Like the text of a newspaper, the parts of a supercomputer and the faces on Mount Rushmore require many instructions to specify their shape or arrangement and consequently have a high information content.[94] These systems are also, not coincidentally, the result of intelligent design, not chance or necessity.

This generalization about the cause of high information content has, ironically, received confirmation from origin-of-life research itself. During the last 40 years, every naturalistic model proposed has failed precisely to explain the origin of genetic information.[95] Thus, mind or intelligence, or what philosophers call "agent causation," now stands as the only cause known to be capable of generating high information content or what Dembski calls "complex specified information."[96]

Because mind or intelligent design is a necessary cause of an information-rich system, one can detect (or, logically, retrodict) the past action of an intelligent cause from the presence of an information-intensive effect, even if the cause itself cannot be directly observed.[97] Since information requires an intelligent source, the pattern of red and yellow flowers spelling "Welcome to Victoria" in the gardens of Victoria harbor in Canada leads visitors to infer the activity of intelligent agents even if they did not see the flowers planted and arranged. Similarly, the specifically arranged nucleotide sequences—the encoded information—in DNA imply the past action of an intelligent mind, even if such mental agency cannot be directly observed.

Moreover, the logical calculus underlying such inferences follows a valid and well-established method used in all historical and forensic sciences. In historical sciences, knowledge of the present causal powers of various entities and processes enables scientists to make inferences about possible causes in the past. When a thorough study of various possible causes turns up just a single adequate cause for a given effect, historical or forensic scientists can make fairly definitive inferences about the past.[98] Several years ago, for example, one of the forensic pathologists from the original Warren Commission that investigated the assassination of President Kennedy spoke out to quash rumors about a second gunman firing from in front of the motorcade. Apparently, the bullet hole in the back of President Kennedy's skull evidenced a distinctive beveling pattern that clearly indicated its direction of entry. In this case, it revealed that the bullet had entered from the rear. The pathologist called the beveling pattern a "distinctive diagnostic" to indicate a necessary causal relationship between the direction of entry and the angle of the beveling.[99] Inferences based on knowledge of necessary causes ("distinctive diagnostics") are common in historical and forensic sciences, and often lead to the detection of intelligent as well as natural causes. Since criminal X's fingers are the only known cause of criminal X's fingerprints, X's prints on the murder weapon incriminate him with a high degree of certainty. In the same way, since intelligent design is the only known cause of high information content, information-intensive systems invariably implicate an intelligent source.

Of course, the adjective "high" in the phrase "high information content" begs a quantitative question, namely, "how high does the information content of a system have to be before it unequivocally justifies a design inference?" This question has recently received a formal answer. Dembski, following and refining the work of earlier probabilists such as Emile Borel, shows that chance can be eliminated as a plausible explanation for specified systems of small probability whenever the complexity of the system exceeds the available probabilistic resources,[100] which are roughly the number of opportunities available to search a given combinatorial space of possibilities in some finite time. He then calculates a universal probability bound of $1/10^{150}$ corresponding to the probabilistic resources inherent in the known universe. This number provides a formal basis for excluding appeals to chance as the best explanation for specified events of probability less than $1/2 \times 1/10^{150}$. Further, since probability is inversely related to information by a logarithmic function, small probabilities translate into high informational measures. The universal small probability bound of $1/10^{150}$ translates into roughly 500 bits of information. Thus, chance can be excluded as an explanation for any specified system or sequence containing more than 500 bits of information. As Richard Dawkins has said, "we can accept a certain amount of luck in our explanations, but not too much."[101] Dembski has answered the question: "how much is, in any case, too much?" Moreover, since systems characterized by complexity (a lack of redundant

order) do not admit explanation by natural laws, and since appeals to prebiotic natural selection presuppose, but do not explain, the origin of high information content, systems with more than 500 bits of novel information content defy reduction to naturalistic explanation. Instead, such systems indicate intelligent design.

Scientists in many fields recognize the connection between intelligence and high information content and make inferences accordingly. Archaeologists assume a mind produced the inscriptions on the Rosetta Stone. Evolutionary anthropologists try to demonstrate the intelligence of early hominids by arguing that certain chipped flints are too improbably specified to have been produced by natural causes. NASA's search for extraterrestrial intelligence (SETI)[102] presupposed that information imbedded in electromagnetic signals from space would indicate an intelligent source.[103] As yet, however, radio astronomers have not found information-bearing signals coming from space. But closer to home, molecular biologists have identified extraordinarily information-intensive sequences and systems in the cell. Consequently, a number of scientists and philosophers of science[104] now suggest that the information in DNA (and the molecular complexity of the cell generally) justifies making what Dembski calls a "design inference."[105]

AN ARGUMENT FROM IGNORANCE?

Against all that has been said, many have maintained that this argument from information content to design constitutes nothing more than an argument from ignorance. Since we do not yet know how biological information could have arisen we invoke the mysterious notion of intelligent design. Thus, say objectors, intelligent design functions, not as an explanation, but as a kind of place holder for ignorance.

