

## Seeking a Signature: A Review of “Signature in the Cell”

BY DENNIS VENEMA

Stephen C. Meyer’s recent tome *Signature in the Cell* (hereafter, *Signature*) represents the “state of the art” for the intelligent design (ID) movement with respect to the origin of biological information. With *Signature*, Meyer claims to have established ID as the best scientific explanation for information in DNA, and thus, to have established the presence of a designing intelligence at the origin of life. The book is a landmark for the ID movement, and, in light of its claims, is of significant interest to Christians in the sciences. If Meyer’s claims indeed are found to have scientific support, they would represent perhaps the most significant scientific advance in the last several hundred years, and at the same time, provide no less than “a blueprint for twenty-first-century biological science.”<sup>1</sup>

### *Signature in the Cell*—Overview

Meyer begins *Signature* with a personal history of his entry into the design movement and his growing interest in what he terms “the DNA enigma—the mystery of the origin of the information needed to build the first living organism.”<sup>2</sup> From there he moves on to an introduction to early origin-of-life research (chap. 2) and a narrative of Watson and Crick’s discovery of the structure of DNA (chap. 3). In chapter 4, Meyer discusses his ideas on the information content of DNA, and in chapter 5, he describes cellular information processing (transcription and translation), presenting these as a “chicken-and-egg” problem for naturalistic origin of life research to explain. In chapters 6 and 7, Meyer outlines his strategy by which he will argue for ID as the best scientific explanation for the information present in DNA.

The core of Meyer’s argument can be found in chapter 7. Here he proposes three criteria for establishing ID as the best explanation for the origin of biological information: evidence that the cause was (1) present at the required time, (2) known to be causally adequate for the effect in question, and (3) the “absence of evidence (despite a thorough search) ... of ... other possible causes.” Meyer also argues that the first criterion can be met if there is only one possible cause of the effect in question:

If there is only one possible cause of a salient piece of evidence, then clearly the presence of that evidence establishes the past existence of its cause.<sup>3</sup>

This, in a nutshell, is the argument of the entire book. The second criterion (that intelligence can be the origin of information) is taken as a given. All that remains is for Meyer to establish with a “thorough search” that intelligence is the *only* possible source of biological information. In so doing, he will argue that ID qualifies as the best *scientific* inference for the information we find in DNA. Of course, the power of this argument lies squarely in the quality of his “thorough search” for alternate causes.<sup>4</sup>

Meyer’s quest for other explanations spans seven chapters, only one of which (at a slim twenty-eight pages) deals with the RNA world, one current hypothesis for the origin of life from abiotic precursors. The remaining six chapters of this section (totaling 123 pages) discuss historical models of abiogenesis that are no longer under serious consideration (if, indeed, they ever were). Having surveyed, to his satisfaction, natural causes for the origin of biological information and found them wanting, Meyer concludes that ID is the best explanation (chap. 15), compares his findings with William Dembski’s “Explanatory Filter” (chap. 16), and argues that his approach is not an argument from ignorance (chap. 17). Importantly, Meyer claims

that he argues not from *absence of knowledge*, but rather from *knowledge of absence* of competing natural explanations:

“True, some of the chapters of this book do argue that, at present, all types of material causes and mechanisms fail to account for the origin of biological information from a prebiotic state. And clearly this lack of knowledge of any adequate material cause does provide part of the grounds for inferring design from information in the cell, although it is probably more accurate to characterize this supposed “absence of knowledge” as knowledge of absence, since it derives from a thorough search for alternative materialistic causes and a thorough evaluation of the results of numerous experiments performed over several decades.”<sup>5</sup>

Meyer then wraps up the book with an argument for ID as science, framed as a rebuttal to the devastating *Kitzmiller vs. Dover Board of Education* ruling in 2005<sup>6</sup> (chap. 18), a chapter comparing his approach to standard science (chap. 19), and a more personal section entitled “Why it Matters” (chap. 20). Here Meyer explains his motivation for engaging the debate:

“... intelligent design, arguably, has theistic implications because intelligent design confirms a major tenet of the theistic worldview, namely, that life was designed by a conscious and intelligent being, a purposive agent with a mind.”<sup>7</sup>

“According to scientific materialism, reality is ultimately impersonal ... though this view of existence proved initially liberating in that it released humans from any sense of obligation to an externally imposed system of morality, it has also proved profoundly and literally dispiriting. If the conscious realities that comprise our personhood have no lasting existence, if life and mind are nothing more than unintended ephemera of the material cosmos, then, as the existential philosophers have recognized, our lives can have no lasting meaning or ultimate purpose. Without a purpose-driven universe, there can be no ‘purpose-driven life.’”<sup>8</sup>

The book also contains an epilogue and two appendices (one discussing ID predictions; the other, multiverse cosmology) which round out its 500-plus pages (excluding endnotes). Whatever else, *Signature* is not a light read.

