

Stephen C. Meyer

The Origin of Life and the Death of Materialism

Alfred North Whitehead once said that “when we consider what religion is for mankind and what science is, it is no exaggeration to say that the future course of history depends upon the decision of this generation as to the relations between them.”¹ Whitehead spoke early in this century at a time when most elite intellectuals believed that science contradicted classical theism with its traditional belief in a divine creation, the uniqueness of man, and the immortality of the human soul. For many intellectuals a scientifically-informed world view was a materialistic world view in which the mere mention of entities such as God, free will, mind, soul, or purpose seemed inherently disreputable. Materialism denied evidence of any intelligent design in nature and any ultimate purpose to human existence. As Whitehead’s contemporary Bertrand Russell put it, “man is the product of causes which had no prevision of the end they were achieving” and which predestine him “to extinction in the vast death of the solar system.”²

It is not hard to see why many intellectuals held this opinion. Despite the now-well documented influence of Christian thinking on the rise of modern science from the time of Ockham to Newton, much of science during the nineteenth century did take a decidedly materialistic turn. Scien-

tific origins theories in particular seemed to support the materialistic vision of an autonomous and self-creating natural world. For example, at the beginning of the nineteenth century the French mathematician Laplace offered an ingenious theory known as the nebular hypothesis to account for the origin of the solar system as the outcome of purely natural gravitational forces. In geology, Charles Lyell explained the origin of the earth’s most dramatic topographical features—mountain ranges and canyons—as the result of slow, gradual, and completely naturalistic processes of change. Most significantly, Darwin’s evolutionary theory sought to show that the blind process of natural selection acting on random variations could, and did, account for the origin of new forms of life without any divine intervention or guidance. According to Darwin, living organisms only *appeared* to be designed by an intelligent creator; nature itself was the real creator. Even in cosmology, a belief in the infinity of space and time obviated any need to consider the question of the ultimate origin of matter. Thus, for scientific materialists at the end of the nineteenth century, the whole history of the universe and life could be told as a seamless,

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or nearly seamless, unfolding of the potentiality of matter and energy. No longer could it be held that a pre-existent mind shaped matter. Rather, modern science showed that matter shaped and created the capacities mind (and not the reverse). God did not create “the heavens and the earth.” The heavens and the earth (i.e., matter) created (via evolution) the minds that created the concept of God.

By the turn of the twentieth century, this once shockingly materialistic approach to science had become the norm. Most twentieth-century scientists have assumed no limits to the explanatory power of materialistic forces. Materialistic modes of thought and assumptions have spread from physics and biology to psychology, sociology, criminology, economics, educational theory, and even theology. Thus, Whitehead would in the end attempt to reconcile science and religion by asserting that even God evolves.

Yet now at the end of the twentieth century, after many wars and genocidal policies pursued in the name of materialistic ideology, the scientific picture of the world is rapidly changing. From the microcosm of the cell and the quantum world, to the macrocosm of an expanding and finely-tuned universe, the materialistic vision of nature now seems incomplete. Even in biology where Darwin’s theory, perhaps more than any other, inspired the possibility of a fully materialistic world view, materialism now seems to be failing as scientists have uncovered an awe-inspiring complexity in even the simplest of living cells. Indeed, nowhere is the inadequacy of materialistic science more evident than in the contemporary discussion of how life in its very “simplest” form might have first originated.

After Darwin published the *Origin of Species* in 1859, many scientists began to think about a problem that Darwin had not addressed,³ namely, how life had arisen in the

first place. 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, where life had first originated. Indeed, by the 1870s with Darwin’s theory of the origin of species, with Laplace’s nebular hypothesis, and Lyellian geology enjoying widespread support, the origin of life remained as the only salient milestone in cosmic history lacking some materialistic explanation.

Yet scientists in the 1870s and 1880s 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. Thus, the German evolutionary biologist Ernst Haeckel would refer to cells as simple “homogeneous globules of plasm.”⁴ To Haeckel, a living cell seemed no more complex than a blob of jello. His theory of how life first came into existence reflected this view. His method likened cell “autogony,” as he called it, to the process of inorganic crystallization.⁵ Haeckel’s English counterpart, T.H. Huxley, proposed a simple two-step method of chemical recombination to explain the origin of the first cell.⁶ Just as salt could be produced spontaneously by adding sodium to chloride, so, thought Haeckel and Huxley, could a living cell be produced by adding several chemical constituents together and then allowing spontaneous chemical reactions to produce the simple protoplasmic substance that they assumed to be the essence of life.

During the 1920s and 1930s a more sophisticated version of this so-called “chemical evolutionary theory” was proposed by a Russian biochemist named Alexander I. Oparin. Oparin had a much more accurate

understanding of the complexity of cellular metabolism, but neither he, nor any one else in the 1930s, fully appreciated the complexity of the molecules such as protein and DNA that make life possible. Oparin, like his nineteenth-century predecessors, 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 (See Figure 1).

Oparin's theory envisioned a series of chemical reactions that he thought would enable a complex cell to assemble itself gradually and naturalistically from simple chemical precursors. Oparin believed that simple gases such as ammonia (NH_3), methane (CH_4), water (H_2O), 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 the earth.⁷ With the aid of ultraviolet radiation from the sun, the ensuing reactions would have produced energy-rich hydrocarbon compounds.⁸ These, in turn, would have combined with 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.⁹ These constituents would eventually arrange themselves into simple cell-like enclosures that Oparin called coacervates.¹⁰ Oparin then proposed a kind of Darwinian competition for survival among his coacervates. Those that developed increasingly complex molecules and metabolic processes would have survived and grown more complicated. Those that did not would have dissolved.¹¹

Thus, cells would have become gradually more complex as they competed for survival over billions of years. Like Darwin,

Oparin employed time, chance, and natural selection to account for the origin of complexity from initial simplicity. Moreover, nowhere in his scenario did "mind" or "intelligent design" or "a Creator" play any explanatory role. Indeed, for Oparin—a committed Marxist¹²—such notions were explicitly precluded from scientific consideration. Matter interacting chemically with other matter, if given enough time and the right conditions, must produce life. Complex cells were thus built from simple chemical precursors without any guiding personal or intelligent agency.

