

Protein Tramples Evolution

Its existence, structure, and function disproves evolutionary theory

PART ONE OF FIVE

NEW ON pathlights.com and evolution-facts.org!

PROTEIN TRAMPLES EVOLUTION

To our many friends on the internet:

There is a broad mass of material on these websites (apparently, more anti-evolution scientific data than is to be found anywhere else on the internet).

In view of the fact that our exposé of the errors of evolutionary theory cover nearly the entire range of scientific endeavor, it seemed best to adequately deal with each field, yet without extensive detail.

However, I recently decided to select a single scientific topic for still more intense analysis. Browsing in my science library, I selected this topic for you. Many other things could have, as easily, been selected; but, because each one is so very tiny, protein makes a good topic for closer scrutiny.

We receive large quantities of genuinely grateful e-mails. This is for you. I know you will like it. You are welcome to copy it, and anything else on this website, to share it with friends or as help in preparing research reports.

I thoroughly enjoyed preparing this research study, as I did when I earlier wrote the entire three-volume, 1,326-page set of books prepared earlier in the 1990s. Any investigation into the true principles of science will always arrive at the same conclusion, and it is a very encouraging one.

This is a copy of a new item we are placing on our websites, **pathlights.com** and **evolution-facts.org**, which are daily being used by large numbers of high school, college, and university students, as well as by others, to disprove evolutionary theory.

As of late August, 2001, we can once again obtain statistics on pathlights.com. It is now receiving nearly 700,000 hits a month. This is over half a million contacts a month, or nearly 22,580 hits every day. The teaching of evolutionary theory is a special method used today, by Satan, to drive people into atheism. We are thankful that we can be used of God to help defend His Creatorship! —*vf*

We are thankful that our entire three-volume set is now on our website, **evolution-facts.org**. Prior to this time, only an extended summary was available on our website, **pathlights.com**.

Click here to go to [Protein Tramples Evolution](#).

PROTEIN TRAMPLES EVOLUTION

ITS EXISTENCE, STRUCTURE, AND FUNCTION DISPROVES EVOLUTIONARY THEORY

Can evolution account for the existence of protein, and what it is doing right now in your body? This is a subject which every student of science should consider.

Proteins are all about the same size, with some longer than others. All are microscopic; so tiny you cannot see one with your naked eye.

Yet each little protein molecule does the most fabulous things. It carries out complicated tasks which require great intelligence. The problem is there is not a nerve cell anywhere in its body. No brains. How can it do what it does?

Each protein has a very complex structure; yet, because there are literally thousands of different protein structures, it would appear to be impossible, by random chance, to produce even one.

How could evolution fit in here?

Do you like challenges? Well, I have one for you. We are going to look at the structure and function of these little things, and see if they could be produced by the randomness of evolutionary activity.

From the latest facts unveiled by microbiology, this is the story of some of your best helpers. Along with their buddies, they keep you alive. Although brief, this is a remarkable story.

This is written for high school and college students, yet many other mature individuals will appreciate it. This will provide you with information you can use in defending your position! You are welcome to copy and use anything on this path-

lights.com website.

Historical background. In the 18th century, chemists came across certain organic substances which were rather strange. They found that heating these materials changed them from the liquid to the solid state instead of the other way around. One example was the white of the egg, another was something they found in milk (casein). Yet another was a component of the blood (globulin).

In the year 1777, Pierre Joseph Macquer, a French chemist, decided to give all these strange substances, which coagulated upon being heated, a common name: *albuminous* (after the word, *albumen*, the name that Pliny had given to egg white.)

In 1839, the Dutch chemist Gerardus Johannes Mulder found that they all contained *carbon, hydrogen, oxygen, and nitrogen*. Proud of the discovery, he named his four-element formula, *protein*, from a Greek word meaning “of first importance.” That is how much he thought of his formula! But it stuck as the name for the strange substances. Over a century later, it would be discovered that it was the substances themselves—proteins (not Mulder’s inaccurate formula)—which were extremely important. They were a key ingredient in all life on earth.

But providing a name for this strange collection of substances did not explain their remarkable structures and some of the amazing things they could do. That would gradually come with time.

Let us now consider several of the many astounding facts about these tiny things:

Proteins are extremely complicated. And so are the amino acids they are constructed from.

By their own definition, evolutionists declare that evolutionary processes are always random, always purposeless, totally lacking in any planned intelligent design, yet the cause of everything in earth and sky.

However, these shuffling, bungling methods of random chance could never produce the intricate formula for even one amino acid, much less a protein that many amino acids are constructed from.

Later in this article, we will provide you with conclusive mathematical evidence that evolutionary theory could never account for a single amino acid or protein.

But, back to our story: By the beginning of the 20th century, biochemists were certain that proteins were giant molecules constructed from amino acids, just as cellulose is built up from glucose and rubber from isoprene units. Yet there is an important difference: Cellulose and rubber are made with just one kind of building block while a protein is

carefully constructed from a variety of different amino acids.

What are proteins? They consist of many smaller units, called *amino acids*, linked together in long chains. Amino acids are organic acids which contain *nitrogen*. They also contain *carbon, hydrogen, and oxygen*. Some also have *sulfur* or *phosphorus*.

Eventually *glycine, leucine, tyrosine, cystine*, and other amino acids were isolated by chemists. By 1935, 19 had been identified. (One comes in two forms, producing a total of 20 essential amino acids.) Gradually, scientists were discovering that they were beginning to delve into one of the most astounding mysteries known to mankind.

Each completed chain of amino acids is called a *peptide*. This is actually a synonym for a complete *protein*. The amino acids are linked together, to form a complete *peptide chain*, which is a protein.

Oh, you say, it should not be too difficult for evolution to produce something like that! But, as an example, consider *hemoglobin*. This is a protein in the blood stream. Hemoglobin contains iron, which is only 0.34 percent of the weight of the molecule. What else is in there? —574 amino acids! All in just one protein! Here is how we know:

Chemical evidence indicates that the hemoglobin molecule has four atoms of iron, so the total molecular weight must be about 67,000. Four atoms of iron, with a total weight of 4×55.85 , comes to 0.34 percent of such a molecular weight. Therefore, hemoglobin must contain about 574 amino acids. This is because the average weight of an amino acid is about 120.

It was through the development of new methods of analyzing amino acids and proteins that scientists gradually learned still more about them. These new methods included the centrifuge, diffusion, paper chromatography, and spectrophotometry.

Using these analytic techniques, here is a sample of what they discovered. This is what is in the blood protein called *serum albumin*:

It contains 15 *glycines*, 45 *valines*, 58 *leucines*, 9 *isoleucines*, 31 *prolines*, 33 *phenylalanines*, 18 *tyrosines*, 1 *tryptophan*, 22 *serines*, 27 *threonines*, 16 *cystines*, 4 *cysteines*, 6 *methionines*, 25 *arginines*, 16 *histidines*, 58 *lysines*, 46 *aspartic acids*, and 80 *glutamic acids*. That is a total of 526 amino acids of 18 different types of amino acids, all built into a single protein with a molecular weight of about 69,000. The only other common amino acid not in serum albumin is *alanine*.

Seriously, now, how could mindless random ac-

tions produce that protein? Yet that is only one of thousands of very different proteins in each living creature.

Are you beginning to see the picture? We must politely but firmly tell our evolutionary friends that, if their theory cannot produce protein, it is a fraud.

The German-American biochemist Erwin Brand suggested a system of symbols for the amino acids. He designated each amino acid generally by the first three letters of its name. Using that shorthand, here is the written formula for *serum albumin*: Gly₁₅ Val₄₅ Leu₅₈ Ileu₉ Pro₃₁ Phe₃₃ Tyr₁₈ Try₁ Ser₂₂ Thr₂₇ CyS₃₂ CySH₄ Met₆ Arg₂₅ His₁₆ Lys₅₈ Asp₄₆ Glu₈₀.

That is what is in one (just one) protein of serum albumin! There are trillions upon trillions of proteins in each animal, and thousands of different kinds. Keep in mind that serum albumin is only an average-size protein; many are much larger.

Do not think that, having laboriously determined the contents of a single protein, the scientists know much about it. Not so. *Learning the formula was only a beginning. Next, they had to figure out the structure and arrangement of a protein molecule!* "Structure" means the chemical arrangement of each amino acid; "arrangement" is the way they are hooked together, in sequence, to form a protein.

Oh, you might say, that should not be too much of a problem. If evolution's random actions can make them in the first place, then biochemists ought to easily figure them out. *That is true!* However, it was only with great difficulty that scientists were able to determine the structural sequence of even one protein. They were discovering that the randomness of their favorite theory could never have produced protein.

The only way biochemists can make a useable protein is by carefully copying the patterns found in living creatures.

Just as scientists cannot do it, so evolutionary development could never invent a workable protein with a new, different formula. Yet the theory says that proteins, like everything else, are supposed to have originated by mindless chance.

The first problem was to ascertain how the amino acids were joined together in the protein-chain molecule. In 1901, the German chemist Emil Fischer managed to link some amino acids in a chain. Mind you, all he did was take existing amino acids and hook them together. He did this by connecting the *carboxyl group* of one amino acid to the *amine group* of the next. Sounds simple enough, but it took years for science just to reach that point.

After struggling for six years in a well-equipped

laboratory, by 1907 Fischer finally managed to hook together ("*synthesize*") a chain made up of 18 of the same amino acids. He did not have a complete protein, nor one in the proper sequence of different amino acids. One of the best brains in Germany took six years to do a little part of that which occurs in a split second in the cell.

Fischer well-knew he did not have a protein molecule, yet he simplistically imagined that this was only because his chain was not long enough. Because he correctly suspected that proteins broke down in the stomach to amino acids, Fischer called his synthetic chains *peptides*, from a Greek word meaning "*digest*."

