

PROTEIN SYNTHESIS AND “FINE TUNING” PARADIGMS FOR THE DISCRETE DEGREES OF DIVINE INFLUX

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INTRODUCTION

Protein synthesis was chosen as a subject for inquiry by the Theistic Science Group in the fall of 2018 at the suggestion of Ian J. Thompson, PhD¹⁰. The focus of the of the group from its inception had been the nature of the *nexus* or interface between the natural and spiritual worlds, as possibly revealed by spiritual correspondences and the workings of Divine influx as explained in the Writings of Emanuel Swedenborg. The biology of protein synthesis was believed to be uniquely suitable for study on the “natural side” of this discussion in virtue of the known science at the molecular, atomic and even quantum levels. It was anticipated that these physical states might be viewed as forms sufficiently sensitive and subtle to receive both “mediate” and “immediate” influx, via “quantum fine tuning,” at the ultimate interface of the spiritual and natural worlds. No less appealing was the idea that protein synthesis, considered from the perspective of spiritual correspondences, might be a window, however tiny, into Divinely generated life forces themselves given the many roles of protein in cell structure and function, as well as protein functions in the extracellular milieu.

And because there must be a continuous connection with the spiritual world in order that every single thing may be kept in being, or constantly come into being, it follows that the purer or more interior things within the natural order, and consequently within the human being, spring from that world, and the purer or more interior things are forms such as are able to receive influx.”
(*Arcana Coelestia* §4524)

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10. Theoretical nuclear physicist; Lawrence Livermore National Atomic Laboratory. 1970–72 B.Sc Auckland University, New Zealand 1973–74 M.Sc Computer Science, Massey University, N.Z. 1975–1979 PhD Theoretical Nuclear Physics, Auckland University

In order to refine the task before us we pursued a more limited line of inquiry in regard to protein synthesis, specifically *protein folding*. The literature on this topic is expansive and has evolved into a complex blend of mathematics (including statistics, geometry, and knot theory), physical chemistry (including thermodynamics and kinetics), organic chemistry, inorganic chemistry, and both classical and quantum physics. The multiple atomic forces and interactions known to fold and stabilize protein each seem to have special electrochemical characteristics making them ripe for speculation as to their unique correspondential indexing, i.e., as targets for the forces of spiritual influx.

Research into the nature of protein folding has pursued three distinct pathways: *in vivo*, in the living cell; *in vitro*, in a test tube (literally in glass); and *in silico*, which is computer driven computation. Using the latter, small novel proteins have been designed and subsequently produced in the laboratory. Given the obvious limitations of conducting experiments in the living cell, *in vitro* research, rather than *in vivo*, had, until the 1980's, dominated the field of protein research. Since then, with the advent of sophisticated protein folding algorithms and supercomputing platforms some progress has been made in sorting out questions confronting researchers in the field. Nevertheless, many basic questions remain, with major problems unresolved.

The best known intra and extra-cellular roles of protein include; signaling, enzymatic action, structure, transport, regulation, storage, and immunity. Clearly, proteins are the basic building blocks and molecular motors of life at the level of the natural world.

Understanding the spiritual cascade of discrete degrees behind the physical degree of life may be a framework that is useful to better understand what is still unknown about protein structure, function and synthesis. —Ian J. Thompson, PhD¹¹

The above quotation reveals a core principle of New Church theistic science: Using principles from the theological writings of Emanuel Swedenborg, in conjunction with contemporary science, enlightened inquiry

11. See papers by Professor Ian J. Thompson preceding and following this paper in this issue of *The New Philosophy* discussing in detail the proposal that "fine tuning" might occur in the discrete degrees of creation on the natural level and that it may be an integral part of how influx works in the physical world.

can transcend the barriers currently facing science, leading to a deeper understanding of nature. Despite the entrenched Enlightenment attitude, banishing “ends” from science, beginning with the publication of *Novum Organum* by Francis Bacon in 1620, some of the leading scientists in the 17th and 18th centuries, including Michael Faraday (1791–1867), and James Clerk Maxwell (1831–1879), were deeply religious, pursuing science in a theistic vein in which ends are implicit in God’s plan. Thomas Huxley (1825–1895), Charles Darwin’s leading apologist, led a vigorous, and ultimately very successful campaign to erase all traces of theism from science both in Europe and in the United States.^{12,13}