The first experimental support for Oparin's hypothesis came in December of 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_2O), and hydrogen (H_2) through a glass vessel containing an electrical discharge chamber.¹³ 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%) 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.¹⁴

Miller's success in producing biologically relevant "building blocks" under ostensibly prebiotic conditions was heralded

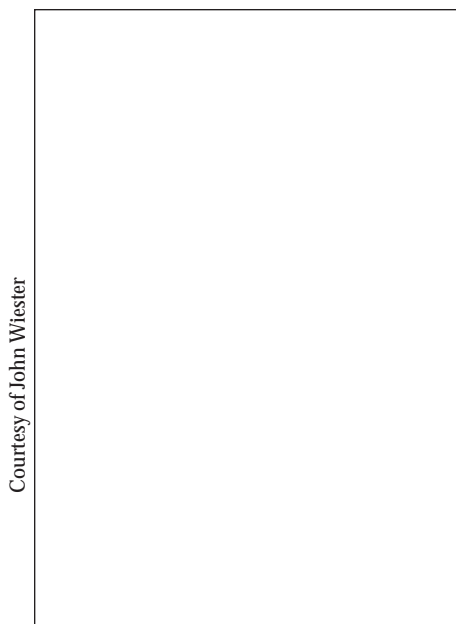
as a great breakthrough. His experiment seemed to provide experimental support for Oparin's chemical evolutionary theory by showing that an important step in Oparin's scenario—the production of biological building blocks from simpler atmospheric gases—was possible on the early earth. Miller's work inspired many similar simulation experiments and an unprecedented optimism about the possibility of developing an adequate naturalistic explanation for the origin of life. Miller's experimental results also received widespread press

ments into an era of discovery and achievement.¹⁶

Indeed, thanks largely to Miller's experimental work, chemical evolution is now routinely presented in both high school and college biology textbooks¹⁷ as the accepted scientific explanation for the origin of life. 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 could have arisen on the early earth.

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.¹⁸ 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.¹⁹ 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, the revolution in the field of molecular biology has revealed so great a complexity and specificity of design in even the "simplest" cells and cellular components as to defy materialistic explanation. Indeed, even scientists known for a staunch commitment to materialistic philosophy now concede that materialistic science in no way suffices to explain the origin of life.²⁰ As Francis Crick has written:

An honest man, armed with all the knowledge available to us now, could only state that in



Courtesy of John Wiester

(Figure 1) Chemical Evolutionary theorists envision life developing from simple chemicals in a series of steps such as these.

coverage in popular publications such as *Time*¹⁵ magazine and gave Oparin's model the status of textbook orthodoxy almost overnight. As one writer put it:

James Watson and Francis Crick unraveled the chemical basis of life.... Stanley Miller discovered how matter and energy could create the building blocks of life without a preexisting cell. Unleashed from paralysis and spurred by the Space Age, research on the origin of life was launched by these... momentous achieve-

some sense, the origin of life appears at the moment to be almost a miracle, so many are the conditions which would have had to have been satisfied to get it going.²⁰

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

When Stanley Miller conducted his experiment simulating the production of amino acids on the early earth, he presupposed that the earth's atmosphere was composed of a mixture of what chemists call reducing gases such as methane (CH₄), ammonia (NH₃), and hydrogen (H₂). 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.²¹ 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 vapor²²—not methane, ammonia, and hydrogen—predominated in the early atmosphere. 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.²³

This new information about the probable composition of the early atmosphere has forced a serious re-evaluation 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, reac-

tions among atmospheric gases will not take place readily and those reactions that do take place will produce extremely low yields of desired biological building blocks. Moreover, even a small amount of atmospheric oxygen will quench the production of biological building blocks and cause any biomolecules otherwise present to degrade rapidly.

An analogy may help to illustrate. Making amino acids in a reducing atmosphere is like getting vinegar and baking soda to react. Because the reaction releases stored chemical energy as heat (i.e. it is "exothermic"), it occurs easily.²⁴ Trying to make biological building blocks in a neutral or oxidizing atmosphere, however, is more like trying to get oil and water (or any two inert chemicals) to react.

Stanley Miller's experiment, and others like his, are only relevant to the origin of life if the reducing conditions he assumed actually existed on the early earth. Since independent geochemical evidence now strongly suggests that chemically hostile conditions prevailed, Miller's experiment cannot be said to "simulate" anything. Miller's work was heralded as a positive test of Oparin's chemical evolutionary scenario because he had selected parameters for his experiment in accord with a then-current understanding of early atmospheric conditions. What made Miller's experiment significant was not the production of amino acids *per se*, but the production of amino acids from presumably plausible prebiotic conditions. As Miller himself stated, "In this apparatus an attempt was made to duplicate a primitive atmosphere of the earth, and not to obtain the optimum conditions for the formation of amino acids."²⁵ Now, however, the situation has changed. The only reason to continue assuming the existence of a chemically-reducing, prebiotic atmosphere is that chemical evolutionary theory requires it. As *Science* magazine's Richard

Kerr put it, “No geological or geochemical evidence collected in the last thirty years favors a strongly reducing primitive atmosphere.... Only the success of the laboratory experiments recommends it.”²⁶

While laboratory simulation experiments have failed to demonstrate the plausibility of chemical evolution, they may have inadvertently demonstrated the necessity of intelligent agency playing an active role in the design of living systems. Ironically, even successful simulation experiments require the intervention of the experimenters to prevent what are known as “interfering cross reactions”²⁷ and other chemically destructive processes.

