

Genetic code as the unity of chemism and semiosis

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Abstract. The paper presents the properties of the genetic code (built from two components: amino acid and nucleotide component) in a new understanding, as the unity of chemism and semiosis. The connection between the two components is established through the three-membered nucleotide associations (three-letter "words"), the codons. In doing so, the Standard Genetic Code Table is viewed as a system-arrangement of strictly balanced and nuanced physico-chemical properties of amino acid molecules, with several "robust" places; robust because they have a high amino acid diversity. Bearing in mind the validity of the "all or nothing" principle in neurophysiology, it is easy to see that a much more general principle is valid in semiosis – "if anything, then everything". If within the genetic code system, along with the coding of a *chemical entity with a chemical entity*, even at least one case of coding a *non-chemical entity with a chemical entity* (and vice versa) could be found, it means that the genetic code is, *per se*, a semiotic system. Among other possible examples of non-chemical entities are events, such as the initiation and/or termination of a possible process (as in protein biosynthesis). With respect to the general principle "if anything, then everything", codons "strive" to reach a high and higher level of diversity in the act of chemical coding of amino acids, so much so that chemical coding in "robust" places turns into its opposite, begins to encode non-chemical entities as well.

Key words: Genetic code, Chemical code, Periodic system, Periodic law, Chemism, Semiosis, Protein amino acids, Mirror symmetry.

1. Introduction

The paper was preceded by two preliminaries: one brief communication (Preliminary 1) and one synopsis (Preliminary 2)¹ [It has already been said in those papers that the genetic code (GC) represents the unity of chemism and semiosis.] Besides that, the said preliminaries were preceded by two papers published in the international peer-reviewed journals, (MMR, 2018a, 2018b). The first paper ("The Cipher of the Genetic Code"), on the example of Rumer's Table of nucleotide doublets, shows that the relationships of the number of nucleotide doublets in distinct subsets and the number of hydrogen bonds in them are such that they represent the unity of "signifiant" and "signifié" (signifier and signified) in De Saussure's sense. In second paper ("Analogies of genetic and chemical code"), it was shown that the chemical code is determined by the Golden mean and the Generalized golden mean (Box 1). As we can see, semiosis was not mentioned in those works, but it was said so, as that it is implied. However, that is not enough, and with this paper we are taking a further and fuller elaboration of the whole problem.

¹ Brief communication in (Rakočević, 2021b: [arXiv:2108.01563](https://arxiv.org/abs/2108.01563) [q-bio.BM]) and Synopsis in (Rakočević, 2021c: DOI [10.31219/osf.io/me8sj](https://doi.org/10.31219/osf.io/me8sj)) (Note: in further citations, instead of "Rakočević", only MMR.)

Comment 1. Semiotic approaches in the interpretation of biological phenomena have been significantly present on the scientific scene since 2008, with the launch of the journal *Biosemiotics*, by Springer Verlag, and the primary engagement of the founding editor M. Barbieri. In several of his papers, published in the journal and outside of it, Barbieri presented the problems encountered by these approaches. It is about the fact that the idea of semiosis is accepted in a very minor way.² And when it was accepted, it was accepted more as a philosophy and not as a science (Barbieri, 2008, 2018, 2019).³ Our approach is different from all others known so far: it concerns only the genetic code, and within it concerns the mirror symmetry and its possible connections and relations with the entities and quantities of the genetic code constituents. (In addition to the molecules mass, the quantities are represented by the number of particles in classes and subclasses of constituents: the number of molecules, atoms, nucleons, protons, neutrons.)

Box 1. Semiotic unity of signifier and signified

MMR, 2018a, pp. 31-32: "Rumer (1966) suggests that encoding [of amino acids] by dinucleotide aggregations is mediated by 'grammatical' formalism (the relation between words and the root of the word), semantics (one-meaning and multi-meaning codon families) and by semiology, i.e. semiotics (the classification of nucleotide doublets after the number of their hydrogen bonds which appear here as 'signifiant' and 'signifié' (signifier and signified) at the same time, that is as their unity (De Saussure, 1985, p. 99-100). ... Ten years later, after the R. Swanson's work [about Gray code model of GC], V. Shcherbak showed that genetic coding is mediated by Pythagorean triple within specific patterns of the number of nucleons in canonical AAs, such patterns that they themselves 'represent analogies with quantum physics' (Shcherbak, 1994)".⁴ [Additional Note 2022: Through the entirety of this paper, additional evidence is provided for the validity of Shcherbak's hypothesis by showing that the analogy he speaks of is realized precisely through the unity of chemism and semiosis.]

MMR, 2018b, p. 297: "... from the relation between these two expressions $[(1^2+2^2+3^2) - (1^1+2^1+ 3^1) = (0 + 2 + 6)]$ follows that the analogies [of genetic and chemical code] are also expressed through determination with the golden and the generalized golden mean ..." (Cf. MMR, 1998a and MMR, 2004b). [Additional Note 2022: Determination of the chemical code (Periodic system of chemical elements, PSE) by Golden mean, see also in Trifonov, Dmitriev, 1981; and in MMR, 1998b. (The shorter Excerpt is given in our website: <http://www.rakocevcode.rs>)

For the full elaboration, we will keep in mind the following basic definitions. We take the notion of *semiosis* from Charles Sanders Peirce, through Charles W. Morris, in the sense that semiosis is "the process in which something functions as a sign" (Morris, 1938, Section II/2, p. 3). On the other hand, the notion of *sign* we take from Ferdinand de Saussure (1985) in the sense

² Barbieri's Appeal that one should not be naive but see that the current science considers the genetic code only a metaphor and not an ontological reality, I accentuated by a *Nota bene*, given in the Introduction of one of my previous papers (MMR, 2018a).

³ "The idea that life is based on signs and codes, i.e., that 'Life is semiosis', has been strongly suggested by the discovery of the genetic code, but so far it has made little impact, and is largely regarded as philosophy rather than science" (Barbieri, 2008c, p.29).

⁴ "The laws of additive-position notation of numbers as a sequence of symbols ... have analogies with quantum physics" (Shcherbak, 1994, p. 476, last passage). As we will show (footnote 12 and 39) we, independently of Shcherbak, presented the same idea (about analogies with quantum physics) within the hypothesis that the genetic code is determined by Boolean spaces.

that "by sign we mean the total resulting from the association of a signifier with a signified. (De Saussure, 1985, pp. 99–100: "Nous entendons par signe le total résultant de l'association d'un signifiant à un signifié")."⁵ By *chemism*⁶ we mean the chemical affinity and chemical reactivity of substances.⁷

Here in the Introduction we present two working hypotheses, for which we will provide evidence within the paper itself. These two hypotheses *per se* are in relation to our previous hypothesis about the (prebiotically) complete genetic code.⁸

Working hypothesis 1: Hypothesis of separate and unified influence of the physical/chemical entities;

Working hypothesis 2: Hypothesis of separate and unified influence of single and double zeroth Boolean triangle.

2. Background and new insights⁹

From the very beginning of my research of the genetic code (MMR, 1987, 1988a, 1988b), I had a hypothesis that there must be a unity of chemism and semiosis. But, to say it publicly at the time, it did not make sense, because I did not have enough arguments. The only thing I dared to do was to present the idea of a possible analogy between the phylogeny of organisms and the diachrony of the human spoken language.¹⁰ Now I have these arguments and here I present how I came to them.

⁵ When we say that something functions as a sign, or about the association of a signifier with the signified, we are actually talking about the same thing, about semiosis. In other words, we agree with the views of both authors.

⁶ "Chemism – chemical affinity or attraction; chemical properties or activities collectively", Webster comprehensive dictionary, international edition, p. 228, J.G. Ferguson publishing company, Chicago, volume one, 1987.

⁷ It is understood that *chemism* is always in relation to *physicism*, in the way that is known in science, and we will not deal with that relation in this work.

⁸ "Hypothesis on a Complete Genetic Code (CGC) ... By this hypothesis, derived from presented facts as we understand them, we support the stand point that genetic code is one and unique, universal, valid for everything living, in fact, it is the condition for origin and evolution of life. Certainly, here we refer to the standard genetic code. According to this hypothesis, regarding other genetic codes (Budisa et al., 1999; Knight et al., 2001) we believe that they present only the expression of a code flexibility and degree of freedom, which is the matter of a separate paper. In correspondence with this, CGC must be based on several key principles. We are going to list only those considered to be the most important: 1. The principle of systemic self-related and self-similar organization. ... 6. Principle of integral influence of all four nature forces (electromagnetic force, gravity, strong and weak nuclear forces)". [MMR, 2004a, Section 7.1, p. 231.]

⁹ The new insights refer both to new insights related to background material, and to completely new insights first announced in this paper.

¹⁰ "From De Saussure's point of view, language (observed in its phylogeny) is a system of words with all the connections and relations between them, and all the changes that have befallen them on the evolutionary path; that is, from an other side, it is a system of macromolecules (nucleic acids or proteins), also with all the connections and relationships between them and changes in the evolutionary path" (MMR, 1988b, p. 64).

In a short period of time, several articles appeared with a possible synergistic influence on the interested researcher. As the first it was the work of R. Swanson (1984) on "A unifying concept for the amino acid code". This article inspired and encouraged me to further researches several questions/problems directly or indirectly contained in it:

1. The first thing this article warned me about is that the two components of the genetic code, the amino acid and the nucleotide components, must be viewed as separated and as unified.

2. From the way R. Swanson presented the connection between the binary Gray code and the natural binary code (in the first case the record in each subsequent codon changes exactly by one different nucleotide; in the second case: there are 6-bit records of pyrimidine-purine properties of codons on a scale from 0 to 63), I concluded two things: first, the Gray code model of the genetic code can be developed into a 6-bit binary tree; and second, Boolean spaces are determinants of the genetic code.¹¹

3. The fact that the amino acid relationships in the Mutation ring (in terms of their position in the protein: inner or outer; and, at the same time, in terms of molecule size: small or large), *mutatis mutandis* is the same ones in the codon ring, is more than surprising. How is it possible that after the evolution of organisms of several hundred million years, the relationships between AAs remain the same; both times with the same *uncertainty*: where the boundary of the accommodation of inner (and also outer) between small and large?¹²

4. Asking questions about a possible 'perfect' genetic code (Box 2) for me was more than encouraging. First on a general plan of asking questions; like Leibniz – is this world the best of all possible; or like Darwin – whether existing organisms are the best adapted organisms of all possible. But the question of possible 'perfection' also led me to a very specific problem – whether the existing terrestrial genetic code is the best of all possible; more specifically, can it be shown that the existing set of protein AAs is more perfect than all possible? And maybe it is the most perfect, and the only possible one?

¹¹ MMR, 2018a, p. 32: "The Genetic code six-bit binary tree represents, per se, the Boolean space, i.e. the Boolean cube B^n ($B= 2$; $n= 0, 1, 2, \dots, 5, 6$) From the chemical point of view, the cases for $n = 2, 3, 4$ are particularly important, where the latter case ($n=4$) represents a display of 16 nucleotide doublets"; p. 41: "The details on how GC can be understood as Boolean space can be seen in two of our studies (Rakočević, 1994, 1997b), both installed on our site"; MMR, 2019, legend of Figure A1, p. 28: "The first three non-negative numbers in the far right column [of Periodic system of numbers, PSN] correspond with the zeroth triangle (0,1,2) in Boolean spaces, and the first four (0,1,2,3) with the logical square."

¹² MMR, 1994, p. 89: "For example, in Mutation ring P falls into the small amino acid region, C into the inner region; but, on the other hand it is 'the fact that proline and cysteine both fall into the large region of the circle' (Swanson, 1984, p. 200). Note that here we have a new type of *synonymy-homononymy* and a new form of uncertainty principle"; p. 9: "It can be demonstrated that the problem of *synonymy-homononymy* in genetic code cannot be resolved independently of the most general nature laws and principles such as the Heisenberg's uncertainty principle and Einstein's relativity theory". [Additional Note, 2022: When I wrote this book (1994) I did not know about the work of V. Shcherbak (1994), in which he hypothesizes that arithmetic regularities in the genetic code contain analogies with quantum physics. (Cf. footnote 4 and 39); it was only later that I came to his work indirectly. (Indirectly, because at that time my country was under sanctions, with a ban on scientific communication.)]

Box 2. The problem of a possible 'perfect' genetic code?

Swanson, 1984, p. 201: "The actual amino acid code and the twenty amino acids it codes for suggest an idealized model coding system and idealized relationships among the amino acids. Using the idealized models, one could construct a 'perfect' genetic code and even choose a different set of amino acids to give a still more even distribution of their physical properties (cf. Figure 4). The purpose of such an effort would be to make comparisons and gain insight into the actual code in use in organisms. In any case, the availability of a theoretical standard for an amino acid code provides a new standpoint for addressing questions of selection vs random drift in the evolution of the code. It also raises new questions: if evolution has moved as far in the direction of a recognizable theoretical ideal as it has, why not farther? Is the ideal too hard to reach? Are the actual code and amino acids better as they are?"

3. Possible natural 'perfect' systems

The idea of a possible 'perfect' genetic code (Box 2), directed my further research in two directions. One direction was to examine the existing set of 20 protein amino acids, asking the question - is it possible that their system-arrangement (system-arrangement of molecules) is subject to two Mendeleevian principles, the principle of continuity and the principle of minimum change; specifically, by arranging the amino acids from the first to the 20th, according to chemical similarity, taking into account the two mentioned principles, whether the expected perfection will be manifested in any way; in other words, will it be one possible Perfect Protein Amino Acid Similarity System (PPAASS) (Box 3).¹³

Box 3. Generating of PPAASS (Perfect Protein Amino Acid Similarity System) in Table 2

MMR, 2019, pp. 12-16: "From a chemical point of view the first step of classification of protein amino acids (AAs), must be the classification into aliphatic and aromatic AAs, where on a hierarchical scale of changes by similarity and complexity, aliphatic AAs must precede the aromatic. For the same reason of the chemical hierarchy, within the class of aliphatic AAs at the beginning must be the hydrocarbon AAs (possessing in the side chain carbon and hydrogen, or hydrogen only, in the case of glycine), and at the end two sulfur AAs ... Two sulfur AAs (as the last in the class of aliphatic amino acids) must be found in direct contact to the aromatic. ...

In the set of aromatic AAs, Phe came the first, as the simplest, followed by Tyr, and Trp, all three with possession of a benzene ring. At the very end ultimately must be His, the only one which does not possess the aromatic benzene ring ...

In the set of hydrocarbon AAs, at the very beginning must be Gly as the simplest AA, followed by Ala as the first possible case of hydrocarbon series with an open carbon chain. At the same time, for chemical reasons, it seems that Gly-Ala can be considered as a pair of AAs. Then comes the pair Val-Pro, both with three carbon atoms in the side chain, rather than Leu and Ile with four carbon atoms. Val with half-cyclic chain precedes Pro. ...After the pair Val-Pro, it follows the pair ... Ile-Leu. ...Finally, it remains to determine the chemical distinctions of AAs in 'between' area. We have already said that sulfur amino

¹³ In previous paper (MMR, 2019, Table 2, p. 14) I only wanted to say that in the question is the Protein Amino Acids System (PAAS). Here, however, the properties of that System are shown to be such that it is necessary to expand the name (PPAASS as in Box 3).

acid pair, Cys-Met, precede aromatic amino acids. As chalcogen¹⁴ AAs, they must be in contact with other two chalcogen amino acids, Ser-Thr. By this, the contact has to be made *via* Cys because it possesses SH group, correspondent to OH group in Ser as well as in Thr. It is to be understood that a pair of oxygen AAs with the hydroxyl (OH) functional group in side chain must be in contact with a pair of two also oxygen AAs, but which possesses the carboxyl (COOH) functional group: Asp-Glu. ...

Returning to the beginning, in the area of hydrocarbon AAs, to the 'point' of the pair Ile-Leu ... further must follow the pair of nitrogen derivatives, Lys-Arg ... Then, chemically speaking, it is very natural that after Arginine comes Gln with its precursor, the glutamic amino acid, both (Gln-Glu) with two carbon atoms in the side chain ... [and then follows] the pair Asn-Asp. With this, chemical sequencing of series of 20 AAs closes, starting from the first, glycine, and ending with very different histidine (Table 2)."

The second direction, concerned the system-arrangement of atoms; in other words, it concerned the Periodic Table of the Elements (PSE). The main question here was whether the reality of the existing Periodic system was consistent with the two said Principles of Mendeleev. Unfortunately, the answer to this question was negative, for at least two reasons. If the essence of the *Periodic law* is that each odd element must be in an odd group of PSE, and each even in an even group, then why are all 14 lanthanides in one and the same, third group, in the real *Periodic Table* (within current science)? And the second reason, if Mendeleev's two principles are valid (and they are valid!), then, from the aspect of neighborhood logic, Hydrogen cannot be in the first but only in the seventh group, as the Helium neighbor from the eighth group.¹⁵

How these two problems can be solved I have presented in one of the previous papers (MMR, 2018b), but that was not the end of the "story". The analysis of both published and manuscript Mendeleev's works suggested that Mendeleev must have had the idea that there must also be a Periodic System of Numbers. The most important facts that point to that are the following. Despite the fact that in the beginning he arranged the elements according to the growing atomic masses ("atomic weights"), in the case of tellurium and iodine he deviated from that principle, putting heavier tellurium (127.6) ahead of lighter iodine (126.9). Proof more that Mendeleev understood the natural order of the elements, consistent with the order in a series of natural numbers, is the fact that in all his tabular representations of PSE, published and hand written (which we find today in the Mendeleev Archive) he marked even and odd groups; also for periods, and for rows within periods.

After these (and other, correspondent) insights, following in Mendeleev's footsteps, it was not difficult for me to present the Periodic System of Numbers, PSN (MMR, 2011, Table 4, p. 826; MMR, 2019, Table A1, p. 28). Unexpectedly, the newly formed PSN immediately, by itself, gave at least two testimonies of the existence of PPAASS (Table 1 in relation to Survey 1, and

¹⁴ The name chalcogen amino acids comes from the fact that they contain oxygen and sulfur, elements of the sixth group of PSE, which is called the group of chalcogen elements, as opposed to the seventh, which is the group of halogen elements.

¹⁵ Along with the neighborhood problem, the issue of the ordinal number and the atom number of the chemical element also arises here (Remark 1).