Researchers would try to link together amino acids. The resulting chains were given the name, "peptides," but they were not real proteins. Any group of amino acids, linked together naturally or artificially, is called a *peptide chain*. But, of course, only the ones produced in nature are genuine, useable proteins.

After years of labor, by 1916 the Swiss chemist Emil Abderhalden had laboriously made a synthetic peptide with 19 amino acids. No one was able to do better until 1946. It was just too difficult—even in million-dollar laboratories—to make the real thing: a genuine protein!

Yet, by this time, chemists were discovering that those little peptide chains were merely tiny fragments, compared with the size of an actual protein molecule. They knew this was true because the molecular weights of proteins were immense.

Compare Abderhalden's 19 amino acids with the 574 amino acids, we mentioned earlier, in a hemoglobin molecule. And hemoglobin is only an average-sized protein.

There could only be one correct arrangement of each protein,—yet there are millions of wrong ways it could be arranged!

The best brains of highly trained men, working in elaborate laboratories, cannot effectively do it. They cannot even produce one new protein by merely changing a single amino acid in it.

The utter randomness of evolution could never come up with the one right combination for each protein.

But consider this: Even if, just one time, evolution could produce one correct protein,—it could never repeat that success again, which it would have to do in order to replicate that correct protein in making millions more of it.

After that, evolution would have to set to work to invent the thousands of other protein formulas used in plants and animals.

But now, let us return to those 19 amino acids of *serum albumin*: The number of possible arrangements, in which 19 amino acids can be placed in a chain (even assuming that only one of each is used—and this is never, never true!), comes to nearly 120 million billion. If you find this hard to believe, try multiplying 19 times 18 times 17 times 16, and so on, down to 1. These are all the possible arrangements.

Yet, in just one average-sized protein, such as serum albumin, we have more than 500 amino acids. The number of possible arrangements of those 500 amino acids comes to 10^{600} . That is a totally impossible amount! It is a quantity so vast that you might as well forget about the possibility of so-called “random selection” producing it even once. The entire universe, packed with subatomic particles, could not hold 10^{600} .

In 1945, the British biochemist Frederick Sanger set to work trying to figure out the sequence of one of the smallest proteins: *insulin*. By slow, painstaking chemical treatments, he and his associates were able to split the insulin protein into individual amino acids. Then they broke separate amino acids at their weaker bonds. Ultimately, they had a lot of pieces. Chemical treatment plus paper chromatography helped them. After years of hard work, by 1952 they had put all the fragments together and arranged them in their proper sequence. They announced their achievement in 1953. For the first time, the complete structure of a protein had been identified. Six years later, in 1959, a second protein, *ribonuclease*, was identified. Since then, improved technology has enabled biochemists to determine additional ones.

Such analyses have shown that, in varying amounts, most proteins contain all 20 amino acids. It is only a few of the simpler fibrous proteins (such as those found in silk and tendons) which are heavily weighted with only two or three types of amino acids.

One important discovery was this: The individual amino acids are lined up in no obvious order. There are no periodic repetitions! Everything is an apparent jumble of amino acids in each sequence;—yet these proteins work, and no other man-made combinations do!

Random chance is not able to produce one useable protein; neither can trained laboratory technicians when they try to invent new proteins. Evolution flunks the test.

Where did these useable proteins come from, if evolution did not produce them? They surely did not make themselves. And man cannot make them either. Yes, a scientist can try to take apart a true amino acid and try to put it back together again in the same order, but he cannot make a new combination which works.

The best that man can do is to imitate what is already there. In 1953, the American biochemist Vincent du Vigneaud succeeded in *synthesizing* a peptide chain exactly like that thought to represent the natural hormone, *oxytocin*. Oxytocin is extremely small and has only eight amino acids.

(The word, “*synthesis*,” is used to describe both the natural hooking together of amino acids into proteins, by constructor proteins, and also man-made productions which are done by carefully copying the chemical sequence found in nature.)

In 1965, *insulin* was synthesized, and later several other proteins.

Each protein is carefully assembled by another protein, from materials lying around. And it never makes a mistake.

This tiny, mindless thing, a single protein, moves around, picking up amino acids here and there and sticking them together. Higher and higher goes the assembly, until that little protein has made another complete protein! But how can this be, since there are no brains in non-neuron cells? There surely are none in that little protein which always carries out this construction project alone. Yet the little fellow does it in a few seconds!

We are confronted here with something beyond our ken. This is not something which the randomness of evolution could ever provide us with. A far higher Intelligence is involved.

When protein is eaten, it is broken down in the stomach into amino acids. These are absorbed by the lacteals in the small intestine and pass into the blood stream. They are then carried to the liver, for processing, and to cells throughout the body. Passing into the cells, they are assembled (“synthesized,” the biochemists call it) into proteins—within the cells!

What assembles them? Other microscopic proteins which were themselves assembled only a short time before. Who taught a protein how to assemble another protein? Think about that awhile. And you say you are still an atheist?

If the constructor protein finds he does not have

Protein Tramples Evolution

**PART TWO
OF FIVE**

Continued from the preceding tract in this series

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the right amount and combination of amino acids lying around, he tells another protein to bring him some more! The messenger goes to the edge of the cell and tells the gatekeeper (another protein) to bring them in, which he does. More about the gatekeeper later.

Keep in mind that each protein consists of hundreds of amino acids, all arranged in a totally complicated order; and each, different protein has a completely different structural sequence than all the others!

Without several days of intense concentration, neither you nor I would be able to memorize the sequence of even one average-sized protein.

Where is the brain in the cell to be able to do this? We are here viewing something that cannot be done; yet it is being done, millions of times a minute, in every cell in your body. If it were to stop for even a minute, you would die.

Then, incredibly, as soon as each protein is assembled in its correct linear sequence, it automatically folds itself into a very definite, but exquisitely complex, shape!

Nearly all types of proteins bend and curve back and forth over, under, and around themselves;—and each protein has a certain pattern it follows. Scientists call these the “fold patterns.” As we will learn below, if the folds do not occur in the proper way, the protein cannot perform its functions properly.

How could evolutionary theory produce those proper fold patterns? It takes brains to do all this; and so-called evolutionary methods are brainless, aimless, and useless as a means of doing anything worthwhile.

Using X-ray diffusion, by 1959 the Austrian-English chemist Max Perutz and his English associate John Kendrew managed to figure out the folded placement of *hemoglobin* and *myoglobin*.

The chemical bonds which link successive carbon atoms in the backbone of the protein are known as *covalent bonds*. (Covalent bonds are formed when two adjoining atoms share their electrons with one another, to complete electron shells.) Nearly all the atoms in the organic compounds, used in living organisms (sugars, fats, amino acids, the nucleotide bases in DNA, etc.), are linked together by covalent bonds.

But there is also another type of chemical bonding of atoms which does not share electrons. This is based on weaker electrostatic forces between neighboring atoms. These are known as *noncovalent bonds*. They are also called *weak chemical bonds*.

The chains of amino acids in a protein are able to bend at the points where these weak bonds are located. They are called *crease points*.

The protein molecules automatically bend by themselves, and always in the proper fold direction. While the protein is being *synthesized* (put together) by another protein, it is positioned in a *linear* (line-length) fashion. But as soon as it is completed, the entire protein folds itself into a special pattern!

This folding takes a fraction of a second; and, when it is completed, the protein molecule has taken the shape of an extremely complicated three-dimensional collection of atoms.

How could evolutionary theory accomplish results like this? And do it repeatedly, trillions of times?

The unfolded protein chain is capable of folding into its native form, without the assistance of any other component of the cell. It folds at those crease points. But how can it know which way to fold at those points? And who planned where those points would be located, so the folding could produce the important results it does? The protein did not figure that out. And why does the new protein wait until it is completely assembled, by another protein, before it folds up? It should be expected to start folding as soon as it was partially made; this, of course, would confuse and stop the rest of the construction.

This would be like origami papers waiting awhile and then automatically folding themselves, and always in the proper fold directions.

The ability of proteins to assemble themselves automatically is a key capability which is essential to their biological role. Without this ability, the proteins could not manipulate or construct. No sort of self-replicating machine could function unless its component machinery was self-assembling.

Can you imagine a machine which can assemble itself? Man is not able to make a robot which is able to assemble itself. As far as we know, proteins are the only self-assembling devices. Yet, having assembled themselves, they are able to carry

out a wide variety of functions. More on this below.

Each type of protein always folds itself into the best pattern for accomplishing the work it is supposed to do! Every new fact about protein seems more fantastic than the preceding one, yet there is more to come.

As soon as the split-second folding is finished, negatively charged groups associate with positively charged groups, to keep everything in place; and the resulting structure is exactly that which is needed for the task it is supposed to do.

Every amino acid in the chain has something sticking out one side. These are important, and are called *side chains* or *fingers*. Some of these side chains are *hydrophobic* and some are *hydrophilic*. The hydrophobic ones do not have an affinity for attachment to water molecules while the hydrophilic ones do.

Now, it is very important that certain cell processes be completed in a water medium while others can only be done where water cannot penetrate. When the protein folds down, it always does it so in exactly the right way, so the water-resisting amino acids are at the center of the folded protein structure and the water-attaching ones are on the outside. In this way, the *hydrocarbon* (water-loving) side chains, on the outside, can carry out chemical, and other, reactions with the watery environment in the cell while the amino acids, in the center, can perform functions in a location where there must be little or no oxygen or hydrogen.

Sounds complicated? It surely is; yet, without it life could not continue. There are hydrophobic amino acids and *lipids* (fats) which must be synthesized, and that can only happen where the water is shut out.