HISTORY

The era of modern protein science began with the 19th century discovery of enzymes, driven by the European brewing and baking industries, both totally dependent at the time on the “largely empirical art of alcoholic fermentation.”¹⁴ The mystery of fermentation was a problem of some urgency given the rapidly rising demand for bread, beer, and wine. For several decades in the middle of the 19th century a debate raged between Louis Pasteur (1822–1895) and Justus von Liebig (1803–1873) as to the nature of fermentation, with Pasteur insisting that living yeast cells were required and Liebig postulating that the active substance in fermentation was a product of the decomposition of yeast. Liebig was closer to the mark and it was not long until the more precise chemical nature of enzymes was elucidated, laying to rest the “vitalism” proposed by Pasteur. By 1860 Moritz Traube (1826–1894) had proposed the idea of “soluble ferments.” Indeed, soon thereafter a pure chemical substance was isolated by Marcelin Pierre Eugene Berthelot (1827–1907), an enzyme which he named *invertase*.¹⁵ While enzymes are only one class of protein, much of the research into the nature

12. Prof. Dan Synnestvedt, as moderator of the panel discussion following the presentations at the “Breaking the Shell” symposium, explained in detail how Thomas Huxley, Charles Darwin’s most noted supporter, conspired successfully to systematically remove all traces of theism from scientific education, first in Europe then in the United States.

13. Matthew Stanley, *Huxley’s Church and Maxwell’s Demon* (Chicago, The University of Chicago Press, 2015).

14. David Dressler, Huntington Potter; *Discovering Enzymes* (New York, Scientific American Library, A division of HPHLP, 1991).

15. *Ibid.* p.139.

of protein folding has focused on them, not least because of their key roles in metabolic pathways. Enzymes are the catalysts that drive the biochemical reactions intrinsic to most life processes at a rate at least one billion times faster than would occur without them (a somewhat theoretical point since there would be almost no life and, therefore, no reactions without them).

Biochemist Christian Anfinsen (1916–1995) shared the 1972 Nobel Prize in chemistry for groundbreaking discoveries deriving from his *in vitro* experimentation with the enzyme *ribonuclease-A*. By first denaturing (unfolding) the active enzyme with a combination of 8M urea and β -mercaptoethanol, then subsequently incubating the unfolded protein (a simple chain of amino acids), in a salt solution at physiologic temperatures, Anfinsen demonstrated that the enzyme *refolded spontaneously* to its original biologically active form. This was an astonishing discovery; the *sequence of the amino acids alone*, comprising the primary polypeptide chain (the unfolded or nascent protein), determines the final folded tertiary active form and, therefore, its function.¹⁶ This has come to be known as “Anfinsen’s Dogma” (or Thermodynamic Hypothesis).¹⁷

LEVINTHAL’S PARADOX

A hotly debated topic in many of the scholarly research and review papers on protein folding is the problem of “Levinthal’s Paradox,” and it has been one of the major issues confronting the Theistic Science Group in our ongoing discussions. Put briefly, Levinthal’s Paradox insists that the time required for the spontaneous folding of an unfolded polypeptide chain (primary form), into the biologically active tertiary form, *by random chance alone*, should be many orders of magnitude greater than the actual, very short times (10^{-3} seconds to several seconds) observed in nature. In fact, for a chain of only one hundred amino acid residues (a relatively small precursor), the calculated time required for complete folding could be many times greater than the age of the universe! The number of possible conformations of the primary form, owing to a great number of degrees of freedom (possible bond angles of the constituent atoms), is so astronomical

16. *Ibid.* p.139.

17. B. Anfinsen, E. Haber, M. Sela, and F. H. White Jr., “The kinetics of formation of native ribonuclease during oxidation of the reduced polypeptide chain.” *Proceedings of the National Academy of Sciences* 47(9) (Sept. 1961): 1309–1314

that the probability of even a relatively simple protein molecule folding successfully, in the very short times observed in nature, would be close to zero. Faced with this conundrum Cyrus Levinthal (1922–1990) postulated that local amino acid sequences, by forming nucleation points, might speed up the process sufficiently. Numerous papers have been published explaining, or even claiming to have solved Levinthal's Paradox.^{18,19,20,21} This is one of many areas where introducing theistic science, using insights provided by the revelation given to Swedenborg, with knowledge of influx and correspondences, may be especially useful. The "intelligent design" scheme, while attractive to many with firm religious convictions simply lacks any real explanatory power in this and many other areas.