Table 2). In segment I of Table 1, the mirroring of the double zeroth Bullean triangle from the last column of PSN is presented, with the formation of *original-image* of the entity. Its specific crossing with the 6-bit binary GC tree results in quantities 02, 13, 24, 16, 05, whose mirror images (segment II in Table 1) appear to be the number of atoms in the five quartets (taken consecutively from Table 2).¹⁶ The classification of amino acids given in Segment III of Table 1 follows from the determination of the Amino acid code¹⁷ by the Golden mean, according to Surveys 2 and 3 and Displays 1 and 2, All four illustrations in correspondence with Survey 4.

Table 2 is viewed in relation to Table 2.1 and Table 2.2, each from the aspect of the given legend. But Table 2.2 also has a special meaning, as a possible response to René Thom's request for the necessity of searching for "natural mathematics" (*Mathematica naturalis*)¹⁸ and a new way of mutually "informing" natural systems.¹⁹ In this sense, the quantities found and presented in this Table (the same ones presented in Table B5: 530, 540, 560, 570) are connected with the quantities presented in Figure 1 (on the right: 031, 041, 061, 071).²⁰

Remark 1: The relationships in Table 2.2 allow us to return to solving one of the key problems of the Periodic system of chemical elements (PSE). It is about whether, in addition to stating the number of protons in the atom of each individual element, its ordinal number should also be stated. It follows from this whether it makes sense to talk about the *atom number* as a sum, in this sense: The *atom number* for hydrogen is 3, since it has one proton in (one) of its atoms and its ordinal number is 1 ($1+1+1 = 3$); for helium ($1+2+2 = 5$); for lithium ($1+3+3 = 7$), and so on.

¹⁶ In the original Table of PPAASS (MMR, 2019, Tab. 2, p. 14), the number of atoms in the side chains of amino acids is given, and here the number of nucleons.

¹⁷ We say "Amino acid code" instead of "Genetic code" in the same way as R. Swanson did (1984). The meaning is depending on what is to be emphasized, the amino acid or nucleotide component of the genetic code.

¹⁸ MMR, 1994, p. 242: "For the researchers of mathematical and logical foundations of the natural codes, several distinctions are necessary ... There are at least two mathematics: *Mathematica instrumentalis* and *Mathematica naturalis* "

¹⁹ René Thom, 1979, last passage: "Sans doute, j'en suis profondément convaincu, les mathématiques 'informent' le monde comme elles 'informent' aussi notre propre structure. Mais ces mathématiques-là ne sont pas celles que nous connaissons, [avec] de l'itération indéfinie des opérations formelles. C'est au contraire dans l'étude des limitations naturelles des formalismes que réside la mathématique de demain." [Additional Note 2022: Our assumption is that Thom means that any mutual "informing" of natural systems inevitably involves semiosis.]

²⁰ Here we have an adequate place to comment on the arbitrariness of the semiotic signifier. Namely, we cannot say that the mentioned quantities have a causal relationship with the properties of AAs, but they are signifiers of those properties in De Saussure's sense. However, the "paradox" was resolved by De Saussure, pointing out that the signifier is arbitrary in relation to the signified, but not arbitrary in the set of possible signifiers. [De Saussure, 1985, p. 100: "Le lien unissant le signifiant au signifié est arbitraire, ou encore, puisque nous entendons par signe le total résultant de l'association d'un signifiant à un signifié nous pouvons dire plus simplement: le signe linguistique est arbitraire. ... Le mot arbitraire appelle aussi une remarque. Il ne doit pas donner l'idée que le signifiant dépend du libre choix ... Nous voulons dire qu'il est immotivé, c'est-à-dire arbitraire par rapport au signifié, avec lequel il n'a aucune attache naturelle dans la réalité."]

4. The unity of standard and mitochondrial Genetic code

One of the greatest, if not the greatest, difficulty and obstacle to the revelation of the unity of chemism and semiosis was the fact of the existence of "deviant genetic codes" (MMR, 2018a, Box 2, p. 41). An additional problem was the mitochondrial GC, which manifested itself as if it were more than an exception. Aware of this, 13 years ago I made a hypothesis that it could be that the two basic GCs, standard and mitochondrial, were generated together and at the same time; certainly synchronously, even if it was in a parallel process (Box 4).

Box 4. The unity of standard and mitochondrial GC

MMR, 2009, Commentary 8, p. 17: "The differences in [Vertebrates] mitochondrial code in relation to standard one are as follows: Isoleucine (I) AUU, AUC; Methionine (M) AUA, AUG; Tryptophan (W) UGA, UGG; 'Stop' codons: UAA, UAG (as in standard one) and AGA, AGG, instead these last two codons to be coded for arginine (R) as in standard genetic code"; Commentary 9, p. 18: "From regularities, harmonic structures and proportions containing within mitochondrial genetic code (see Appendix C) [here: Survey 5.3] it follows that standard and mitochondrial code possess a parallel and collective prebiotic evolution;²¹ collective in the sense of a unity and harmonized dynamic of PIS and NIS (Protein Interactive System and Nucleotide Interactive System)" [*Additional Note 1* (2022): When I wrote "interactive", it means the exchange of "information" between two systems in sense of René Thom's position (as in footnote 19).

4.1. Mapping the relationships from PPAASS into Tables of Standard and Mitochondrial Genetic Code

In order to understand the mapping of the PPAASS into the Table of the Standard Genetic Code (SGC), except two system-arrangements that we are talking about, it should have in mind the analogies of the genetic and chemical code. This is because these analogies are valid only for the SGC, in which 61 codons code for chemical entities (AAs)²², and three codons for non-chemical ones (three "stop" codons). By this, the basic setting of the analogy is in the following: 25 codons coding for less complex amino acids versus 25 unstable chemical elements. On the other hand there are 36 codons coding for more complex amino acids versus 36 stable chemical elements. It is not unimportant fact that in three "stop" codons (within their four bases) there are

²¹ The term "evolve" in prebiotic conditions, then, as in all my later works, I use in the sense of "generate". Everything is "given" by the structure of AA molecules (PPAASS, Box 3) and their connection with nucleotide bases, as I stated in the Scenario of generating GC constituents – amino acid and nucleotide. [MMR, 2018a, p. 33: "We find that aromatic hydrocarbons provide precursors for all four Py-Pu bases and all four aromatic AAs ..."; MMR, 2004a, p. 232: "However, if the principle of 'chance' brings into relation the principle 'All or Nothing', then ... it is the matter of pure 'chance' ... if some of 'NOTHING'-aggregations would gain the characteristic of self-reproduction by which it would become 'EVERYTHING'-aggregation. It could happen that CGC [Complete Genetic Code, as prebiotic] has never been assembled, so there would be no origination of life on our planet."

²² As is known one of these 61 codons (AUG) encodes both, a chemical and a non-chemical entity: AA methionine and the initiation of protein synthesis in eukaryotes. [The initiation coding in prokaryotes is performed by GUG and UUG codons, what is an example of the existence of deviant genetic codes (MMR, 2018a, Box 3 and footnote 8 in this paper).]

[(128 x 1) x 01] of atoms, and within 61 amino acid codons [(128 x 2) x 10]. (Cf. Fig. 4, p. 37 in: MMR, 2018a.)

All of the above is about insight into the general level of nuancing and balancing in establishing a connection between the two codes. However, there are also lower, finer levels of analogy, where the quantity 25 is splitted into 8 and 17, and the quantity 36 into 10 and 26, or into 13 and 23 quantities (number of isotopes and number of codons, respectively) (Box 5 and legend of Table 3).

Box 5. Compatibility of genetic and chemical code

MMR, 2018b, p. 296, paragraph 1: "The 25 codons encode the AAs of the less complexity (2AAs + 4AAs) [(GP) + (ALVI)] which have only carbon and hydrogen (glycine – only hydrogen!) in the side chain; and 36 codons encode the AAs of greater complexity which have, except C and H, some other elements (N, O or S)"; p. 296, paragraph 2: "From a total of 61 multi-isotope elements, the 25, except stable isotopes, possess unstable primordial isotopes ...; and 36 multi-isotope elements possess only stable isotopes (they do not have unstable primordial isotopes)"

MMR, 2018b, p. 296, paragraph 1: "The number of codons for encoding less complex AAs corresponds to the solutions of the first linear equation ($x_1 = 8$ and $y_1 = 17$): two nonstandard hydrocarbon AAs (GP) are encoded with 8 codons, and four standard hydrocarbon AAs (ALVI) with 17 codons. On the other hand, the number of codons for encoding more complex AAs corresponds to the solutions of the second linear equation ($x_2 = 10$ and $y_2 = 26$): six AAs (CMFYWH) which do not have a 'mapping' of functional groups from the 'head' to the 'body' (side chain), are encoded with 10 codons, and the eight AAs (STDENQKR) which have a mapping of functional groups from the 'head' to the 'body', are encoded with 26 codons.

MMR, 2018b, p. 296, paragraph III: "Further distributions are carried out through distinctions into odd and even elements – the odd elements within the odd groups and the even elements within the even groups, in both cases are in accordance with the model (the shaded part in Survey 3a). In accordance with the solutions of the first linear equation ($x_1 = 8$ and $y_1 = 17$), the 8 unstable and odd elements are within the odd groups, and 17 unstable and even elements within the even groups. On the other hand, according to the solutions of the second linear equation ($x_2 = 13$ and $y_2 = 23$), the 13 stable and odd elements are in odd groups and 23 stable and even elements in even groups." [*Additional Note 2022*: That this last result exists also in the genetic code was not announced in our previous work (MMR, 2018b, Surveys 2a and 3a, p. 296), but now it is revealed for the first time (see legend of Table 3).]

By comparing the structure of PPAASS (Table 2) with the structure of SGC Table, we find that relations are established not through positions rich in similarity, but rather through positions with high amino acid diversity. So, in PPAASS, the only two sulfur amino acids are found between hydrocarbon aliphatic, and aromatic amino acids; in SGC Table those two sulfur amino acids, with the neighbor amino acids (M-I, CW), make very high diversity. And right in the neighborhood of those places we have the appearance of coding of non-chemical entities.

It is very important to realize that here the high level of diversity does not only come from sulfur amino acids but also from their neighbors. Isoleucine, together with leucine, is the only pair of structural isomers in the set of protein amino acids; they have the same chemical composition, but a different molecular structure. However, leucine belongs to the subset of

amino acids of the alanine stereochemical type (of which there are 16), while isoleucine belongs to the subset of amino acids of the valine type (in which there are only two of them: valine and isoleucine). The connection between the "head" and the "body" (between the amino acid functional group and the side chain) in amino acids of the first subset is established through the primary, and in the second type through the secondary carbon atom.²³ [This is a small nuance in distinguishing structures, but with great consequences in distinguishing the physico-chemical properties of amino acid molecules, as well as the semiotic properties of the corresponding chemical and non-chemical entities.]²⁴ As for the increase in diversity by the presence of tryptophan, it is not only because it has the most atoms in the side chain (18), but also because it is the only one of the four aromatic amino acids that has two rings in the molecule: benzene as carbocyclic, and pyrrole as heterocyclic.

We find a similar state of increased diversity in the third column of the Standard Genetic Code Table, where tyrosine and histidine are located next to each other. Tyrosine is the only one of the four aromatic amino acids that has a functional group attached to a ring. On the other hand, histidine is the only one of the four aromatic amino acids that has a 5-membered ring instead of a 6-membered one. And right there, between these two amino acids, two "stop" codons appear.²⁵

Taken together, we find the following state of affairs. Respecting the general biological principle "all or nothing" ("if anything, then everything"), codons "tend" to reach a higher and higher level of diversity, in the act of chemical coding of amino acids; so much so that chemical coding in places "wounded" by diversity turns into its opposite, begins to code non-chemical entities as well.

On the other hand, when the mitochondrial genetic code continues to heal the "robustness" caused by increased diversity (especially in the case of arginine as an "intruder"),²⁶ then full

²³ It is obvious that there was a mistake in the naming of these two amino acids. The iso-butyl group is not in isoleucine, but in leucine.

²⁴ We find a similar nuancing through the neighborhood of two carbon atoms in one fundamental classification of canonical AAs (classes I and II, each with 10 of AAs). Namely, there is a distinction of canonical amino acids in correspondence with two classes (I & II) of enzymes aminoacyl-tRNA synthetases, which attach amino acids (10 vs 10) to the 2'- and 3'-OH of the tRNA terminal adenosine, respectively (Survey 4, p. 290 in: MMR, 1998a, in relation to Survey 5 in this paper). Only one exception is phenylalanyl-tRNA synthetase, which belongs to Class II but attaches phenylalanine to the 2'-OH. [Phenylalanine is also an exception from the aspect of amino acids pairing, in the sense that it, as non-polar, makes the pair with tyrosine, as polar AA. In all other cases amino acids are paired (within four stereochemical types): non-polar with non-polar and polar with polar (Rakočević and Jokić, 1996, Survey 1, p. 346).] (About the mentioned two classes of AAs see in: Wetzel, 1995 and Rakočević, 1997a.)

²⁵ Corresponding situation in PPAASS: tyrosine, which has a functional group attached to the ring, separates phenylalanine and tryptophan, which do not have such a group. On the other hand, histidine, although the smallest of the four aromatic amino acid molecules, appears as the last in the sequence of similarity, which means the most different compared to the first amino acid, glycine.

²⁶ Jukes, 1973, p 24: "I have suggested that arginine displaced ornithine during the evolution of protein synthesis"; Jukes, 1974, p. 331: "It is speculated that arginine is an 'intruder' into the genetic code, and that it may have displaced another amino acid such as ornithine, or may even have displaced lysine from some of its previous codon assignments".

compatibility of the standard genetic code and mitochondrial is achieved (Surveys 5.3 and 5.4).
[Box 6]

Box 6. The genetic code Enigma of Koonin and Novozhilov (2009)

"The existence of variant codes and the success of experiments on the incorporation of unnatural amino acids ... indicates that the genetic code has a degree of evolvability. However, all these deviations involve only a few codons, so in its main features, the structure of the code seems not to have changed through the entire history of life ... The existence of variant codes and the additional, experimentally revealed flexibility of the code ... presents a challenge to the frozen-accident view. Indeed, the fact that there seem to be ways to 'sneak in' changes to the standard code, and yet, the same limited modifications seem to have evolved independently in diverse lineages suggest that the code structure could be nonaccidental." (Koonin and Novozhilov, 2009, p. 101).

Note 2022: We can imagine a scene when a change of articulation "sneaked" into the inarticulate oral voices of the proto-man. The first possible articulate "word" was created; and completely by chance it made a connection with one of the things nearby. Then between the second word and the second thing, the third word and the third thing, and so on, until the formation of the proto-speech (language) with which the members of the cave and surrounding caves began to communicate. Analogously, we can imagine that in some prebiotic aggregation of molecules and macromolecules, some completely random non-chemical "event" interrupted the further "insertion" of molecules into the macromolecule. Any chemical entity (chemical "event", chemical reaction, etc.), due to the nature of chemistry, could not stop further chaining: either the chaining would continue to "infinity", or a "knot" would be formed, generated by a set of completely random chemical reactions. The a macromolecule, stopped in further "chaining", could have been the first possible candidate, capable of, together with its initial molecule in the chain, and the molecules between the two points, achieving reproduction, autopoiesis, or whatever else, seen through the eyes of Oparin, Haldane, Maturana and Varela or someone else.

Comment 2. The way Koonin and Novozhilov talk about variant codes (Box 6), and I about deviant codes (MMR, 2018a, Box 2), is actually, *mutatis mutandis*, one and the same way. From the potential source of the genetic code (PPAASS in Table 2, with a large degree of freedom), changes are generated during the evolution of organisms, which can "sneak" into the standard GC, with new balances and nuances of the number of particles within the AA molecule.

5. Formal determinations as the essence of the genetic semiotic process

In the previous Section 4.1, it was shown that in the mapping of PPAASS into Tables of Standard and Mitochondrial GC, the key relation is the establishment of a connection between chemical and non-chemical entities; variation of amino acid diversity, on the one hand, and events of *initiation* and *termination* of protein synthesis, on the other hand (*Proof of semiosis*

1)²⁷. And it was also shown that there is a strict correspondence between the number of codons in the genetic code and the number of isotopes in the chemical code (*Proof of semiosis 2*)²⁸

As we can see it is *per se* clear that none of the above does not represent a causal relationship, but they certainly represent the unity of the formal and the essential.²⁹ In such a state of affairs, it makes sense to look for other possible cases of such unity, which we do in the next two sections.

5.1. Determination by the Golden Mean

Already in our first work on the GC, published in an international peer review journal (Rakočević and Jokić, 1996), referring to the works of V. Shcherbak (1993, 1994) and A. Verkhovod (1994)³⁰, we presented in the very title that in the set of protein amino acids, there is a "synchronic determination with chemical characteristics, atom and nucleon number". It was a second way to express the existence of the unity of hemism and semiosis, because at that time it was not allowed to be said openly (cf. Section 2, first paragraph; and Additional Note in footnote 12). In further researches, working mostly alone and independently, I consistently implemented this idea in all my works.

Posmatramo Survey 2, gde pozicije sedam "zlatnih" aminokiselina slede iz determinacije Zlatnim presekom na šesto-bitnom binarnom drvetu; tako, kako je ovde pokazano u Survey 2.1 (MMR, 1998a, Figure 1 and Table 2). From Survey 2 follow cyclically dependent or linearly dependent distinction and classifications of amino acids; cyclically dependent as in Figure 1 (on the left), and linearly dependent as in Survey 3 and Displays 1 and 2. Both follow only on the condition that the order of the "golden" AAs is changed, so that it is in accordance with the two principles of Mendeleev, the principle of continuity and the principle of minimum change. The first and most important among all those system-arrangements is CIPS (Cyclic Invariant Periodic System: Figure 1, on the left), which is created "automatically", by the very act of "dictating" Mendeleev's principles.

²⁷ The question of the origin of life is the question of the origin of an independent unicellular organism – amoeboid and/or non-amoeboid. In both cases, the next question that arises is the synthesis of the basic (organic) cell builder. And, any builder in question, its creation (synthesis) is inevitably determined by *initiation* and *termination*. (Barbieri, 2008c, p. 29: "Semiosis not only is a fact of life but is the fact that allowed life to emerge from inanimate matter".)

²⁸ We say "correspondence" referring to the previously presented analogy of one and the other code (MMR, 2018b), but also to their possible unity, which future research should tell about.

²⁹ MMR, 2004a, Section 8, p. 233: "On the other hand, the existence of such a harmonic structure with unity of a determination with physical–chemical characteristics and atom and nucleon number at the same time appealed to Aristotle and to his idea of unity of form and essence."