And yet, as Dembski has demonstrated, we often infer the causal activity of intelligent agents as the best explanation for events and phenomena.[106] Moreover, we do so rationally, according to objectifiable, if often tacit, information and complexity-theoretic criteria. His examples of design inferences—from archaeology and cryptography to fraud detection and criminal forensics—show that we make design inferences all the time and we often do so for a very good reason.[107] Intelligent agents have unique causal powers that nature does not. When we observe effects that we know only agents can produce, we rightly infer the presence of a prior intelligence even if we did not observe the action of the particular agent responsible. In other words, Dembski has shown that designed events leave a complexity and information-theoretic signature that allows us to detect design reliably.[108] When these criteria are present, scenarios involving design constitute better explanations than those that rely exclusively on chance and/or deterministic natural processes.

While admittedly the design inference does not constitute a proof (nothing based upon empirical observation can), it most emphatically does not constitute an

argument from ignorance. Instead, the design inference from biological information constitutes an "inference to the best explanation."

Recent work on the method of "inference to the best explanation"[109] suggests that determining which among a set of competing possible explanations constitutes the best depends upon assessments of the causal powers of competing explanatory entities. Causes that have the capability to produce the evidence in question constitute better explanations of that evidence than those that do not. This essay has evaluated and compared the causal efficacy of three broad categories of explanation—chance, necessity, (and chance and necessity combined), and design—with respect to their ability to produce high information content. As we have seen, neither chance nor necessity (nor their combination) seems to possess the ability to produce biological information in a prebiotic context. This result comports with our ordinary uniform human experience. Brute matter—whether acting randomly or by necessity—does not have the capability to produce information-intensive systems or sequencing.

Yet it is not correct to say that we do not know how information arises. We know from experience that intelligent agents create information all the time. Indeed, experience teaches that whenever high information content is present in an artifact or entity whose causal story is known, invariably creative intelligence—design—has played a causal role in the origin of that entity. Thus, the inference to design does not depend upon our ignorance, but instead upon our knowledge of the demonstrated causal powers of nature and agency, respectively. Recent developments in the information sciences formalize this knowledge, helping us to make inferences about the causal histories of various artifacts, entities, or events based upon the information-theoretic signatures they exhibit.[110] Knowledge of established cause-effect relationships, not ignorance, justifies the design inference as the best explanation for the origin of biological information in a prebiotic context.

Objectors complain, of course, that future inquiry may uncover other natural entities possessing as yet unknown causal powers. They object that the design inference presented here depends upon a negative generalization—purely physical and chemical causes cannot produce high information content—that future discoveries may well later falsify. We should "never say never," they say. Yet science often says never, even if it cannot say so for sure. Indeed, negative or proscriptive generalizations play an important role in science. As many scientists and philosophers of science have pointed out, scientific laws often tell us not only what does happen, but also what does not happen.[111] The conservation laws in thermodynamics, for example, proscribe certain outcomes. The first law tells us that energy is never created or destroyed. The second tells us that the entropy of a closed system will never decrease over time. Those who claim that such "proscriptive laws" do not constitute knowledge simply because they are based upon past, but not future, experience will not get very far if they want to use their skepticism to justify funding for, say, research on perpetual motion machines.

Moreover, without proscriptive generalizations, without knowledge about what possible causes can and cannot produce, historical scientists could never make any determinations about the past. As work on the method of the historical sciences has shown, reconstructing the past requires making inferences from present effects back to past causal events.[112] Yet historical scientists judge the plausibility of such inferences against our knowledge of the causal powers of competing possible causes. Making inferences about the best historical explanation requires a progressive elimination of competing causal hypotheses. Deciding which causes can be eliminated from consideration requires knowing what effects a given cause can, and especially cannot, produce. If we can never say that certain entities do not possess certain causal powers, then we can never eliminate them—even provisionally—from consideration. And thus, we could never make historical inferences. Yet we do so all the time.

Recently, those investigating the cause of the TWA plane crash over Long Island eliminated a Navy missile as the cause of the crash because none of the Navy ships within missile range had missile-launching capability. We may later learn otherwise, or we may later learn that ships without missile launching capability can launch them after all, but for now other explanations seem better. Indeed, to determine the best explanation we do not need to say "never, for sure." We only need to say that a given postulated cause is best given all that we know at present about the demonstrated causal powers of competing entities or agencies. That cause C can produce effect E makes it a better explanation of E than some other cause D that has never produced E and which seems incapable of doing so on theoretical grounds, even if D may later demonstrate causal powers of which we are presently ignorant.

Thus, the objection that the design inference constitutes an argument from ignorance reduces in essence to a restatement of the problem of induction. Yet one can make this objection against any scientific law or explanation, or any historical inference that takes our knowledge of natural laws and causal powers into account. As Barrow and Tipler have noted, to criticize design arguments, as Hume did, simply because they assume the uniformity and (normative character) of natural law cuts just as deeply against "the rational basis of any form of scientific inquiry."[113] Our knowledge of what can and cannot produce high information content may later have to be revised, but so might the laws of thermodynamics. Inferences to design may also later prove incorrect, but so may inferences implicating various natural causes. Such a possibility does not stop scientists from making generalizations about the causal powers of various entities or using these generalizations to identify probable or most plausible causes in particular cases. Inferences based upon past and present experience constitute knowledge (albeit provisional), not ignorance. Those who object to such inferences object to *scienc*e as much as they object to a particular science-based hypothesis of design.