THE PROCESS

Proteins form in discrete stages beginning with a code transcribed from DNA onto messenger RNA (mRNA). Three DNA nucleotide bases code for one amino acid. The mRNA carries the three codon ribonucleotide code to ribosomes, both on the endoplasmic reticulum (an extension of the nuclear membrane), and within the extra nuclear cytoplasm. Ribosomes use transfer RNA (tRNA) to begin forming peptide bonds, linking individual amino acids in the precise sequence directed by mRNA (as coded from the appropriate segment of DNA), to form a polypeptide chain known as the "primary form." The primary form will begin to change its conformation from a simple string of amino acids into more complex "secondary forms" either co-translationally (as it is exiting the ribosome), or after emergence from the ribosome. The secondary forms are described as alpha-helices and beta-sheets (or strands). These forms may persist in structural proteins by repetitive linking, but in the case of enzymes and many other proteins, further complex folding will yield "tertiary" or "native" forms. These are

18. A.V. Finkelstein, S.O. Garbuzynskiy, "Solution of Levinthal's paradox is possible at the level of the formation and assembly of protein secondary structures." *Biophysics* 61(1), (January 2016): 1–5

19. Barry Honig, "Protein folding: from Levinthal's Paradox to structure prediction." *Journal of Molecular Biology* 293 (1999): 283–293

20. Arieh Ben-Naim, "Levinthal's Paradox revisited, and dismissed." *Open Journal of Biophysics* 2, (2012): 23–32

21. Alexey V. Melkikh, Dirk K.F. Meijer, "On a generalized Levinthal's Paradox: the role of long and short range interactions in complex bio-molecular reactions, including protein and DNA folding." *Progress in Biophysics and Molecular Biology* 132 (January 2018): 57–79

the biologically active forms. Not uncommonly the tertiary forms will link to form “quaternary” molecules, examples being *lectin* in plants and *hemoglobin* in birds and mammals. The forces responsible for forming and stabilizing these biologically active forms will be what concerns us most for of the remainder of this article.

The Swedish chemist Jöns Jacob Berzelius (1779–1848) had the remarkable insight to conclude that:

electrical and chemical relationships are one and the same thing, and that the affinities that are finally selected during chemical reactions merely the result from the movement of atoms toward more perfect reciprocal electrical relationships.²²

That electrical forces are behind all chemical reactions, both organic and inorganic, is a critical point in the discussion of how influx may descend into creation, via a process of “fine tuning.” A fundamental constant of nature, known as the “fine structure constant,”²³ $\alpha = e^2 / hc / 2\pi \approx 1/137$, characterizes the strength of the electromagnetic interaction between elementary charged particles. The fine structure constant, incorporating the electric charge “*e*” as a variable in the equation, may possibly have varied by small amounts over astronomical time scales.²⁴ Ian Thompson has theorized that *if the fine structure constant can vary at all* then it might do so *locally* over very short time scales, in ways sufficient to influence the very “finest things of nature,” thereby playing a key role in the cascade of discrete degrees responsible for the perpetual creation of the natural world, including the myriad biochemical pathways involved in life processes.²⁵

Also, they do not know what correspondence is and what influx is, and that when the spiritual flows into the organic forms belonging to the body, it establishes the living workings such as occur there. Nor do they know that without such influx and correspondence *not even the smallest parts of the body* can have life or be set in motion. (*Arcana Coelestia* §3629)

22. David Dressler, Huntington Potter *Discovering Enzymes* (New York: Scientific American Library, A division of HPHLP, 1991).

23. Nicholas Mee, *Higgs Force* (Marple: Quantum Wave Publishing, 2012).

24. John D. Barrow, John K. Webb, “Inconstant Constants.” *Scientific American Special Editions 16 1s* (February 2006): 64–71.

25. Ian Thompson proposes that by varying the electric charge at these fundamental levels locally, influx might be able to alter the path of reactions (according to need) thereby having a causal effect in biological processes. Once again, see his papers in this issue for a more in depth examination.

The role of water as a solute in the protein folding process continues to be a critical area of research. The dielectric constants (static dielectric permittivities, $[\epsilon]$) of surrounding water and charged amino acid residues are integral properties of the electrostatic interactions driving the behavior of protein folding and denaturation.²⁶ Given this background, the multiple electrostatic forces and interactions participating in protein folding will now be set forth along with *speculation* as to their spiritual level representations (correspondences).