³⁰ The main result of Shcherbak (determination of GC by the Pythagorean triple: 3–4–5) is now shown as a key connecting quantity-entity between the essential quantity-entities located in the last column of the Periodic System of Numbers (PSN); of the zeroth Boolean triangle (0-1-2) and the logical square (0-1-2-3), on the one hand, as well as with Plato's four (3-4-5-6), on the other. The main result of Verkhovod I incorporated in Figure 4, p. 37, in (MMR, 2018a).

And we can stop here already, because the evidence of semiosis, that is, the unity of chemism and semiosis, is more than obvious. First, the golden mean determination is not a causal relationship *per se*. By searching the set of all sciences known so far, the only place where one could find an understanding (and justification) of such a phenomenon – "mixing" of causal and non-causal relations – is *semiotics* (according to Peirce), that is, *semiology* (according to De Saussure). If that science did not exist, some new Pierces–Saussures would have to invent it. [*Proof of semiosis 3*: The facts about the determination of distinctions and classifications of AAs by the Golden mean can hardly be understood otherwise than as the presence of semiosis in GC.]

5.2. Determination by the diagonal of PSN

In Figure 1 (on the right) we find four quintets of amino acids with quantities of numbers 31, 41, 61, 71 also as number of atoms. Indirectly, we find two more pairs of non-alanine stereochemical type amino acids with 11 and 21 atoms, and in addition two and two columns of alanine-type of amino acids with 81 and 91 atoms, respectively. All together: 11, 21, 31, 41, (...),³¹ 61, 71, 81, 91 atoms in amino acid molecules; exactly as we find in the right diagonal within the PSN. [*Proof of semiosis 4*: It is immediately obvious that it is not possible to find causal reasons (from the aspect of physics and chemistry)³² for the fact that the number of atoms in the five quintets of a specific system-arrangement is such that it corresponds to the mirror image as shown in Table 1; *Proof of semiosis 5*: It would be pointless to look for causal reasons for the fact that a system-arrangement of AAs as shown in Figure 1 (on the right) is possible: to obtain the quantities of the number of atoms, such that, in all cases, the number 1 is at the end of each individual numerical record of the number of atoms, and that all this corresponds to the right diagonal of the Periodic System of Numbers.]

6. Cyclic and open structures

In completing the sample of works that had a synergistic impact on possible further researches were the works published in the following year after the work of R. Swanson (1984) was published; the work of R. Doolittle (1985) and the work of V. Sukhodolets (1985). R. Doolittle, inspired by R. Swanson's idea of the existence of a codon ring, presented an amino acid ring (Doolittle, 1985; MMR, 1988b, Fig. 33, p. 128) determined by the size and polarity of molecules, regardless of their position and order in the Standard Genetic Code Table (Doolittle,

³¹ We do not know why the quantity 51 does not appear as the number of atoms, but we can see that it alone has no corresponding pair member to complement up to 102, while all the remaining quantities are actually pair members within the set of four pairs that complement up to 102 atoms, which is otherwise half the number of atoms in twenty amino acids (204 atoms in their side chains). [(11 + 91 = 102), (21 + 81 = 102), (31 + 71 = 102), (41 + 61 = 102).]

³² In all the following examples concerning "Proof of semiosis" the immediate obviousness and aspects of physics and chemistry will go without saying.

1985).³³ On the other hand, in the same year, V. Sukhodolets (1985) presented a specific system-arrangement of amino acids, in a rectangular form (also independent of their position in GC Table), from the aspect of the number of hydrogen atoms that each amino acid individually possesses.

Remark 2: Unexpectedly, two amino acids that Doolittle previously (together with Kyte) (Kyte and Doolittle, 1982), on the hydropathy scale, marked as polar (proline and threonine), here, in the amino acid ring, he marked as non-polar (Doolittle, 1985; MMR, 1988b, Fig. 33, p. 128) (cf. Remark 4).

The Doolittle's amino acid ring was then an inspiration and a stimulus for me personally in wondering if a correspondent ring could be made while following the order of the amino acids in the Crick's Table of the Genetic Code.³⁴ Even more than that, will one such ring (Coding ring) be in correspondence with the Mutation ring (with the evolution of organisms), with the essentiality of amino acids and with Boolean spaces. The answer was positive and is presented in Preliminary 2 (MMR, 2021c, Figs A1–A4, pp. 16-19). [*Proof of semiosis 6:* It is not possible to find causal reasons for the fact that one half of the Mutation Ring contains amino acids belonging to Boolean space-3, and the other half to Boolean space-4; also, that one half contains non-essential amino acids and the other half essential and/or semi-essential ones³⁵; *Proof of semiosis 7:* It is not possible to find causal reasons for the fact that one (smaller) part of the Coding ring³⁶ contains amino acids belonging to Boolean space-3, and the other (larger) part to Boolean space-4.]

The Codon ring, the Mutation ring, the Coding ring, the Amino acid ring, represent, *mutatis mutandis*, cyclic structures, the cyclic arrangement of AAs based on their physico-chemical properties. On the other hand, the amino acid system-arrangement of V. Sukhodolets (1985) represents one rectangular structure, with two outer and two inner rows of 10 AAs each (Figure 2). Here, the unity of chemistry and semiosis is expressed through one specific homonymy of quantities. Quantities that we know to represent the number of neutrons (569) and the number of protons (686) in a set of 20 amino acids (in their side chains), appear here as quantities of the total number of nucleons (without distinction between protons and neutrons); namely: in two

³³ MMR, 2000, in Introduction: "Doolittle (1985, p. 76) has shown that a possible classification of protein amino acids must be 'based on the size of the amino acid's side chain and on the degree to which it is polarized'. ([arXiv:q-bio/0611004](https://arxiv.org/abs/q-bio/0611004) [q-bio.BM])

³⁴ I call the Table of the standard GC as Crick's Table because he was the first to give a complete elaboration of the genetic code in two of his works (Crick, 1966, 1968).

³⁵ MMR, 2021c (Preliminary 2: Figs A1, A2, A3, pp. 16-17): Space-3 in Boolean cube, B^3 . In Figure A1 we see a perfect system of essentiality, which is realized through the robustness of the "intruder", arginine (DOI [10.31219/osf.io/me8sj](https://doi.org/10.31219/osf.io/me8sj)) [See footnote 26 for why arginine is an "intruder".]

³⁶ MMR, 2021c (Preliminary 2: Fig. A1 in relation with Tab. A3): The following balance is observed. On the right side of the system-arrangement of essentiality, in Figure A1, there are 8 essential AAs, four in Boolean space-4, and four in space-3. There are a total of 102 atoms in their side chains. To the left of these are non-essential and semi-essential AAs, also with 102 atoms. The binary values of the codons, belonging to the amino acids, conditioned this strict distinction; which, of course, cannot be a causal relationship, but only a semiotic one.

outer rows (with 10 AAs) as the quantity of the number of neutrons, and in the two inner rows (also with 10 AAs) as the quantity of the number of protons.

This division of the number of nucleons is accompanied by the simultaneous division of the number of hydrogen atoms (also in two and two rows) into approximately two equal parts differing the least possible, by one atom (58/59). At the same time, it is shown that the total number of atoms in the entire molecule of all 20 protein amino acids, hydrogen atoms versus non-hydrogen atoms, is so great that it differs by one second-order unit (197 vs 187).

Given the fact that we find this division also as division of all atoms, and not just hydrogen atoms, in one other system-arrangements of 6 plus 5 AAs within the interspace of 23 AAs in Standard Table of GC [Solution (1)]³⁷, we can say that this fact of quantities homonymy is also an "indication" of semiosis and the proof of its presence (*Proof of semiosis 8*). Finally, the very space of the overall system-arrangement manifests itself as a semiotic signifier in the sense of De Saussure and Charles Pierce.³⁸ In one separate part of the space (shaded in Figure 2) there are AAs with even numbers of both nucleons and hydrogen atoms, and in the other (larger) part AAs with odd numbers of the quantities of mentioned particles (*Proof of semiosis 9*). [Also, the number of non-hydrogen atoms occurs with a change for one second-order unit (in relation to the hydrogen atom number), and two second-order units, respectively: 48 vs 58 and 39 vs 59.]³⁹

Remark 3: In Solution (1) there appears a "phantom" quantity⁴⁰, as a De Saussure's type of signifiers, originating from the three duplicated AAs (LSR 35) in the standard Table of GC. Here it is in the function of balancing and nuancing⁴¹ in determining the quantities 117 and 87 of the number of hydrogen and non-hydrogen atoms, respectively. And we also had it in the previous work when it (within the modified Rumer Table) enabled insight into the existence of a third "hidden" quantity, where all three (60, 66, 78) participate in the determination of GC by the golden mean (MMR, 2018a, Table 2B, p. 34).⁴²

³⁷ MMR, 2013a, Table 4: "In amino acids (within their side chains), in left/right areas [LIMADE / SYRSR] there are 369-33/369 nucleons and 58/59 atoms, respectively". [*Additional Note, 2022:* Within the outer/inner areas (FL+CW+V+G / P+T+HQ+NK) the division of the number of nucleons and atoms is 369/369 and 61/61, respectively.]

³⁸ The statement that "the very space of the overall system-arrangement manifests itself as a semiotic signifier" applies, *mutatis mutandis*, to all illustrations in Appendices A, B, C and, especially, to the illustrations in Appendix D.

³⁹ All of these listed changes for a first-order, second-order, third-order unit, separately and/or together, which we consistently carry out throughout the paper, are there to show the justification of the hypothesis of V. Shcherbak about analogies with quantum physics (1994). Indeed, all these regularities of nuancing and balancing of the number of particles, accompanied by changes in physical and chemical properties, are actually analogies with quantum physics. (Cf. footnote 4 and 12.)

⁴⁰ "Phantom pain is pain that feels like it is coming from a body part that is no longer there. Doctors once believed this post-amputation phenomenon was a psychological problem, but experts now recognize that these real sensations originate in the spinal cord and brain." <https://www.mayoclinic.org/diseases-conditions/phantom-pain/symptoms-causes/syc-20376272>

⁴¹ Nuancing and balancing explained in the previous work (MMR, 2018a, Definitions 1 and 2 on page 33).

⁴² In the modified Rumer's Table, the "phantom" quantity 35 appears in its entirety, although only two amino acids are present in the significant column (L and R from LSR). Here, in Solution (1), only one AA is present (L from LSR), and the quantity 35 as a whole. We have something similar in the determination of the molecules mass of

To the relationships presented in Figure 2, analogous relationships are found in Table 3, where the four types of diversity of AAs are represented. Within two "outer" areas (10 AAs) the number of atoms, in the whole molecules, is 180, which is a homonymous designation for the number of atoms in all 20 AAs, in their "heads". On the other hand, there are 204 atoms in the two inner ones (also 10 AAs), which is a homonymous designation for the number of atoms in all 20 AAs, in their "bodies". At the same time, it is shown that the total number of atoms in the entire molecule of all 20 protein amino acids, hydrogen atoms versus non-hydrogen atoms, is so much that it differs by one of the second-order unit (197 vs 187). [The relationships in Figure 2 and Table 3 support *Working hypothesis 1.*]

7. Minimum signifiers – maximum meanings

In Solutions (1) to (6), in relation to Figures 3 and 4, and Survey 5, we see how all the key distinctions of AAs, both in the Table of the Standard Genetic Code and outside the Table (from the aspect of physico-chemical properties: polarity / non-polarity of AAs), take place in relation to half the number of atoms in the side chains of 20 amino acids (102), and the division into the number of hydrogen (117) and non-hydrogen atoms (87). Based on what we know about Heraclitus' changes in nature, especially about the randomness of prebiotic chemical reactions as well as of randomness of mutations within living organisms, the only thing we can say is that this division has no causal basis, rather it is a pure semiotic occurrence (*Proof of semiosis 10*).

This happens both in the set of 23 [Solutions (1) to (4)] and in the set of 20 amino acids [Solutions (5) to (7)]. In Solution (5), the 20 protein amino acids are distinguished into polar, non-polar and semi-polar. There are 10 strictly polar; they are polar from both the hydrophathy aspect and the cloister energy aspect. There are seven strictly non-polar ones, and three more semi-polar ones are added here, which we can say are not polar. But in order to fully understand the polarity, non-polarity and semi-polarity of protein amino acids, it is necessary to first solve the puzzle posed by Russell F. Doolittle (Remark 2).

Independently of Russell F. Doolittle, two other authors, B. G. Konopelchenko and Yu. B. Rumer showed that proline can also be expressed as a non-polar amino acid. They reached this result by relating the polarity scale of amino acids C.R. Woese and the analogue scale of M. V. Volkenstein. [(Konopelchenko and Rumer, 1975, p. 474: M. V. Volkenstein, *Genetika*, N° 4, 119 (1966). C.R. Woese, D. H. Dugre et al., In: *Cold Spring Harbor Simp. Quant. Biol.*, v. 31, 723 (1966)].] This result of theirs allowed me to, in a previous paper (MMR, 2004a), resolve the issues of distinguishing polar and non-polar AAs, nuancing and balancing their properties in a harmonious system-arrangement (Tables D1 and D2).

AAs through the abundance of corresponding isotopes. Although only the first, the lightest isotope, with its abundance generally greater than 99%, participates in the molecules mass, nevertheless Table D1 shows us that the isotopic nuancing and balancing are such that it is as if all the remaining isotopes participate with 100% of their nucleons, as in reality is the case only with the first isotope. [Note: In the previous work, with the status of Preliminary 1 for this paper (MMR, 2021b, Tables 1 – 3), we showed that the integer number of the sum of molecules masses of protein amino acids is determined via the third perfect number, what is also a case of determination through the signifiers of the De Saussure's type.]

Apart from the aspect of polarity/non-polarity, proline proves to be unique in another interesting and significant way. Namely, it appears as one of the important determinants of p-adic properties of the genetic code (Dragovich and Dragovich, 2009, 2010; Dragovich and Mišić, 2019; Dragovich et al, 2021). It is that p-adic properties are most easily and best observed by comparing the standard genetic code and the vertebrate mitochondrial code; but, provided that they are viewed in the form of two tables: the Table of the classic presentation with phenylalanine in the starting position; and the Table, with proline in the starting position.⁴³ Only then is it noticed that this second Table shows full and complete symmetry. In other words, it turns out that the mitochondrial code is the most symmetrical in the set of genetic codes so far found; and that as such, apart on the symmetry, it also testifies to significant p-adic properties of all genetic codes.

If, in future researches, a semiotic analysis was to be included in these comparisons, it could be shown, according to our assumption, that for such a (possible) analysis, the important fact is that phenylalanine is a derivative of benzene (a very stable six-membered ring), the simplest compound in the class of aromatic hydrocarbons, arenes; and proline as derivative of cyclopropane (a very unstable three-membered ring), the simplest compound in the class of alicyclic hydrocarbons.

Remark 4: Even without measurement, it is immediately obvious, from the molecular structure itself, that four amino acids, in a set of 20 protein ones, are semi-polar (G, P, T, W). Glycine has a side chain of only one hydrogen atom, which is non-polar. However, from the fact that it directly binds to a polar amino acid functional group ("head" i.e. "standard block") its polarity follows; but both taken together give ambivalence, i.e. semi-polarity. As far as proline is concerned, it has three methylene groups responsible for non-polarity, but the fact that one such group binds to the polar amino group in the "head" of the amino acid indicates its ambivalence. Furthermore, threonine, despite being polar in terms of hydrophathy (Kyte and Doolittle, 1982) and cloister energy (Swanson, 1984), has a non-polar part in its structure. Namely, it is the only one of the 16 amino acids of the alanine stereochemical type where in the CH₂ "dividing screen" (placed between the head and body of the amino acid molecule)⁴⁴ one hydrogen atom is substituted by a non-polar CH₃ group. Finally, tryptophan is the only amino acid with two rings: a non-polar benzene ring and a polar pyrrole one. [Through the act of head-body binding, the proline molecule acquires the form of a pyrrolidine ring to which one carboxyl group is bound. It follows from this fact that proline has an NH group in the head, instead of NH₂. However, when calculating the number of atoms and nucleons in the proline molecule, everything must be reduced to a common general pattern. Hence, it is rightly assumed that there are 8 instead of 9 atoms in the side chain of proline.]⁴⁵

⁴³ Apart with the starting position, the relationship between these two Tables is determined by the entire "beginning – end" diagonal: [FL – (P – NK) – G] vs [P – (NK – FL) – G].

⁴⁴ In chemistry textbooks, the structural formula of threonine is written in such a way that it is not seen that the CH₃ group, as a substituent, is contained in the "screen" (which separates the head and body of the amino acid molecule). In other words, it does not take into account the fact that there are four stereochemical types of protein amino acids, without what the genetic code cannot be understood.

⁴⁵ "The only exception from the general structure of amino acids is provided by proline. It holds its own side chain with two bonds and has one less hydrogen inside the standard block. However, an imaginary borrowing of one nucleon from the proline side chain in favor of its block brings the block nucleon number to the standard 73 + 1 = 74, whereas the side chain nucleon number becomes 42 – 1 = 41" (shCherbak, 2008, p. 162).

The results presented in solutions (8) and (9) confirm our second working hypothesis on the separate and unified influence of single and double zeroth Boolean triangle (Survey 6 and 6.1). By this, the missing values $X = 6$, $Y = 2$ can be found in the original Crick's as well as original Rumer's Table (Table 4 and 5, respectively). The values corresponding to them, which we have already discussed in the previous work (MMR, 2018a, Comment 9 and Survey 2) can be found in Tables 6 and 7.