NOTES

1. Elliot Sober, *The Philosophy of Biology* (Boulder: Westview Press, 1993), 44.
2. Sober, *The Philosophy of Biology*, 44.
3. Darwin's only speculation on the origin of life is found in an unpublished 1871 letter to Joseph Hooker. In it he sketched the outlines of the chemical evolutionary idea, namely, that life could have first evolved from a series of chemical reactions: "It is often said that all the conditions for the first production of living organisms are now present, which could ever have been present. But if (and oh! what a big if!) we could conceive in some warm little pond, with all sorts of ammonia and phosphoric salts, light, heat, electricity, etc., that a protein compound was chemically formed ready to undergo still more complex changes, at the present such matter would be instantly devoured or absorbed, which would not have been the case before living creatures were formed." Cambridge University Library, Manuscripts Room, Darwin Archives, Letter to Hooker February, 1871. Courtesy Peter Gautrey.
4. Ernst Haeckel, *The Wonders of Life*, trans. Joseph McCabe (London: Watts, 1905), 111; Thomas Henry Huxley, "On the Physical Basis of Life," *Fortnightly Review* 5 (1869): 129-45.
5. Ernst Haeckel, *Generelle Morphologie der Organismen*, vol. 1 (Berlin: G. Reimer, 1866), 179-80; Ernst Haeckel, *The History of Creation*, vol. 1 (London: Kegan, Paul, Trench, Trubner & Co., 1892), 411-13; Huxley, "On the Physical Basis of Life," 138-39; Harmke Kamminga, "Studies in the History of Ideas on the Origin of Life," (Ph.D. diss., University of London, 1980), 60, 61.
6. Alexander I. Oparin, *The Origin of Life*, trans. Sergius Morgulis (New York: MacMillan, 1938), 64-103; Stephen C. Meyer, "Of Clues and Causes: A Methodological Interpretation of Origin of Life Studies," (Ph.D. diss., Cambridge University, 1991), 174-79, 194-98, 211, 212.
7. Oparin, *Origin of Life*, 98, 107, 108.
8. Oparin, *Origin of Life*, 133-35.
9. Oparin, *Origin of Life*, 148-59.
10. Oparin, *Origin of Life*, 195-96.
11. Loren R. Graham, *Science and Philosophy in the Soviet Union* (New York: Alfred A. Knopf, 1972), 260-63, 269, 272, 286-96; Lazcano Araujo, interview with Alexander I. Oparin in Mexico City newspaper *Uno Mas Uno*, May 7, 1981, 19.
12. Stanley L. Miller, "A Production of Amino Acids Under Possible Primitive Earth Conditions," *Science* 117 (1953): 528-29.
13. Robert Shapiro, "Prebiotic Ribose Synthesis: A Critical Analysis," *Origins of Life and Evolution of the Biosphere* 18 (1988): 71-95; Charles B. Thaxton, Walter L. Bradley, and Roger L. Olsen, *The Mystery of Life's Origin* (New York: Philosophical Library, 1984), 24-38; Charles B. Thaxton and Walter L. Bradley, "Information and the Origin of Life," in *The Creation Hypothesis: Scientific Evidence for an Intelligent Designer*, ed. J. P. Moreland (Downers Grove, Ill.: InterVarsity Press, 1994), 173-210; James P. Ferris, "Prebiotic Synthesis: Problems and Challenges," *Cold Springs Harbor Symposia on Quantitative Biology* 52 (1987): 30ff; Kaoru Harada and Sidney W. Fox, "Thermal Synthesis of Amino Acids from a Postulated Primitive Terrestrial Atmosphere," *Nature* 201 (1964): 335-37; Richard Lemmon, "Chemical Evolution," *Chemical Review* 70 (1970): 95-96.
14. See, for example, Bruce Alberts and Dennis Bray et al., *Molecular Biology of the Cell* (New York: Garland, 1983), 91-141; see also Albert L. Lehninger, *Biochemistry* (New York: Worth Publishers, 1975), 23.
15. As the result of geological and geochemical studies of the earliest Precambrian rocks scientists now question whether an oceanic medium full of biological precursors—i.e., the so-called

"prebiotic soup" required by Oparin's scenario—ever existed. In 1973, two scientists, Brooks and Shaw, argued that if an amino and nucleic acid-rich ocean had existed, it would have left large deposits of nitrogen rich minerals (nitrogenous cokes) in metamorphosed Precambrian sedimentary rocks. No evidence of such deposits exists, however. In the words of Brooks, "the nitrogen content of early Precambrian organic matter is relatively low (less than .015%). From this we can be reasonably certain that: there never was any substantial amount of 'primitive soup' on Earth when Precambrian sediments were formed; if such a soup ever existed it was only for a brief period of time." Jim Brooks, *Origins of Life* (Sidney: Lion, 1985), 118.