The end result is a protein which has folded itself into a tight water-avoiding ball, yet one in which the outside is in water and able to interact efficiently with it, so it can take in needed substances.

Water itself is another marvel which we do not have the space to discuss here. It was designed to be unable to dissolve lipids (fats and oils) and compounds containing hydrocarbon chains. In addition, it is not a good medium in which to synthesize organic substances. So those functions must be done in the center of the protein molecule, where water has been excluded.

(You might wonder why water has this apparent flaw. It was intentionally designed in this manner and is not a flaw. The organs in your body could not accomplish their work if the lipids in them could be dissolved by water. Modern planographic

printing presses use this same formula: They can only print on paper because water and oil do not mix.)

Think about this for a minute. The “water-proofed” amino acids are carefully placed in just the right portions of that long protein chain. The strong and weak bonds are placed at just the right points so that, when the protein automatically folds itself, the outer portions will wrap themselves in exactly the proper manner so that, on all sides, the water-excluding portions will be completely enclosed.

In view of the complicated manner in which the proteins fold in upon themselves, it would take months for a scientist to figure out how to fold one so that the watertight portions would be in the middle and the right arrangement of strong and weak bonds would be on the outside. Yet the little proteins are quickly made in a brainless cell which just as quickly, and correctly, folds in upon themselves.

This reads like fantastic science fiction. But it is true, and without it you would not be alive. There is more:

It is vital that some of the little fingers which protrude from the folded protein have both strong and weak bonds. The strong bonds are needed exactly at those points where the protein needs to solidly bind with other like proteins. The weak bonds must be located at just those places where the protein must temporarily hook up with various substances.

For example, a muscle protein must be able to solidly bond with neighboring ones, yet be able to absorb needed nutrients. The little fingers have to be located in just the right places.

How could this be planned out in advance?

It is the proteins which carry out all the atomic manipulations on which life depends. Yet in order to do it, each protein must be able to permanently or temporarily make contact with other molecules. Whether they be proteins, amino acids, or miscellaneous chemical supplies, the substances with which the protein makes contact are called *ligands*.

Nearly all these associations between a protein and its ligand are done by means of the weak chemical bonds. Since each weak bond is rather frail, the contact must be made using several weak-bond points on the protein.

If those bonds were either weaker or stronger, the proteins could not carry out their work. If the contact was a little weaker, contact could not be properly made; if a little stronger, the two would lock together so solidly, they could never separate.

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In the structure of every part of the physical organism, you will find that every detail has been perfectly worked out! We observe highly intelligent planning, not aimless chance.

Just as the strong and weak atomic forces must be exactly as they are, in order for all atomic structures to function properly, so the difference in strength between the strong and weak bonds on the protein must be just right.

It turns out that the strong bonds are about 20 times stronger than the weak bonds; this is just the amount needed, so portions of the protein can bind while other portions can make fast contacts with other substances.

How fast?

The interactions of a single protein with other substances can occur several times a second. The case of enzymatic action produces results as often as 10^6 times per second! That is a million actions a second!

But since nearly every function in the body depends on the activity of these proteins, one can understand why they have a lot of work to do and need to be able to do it quickly. Tissue is constantly being worn out and must be replaced. Food must be processed. Waste must be eliminated. Manifold processes are repeated constantly, just to keep you alive and well.

Who thinks evolution should get the credit for this?

The protein molecules have, what scientists call, *metastability*. This is the ability to rapidly change shape, in order to adapt to changing circumstances around them.

It is the weak bonds which hold the protein in its characteristic shape. Under the stress of very minor physical or chemical challenges, these bonds give way. This makes each protein fragile. Yet it is a necessary quality.

If the temperature is increased only a few degrees, the proteins unfold. If the chemical environment is changed a little, they unravel. If another molecule is attached to them, they change shape. In the midst of stability, there is a necessary instability. If this were not so, the protein structures would not be aroused to go into action in time of injury or crisis in the cell.

Yet there are other reasons why metastability is so important.

Because the protein can quickly respond to what is happening around it, vital functions can occur which otherwise would be impossible.

The arrangement of a protein is subtly affected as soon as it binds to another molecule. Any such interaction will cause molecular distortions which will be transmitted throughout the entire molecule and affect, not only its shape, but its functioning.

Each time a protein temporarily connects with a ligand, the protein reacts to chemical data from the ligand. This causes the protein to do something which often affects the ligand.

When the protein is making contact with several different ligands at the same time, it is receiving, integrating, and outputting data or chemicals simultaneously, yet separately, to this one or that one!

And some people suppose all this is supposed to have come from evolution?

The protein is able to integrate information from several different chemical inputs, each being determined by the concentration in the cell of a particular chemical.

This astounding function of the protein molecule is called *allostery*. It enables the protein to do three things at once: (1) produce chemical reactions upon another substance, (2) receive and integrate within itself special information, and (3) increase or lessen its own chemical reactivity in relation to that information. Jacques Monod called this remarkable ability, "the second secret of life" (*J. Monod, Chance and Necessity*).

Because of this, proteins are not only capable of carrying out a specific chemical reaction, but are also able to integrate and intelligently respond to changes in their chemical environment.

The protein molecule is a self-adjusting miniature machine!

Allostery is the ability to self-regulate, and this is what the proteins can do. They must be ever aware of constant changes, in the cell, and able to react to them.

Because of this ability, proteins are far in advance of any artificial device which man could make—and certainly far in advance of anything that the mindlessness of evolution could produce. In even the most advanced man-made machines, the regulating functions of a machine are always separate from the working parts. In an oven, the regulator (thermostat) and heater (functional unit) are separate; in a protein, they are united. This allosteric function is vital to enzymatic action.

The amazing protein molecule is able to carry out the most complicated enzymatic activity automatically, yet all the while being able to adjust that activity to meet the needs of the situation.

Catalysis was a function which scientists began discovering toward the end of the 18th century. When they started studying chemical reactions, they discovered that the *reaction rate* (time it took for a chemical to respond to an effect) could be greatly speeded up if there were small changes in the environment. For example, the Russian chemist Kirchoff found that starch could be converted to sugar in the presence of acid; yet, while the acid speeded up the process, it was not itself consumed. The same amount of acid was still there. The acid was a *catalyst*. The substance which it acted upon was the *substrate*.

Then it was discovered that there were catalysts in the organic world. Bread dough, left to itself and kept from contamination, will not rise. But add a little yeast (*leaven* comes from the Latin word, "rise") and bubbles appear, lifting and lightening the dough.

In 1777, the Scottish physician Edward Stevens took fluid from the stomach and found it would dissolve protein. In 1834, the German naturalist Theodore Schwann isolated a substance he called *pepsin* (Greek for "digest") from the stomach acid.

In 1930, John Northrop, working at the Rockefeller Institute, established that all the enzymatic functions in living tissue were carried out by proteins.

It is now known that there are over 2,000 different protein enzymes, and they are all unmatched by any other substance for efficiency and specificity. Each protein, which works as an enzyme, works with just one type of substance.

Catalase is the protein enzyme which catalyzes the breakdown of *hydrogen peroxide* to water and oxygen. Yet this can also be done by *iron filings* or *manganese dioxide*. But, weight for weight, catalase accelerates the rate of breakdown faster than an inorganic catalyst can. Fast? Yes, fast! Each molecule of catalase can bring about the breakdown of 44,000 molecules of hydrogen peroxide per second while operating at a temperature of 0° C.

How is that for business efficiency? Something the random actions of evolutionary theory could never accomplish. Tell me where I can hire a worker who can do forty-four thousand things a second, and I will hire him.

(The protein enzymes can do this because an extremely small dilution of them is needed to effect such changes. How that can be is not known, since the enzymes do not give off, or lose, any substances in the process.)

Do not underestimate the need for continual enzymatic activity in your body! *Cyanide*, one of the most

deadly of all poisons, kills people by stopping their enzymatic proteins from working. Without multiplied trillions of them every moment, you would die within 10 seconds. Nearly every other major poison also kills by stopping the enzymatic action of proteins. (An exception is *carbon monoxide* which locks with hemoglobin, keeping it from carrying oxygen to the cells.)

As noted earlier, it is a remarkable fact that each type of protein enzyme only acts on one type of substance. That makes them ideal catalysts. Catalase only breaks down hydrogen peroxide and nothing else; yet inorganic catalysts, such as iron filings and manganese dioxide, will break down hydrogen peroxide and also a variety of other substances. If catalase did that, it would be harmful in the body.

In living tissue, everything is perfectly designed. In contrast, the utter randomness of evolutionary processes accomplishes nothing worthwhile. Randomness never does.

There is far more that we could say about protein enzymes and their substrates, but let us now turn our attention to other wonders of protein.

Keep in mind that it is because of the allosteric quality of proteins that they can accomplish so much as enzymes. The actual activity of individual enzymes are self-regulated, so the protein can increase or decrease its catalytic activity as it is needed.

Another amazing function of proteins is that those tiny things regulate the metabolism of the entire body.

A living body is a chemical plant and must be able to take in oxygen, water, carbohydrates, fats, proteins, minerals, and other raw materials. It must be able to process them and also destroy bacteria and eliminate wastes, such as carbon dioxide and urea. Each of these functions requires extremely complicated actions, yet they are vital to existence. All this is done by those fabulous little protein molecules.

Thousands of protein-induced actions and reactions must take place for each accomplishment, regardless of how small. Every major conversion in the body involves a multitude of steps and many enzymes.

Someone will say that life began with bacteria and evolved over long aeons; so there was lots of time for proteins and enzymes to be invented. Not so. The simplest organisms have lots of protein, and carry out many enzymatic functions. Even an apparently simple organism, such as the tiny bacterium, must make use of many thousands of separate enzymes and reactions. All this complexity is vital to existence. Without it, the creature would quickly die.