The results presented in solutions (10) and (11) were taken from Solutions 5 – 8 of the previous work (MMR, 2018a, p. 45) to be presented here in a slightly more sophisticated form; to present their connection with the space of the standard Table of GC (Figures 5 and 6) thus showing the presence of semiosis. If, namely, it can be shown that the distinction of polar/non-polar space on the one hand, and inner/outer space on the other hand, is such that it is determined by a change for the first and second order-unit, then this is nothing more than a confirmation, actually a fact, that the genetic code represents the unity of chemism and semiosis.

$$\begin{aligned} (\text{FL CW V G}) 61 + (\text{PT HQ NK}) 61 &= 122 \text{ [122 - (LSR 35) = 87]} \\ (\text{LIMADE}) 58 + (\text{SYRSR}) 59 &= 117 \text{ (MMR, 2013a, Tab. 3 and 4)} \end{aligned} \quad (1)$$

$$\begin{aligned} (\text{GFLPNK 59}) + (\text{VCWTHQ 63}) &= 122 \text{ (MMR, 2018a, Tab. 2B, p. 34)} \\ (\text{AYRIM 60}) + (\text{LSRSDE 57}) &= 117 \text{ (here: Survey 2)} \end{aligned} \quad (2)$$

$$\begin{aligned} (\text{FLLIMV}) 74 + (\text{CWRSRG}) 63 &= 137 \text{ [Outer columns in GC Table]} \\ (\text{SPTA 25}) + (\text{YHQNKDE 77}) &= 102 \text{ [Inner columns in GC Table]} \end{aligned} \quad (3)$$

$$\begin{aligned} (\text{FLSYCW}) 70 + (\text{VADEG 32}) &= 102 \text{ [Outer rows in GC Table]} \\ (\text{LPHQR 60}) + (\text{IMTNKSR 77}) &= 137 \text{ [Inner rows in GC Table]} \end{aligned} \quad (4)$$

$$\begin{aligned} (\text{KR-ST-DE-NQ-YH}) 107 \text{ (117 - 10)} &\text{ [They are polar]} \\ (\text{GP-AL-VI-CM-FW}) 97 \text{ (87+10)} &\text{ [They are not polar: non-polar + semi-polar]} \end{aligned} \quad (5)$$

$$\begin{aligned} (\text{GSYW ADMR EF}) 102 &\text{ [Four diversity types: above] (MMR, 2011a, Fig. 3)} \\ (\text{PHLK NQVI CT}) 102 &\text{ [Four diversity types: below in the mentioned Fig. 3]} \end{aligned} \quad (6)$$

$$\begin{aligned} (\text{GACMP SDTQH YMEVL}) 127 \text{ [117 + 10]} &\text{ [Four diversity types: left]} \\ (\text{WRFIK}) 77 \text{ [87 - 10]} &\text{ [Four diversity types: right in the mentioned Fig. 3]} \end{aligned} \quad (7)$$

$$\begin{aligned} \text{(n) } 2\text{F}+2\text{L}+4\text{L}+3\text{I}+1\text{M}+4\text{V}+4\text{A}+4\text{P}+2\text{C}+1\text{W}+4\text{G} &= 31 \text{ molecules; } \boxed{11} / \underline{10} \text{ AAs} \\ 28+26+52+39+11+40+16+32+32+10+18 +04 &= \mathbf{276} \text{ [2X6] atoms (X = 6, 7, 8)} \\ \text{(p) } 4\text{S}+4\text{T}+2\text{Y}+2\text{H}+2\text{Q}+2\text{N}+2\text{K}+2\text{D}+2\text{E}+4\text{R}+2\text{S}+2\text{R} &= 30 \text{ molecules; } \boxed{12} / \underline{10} \text{ AAs} \\ 20+32+30+ 22+ 22+ 16+ 30+ 14+ 20+68+10 +34 &= \mathbf{318} \text{ [3Y8] atoms} \end{aligned} \quad (8)$$

$$[6-7-8] - [0-1-2] = 6-6-6$$

$$\begin{aligned} \text{(n) } 2\text{F}+2\text{L}+4\text{L}+3\text{I}+1\text{M}+4\text{V}+4\text{A}+4\text{T}+4\text{P}+2\text{C}+1\text{W}+4\text{G} &= 35 \text{ molecules; } \boxed{12} / \underline{11} \text{ AAs} \\ 28+26+52+39+11+40+16+32+32+10+18 +04 &= \mathbf{308} \text{ [3Y8] atoms (Y = 0, 1, 2)} \end{aligned}$$

$$\text{(p) } 4\text{S}+2\text{Y}+2\text{H}+2\text{Q}+2\text{N}+2\text{K}+2\text{D}+2\text{E}+4\text{R}+2\text{S}+2\text{R} = 26 \text{ molecules; } \boxed{11} / \underline{9} \text{ AAs}$$

$$20+30+22+22+16+30+14+20+68+10+04+34 = \mathbf{286} [2X6] \text{ atoms} \quad (9)$$

$$(n) \mathbf{2F+2L+4L+3I+1M+4V+4A+2C} = 22 \text{ molecules; } \mathbf{8} / \mathbf{7} \text{ AAs}$$

$$28+26+52+39+11+40+16+10 = \mathbf{222} \text{ atoms } [420]$$

$$(o) \mathbf{3I+1M+4V+4A+2Y+4R+1W+2C} = 21 \text{ molecules; } \mathbf{8} / \mathbf{8} \text{ AAs}$$

$$39+11+40+16+30+68+18+10 = \mathbf{232} \text{ atoms } (421) \quad (10)$$

$$(p) \mathbf{4S+4P+4T+2Y+2H+2Q+2N+2K+2D+2E+1W+4R+2S+2R+4G} = 39 \text{ molec.; } \mathbf{15} / \mathbf{13} \text{ AAs}$$

$$20+32+32+30+22+22+16+30+14+20+18+68+10+34+04 = \mathbf{372} [723] \text{ atoms}$$

$$(i) \mathbf{2F+2L+4L+4S+4P+4T+2H+2Q+2N+2K+2D+2E+2S+2R+4G} = 40 \text{ molec.; } \mathbf{15} / \mathbf{13} \text{ AAs}$$

$$14+26+52+20+32+32+22+22+16+30+14+20+10+34+04 = \mathbf{362} (722) \text{ atoms} \quad (11)$$

$$(i) \mathbf{3I+1M+4V+4P+4T+4A+2Y+2H+2Q+2N+2K+2C+1W+4R} = \mathbf{37} \text{ molecules}$$

$$39+11+40+32+32+16+30+22+22+16+30+10+18+68 = \mathbf{386} (719) \text{ atoms}$$

$$(o) \mathbf{2F+2L+4L+4S+2S+2R+4G+2D+2E} = \mathbf{24} \text{ molecules}$$

$$28+26+52+20+10+34+04+14+20 = \mathbf{208} (424) \text{ atoms} \quad (12)$$

Explanation of Solutions (1) and (2)

In Solution (1), in the first row there are the AAs from the four corner squares of the Table of GC. At the same time, they are AAs from the first row of the upper and the first row of the lower quartet of Rumer's modified Table. AAs from the four central squares are added to them, which at the same time belong to the second row of both quartets of Rumer's modified table (MMR, 2013a, Tab. 3). In the second row of Solution (1), and both rows of Solution (2) are listed the possibilities of meaningful readings of the original and modified Rumer's Table, compared to the standard Table of the genetic code. In the original Rumer's Table, the corner and central squares are not observed separately, but together, as the left and right diagonals of the standard GC Table.

8. Relationships within SSAAPP (Similarity System of Amino Acid Perfect Pairs)

We look at Table 8. Near the top there are 10 AAs pairs with a strictly determined order based on chemical complexity. Analogous to the order of individual amino acids in Table 2 from the first to the 20th, here is the order from the first to the 10th pair. The only difference is that there the order is given based on chemical similarity (chemical properties and structure of molecules) and here it is given based on the complexity of amino acid molecules. Amino acids of alanine stereochemical type come first, and only then amino acids from non-alanine types (GV and PI).⁴⁶ Within the alanine type, AAs of lower diversity level come first: three less complex and then three more complex pairs (as in Segment III of Table 1). At the very end, there are four

⁴⁶ The pairs are the same as those found in Survey 2 (resulting from the Golden mean determination), except in the case of two carboxylic amino acids (carboxylic from the side chain aspect) and their amides: here each of the two carboxylic AAs is paired with its amide (DN, EQ).

chalcogen AAs (SC and TM) with a higher level of diversity due to the presence of sulfur (in two sulfur AAs, cysteine and methionine) from the third PSE period.

Each pair has its own column. In those columns, the pairs are repeated as many times as necessary to obtain a system-arrangement analogous to quantum physics, with the start of the quantitative state 111, analogous to Hund's half-filling of electronic orbitals in atoms. But, what is particularly interesting, and even more than that – particularly important, is the fact that significant⁴⁷ shading and balancing takes place not only in the number of atoms, but also in the sums of ordinal numbers by columns, those numbers that are, or that are not selected. (*Proof of semiosis 11.*)⁴⁸

When we say that in columns (of Table 8) "the pairs are repeated as many times as necessary", then it is not known whether that means a total coincidence and arbitrariness, or strict "intention". But just such a contradiction is what reflects the essence of language as such, be it natural spoken language, genetic language⁴⁹, or any other⁵⁰, whose essence De Saussure himself suggests to us:

"Si par rapport à l'idée qu'il représente, le signifiant apparaît comme librement choisi, en revanche, par rapport à la communauté linguistique qui l'emploie, il n'est pas libre, il est imposé. La masse sociale n'est point consultée, et le signifiant choisi par la langue, ne pourrait pas être remplacé par un autre. Ce fait, qui semble envelopper une contradiction, pourrait être appelé familièrement 'la carte forcée'. On dit à la langue: 'Choisissez!' mais on ajoute: 'Ce sera ce signe et non un autre.' Non seulement un individu serait incapable s'il le voulait, modifier en quoi que ce soit le choix qui a été fait, mais la masse elle-même ne peut exercer sa souveraineté sur un seul mot; elle est liée à la langue telle qu'elle est" (De Saussure, 1985, p. 104).

The citing this quote from De Saussure (1985, p. 104), besides being done because of the said contradiction contained in languages as semiotic systems, is also related to an even more significant issue, the problem of a possible *Perfect genetic code* (Box 2).⁵¹ One should connect

⁴⁷ The sums of selected and/or unselected ordinal numbers of amino acid pairs that, according to some rule, correspond to the sums of the number of atoms (or other particles) are significant; and in addition, both sums correspond to chemical distinctions and/or classifications of amino acid molecules.

⁴⁸ Of course, there is more evidence in the paper, but we will not list them further. The reader will determine them himself, if they really are the Proofs.

⁴⁹ MMR, 1988b, p. 4: "The founder of structural linguistics, Ferdinand de Saussure, as early as 1908 said everything about the universal in language, whether natural speech language, or language in other sign systems; even about the interdependence of language units ... By genetic language we mean the system of nucleotide sequences in nucleic acids and a system of amino acid sequences in proteins."

⁵⁰ De Saussure, 1985, p. 33: "On peut donc concevoir *une science qui étudie la vie des signes* ...; nous la nommerons *sémiologie*. Elle nous apprendrait en quoi consistent les signes, quelles lois les régissent. ... La linguistique n'est pas qu'une partie de cette science générale, les lois que découvrira la sémiologie seront applicables à la linguistique, et celle-ci se trouvera ainsi rattachée à un domaine bien défini ..."

⁵¹ MMR, 2021a, Section 7, p. 7: "Based on the principles of similarity and self-similarity ... there is no other organic molecule whose functional groups best reflect the chemical content of the 'Island of life' [in PSE] (carbon, nitrogen, oxygen, hydrogen, C, N, O, H) (Box 15)"; MMR, 2021a, Box 15, p. 37: "The facts we present in this paper on the

De Saussure's views with R. Swanson's views on a possible perfect genetic code and test the SSAAP presented in Table 8. Even at first glance it becomes clear that both are right: there is a perfect genetic code, just as we find it (in Table 8), which reflects the analogy with half-filled and filled quantum levels in atoms. At the same time, the perfection is such that no individual-researcher, or community ("mass") of researchers, can change anything.

9. Concluding remarks

In addition to the nucleotide, the second component of the genetic code are the 20 protein AAs, whose essential characteristic, chirality, is considered in current science only from the aspect of asking why only their left enantiomers were "selected" and not the right ones; or, why not both? The question of polarized light and mirror symmetry, determinants of enantiomerism, has not been considered from a possible wider aspect, and biological significance. And then, independently, papers were published on exactly those two topics. First, it was shown that there is hyperpolarized light with a great biological and biomedical impact (Koruga, 2017, 2018). It was then shown that, in addition to the mirror symmetry of amino acid molecules, there is also mirror symmetry of the number of atoms in subsets of 20 standard protein AAs (MMR, 2018a, b; 2019, 2021b, c).

In this paper, however, we show that the mirror images of the number of atoms are actually semiotic signifiers (signifiers of the signified), in the sense of understanding semiotics/semiology according to Charles Sanders Peirce and Ferdinand de Saussure. In doing so, the procedure of showing and proving is as follows. By the theoretical analysis of the physico-chemical properties of protein AAs is first generated PPAASS (Perfect Protein Amino Acid Similarity System): GAVPILKRQE / NDSTCMFYWH, and then the significant crossing procedure is approached. A 6-bit binary tree of GC, its path of greatest change (101010), is crossed with a double zeroth Boolean triangle, enlarged by its own mirror image, with superposition at the "touch" point of the original and the mirror image (00-11-22-11- 00).

The result of crossing is unique, but visible only after applying additional "hidden" procedures. The original binary record is taken as two numbers (101 and 010) (5 and 2), so the smaller number is added three times and the larger number twice to the extended Boolean triangle, resulting in (02-13-24-16-05). The mirror images of the obtained two-digit numbers fully correspond to the number of atoms in five quartets of the PPAASS arrangement (in side chains of 20 AAs molecules): GAND 20, VPST 31, ILCM 42, KRFY 61, QEWH 50.

As a second manner, the double zeroth Boolean triangle is added to the single one (00-11-22 + 2-1-0), and the obtained result (02-12-22) is put in relation to the number of atoms (in 61 AK molecules: 330 and 264), in the rows of the modified Crick's Table of GC (MMR, 2004a, Table 3a, p. 224) (Table 6 in this paper) and in the columns of the modified Rumer's Table (MMR,

existence of the 'Island of Life' in PSE, in the space of the first (and simplest) non-metal elements, are a prerequisite for a possible deeper elaboration of the idea on life as such, anywhere in the Universe to exist, must be based on Glycine. (From 'selection pressure' of the Periodic System results a 'Glycine Life'.)" DOI [10.31219/osf.io/bpqtz](https://doi.org/10.31219/osf.io/bpqtz)

2018a, Table 2B, p. 34) (Table 7 in this paper) : $330 - 02 = 328$; $330 - 12 = 318$; $330 - 22 = 308$, i.e. $264 + 02 = 266$; $264 + 12 = 276$; $264 + 22 = 286$. The obtained results represent the number of atoms in columns and rows within the two remaining significant GC Tables: the original Crick's Table (Table 4 in this paper) and the original Rumer Table (Table 5 in this paper); as well as in some significant classes of amino acids. (Cf. Solutions 8 and 9; Surveys 5.2; 7 and 7.1; Tables 8 and 9.) [Generally speaking, both mentioned research approaches (polarized light and mirror symmetry, respectively) correlate with holistic approaches in science (Raković et al, 2011).]

*

Just as we can never know why the protolanguage of any group of human terrestrial languages was formed by the words it was formed from, and not by some other and different one, so we will never be able to know why the constituents of the terrestrial genetic code were chosen to allow the generation of such a system-arrangement that manifests itself as an image of a mirror image – in the manner and process presented in Table 1. The only thing we can find out are the facts that confirm that this is so, in the case of the terrestrial genetic code.

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TABLES

Table 1. Generating of Genetic code as an "image of mirror image"

I	$[(010 101) \text{ as } (2 5)]; [(3 \times \underline{2} \text{ and } 2 \times \underline{5}):$ $00-11-22 22-11-00 \rightarrow 00-11-22-11-00 \rightarrow$ $\rightarrow 02, 13, 24, 16, 05$	
II	$[(1G 01 + 2A 04) + (11N 08 + 12D 07)] = 20 02$ $[(3V 10 + 4P 08) + (13S 05 + 14T 08)] = 31 13$ $[(5I 13 + 6L 13) + (15C 05 + 16M 11)] = 42 24$ $[(7K 15 + 8R 17) + (17F14 + 18Y 15)] = 61 16$ $[(9Q 11+10E 10) + (19W18 + 20H 11)] = 50 05$ $(51 \pm 1) \qquad \qquad \qquad (51 \pm 1)$	
III	Alanine stereochem. type: less complex: AL, KR, FY more complex: DE, NQ, HW middle complex: SC, TM	Non-alanine st. types: less complex: G more complex: P middle complex: V-I

Explanation of area I: Crossing the 6-bit binary tree of GC (MMR, 1998a, Fig. 1), its path of the largest change (101010), with a double zeroth Boolean triangle (taken from the last column of PSN), with superposition at the "touch" point of the original and the mirror image (00-11-22-11-00) gives unique results. Original binary notation (101010) is taken as two numbers (101 and 010) (5 and 2), so the smaller number is added three times, and the larger one twice, resulting in (02-13-24-16-05). The mirror image of the obtained two-digit numbers fully corresponds to the number of atoms in the five quartets of the PPAASS arrangement (in side chains of 20 AK molecules): GAND 20, VPST 31, ILCM 42, KRFY 61, QEWH 50, as it is shown in area II. [The number of atoms, as mirror images, appear to be semiotic *signifiers* of the physico-chemical properties of amino acids, which appear as signified; both notions in the sense of understanding the semiotics/semiology, according to Charles Sanders Peirce and Ferdinand de Saussure.] *Explanation of area II:* Five amino acid quartets, taken from the PPAASS arrangement, presented in Table 2. The ordinal number of amino acid is listed in the index, and the number of atoms is given to the right of the amino acid label. At the very bottom, the number of atoms in the two decades of the PPAASS arrangement is indicated. *Explanation of area III:* The classification of amino acids, resulting from the determination of amino acid positions on the six-bit binary tree. [The Golden mean as De Saussurean *signifier*, and the physico-chemical properties of amino acids as *signified*.] (Cf. the right side of Survey 3.)

Table 2. The order within Perfect Protein Amino Acid Similarity System (PPAASS)

(1)	G	01	58	N	(11)
(2)	A	15	59	D	(12)
(3)	V	43	31	S	(13)
(4)	P	41	45	T	(14)
(5)	I	57	47	C	(15)
(6)	L	57	75	M	(16)
(7)	K	72	91	F	(17)
(8)	R	100	107	Y	(18)
(9)	Q	72	130	W	(19)
(10)	E	73	81	H	(20)
		157		240	(614)
		374		484	(641)
		531		724	

The perfection follows from the interrelationship of amino acids, as shown in Box 3. Compared to the original (MMR, 2019, Tab. 2, p. 14), where the number of atoms in the amino acid side chain is given, here that is the number of nucleons. Some calculation: $724 - 614 = 110$ ($111 - 1$); $641 - 531 = 110$ ($111 - 1$). First decade: odd / even positions: 245 / 286; second decade: odd / even positions: 357 / 367 ($245 + 367 = 111 + 1$) ($286 + 357 = 641 + 2$) ($367 - 357 = 11$). Semiotic relations, as "quantities stacking" [(1:9), (2:8), (3:7) ...] are shown in Appendix A.