## Rationale for a Thorough Scientific Critique

So, does Meyer’s scientific case hold together? I would say no. It suffers from what I perceive as fatal flaws that scuttle Meyer’s case for a design inference as the best explanation for the origin of biological information. While there is much that could be said about less important issues in *Signature* (e.g., Is ID “scientific creationism”? Poor theology?), I will focus this review on the core of Meyer’s scientific case for design. Meyer claims to have achieved a scientifically robust argument that establishes intelligent intervention as the best *scientific* explanation for the information content of DNA. Accordingly, this argument should be evaluated on its scientific merit. However, be forewarned: in what follows, I focus on what I see as serious scientific flaws in *Signature*, and leave what praise I have for the book (and there is some) left unsaid. I do this not out of disrespect, but rather out of respect. Meyer has presented his case, and he deserves to have this case thoroughly tested. If it can stand, so be it. If it cannot, then this critique

may be useful to him in the future as he continues his work. In either case, my platitudes will avail nothing; only scientific critique has lasting merit.

### No Biological Information by Natural Means?

The first fatal flaw, as I see it, is that Meyer claims there is no known natural mechanism that can add information to DNA. This claim is key to the entire argument, since Meyer cannot claim information as the direct action of a designing intelligence at the origin of life unless he rules out all natural causes that may add information to DNA. In doing so, he has to deny natural selection as such a mechanism:

“Since the case for intelligent design as the best explanation for the origin of biological information necessary to build novel forms of life depends, in part, upon the claim that functional (information-rich) genes and proteins cannot be explained by random mutation and selection, this design hypothesis implies that selection and mutation will not suffice to produce genetic information and that, consequently, functional sequences of amino acids within protein sequence space will be extremely rare rather than common. Axe’s mutagenesis experiments have tested, and continue to test, this prediction of ID theory.”<sup>9</sup>

Meyer’s main argument for the inability of random mutation coupled with natural selection (hereafter, “RM + NS”) to add information to DNA is based on the research of Douglas Axe, a scientist currently working at the Discovery Institute’s Biologic Institute.<sup>10</sup> Meyer claims that Axe’s work demonstrates that proteins are rare in sequence space—and argues therefore that functional proteins cannot be converted to different functions through RM + NS due to the intervening nonfunctional space between islands of function. There are several reasons why Axe’s work cannot be used as evidence for such an assertion.

The most obvious issue is that the rarity or commonality of function in protein sequence space is irrelevant to the discussion. What counts is whether functional sequences in protein space are *isolated* from each other in a way RM + NS cannot bridge.<sup>11</sup> This, as far as I can tell, is, in fact, what Meyer is arguing, though he does not appear to understand the distinction and conflates the two ideas in *Signature*. Even if one accepts Axe’s work uncritically, it only attempts to evaluate the rarity of functional sequences, not their evolutionary isolation. There are several very important differences between Axe’s work and a natural protein exploring sequence space through RM + NS.<sup>12</sup> First, the protein Axe used as a “test bench” was intentionally “hamstrung” with multiple mutations to render it far less functional than its natural counterpart. Secondly, the cellular environment for this altered protein was held constant, whereas proteins exploring sequence space through RM + NS experience drift in their cellular environment as well as in their own sequences. Thirdly, and most significantly, Axe did not mutate his test protein with single point mutations, but rather by adding partially randomized groups of ten amino acids at a time, something that does not resemble natural processes. While these features of Axe’s work are useful standardizations for estimating the relative rarity of function protein folds in his specific experimental setup, they render his work irrelevant to the issue of evolutionary isolation of functional sequences. Axe himself does not draw this conclusion from his work in the paper in question, and it is inappropriate for Meyer to attempt to do so. Moreover, Meyer ignores (or is unaware of) research in this area that is directly relevant to his argument. There is a large body of evidence from structural biology studies that proteins do transition between varied structures and functions across evolutionary time.<sup>13</sup> If Meyer wishes to justify his argument, he needs to address this evidence.