Evolution says a little improvement happened here.

Protein Tramples Evolution

**PART THREE
OF FIVE**

Continued from the preceding tract in this series

and another advance there, and gradually a living creature came into existence. That is another fiction. In reality, everything had to be in place all at once in each plant and animal. All its organs, proteins, and structures had to be there in the beginning, in order for it to exist. Nothing could be left out or added later.

A small army of proteins carry out complicated organic cycles. It has taken years of laborious labor, by a small army of researchers, to figure out the various *metabolic cycles*. In each one, proteins change one substance to others, and then to yet others, and then still others. Every step is complex, yet the finished result is always perfect.

How can this be done, when different proteins which never meet each other take part in the different steps? And, as you know, none of the proteins live very long; and none of them teach the new proteins they construct how to do the work they are going to do! There are no classroom teachers in the cell, for all the students have no brains; yet they all know exactly what to do!

Are you going to keep believing those who tell you that evolution is responsible for this!

The *Krebs cycle* is used to reduce lactic acid to carbon dioxide and water. There is the *urea cycle*, the *fatty-acid oxidation cycle*, and many others. All are vital to existence and each is so complicated, that it took years for researchers to figure them out.

How efficient are these cycles? They produce outstanding performance! For example, in 1941, the German-American chemist Fritz Lipmann discovered that carbohydrate breakdown yields certain phosphate compounds which are stored. We now know that this cycle stores unusual amounts of energy in, what came to be known as, the *high-energy phosphate bond*. This is transferred to energy carriers present in all cells. The best known of these carriers is *adenosine triphosphate* (ATP). They store the energy in small, readily used packets. When needed, the phosphate bond is hydrolyzed off and the energy is available for quick chemical energy required in the building of proteins from amino acids, the electrical energy needed for nerve impulse transmission or muscle contraction, etc.

Everywhere you turn in biology, you find new wonders which the doddering effects of evolutionary theory could never produce.

Men in their high-tech laboratories cannot as efficiently duplicate these protein functions. Seriously now, if a trained scientist, working in a million-dollar fully equipped facility, cannot improve on what the little proteins easily and rapidly do, then how could random

motions of molecules produce those proteins in the first place? It could not be done.

Multiplied trillions of individual proteins are not only in each animal, but also in each plant. There is no way that evolutionary theory could have put them there.

Yes, plants as well as animals! Every living creature has proteins in it; there are no exceptions.

The proteins in plants build carbohydrates, fats, and proteins from simple molecules, such as carbon dioxide and water. This synthesis calls for an input of energy, and the plants get it from the most copious possible source: sunlight.

Certain proteins in green plants convert the energy of sunlight into the chemical energy of complex compounds—and that chemical energy supports all life forms (except for certain bacteria).

This process is called *photosynthesis* (Greek for “put together by light”).

These plant proteins take *carbon dioxide* from the air, mix it with *sunlight* from the sky and *water* taken up from the root;—and, presto! *carbohydrates*, the basic food of life, are produced. (The plant itself also needs *nitrates*, *phosphates*, and certain other substances from the soil for normal growth.)

In 1817, two French biochemists (Pierre Pelletier and Joseph Caventou) isolated the substance that gives the green color to plants. They named it *chlorophyll* (Greek for “green leaf”). In 1865, the German botanist Julius von Sachs showed that chlorophyll is not found all through plant cells (even though leaves appear uniformly green), but only in extremely small bodies called *chloroplasts*. Here are more protein friends; in them photosynthesis takes place. It is only here that the plant uses chlorophyll.

Inside the amazing chloroplast, you will find, what some scientists describe as, little stacks of coins. These are the *lamellae*. In most types of chloroplasts, these lamellae thicken and darken in places to produce *grana*—which contain the chlorophyll. This is only mentioned to reveal a hint of the utter complexity of these protein structures!

How could the purposeless meanderings of evolution produce something like this? Yet the chlorophyll and the chloroplasts had to be there on the first day each plant came into existence—or it would have immediately died. This is because the process of photosynthesis provides food not only for animals, but for plants as well.

It was not until 1954 that the Polish-American biochemist Daniel Arnon, working with spinach leaves,

managed to isolate chloroplasts intact. He discovered that inside each tiny one is not only chlorophyll, but a large collection of specialized protein enzymes, related protein, and other substances. All of them are carefully and intricately arranged. If you think that everything is arranged well under the hood of a modern automobile, you ought to take a look inside a sub-microscopic chloroplast.

How did all that perfect order and well-functioning organization come into existence? Not through the slow, dawdling inattention of evolution!

Research by scientists, stretching from 1906 to 1960, was conducted in order to figure out what was in chlorophyll. This strange protein substance was found to have a *porphyrin ring* structure basically like that of *heme* (the oxygen-carrying substance in blood *hemoglobin*). The difference was that chlorophyll had a *magnesium* atom at the center of the ring instead of an *iron* atom.

Meanwhile, other researchers were trying to learn how chlorophyll carried on its catalytic work. By the 1930s, all that was known was that carbon dioxide and water go in and oxygen comes out. Only intact chloroplasts performed the functions, so researchers were stumped as to what was happening inside.

If the best brains in the scientific world can hardly figure out the matter, how could the fooleries of evolution produce it?

The use of radioactive tracers (especially carbon 14) and the development of gas and paper chromatography greatly helped. Using these new tools, one of the scientists' first discoveries was the lightning speed with which the tiny protein substances within the chloroplast carried on their work! An incredible amount of complicated work is done within seconds.

Well, by now you probably want to know the answer to the riddle. *Here is how proteins in the chloroplast produce carbohydrates*,—and you cannot thank evolutionary processes for giving the process to us:

Carbon dioxide is added to the normal five-carbon *ribulose diphosphate*, making a six-carbon compound. This quickly splits in two, creating three-carbon *glyceryl phosphate*. A series of reactions involving *sedoheptulose phosphate* and other compounds then puts two *glyceryl phosphates* together, to form the six-carbon *glucose phosphate*. Meanwhile, *ribulose diphosphate* is regenerated and is ready to take on another *carbon-dioxide* molecule. This cycle is repeated six more times. Each one supplies one carbon atom (from the *carbon dioxide*) and produces a molecule of *glucose phosphate*. Then the six cycles are repeated over and over again.

Now you can go home and try to do it yourself. If a brainless protein learned it by random chance, surely you ought to be able to improve on the process. I guarantee that, if you succeed in doing it more efficiently, you will make half a billion dollars for yourself.

The catalytic action of the chlorophyll uses the en-

ergy of sunlight to split a molecule of water into hydrogen and oxygen, a process called *photolysis* (Greek for "loosening by light"). In this way radiant energy of sunlight is converted into chemical energy. The resultant hydrogen and oxygen molecules contain more chemical energy than did the water molecule from which they came.

Sounds complicated? It is. Surely there must be some other way to do it. No one has found that way, or any way, to produce carbohydrates. But there is a way to break up water molecules into hydrogen. However, it takes a lot of energy: The water must be heated to 2,000° C. or a strong electric current must be sent through it. Yet chlorophyll does it at ordinary temperatures and with energy from relatively weak light.

Neither mindless evolution nor intelligent men can do what millions of little proteins regularly do. Yet those tiny proteins have no brains. They cannot talk, they cannot see, they cannot think. Each protein is just a collection of amino acids, without one nerve cell being present anywhere in their tiny structure.

We are here confronted with an Intelligence beyond that of man or nature. A great Designer is at work.

Under ideal conditions, plants have a near 100 percent efficiency in producing energy. Astounding! Pooling all our vast human intelligence and technology, if we could somehow match that with machines which could produce high-efficiency energy from sunlight, we could solve all our fuel problems! Every one of them. The only waste would be lots of extra oxygen! And we could sure use that.

But the greatest brains among us are unable to do what the diminutive protein molecule in the leaf does with ease, and all without the help of evolution.

The action of plant proteins also provides us with our oxygen. The scale on which the earth's green plants manufacture organic matter and release oxygen is enormous. It is estimated that, each year, they combine a total of 150 billion tons of carbon (from carbon dioxide) with 25 billion tons of hydrogen (from water) and liberate 400 billion tons of oxygen. Plants of forest and field produce about 10 percent of this oxygen, and one-celled plants and seaweed in the oceans provide us with the other 90 percent.

Amino acids in animals are only composed of L-amino acids. This is an extremely important point in the ongoing creation-evolution debate.

It is impossible for man to synthesize amino acids, without producing an equal number of left-handed (L) and right-handed (D) amino acids. Yet animals can only use the left-handed form. The chemical composition of both is identical; the difference is which side the important side chain, or finger, protrudes from.

Evolutionists, desperate to prove the validity of Darwin's theory, have repeatedly tried to produce only

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L-amino acids. But they cannot do it.

It has been scientifically proven that an animal will be crippled or die if it has any D-amino acids in it. Yet, even though both types of amino acids are formulated in equal amounts in the laboratory, both chemical and X-ray analysis reveals that only the left-handed form is produced in animals. Is not that a remarkable fact!

If the random processes of evolution really did produce amino acids, then we would have even amounts of both kinds; always.

There is a little mystery here: Why are only L-amino acids found in animals?

The answer is that they are the only kind which are biologically useful: In the left-handed form, the side chains stick out alternately on one side of the central line and then the other. A chain composed of a mixture of both isomers would not be stable. This is due to the fact that, whenever an L-amino acid and a D-amino acid are next to each other, two side chains would be sticking out on the same side, crowding them and straining the bonds.