FORCES AT WORK

There had been much debate in the latter half of the 20th century as to the roles of the multiple electrostatic forces and molecular interactions, especially as to which might be dominant in the protein folding process. While this discussion continues up to the present time, it became apparent by the mid 1980's that there was a hierarchy of forces and interactions, both electrostatic and hydrophobic, and that the hydrophobic interactions, by thermodynamic considerations, were most likely dominant. Given the correspondence of oils (hydrocarbon chains and organic fatty acids) to *love*,²⁷ one can envision the hydrophobic amino acids and their oil-like domains, by generating the "hydrophobic effect" central to protein folding, conforming closely to the action of love.

Thus, the whole body is an organ composed of the deepest arcana belonging to everything which exists within the natural world, and its formation is determined by *hidden forces by which all things act* and the wonderful manner in which they flow. (*Arcana Coelestia* §4523)

26. J W Pitera, M Falta, W F van Gunsteren, "Dielectric properties of proteins from simulation: the effects of solvent, ligands, pH, and temperature." *Biophysics Journal* 80(6) (June 2001): 2546–55

27. *Arcana Coelestia* §4581(4) in addition to many other places in the Writings of Emanuel Swedenborg where oil and fat are described as corresponding to "love." Divine love is the driving force in creation that actualizes when *informed* by Divine wisdom. See: Ian Thompson. *Starting Science From God* (Pleasanton: Eagle Pearl Press, 2011), where *love* is described as propensity, disposition, and desire to achieve useful ends. *It is substance itself.*

HIERARCHY OF FORCES

(WEAKEST TO STRONGEST)

- van der Waals forces
- Hydrogen bonds
- Ionic bonds (salt bridges)
- Peptide bonds
- Covalent bonds
- Hydrophobic interactions (not electrostatic)

The *van der Waals* interactions are the result of continuous slight fluctuations in the electron clouds surrounding atoms. “These fluctuations cause transient electric dipoles (two separate charges within a slightly varying proximity having a mutual influence) which participate in electrostatic interactions as they flicker in and out of existence.”²⁸ The dipoles can induce additional dipoles in neighboring chemical groups giving rise to “a significant attractive force between otherwise neutral atoms.”²⁹ Almost all of the atoms in the interior of a protein molecule participate in this weak but essentially ubiquitous force giving rise to a collective effect of major significance.

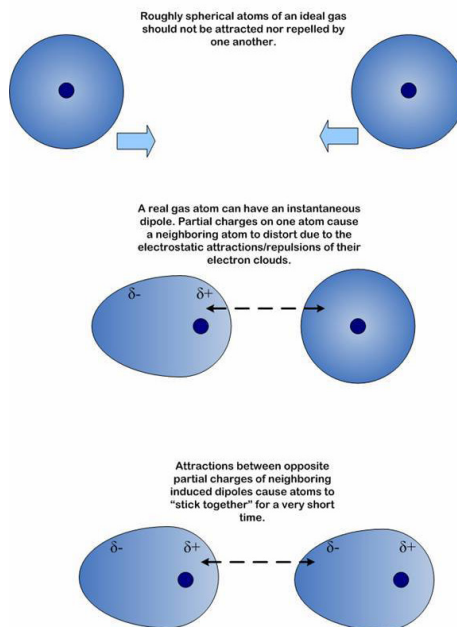
Speculation as to the spiritual representation of the van der Waals force might lead to thoughts of *bare facts, or first order phenomenological perceptions at the sensual/corporeal level*. Consider viewing a nursery full of newborn infants waving their limbs in response to infantile reflexes (perhaps they see angels?) as they probe and learn with nascent consciousness and innocence a strange new world. Lowest level facts will not exist in total isolation and tend to associate or disassociate, build or vanish, depending on the cognitive needs of the moment and the affectional states attached to them, much like the moving electron clouds giving rise to the transient electric dipoles of the van der Waals force.

28. David Dressler, Huntington Potter. *Discovering Enzymes* (New York: Scientific American Library, A division of HPHLP, 1991)..

29. *Ibid.* p.136..

Figure 1, right. Illustration of the van der Waals interaction³⁰

Hydrogen bonds are stronger than the van der Waals interactions. They arise as a result of one atom of a pair of atoms having a stronger charge than the other causing an unequal sharing of the electron cloud.³¹ Hydrogen bonds, while only of moderate strength, are numerous and, therefore, contribute to the conformational stability of a protein molecule.³² Precisely how much hydrogen bonds contribute to the folding process has been a matter of much debate in the protein folding literature.³³ Here we could suppose that hydrogen bonding corresponds to the *natural knowledges* common to our lives. Like these "scientifics" (external truths), hydrogen bonds are plentiful. One might also picture them as being at the level of "*apparent* causes and effects." This would equate to a union of good and truth at a very natural, primitive level, with the unequal sharing of electron clouds, in this case relating to the *appearance of truth preceding* and appearing to prevail over good. One can see this level as being represented by "Egypt" and especially the sojourning in Egypt, as that phase in life where natural knowledges must be acquired as a necessary foundation for the subsequent acquisition of rational, more interior knowledges. Perhaps this atomic/molecular force, ubiquitous in the building of protein, seen in relation to human development, might be not unlike early *childhood curiosity*, attempting to link the known to the unknown, thereby generating the never-ending question "why?"