Assume for the moment that the reducing gases used by Stanley Miller do actually simulate the conditions on the early earth. Would his experimental results, then, support chemical evolution? Not necessarily. Miller-type simulation experiments have invariably produced non-biological substances in addition to biological building blocks such as amino acids and nucleic acid bases. Without human intervention, these other substances will react readily with biologically relevant building blocks to form a biologically irrelevant compound—a chemically insoluble sludge.²⁸ To prevent this from happening and to move the simulation of chemical evolution along a biologically promising trajectory, experimenters remove those chemicals²⁹ that degrade or transform amino acids into non-biologically relevant compounds. They must also artificially manipulate the initial conditions in their experiments. Rather than using both short and long-wavelength ultraviolet light (UV) which would be present in any realistic atmosphere, they use only short-wavelength UV. Why? The presence of the long-wavelength UV light quickly degrades amino acids.³⁰ Thus, investigators have routinely manipulated chemical conditions both before and after performing “simulation” ex-

periments in order to protect their experiments from destructive naturally occurring processes. Such manipulations constitute what chemist Michael Polanyi called a “profoundly informative intervention.”³¹ They seem to simulate, if anything, the need for an intelligent agent to overcome the randomizing influences of natural chemical processes—processes that lead inexorably, under realistic conditions, to biochemical deadends.

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 materialistic evolutionary thinking.

In the early 1950s, the 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.³² 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 or as structural components in the cell) depends upon the specific sequencing of the individual amino acids,³³ just as the meaning of an English text depends upon the sequential arrangement of the letters. 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 “hand-in-glove” fit with other molecules in the cell, enabling it to catalyze specific chemical reactions or to build specific structures within the cell. The proteins histone 3 and 4, for example, fold into well-defined three-dimensional shapes with a precise distribution of positive charges around their exteriors. This shape and charge distribution enables them to form part of the spools or nucleosomes that allow DNA to coil efficiently around itself and to store information.³⁴ Indeed, the information storage density of DNA, thanks in part to nucleosome spooling, is several trillion times that of our most advanced computer chips.³⁵

To get a feel for the specificity of the three-dimensional charge distribution on these histone proteins, imagine a large wooden spool with grooves on the surface. Next, picture a helical cord made of two strands. Then, visualize wrapping the cord around the spool so that it lies exactly into perfectly hollowed-out grooves—thicker parts nestling into deeper grooves, thinner parts into more shallow ones. In other words, the irregularities in the shape of the cord exactly match irregularities in the hollow grooves. In the case of histone and DNA, there aren’t actually grooves, but there is an uncanny distribution of positively charged regions on the surface of the histone proteins that exactly matches the negatively charged regions of the double stranded DNA that coils around it.³⁶ Proteins that function as enzymes or that assist in the processing of information stored on DNA strands often have an even greater specificity of fit with the molecules to which they must bind. Indeed, almost all proteins function as a result of an extreme “hand-in-glove” three-dimensional specificity that derives from the precise sequencing of the amino acid building blocks.

The discovery of the complexity and specificity of protein molecules has raised serious difficulties for chemical evolutionary theory, even if an abundant supply of amino acids is 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 sequencing 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.

During the 1950s and 60s, at roughly the same time molecular biologists began to determine the structure and function of many proteins, scientists were able to explicate the structure and function of DNA, the molecule of heredity. After Watson and Crick elucidated the structure of DNA in 1953,³⁷ molecular biologists soon discovered how DNA directs the process of protein synthesis within the cell. 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 millions of specifically arranged chemicals 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).

As in the case of protein, the sequence specificity of the DNA molecule strongly resembles the sequence specificity of human codes or languages. 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 messages that direct protein synthesis within the cell. Whereas the function of the protein molecule derives from the specific arrangement of twenty different amino acids (a twenty-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 the construction of one amino acid. This process proceeds as long chains of nucleotide triplets (the genetic message) are first copied during a process known as DNA replication and then transported (by the molecular messenger m-RNA) to a complex organelle called a ribosome.³⁸ There at the ribosome site, the genetic message is translated with the aid of an ingenious adaptor molecule called transfer-RNA to produce a growing amino acid chain³⁹ (See Figure 3). 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.

The explication of this system by molecular biologists in the 1950s and 1960s has raised the question of the ultimate origin of the specificity—the information—in both DNA and proteins. Indeed, many scientists now refer to the information problem as the “Holy Grail” of origin-of-life biology.⁴⁰ As Bernd-Olaf Koppers recently stated, “the problem of the origin of life is clearly basically equivalent to the problem of the origin of biological information.”⁴¹ As mentioned previously, the information contained or expressed in natural languages and computer codes is the product of intelligent minds. Minds routinely create informative arrangements of matter. Yet since the mid-nineteenth-century scientists have sought to explain all phenomena by reference to exclusively material causes.⁴² Since the 1950s,

three broad types of naturalistic explanation have been proposed by scientists to explain the origin of information.

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 pro



Courtesy of Doug Stevens and Insight magazine

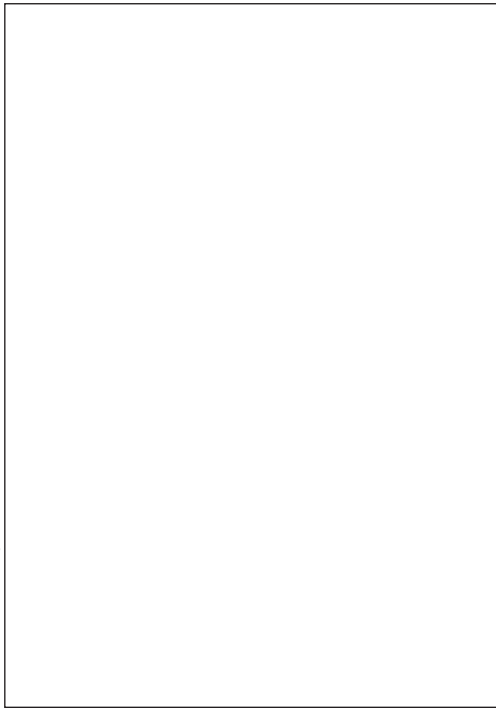
(Figure 2) A DNA molecule and the genetic text it contains. The DNA molecule stores information in the form of many specifically arranged chemicals called nucleotides (represented by A, T, G, and C). The genetic text (pictured as a scroll on the far right) is read along the spine or long axis of the molecule.

teins, DNA, and RNA (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 biopolymer* to account for the emergence of their specificity.⁴³ Others invoked the idea of a chance formation for these large information-bearing molecules by speaking of them as “frozen accidents.”⁴⁴

While many outside origin-of-life biology may still invoke “chance” as a causal

explanation for the origin of biological information, few serious researchers⁴⁵ still do. 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.