You will recall that we earlier learned that those side chains are vital in holding neighboring peptide chains together. Wherever a negatively charged side chain on one chain is near a positively charged side chain on its neighbor, an electrostatic link is formed. The side chains also provide hydrogen bonds that can serve as links. The binding together of the polypeptide chains accounts for the strength of protein fibers. It explains the remarkable toughness of spider webs and the fact that *keratin* can form structures as hard as fingernails, tiger claws, alligator scales, and rhinoceros horns. (A *polypeptide* is the scientific word for a group of proteins which have linked themselves together.)

The questions keep piling up in our mind: How can the cell know what kind of protein to assemble from the amino acids? How can its component proteins know what types are needed and how much of each? How can they know the correct sequence? How can they know how to put everything together properly?

That which they do is far more complicated than assembling Tinker Toys or Legos. Indeed, it would be equivalent to one man, without any previous instruction, ordering all the needed supplies and, then, without any help, building houses, one right after the other. Yes, some men have done that; but they had large cerebrums to think with and large cerebellums, so they could coordinate their movements. The little protein lacks all this.

We really do not know how the little fellow manages; yet, given a steady flow of raw materials from the blood stream, he always selects the type and amount of amino acids needed to construct whatever kind of material is needed.

Proteins are also used for DNA recognition. Aside from RNA, only proteins have the ability to read the

DNA code and make use of it.

Proteins do everything in the cell, except carry the genetic code. Only the DNA has that, and DNA is structured differently than protein. It is not composed of amino acids, and is much longer than any protein. (A fully extended DNA molecule would be about six and a half feet in length.)

A quick review is here in order. In 1869, the Swiss biochemist Friedrich Miescher found something in the cell which was not a protein, so he named it *nuclein*. Twenty years later, when it was found to be strongly acid, it was renamed *nucleic acid*,

About the turn of the century, the German biochemist Albrecht Kossel isolated four nitrogen-containing compounds in it; which he named, *adenine*, *guanine*, *cytosine*, and *thymine*. There were large numbers of them in each nucleic acid.

But in 1911, the Russian-born American biochemist Phoebus Levene, in America, found that there were two types of nucleic acid in the cell! One he named *ribonucleic acid* (RNA); the other *deoxyribonucleic acid* (DNA).

By the 1940s, it appeared likely that DNA, the stringy substance in the *cell nucleus*, contained the genes. Then, in 1953, Francis Crick and James Watson used a British scientist's X-ray photograph (without her permission) to establish that DNA was a *double helix*—two sugar-phosphate backbones winding like a double-railed spiral staircase up the same vertical axis, complete with horizontal steps. The rest is history.

It is now known that, not only can RNA transmit data from the DNA code, but proteins can decode the DNA also. Proteins are ideally suited for this task, since each one has an *alpha helix*, a single twisting strand of chemicals; whereas the DNA is a double twisting strand. This alpha helix fits almost perfectly into the major groove of the DNA helix. When they come together, the left-handed side chains of the amino acids project outward and make contact with the DNA code.

In this manner, the protein obtains data from the DNA, which takes it elsewhere for use in constructing something.

Now let us consider this a little more closely:

In order for the protein "to read" a particular base sequence in a particular region of the DNA, it has to know where to go to find that information. But how can it do that, since the DNA has an enormous coiled length? How does the little protein know how to find the information section on the DNA that it is looking for? These are problems which evolutionary textbooks avoid. The sheer immensity of this needle-in-a-haystack search is staggering.

How can the protein even carry on the search, when it has no eyes (there is total darkness anyway) and the protein does not have the sense to know what it is looking for?

It has been suggested that the protein searches along

the protuberances of DNA, until it finds certain ones. How can the protein have time to search six and a half feet of coding, when research shows it locates and uses data from the code at breakneck speed!

One might reply that it knew what pattern to look for. Well first, if that is so, why bother to look for a pattern the protein already knows? Second, how could the hapless protein know where, on the vast length of DNA, to go find that particular section?

There are great mysteries connected with every aspect of living creatures, mysteries which defy explanation. It is not enough to blithely mouth the evolutionary line, that random changes (“natural selection”) and “harmless” chance mutations (none are harmless) have produced everything;—and because everything exists, that proves it must be so! This is circular reasoning.

The truth is that evolutionary theory is what Karl Popper, the leading scientific philosopher of the 20th century, says it is: a philosophical theory which is unrelated to scientific facts. Creationism, on the other hand, agrees with the scientific facts.

The protein is searching for a certain coding pattern which employs four DNA chemicals. Given the existing energy levels of the weak chemical bonds involved in protein-DNA binding, protein recognition complexes can bind reversibly to DNA sequences up to 15 bases long, but not to lengths much greater. In addition, because of the natural twist in the DNA double helix, protein recognition motifs, such as the alpha helix, can only feel along about 4 bases in the DNA double helix at a time.

With such a narrowed baseline to work with, how could the little protein be expected to ever find what it is looking for in six and a half feet of DNA ribbon?

Do not take for granted the miracle which happens continually in your body. It is totally astounding. Instead of ignoring God, people ought to praise Him.

Amazingly, a diverse number of proteins is made from various combinations of those 20 kinds of amino acids.

Some proteins which are constructed take the form of extremely hard materials—such as hair, nails, and feathers. Others are the tough tendons that attach muscles to bone. Then there are the fibrous sheaths which encase the various compartments and organs in the body.

Other proteins are rubberlike elastic materials that surround the major arteries or constitute the smooth elasticity of skin.

Still others form totally transparent materials which become the lens of the eye.

Do not listen to the suggestion that evolution could

provide us with such wonders. Everything had to be in place right at the beginning; so all these marvelous structures and functions were operating from ground zero.

Yet another question confronts us: How can all the above diverse things be made from the various combinations of the *same 20 amino acids*?

Do not hurry away from such questions too quickly. It is a mark of a wise man that he takes time to think while the shallow mind, fearful to confront facts, can only parrot what it has been taught.

Proteins do a seemingly endless variety of things. Here is an even deeper view of this astounding subject:

Some act as catalysts, speeding up the rates of chemical reactions billions of times. Working together in teams (how do they know to work together in teams?), proteins build up all the chemical components of the cell, including complex *lipids* and *carbohydrates*.

Proteins not only build up; they also break down. They can utilize their catalytic powers to break down the cells' macromolecular constituents back into simple organic compounds.

Through their catalytic abilities, proteins provide energy for the cell. They arrange for the fuel to fire the *mitochondria*, the energy batteries of the cell. They also build the mitochondria. And what is it made of? Like most everything else in the cell (with the exception of the DNA, RNA, water, lipids, and chemicals), those batteries are composed of specialized protein (in this case, wrapped around an energy drop of *lipid*). (In plants the energy provider is another type of protein, the *chlorophyll*.)

Proteins form the primary components of the contractile assemblies in the *muscles*. Without them, the organism could not move.

Out of a selection of amino acids, proteins construct all the tubular and wrapping systems of the body. This includes *cell walls*, *cellular tubes*, *membranes*, *blood vessels*, *capillaries*, and *lymph vessels*. The entire tubular transportation system of the body is made of protein and constructed, by proteins, from amino acids.

Proteins are also the *transporters* within the cells. They are the stevedors that lug everything around! Who tells them what, where, when, and how much to carry?

I will tell you the answer to that one, yet it only presents a bigger question: Another protein (often a constructor) moves over to the transporter, touches him momentarily, and the transporter then knows exactly what to get and how much is needed.

When trying to find answers to the mysteries within

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**PART FOUR
OF FIVE**

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the living cell, you will be disappointed if you look to evolutionary theory for solutions. In order to find them, you must look higher.

Proteins are generally the *messengers*, carrying messages from the DNA or from one part of the cell to another. (RNA is also a cell messenger.) Proteins are also the *chemical messengers*! Manufactured in one site in the cell, they then travel to other locations, where they bind to some other molecule to cause an appropriate message response.

Not only do proteins send the messages via other traveling proteins, they also receive them. How is a protein smart enough to know how to send a message, how to carry one somewhere, how to receive it, or how to provide an appropriate response?

Proteins are also the gates and pumps in the cell! As gatekeepers, they know when to open the gates. How do they open the gate, so outside substances can enter the cell? They do it by going to the cell wall (which consists of more protein) and telling it to open up! Obediently, it does so, just the right amount and long enough to admit the right substances from the *capillary* outside. In some cases, more than one wall has to be penetrated.

How do the proteins operate as pumps? The message is given to the gatekeeper to admit such and such amino acids and a certain amount of specified minerals, etc. Having told the walls to open up, the gatekeeper then begins a pumping action—and pumps construction materials and other supplies into the cell from the supply flowing through the capillary outside. Of course, only the correct materials and quantities are brought in. Then protein transporters are called over, which carry them to where they are needed.

Inside the cell, other proteins provide internal walls, gates, and pumps. They open and close chemical channels and actively pump chemicals from one side to another.

The little proteins must also haul waste materials (carbon dioxide, lactic acid, urea, etc.) to the gatekeeper, so it can be shipped out through the capillaries to the liver and/or kidneys for processing, recycling, or disposal.

The list of structural and functional properties of proteins is seemingly endless.

—And there are people out there who imagine that evolution produced all this! Seriously now, what is happening every moment in your quintillions of cells is no fairy tale, but evolution surely is. It could never provide you with the complexity that is taking place inside you!

Just as aimless people are useless in society, so purposeless evolution is worthless as a causative agent of anything in our world or out of it.

There is nothing that man has produced which can faintly match all the things proteins can do. Some man-made polymers can do a few things. For example, *nylon* has the elasticity and strength of collagen. *Chitan* (a carbohydrate polymer) is similar to nails and hair. *Perspex*, a plastic, has transparency similar to the crystal in the eye.