30. <https://learnbiochemistry.files.wordpress.com/2011/09/image003.jpg?w=584>, licensed under CC BY-SA.

31. Ibid. p.131.

32. . Ibid. pp.131–132.

33. C N Pace, H Fu, K L Fryar, et. al., "Contribution of hydrogen bonds to protein stability." *Protein Science* 5 (May 2014), 652–661

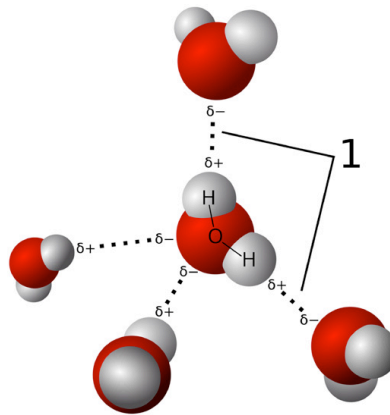


Figure 2: Hydrogen bonds form when one atom of a pair of atoms has a stronger nuclear force than the other resulting in an unequal sharing of the electron cloud.³⁴

Stronger still than hydrogen bonds are *ionic bonds or salt bridges*. These forces arise from oppositely charged amino acid side chains being in close proximity.³⁵ The strength of an ionic bond can be expressed by the equation $F = q_1q_2 / (d^2 \epsilon)$, where “ q_1 ” and “ q_2 ” represent the charges on the adjacent amino acid side chains, “ d ” the distance between them, and “ ϵ ” the dielectric constant of the solvent. The larger the “ ϵ ” the smaller the electrostatic attraction. Once again, we see a theoretical opportunity for subtle, local, brief changes in the electric charge, owing to transient fluctuations in the fine structure constant, to influence a biological process. The Heavenly Doctrines teach that salt, in a good sense, corresponds to an affection for truth. Since ionic bonding forms a salt we might well imagine that it corresponds to a relationship in mental states based on *affection for truth*. In regard to correspondences, we may now be at the level of *cognitions*, with an *affection for truth* participating in this higher level of mental awareness.

34. https://upload.wikimedia.org/wikipedia/commons/thumb/c/c6/3D_model_hydrogen_bonds_in_water.svg/1200px-3D_model_hydrogen_bonds_in_water.svg.png

35. David Dressler, Huntington Potter. *Discovering Enzymes* (New York: Scientific American Library, A division of HPHLP, 1991).

PROTEIN SYNTHESIS AND "FINE TUNING" PARADIGMS

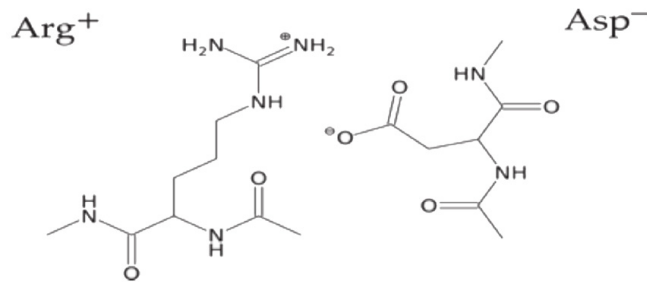


Figure 3: Ionic bonds form between a negatively charged oxygen and positively charged amino group (salt bridge).
(public domain)

One might suppose that yet another intractable problem for modern science, the "hard problem" of consciousness itself, as described by David Chalmers,³⁶ may be approached by integrating many of the aspects of protein folding as described in this paper with modern neuroscience and the revelations given to Swedenborg regarding the human mind. The salt produced by ionic bonding, representing an affection for truth, might at the molecular level, be at least a partial means of orienting the protein folding cascade in such a way that permits (or prepares the way for) the appearance of consciousness. Current research seems to confirm the role of local protein synthesis at the neuronal level of dendrites and synapses in creating the *biological substrate* of memory and conscious awareness. How entirely appropriate that the Theistic Science Group studied protein folding for an entire year prior to beginning inquiry into the "mind body problem."