Courtesy of I.L. Cohen of New Research Publications



(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.

Various methods of calculating probabilities have been offered by Morowitz, Hoyle, Cairns-Smith, Prigogine, Yockey, and more recently, Robert Sauer.⁴⁶ For the sake of argument these calculations have generally assumed extremely favorable prebiotic conditions (whether realistic or not) 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."⁴⁷ 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.⁴⁸

Consider the probabilistic hurdles that must be overcome to construct even one short protein molecule of about one hundred amino acids in length. (A typical protein consists of about 300 amino acids, and some are considerably longer).⁴⁹

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; further, peptide and non-peptide 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: $(1/2 \times 1/2 \times 1/2 \times 1/2) = 1/16$ or $(1/2)^4$. The probability of building a chain of 100 amino acids in which all linkages involve peptide bonds 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 acids, yet the right-handed and left-handed isomers occur in nature with roughly equal frequency. Taking this into consideration increases the improbability of attain-

ing 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 is now $(1/4)^{100}$ or roughly 1 chance in 10^{60} .

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. In some cases, even changing one amino acid in a sequence can result in a loss of protein function. Moreover, because there are twenty 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 non-proteineous 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 is $(1/20)^{100}$ or roughly 1 chance in 10^{130} .

We know now, however, that some sites along the chain do tolerate several of the twenty 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 acids⁵⁰ in several functioning proteins at random is still "vanishingly small," roughly 1 chance in 10^{65} —an astronomically large number.⁵¹ (There are 10^{65} atoms in our galaxy). In light of these results, biochemist Michael Behe has compared the odds of attaining proper sequencing in a 100 amino acid length pro-

teins to the odds of a blindfolded man finding a single marked grain of sand hidden in the Sahara Desert, not once, but three times.⁵² Moreover, if one also factors in the probability of attaining proper bonding and optical isomers, the probability of constructing a rather short, functional protein at random becomes so small as to be effectively zero (1 chance in 10^{135}) even given our multi-billion-year-old universe. Sauer's calculations, thus, simply reinforce the opinion that has prevailed since the mid-1960s within origin-of-life biology: chance is not an adequate explanation for the origin of biological specificity. 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 [chance] 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.⁵³

At nearly the same time that many researchers became disenchanted with "chance" explanations, theories of pre-biotic natural selection also fell out of favor. Such theories allegedly overcome the difficulties of pure chance by providing a mechanism by which complexity-increasing events in the cell might be preserved and selected. Yet these theories share many of the difficulties that afflict purely chance-based theories.

Oparin's revised theory, for example, claimed that a kind of natural selection acted upon random polymers as they formed and changed within his coacervate protocells.⁵⁴ As more complex molecules accumulated, they presumably survived and reproduced more prolifically. Nevertheless, to many, Oparin's discussion of differential reproduction seemed to presuppose a pre-existing 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. Thus, many rejected the postulation of prebiotic natural selection as question begging.⁵⁵ Functioning nucleic acids and proteins (or molecules approaching their complexity) seemed necessary to self-replication, which in turn seemed necessary to natural selection. Yet Oparin invoked natural selection to explain the origin of proteins and nucleic acids. As the evolutionary biologist Dobzhansky would proclaim, “prebiological natural selection is a contradiction in terms.”⁵⁶ 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.⁵⁷

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 there is some means of selecting them after they have been produced. Natural selection can only select what chance 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 the problem by claiming that the first polymers need not have been terribly specific. But this claim raises doubts about whether self-replication (and thus, natural selection) could have proceeded at all. The mathematician Von Neumann, for example, showed that any system capable of self-replication would need to contain sub-systems that were functionally equivalent to the information storage, replicating and processing systems found in extant cells. His calcula-

tions⁵⁸ and similar ones by Wigner,⁵⁹ Landsberg,⁶⁰ and Morowitz,⁶¹ showed that random fluctuations of molecules in all probability would not produce the minimal complexity needed for even a primitive replication system. Indeed, the improbability of developing a replication system vastly exceeds the improbability of developing the protein and DNA components of such a system.⁶² For this reason, most scientists now dismiss appeals to prebiotic natural selection as essentially indistinguishable from appeals to chance.

Because of these difficulties, many origin-of-life theorists after the mid-1960s attempted to address the problem of the origin of biological information in a completely new way. Rather than invoking prebiotic natural selection or “frozen accidents,”⁶³ many theorists suggested that the laws of nature and chemical attraction may themselves be responsible for the information in DNA and proteins. Some have 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.⁶⁴ 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.⁶⁵ Just as electrostatic forces draw sodium ions (Na⁺) and chloride ions (Cl⁻) together into a highly-ordered pattern within a crystal of salt (NaCl), so too might amino acids with special affinities for each other arrange themselves to form proteins. This idea was developed in a book called *Biochemical Predestination* by Kenyon and Steinman in 1969. They argued that the origin of life might have been “biochemically predestined” by the properties of attraction that exist between constituent chemical parts, particularly between amino

acids in proteins.⁶⁶

In 1977, another theory of self-organization was proposed by Prigogine and Nicolis, but based on a thermodynamic characterization of living organisms. In their book *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.⁶⁷ 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; and thermal energy flowing through a heat sink will generate distinctive convection currents or “spiral wave activity.” Prigogine and Nicolis then 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 available, biochemical building blocks might arrange themselves into highly ordered patterns.

For many current origin-of-life scientists, self-organizational models⁶⁸ now seem to offer the most promising approach to explaining the origin of biological information. 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, Professor Dean Kenyon, has now explicitly repudiated such theories as both incompatible with empirical findings and theoretically incoherent.⁶⁹

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).⁷⁰ Nevertheless, these differences do not correlate to actual sequencing in large classes of known proteins.⁷¹ 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 phosphate 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 nucleotide bases that run along the spine of the helix. Yet it is precisely along this axis of the molecule that the genetic instructions in DNA are encoded.⁷²

In other words, the chemical constituents that are responsible for the message text in DNA do not interact chemically in any significant way. Just as the letters in a Scrabble game can be combined and recombined in any way to form various sequences, so too can each of the four nucleotide bases attach to any site on the DNA backbone with equal facility, making all sequences equally probable (or improbable). Thus, chemical bonding affinities cannot explain the sequential ordering of the nucleotide bases along the spine of the DNA because *there are no chemical bonds* be-

tween the nucleotides that make the message text. Because the same holds for RNA molecules, researchers who speculate that life began in an “RNA world,” have also failed to solve the sequencing problem⁷³—i.e., the problem of explaining how the information present in all functioning RNA molecules could have arisen in the first place.