16. Though Oparin did not specify when he believed life first emerged, the gradual process of evolutionary development he described clearly implied that Earth had long existed in a lifeless state (perhaps several hundreds or even thousands of million years) in order to allow for the gradual development of molecular and metabolic complexity via natural selection. After the 1960s, however, a series of new fossil finds forced scientists to revise progressively downward their estimates of the time available for chemical evolution on Earth. Fossilized mats of stromatolites and the remains of various one-celled microorganisms were found in some of the world's oldest Precambrian rocks in Australia, South Africa, and Greenland. These finds suggested that one-celled life first existed at least as early as 3.5 billion, and perhaps as early as 3.85 billion years ago, or within as few as 150 million years of Earth's cooling according to geological and astronomical estimates. This drastic diminution of the time considered available for the occurrence of chemical evolution challenged the plausibility of Oparin's assumption of a long-lifeless terrestrial environment. It also calls into question all chemical evolutionary theories that rely heavily on time and chance to explain the origin of biological complexity. J. William Schopf and Elso S. Barghoorn, "Algae-like Fossils from the Early Precambrian of South Africa," *Science* 130 (1967): 508-11; J. Brooks and G. Shaw, *Origin and Development of Living Systems* (New York: Academic Press, 1973), 267-305, 361; Richard E. Dickerson, "Chemical Evolution and the Origin of Life," *Scientific American* 229 (1978): 70; Andrew H. Knoll and Elso S. Barghoorn, "Archean Microfossils Showing Cell Division from the Swaziland System of South Africa," *Science* 198 (1977): 396-98; D. R. Lowe, "Stromatolites 3,400-Myr-old from the Archean of West Australia," *Nature* 284 (1980): 441-43; M. R. Walter, R. Buick, and J. S. R. Dunlop, "Stromatolites 3,400-3,500 Myr old from the North Pole area, Western Australia," *Nature* 284 (1980): 443-45; J. Brooks, *Origins of Life,* 104-16; John M. Hayes, "The Earliest Memories of Life," *Nature* 384 (1996): 21-22; S. J. Mojzsis, G. Arrhenius, K. D. McKeegan et. al., "Evidence for Life on Earth Before 3,800 Million Years Ago," *Nature* 384 (1996): 55-59; H. D. Pflug and H. Jaeschke-Boyer, "Combined Structural and Chemical Analysis of 3,800-Myr-old Microfossils," *Nature* 280 (1979): 483-86; D. Bridgewater, J. H. Allart, J. W. Schopf et al., "Microfossil-like Objects from the Archaean of Greenland: A Cautionary Note," *Nature* 289 (1981): 51-56; Kevin A. Maher and David J. Stevenson, "Impact Frustration of the Origin of Life," *Nature* 331 (1988): 612-14; Thaxton et al., *Mystery of Life's Origin*, 69-72.

17. Francis Crick, *Life Itself* (New York: Simon and Schuster, 1981), 88. Robert Shapiro, *Origins* (London: Heinemann, 1986).

18. Klaus Dose, "Origin of Life: More Questions than Answers," *Interdisciplinary Science Reviews* 13 (1988): 348-56, esp. 348.

19. Miller, "A Production of Amino Acids," 528-29.

20. James C. G. Walker, *Evolution of the Atmosphere* (New York: Macmillan, 1977), 210, 246; James C. G. Walker, *Pure Applied Geophysics* 116 (1978): 222; Richard A. Kerr, "Origin of Life: New Ingredients Suggested," *Science* 210 (1980): 42-43; Thaxton et al., *Mystery of Life's Origin*, 73-94.

21. L. C. Berkner and L. L. Marshall, "On the Origin and Rise in Concentration in the Earth's Atmosphere," *Journal of Atmospheric Science* 22 (1965): 225-61; R. T. Brinkman, "Dissociation of

Water Vapor and Evolution of Oxygen in the Terrestrial Atmosphere," *Journal of Geophysical Research* 74 (1969): 5354-68; Erich Dimroth and Michael M. Kimberly, "Pre-Cambrian Atmospheric Oxygen: Evidence in Sedimentary Distribution of Carbon Sulfur, Uranium and Iron," *Canadian Journal of Earth Sciences* 13 (1976): 1161-85; J. H. Carver, "Prebiotic Atmospheric Oxygen Levels," *Nature* 292 (1981): 136-38; H. D. Holland, B. Lazar, and M. McCaffrey, "Evolution of Atmosphere and Oceans," *Nature* 320 (1986): 27-33; J. F. Kastings, S. C. Liu, and T. M. Donahue, "Oxygen Levels in the Prebiological Atmosphere," *Journal of Geophysical Research* 84 (1979): 3097-3102; Kerr, "Origin of Life: New Ingredients Suggested," 42-43; Thaxton et al., *Mystery of Life's Origin*, 73-94.