Beyond the evidence from structural biology, evidence from comparative genomics also strongly supports the hypothesis that the orthologous proteins we see in related species are indeed modified versions of an ancestral sequence. Consider the example of insulin sequences in various species and their conservation at the nucleotide level as well as at the amino acid level.<sup>14</sup> These sequences, when compared across widely diverged species, produce the exact pattern one would predict if they were, in fact, the results of an ancestral protein sequence “exploring sequence space” across evolutionary time through random point mutations and purifying selection of its nucleotide code. If Meyer wants to argue that Axe’s work demonstrates that proteins cannot explore sequence space through RM+NS, he needs to address this pervasive pattern. As we shall see, however, Meyer does not tackle this evidence or, for that matter, any evidence relevant to common ancestry.

Meyer’s denial of RM + NS as an information generator notwithstanding, in a discussion about evolutionary computer simulations, Meyer makes the following claim:

“If computer simulations demonstrate anything, they subtly demonstrate the need for an intelligent agent to elect some options and exclude others—that is, to create information.”<sup>15</sup>

Employing this argument, Meyer claims that any mechanism that prefers one variant over another creates information. As such, the ample experimental evidence for natural selection as a mechanism to favor certain variants over others certainly qualifies as such a generator. Meyer, however, makes no mention of evidence for natural selection in the book. The closest Meyer comes to discussing this issue is in the same section on computer simulations:

“Nothing in nature (biology or chemistry) corresponds to the role that the computer plays in selecting functionally non-advantageous sequences that happen to agree ‘one bit better’ than others with a target sequence.”<sup>16</sup>

This statement, while technically true, is misleading. It is technically true that nothing in nature distinguishes between nonfunctional sequences. It is misleading to suggest, however, that natural selection cannot work because it has no way of attaining a future idealized target. What natural selection can do, and do very well, is select between variants within a population, based on differential reproductive success. As such, it is not working toward a future target, but rather disproportionately preserving the most successful variants in a given generation. Natural selection works not because it has *foresight*, but because it has *hindsight*: sequences converge on highly functional sequences not because they “know” where they are going, but because they “know” where they have been, and they use this sequence as the starting point for exploring sequence space. As mutations “explore” the space around a previously selected sequence, variants that have an increase in function relative to the environment at that point in time are again selected. This process, as it is repeated, can rapidly converge on sequences highly suited to their tasks.

I happened to be teaching an upper-level class on immunology while I was reading *Signature*. The differences between Meyer’s arguments against RM + NS as a generator of information and the process by which the human body produces specific antibodies stood in sharp contrast for me. An overview of this process recently appeared in this journal,<sup>17</sup> and I was pleased to see that this issue was raised on the ASA blog discussing *Signature*.<sup>18</sup> Antibodies are generated through successive rounds of mutation and

selection. In the first instance, antibody gene segments are spliced together to form a coding sequence for the variable tip of the antibody; this process also includes the addition of random nucleotides in the joints between the segments. Each antibody-producing cell (a B cell) makes one antibody through this process. Of the vast numbers of antibodies produced, the few that bind foreign material trigger the selective reproduction of the B cells that harbor them. This replication is accompanied by further random mutation of the originally selected antibody sequence, and the resulting cells with the strongest binding antibodies are selected (and the process may repeat if the same pathogen attacks the host again in the future). Through this process of repetitive mutation and selection, an antibody progresses from relatively weak affinity to very strong affinity—a feature that greatly improves its function as an agent to fight infection. By any reasonable definition, this is an increase in biological information, but it proceeds effectively (a) through random mutation and a form of natural selection, and (b) with no planned target in mind, only repetitive selection for the best variants at any given time. What “creates” the information is the *environment*: the presence of the specific pathogen elects certain B cells and excludes others. By Meyer’s definition, the pathogen is the antibody designer.