Table 2.1. Relationships in PPAASS (I)

(1)	G	01	58	N	(11)	133
(2)	A	15	59	D	(12)	
(3)	V	43	31	S	(13)	160
(4)	P	41	45	T	(14)	
(5)	I	57	47	C	(15)	236
(6)	L	57	75	M	(16)	
(7)	K	72	91	F	(17)	370
(8)	R	100	107	Y	(18)	
(9)	Q	72	130	W	(19)	356
(10)	E	73	81	H	(20)	
		531			724	
				530 /	725	

Shaded areas correspond to the first, third and fifth rows, and unshaded to the second and fourth in Table 1. The rectangular boxed areas represent the changes for the 3rd, 2nd and 1st order-unit, respectively, as we find in the 2nd and 6th areas in Table A1, related to Table A2. The uniqueness of proline and threonine is presented in the Solutions (8) and (9) and in Remark 4.

Table 2.2. Relationships in PPAASS (II)

on		an	pn		pn	an		on
(1)	G	01	01		31	08	N	(11)
(2)	A	04	09		31	07	D	(12)
(3)	V	10	25		17	05	S	(13)
(4)	P	08	23		25	08	T	(14)
(5)	I	13	33		25	05	C	(15)
(6)	L	13	33		41	11	M	(16)
(7)	K	15	41		49	14	F	(17)
(8)	R	17	55		57	15	Y	(18)
(9)	Q	11	39		69	18	W	(19)
(10)	E	10	39		43	11	H	(20)
<u>055</u>		102	<u>298</u>		<u>388</u>	102		<u>155</u>
$\text{on} + \text{an} + \text{pn} = 210 + 204 + 686 = 1100$								
Odd / Odd:								
[GVIKQ: $25 + 50 + 139 = 214$ / NSCFW: $75 + 50 + 191 = 316$] → <u>530</u>								
Lst / Fst:								
[LKRQE: $40 + 66 + 207 = 313$ / NDSTC: $65 + 33 + 129 = 227$] → <u>540</u>								
Fst / Lst:								
[GAVPI: $15 + 36 + 91 = 142$ / MFYWH: $90 + 69 + 259 = 418$] → <u>560</u>								
Evn / Evn:								
[APLRE: $30 + 52 + 159 = 241$ / DTMYH: $80 + 52 + 197 = 329$] → <u>570</u>								
<u>910</u> (10 x 220) <u>1290</u>								
(1290 – 910 = 2 x 190)								

Summations of ordinal number, number of atoms and number of protons. The system-arrangement is directly corresponding to the system-arrangement in Table B5, and indirectly with the system-arrangement on the right side of Figure 1 (530 vs 031 etc.).

Table 2.3. Data for Table 2.2

	G	A	V	P	I	L	K	R	Q	E	
on	1	2	3	4	5	6	7	8	9	10	55
an	1	4	10	8	13	13	15	17	11	10	102
pn	1	9	25	23	33	33	41	55	39	39	298
all	3	15	38	35	51	52	63	80	59	59	455
	N	D	S	T	C	M	F	Y	W	H	
on	11	12	13	14	15	16	17	18	19	20	155
an	8	7	5	8	5	11	14	15	18	11	102
pn	31	31	17	25	25	41	49	57	69	43	388
all	50	50	35	47	45	68	80	90	106	74	645
<p>(55 + 155 = 210) (102 + 102 = 204) (298 + 388 = 686 [686 + 569 = 1255] [210 + 204 + 686 = 1100 = 5 x 220]</p> <p>(645 - 455 = 190) (388 - 298 = 90) (102 - 102 = 00) (155 - 55 = 100)</p> <p>(Cf. results 910 and 1290 in last row of Table 2.2.)</p>											

Designations as in Table 2.2; on: ordinal number; an: atom number; pn: proton number.

Table 3. Four types of diversity of protein amino acids

G ₀₅ P ₀₉	A ₀₇ L ₁₃ V ₁₁ I ₁₃	C ₀₇ M ₁₁ F ₁₁ Y ₁₁ W ₁₂ H ₀₉	R ₁₄ K ₁₄ Q ₁₀ N ₀₈ E ₀₉ D ₀₇ T ₀₉ S ₀₇
01 08	04 13 10 01	05 11 14 15 18 11	17 15 11 08 10 07 08 05
10 17	13 22 19 22	14 20 23 24 27 20	26 24 20 17 19 16 17 14
14/27/13	44 / 76 / 32	61 / 128 / 67	78 / 153 / 75
(27+153 = 180) (76+128 = 204)			
(14+78 = 92) / (44+61 = 105) → 197 Hydrogen atoms (13+75 = 88) / (32+67 = 99) → 187 Non-hydrogen atoms			

MMR, 2018b, Solution 4, p. 297: "Within four diversity types of 2-4-6-8 AAs there is the number of atoms as follows. Within four standard hydrocarbon AAs there are 76 atoms; in two non-standard are 27 atoms; in eight AAs with 'mapping' functional groups from the head to the body there are 153 atoms; in the six AAs without the 'mapping' are 128 atoms. And then a balance: in two inner groups (with 10 AAs) there are 204 atoms as in 20 AAs side chains. On the other hand, in two outer groups (also with 10 AAs) there are 180 atoms as in 20 AAs heads." [Additional Note 1 (2022): In the fourth group, arginine is an "intruder" because its mapped amino group is located within the bulky guanidino group. (Cf. footnote 26); Additional Note 2: In the first row, the designations of AAs with the number of hydrogen atoms in the index. In the second row, the number of atoms in the side chain of AA. In the third row, the total number of atoms in the amino acid molecule; Additional Note 3: Number of coding codons for AAs, by types: I (8), II (17), III (10), IV (26); another variant for type III and IV: shaded (chalcogen) AAs with 13 and the remaining with 23 codons. (The existence of chalcogen AAs as an independent system see in Figure 1 and Display 2). The remaining AAs in type III are aromatic AAs; in type IV: four electric charged AAs, basic K-R and acidic D-E, plus two carboxyl group derivatives, amides N-Q. (Amides are related to two bases through the amino group, which explains why bases do not have derivatives of their own; they do not have because the effect of the principle of self-similarity alone is fully realized by this relation).]

Table 4. The original Crick’s Table in a new arrangement-form

1 st	2nd letter				3 rd		
	U	C	A	G			
U	UUU F	UCU S	UAU Y	UGU C	U C A G	132	328
	UUC F	UCC S	UAC Y	UGC C			
	UUA L	UCA S	UAA *	UGA *			
	UUG L	UCG S	UAG *	UGG W			
	54	20	30	28			
C	CUU L	CCU P	CAU H	CGU R	U C A G	196	
	CUC L	CCC P	CAC H	CGC R			
	CUA L	CCA P	CAA Q	CGA R			
	CUG L	CCG P	CAG Q	CGG R			
	52	32	44	68			
A	AUU I	ACU T	AAU N	AGU S	U C A G	172	
	AUC I	ACC T	AAC N	AGC S			
	AUA I	ACA T	AAA K	AGA R			
	AUG M	ACG T	AAG K	AGG R			
	50	32	46	44			
G	GUU V	GCU A	GAU D	GGU G	U C A G	94	266
	GUC V	GCC A	GAC D	GGC G			
	GUA V	GCA A	GAA E	GGA G			
	GUG V	GCG A	GAG E	GGG G			
	40	16	34	04			
	196	100	154	144			
	296		298				

Table 5. The original Rumer's Table in a new arrangement-form

I-II			I-II				
GG	GGGG	36	UU	FLL	98	134	276
AC	TTTT		CA	HHQQ			
CC	PPPP	72	AA	NNKK	74	146	318
GU	VVVV		UG	CC*W			
CG	RRRR	88	AU	IIM	84	172	
UC	SSSS		GA	DDEE			
GC	AAAA	68	UA	YY**	74	142	
CU	LLLL		AG	SSRR			
264			330			594	
<p>[264 = (8 x 33) ± 0] [330 = (10 x 33) ± 0] [296 = (9 x 33) - 1] [298 = (9 x 33) + 1]</p>							

Table 6. The modified Crick's Table in a new arrangement-form

I-III	II = Py		I-III	II = Pu			
Py-Py	FLL SSPP	80	Py-Py	YYHH CCRR	96	176	330
Py-Pu	LLL SSPP	78	Py-Pu	**QQ *WRR	74	152	264
Pu-Py	IIVV TTAA	70	Pu-Py	NNDD SSGG	42	112	
Pu-Pu	IMVV TTAA	68	Pu-Pu	KKEE RRGG	86	154	
		296			298	594	
<p>[264 = (8 x 33) ± 0] [330 = (10 x 33) ± 0] [296 = (9 x 33) - 1] [298 = (9 x 33) + 1]</p>							

Table 7. The modified Rumer's Table in a new arrangement-form

I-II			I-II						
GG	GGGG	44	UU	FLL	82	126	298		
GU	VVVV		UG	CC*W					
CC	PPPP	<i>64</i>	AA	NNKK	<i>90</i>	<i>154</i>			
AC	TTTT		CA	HHQQ					
GC	AAAA	<i>68</i>	UA	YY**	<i>74</i>	<i>142</i>			296
CU	LLLL		AG	SSRR					
CG	RRRR	88	AU	IIM	84	172			
UC	SSSS		GA	DDEE					
264			330			594			
<p>[264 = (8 x 33) ± 0] [330 = (10 x 33) ± 0] [296 = (9 x 33) - 1] [298 = (9 x 33) + 1]</p>									

Table 7.1. Interrelationships of AAs and the number of atoms in their side chains, according to Tables 4 – 7 (I)

From Rumer's modif. Table ("264")	From Crick's modif. Table ("264")	From Rumer's modif. Table ("330")	From Crick's modif. Table ("330")
<u>GG</u> <i>GG</i> <u>VV</u> <i>VV</i>	<i>LLL</i> <i>SSPP</i>	<i>FF LL</i> <i>CC * W</i>	<i>FF LL</i> <i>SS PP</i>
<u>PP</u> <i>PP</i> <u>TT</u> <i>TT</i>	<u>II</u> <i>VV</i> <i>TTAA</i>	<u>NN</u> <i>KK</i> <i>HH QQ</i>	<i>KK EE</i> <u>RR</u> <u>GG</u>
<u>AA</u> <i>AA</i> <i>LLL</i>	** <u>QQ</u> <i>*W RR</i>	<i>YY **</i> <i>SS RR</i>	<i>YY HH</i> <i>CC RR</i>
<u>RR</u> <i>RR</i> <i>SSSS</i>	<u>NN</u> <u>DD</u> <i>SSGG</i>	<u>II</u> <i>IM</i> <u>DD</u> <i>EE</i>	<i>IM VV</i> <u>TT</u> <u>AA</u>
----- 96 / 168	----- 96 / 168 (264)	----- 96 / 234	----- 96 / 234 (330)
2 x 48 / 84 x 2 234 – 168 = 66		234 – 96 = 60 + 78	

Table 7.2. Interrelationships of AAs and the number of atoms in their side chains, according to Tables 4 – 7 (II)

$2 \times 12 / 21 \times 2$ $(1 \times 24 / 42 \times 1) [+ 18]$	$42 + 12 = 54$ $54 + 12 = 66$	$54 \times 2 = 108$
$2 \times 24 / 42 \times 2$ $(1 \times 48 / 84 \times 1) [+ 36]$	$84 + 24 = 108$ $108 + 24 = 132$	$108 \times 2 = 216$
$2 \times 48 / 84 \times 2$ $(1 \times 96 / 168 \times 1) [+ 72]$	$168 + 48 = 216$ $216 + 48 = \boxed{264}$	$216 \times 2 = \underline{\underline{432}}$
$2 \times 96 / 69 \times 2$ $(1 \times 192 / 138 \times 1) [- 54]$	$138 + 96 = \underline{\underline{234}}$ $234 + 96 = \boxed{330}$	$234 \times 2 = 468$ $468 = 496 - 28$

On the left: Multiplication of the number 12 within the arithmetical logical square, according to (MMR, 1994, p. 235).

Table 7.3. Interrelationships of AAs and the number of atoms in their side chains, according to Tables 4 – 7 (III)

$(66 = 2 \times 33), (132 = 4 \times 33), (264 = \underline{8} \times 33), (330 = \underline{10} \times 33)$ $\text{033} \text{330}$ $264 + 330 = 594 = 297 \times 2 [297 = \underline{9} \times 33]$ $234 + 432 = 666$	
$18 = 2 \times 9$ $36 = 4 \times 9$ $54 = 6 \times 9$ $72 = 8 \times 9$	$6 + 7 = 13$ $66 + 77 = 143$ $666 + 777 = 1443$ $13 \times 777 = 10101$ $13 \times 666 = 8658$
$10101 = 273 \times 37$ $8658 = 234 \times 37$ $8658 : 6 = 1443$	$10101 - 8658 = 1443$

Table 8. The order within the System of Amino Acid Pairs (SAAP)
based on chemical complexity

1	2	3	4	5	6	7	8	9	10			
AL	KR	FY	DN	EQ	HW	SC	TM	GV	PI	→	204	
AL	2	FY	DN	EQ	HW	7	8	9	10	→	111	19 / 36
											11	
1	KR	FY	4	EQ	6	7	TM	GV	PI	→	122	37 / 18
											11	
AL	KR	FY	DN	EQ	HW	7	8	9	10	→	133	21 / 34
											10	
AL	2	FY	DN	EQ	6	SC	TM	GV	10	→	144-1	37 / 18
												220
3/1	4/4	12/0	12/4	20/0	12/12	7/21	16/16	18/18	10/30		233/276 509	114/106 220
											odd (233+11) / (276 - 11) even	
↓ [51	(64	116)	↓ 45]	84	↓ 58	↓ 10	38	↓ 22	↓ 21			
$51+64+116+45 = 276) / [84 + 58 + 10 + 38 + 22 + 21 = 233]$ $(51 + 45 = \underline{133} - 37) (64 + 116 = \underline{143} + 37) [58+10 +22+ 21 = \underline{111}] [\underline{84} + \underline{38} = \underline{122}]$												
Columns: odd (60 / 40) (54 / 66) even → (110 - 10) [110 + 10] Rows: odd (40 / 70) (74 / 36) even → (110) [110]												
$233 + 276 = (2 \times \mathbf{204}) + 0101 [0101 + 1010 = 1111] [1111 - 01 = 1110]$ $[(1110, \text{as the number of nucleons in 15 AAs (Shcherbak, 1994)}]$ $233 + 276 = 255 + 254 [233 = 255 - 022; 276 = 254 + 022] [022 / \mathbf{220}]$												

Table 8.1. The relationships of selection / non-selection of ordinal numbers in SAAP

Columns				Rows			
Odd		Even		Odd		Even	
yes	no	yes	no	yes	no	yes	no
60	40	54	66	40	70	74	36
	<u>20</u> →	-----		←	<u>30</u>		
		54	→	<u>20</u>	←	74	
			66	→	<u>30</u>	←	36

The ratio 30:20 as 3:2, in correspondence with Golden Mean. (Moore, 2004, p. 211: "Our concern here is the study of the sequence {gn} of 'golden numbers'. A computer analysis of this sequence of roots indicated that the odd-indexed subsequence of {gn} was monotonically increasing and convergent to 3/2 from below, while the even-indexed subsequence was monotonically decreasing and convergent to 3/2 from above".)

Table 9. The selection of amino acid pairs through ordinal number in SAAP

VII	(1 SC) ₁₀	X	(1 PI) ₂₁	<i>17</i>	31
II	(2 KR) ₆₄	VI	(2 HW) ₅₈	25	182
VIII	(2 TM) ₃₈	IX	(2 GV) ₂₂		
I	(3 AL) ₅₁	IV	(3 DN) ₄₅	<i>05</i>	96
III	(4 FY) ₁₁₆	V	(4 EQ) ₈₄	<i>08</i>	200
<i>21</i>		<i>34</i>		<i>55</i>	<i>509</i>
[509 = 233 + 276] [(233 = 231 + 2); 276 = 278 - 2]					
(a) 1, 2, 3 (a) 7, 8		(b) 4, 5, 6 (b) 9, 10		509 = 408 + 0101 408 = 204 x 2	
<i>17 + 08 = 25</i> <i>25 + 05 = 30</i>			31 + 200 = 231 (out) 182 + 96 = 278 (in)		
(a) → <i>21</i> (b) → <i>34</i>			(a) 279 (left) (b) 230 (right)		
<i>30 - 21 = 9</i> ["0"] <i>34 - 25 = 9</i> ["0"]			279 - 278 = 1 231 - 230 = 1		

The ordinal numbers as Roman numbers.

The result 21, 34, 55 as a unique Fibonacci sequence.

Table 9.1. The uniqueness of the Fibonacci sequence: 21, 34, 55

...					<p style="text-align: center;">...</p> <p style="text-align: center;">(21 - 4 = 17) (34 : 2 = 17)</p> <p style="text-align: center;">(21 - 4 = 17) (34 : 2 = 17)</p> <p style="text-align: center;">(34 : 2 = 17) (55 - 4 = 51)</p> <p style="text-align: center;">(51 = 3 x 17)</p> <p style="text-align: center;">On the determination of the genetic code with quantities 17, 34 and 51, see in (MMR, 2021a, Surveys 1 - 3)</p> <p style="text-align: center;">...</p>
05	:	08	=	5 / 8	
08	:	13	=	8 / 4	
13	:	21	=	4 / 3	
21	:	34	=	3 / 7	
21	:	34	=	3 / 7	
34	:	55	=	7 / 1	
55	:	89	=	1 / 8	
89	:	144	=	8 / 9	
...					