But, aside from protein, no other natural or man-made molecules even remotely has such a diversity of properties. Nothing else can match the catalytic powers of proteins. Nothing else can equal the ability of protein to discriminate and make decisions on a molecular level. Each protein is able to interact with unerring specificity with another one.

It would not be possible for the clumsy randomness of so-called evolution to produce useable amino acids and proteins.

We know this because of studies made over a period of years into *abnormal hemoglobin*. It has been discovered that there is a flaw in the protein chains, due to earlier mutations.

Yet evolutionists tell us it is mutations which have produced evolutionary development! This is simply not true. Scientists who deal with the effects of mutations will tell you that 99.99 percent of all mutations produce crippling and often lethal effects on the organism. Mutations do not improve; they destroy. See chapter 14 in the present author's three-volume, *Evolution Disproved Series*, for extensive evidence of this.

About 9 percent of the black people in America have the trait for sickle cell anemia, and 0.25 have the disease. In some localities in Central Africa, as much as a quarter of the black population shows the trait. It is commonly recognized, by scientists, that the sickle cell gene arose as a mutation in Africa and has been inherited ever since by individuals of African descent.

Researchers have found that normal hemoglobin has *glutamic acid* at the seventh point in just one of its many peptide chains; whereas the sickle cell form has *valine* at that point. Just *one* little chemical difference in *one* amino acid; that is what makes sickle-cell blood cells different than regular blood cells. But the entire hemoglobin molecule has nearly 600 amino acids! Just one flaw in one amino acid, out of a total of almost 600 amino acids; yet it results in a disease which generally results in an early death.

In view of this, it would be impossible for the hap-

hazard method of development, known as “evolution,” to produce useable protein. All the amino acids, and the protein structures they are built up into, have to be perfect or there is sickness, infirmity, and death. This is an important evidence that evolution could never produce worthwhile amino acids or proteins.

“Evolution” is misnamed. If it were called what it actually is, “Uselessness,” no one would be fooled by it. Yet the latter name exactly fits the evolutionary definition! Evolutionists declare it to be totally random, without any plan or purpose.

(At this juncture, it should be noted that evolutionists cite two evidences that mutations produce favorable results: [1] antibiotic-resistant bacteria, and [2] sickle-cell anemia. Let us briefly consider both:

First, mutations are not the cause of resistant strains of bacteria. They are just that: *strains*. Within the DNA coding of each life form, there is room for a wide variety of, what are variously called, hybrids, variations, varieties, or breeds. Chrysanthemums, roses, and dogs are excellent examples. Many varieties can be produced, but each one remains within its own species. Like peppered moths, there are also many varieties of a given bacteria which, when one form is more easily attacked, other forms temporarily increase in number. But both forms were in the DNA to begin with. This is not a mutation, but a species variation.

Second, Africans with sickle-cell anemia are less likely to die of malaria. Therefore it is sometimes claimed that sickle-cells (which are, indeed, caused by a mutation) are a beneficent mutation. Not so, for people with this condition always live shorter lives; during which time, their cells are unable to adequately obtain oxygen and nutrients from the red blood corpuscles. See the author’s chapter on *Mutations* for much more on this.)

Let us now turn our attention to mathematics. Here we find the most devastating rebuttal of evolutionary causation of amino acids, proteins, and DNA:

The mathematical probabilities that evolution could produce amino acids, proteins, and DNA are totally impossible of attainment. Many thinking scientists have established this fact. All living creatures are alive because they contain massive quantities of these complicated substances; therefore we can know that no living creatures came into existence because of evolution.

In Volume Two (*The Origin of Life*) of the present author’s three-volume set (*The Evolution Disproved Series*), you will find in chapter 10 (*DNA and Protein*) an extensive rebuttal of the possibility that amino acids, protein, and DNA could result from the randomness of evolution. As you will find throughout the entire set, that chapter is filled with quotations from reputable scientists. You will want to read them. Only a brief summary of that three-volume set is currently found on our website, pathlights.com. We are in the process

of gradually placing the entire three-volume set on the site.

That which you have already read in this present study was not taken from that three-volume collection of material. But now we will consider some data from chapter 10, relating to the mathematical possibilities that evolution could produce even one DNA, amino acid, and protein.

Here are some big numbers to help you grasp the utter immensity of the gigantic numbers which evolution would need in order to produce living tissue: *Ten billion years is 10^{18} seconds. The earth weighs 10^{26} ounces. From one side to the other, the universe has a diameter of 10^{28} inches. There are 10^{80} elementary particles in the universe* (subatomic particles: electrons, protons, neutrons, etc.). Compare those enormously large numbers with the *inconceivably larger* numbers, presented below, which would be required for a chance formulation of the right mixture of amino acids, proteins, and all the rest out of totally random chance combined with raw dirt, water, and so forth.

Mathematicians have shown that evolutionary processes could never produce even one amino acid.

When we discuss amino acid formulas, we are faced with a formidable barrier:

(1) There are 20 amino acids. (2) There are 300 amino acids in a specialized sequence in each medium protein. (3) There are billions upon billions of possible combinations! (4) The right combination from among the 20 amino acids would have to be brought together in the right sequence—in order to properly make one useable protein.

The chances of getting accidentally synthesized left amino acids for one small protein molecule is one chance in 10^{210} . That is a number with 210 zeros after it! Such probabilities are indeed impossibilities. The number is so vast as to be totally out of the question.

How long would it take to walk across the 10^{28} inches, from one side of the universe to the other side? Well, after you do it, you would need to do it billions of times more before you would even have time to try all the possible chance combinations of putting together just ONE properly sequenced left-only amino acid protein in the right order.

The possible arrangements of the 20 different amino acids is 2,500,000,000,000,000,000. If evolutionary theory is true, every protein arrangement in a life form has to be worked out by chance until it works right—first one combination and then another until one is found that works right. But by then the organism will have been long dead, if it ever had been alive!

Once the chance arrangements hit upon the right combination of amino acids for a single protein—the same formula would have to somehow be repeated for the other 19 proteins. And then it will somehow have to be correctly transmitted to offspring!

Each red blood cell (RBC) has about 280 million molecules of hemoglobin, and it would take about 1,000 red blood cells to cover the period at the end of this sentence. Because amino acids can exist in two forms (left and right) and in different sequences, there are 10^{300} possible ways hemoglobin could be arranged. But only one arrangement would succeed in producing and maintaining life. More on the hemoglobin odds, below.

Here is what Fred Hoyle, one of the most distinguished 20th century British scientists, says about the likelihood of amino acids being produced by mutations:

“If only ten amino acids of particular kinds are necessary at particular locations in a polypeptide chain for its proper functioning, the required arrangement (starting from an initially different arrangement) cannot be found by mutations, except as an outrageous fluke. Darwinian evolution is most unlikely to get even one polypeptide right, let alone the thousands on which living cells depend for their survival. This situation is well-known to geneticists and yet nobody seems prepared to blow the whistle decisively on the theory.”—*F. Hoyle and N. Wickramasinghe, Evolution from Space, p. 148.*

Mutations could not be the cause of evolution; for they would, in one instant, have to produce all the coding and content of every necessary type of protein molecule in the creature.

How then did the amino acids ever become coded into complicated protein chains? How did it originally happen?

“But the question arises as to how these amino acids could have become joined together into polypeptide chains. It is commonly assumed today that life arose in the oceans, J. B. S. Haldane’s ‘dilute hot soup’ providing a supposedly appropriate medium.

“But even if this soup contained a goodly concentration of amino acids, the chances of their forming spontaneously into long chains would seem remote . . . The probability of forming a polypeptide of only ten amino acid units would be something like 10^{20} . The spontaneous formation of a polypeptide of the size of the smallest known proteins seems beyond all probability. The calculation alone presents serious objection to the idea that all living systems are descended from a single protein molecule, which was formed as a ‘chance’ act—a view that has been frequently *entertained*.”—*H. Blum, Time’s Arrow and Evolution, p. 158.*

Mathematicians have shown that evolutionary processes could never produce even one protein. *We have considered the math of amino acids; we will next consider proteins:*

The probability of forming 124 specifically sequenced proteins of 400 amino acids, each by chance, is 1×10^{64489} . That is a big number!

The probability of those 124 specifically sequenced

proteins (consisting of all left-handed amino acids) being formed by chance, if every molecule in all the oceans of 10^{31} planet earths was an amino acid and these kept linking up in sets of 124 proteins every second for 10 billion years, would be 1×10^{78436} . And that is another big number! It is a one followed by 78,436 zeros!

As mentioned earlier, such ‘probabilities’ are impossibilities. They are fun for math games, but nothing more. They have nothing to do with reality. Yet such odds would have to be worked out in order to produce just 124 proteins! Without success in such odds as these, multiplied a million-fold, evolution would be totally impossible.

Even assuming that millions of complete amino acids were at hand to select from (and in nature they never are), there are still 41,000 possible codes; yet only one would fit each protein:

“The problem of synthesizing one simple protein of about 300 amino acids has been cited. A chain of 1,000 nucleotides made of the four basic units might exist in any of 41,000 ways, but only one will form the protein being sought. The chance that the correct sequence would be achieved by simple random combination is said to be so small that it would not occur during billions of years on billions of planets, each covered by a blanket of a concentrated watery solution of the necessary amino acids.”—*W. Stokes, Essentials of Earth History, p. 186.*

The mathematical impossibility of chance production of just one of the many blood proteins (*cytochrome C*) testifies to the impossibility of chance producing even one living being:

“The number of sequences of *cytochrome C* is now 7.25×10^{60} ; the number of sequences for 101 sites is 3.4×10^{160} . Therefore the probability of selecting a member of the *cytochrome C* family with the same optical isomers in a given set of 101 rolls of the icosahedral dice is 2.15×10^{94} .”—*H. Yockey, “A Calculation of the Probability of Spontaneous Biogenesis by Information Theory,” in Theoretical Biology, pp. 377-387.*

Evolutionists answer this by saying that evolution first formed the simplest organism, and it gradually “evolved.” Of course, that would mean changing all its DNA, amino acid, and protein codes into the ones needed for a new creature! How ridiculous to imagine that this could be done. In spite of erroneous reports, no missing links have ever been found.