While antibody generation is a particularly compelling case of natural processes increasing biological information, the same principles are seen time and again with RM + NS at the population level. For example, the work of Richard Lenski and colleagues on long-term evolution of *E. coli* has documented numerous mutations that have increased biological fitness within their experimental populations which have arisen through spontaneous mutations.<sup>19</sup> Other examples abound: the mutation and selection of the nylonase enzyme (which allowed its host to metabolize nylon),<sup>20</sup> the production of an antifreeze protein in fish from an enzyme gene,<sup>21</sup> and other examples of proteins arising *de novo* through mutation.<sup>22</sup>

Therefore, the demonstration that RM + NS can add information to DNA without the intervention of a designer means that Meyer’s argument for the exclusivity of intelligence in producing biological information fails. As such, RM + NS now becomes a candidate for the origin of biological information from nonliving precursors. What is required, of course, is a plausible pathway leading from nonliving precursors to a replicating entity capable of variation on which natural selection can act.

## Abiogenesis: God’s Last Gap?

While Meyer is correct that no complete mechanism for abiogenesis has yet been put forward, his argument here suffers from additional major flaws: he focuses disproportionately on outdated, discarded origin-of-life hypotheses, gives current science on the issue short shrift, and does not fairly represent the science he does discuss. For example, the major model favored by many scientists is the “RNA world” hypothesis, yet Meyer spends little time on it. Other current models, such as “metabolism first” hypotheses,<sup>23</sup> receive no attention at all. This seriously compromises Meyer’s argument, since his conclusion of design depends on his assertion that he has performed a “thorough search” to exclude all natural alternatives to intelligent intervention at the origin of life. Yet his search is not extensive, but selective and misleading at several key points.

In total, Meyer discusses origin-of-life hypotheses in a section spanning four chapters totaling approximately 150 pages. Of this section, the only current origin-of-life model (the RNA world) merits a slim chapter of twenty-eight pages; the remainder is a review of outdated ideas which he uses to argue that biological information cannot be assembled by chance alone or through self-assembly of the monomers that make up proteins or nucleic acids. The length of time Meyer spends on these various discredited origin

-of-life hypotheses (if, indeed, several of them were ever serious contenders) suggests he is either attempting to inflate the appearance of their importance to his nonspecialist audience or that he himself is not capable of evaluating them at their key points.

Once Meyer does arrive at discussing a current model (the RNA world hypothesis), he does so without mentioning several key pieces of evidence in its favor. Indeed, the discussion is not so much a description of the hypothesis as it is a polemic against it. Further, it is a flawed polemic. The first and most obvious error is that Meyer claims that the RNA world must explain a transition from an RNA-based enzyme for protein synthesis to a protein enzyme in the modern system. The error is, of course, that the “modern” system uses an RNA enzyme for protein synthesis: the enzymatic core of the ribosome (i.e., the portion of the complex that catalyzes peptide bond formation) is a ribozyme, not a protein enzyme. The modern ribosome uses proteins to stabilize and direct peptide bond formation, but they do not perform an enzymatic role.<sup>24</sup> Meyer, however, claims that modern ribosomes are “protein dominated” and presents this as a hurdle for the RNA world to explain.

While Meyer’s lack of depth in modern origin-of-life research appears in several places, one key error relevant to the RNA world hypothesis arises on multiple occasions. A rhetorical thread that Meyer weaves throughout the book is that the genetic code is arbitrary: that, in principle, any codon could have been assigned to any amino acid since there is no physical connection between them. Meyer claims that this feature of the translation apparatus is a “mystery” for origin-of-life research:

“Self-organizational theories have failed to explain the origin of the genetic code for several reasons. First, to explain the origin of the genetic code, scientists need to explain the origin of the precise set of correspondences between specific nucleotide triplets in DNA (or codons on the messenger RNA) and specific amino acids (carried by transfer RNA). Molecular biologists have failed to find any significant chemical interaction between the codons on the mRNA (or the anticodons on the tRNA) and the amino acids on the acceptor arm of tRNA to which the codons correspond. This means that the forces of chemical attraction between amino acids and these groups of bases do not explain the correspondences that constitute the genetic code ... the code is physically and chemically arbitrary. All possible codes are equally likely; none is favored chemically.”<sup>25</sup>