For those who want to explain the origin



(Figure 4) The bonding relationships between the chemical constituents of the DNA molecule. Sugars (designated by the pentagons) and phosphates (designated by the circled Ps) are linked chemically. Nucleotide bases (As, Ts, Gs, and Cs) 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 message-bearing spine of the helix.

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 the forces of

attraction between the constituents in DNA, RNA, and protein do not explain the sequence specificity of these large information-bearing biomolecules.

Significantly, information theorists insist 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 probable 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 likely drag thymine (T) along with it.⁷⁴ Every time cytosine (C) found a slot, guanine (G) would 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 se-

quences—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 repetitive and highly ordered, 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 and 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.⁷⁵ (emphasis added)

So, if chemists had found that bonding affinities between the nucleotides in DNA produced nucleotide sequencing, they would also have 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.⁷⁶ Bonding affinities, to the extent they exist, mitigate against the maximization of infor-

mation.⁷⁷ 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).⁷⁸ He concedes that energy flowing through a system may produce highly ordered patterns. Strong winds form swirling tornados 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 doesn’t need explaining. What needs explaining 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! Our neighbor’s 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. It is complex because its characters do not follow a rigidly repeating or predictable pattern—i.e., it is aperiodic. 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. Systems that are characterized by both specificity and complexity (what information theorists call “specified complexity”) have “information content.” Since such systems

have the qualitative feature of aperiodicity or complexity, 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 specified complexity or 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 highly specified and complex, just like meaningful English sentences.

Conflating order and information (or specified complexity) 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 energy alone 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.⁷⁹

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 is neither deducible from the properties of the material medium nor attributable to them. The properties of matter do not explain the origin of information.

To amplify the 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 to convey the same message. The information in the headline could have been written with chalk on a board, with neon-filled tubes in a series of signs, or by a skywriter over New York Harbor. Clearly, the 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. This November the *Times* will use ink and English characters to tell the reading public that either a Democrat, a Republican, or a Third-Party candidate has won the Presidential election. Yet the properties of the ink and the twenty-six letters available to the typesetter will not determine which headline will be broadcast by the *Times*. Instead, the ink and English characters will permit the transmission of whatever headline the election result requires, 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 determine the meaning of the text. In short, the message transcends the properties of the medium.

The information in DNA also transcends the properties of its material medium. 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 synthesis of naturally occurring proteins). Thus, again, the prop-

erties of the constituents do not determine the function—the information transmitted—by the whole. As Michael Polanyi has said: “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.”⁸⁰

If the properties of matter (i.e., the medium) do not suffice to explain the origin of information, what does? Blind chance is, of course, a possibility but *not*, as we have seen in the case of DNA and proteins, where the amount of information (or the improbability of arrangement) gets too great.⁸¹ 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 invariably fail as the numbers of letters required to make a 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 information. But this suggestion betrays confusion on two counts. First, scientific laws don’t generally explain or cause natural phenomena, they describe them. For example, Newton’s law of gravitation described, but did not explain, the attraction between planetary bodies. Second, to say that scientific laws describe, or generate, an informational sequence, is essentially a contradiction in terms. Such patterns as laws describe are necessarily highly ordered, not complex. Thus, like crystals, all law-like patterns have an extremely limited capacity to convey information. One might, perhaps, hope to find a complex set of material conditions capable of regularly generating high information content, but everything we know suggests that the complexity and information content of such conditions would have to equal or exceed

that of the system produced,⁸² thus begging the question about the ultimate origin of information.

Instead, our experience with information-intensive systems (especially codes and languages) indicates that such systems always come from an intelligent source—i.e., from mental or personal agents, not chance or material necessity. This generalization holds not only for the information present in languages and codes but also for the non-grammatical 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 arrangement⁸³ and, consequently, have a high information content. All these systems are also, not coincidentally, the result of intelligent design, not chance or material forces.

Our generalization about the cause of information has, ironically, also received confirmation from origin-of-life research itself. During the last forty years, every naturalistic⁸⁴ model proposed has failed to explain the origin of information—the great stumbling block for materialistic scenarios. Thus, mind or intelligence or what philosophers call “agent causation,” now stands as the only cause known to be capable of creating an information-rich system, including the coding regions of DNA, functional proteins, and the cell as a whole.

Because mind or intelligent design is a necessary cause of an informative 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.⁸⁵ Since information requires an intelligent source, the flowers spelling “Welcome to Victoria” in the gardens of Victoria harbor lead 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.

Scientists in many fields now recognize the connection between intelligence and information 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.⁸⁶ N.A.S.A.'s search for extraterrestrial intelligence (S.E.T.I.)⁸⁷ presupposes that the presence of information imbedded in electromagnetic signals from space would indicate an intelligent source.⁸⁸ As yet, radio-astronomers have not found information-bearing signals coming from space. But molecular biologists, looking closer to home, have identified encoded information in the cell. Consequently, a growing number of scientists⁹¹ now suggest that the information in DNA justifies making what probability theorist William Dembski and biochemist Michael Behe call "the design inference."⁸⁹

During the last forty years, molecular biology has revealed a complexity and intricacy of design that exceeds anything that was imaginable during the late-nineteenth century. We now know that organisms display any number of distinctive features of highly-engineered, information-processing systems: information storage and transfer capability; functioning codes;⁹⁰ sorting and delivery systems;⁹¹ regulatory and feedback loops; signal transduction circuitry;⁹² and everywhere, complex, mutually-interdependent networks of parts. Indeed, the complexity of the biomacromolecules discussed in this essay does not begin to exhaust the

full complexity of design inherent in living organisms.