22. Horace Judson, *Eighth Day of Creation* (New York: Simon and Schuster, 1979), 213, 229-35, 255-61, 304, 334-35.
23. Bruce Alberts and Dennis Bray et al., *Molecular Biology of the Cell*, 91-141.
24. James Watson and Francis Crick, "A Structure for Deoxyribose Nucleic Acid," *Nature* 171 (1953): 737-38.
25. Ernest Borek, *The Code of Life* (New York: Columbia University Press, 1965), 184.
26. Bruce Alberts and Dennis Bray et al., *Molecular Biology of the Cell*, 108-9.
27. Charles B. Thaxton and Walter L. Bradley, "Information and the Origin of Life," 190.
28. Bernd-Olaf Küppers, *Information and the Origin of Life* (Cambridge, Mass.: MIT Press, 1990), 170-72.
29. Neal C. Gillespie, *Charles Darwin and the Problem of Creation* (Chicago: University of Chicago Press, 1979); Stephen C. Meyer, "Demarcation and Design: The Nature of Historical Reasoning" in *Facets of Faith and Science*, vol. IV, *Interpreting God's Action in the World* (Lanham, Md.: University Press of America, 1996), 91-130; Stephen C. Meyer, "The Methodological Equivalence of Design and Descent: Can There Be a Scientific Theory of Creation?," in *The Creation Hypothesis: Scientific Evidence for an Intelligent Designer*, 67-112; Stephen C. Meyer, "Laws, Causes, and Facts: A Response to Professor Ruse," in *Darwinism: Science or Philosophy?*, ed. Jon Buell and Virginia Hearn (Dallas: Foundation for Thought and Ethics, 1994), 29-40; Stephen C. Meyer, "A Scopes Trial for the '90's," *Wall Street Journal*, December 6, 1993, A14; see also "The Harmony of Natural Law," *Wall Street Journal*, January 17, 1994, Letters to the Editor Section, A9; Michael Ruse, "Creation Science is Not Science," *Science, Technology and Human Values* 7 (1982): 72-8.
30. Kamminga, "Studies in the History of Ideas on the Origin of Life," 326; Alexander I. Oparin, *Genesis and Evolutionary Development of Life*, trans. Eleanor Maass (New York: Academic Press, 1968), 146-47.
31. Francis Crick, "The Origin of the Genetic Code," *Journal of Molecular Biology* 38 (1968): 367-79; Kamminga, "Studies in the History of Ideas on the Origin of Life," 303-4.
32. George Wald, "The Origin of Life," *Scientific American* 191 (August 1954): 44-53; Shapiro, *Origins*, 121.
33. Christian de Duve, "The Constraints of Chance," *Scientific American* (January 1996): 112; see especially Crick, *Life Itself*, 89-93.
34. Hubert P. Yockey, *Information Theory and Molecular Biology* (Cambridge: Cambridge University Press, 1992), 246-58; Hubert P. Yockey, "Self Organization, Origin of Life Scenarios and Information Theory," *Journal of Theoretical Biology* 91 (1981): 13-31; Harold J. Morowitz, *Energy Flow in Biology* (New York: Academic Press, 1968), 5-12; A. G. Cairns-Smith, *The Life Puzzle* (Edinburgh: Oliver and Boyd, 1971), 92-96; Fred Hoyle and Chandra Wickramasinghe, *Evolution from Space* (London: J. M. Dent, 1981), 24-27; Shapiro, *Origins*, 117-31; J. Bowie and R. Sauer,

"Identifying Determinants of Folding and Activity for a Protein of Unknown Sequences: Tolerance to Amino Acid Substitution," *Proceedings of the National Academy of Sciences USA* 86 (1989): 2152-56; J. Bowie, J. Reidhaar-Olson, W. Lim, and R. Sauer, "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitution," *Science* 247 (1990): 1306-10; J. Reidhaar-Olson and R. Sauer, "Functionally Acceptable Solutions in Two Alpha-Helical Regions of Lambda Repressor," *Proteins, Structure, Function, and Genetics* 7 (1990): 306-16.

35. Ilya Prigogine, Gregorie Nicolis, and Agnes Babloyantz, "Thermodynamics of Evolution," *Physics Today*, November 1972, 23. Prigogine's statement in full is: "The probability that at ordinary temperatures a macroscopic number of molecules is assembled to give rise to the highly ordered structures and to the coordinated functions characterizing living organisms is vanishingly small. The idea of spontaneous genesis of life in its present form is therefore highly improbable, even on the scale of the billions of years during which prebiotic evolution occurred."
36. Cairns-Smith, *Life Puzzle*, 95.
37. Alberts et al., *Molecular Biology of the Cell*, 118.
38. Actually, Sauer counted sequences that folded into stable three-dimensional configurations as functional, though many sequences that fold are not functional. Thus, his results actually underestimate the probabilistic difficulty.
39. Reidhaar-Olson and Sauer, "Functionally Acceptable Solutions in Two Alpha-Helical Regions of Lambda Repressor," 306-16; Michael Behe, "Experimental Support for Regarding Functional Classes of Proteins to be Highly Isolated from Each Other," in *Darwinism: Science or Philosophy?*, 60-71. See also Yockey, *Information Theory and Molecular Biology*.
40. Emile Borel, *Probabilities and Life*, trans. M. Baudin (New York: Dover, 1962), 28; William A. Dembski, "The Design Inference: Eliminating Chance through Small Probabilities" (Ph.D. diss., University of Illinois, 1996), 54, 196-97.
41. Elizabeth Pennisi, "Seeking Life's Bare Genetic Necessities," *Science* 272 (1996): 1098-99; Arcady Mushegian and Eugene Koonin, "A Minimal Gene Set for Cellular Life Derived by Comparison of Complete Bacterial Genomes," *Proceedings of the National Academy of Sciences* 93 (1996): 10268-73; Carol J. Bult, Owen White, Gary J. Olsen et al., "Complete Genome Sequence of the Methanogenic Archaeon, *Methanococcus Jannaschi*," *Science* 273 (1996): 1058-72.
42. Dembski, *The Design Inference*, 153-215.
43. Peter T. Mora, "Urge and Molecular Biology," *Nature* 199 (1963): 212-19.
44. Oparin, *Genesis and Evolutionary Development of Life*.
45. Christian de Duve, *Blueprint for a Cell: The Nature and Origin of Life* (Burlington, N.C.: Neil Patterson Publishers, 1991), 187.
46. Peter T. Mora, "The Folly of Probability," in *The Origins of Prebiological Systems and of their Molecular Matrices*, ed. Sidney W. Fox (New York: Academic Press, 1965), 39-64; Ludwig von Bertalanffy, *Robots, Men and Minds* (New York: George Braziller, 1967), 82; Graham, *Science and Philosophy in the Soviet Union*, 291-92.
47. Theodosius Dobzhansky, discussion of Gerhard Schramm's paper in *The Origins of Prebiological Systems and of their Molecular Matrices*, 310.
48. Howard H. Pattee, "The Problem of Biological Hierarchy," in *Toward a Theoretical Biology*, vol. 3, ed. C. H. Waddington (Edinburgh: Edinburgh University Press, 1970), 123.
49. John Von Neumann, *Theory of Self-reproducing Automata*, ed. and completed by A. Berks (Urbana: University of Illinois Press, 1966).