This point is a major one for Meyer: if the code is chemically arbitrary, then there can be no mechanistic pathway leading to it from nonliving chemical precursors. However, Meyer either avoids, or is simply unaware of,<sup>26</sup> a significant amount of research in this area that *has* demonstrated chemical interactions between amino acids and their cognate anticodons or codons.<sup>27</sup> This productive area of research was recently reviewed in extensive detail.<sup>28</sup> In brief, several amino acids directly bind RNA sequences corresponding to their anticodon or codon. This finding is strong evidence that the genetic code was established, at least in part, by the exact sort of chemical interactions that Meyer explicitly denies have ever been found. If, indeed, the genetic code was arbitrary, there would be no reason to expect these correspondences; conversely, their presence is good evidence that the modern genetic code passed through a “stereochemical era” where proteins were synthesized by direct organization on an RNA template, consonant with the hypothesis that RNA was the original genetic material.<sup>29</sup> While he does mention one discarded direct-coding hypothesis from the 1950s,<sup>30</sup> there is no mention of this more recent, and relevant, data. Meyer’s failure to address this research, while claiming that such evidence does not exist, is a serious flaw in his argument.

## What of Common Ancestry?

An additional flaw in Meyer’s work is that it almost completely avoids the issue of common ancestry. Surely, in a study attempting to eliminate a natural origin for biological information, the evidence for how biological information has been transmitted and modified by natural processes would be highly relevant. I found it very odd that in *Signature’s* five hundred pages, no DNA evidence for common ancestry is discussed. The only time Meyer broaches the issue is to claim that his work on the information content of DNA is compatible with all ID models: those that accept common ancestry, and those that deny it. Here, too, Meyer avoids a huge body of genetics evidence that overwhelmingly favors common ancestry<sup>31</sup> and has been described as such by the only well-known ID advocate who accepts it.<sup>32</sup> Meyer is claiming that his analysis, while robust enough to rule out all natural mechanisms for the origin of information in DNA, is insufficient to adjudicate between two competing ideas about the transmission of genetic information currently advocated *within* the ID movement. Put more simply, it means that ID as an explanatory framework is insufficiently powerful to test a hypothesis for which there is much relevant evidence. Given the strength of that evidence, this waffling on Meyer’s part can only be for the benefit of the ID “big tent” approach or because he personally rejects common ancestry.<sup>33</sup> A serious scientific work would not equivocate on such a well-supported area of research: at a minimum, it would engage the relevant evidence even if it argued for a conclusion at odds with the consensus. Meyer simply avoids the evidence altogether.

## Odds and Ends

Although other flaws are less serious in and of themselves, they are still indicative of the level of argumentation in the book, as well as of the quality of its peer review. For example, it was in chapter three that I first arrived at what I now call a “Behe moment” when reading antievolutionary literature. In Michael Behe’s book *Edge of Evolution*, he makes a few obvious “rookie errors” when discussing how probabilities work in population genetics.<sup>34</sup> This, for me, was the clear signal that the book was written by an amateur in the field and not adequately peer reviewed. In *Signature*, this moment arrived when Meyer calls *Pneumococci* a bacterium *and* a virus in the same paragraph.<sup>35</sup> This impression was confirmed anew when Meyer describes, over the course of several pages, his epiphany that DNA bases do not have bonds between them and thus cannot selforganize into specified sequences. This “epiphany” is something that biology majors learn (or at least, *should* learn) in their introductory courses. This theme continued apace in the figure describing translation.<sup>36</sup> *Signature* shows tRNAs aligning to the mRNA in a 5' to 5' orientation, tRNAs with codon instead of anticodon sequences, and several inappropriate nucleotide pairings: all very basic mistakes. In short, *Signature* clearly was not written or peer reviewed by individuals with a working knowledge of molecular biology.

Now, these issues in and of themselves would not be a serious problem for *Signature*, if not for the fact that the strength of Meyer’s argument rests entirely on his assertion that he has made a thorough search through all proposed mechanisms for generating biological information through natural means and found them lacking. Meyer is asking his audience to trust him that his analysis is thorough and sound. However, that Meyer’s understanding of molecular biology appears to be at or below a first-year college level should give even the most pro-ID reader pause here. It means that Meyer, well intentioned though he may be, is simply not equipped to grapple with these issues beyond an introductory textbook level. Nor has Meyer sought the advice of those who are able to do so. And as we have seen, Meyer has made neither a

thorough search for the origin of biological information by natural mechanisms, nor a fair assessment of current origin-of-life research.