Forget about the possibility of “a simple organism” first being evolved. NASA scientists have settled the matter for all time to come: There is no such thing as a “simple” organism! McCann tells us what NASA scientists have discovered:

“At one point in the space program, in anticipation of forthcoming contacts with other celestial [living] bodies, a determination was made for the makeup of the most meager, unadorned possible form of life based on what we know about present, earth-bound creatures.

Let us use figures derived from this hypothetical, simple organism. To simplify matters further, we will consider just one aspect—the protein makeup of such a simple creature.

“Thinking in minimal terms, it was the decision of the space scientists working on this problem that this simplest possible form of life would have to possess *no less than 124 different proteins*. It was also concluded that these proteins would each be composed of an average of 420 properly arranged subunits, called amino acids.

“In reality, this is a very conservative estimate of the proteins required in the formation of something alive. The simplest form of life actually known to exist on earth today is composed of 625 diverse proteins. Bacteria possess upwards of 2,000 different proteinaceous compounds, and the cells of man are estimated to harbor at least 100,000 proteins of assorted makeup. [There are billions of proteins in man, but McCann means 100,000 different types of protein.]

“[The author then mentions a lengthy list of non-protein requirements for organic life on earth, and the fact that all but one type of amino acid in the proteins must be left-handed ones].

“What then is the probability that just one average protein consisting of 400 left oriented amino acids will fall into place from a mixture offering equal numbers of left and right oriented amino acids? This means having it take place under conditions thought to have occurred at the time life arose.

“The probability of this happening calculates out to be one chance in ten followed by 114 zeros! This figure should be compared then with the probability of one chance in ten followed by 49 zeros, which labels the portal beyond which lies the realm of the impossible, as previously mentioned. Thus, we are taken far beyond the bounds of that which is possible, in expecting just ONE protein to assemble itself unassisted.

“In comparing the previous numbers, it should be realized that each time a zero is added, the chances get smaller by a factor of tenfold. This means that by adding two zeros, the chances become 100 times smaller; three zeros makes the chances 1,000 times smaller; four zeros makes the chances 10,000 smaller, etc.

“It might be interesting to know the computed chances of obtaining the necessary left arrangement for ALL the amino acids in ALL 124 proteins of our reference organism. It comes out to be one chance in 10 followed by 14,135 ZEROS!

“To get an idea of the scope of this last number, if the figure is written on a blackboard with normal sized numerals, the blackboard would have to be one quarter mile in length! It means that we have gotten a figure

so far beyond the statistical limits of obtainability as to be stupefying.

“[The author goes on to explain that all of the 20 variant amino acids in those 124 proteins *would then need to be arranged in their proper sequence!* He then mentions other factors which complicate the matter still further. You may want to read McCann’s entire *book*.]”—Lester J. McCann, *Blowing the Whistle on Darwinism*, pp. 60-62.

Fred Hoyle openly and honestly recognized this in a number of his writings. He wrote, in *New Scientist*, that 2,000 different and very complex enzymes are required for a living organism to exist. Then he added that not a single one of these could be formed by random, shuffling processes in even 20 billion years!

The *Dixon-Webb calculation* explains how evolution can make a protein: In 1964 Malcolm Dixon and Edwin Webb (on page 667 of their standard reference work, *Enzymes*) warned fellow scientists that, in order to get the needed amino acids in close enough proximity to form a given protein molecule, a total volume of amino acid solution equal to 10^{50} times the volume of our earth would be needed! That would be 1 with 50 zeros after it is multiplied by the contents of a mixing bowl. And the size of the bowl would be so large that Planet Earth could fit in it!

That is what two knowledgeable scientists say would be needed to arrive at the proper combination of amino acids to make just one protein molecule. Please remember that this is assuming the mixing bowl (times one with 50 zeros) *was filled with amino acids to begin with!* Nothing is said here about how they would initially be made.

After using the above method to obtain *one protein molecule*, what would it take to produce *one hemoglobin (blood) molecule* which contains 574 specifically coded amino acids?

On page 279 of their *Introduction to Protein Chemistry*, S. W. Fox and J. F. Foster explain how that would have to be done. First, large amounts of random amounts of all 20 basic types of already formed protein molecules would be needed. In order to succeed at this, enough of the random protein molecules would be needed to fill a volume 10^{512} times the volume of our entire known universe! And all that space would be packed in solid with protein molecules. In addition, all of them would have to contain only left-handed amino acids.

Then and only then might random chance be able to produce just the right combination, close to each other, of the proteins needed for one hemoglobin molecule, with the proper sequence of 574 left-handed amino acids!

Not even very simple codes can be duplicated by random activity. The truth is that duplicating even simple things by happenstance is nearly impossible. Some monkey business will help demonstrate that randomly producing even a very simple code sequence—far less complicated than that found in a single amino acid, protein, or DNA molecule—cannot be done:

“Assume that a monkey types randomly at a typewriter which has 60 keys: 26 small letters, 26 capital letters, a space, full stop, comma, colon, semicolon, two brackets and a question mark. Suppose that the monkey is to produce the word, ‘monkey.’

“Now the chances of the monkey typing the letter ‘m’ is 1 in 60; and of typing the two letters (‘mo’) is $(1/60)^2$; i.e., 1 in 3,600 ($1/60 \times 1/60$). Hence the chances of the monkey typing the word, ‘monkey,’ randomly is $(1/60)^6$; i.e., 1 in 46,656,000,000.

“To type on such a typewriter the title, ‘*Monkeys and Typewriters*,’ would take a million monkeys over a thousand million million million years (i.e., 1027 years) with each monkey typing at a rate of a hundred thousand million million (i.e., 1017) times as long as the age of the universe imagined by cosmologists.”—A. J. Monty White, “*Monkeys and Typewriters*,” in *Creation Research Society Quarterly*, September 1974, p. 128.

All the monkeys in the world could not accomplish the task!

“That these sequences of coordinated reactions—and there are literally thousands of them in the human body—should all have arisen by chance mutation of single genes is, in the highest degree, unlikely.

“It is as if we expected the famous monkeys who inadvertently typed out the plays of Shakespeare, to produce the works of Dante, Racine, Confucius, Tom Wolfe, the *Bhagavad Gita* and the latest copy of *Punch* in rapid succession.”—G. R. Taylor, *Great Evolution Mystery*, p. 184.

The letter code sequences of all the writings of William Shakespeare are not as complicated as the DNA and protein codes in your body! Yet, as two leading scientists explain, the randomness of evolutionary processes could not produce them:

“No matter how large the environment one considers, life cannot have had a random beginning. Troops of monkeys thundering away at random typewriters could not produce the works of Shakespeare, for the practical reason that the whole observable universe is not large enough to contain the necessary monkey hordes, the necessary typewriters, and certainly the waste paper baskets required for the deposition of wrong attempts. The same is true for living material.”—Fred Hoyle and Chandra Wickramasinghe, *Evolution from Space*, p. 148.

For much more on the mathematical probabilities of a random cause of amino acids, proteins, and DNA, the present author refers you to his book, *The Origin*

of Life, Vol. 2, pp. 271 - 286, 298 - 304. (Click on [Bookstore](#), and then on [Creation Books](#). The three-volume set is at the top and separate sections of it, in smaller booklet form, are below.)

Still more facts about protein and the possibility of it being caused by the random processes of so-called evolution. Here are but a few of the many other points cited in the above chapter:

- Dr. C. Haskins, writing in *American Scientist* (59 [1971], pp. 298) noted that evolution would not only have to produce these biologic codes, but it would simultaneously have to produce the *translation package* to interpret them. Several other writers discuss this; for example, J. Monod, *Chance and Necessity*, p. 143.

- *Messenger RNA* is also needed. So evolution would have to simultaneously produce not only the incredibly complex DNA code, but also the RNA molecules. Without them, DNA could not be effectively used.

- There is an intermediating substance between DNA and the proteins, called *tRNA*. The complexity gets worse! Each of the 20 proteins requires a different tRNA. This tRNA is the “biological compiler” which enables the protein to obtain the needed DNA data.

- There are also *DNA indexes*. DNA is a data bank, but the indexes, which are different than the translators, tell the protein how to locate needed data.

- There is also *cell switching*. The cell has to be able to switch its DNA from one process to another. Pitman discusses this on p. 124 of his book, *Adam and Evolution*.

- To make matters worse for evolution, each characteristic in a living organism is controlled by many genes. How could randomness devise all these matching and interlocking codes? See G. R. Taylor, *Great Evolution Mystery*, pp. 165-166 for more on this. Eye color in *Drosophila* (the fruit fly) depends on 14 genes. Over 30 reactions are needed in making human blood (p. 183).

- All the codes (DNA, RNA, tRNA, translator, amino acid, protein) would have to be instantaneously set in place within the organism—as soon as it began existing. Several scientists discuss this problem, but without providing a solution.

- Classical quantum mechanical principles, as demonstrated by Wigner, reveals that the probability of a self-reproducing state is zero. In everyday language, even if evolution made all those codes in one moment, it could not get them to reproduce themselves. See P. T. Mora, “*The Folly of Probability*,” in S. W. Fox (ed.), *Origins of Prebiological Systems and their Molecular Matrices*, p. 65.