Peptide bonds link amino acids to form the **backbone** of the protein structure and are intermediate in strength between single and double bonds.^{37,38} These bonds are formed when an amino (NH₂) group and carboxyl (COOH) group of adjacent amino acids link, releasing a molecule of H₂O in the process. These bonds resist rotation. The various characteristics of the peptide bond suggest a correspondence to the *rational mind* which links the

36. David Chalmers, "Facing up to the problem of consciousness." *Journal of Consciousness Studies* 2(3), (1995): 200-219.

37. David Dressler, Huntington Potter. *Discovering Enzymes* (New York: Scientific American Library, A division of HPHLP, 1991).

38. Consider the internal sense of the Jacob and Esau story, (Genesis 25: 19-34) as revealed in the *Arcana Coelestia* §3491-3604; Jacob gripping the heel of Esau, as the twins are born, represents good linked to and preceding truth.

spiritual and natural minds, generating what is truly human thought. Like a water molecule (water corresponds to truth) deriving from the formation of the peptide bond, truth comes to the fore in rational thought.

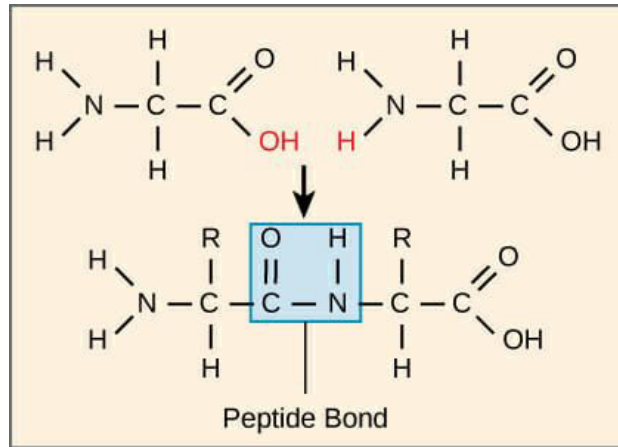


Figure 4. Peptide bonds form the backbone of the protein molecule. They are strong bonds, intermediate in strength between single and double bonds. They resist rotation. A molecule of H₂O is released in the formation of this bond.³⁹

Covalent bonds are very strong chemical bonds with strictly limited rotation. They arise between atoms sharing electron clouds in their outer or valence shell. They are strongest between atoms of similar electronegativities. The nature of the covalent bond suggests the *marriage of good and truth*, a foundational relationship in New Church doctrine, which teaches that similarity of thought and affection between husband and wife reinforces the marriage bond. The *good and truth paradigm* is central to the entire process of creation, including the perpetuation (sustaining) of all that exists in the natural and spiritual worlds. The idea of mutual love, at a very fundamental level of nature, is plain when contemplating covalent bonds.

39. <https://biologydictionary.net/peptide-bond/#foobox-1/0/Peptide-Bond-Formation.jpg>

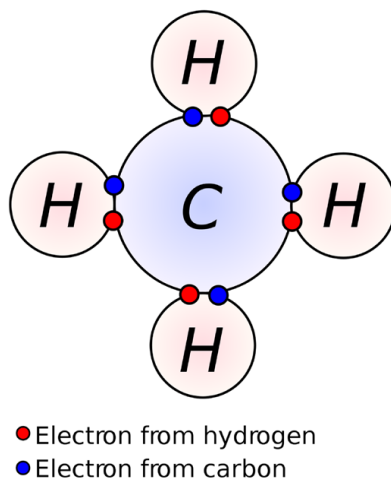


Figure 5. Covalent bonds are formed between two non-metal atoms sharing electron clouds in the outer or valence shell.⁴⁰

The amino acids with aromatic side chains; phenylalanine, tyrosine, tryptophan and histidine, including the other hydrophobic amino acids, are key to the *hydrophobic interactions*. These interactions are primary drivers of protein folding via the mechanism of hydrophobic collapse.⁴¹ To repeat what was stated previously, hydrophobic amino acid aggregates have oil-like characteristics. Oils and fats have a correspondence to love, and love precedes and is interior to truth. Consider that the heart which corresponds to love is interior and relatively central in the body. The hydrophobic amino acid residues likewise, by local thermodynamic conditions, are mostly driven into the interior core of the protein molecule where they are surrounded by the hydrophilic (polar or electrically charged) amino acids. (The water attracting hydrophilic amino acids would have a correspondence to truth).