## Concluding Thoughts

In some ways, the disappointment for me in reading *Signature* was its too obvious weaknesses. An ID argument with some scientific teeth to it would be intellectually invigorating, and I expected *Signature* would deliver more than it did. It has no theory of design, and no vigorous hypotheses to advance the movement. As Randy Isaac noted in an ASA blog, Meyer's predictions do not distinguish between ID and other hypotheses:

“It is laudable that Meyer takes the step to explore predictions that ID would make. Predictions that are testable are a vital part of the scientific process. But just making a prediction isn't sufficient to indicate viable science. Astrologers and tasseologists can also make predictions and sometimes they may be right. Predictions must also be based on causal factors that are understood independently to exist and whose adequacy can be independently verified. The predictions must clearly differentiate between competing hypotheses. It is unfortunate that this set of dozen predictions is very weak on all counts.”<sup>37</sup>

Effectively, Meyer requests that we trade pursuing an ongoing area of productive research for his pronouncement that it will never succeed. Not so. Biologists know full well that natural mechanisms can add functional information to DNA sequences, and it thus makes good sense to look for pathways that exploit these mechanisms at the origin of life. True, research in this field has not solved the origin-of-life problem, and there are several competing hypotheses on the table, all with some experimental support. Quite a lot has been accomplished in this area in the last few decades, and it is a reasonable expectation that further research will continue to pay dividends. To halt research in this field and to label it “design” (and therefore unsolvable) accomplishes nothing scientifically, especially when there is no workable theory of design to guide future work.

While popular-level books written by nonspecialists can be very helpful to a lay audience if they are carefully reviewed by experts and adhere to consensus science, *Signature* is not such a book. Like *Edge of Evolution* before it, *Signature in the Cell* represents a layman's attempt to overturn an entire field of research based on a surface-level understanding (and, at times, significant misunderstanding or ignorance) of the relevant science, published in a form that bypasses review by qualified peers, and that is marketed directly to a nonspecialist audience. This is not good science, nor science in any meaningful sense. If ID is going to advance as an intellectual framework, it simply must do better. I, for one, would be fascinated by a scientifically plausible design argument. It would demonstrate that something is fundamentally wrong with the interpretation of very wide swaths of data across numerous disciplines. That would not be a scientific problem, but rather a monumental scientific opportunity that would reshape research for decades to come. Such times are the occasions of scientific legend—careers to be made, Nobel prizes to be won. Alas, *Signature* is not that argument. I do recommend it for those who follow the ID literature, for it represents the current state-of-the-art in ID thought for an important area of biology. However, for those of us waiting for the science behind ID, it looks as if the wait goes on.