Figures

5	F₁₄	Y₁₅	S ₀₅	T₀₈	L ₁₃	A ₀₄	G ₀₁	031	
4	L ₁₃	A ₀₄	D ₀₇	E ₁₀	M ₁₁	C₀₅	P ₀₈	041	
3	Q₁₁	N₀₈	K ₁₅	R ₁₇	Q ₁₁	N ₀₈	V ₁₀	061	
2	P ₀₈	I ₁₃	F ₁₄	Y ₁₅	W ₁₈	H ₁₁	I ₁₃	071	
1	T₀₈	M₁₁	103						204
1	S₀₅	C₀₅	91			81	GV	11	
2	G ₀₁	V ₁₀					PI	21	
3	D₀₇	E₁₀	S ₀₅	T ₀₈				32	
4	K ₁₅	R ₁₇	D ₀₇	E ₁₀	M ₁₁	C ₀₅			
5	H₁₁	W₁₈					Q ₁₁	N ₀₈	
$(\text{GSTPQLF } \mathbf{60})_7 + (\text{VCMINAY } \mathbf{66})_7 + (\text{DE KR HW } \mathbf{78})_6 = 204$ $[66 - 60 = (\mathbf{1} \times 6)] [78 - 66 = (\mathbf{2} \times 6)] [78 - 60 = (\mathbf{3} \times 6)]$									

Figure 1. From (MMR, 2019, Figure 1, p. 6) with further elaboration. The left illustration: Cyclic Invariant Periodic System (CIPS) of canonical AAs, with the number of atoms in the side chain: in the middle area there are chalcogen AAs (S, T & C, M); follow in next cycle the AAs of non-alanine stereochemical types (G, P & V, I); then two double acidic AAs with two their amide derivatives (D, E & N, Q); follow two original aliphatic AAs with two amine derivatives (A, L & K, R); and, finally, four aromatic AAs (F, Y & H, W) – two up and two down. The mentioned five classes belong to two superclasses: primary superclass in light areas and secondary superclass in dark areas. (Further classification of CIPS in Appendix C.). The right illustration as in legend of Figure 9, p. 834 in: MMR, 2011. [Cf. the right diagonal of PSN in: MMR, 2019, Fig. A1, p.28.]

G ₀₁ 01	A ₀₃ 15	S ₀₃ 31	D ₀₃ 59	C ₀₃ 47	(13)	153	(59 / 58) 569 / 686 39 / 48
N₀₄ 58	P ₀₅ 41	T ₀₅ 45	E ₀₅ 73	H ₀₅ 81	(24)	298	
Q₀₆ 72	V ₀₇ 43	F ₀₇ 91	M ₀₇ 75	Y ₀₇ 107	(34)	388	
W₀₈ 130	R₁₀ 100	K₁₀ 72	I ₀₉ 57	L ₀₉ 57	(46)	416	
(569 / 686) as neutron / proton number				04 + 06 + 08 + 10 + 10 = 38			
569 – 59 = 627 – 117 [117 x 2 = 234 / 432]				117 – 38 = 79			
686 – 58 = 628 [432 = 58+72+130+100+72]							
[(59 + 40 = 99 / 58 + 40 = 98)] [(39 + 50 = 89 / 48 + 50 = 98)]							204
[(99 + 98) (89 + 98) → 197 H & 187 non-H] [384 total]							180
							↓
							384

Figure 2. MMR, 2011, Table 7, p. 830: "The Sukhodolets' system of amino acids in a 4 x 5 arrangement. The Sukhodolets' Table, with a minimal modification (Sukhodolets, 1985): the system of 4 x 5 AAs. The shadow space: AAs with even number of hydrogen atoms (4, 6, 8, 10); the non-shadow space: AAs with odd number of hydrogen atoms (1, 3, 7, 9, 11). In brackets [in index]: number of hydrogen atoms and out of brackets [out of index] the number of nucleons. Nucleon number through a specific 'simulation': 569 within two outer rows, as the number of neutrons, 569, in all 20 AAs – within their side chains; and 686 nucleons within two inner rows, as the number of protons, 686, in all 20 AAs – within their side chains. [The 'simulation' as a holistic information within a part about the whole? (Rakočević, 2011b).] Within 20 side chains of amino acid molecules there are 569 neutrons as well as 569 non-hydrogen protons. Within 20 side chains of amino acid molecules there are 117 hydrogen protons, what means 117 hydrogen atoms at the same time (117 = 59 + 58)." [Additional Note, 2022: In relation to the original, several new calculations and elaborations have been added, the meaning of which is clear when compared.]

1st	2nd letter								3rd
	U		C		A		G		
U	UUU UUC UUA UUG	F ₁₄ L ₁₃	UCU UCC UCA UCG	S ₀₅	UAU UAC UAA UAG	Y ₁₅ CT	UGU UGC UGA UGG	C ₀₅ CT W ₁₈	U C A G
C	CUU CUC CUA CUG	L ₁₃	CCU CCC CCA CCG	P ₀₈	CAU CAC CAA CAG	H ₁₁ Q ₁₁	CGU CGC CGA CGG	R ₁₇	U C A G
A	AUU AUC AUA AUG	I ₁₃ M ₁₁	ACU ACC ACA ACG	T ₀₈	AAU AAC AAA AAG	N ₀₈ K ₁₅	AGU AGC AGA AGG	S ₀₅ R ₁₇	U C A G
G	GUU GUC GUA GUG	V ₁₀	GCU GCC GCA GCG	A ₀₄	GAU GAC GAA GAG	D ₀₇ E ₁₀	GGU GGC GGA GGG	G ₀₁	U C A G
87 (100) [555] light area					117 (139) [888] dark area				

Figure 3. From (MMR, 2004a, Fig. 5, p. 226): "The nucleon number balance within two complementary parts (sub-systems) of Standard Genetic Code Table. Up, in 12 AAs molecules (side chains), there are 888 nucleons (in first nuclide). ... Down, in 11 AAs molecules (side chains), there are 555 nucleons. [Additional Note, 2022: Here, the number of atoms is also calculated by counting duplicated amino acids only where they appear for the first time. This gives the number of atoms in the set of 20 instead of 23 amino acids. As we can see, in that case the number of atoms in two areas is 117/87, what corresponds to the division into the number of hydrogen and non-hydrogen atoms, respectively. Again we have an example of the validity of the principle – minimum signifiers, maximum meanings. On the other hand, when the duplicated amino acids remain duplicated, then, in the dark area, we have a third-order-unit change, in relation to the total number of atoms, in the side chains of 23 amino acids.]

1st	2nd letter								3rd
	U		C		A		G		
U	UUU UUC UUA UUG	F ₁₄ L ₁₃	UCU UCC UCA UCG	S ₀₅	UAU UAC UAA UAG	Y ₁₅ CT	UGU UGC UGA UGG	C ₀₅ CT W ₁₈	U C A G
C	CUU CUC CUA CUG	L ₁₃	CCU CCC CCA CCG	P ₀₈	CAU CAC CAA CAG	H ₁₁ Q ₁₁	CGU CGC CGA CGG	R ₁₇	U C A G
A	AUU AUC AUA AUG	I ₁₃ M ₁₁	ACU ACC ACA ACG	T ₀₈	AAU AAC AAA AAG	N ₀₈ K ₁₅	AGU AGC AGA AGG	S ₀₅ R ₁₇	U C A G
G	GUU GUC GUA GUG	V ₁₀	GCU GCC GCA GCG	A ₀₄	GAU GAC GAA GAG	D ₀₇ E ₁₀	GGU GGC GGA GGG	G ₀₁	U C A G
124 (137) [888-42] dark [888-42] - 57 = 789					115 (102) [555+42] light [555+42] + 57 = 654				

Figure 4. Here we have a splitting of the space of the Standard Genetic Code Table in the same way as in the previous Figure 3, only in the opposite direction. Also here we find the same signifiers, but different meanings. First of all, we find the atom quantities 137 / 102 in the two outer and two inner columns, as well as in the two inner and two outer rows, respectively (out: 137 / in: 102 in columns and vice versa in rows). [Cf. Solutions (3) and (4)]. In both cases on the scene is the presence of the "phantom" quantity (137 = 102 + 35) (35 comes from LSR). Reduced to a set of 20 amino acids, the quantities are 124 in dark area and 80 atoms in light area. The 80 plus "phantom" quantity 35 equals 115; the same ones results we find in Rumer's modified Table (MMR, 2018a, Table 2B, p. 34), as well as in the new arrangement of Rumer's Table (Survey 6), changed by ± 1 . The number of nucleons (reduced to a set of 20 amino acids): 789 in dark area and 466 in light area. The 466 plus "phantom" quantity 188 equals 654; together (789 / 654) as in original Crick's Table, according to A. Verkhovod's calculation, as we showed in the previous work (MMR, 2018a, Fig. 4, p. 37).

1st	2nd letter						3rd		
	U		C		A			G	
U	UUU	F ₁₄	UCU	S ₀₅	UAU	Y ₁₅	UGU	C ₀₅	U C A G
	UUC		UCC		UAC		UGC		
	UUA	UCA	UAA		UGA	CT W ₁₈			
	UUG	UCG	UAG		UGG				
C	CUU	L ₁₃	CCU	P ₀₈	CAU	H ₁₁	CGU	R ₁₇	U C A G
	CUC		CCC		CAC		CGC		
	CUA		CCA		CAA	CGA			
	CUG		CCG		CAG	CGG			
A	AUU	I ₁₃	ACU	T ₀₈	AAU	N ₀₈	AGU	S ₀₅	U C A G
	AUC		ACC		AAC		AGC		
	AUA	ACA	AAA		AGA	R ₁₇			
	AUG	ACG	AAG		AGG				
G	GUU	V ₁₀	GCU	A ₀₄	GAU	D ₀₇	GGU	G ₀₁	U C A G
	GUC		GCC		GAC		GGC		
	GUA		GCA		GAA	GGA			
	GUG		GCG		GAG	GGG			

Figure 5. The splitting of the space of the Standard Table of GC into the space of non-polar and space of polar amino acids. [Non-standard Tables for non-standard genetic codes we see only as deviations, i.e. exceptions and degrees of freedom in changes, in relation to the standard genetic code (MMR, 2018a, Box 2, p. 41.) Dark area: nonpolar space with number of the particles (molecules, atoms in side chain and atoms in whole molecule, in the set of 61 amino acid molecules): 22 / 222 / 420 versus 21/ 232 /421 within Outer space in Fig. 6; light area: polar space with 39 / 372 /723 versus 40/ 362 /722 within Inner space in Fig. 6. Notice that the polarity is given on the basis of hydrophathy (Kyte and Doolittle, 1982).

1st	2nd letter						3rd		
	U		C		A			G	
U	UUU UUC UUA UUG	F ₁₄ L ₁₃	UCU UCC UCA UCG	S ₀₅	UAU UAC UAA UAG	Y ₁₅ CT	UGU UGC UGA UGG	C ₀₅ CT W ₁₈	U C A G
C	CUU CUC CUA CUG	L ₁₃	CCU CCC CCA CCG	P ₀₈	CAU CAC CAA CAG	H ₁₁ Q ₁₁	CGU CGC CGA CGG	R ₁₇	U C A G
A	AUU AUC AUA AUG	I ₁₃ M ₁₁	ACU ACC ACA ACG	T ₀₈	AAU AAC AAA AAG	N ₀₈ K ₁₅	AGU AGC AGA AGG	S ₀₅ R ₁₇	U C A G
G	GUU GUC GUA GUG	V ₁₀	GCU GCC GCA GCG	A ₀₄	GAU GAC GAA GAG	D ₀₇ E ₁₀	GGU GGC GGA GGG	G ₀₁	U C A G

Figure 6. The "left" splitting of the space of the Standard Table of GC into outer and inner space. Dark area: outer space with number of the particles within belonging amino acids (molecules, atoms in side chain and atoms in whole molecule, in the set of 61 amino acid molecules): 21 / 232 / 421 versus 22 / 222 / 420 within non-polar space in Fig. 5; light area: inner space with 40 / 362 / 722 versus 39 / 372 / 723 within polar space in Fig. 5.

1st	2nd letter				3rd
	U	C	A	G	
U	UUU UUC F UUA UUG L	UCU UCC S UCA UCG	UAU UAC Y UAA UAG CT	UGU C UGC UGA CT UGG W	U C A G
C	CUU CUC L CUA CUG	CCU CCC P CCA CCG	CAU CAC H CAA CAG Q	CGU CGC R CGA CGG	U C A G
A	AUU AUC I AUA AUG M	ACU ACC T ACA ACG	AAU AAC N AAA AAG K	AGU AGC S AGA AGG R	U C A G
G	GUU GUC V GUA GUG	GCU GCC A GCA GCG	GAU GAC D GAA GAG E	GGU GGC G GGA GGG	U C A G

Figure 7. The splitting into the space of non-polar and polar amino acids. In relation to the Figure 5, here AAs PTWG are attached to the non-polar space as in Solution (9).

1st	2nd letter							3rd	
	U		C		A		G		
U	UUU UUC UUA UUG	F L	UCU UCC UCA UCG	S	UAU UAC UAA UAG	Y CT	UGU UGC UGA UGG	C CT W	U C A G
C	CUU CUC CUA CUG	L	CCU CCC CCA CCG	P	CAU CAC CAA CAG	H Q	CGU CGC CGA CGG	R	U C A G
A	AUU AUC AUA AUG	I M	ACU ACC ACA ACG	T	AAU AAC AAA AAG	N K	AGU AGC AGA AGG	S R	U C A G
G	GUU GUC GUA GUG	V	GCU GCC GCA GCG	A	GAU GAC GAA GAG	D E	GGU GGC GGA GGG	G	U C A G

Figure 8. The "right" splitting of the space of the Standard Table of GC into outer and inner space. The sum $2F+2L+4L+4S+2S+2R+4G+2D+2E$ equals 208 atoms as in Solution (12).

SURVEYS

Survey 1. The source of PPAASS mirror symmetry

(0)	(1)	(2)	(3)	(4)	(5)	(6)
00	02	04	06	08	10	12
11	13	15	17	19	21	23
22	24	26	28	30	32	34
11	16	21	26	31	36	41
00	05	10	15	20	25	30
44	60	76	92	108	124	140
	12	14	16	18	20	22
	23	25	27	29	31	33
	34	36	38	40	42	44
	41	46	51	56	61	66
	30	35	40	45	50	55
	140	156	172	188	204	220
	22	24	26	28	30	32
	33	35	37	39	41	43
	44	46	48	50	52	54
	66	71	76	81	86	91
	55	60	65	70	75	80
	220	236	252	268	284	300
	32	34	36	38	40	42
	43	45	47	49	51	53
	54	56	58	60	62	64
	91	96	101	106	111	116
	80	85	90	95	100	105
	300	316	332	348	364	380
	42	44	46	48	50	52
	53	55	57	59	61	63
	64	66	68	70	72	74
	116	121	126	131	136	141
	105	110	115	120	125	130
	380	396	412	428	444	460
	...					

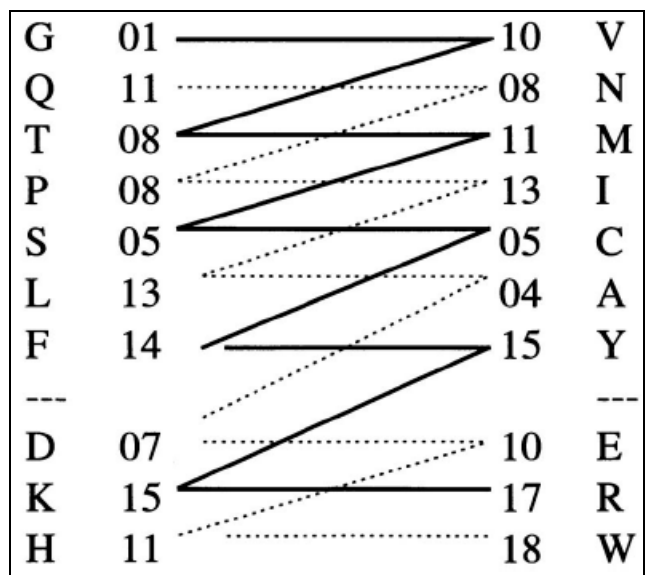
(10) 204, (11) 220 / (15) 284, (16) 300

(220 + 284 = **504**) (204 + 300 = **504**)

(00) 204, (01) 220 / (10) 284, (11) 300

MMR, 2019, Table A3, p. 30 [PAAS (Protein Amino Acid System)]: "The arrangement represents the Table of distinct 2-5 adding (TDA) with starting column 00-11-22-11-00 which follows from PSN (Periodic system of numbers: Figure A1) in decimal number system by overlapping the real sequence of doubled the first possible triangle in Boolean space (0-1-2) with its mirror image through compression and superposition at the point "22". In the 10th step we have a realization of the sequence (20-31-42-61-50), the same with the number of atoms in five AAs classes (20, 31, 42, 61, 50) as it is here presented: all five results in the 10th step are mirror image of the first step". (Cf. Table 1, segment I and II in this paper.) [Additional Note, 2022: The Table is extended from the original to show how in the *fifth step* of the *fifth cycle* the zeroth quantity 44 "experiences" its own self-similar enlargement. At the bottom is added a calculation that shows that in the tenth step, not only the quantity of the number of atoms in the side chains of 20 AAs (204) is realized, but also a kind of "logical square" whose two positions are occupied by the first friendly pair of numbers (220, 284).]

Survey 2. System-arrangement of AAs as a result of Golden Mean determination



From (MMR, 1998a, Survey 2.1, p. 289): "Atom number balance directed by Golden mean route on the binary-code tree. First seven amino acids on the left are 'golden' amino acids; arrangement-ordering follows from the ordering given in [Binary tree of GC (MMR, 1998a, Fig. 1, p. 284)]. On the right are their complements; below are three amino acid pairs as non-complements. On the first zigzag (full) line there are 102-1 whereas on the second (dotted) line 102+1 atoms. Arithmetic mean for both: 102±1."

Survey 2.1. "The amino acids in Golden mean power positions within the sequence 0–63 on the binary-code tree"

ϕ^0	ϕ^1	ϕ^2	ϕ^3	ϕ^4	ϕ^{5-7}	ϕ^8	ϕ^9
G	Q	T	P	S	L	L	F
63	39-38	25-24	15-14	10-09	06-02	02-01	01-00
63	38.94	24.06	14.87	9.19	5.68 – 2.17	1.34	0.83

From (MMR, 1998a, Table 2, p. 288): "First row: Golden mean powers within first 'cycle' in module 9. Second row: amino acids in the positions marked in third row, taken from the binary-code tree in Fig. 1. Fourth row: the values of the Golden mean powers within the interval 0–63."