50. Eugene Wigner, "The Probability of the Existence of a Self-reproducing Unit," in *The Logic of Personal Knowledge* (London: Kegan and Paul, 1961), 231-35.
51. P. T. Landsberg, "Does Quantum Mechanics Exclude Life?," *Nature* 203 (1964): 928-30.
52. Harold J. Morowitz, "The Minimum Size of the Cell," in *Principles of Biomolecular Organization*, ed. Maeve O'Connor and G. E. W. Wolstenholme (London: Churchill, 1966), 446-59; Morowitz, *Energy Flow in Biology*, 10-11.
53. Mora, "Urge and Molecular Biology," 212-19.
54. Richard Dawkins, *The Blind Watchmaker* (London: Longman, 1986), 47-49.
55. Bernd-Olaf Küppers, "On the Prior Probability of the Existence of Life," in *The Probabilistic Revolution*, ed. Kruger et al., (Cambridge, Mass.: MIT Press, 1987), 355-69.
56. Küppers, "On the Prior Probability of the Existence of Life," 366.
57. Küppers, "On the Prior Probability of the Existence of Life," 366.
58. Dawkins, *The Blind Watchmaker*, 47-49.
59. Paul Nelson, "Anatomy of a Still-Born Analogy," *Origins & Design* 17, no. 3 (1996): 12.
60. Christian de Duve, "The Beginnings of Life on Earth," *American Scientist* 83 (1995): 437.
61. Morowitz, *Energy Flow in Biology*, 10-11.
62. Gary Steinman and Marian N. Cole, "Synthesis of Biologically Pertinent Peptides Under Possible Primordial Conditions," *Proceedings of the National Academy of Sciences, USA* 58 (1967): 735-41; Gary Steinman, "Sequence Generation in Prebiological Peptide Synthesis," *Archives of Biochemistry and Biophysics* 121 (1967): 533-39; for more recent criticism see R. A. Kok, J. A. Taylor, and W. L. Bradley, "A Statistical Examination of Self-Ordering of Amino Acids in Proteins," *Origins of Life and Evolution of the Biosphere* 18 (1988): 135-42.
63. Dean Kenyon and Gary Steinman, *Biochemical Predestination* (New York: McGraw-Hill, 1969), 199-211, 263-66.
64. Ilya Prigogine and Gregorie Nicolis, *Self-Organization in Non-Equilibrium Systems* (New York: John Wiley, 1977), 339-53, 429-47.
65. Stuart Kauffman, *The Origins of Order* (Oxford: Oxford University Press, 1993), 285-341.
66. Christian de Duve, *Vital Dust: Life as a Cosmic Imperative* (New York: Basic Books, 1995), 428-37. For extensive technical critique of de Duve's metabolism first proposals see Leslie E. Orgel, "The Origin of Life: A Review of Facts and Specifications," *Trends in Biochemical Sciences* 23 (1998): 491-95.
67. See Kenyon in Thaxton, Bradley, and Olsen, *The Mystery of Life's Origin*, v-viii; Dean Kenyon and Gordon Mills, "The RNA World: A Critique," *Origins & Design* 17, no. 1 (1996), 12-6; Dean Kenyon and Percival W. Davis, *Of Pandas and People: The Central Question of Biological Origins* (Dallas: Haughton, 1993); Meyer, "A Scopes Trial for the 90's"; Kok et. al., "A Statistical Examination of Self-Ordering Amino Acids in Proteins," 135-42.
68. Steinman and Cole, "Synthesis of Biologically Pertinent Peptides Under Possible Primordial Conditions," 735-41; Steinman, "Sequence Generation in Prebiological Peptide Synthesis," 533-39.
69. Kok et al., "A Statistical Examination of Self-Ordering Amino Acids in Proteins," 135-42.
70. Alberts et al., *Molecular Biology of the Cell*, 105.
71. It should be noted that the "RNA World" scenario was not devised to explain the origin of the sequence of specificity of biomacromolecules. Rather, it was proposed as an explanation for the origin of the interdependence between nucleic acids and proteins in the cellular information