Everything in the universe that is in harmony with God's plan relates to goodness and truth. (*New Jerusalem and its Heavenly Doctrine* §11)

There are always two forces which . . . keep everything in its connection and in its form, namely a force acting from without, and a force acting from within, in the midst of which forces is the object itself which is being held together by them. (*Arcana Coelestia* §3628 [2])

40. https://en.wikipedia.org/wiki/Covalent_bond

41. Ken A. Dill, "Dominant forces in protein folding," *Biochemistry*, 29(31), (Aug. 1990)

Again, we might think of Divine love as being represented by the oil like hydrophobic protein domains, while Divine truth can be seen as corresponding to the hydrophilic domains. The several electrostatic interactions described above are more significant in the polar hydrophilic domains than in the non-polar hydrophobic domains.

The quantum physics of water is key to the hydrophobic interaction. Molecular layers of water known as the “protein hydration layer” are bound externally to the protein molecule with a thickness varying between 5 Å and 20 Å. It is of interest that the dielectric constant of bulk water is 78 whereas that of the protein hydration layer is only 40.⁴² Perhaps one can envision a variation in the *quality of truth* here; more interior truth being represented by the protein hydration layer, with the *lower dielectric constant* (permitting a stronger attraction) representing a strengthened affirmative principle, or perhaps a more mature level of rationality. This, in turn, might imply a lowered threshold (would a lower “ ϵ ” increase the *probability* of enlightenment?) for the skeptical mind accepting genuine truth. That there is an astonishingly rapid exchange of water molecules between the hydration layer and the surrounding aqueous environment (bulk water solvent), in the femtosecond (10^{-15} second) range, is a testament to how unlike the natural world of our everyday experience is the world of protein folding, and how closely it approximates the “finest things of nature” described by Swedenborg in the 18th century.

Hydrophobic amino acid domains, prior to collapsing into the core, unlike the polar domains, are bounded externally by “ordered cages” of water which are crystalline or ice-like. This ordering of the water molecules results in a very *local loss of entropy* in the system. When hydrophobic residues coalesce, the water cages are dispersed resulting in a *positive entropy locally* and the *favorable free energy* needed to drive the hydrophobic residues into the interior of the protein molecule.^{43,44,45}

42. S Mondal, “Protein hydration dynamics: much ado about nothing?” *Journal of Physical Chemistry Letters*, 8 (2017) 4878–4882.

43. Ibid.

44. W Kauzmann, “Some factors in the determination of protein denaturation.” *Advances in Protein Chemistry* 14(1), (1959), 1–63

45. M Charton, B I Charton, “The structural dependence of amino acid hydrophobicity parameters.” *Journal of Theoretical Biology*, Elsevier BV 99(4), (Dec. 21, 1982), 629–644

CHAPERONE PROTEINS

Chaperone proteins have multiple intra-cellular roles in the synthesis, preservation, and degradation of proteins. Many chaperone proteins fall into the large family of "heat shock proteins" (HSPs). HSPs are recognized as a class of proteins that are rapidly synthesized in response to stress, including non-physiologic thermal conditions. Proteins may be denatured when exposed to higher than normal temperatures and HSPs function to preserve the native or active 3-D conformation by preventing denaturation. Chaperone proteins are molecular assistants integral to many phases of the biogenesis of larger proteins. From the moment they begin to exit from the ribosome as primary forms, the simple polypeptide chains are vulnerable to premature and incorrect folding. Chaperone molecules function as "nurse maids," preventing mis-folding by restricting the formation of defective folding intermediates.⁴⁶ During the assembly of larger complexes, chaperones prevent non-productive protein to protein aggregation, promoting successful folding. As "hospice nurses" chaperones remove redundant or defective proteins by transporting them to lysosomes and through the ubiquitin-proteasome system (UPS) for degradation and recycling.⁴⁷

Different classes of HSPs may interact such as HSP 40 with HSP70 in the ubiquitin-proteasome system for removal of misfolded proteins. Increasing HSP levels has been shown to be effective in reducing toxic aggregation of proteins thereby preventing diseases these aggregates are known to cause.⁴⁸ A special class of HSPs, Group I chaperonins (HSP 60s), form a cage that encloses proteins (no larger than 60 kDa) for folding. During encapsulation certain proteins are passively prevented from aggregating and other proteins are folded more efficiently and quickly. It is possible that chaperonins are able, via thermodynamic interactions with hydrophobic domains, to eliminate entropic and enthalpic barriers to folding.⁴⁹

The aim here is to show a possible correspondence between the various classes of chaperone proteins and celestial and spiritual angels, as well as the good spirits that protect us from the time we are tender, vulnerable

46. F Ulrich Hartl, Andreas Bracher, Manajit Hayer-Hartl, "Molecular chaperones in protein folding and proteostasis." *Nature* 475 (July 2011) 324-332

47. Ibid.

48. Ibid.

49. Ibid.

newborns, through subsequent stages of maturation, encouraging in various ways entirely unperceived by us, the most useful and productive lives possible, eventually assisting in the transition to the next world.