Survey 3. "Golden" amino acids, their complements and non-complements

F 14		15 Y	F	Y
L 13	(65)	04 A	L (78)	A
Q 11		08 N	K	R
P 08		13 I	P	I
T 08		11 M	T	M
	(61)		(61)	
S 05		05 C	S	C
G 01		10 V	G	V
D 07		10 E	D	E
K 15	(78)	17 R	Q (65)	N
H 11		18 W	H	W

From (MMR, 2018a, Survey 3, p. 39): "Golden amino acids, their complements and non-complements. Presented is the modified Survey 2.1, given in Rakočević, 1998a, p. 289. Originally, 'Golden' amino acids (dark tones) are given in the order they have on the binary tree; and here according to the growing mass of their molecules. Opposite the 'golden' AAs, there are their complements, and at the bottom non-complements. The number of atoms in side chains of amino acids is as follows: GSTPQLF = 60, VCMINAY=60 + (1×6) = 66, DEKRHW = [60 + (1×6)] + (2×6) = 78. Here, however, is shown that one other distinction is possible with the same patterns of the number of atoms (self-identity!); such a change that leads to a minimum change, for±1." [Additional Note 2022: The right-hand side is added here, primarily to show the meaning of the chemical classification into less complex and more complex amino acids as given in Table 1, segment III; and, on the other hand, to demonstrate the effect of determination by the golden mean: to balance and nuance so that one more complex and one less complex pair of amino acids exchange the places.]

Survey 4. The classification of AAs through a synthetic influence of seven physico-chemical parameters

		IV	III	II	I		IV	III	II	I
6	(-)	G	T	-	-		G-V	T-M	P-I	K-R
5	(-)	S	D	P	K		S-C	D-N	H-W	
4	(-)	Q	N	H	-		Q-E	Y-F		
3	(±)	E	Y	W	R		A-L			
3	(±)	A	F	-	-		G-V	T-M	P-I	K-R
4	(+)	L	-	-	-		S-C	D-N	H-W	
5	(+)	C	-	I			Q-E	Y-F		
6	(+)	V	M	-			A-L			

From (MMR, 2000, left Table 3 and right Table 4, p. 6): In order to obtain these two system-arrangements, it should start from the Table 1 in original paper, which lists ten pairs of amino acids [G-V, S-C, T-M, P-I, A-L, D-E, N-Q, K-R, H-W, F-Y], according to how they are handled by two classes of enzymes, the aminoacyl-tRNA synthetases. In next Table (Table 2 in original paper), pairs of AAs are linked to the values of the parameters that determine them: five physico-chemical ones (hydropathy, hydrophobicity, enzymatic influence, acidity-basicity and basicity-acidity), and one formal, non-causal one, which concerns the position of amino acids into the inner/outer space of the standard Table of GC. In Table 3 there (the left side here, in Survey 4) it is shown by rows how many times the lower value of the parameter appears ('-'), and how many times the higher one ('+'). In the third row, the mark ('±') shows that in three parameters a higher value appears, and in three the lower ones. From Table 3 follows Table 4 (right side here); follows the classification of amino acids, *mutatis mutandis*, the same one that we find in Segment III of Table 1 in this paper. (Notice that the upper four rows, in left side, contain polar amino acids with negative values for hydropathy, while the lower four rows contain non-polar amino acids with positive values.) [Additional Note 2022: Within this paper the right side is repeated, with a shading, to indicate the following relationships. In the first diagonal, reading from right to left, we find the pair of A-L, the only two aliphatic hydrocarbon amino acids in the set of 16 amino acids of the alanine stereochemical type, together with the amino derivatives K-R. Associated with them is the less complex pair from the set of four aromatic amino acids, the pair of carbocyclic aromatic amino acids, F-Y. In the second diagonal is the pair D-E, the only two carboxylic amino acids (carboxylic from the aspect of the side chain) and two of their amide derivatives, N-Q. Associated with them is the more complex pair from the set of four aromatic amino acids, the pair of heterocyclic aromatic amino acids, H-W. In the next diagonal are four chalcogen amino acids, in the neighborhood of which there are also four amino acids of non-alanine stereochemical types, in the same manner as on the right side of Survey 3.]

Survey 5. Relations between standard and Mitochondrial genetic code

073	F ₉₁	(14/15)	107 Y	079	
235	L ₅₇	(13/04)	15 A	172	
087	Q ₇₂	(11/08)	58 N	085	
160	P ₄₁	(08/13)	57 I	121	079
168	T ₄₅	(08/11)	75 M	043	085
243	S ₃₁	(05/05)	47 C	081	
184	G ₀₁	(01/10)	43 V	168	
087	D ₅₉	(07/10)	73 E	093	
091	K ₇₂	(14/17)	100 R	265	172
081	H ₈₁	(11/18)	130 W	044	087
$(121 + 43 + 265 + 44 = 473)$ $(79 + 85 + 172 + 87 = 423)$ $[473 - 423 = 50] [473 + 423 = 896 = 496 + 400]$ $400 = 300 + 100$					

Two columns of protein AAs (column "F" and column "Y") are given within the bold framed system-arrangement. In the column to the left of column "F" and to the right of column "Y" data are given for the number of atoms in the corresponding codons. The differences for the mitochondrial code are given in the added "thin" column, far right. In the amino acid symbol index data are given for the number of nucleons in the side chain. The number of atoms in the side chain of the amino acid is indicated in the central column. The order of amino acids in column "F" is dictated by the "golden" amino acids, from G to F (according to Survey 2.1, in the first arrangement, and to Survey 3 in the second arrangement), while the order in column "Y" is dictated by the chemical complements of "golden" amino acids. At the very bottom is the calculation and the calculated difference in the number of atoms in the coding codons for the two codes (50). The relation to the third perfect number (496) and the fourth vertices ("300") of the significant logical square in Survey 1 is also indicated [204-220-284-**300**]. The boxed two and two amino acids concern the differences between the two classes of synthetases.

Survey 5.1. Relationships in the standard Genetic Code

073 F	Y 079	073 F	Y 079
235 L	A 172	235 L	A 172
087 Q	N 085	087 Q	N 085
160 P	I 121	160 P	I 121
168 T	M 043	168 T	M 043
243 S	C 081	243 S	C 081
184 G	V 168	184 G	V 168
087 D	E 093	087 D	E 093
091 K	R 265	091 K	R 265
081 H	W 044	081 H	W 044
1446 / 1114	332 330 <u>02</u>	1445 / 1115	
1446 - 1114 = 332		1445 - 1115 = 330	
1409 / 1151 → Cf. Surv. 5 and 5.2;			

From (MMR, 2009, Table B.6, p. 29): "Golden the number of molecules in proportion 1:1 on the left and 2:3 on the right. The atom number balance within coding codons (Py-Pu bases), regarding both arrangements, as 1114:1115 and 1446:1445."

Survey 5.2. Relationships in the mitochondrial Genetic Code

073 F	Y 079	073 F	Y 079
235 L	A 172	235 L	A 172
087 Q	N 085	087 Q	N 085
160 P	I 079	160 P	I 079
168 T	M 085	168 T	M 085
243 S	C 081	243 S	C 081
184 G	V 168	184 G	V 168
087 D	E 093	087 D	E 093
091 K	R 172	091 K	R 172
081 H	W 087	081 H	W 087
1409 / 1101 1409 – 1101 = 308	328 308 20	1419 / 1091 1419 – 1091 = 328	

From (MMR, 2009, Table C.1., p. 33): "The mitochondrial genetic code; for the relation to the standard one cf. Table B.6 [here: Survey 5.1] and see Comments 8 and 9 [here: Box 4]. As in standard code [Survey 5.1] here we have the same proportions: the number of molecules in proportion 1:1 on the left and 2:3 on the right. The atom number balance within coding codons (Py-Pu bases), regarding both arrangements, as **1409:1419** and **1101:1091**[with the differences for ± 10]. (*Additional Note 1 (2022):* Quantities 308 and 328 ...) as in (Solution 9, Tab. 4 and Survey 7) [*Additional Note 2: 308 = 4 x 77 (308 = 266 + 42)*]

Survey 5.3. LIPS (Linear Invariant Perfect System) I

073	F ₉₁		₁₀₇ Y	079
235	L ₅₇		₁₅ A	172
087	Q ₇₂		₅₈ N	085
160	P₄₁		₅₇I	079
168	T ₄₅		₇₅ M	085
243	S ₃₁		₄₇ C	081
184	G₀₁		₄₃V	168
087	D ₅₉		₇₃ E	093
091	K ₇₂		₁₀₀ R	172
081	H ₈₁		₁₃₀ W	087
$550 + (550 + 155) = 1255$ $\underline{1255} \qquad \qquad \qquad 1255$				

From (MMR, 2009, Table C.2., p. 34): "Two columns of AAs with two and two columns of numbers; outer: number of atoms within coding codons (Py-Pu bases); inner [in index]: number of nucleons within amino acid molecules (side chains). As in Table C.1 here we have the same proportion for the number of molecules, 2:3, but the proportion for the number of atom is 1:1. But relations between atom number within codons and nucleon number within amino acid molecules is noteworthy in a special respect: the number of atom 2 x 1255 and the number of nucleons 1 x 1255?! (Within the columns, on the left: 550 and on the right 550+155.) If the Nature is still of a great 'N', and then is – too much!"

Survey 5.4. LIPS (Linear Invariant Perfect System) II

073	F ₉₁		₁₀₇ Y	079
235	L ₅₇		₁₅ A	172
087	Q ₇₂		₅₈ N	085
160	P₄₁		₅₇I	079
168	T ₄₅		₇₅ M	085
243	S ₃₁		₄₇ C	081
184	G₀₁		₄₃V	168
087	D ₅₉		₇₃ E	093
091	K ₇₂		₁₀₀ R	172
081	H ₈₁		₁₃₀ W	087
$378 \qquad + \qquad 877 = 1255$ $\underline{1255} \qquad \qquad \qquad 1255$				

Survey 6. Further elaboration of Rumer's Table

6,4 / 5,5 hb			
01 G 01		10 V 13	
02 F 14		05 C 14	
03 L 13	59/63	18 W 15	
04 P 08	(122)	08 T 16	
05 N 08		11 H 17	
06 K 15	(116/123)	11 Q 18	
07 A 04		13 L 19	
08 Y 15		05 S 20	
09 *		17 R 21	
10 R 17	60/57	05 S 22	
11 I 13	(117)	07 D 23	
12 M 11		10 E 24	
Odd / Even arrangement			
54 (130) 76 (141)			
65 (109) 44 (98)			
119/120			

The Table comes from the previous preprint work (MMR, 2013b, Table A3, p. 30) where it only had a title, and here it gets the legend. From Rumer's Table, its modified form (MMR, Table 2B, p. 34), we take here only the amino acids (without corresponding nucleotide doublets), with their ordinal number. In doing so, we find the odd and even summation quantities there (115/124) here in one cross-link, changed by ± 1 . [$59 + 57 = 116$ and $63 + 60 = 123$.] In addition, it is a change for ± 1 also in comparison to the standard Table of GC, as shown in Solution (1), in this paper (116/123 versus 117/122). Quoting this result from Solution (1), we would like to draw attention to another fact, to the role played by the "phantom quantity" (LSR 35) in the balancing and nuancing of the number of particles, which also appears in a different way in the modified Rumer's Table (MMR, 2018a, Table 2B, p. 34). [Note: All these reorganizations of amino acid system-arrangements, followed by changes for first and/or second-order units in the records of the number of atoms, are only a confirmation of the presence of semiosis in the genetic code, more precisely a confirmation of the unity of chemism and semiosis.]

Survey 7. Adding a singlet zeroth Boolean triangle to the doublet one

22 + 0 = 22		330 - 02 = <u>328</u>
11 + 1 = 12		330 - 12 = <u>318</u>
00 + 2 = 02		330 - 22 = <u>308</u>
22 - 2 = 20		264 + 02 = <u>266</u>
11 - 1 = 10		264 + 12 = <u>276</u>
00 - 0 = 00		264 + 22 = <u>286</u>
328 + 266 = 594	328	332
318 + 276 = 594	308	330
308 + 286 = 594	<u>20</u>	<u>02</u>

Survey 7.1. The relations of the quantities 330 and 264, as the number of atoms within the rows of modified Crick's Table of GC (MMR, 2004a)

$(9 + 1) \times 33 = 330$ $(9 \pm 0) \times 33 = 297$ $(9 - 1) \times 33 = 264$
$300 + \underline{30} = 330$ $284 - \underline{20} = 264$
$300 - 02 = \underline{298}$
$298 - 02 = \underline{296}$ $298 - 12 = \underline{286}$ $298 - 22 = \underline{276}$

DISPLAYS

Display 1. Determination of amino acid positions by the Golden mean: relation to the number of all atoms in the side chains of 20 amino acids (I)

F ₁₄	Y ₁₅	F ₁₄	Y ₁₅
L ₁₃	A ₀₄	L ₁₃ (65)	A ₀₄
Q ₁₁	N ₀₈	Q ₁₁	N ₀₈
P₀₈ (60) (66)	I₁₃		
<i>T₀₈</i>	<i>M₁₁</i>		
<i>S₀₅</i>	<i>C₀₅</i>	P₀₈	I₁₃
G₀₁	V₁₀	<i>T₀₈</i>	<i>M₁₁</i>
[y a n & f l q] → 65		(61)	
[y a n & i m c v] → 66			
[p t s g & f l q] → 60		<i>S₀₅</i>	<i>C₀₅</i>
[p t s g & i m c v] → 61		G₀₁	V₁₀
		66 – 01 = 65	
		60 + 01 = 61	
D ₀₇	E ₁₀	D ₀₇	E ₁₀
K ₁₅ (78)	R ₁₇	K ₁₅ (78)	R ₁₇
H ₁₁	W ₁₈	H ₁₁	W ₁₈

It is about determination of the positions of AAs on the binary tree of GC (MMR, 1998a, Fig. 1). illustration on the left: "The Cyclic Invariant Periodic System (CIPS) of canonical AAs. ... At the index – the atom number within amino acid side chains. In the middle position there are chalcogen AAs (S, T & C, M); follow – in next 'cycle' – the AAs of non-alanine stereochemical types (G, P & V, I), then two double acidic AAs with two their amide derivatives (D, E & N, Q), the two original aliphatic AAs with two amine derivatives (A, L & K, R); and, finely, four aromatic AAs (F, Y & H, W) – two up and two down. The said five classes belong to two superclasses: primary superclass in light areas and secondary superclass in dark areas [as in Figure 1 in this paper]. Notice, that each amino acid position in this CIPS is strictly determined and none can be changed" (MMR, 2011, Figure 6, p. 832). Illustration on the right: as left side in Survey 3.

Display 2. Determination of amino acid positions by the Golden mean: relation to the number of all atoms in the side chains of 20 amino acids (II)

F₁₄	Y₁₅	F₁₄	Y₁₅
L₁₃	A₀₄	L₁₃	(78) A₀₄
Q₁₁	N₀₈	K₁₅	R₁₇
P₀₈	(60) (66) I₁₃		
T₀₈	M₁₁		
S₀₅	C₀₅	P₀₈	I₁₃
G₀₁	V₁₀	T₀₈	M₁₁
(yar flk) ₇₈ - (erw dkh) ₇₈ = 0		(61)	
(yan imcv) ₆₆ - (enw dqh) ₆₅ = 1		S₀₅	C₀₅
[p t s g & f l q] → 60		G₀₁	V₁₀
[p t s g & i m c v] → 61			
D₀₇	E₁₀	D₀₇	E₁₀
K₁₅	(78) R₁₇	Q₁₁	(65) N₀₈
H₁₁	W₁₈	H₁₁	W₁₈

Compared to the previous Display 1, the novelty is the right side, which corresponds to the right side of Survey 3

Display 5. Determination of amino acid positions by the Golden mean: relation to the number of non-hydrogen atoms within the side chains of 20 AAs (I)

F ₀₇		Y ₀₈	F ₀₇		Y ₀₈
L ₀₄		A ₀₁	L ₀₄	(29)	A ₀₁
Q ₀₅		N ₀₄	Q ₀₅		N ₀₄
P₀₃	(24)	(26)	I₀₄		
T ₀₃					
S ₀₂			P₀₃		I₀₄
G₀₀			T ₀₃		M ₀₄
				(21)	
			S ₀₂		C ₀₂
			G₀₀		V₀₃
D ₀₄		E ₀₅	D ₀₄		E ₀₅
K ₀₅		R ₀₇	K ₀₅	(37)	R ₀₇
H ₀₆		W ₁₀	H ₀₆		W ₁₀

Display 6. Determination of amino acid positions by the Golden mean: relation to the number of non-hydrogen atoms within the side chains of 20 AAs (II)

F ₀₇		Y ₀₈	F ₀₇		Y ₀₈
L ₀₄		A ₀₁	L ₀₄	(32)	A ₀₁
Q ₀₅		N ₀₄	K ₀₅	⋮	R ₀₇
P₀₃	(24)	(26)	I₀₄	⋮	I₀₄
T ₀₃		M ₀₄	(11)	⋮	M ₀₄
S ₀₂		C ₀₂	P₀₃	⋮	I₀₄
G₀₀		V₀₃	T ₀₃	⋮	M ₀₄
			(21)	⋮	
			S ₀₂		C ₀₂
			G₀₀		V₀₃
D ₀₄		E ₀₅	D ₀₄		E ₀₅
K ₀₅	(37)	R ₀₇	Q ₀₅	(34)	N ₀₄
H ₀₆		W ₁₀	H ₀₆		W ₁₀

Table A2 Results of summarization in Table A1

(a)	Decimal	(b)		Binary	
667	(07 x 07)	716)		667	(111 x 111) 716
597	(01 x 61)	658		597	(111101) 658
	(110)				
641	(01 x 10)	651		641	(01 x 1010) 651
631	(01 x 11)	620		631	(01 x 1011) 620
	(21)				
632	(00 x 00)	632		632	(000 x 000) 632
623	(00 x 00)	623		623	(000 x 000) 623
624	(01 x 11)	635		624	(01 x 1011) 635
614	(01 x 10)	604		614	(01 x 1010) 604
	(21)				
588	(07 x 07)	539		588	(111 x 111) 539
	(49)				

[5678 – 61 / 5678] [(716 = 496 + 220) (21 + 21 = 42)]

[5678 – 3456 = **2222**] [3456 – 1234 = **2222**]

The quantity 5678 - 61 represents the sum of the results given in column (a), while the quantity 5678 is analogous sum of the results in column (b). The quantity 3456 represents the sum of the codon nucleotides atoms within the two inner and two outer columns of the GC Table (MMR, 2018a, Fig. 4, p.37).