## Notes

1. As claimed by Steve Fuller on *Signature's* dust jacket.
2. Meyer, *Signature*, 14.
3. *Ibid.*, 167.
4. As we shall see, this search leaves much to be desired.
5. Meyer, *Signature*, 376.
6. The *Kitzmiller* decision is available online at [www.talkorigins.org/faqs/dover/kitzmiller\\_v\\_dover\\_decision.html](http://www.talkorigins.org/faqs/dover/kitzmiller_v_dover_decision.html) (last accessed September 28, 2010). Additionally, transcripts of the *Kitzmiller* case are available online at several locations including [www.talkorigins.org/faqs/dover/kitzmiller\\_v\\_dover.html](http://www.talkorigins.org/faqs/dover/kitzmiller_v_dover.html) and [http://ncse.com/webfm\\_send/73](http://ncse.com/webfm_send/73) (last accessed September 28, 2010).
7. Meyer, *Signature*, 443.
8. *Ibid.*, 449. I agree with Meyer here, as far as it goes, but I disagree that finding a “natural” explanation is equivalent to finding a “purposeless” explanation. I view both nature and the supernatural as part of the providence of God and as appropriate means of divine action in the cosmos, since God is the Author of nature.
9. *Ibid.*, 495.
10. See <http://biologicinstitute.org/people/> (last accessed September 28, 2010).
11. I was pleased to see that this point was also picked up by Steven Matheson. See <http://sfmatheson.blogspot.com/2010/05/bread-and-circus-signature-in-cell-at-28.html> (last accessed September 28, 2010).
12. See <http://aghunt.wordpress.com/2008/12/26/axe-2004-and-the-evolution-of-enzyme-function/>
13. N. V. Grishin, “Fold Change in Evolution of Protein Structures,” *Journal of Structural Biology* 134 (2001): 167–85; and T. Newlove, J. H. Konieczka, and M. H. J. Cordes, “Secondary Structure Switching in Cro Protein Evolution,” *Structure* 12 (2004): 569–81.
14. For example, see Figure 1A in D. R. Venema, “Genesis and the Genome: Genomics Evidence for Human-Ape Common Ancestry and Ancestral Hominid Population Sizes,” *Perspectives on Science and Christian Faith* 62, no. 3 (2010): 166–78.
15. Meyer, *Signature*, 283.
16. *Ibid.*, 282.
17. C. Story, “The God of Christianity and the G.O.D. of Immunology,” *Perspectives on Science and Christian Faith* 61, no. 4 (2009): 221–32.
18. See [www.asa3online.org/Book/category/books/sitc/](http://www.asa3online.org/Book/category/books/sitc/) (last accessed September 28, 2010).
19. See <http://myxo.css.msu.edu/> (last accessed September 28, 2010) for an extensive listing of research publications presenting data from the Lenski group.
20. S. Ohno, “Birth of a Unique Enzyme from an Alternative Reading Frame of the Preexisted, Internally Repetitious Coding Sequence,” *Proceedings of the National Academy of Sciences USA* 81 (1984): 2421–5.
21. A discussion of this example written at a level accessible to nonspecialists is found in S. B. Carrol, “In Cold Blood: The Tale of the Icefish,” in *Into the Jungle: Great Adventures in the Search for Evolution* (San Francisco, CA: Pearson [Benjamin Cummings], 2009).
22. For example, T-urf13. See <http://pandasthumb.org/archives/2007/05/on-the-evolutio-1.html> (last accessed September 28, 2010).
23. For example, L. E. Orgel, “Self-Organizing Biochemical Cycles,” *Proceedings of the National Academy of Sciences USA* 97 (2000): 12503–7.
24. For a recent review on ribosome structure and function, see V. Ramakrishnan, “What We Have Learned from Ribosome Structures,” *Biochemical Society Transactions* 36 (2008): 567–74.
25. Meyer, *Signature*, 246–7, 248.
26. Frankly, I suspect the latter. My overall impression of Meyer’s grasp of molecular/cell biology after reading *Signature* is that he has an approximately introductory college-level understanding of the field. See further discussion of this point below.
27. For this point and direction to relevant literature I am indebted to Arthur Hunt, whose excellent blog, *The RNA Underworld* at <http://aghunt.wordpress.com/> (last accessed September 28, 2010) is on my regular reading list. See <http://>

ag hunt.wordpress.com/2010/01/03/signature-inthe-cell/ (last accessed September 28, 2010) for a thorough discussion of this problem with Meyer’s argument.

28. M. Yarus, J. J. Widmann, and R. Knight, “RNA-Amino Acid Binding: A Stereochemical Era for the Genetic Code,” *Journal of Molecular Evolution* 69 (2009): 406–29.
29. Ibid.
30. The “direct template model” of Gamow; see Meyer, *Signature*, 114.
31. I review multiple lines of evidence for human-chimpanzee common ancestry in D. R. Venema, “Genesis and the Genome: Genomics Evidence for Human-Ape Common Ancestry and Ancestral Hominid Population Sizes,” *Perspectives on Science and Christian Faith* 62, no. 3 (2010): 166–78.
32. M. Behe, *The Edge of Evolution: The Search for the Limits of Darwinism* (New York: Free Press, 2007).
33. Though Meyer later claims, as one of his ID “predictions,” that the fossil record should show “discrete infusions of information into the biosphere at episodic intervals” seems to tip his hand as to the model he prefers.
34. See <http://sfmatheson.blogspot.com/2010/04/behe-andprobability-one-more-try.html> (last accessed September 28, 2010).
35. Meyer, *Signature*, 66.
36. Ibid., 128, Figure 5.7.
37. See [www.asa3online.org/Book/2010/04/13/id-predictionssummary/](http://www.asa3online.org/Book/2010/04/13/id-predictionssummary/) (last accessed September 28, 2010).