To enable the cause to exist the end must act on the level where the cause belongs, calling on assistant means to help it -the end- to bring the cause into existence, and to enable the effect to exist the cause likewise must act on the level where the effect belongs, by calling on assistant . . . (*Arcana Coelestia* §5131)

The HSP90 class of chaperones is unique in its role as molecular switches, regulating cell cycling and development. These protein molecules actually have a dual role in that they also deal with cellular response to stress. Researchers in HSP90 function claim that it provided “. . . the first evidence for an explicit molecular mechanism that assists the process of evolutionary change in response to the environment.”⁵⁰ Experiments revealed that, “populations contain a surprising amount of unexpressed genetic variation.” therefore, it was seen that HSP90 acted as a, “capacitor for the *conditional release of stores of hidden morphogenic variation . . .*” This means that environmental conditions, in some specific circumstances can, “. . . uncover (a) previously silent variation.”⁵¹ The implications of this are astonishing! Divine providence has produced a mechanism to protect a species with entirely hidden defenses, only being expressed in times of major stress. Is it possible as conjectured, that this, “. . . allow(ed) the rapid morphological radiations that are found in the fossil record.”?⁵²

All natural things representatively picture those that exist among the spiritual things to which they correspond, and these in turn picture those that exist among heavenly things in which they have their origin. (*Arcana Coelestia* §2991)

The theme of the 2019 Theistic Science symposium was “Breaking the Shell (from the inside).” Modern science has been hamstrung by either ignorance or willful denial of the nature of Divine creation at all levels and as such, despite ever higher mountains of data, some very basic questions continue to frustrate scientists, and will continue to challenge them indefinitely. When confronted by seemingly intractable puzzles the response generally is, “Just give us more time!” Life will never be produced

50. Suzanne L Rutherford, Susan Lindquist. “HSP90 as a capacitor for morphological evolution.” *Nature* 396 (November 1998) 336–342

51. Ibid.

52. Ibid.

de novo in the laboratory; “artificial intelligence” will never integrate human subjectivity nor approach the capabilities of the truly rational mind. As the Theistic Science Group, we hope that our ongoing endeavors, as an open-minded circle of curious and inquiring minds, by integrating the Divine revelation transmitted through Emanuel Swedenborg with the natural truths coming to us through scientific discovery, will “break the shell from the inside.” As Ian Thompson explained to the high school students at the Kempton New Church School last year, there are avenues of inquiry that are futile and should not be pursued and there are others that are fertile and hold great promise.

“Intelligent design” has developed a negative connotation among New Church thinkers, a reputation that its proponents have brought on themselves. This is the case for two reasons:

First, while they do assign a place for “intelligence” in creation, they are at a loss to explain in any rational terms how the process(es) actually work. Secondly, the intelligence referred to as “the designer” is invoked much of the time only to fill the perceived voids where science has failed to yield an explanation. In modern science, effects continue to be confused with causes and there is a complete ignorance of *discrete degrees* and the importance of *ends*, knowledges of which are pre-requisite to understanding the cascade of Divine influx into the ultimates of the natural world.

No doubt portraying the atomic and molecular interactions active in protein folding as having representatives in human psychology and human spiritual development will be thought by many readers to be quaint, fanciful, even bizarre. However, consider the following quotation:

Everything in nature has relation to the human form and has significance thence.
[emphasis added] (*Arcana Coelestia* §9555)

In order to appreciate the concept of how the human form is reflected in all of nature more fully please refer to the paper in this issue by the Rev. Dr. Reuben Bell.⁵³ In addition, might observing the behavior of a kinesin protein molecule “walking” in a style closely approximating that of a human, as it transports an endorphin molecule along a microtubule, tend to validate the above quotation? <https://www.youtube.com/watch?v=FJ4N0iSeR8U>

53. Reuben P Bell. *Intelligent Default: Swedenborg’s Theistic Science and the Problem of Organic Form* (Bryn Athyn: Swedenborg Scientific Association, 2019).

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