Table A3. The algorithm for generating the number of nucleons (1255) in 20 AAs

$367 - 444 = -77$ $[(+811) + (+1699)] = 1255 \times 2$ $[(+367) + (+2143)] = 1255 \times 2$ $[(-077) + (+2587)] = 1255 \times 2$ $1255 \times 2 = 2510$	(1) $22\mathbf{3} / \mathbf{1}44$ (2) $44\mathbf{5} / \mathbf{3}66$ (3) $66\mathbf{7} / \mathbf{5}88$ (4) $88\mathbf{9} / \mathbf{7}AA$	223 121 $144 (367)$ $445 \quad 444$ 121 $366 (811)$
$(1-3), (3-5), (5-7), (7-9)$ $(2-4), (4-6), (6-8), (8-A)$		$\mathbf{667} \quad 444$ 121 $\mathbf{588 (1255)}$
$223 - 144 = \mathbf{79}$ [$79 - 11 = 68$] ($68 \times 3 = \mathbf{204}$) $445 - 366 = \mathbf{79}$ ($121 - 79 = 42$) $667 - 588 = \mathbf{79}$ $121 + 79 = 200$...		$889 \quad 444$ 121 $7AA (1699)$...

Table A5. Number of atoms in the nine areas of Table A4

IX	101 / 103	(2)	[2]	IX + I = 10
I	99 / 105			
II	97 / 107	(0)	[3]	II + III + VI = 11
III	97 / 107			
VI	97 / 107			
VII	96 / 108	(1)	[3]	VII + VIII + V = 20
VIII	95 / 109			
V	94 / 110			
IV	92 / 112		[1]	IV = 04
$[10 + 11 = 22 - 1]$ $[20 + 04 = 23 + 1]$				

Appendix B. Quantitative relations in PPAASS, expressed through the number of nucleons

Table B1. Number of nucleons in 20 AAs, ordered by chemical similarity, according to Table 2 and in relation with Table A1 (I)

<u>623</u>	<u>632</u>	631	<u>623</u>	<u>632</u>		<u>641</u>	<u>614</u>
G N	G N		G N	G N		G N	G N
A D	A D		A D	A D		A D	A D
V S	V S		V S	V S		V S	V S
P T	P T		P T	P T		P T	P T
I C	I C		I C	I C		I C	I C
L M	L M		L M	L M		L M	L M
K F	K F		K F	K F		K F	K F
R Y	R Y		R Y	R Y		R Y	R Y
Q W	Q W		Q W	Q W		Q W	Q W
E H	E H		E H	E H		E H	E H

Table B2. Number of nucleons in 20 AAs, ordered by chemical similarity, according to Table 2 and in relation with Table A1 (II)

<u>651</u>	<u>641</u>	632	631	<u>620</u>		<u>604</u>	<u>614</u>		<u>624</u>
G N	G N		G N	G N		G N	G N		G N
A D	A D		A D	A D		A D	A D		A D
V S	V S		V S	V S		V S	V S		V S
P T	P T		<u>P</u> T	<u>P</u> T		P T	P T		P T
I C	I C		I C	I C		I C	I C		I C
L <u>M</u>	L <u>M</u>		L M	L M		<u>L</u> M	<u>L</u> M		L M
K <u>F</u>	K <u>F</u>		K F	K F		<u>K</u> F	<u>K</u> F		K F
R Y	R Y		R Y	R Y		R Y	R Y		R Y
Q W	Q W		Q W	Q W		Q W	Q W		Q W
E H	E H		E H	E H		E H	E H		E H

Table B3. Number of nucleons in 20 AAs, ordered by chemical similarity, according to Table 2 and in relation with Table A1 (III)

635	634	632	631	641		623	624		614
G N	G N		G N	G N		G N	G N		G N
A D	A D		A D	A D		A D	A D		A D
V S	V S		V S	V S		V S	V S		V S
P T	P T		P T	P T		P T	P T		P T
I C	I C		I C	I C		I C	I C		I C
L M	L M		L M	L M		L M	L M		L M
K F	K F		K F	K F		K F	K F		K F
R Y	R Y		R Y	R Y		R Y	R Y		R Y
Q W	Q W		Q W	Q W		Q W	Q W		Q W
E H	E H		E H	E H		E H	E H		E H

Table B4. Number of nucleons in 20 AAs, ordered by chemical similarity, according to Table 2 and in relation with Table A1 (IV)

597	658		539	716		667	588
G N	G N		G N	G N		G N	G N
A D	A D		A D	A D		A D	A D
V S	V S		V S	V S		V S	V S
P T	P T		P T	P T		P T	P T
I C	I C		I C	I C		I C	I C
L M	L M		L M	L M		L M	L M
K F	K F		K F	K F		K F	K F
R Y	R Y		R Y	R Y		R Y	R Y
Q W	Q W		Q W	Q W		Q W	Q W
E H	E H		E H	E H		E H	E H

$[658 - 597 = (60+1)]$ $[667 - 588 = (78+1)]$
 $[716 - 539 = (66 + 111)]$

Table B5. The sums of atoms, protons and ordinal number in 20 AAs, ordered by chemical similarity in Table 2.2 (I)

<u>530</u>		<u>540</u>		<u>560</u>		<u>570</u>
G N		G N		G N		G N
A D		A D		A D		A D
V S		V S		V S		V S
P T		P T		P T		P T
I C		I C		I C		I C
L M		L M		L M		L M
K F		K F		K F		K F
R Y		R Y		R Y		R Y
Q W		Q W		Q W		Q W
E H		E H		E H		E H
(10 x 220 = 25 x 88)						

Table B6. The sums of atoms, protons and ordinal number in 20 AAs, ordered by chemical similarity in Table 2.2 (II)

20 x 88						
GN		G N		GN		GN
AD		A D		AD		AD
VS		V S		VS		VS
PT		P T		PT		PT
IC		I C		IC		IC
LM		L M		LM		LM
KF		K F		KF		KF
RY		R Y		RY		RY
QW		Q W		QW		QW
EH		E H		EH		EH
30 x 88						

Appendix C. Results of Golden Section determination

Table C1. Relationships to two classes of Aminoacyl-tRNA synthetases: all atoms

28	09 19	G_{01} P_{08} A_{04} K_{15}	(2) (4)	23 30	V_{10} I_{13} L_{13} R_{17}	53	81
53	13 15 25	S_{05} T_{08} D_{07} N_{08} H_{11} F_{14}	(1) (3) (5)	16 21 33	C_{05} M_{11} E_{10} Q_{11} Y_{15} W_{18}	70	123
81						123	204
$G_{01} + A_{04} + S_{05} + D_{07} + H_{11} = 28$ $V_{10} + L_{13} + C_{05} + E_{10} + Y_{15} = 53 \quad [81]$ $P_{08} + K_{15} + T_{08} + N_{08} + F_{14} = 53$ $I_{13} + R_{17} + M_{11} + Q_{11} + W_{18} = 70 \quad [123]$							

Table C2. Relationships to two classes of Aminoacyl-tRNA synthetases: hydrogen atoms

19	06 13	$G_{01} P_{05}$ (2) 16 $A_{03} K_{10}$ (4) 19	$V_{07} I_{09}$ $L_{09} R_{10}$	35	54
27	08 07 12	$S_{03} T_{05}$ (1) 10 $D_{03} N_{04}$ (3) 11 $H_{05} F_{07}$ (5) 15	$C_{03} M_{07}$ $E_{05} Q_{06}$ $Y_{07} W_{08}$	36	63
46				71	117
$G_{01} + A_{03} + S_{03} + D_{03} + H_{05} = 15$ $V_{07} + L_{09} + C_{03} + E_{05} + Y_{07} = 31 \text{ [46]}$ $P_{05} + K_{10} + T_{05} + N_{04} + F_{07} = 31$ $I_{09} + R_{10} + M_{07} + Q_{06} + W_{08} = 40 \text{ [71]}$ $(15 + 40 = 54 + 1) \quad (31 + 31 = 63 - 1)$					

Table C3. Relationships to two classes of Aminoacyl-tRNA synthetases: non-hydrogen atoms

09	03 06	$G_{00} P_{03}$ (2) $A_{01} K_{05}$ (4)	07 11	$V_{03} I_{04}$ $L_{04} R_{07}$	18	27
26	05 08 13	$S_{02} T_{03}$ (1) $D_{04} N_{04}$ (3) $H_{06} F_{07}$ (5)	06 10 18	$C_{02} M_{04}$ $E_{05} Q_{05}$ $Y_{08} W_{10}$	34	60
35					52	87
$G_{00} + A_{01} + S_{02} + D_{04} + H_{06} = 13$ $V_{03} + L_{04} + C_{02} + E_{05} + Y_{08} = 22 \text{ [35]}$ $P_{03} + K_{05} + T_{03} + N_{04} + F_{07} = 22$ $I_{04} + R_{07} + M_{04} + Q_{05} + W_{10} = 30 \text{ [52]}$ $(13 + \underline{30} = 43) \quad (22 + \underline{22} = \underline{44})$ $(\underline{30} \text{ as } \frac{1}{2} 60) \quad (27 \text{ as } \frac{1}{2} 54) \quad (54 = \underline{44} + 10)$						

Appendix D. Harmonic structures of the genetic code

Table D1. "The harmonic structure with two 'acidic' and three 'basic' amino acid quartets"

					a	b	c	d	M
D	N	A	L	→	189	189	221	221+3	485.49=485
R	F	P	I	→	289	289	341	341+0	585.70=586
K	Y	T	M	→	299	299	351	351+2	595.71=596
H	W	S	C	→	289	289	331	331+1	585.64=586
E	Q	G	V	→	189	189	221	221+3	485.50=485
					1255	1255	1465	1465+9	2738.04
					$1255 + 1465 + (1465 + 9) = 2738 + (1465 - 9)$				

MMR, 2004a, Table 1, p. 223: "Four choices after four types of isotopes: (a) The number of nucleons within 20 AAs side chains, calculated from the first, the lightest nuclide (H-1, C-12, N-14, O-16, S-32). (b) The number of nucleons within 20 AAs side chains, calculated from the nuclide with the most abundance in the nature [the same patterns as in (a): H-1, C-12, N-14, O-16, S-32; at heavier nuclides of other bioelements the data by (a) and (b) are not the same]. (c) The number of nucleons within 20 AAs side chains, calculated from the nuclide with the less abundance in the nature (H-2, C-13, N-15, O-17, S-36); (d) The number of nucleons within 20 AAs side chains, calculated from the last, the heaviest nuclide (H-2, C-13, N-15, O-18, S-36). (M) The AAs molecule mass. Notice that (d) is greater from (c) for exactly one modular cycle (in module 9) and that total molecules mass is equal to $[2(37 \times 37)]$. Notice also that molecule mass within five rows is realized through the same logic-patterns of notations as the first nuclide, i.e. isotope." [Additional Note 2022: A calculation that is not in the original has been added at the very bottom, to indicate the "phantom" quantities of some of the isotopes (Remark 3).]

Table D2. "The polar and non-polar amino acids"

D	N	A	L	D 07	N 08	A 04	L 13	→	32	84
R	F	P	I	R 17	P 08	F 14	I 13	→	52	
K	Y	T	M	K 15	Y 15	T 08	M 11	→	49	120
H	W	S	C	H 11	W 18	S 05	C 05	→	39	
E	Q	G	V	E 10	Q 11	G 01	V 10	→	32	
60	66	78		↓	↓	↓	↓			
				60	60	32	52			
				120		84				
$(84 = 173 + 11) / (120 = 131 - 11)$ [Cf. Tab. D3]										

Illustration on the right: "The splitting into polar (light ton) and non-polar (bold, dark ton) AAs. The polarity as hydrophathy, i.e. as hydrophathy index. (After Table 2 in Kyte and Doolittle, 1982, p. 110). The number of atoms within AAs molecules (side chains) in first two rows as well as in second two columns is identical (84 atoms). The same is valid for second three rows in relation to first two columns (120 atoms)." (MMR, 2004a, Table 4, p. 225.)

Table D3. A variant of '4 x 5' AAs system: the splitting into two subsystems: inner and outer

D	E	Y	S	T	$(6 \times 6) \pm 0$ $(6 \times 6) + 1$
N	Q	G	C	M	
A	L	F	V	I	
K	R	P	H	W	
$(66) \pm 0$			$(66) - 1$		
$(66 + 65 = \mathbf{131}) / (36 + 37 = \mathbf{73})$ [$131 = 120 + 11$ and $73 = 84 - 11$] $(\mathbf{84} = 173 + 11) / (\mathbf{120} = 131 - 11)$ [Cf. Tab. D2]					

MMR, 2004a, Table 9, p. 229: "This system follows from the system in Table 4 [Table D2 here]. First row (down): N-ended AAs [apart from hydrogen and carbon, they also have nitrogen in side chain]. Second row: solely C-ended AAs [apart from hydrogen, they also have carbon]. Last row (up): O-ended AAs [apart from hydrogen and carbon, they also have oxygen]. First to last row: remaining five AAs (one solely H-ended, two S-ended and two N-, O-ended, all five as a 'combination'. Within the cross there are only the exceptions: horizontally five the mentioned combining AAs; vertically: Y as aromatic within aliphatic AAs; G without carbon; F as aromatic within aliphatic AAs; and, finally, P as cyclic aliphatic amino acid. In the system there is a balanced proportionality as follows: within horizontal leg of the cross there are $(6 \times 6) \pm 0$ of atoms, and within vertical leg (without glycine), there are $(6 \times 6) + 1$. Without cross: on the left there are $(66) \pm 0$ and $(66) - 1$ on the right..." [Additional Note 2022: Notice the mathematical operation: multiplication as abbreviated addition of equal adders vs abbreviated addition of equal adders by positions of the number record.]

G 01	S 05	Y 15	W 18	39	78	102
A 04	D 07	M 11	R 17	39		
C 05	T 08	E 10	F 14	37	24	102
N 08	Q 11	V 10	I 13	42	13	
P 08	H 11	L 13	K 15	47	89	
26	42	59	77			
16		17	18			
(1 x 68)		(2 x 68)				

Figure D1. From (MMR, 2011, Figure 3, p. 828): "A specific classification and systematization of amino acids which follow from four diversity types (Figure 2). In the shadow space there are 20 AAs with atom number in molecules side chains. Within first two and last two columns: 1 x 68 and 2 x 68 atoms, respectively. Within two inner and two outer columns: 102 ± 1 atoms. Regarding at the rows: there are 78 atoms within first two and $78 + 11 = 89$ within last two rows; within first half of the middle row 13, and within the second one $13 + 11$ atoms. Within two halves of shadow spaces (light and dark) there is also a specific balance: 102 ± 00 atoms. All amino acid sequences are of the growing series from the aspect of number of atoms; all but one, in which Q-11 precedes V-10, because different stereochemical types have been distinguished: NQ belongs to alanine but V-I to valine type."

F 14	15 Y	F 14	15 Y
L 13	04 A	L 13	04 A
Q 11	08 N	Q 11	08 N
P 08	13 I	P 08	13 I
T 08	11 M	T 08	11 M
S 05	05 C	S 05	05 C
G 01	10 V	G 01	10 V
D 07	10 E	D 07	10 E
K 15	17 R	K 15	17 R
H 11	18 W	H 11	18 W

1 x 68 / 68 x 2

Figure D2. From (MMR, 2009, Table B.2., p. 26): "The number of amino acid molecules in proportion 2:3 and the number of atoms within side chains 1:2. On the right: the quantum '1 x 68' make the aliphatic 'golden' AAs [without aromatic F] plus (D & K), and the quantum '2 x 68' all others. On the left: the quantum '1 x 68' make four AAs (G, P and V, I) of non-alanine stereochemical type (larger diversity!) plus two and two AAs – two double acidic (D, E) and only two amides (N, Q), what means a very specific diversity; and the quantum '2 x 68' all other AAs."

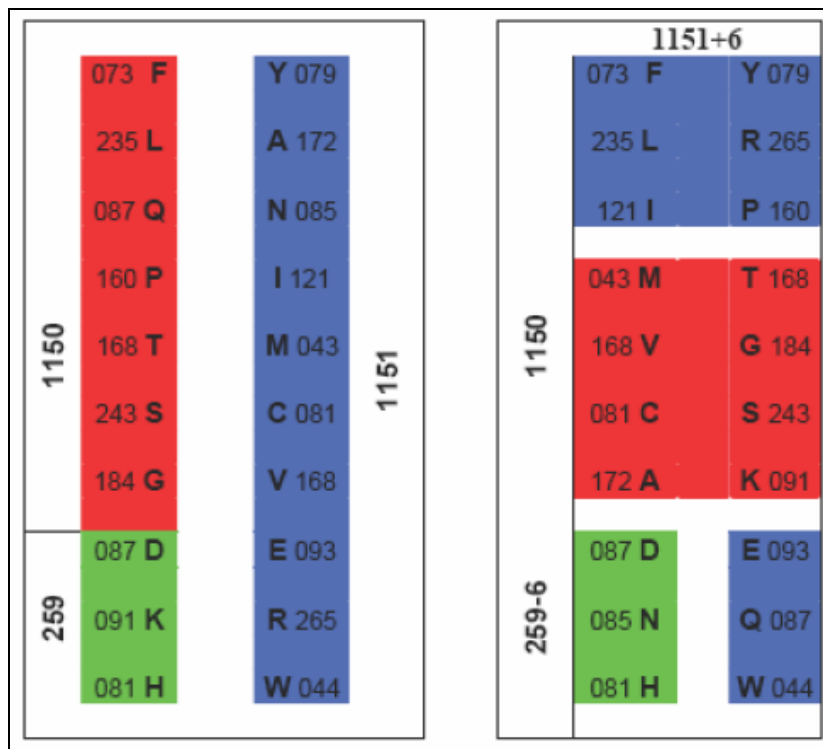


Figure D3. From (MMR, 2009, Table B.3 on the left and Table B.4 on the right, p. 27). The illustration on the left: "The block-aufbau principle as well as the principle of self-similarity are on the scene: the quantum of 1150 atoms within coding codons (their Py-Pu bases) for seven 'golden' AAs (red block) in relation to the same such quantum valid for eight AAs in the system over there in Table B.4. At the same time the principle of minimum change is valid: 1150 versus 1151 (blue block). Notice also these relations: $1151 + 259 = 1410$ ('golden' AAs versus 'non-golden' AAs in relation to $1150:1410$). Quantum '1150' make all seven 'golden' AAs." The illustration on the right: "The self-similarity through the same patterns: the seven nonpolar AAs (F, L, I, M, V, C, A) play the role of seven 'golden' AAs (F, L, Q, P, T, S, G) in previous Table (Table B.3). The polar/nonpolar AAs after (Kyte & Doolittle, 1982). The quantum '1150' make three 'golden' AAs (T, G, S) together with three their complements (M, V, C) plus two other – A & K (Alanine as first possible hydrocarbon amino acid; lysine as a simple amine derivative – the simpler of total two: K and R)."