The materialistic science we have inherited from the late-nineteenth century, with its exclusive conceptual reliance on matter and energy, could neither envision nor can it now account for the biology of the information age. As Werner Gitt has said, throughout the natural sciences "energy and matter are considered to be basic, universal quantities. But the concept of information has become just as fundamental and far reaching...information has rightly become known as the third fundamental quantity."⁹³ As Norbert Weiner put it, "Information is information, neither energy nor matter. No materialism that fails to take account of this can survive the present day."⁹⁴

The molecular biology of the cell raises the possibility that "no materialism" will survive the revolution beginning to take root in science. While established journals and institutions continue to propagate the orthodoxies of a generation ago, many scientists, philosophers of science, and mathematicians have begun to challenge these views and to formulate alternative approaches. Recent work in probability theory has defined information more precisely and articulated clear mathematical criteria for the identification of intelligently designed systems,⁹⁵ thus providing a theoretical framework for a new science based upon the reality of design. A new book on the "irreducible complexity" of biochemical systems explains why gradual undirected evolution cannot produce such systems, and suggests intelligent design as the most viable scientific explanation.⁹⁶ A new peer-reviewed journal, *Origins & Design*, opens this spring with a seminal article by a former chemical evolutionist-turned-design-advocate.⁹⁷ Other work in progress promises to reshape our conception, not only of living things, but of our science and ourselves. If the simplest life owes its origin to

an intelligent Creator, then perhaps man is not the “cosmic orphan” that twentieth-century scientific materialism has suggested. Perhaps then, during the twenty-first century, the traditional moral and spiritual foundations of the West will find support from the very sciences that once seemed to undermine them.

Notes

1. Whitehead, *Science and the Modern World* (N.Y.: Macmillan, 1926) 260. 2. Russell quoted in Conant, *Modern Science and Modern Man*, (N.Y.: Doubleday Anchor, 1953) 139-140. 3. Darwin's only published speculation on the origin of life is found in a Feb., 1871 letter to Joseph Hooker. Cambridge University Library, Darwin Archives. Courtesy Peter Gautrey. 4. Haeckel, *The Wonders of Life* (1905) 111. Huxley, “On the Physical Basis of Life,” *The Fortnightly Review* 5 (1869) 129-45. 5. Haeckel, *Generelle Morphologie der Organismen*, vol. 1 (Berlin, 1866) 179-80, and *The History of Creation* (Trans. E.R. Lankester, London, 1892) 411-13. Kamminga, *Studies in the History of Ideas on the Origin of Life* (Ph.D Thesis, Univ. of London, 1980) 60-1. 6. Huxley, (1869) 138-9. 7. Oparin, *The Origin of Life* (Trans. S. Morgulls, 1938) 64-103. 8. *Ibid.*, 98, 107, 108. 9. *Ibid.*, 133-5. 10. *Ibid.* 148-59. 11. *Ibid.* 195-6. 12. Graham, *Science and Philosophy in the Soviet Union* (London, 1973) 262-63. Araujo, Interview with A.I. Oparin in *Uno Mas Uno* (Mexico City, May 7, 1981) 19. 13. Miller, “A Production of Amino Acids under Possible Primitive Earth Conditions” *Science* 117 (1953) 528-9. 14. Thaxton, *et al.*, *The Mystery of Life's Origin* (Dallas, 1992) 182. Shapiro, “Prebiotic Ribose Synthesis: A Critical Analysis” *Origins of Life and Evolution of the Biosphere* 18 (1988) 71-95. Ferris, “Prebiotic Synthesis: Problems and Challenges,” *Cold Spring Harbor Symposia on Quantitative Biology* 52 (1987) 30ff. Thaxton *et al.* (1992) 24-38. Harada and Fox “Thermal Synthesis of Amino Acids from a Postulated Primitive Terrestrial Atmosphere,” *Nature* 201 (1964) 335. Lemmon, (1970) 95-6. 15. See Shapiro, *Origins* (London: Heinemann, 1986) 98. 16. *Ibid.*, xvii. 17. See, for example, Alberts, *et al.*, *Molecular Biology of the Cell* (N.Y.: Garland, 1983) 4. Lehninger, *Biochemistry* (N.Y.: Worth, 1975) 23. 18. 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. Brooks, *Origins of Life* (Sidney: Lion, 1985) 118. 19. 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. Schopf and Barghoorn, “Alga-like Fossils from the Early Precambrian of South Africa,” *Science* 156(1967) 508-11. Brooks and Shaw, *Origin and Development of Living Systems* (N.Y.: Academic Press, 1973) 267-305, 361. Dickerson, “Chemical Evolution and the Origin of Life,” *Scientific American* (1978) 70. Knoll and Barghoorn, “Archean Microfossils Showing Cell Division from the Swaziland System of South Africa,” *Science* (1977) 396-8. Lowe, “Stromatolites 3,400-myr old from the Archean of Western Australia,” *Nature* 284 (1980) 441-3. Walter, *et al.*, (1980) 443-5. Brooks, *Origins of Life* (Sidney: Lion, 1985) 104-16. Remains of various one-celled microorganisms in the world's oldest Precambrian rocks suggest that one-celled life first existed as early as 3.85 billion [Pflug and Jaeschke-Boyer, “Combined Structural and Chemical Analysis of 3,800 myr-old microfossil,” *Nature* 280 (1979) 483-86. Bridgewater, *et al.* (1981) 51-3] years ago or within as few as 150 million years of the earth's cooling. Maher and Stevenson, “Impact Frustration of the Origin of Life,” *Nature* 33 (1988) 612-14. Brooks and Shaw, (1973) 73. Thaxton, *et al.* (1992) 20. Crick, *Life Itself* (N.Y.: Simon and Shuster, 1981) 88. 21. Miller, (1953) 528-9. 22. Walker, *Evolution of the Atmosphere* (N.Y.: Macmillan, 1977) 210, 246. Walker, *Pure Applied Geophysics* 116 (1978) 222. Kasting *et al.*, “Oxygen Levels in the Prebiological Atmosphere,” *Journal of Geophysical Research* 84 (1979) 3097-3102. Kerr, “Origin of Life: New Ingredients Suggested,” *Science* 210(1980) 42-3. Thaxton, *et al.* (1992) 73-94. 23. Berkner and Marshall, “On the Origin and Rise of Oxygen Concentration in the Earth's Atmosphere,” *Journal of Atmospheric Science* 22 (1965) 225. Brinkman, “Dissociation of Water Vapor and Evolution of Oxygen in the Terrestrial Atmosphere,” *Journal of Geophysical Research* (1969) 5355. Dimroth and Kimberly, “Precambrian Atmospheric Oxygen: Evidence in Sedimentary Distribution of Carbon, Sulfur, Uranium, and Iron,” *Can. Jour. of Earth Sci.* 13 (1976) 1161. Carver, “Prebiotic Atmospheric Oxygen Levels” *Nature* 292 (1981) 136. Holland, *et al.*, “Evolution of the Atmosphere and Oceans,” *Nature* 320 (1986) 27-33. Kerr, (1980) 42-3. Thaxton, *et al.* (1992) 73-94. 24. Thaxton and Bradley (1994) 184, have shown that polymerizing amino acids under reducing conditions releases 200 kcal of energy per mole, whereas polymerizing amino acids in neutral conditions requires an input of 50