processing system. In all extant cells, building proteins required instructions from DNA, but information on DNA cannot be processed without many specific proteins and protein complexes. This poses an obvious "chicken-or-egg" dilemma. The discovery that RNA (a nucleic acid) possesses some limited catalytic properties (as modern proteins do) suggested a way to split the horns of this dilemma. By proposing an early Earth environment in which RNA performed both the catalytic (i.e., enzymatic) functions of modern proteins and the information storage function of modern DNA, "RNA first" advocates sought to formulate a scenario making the functional interdependence of DNA and proteins unnecessary to the first living cell. In so doing, they sought to make the origin of life a more tractable problem from a chemical evolutionary point of view. In recent years, however, many problems have emerged with the RNA world. (See: Shapiro, "Prebiotic Ribose Synthesis: A Critical Analysis," 71-95; Millas and Kenyon, "RNA World: A Critique," 9-16.) To name just one, RNA possesses very few of the specific catalytic properties necessary to facilitate the expression of the genetic information on DNA. In any case, by addressing a separate problem the RNA world presupposed a solution to, but did not solve, the sequence specificity or information problem. A recent article heralding a breakthrough for "RNA world" scenarios makes this clear. After reporting on RNA researcher Jack Szostak's successful synthesis of RNA molecules with some previously unknown catalytic properties, science writer John Horgan makes a candid admission: "Szostak's work leaves a major question unanswered: How did RNA, self-catalyzing or not, arise in the first place?" John Horgan, "The World According to RNA," *Scientific American*, January 1996, 27; Arthyr J. Zaug and Thomas R. Cech, "The Intervening Sequence RNA of *Tetrahymena* is an Enzyme," *Science* 231 (1986): 470-75; Thomas R. Cech, "Ribozyme Self-replication?," *Nature* 339 (1989): 507-08.

72. This, in fact, happens where adenine and thymine do interact chemically in the complementary base pairing across the message-bearing axis of the DNA molecule. Recent experiments have also shown that deoxyribonucleoside 5' triphosphates (i.e., the nucleotide bases joined with necessary sugar and phosphate molecules) will form repetitive sequences in solution even when polymerization is facilitated by a polymerizing enzyme such as DNA polymerase. N. Ogata and T. Miura, "Genetic Information 'Created' by Achaebacterial DNA Polymerase," *Biochemistry Journal* 324 (1997): 667-71.
73. Michael Polanyi, "Life's Irreducible Structure," *Science* 160 (1968): 1308-12, esp. 1309.
74. The information-carrying capacity of any symbol in a sequence is inversely related (by a negative logarithm function) to the probability of its occurrence. The informational capacity of a sequence as a whole is inversely proportional to the product of the individual probabilities for each member in the sequence. Since chemical affinities between constituents ("symbols") increase the probability of the occurrence of one given another (i.e., necessity increases probability), such affinities decrease the information carrying capacity of a system in proportion to the strength and relative frequency of such affinities within the system.
75. Fred I. Dretske, *Knowledge and the Flow of Information* (Cambridge, Mass.: MIT Press, 1981), 12.
76. Yockey, "Self Organization, Origin of Life Scenarios and Information Theory," 18.
77. Orgel has drawn a similar distinction between order and/or the randomness that characterizes inanimate chemistry and what he calls the "specified complexity" of informational biomolecules. Leslie E. Orgel, *The Origins of Life* (New York: John Wiley, 1973), 189ff. See also Thaxton et al., *The Mystery of Life's Origin*, 130ff.
78. In the most general sense, a specification is a pattern or description of an event that is conditionally independent of the event that it describes. Thus, an event is specified if it conforms to a conditionally independent pattern or description. In both a linguistic and biological context, a specification is a match or convergence between an event and an independent functional requirement. For a formal account of specification see Dembski, "The Design Inference," 53-73.