- Just one average protein (*tryptophan synthetase A*) has 2,015 separate units, yet it is just one of the millions of functioning proteins in your body. How could evolution organize 2,015 units in their proper sequence?

1 • In a famous statement, Charles Darwin suggested
2 that life began “in a warm little pond.” In view of what
3 we know today about microbiology, would you not agree
4 that Charles, living back in the 19th century, did not
5 know what he was talking about?

• All biologically useful amino acids are L-forms, all sugars are D-forms, and all fats are in cis-forms; yet random production of each of them by evolution would produce equal amounts of two alternate forms.

• Julian Huxley, one of the foremost proponents of mutational evolution, estimated that production of each new species would take millions of mutational steps. Yet, if you will read the present author’s chapter on *Mutations*, they are always harmful. The best places to produce Huxley’s mutational “improvements” would be high-radiation locations. In the 20th century, the three best places were: (1) The jars of irradiated fruit flies; but the flies are always damaged, not improved by the mutational changes. (2) The August 6, 1945, nuclear explosion at Hiroshima. It produced many horrors, but no evolutionary improvements to man, beast, or plants. (3) The April 27, 1990, Chernobyl nuclear meltdown. Over 800,000 children urgently needed medical treatment and livestock were born with terrible abnormalities. None of Huxley’s improvements occurred.

Mutational damage to the DNA code can only produce flaws (such as sickle-cell anemia); it cannot produce new species.

• It was not until the 1960s, when biomathematicians had powerful computers available to them for research, that they could figure out the probabilities of evolution having had occurred in the preceding billions of years. Prior to that time, they could only guess. But, using computers, they discovered that evolutionary development of organic structures, codes, and functions was impossible.

The 1967 *Wistar Symposium* in Philadelphia, attended by leading scientists and mathematicians from around the world, discussed this fact. No scientist was able to repudiate it. Yet the public was never told the truth. Instead, the gullible masses continued to be pointed to such things as prior existence of dinosaurs, previous glaciation, and back-and-forth variations in the peppered moth as evidence of evolution!

It was repeatedly admitted at the Wistar Institute that computers had proven the impossibility of evolution—even in billions of years—to produce living things. Many mathematical calculations were cited.

One Wistar speaker, M. Eden, said that the code within the DNA molecule is actually arranged in a structured form, like words in a language. Letters in a language are structured in a certain sequence, and only because of the sequence can they have meaning. Eden then went on to explain that DNA, like other languages, cannot be tinkered with by *random* variational changes; if done, the result will always be confusion.

“No currently existing formal language can tolerate

random changes in the symbol sequences which express its sentences. Meaning is invariably destroyed.”—M. Eden, “*Inadequacies of Neo-Darwinian Evolution as a Scientific Study*,” in *Mathematical Challenges to the New-Darwinian Interpretation of Evolution*, p. 11.

• The instructions in DNA would fill a thousand 600-page books (Rick Gore, *National Geographic*, September 1976). Imagine evolution producing that book!

• Francis Crick, the co-discoverer of DNA propounded, what he called, the “*central dogma*.” It is this: Data can come from the DNA to the cell, not the other way around. (See Richard Milner, *Encyclopedia of Evolution*, p. 77.) That means that one species cannot change to another one; there is no transmission of acquired characteristics. Scientists claim to have rejected Lamarckism (the inheritance of acquired characteristics), yet evolutionists cling to it. (Darwin admitted in a letter that he believed it.)

• Francis Crick, himself, the co-discoverer of DNA, later wrote a book repudiating the possibility that DNA could be produced by evolutionary processes! He said the code was too complicated for random production of it.

• You can now ignore the evolutionary claim that life began with the lowest, simplest form of life, which is the amoeba. “Some specials of the unjustly called ‘primitive’ amoebas have as much information in their DNA as 1,000 *Encyclopedia Britannicas*” (R. Dawkins, *The Blind Watchmaker*, p. 116). That means that not even an amoeba could be produced by evolution!

• Evolutionists imagine that time could solve the problem. Given enough time, they say, the impossible could become possible. But Pitman explains that time works directly against success!

“Time is no help. Biomolecules outside a living system tend to degrade with time, not build up. In most cases, a few days is all they would last. Time decomposes complex systems. If a large ‘word’ (a protein) or even a paragraph is generated by chance, time will operate to degrade it. The more time you allow, the less chance there is that fragmentary ‘sentence’ will survive the chemical maelstrom of matter.”—Michael Pitman, *Adam and Evolution*, p. 233.

• Attempting to prove something by the argument that it could be done in near infinite time and that a vast number of polymers were available to make it happen is a desperate, self-defeating argument. “This is to invoke probability and statistical considerations when such considerations are meaningless” (P. T. Mora, *et al.*, p. 45).

All the above is only a hint of all that you will find in our three-volume set on this subject. (Click on [Bookstore](#), and then on [Creation Books](#). The three-volume set is at the top and separate sections of it, in smaller booklet form, are below.)

As we are able, we will put the complete set on this pathlights.com website. At the present time, only a brief

summary is online.

Conclusion. So we find it is impossible for evolution to produce protein or DNA. That settles that. Well, we didn't need protein anyway,—or did we?

Let me serve you a nice dinner of broccoli, a little dish of beans, a slice of whole wheat bread, with a little salt and vegetable oil. A wholesome meal. After chewing it well, you swallow it. Your tongue and mouth are made of protein. Down the meal goes to your stomach and small intestines, where it is acted on by digestive juices. Both the gullet, stomach, intestines, and the organs producing those juices are made of protein.

Through the lacteals, the food is absorbed into your blood stream, thence to travel all over your body—to nourish your liver, heart, brain, muscles, skin, lymphatics, glands, and all your other body organs. Along with the blood cells, arteries, and veins, all those organs are also made of protein.

Since evolution cannot produce protein, let's get rid of it. So there you stand in front of me, with all your protein gone. Nothing is left but bones, with some fat and chemically diluted water draining down onto the floor.

So apparently you need protein, after all! Well, you did not get it from "evolutionary development"!

If you decide to read my three-volume book, it will explain that nothing else in this world was made by evolution either. (You will there learn that stellar and geological facts also disprove evolutionary theory.)

Not only amino acids, proteins, and DNA,—but everything else about us reveals careful planning by a Higher Intelligence, not random purposeless as the cause.

You need to stop believing the errors of these men who preach evolution. They are stuck with an outmoded mid-19th century theory that was devised when almost nothing was known about proteins, genetics, or microbiology. And they are ashamed to admit that modern research has shown evolution to be a hoax. Although they choose to defend an error, you do not have to be part of it.

Instead, go alone by yourself, kneel down and ask God, who made you and keeps you alive every moment, to forgive you of your sins. Ask Him to accept you as His little child. He will do it, and you will experience a new peace in your heart you have never had before.

But do not stop there. Get a Bible and read in it every day and obey it. Through the enabling grace of Jesus Christ, obey God's Ten Commandment law. He will help you live a clean, godly life.

Is not this what you really want?

E-mail me at our pathlights.com address, and ask for books to help you in this matter, and I will send

some.

— Vance Ferrell

For further study. The data in the first two-thirds of this article were based on the following sources:

J. Monod, *Chance and Necessity*. London: Collins (1972).

G. Stix, "Waiting for Breakthroughs." *Scientific American* 274(4):78-83 (1996).

N.P. Pavletich and C.O. Pabo, "Zinc Finger-DNA Recognition: Crystal Structure of a Zif 268-DNA Complex at 2.1 Å." *Science* 252:809-817 (1991).

M. Suzuki and N. Yagi, "DNA Recognition Code of Transcription Factors in the Helix Turn Helix, Probe Helix, Hormone Receptor and Zinc Finger Families." *Proc. Natl. Acad. Sci. USA* 91:12357-12361 (1994).

"News and Views," *Nature Structural Biology* 4:424-427 (1997).

Isaac Asimov, *Photosynthesis*. New York: Basic Books (1969).

C.O. Pabo and R.T. Sauer, "Protein DNA Recognition." *Annual Review of Biochemistry* 53:293-321; see pp. 313-314 (1984).

J. Watson, *The Molecular Biology of the Gene*, 3rd ed. (Menlo Park, Calif.: W.A. Benjamin). Chap. 4 contains a discussion of the role and biochemical significance of weak bonds (1976).

Ernest Baldwin, *Dynamic Aspects of Biochemistry* (5th ed.). New York: Cambridge University Press (1967).

Y. Cho, *et al.*, "Crystal Structure of a p53 Tumor Suppressor-DNA Complex: Understanding Tumorigenic Mutations." *Science* 265:346-355 (1995).

Ernest Baldwin, *The Nature of Biochemistry*. New York: Cambridge University Press (1962).

M. F. Perutz, "X-Ray Analysis: Structure and Function of Enzymes." *European Journal of Biochemistry* 8:455-466 (1969).

Harold A. Harper, *Review of Physiological Chemistry* (8th ed.). Los Altos, Calif., Lange Medical Publications (1961).

Martin Kamen, *Isotopic Tracers in Biology*. New York: Academic Press (1957).

Karlson, P., *Introduction to Modern Biochemistry*. New York: Academic Press (1963).

G.J. Narilkar and G. Herschlag, "Mechanistic Aspects of Enzymic Catalysis." *Annual Review of Biochemist*, 66:19-59 (1977).

Albert L. Lehninger, *Biochemistry* (2nd ed.). New York: Worth Publishers (1975).

I. Hirao and A. D. Ellingron, "Re-creating the RNA World." *Current Biology* (1995).

Albert L. Lehninger, *Bioenergetics*. New York: Benjamin Company (1965).

Nature Structural Biology, 5:100 (1998).

M. Ptashne, *A Genetic Switch*. Palo Alto, Calif.: Blackwell Scientific Publications (1986).