kcal energy/mole. 25. Miller (1953) 529. 26. Kerr (1980) 42. 27. See Kenyon's preface in Thaxton, *et. al.* (1992) v-viii, and Thaxton, *et. al.* (1992) pp. 99-112. 28. Kenyon in Thaxton, *et. al.* (1992) vi. 29. Thaxton, *et. al.* (1992) 102. 30. Thaxton and Bradley (1992) 184. Thaxton, *et. al.* (1992) 100-1. 31. Polanyi, "Life's Irreducible Structure," *Science* 160 (1968) 64. 32. Portugal and Cohen, (1977) 307. 33. Alberts, *et. al.* (1983) 91-141. 34. Lodish, *et. al.*, (1993) 347-8. 35. Gitt "Information: The Third Fundamental Quality," *Seimens Review* 56 (1989) 4. 36. Lodish, *et. al.*, (1993) 347-8. 37. Watson and Crick "A Structure for Deoxyribose Nucleic Acid," *Nature* 171 (1953) 737. 38. Borek (1969) 184. 39. Alberts, *et. al.* (1983) 108-9. 40. Thaxton and Bradley (1994) 190. 41. Koppers (1990) 170-72. 42. Gillespie, *Charles Darwin and the Problem with Creation* (Chicago, 1983). Meyer, "Demarcation and Design: The Nature of Historical Reasoning," in *Facets of Faith and Science* Vol. 4: Interpreting God's Action in The World, (UPA, 1996). Meyer, "The Methodological Equivalence of Design and Descent: Can There be a Scientific Theory of Creation?" in *The Creation Hypothesis*, ed. Moreland (Intervarsity Press, 1994) 67-112. Meyer, "Laws, Causes, and Facts: A Response to Professor Ruse," in *Darwinism: Science or Philosophy*, ed. Buell and Hearn (Foundation for Thought and Ethics: Dallas, 1994) 29-40. Meyer, "A Scopes Trial for the '90s," *The Wall Street Journal* (12/6/93) A. See also, "The Harmony of Natural Law," (1/17/94) Letters to the Editor, A9. Johnson, *Darwin on Trial* (Washington, D.C.: Regnery Gateway, 1991). Ruse (1982). 43. Kamminga, (1980) 326. Oparin, *Genesis and Evolutionary Development of Life* (1968) 146-47. 44. Crick, "The Origin of the Genetic Code," *Journal of Molecular Biology* 38 (1968) 367-79. Kamminga, (1980) 303-4. 45. De Duve, "The Constraints of Chance" *Scientific American* (1/96) 112. 46. Morowitz, *Energy Flow in Biology* (N.Y.: Academic Press, 1968) 5-12. Cairns-Smith, *The Life-Puzzle* (Edinburgh: Oliver and Boyd, 1971) 92-6. Hoyle and Wickramasinghe, *Evolution from Space* (London: J.M. Dent, 1981) 24-7. Shapiro, (1986) 117-31. Yockey, "Self-organization Origin of Life Scenarios and Information Theory," *J. Theor. Biol.* 91 (1981) 13-31. Yockey, *Information Theory and Molecular Biology* (Cambridge, 1992) 246-58. Bowie and Sauer, "Identifying Determinants of Folding and Activity for a Protein of Unknown Structure," *Proceedings of the National Academy of Sciences USA* (1989) 2152-6. Bowie, *et. al.* "Deciphering the Messages in Protein Sequences: Tolerance to Amino Acid Substitution," *Science* 247 (1990) 1306-10. Reidhaar-Olson and Sauer (1990) 306-16. 47. Prigogine, *et. al.*, (1972) 23. 48. Cairns-Smith, (1971) 95. 49. Alberts, *et. al.* (1983) 118. 50. 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. 51. Reidhaar-Olson and Sauer "Functionally-acceptable Substitutions in Two Alpha-Helical Regions of Lambda Repressor," *Proteins: Structure, Function, and Genetics* 7 (1990) 306-16. 52. Behe, "Experimental Support for Regarding Functional Classes of Proteins to be Highly Isolated from Each Other," *Darwinism: Science or Philosophy* (1994) 68-9. 53. Mora, "Urge and Molecular Biology," *Nature* 199 (1963) 215. 54. Oparin (1968) 146-7. 55. Mora, "The Folly of Probability," *The Origins of Prebiological Systems and of Their Molecular Matrices* (N.Y.: Academic Press, 1965) 311-12. Bertalanffy, *Robots, Men and Minds* (N.Y.: Braziller, 1967) 82. 56. Dobzhansky, Discussion of G. Schramm's paper (see note 55) 310. 57. Pattee, "The Problem of Biological Hierarchy," *Towards A Theoretical Biology*, vol. 3 (Edinburgh, 1970) 123. 58. Von Neumann, "Theory of Self-Reproducing Automata," (Ill., 1966) 59. Wigner "The Probability of a Self-Reproducing Unit," *The Logic of Personal Knowledge* (London: Kegan and Paul, 1961) 231-5. 60. Landsberg "Does Quantum Mechanics Exclude Life?" *Nature* 203 (1964) 928-30. 61. Morowitz, "The Minimum Size of the Cell," *Principles of Biomolecular Organization* (1966) 446-59, (1968) 10-11. 62. Mora (1963) 215. 63. Crick (1968) 367-79. Kamminga (1980) 303-4. 64. Morowitz (1968). 65. Steinman and Cole, *Proc. Acad. Nat. Sci. US* (1967) 735-41. Steinman "Sequence Generation in Prebiological Peptide Synthesis," *Arch. Biochem. Biophys.* 121 (1967) 533-9. For recent criticism see, Kok, *et. al.* (1988) 135-42. 66. Kenyon and Steinman, *Biochemical Predestination* (N.Y.: McGraw-Hill, 1969) 199-211, 263-6. 67. Prigogine and Nicolis, *Self Organization in Nonequilibrium Systems* (N.Y.: Wiley, 1977) 339-53, 429-47. 68. See, for example, Kauffman, *The Origins of Order* (Oxford, 1993), De Duve, *Vital Dust: Life as a Cosmic Imperative* (N.Y.: Basic Books, 1995). 69. Kok, *et. al.*, "A Statistical Examination of Self Ordering of Amino Acids in Proteins," *Origins of Life and Evolution in the Biosphere* 18 (1988) 135-142. 70. Steinman and Cole (1967) 735-741. Steinman (1967) 533-539. 71. Kok, *et. al.* (1988) 135-142. 72. Alberts, *et. al.* (1983) 105. 73. A recent article heralding a breakthrough for "RNA world" scenarios makes this clear. After telling how RNA researcher Jack Szostak had succeeded in engineering RNA molecules with a broader range of catalytic properties than previously known, 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?" Horgan "The World According to RNA," *Scientific American* (1/96) 27. Shapiro (1988) 71-95. Zaug and Cech, *Science* 231 (1986) 470-