79. Thaxton and Bradley, "Information and the Origin of Life," 173-210; Thaxton et al., *The Mystery of Life's Origin*, 127-66; Yockey, *Information Theory and Molecular Biology*, 242-93.
80. Hubert P. Yockey, "A Calculation of the Probability of Spontaneous Biogenesis by Information Theory," *Journal of Theoretical Biology* 67 (1977): 377-98, esp. 380.
81. Interview with George Williams in *The Third Culture: Beyond the Scientific Revolution*, ed. John Brockman (New York: Simon and Schuster, 1995), 42-3.
82. Interview with G. Williams in *Third Culture*, 42-43.
83. George C. Williams, *Natural Selection: Domains, Levels and Challenges* (New York: Oxford University Press, 1992), 11.
84. Polanyi, "Life's Irreducible Structure," 1309.
85. Manfred Eigen, *Steps Toward Life* (Oxford: Oxford University Press, 1992), 12.
86. J. C. Walton, "Organization and the Origin of Life," *Origins* 4 (1977): 16-35; Mora, "The Folly of Probability," 41.
87. See John Maynard Smith, "Hypercycles and the Origin of Life," *Nature* 280 (1979): 445-46.
88. Freeman J. Dyson, *Origins of Life* (Cambridge: Cambridge University Press, 1985), 9-11, 35-39, 65-66, 78.
89. See discussion in Shapiro, *Origins*, 161.
90. Dembski has recently attempted to formalize this tendency as a general "law of information conservation." See his "Intelligent Design as a Theory of Information," presented to the "Naturalism, Theism and the Scientific Enterprise" conference at the University of Texas, Austin, February 22, 1997. Available on the Internet at http://www.dla.utexas.edu/depts/philosophy/faculty/koons/ntse/papers/Dembski.txt. See also Dembski, "The Design Inference," 153-215.
91. Kauffman, *The Origins of Order*, 285-341.
92. See Thaxton et al., *The Mystery of Life's Origin*, 127-43.
93. This qualification means to acknowledge that chance can produce low levels of information.
94. Defining information as the number of instructions required to specify a structure or sequence allows scientists to distinguish sequences that are merely mathematically improbable from functional sequences or meaningful text. Classical information theory as developed in the 1940s by Claude Shannon could not distinguish merely improbable sequences from those that conveyed a message (e.g., "we hold these truths to be self-evident. . . ." vs. "ntnyhiznlhteqkhgdsjh"). Shannon's theory could measure the "information carrying capacity" of a given sequence of symbols, but not the "information content." This is significant because random (natural) processes might produce an improbable but unspecified system. Nevertheless, recent reformulations of the design argument based on the presence of information in DNA have been based upon evaluations of information content, or what Dembski has called "specified information," not carrying capacity. As such, they do not commit the fallacy of equivocation. The argument asserts that the presence of high information content (in whatever context, semantic, structural, or computational) implicates a prior intelligent cause. It does not claim that information-carrying capacity (i.e., unspecified information or brute complexity) does. Moreover, Dembski has recently given a formal and generalized account of specification. His treatment makes it possible to distinguish specified and unspecified information and makes the notion of specification applicable beyond its original computational context. Gregory J. Chaitin, "On the Length of Programs for Computing Finite Binary Sequences," *Journal of the Association of Computing Machinery* 13 (1966): 547-69; Andrei N. Kolmogorov, "Three Approaches to Quantitative Definition of Information," *Problemy Peredachi Informatsii* (in translation) 1, no. 1 (1965): 3-11; Dembski, *The*

Design Inference, 115-52; Thaxton and Bradley, "Information and the Origin of Life," 200-10; Thaxton et al., *The Mystery of Life's Origin*, 127-66.

95. For a good summary and critique of different naturalistic models see especially Dose, "Origin of Life: More Questions than Answers," 348-56; Yockey, *Information Theory and Molecular Biology*, 259-93; Thaxton et al., *The Mystery of Life's Origin*, 24-38; Shapiro, *Origins*. For a contradictory hypothesis see Kauffman, *The Origins of Order*, 287-341.
96. Dembski, "Intelligent Design as a Theory of Information."
97. Meyer, "Of Clues and Causes: A Methodological Interpretation of Origin of Life Studies," 77-140.
98. Meyer, "Of Clues and Causes: A Methodological Interpretation of Origin of Life Studies," 77-140; Elliott Sober, *Reconstructing the Past* (Cambridge, Mass.: MIT Press, 1988), 4-5; Michael Scriven, "Causes, Connections, and Conditions in History," in *Philosophical Analysis and History*, ed. W. Dray (New York: Harper & Row, 1966), 249-50.
99. See transcript of the *McNeil-Lehrer NewsHour*, May 19, 1992.
100. Dembski, "The Design Inference," 153-215; Borel, *Probabilities and Life*, 28.
101. Dawkins, *The Blind Watchmaker*, 139.
102. Less exotic (and more successful) design detection occurs routinely in both science and industry. Fraud detection, forensic science, and cryptography all depend upon either the tacit or explicit application of probabilistic and information-theoretic criteria for detecting intelligent design. John Noble Wilford, "An Ancient 'Lost City' is Uncovered in Mexico," *New York Times*, February 4, 1994, A10; A. W. F. Edwards, "Are Mendel's Results Really Too Close?" *Biological Reviews* 61 (1986): 295-312; Philip J. Hilts, "Plagiarists Take Note: Machine is On Guard," *New York Times*, January 7, 1992, C9; Wayne Patterson, *Mathematical Cryptology for Computer Scientists and Mathematicians* (Towoya N.J.: Rowman and Littlefield, 1987).
103. Thomas R. McDonough, *The Search for Extraterrestrial Intelligence: Listening for Life in the Cosmos* (New York: Wiley, 1987).
104. William A. Dembski, ed., *Mere Creation: Science, Faith and Intelligent Design* (Downers Grove, Ill: InterVarsity Press, 1998); Michael J. Behe, *Darwin's Black Box* (New York: The Free Press, 1996); see also Michael Behe, "Molecular Machines: Experimental Support for the Design Inference," presented to American Scientific Affiliation Intelligent Design Symposium, August 9, 1993. For review of the symposium see: Paul Nelson, *Origins Research* 15, no. 2 (1994): 1, 6-14. Dembski, "The Design Inference"; Kenyon and Davis, *Of Pandas and People*, 55-8; Kenyon and Mills, "The RNA World: A Critique," 9-16; G. Ayoub, "On the Design of the Vertebrate Retina," *Origins & Design* 17, no. 1 (1996): 19-22; Michael Denton, *Evolution: A Theory in Crisis* (London: Adler and Adler, 1986), 326-43; Edmund Jack Ambrose, *The Nature and Origin of the Biological World* (New York: Halstead Press, 1982).
105. Dembski, "The Design Inference"; see also Behe, *Darwin's Black Box*, 196-97.
106. Dembski, "The Design Inference," 1-25.
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