5. Cech (1989) 507-8. 74. 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. 75. Polanyi, (1968) 1309. 76. The information carrying capacity of any symbol in a sequence is inversely proportional 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. 77. Yockey (1981) 18. 78. 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. Orgel, *The Origins of Life on Earth* (N.Y.: Wiley, 1973) 189ff. See also Thaxton, et. al. (1992) 130ff. 79. Yockey, "A Calculation of the Probability of Spontaneous Biogenesis by Information Theory," *J. Theor. Biol.* 91 (1977) 380. 80. Polanyi (1968) 1309. 81. See Dembski, *The Design Inference: Eliminating Chance Through Small Probabilities* (U. of Ill. Ph.D. Thesis, 1996) for a thorough explication of the criteria by which quantitative judgements about the efficacy of chance can be made. 82. J.C. Walton has argued that the self-organization produced in Prigogine-style convection currents does not exceed the organization or information of the experimental apparatus used to create the currents. Walton (1977) 16-35. Mora (1965) 41. Similarly, Maynard-Smith and Dyson show that Manfred Eigen's so-called hypercycle model for generating information naturalistically, is subject to this same law of information loss. 83. Defining information as the number of instructions required to specify a structure 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 or complex sequences from those that conveyed a message (e.g., "we hold these truths to be self-evident..." v. "ntnyhiznlhteqkhdjsjh"). 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, not carrying capacity. As such, they do not commit the fallacy of equivocation. See Thaxton and Bradley (1994) 200-10. 84. For a good summary and critique of different approaches see especially, Dose "The Origin of Life: More Questions than Answers," *Interdiscipl. Sci. Rev.* 13 (1988) 348-56. Yockey (1992) 259-93, Thaxton, et. al. (1992), Shapiro (1986). For a contradictory hypothesis see Kauffman (1993) 287-341. 85. Meyer, *Of Clues and Causes: A Methodological Interpretation of Origin of Life Studies* (Cambridge Univ. Ph.D. Thesis, 1990) 79-99. 86. Less exotic (and more successful) design detection occurs routinely in both science and industry. Fraud detection, forensic science, and cryptography all depend upon the application of probabilistic or information theoretic criteria of intelligent design. Wilford, "An Ancient 'Lost City' is Uncovered in Mexico," *The New York Times* (2/4/94) A 10. Edwards, A.W.F. (1986) 295-312. Hilts, Philip J., "Plagiarist Take Note: Machine is on Guard," *The New York Times* (1/7/92) C9. Patterson, W., *Mathematical Cryptology for Computer Scientists and Mathematicians* (N.J.: Rowman & Littlefield, 1987). 87. McDonough, *The Search for Extraterrestrial Intelligence* (N.Y.: Wiley, 1987). 88. Behe, *Darwin's Black Boxes* (N.Y.: The Free Press, 1996). Kenyon and Mills, "The RNA World: A Critique," *Origins & Design* 17 (1996) 12-16. Ayoub, "On the Design of the Vertebrate Retina," *Origins & Design* 17 (1996) 19-22. Dembski (1996). Moreland, et. al. *The Creation Hypothesis* (Downers Grove, IL.: Intervarsity Press, 1994). Bradley, "Thermodynamics and the Origin of Life," *Perspectives on Science and Christian Faith* 40 (1988) 72-83. Augros, R. and Stanciu, G., *The New Biology* (Boston: Shambala, 1987). Denton, M., *Evolution: A Theory in Crisis* (London: Adler and Adler, 1986) 326-343. Thaxton, et. al. (1994). Ambrose, E.J., *The Nature and Origin of the Biological World* (N.Y.: Halstead Press, 1982). Thaxton, et. al. (1992). Walton (1977) 16-35. 89. Dembski (1996). Behe (1993). 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, forensic scientists can make fairly definitive inferences about the past. Meyer (1990) 79-99. Sober (1988) 4-5. Scriven (1966) 249-50. 90. Wolfe, *Molecular and Cell Biology* (C.A.: Wadsworth, 1993) 671-9. 91. Wolfe (1993) 835-44. 92. Wolfe (1993) 237-53. 93. Gitt (1989) 2. 94. Quoted in Gitt (1989) 5. 95. Dembski (1996). 96. Behe, (1996). 97. Kenyon and Mills (1996) 12-16.