SEMIOTIC NATURE OF GENETIC CODE

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Semiotic nature of Genetic code

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Abstract. In some previous works (2018a,b; 2019, 2021a,b, 2022) we presented a new type of mirror symmetry, expressed in the set of protein amino acids; such a symmetry, that it simultaneously represents the semiotic essence of the genetic code. In this paper we provide new evidences that the genetic code represents the unity of chemism and semiosis.

Keywords: Genetic code, Chemical code, Periodic system of chemical elements, Periodic system of numbers, Chemism, Semiosis, Protein amino acids, Mirror symmetry.

1. Introduction

My understanding of the genetic code as a semiotic system began 35 years ago with the publication of the book *Genes, molecules, language* (Rakočević, 1988).[1] But then it could not be said publicly, because the time had not come for a possible new paradigm.[2] However, the very title of the book suggests that it is about semiotics, i.e. about semiology; also in relation to the chemical code, as I looked at PSE already in older works (MMR, 1990, 1991), and in newer ones (MMR, 2018a and 2018b); language, as natural human spoken language. [A minimal excerpt from that book (translated from Serbian), is here in Box 1.]

In the mentioned previous two works, the new paradigm is more than hinted at. Thus, in the first paper (MMR, 2018a, Nota bene, p. 32), agreeing with the progenitor of biological semiotics (biosemiotics) M. Barbieri (2008, 2018) that GC is not a metaphor but an entity,[3] and a semiological entity at that, I supported that idea with even more pronounced "arbitrariness", which are semiological in themselves, the essence of all semiological systems, with the cipher of the genetic code and the key to the cipher.

[1] In further citations, instead of "Rakočević", only MMR.

[2] In those years (the eighties and nineties of the XX century), instead of speaking about the unity of chemism and semiosis in natural codes, I only dared to speak (and write) about *The universal code of Nature* (MMR, 1997c).

[3] "It is a fact that the genetic code has been universally accepted into Modern Biology, but let us not be naive about this: what has been accepted is the name of the genetic code, not its ontological reality ..., the genetic code is a metaphorical entity, not a real code " (Barbieri, 2018, p. 2).

Box 1. Excerpts from the book "Genes, molecules, language" (MMR, 1988)

MMR, 1988, on page 4: “The way in which [Mendel] arrived at scientific conclusions is closer to the methodology of scientific reasoning in information theory and systems theory than to the methodology of reasoning in classical biology. Darwin's entire work also has a systemic character. ... The founder of structural linguistics, Ferdinand de Saussure, already in 1908 said everything about the universal in language, either natural speech or the language of 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.”

On p. 64: “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”] “Therefore, it is not about any norms that are prescribed, but the laws of language, the laws of synchrony and diachrony, independent of "agreements about language, from the norms prepared by experts and specialists"... "The laws of synchrony and diachrony have a universal character". Saussure well observed the universal character of phenomena in language, in the same way as Darwin, when it comes to the laws of evolution of organisms.

"... On ne pourrait concevoir un tel changement [lors de l'introduction de normes dans la langue] que par l’intervention de spécialistes, grammairiens, logiciens, etc.; mais l’expérience montre que jusqu’ici les ingérences de cette nature n’ont eu aucun succès" (De Saussure, 1985, p. 107). "How poor will his (of man) products be, compared with those accumulated by nature during whole geological periods." (Darwin, 1859, p. 66) [*Origin of Species*: second British edition (1860), page 84.] Many more such, almost identical statements, can be found in *The origin of species* and *Cours de linguistique general*, with Darwin talking about organisms and Saussure about language.”

On p. 65: “This universality in language, which can also be revealed in other phenomena, was emphasized by linguists even after De Saussure, especially Louis Hjelmslev. In his famous monograph, a scientific study, *Prolegomena to the Theory of Language*, he says: ‘In a new sense, it seems that it is as fruitful as it is necessary to establish a certain common point of view for a whole range of sciences, from literature science, through the science of art, musicology and general history, to logic and mathematics, wouldn't they all, from such a common platform, focus on the problem defined by linguistics. Each of them will be able to contribute to the general science of language in their own way if they try to investigate to what extent and in what way their subject can be subjected to an analysis that would be in accordance with the requirements of language theory, so perhaps new light could be shed on these disciplines, encourage them to do their own self-reflection. In this way, through all-round fruitful cooperation, it would be possible to arrive at a kind of general encyclopedia of sign structures’ (Hjelmslev, 1980, p. 101)”.

On p. 223: “This Ideas for possible research into the scientific problems that are the subject of this study began in the early seventies, when I came across literature on such biochemical processes as the *transcription* and *translation* of genetic informations from one macromolecular language to another...”

2. A new elaboration

In the previous work (MMR, 2021a)[4] we presented a new type of mirror symmetry, expressed through the number of atoms in the set of 20 protein amino acids (AAs), arranged by chemical similarity into two columns and 10 rows (Tables 1 and 2) (Tables 1 in relation to Table 3; Table 2 in relation to Figure 1); the 10 rows with 5 quarters (Table 2) and two columns with 4 quintets (Table 4). Mirroring itself is created by crossing the last column of the periodic system of numbers (PSN, Figure 2) and the path of the largest change on the 6-bit binary tree (Table 2). That fact alone justifies the title of this paper. Another reason for title justification lies in the fact that in most of the illustrations of that previous paper (MMR, 2021a) the unity of chemism and semiosis is presented.

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 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".) By chemism we mean the chemical affinity and chemical reactivity of substances.

However, independently of the mentioned previous paper MMR, 2021a), we also presented the argumentation about the unity of chemism and semiosis in other papers, some of which were published before (MMR, 2018a, 2018b) and some after (MMR, 2021b, 2022) the cited work.

[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, pp. 99-100)".]

But what is most interesting is that the argumentation for the validity of the claim (attitude) contained in the title of this paper found already in the first results of genetic code researches. We mention examples. Codon AUG, as a chemical entity, encodes the amino acid methionine as a corresponded chemical entity; however, in parallel, it encodes a non-chemical entity, actually an event – the initiation of protein synthesis. And, second

[4] Brief communication in: arXiv:2108.01563v4 [q-bio.BM]. Along with this quote, it should also be said that this is the fourth step on the way to the definitive version of the paper. The first three steps are listed in my website, under the same title. (http://www.rakocevcode.rs)

example: the codons AGA and AGG in the standard genetic code encode the amino acid arginine, while in the mitochondrial code, they encode an event: the termination i.e. the end of protein synthesis. All together, we see that in the genetic code there is a unity of chemical and non-chemical entities.

3. New insights

In this paper, we continue to present new examples of the said new type of mirror symmetry in a set of 20 protein AAs. So, let us look at the PPAASS arrangement in Table 1 (Box 2), where we find something that cannot be expected from the aspect of everything that is known so far about causality in the natural sciences, primarily physics and chemistry. We find a strict mirror symmetry of quantities more than strangely obtained – by summing the ordinal number of each individual amino acid, the number of atoms in the amino acid molecule and the number of protons in those atoms (in the side chain of AA). It is strange and unbelievable, but at the same time it is also a serious fact. The essence – the chemical properties of similarity of AAs – is strict, but the form (semiosis) is also strict;[5] and in fact, the semiotic *sign* is also strictly constructed, as a unity of the *signifier* – the mirror image of the sum of the quantities indicated above and the *signified*, as the real chemical entities.[6]

Box 2. The PPAASS arrangement (Perfect Protein Amino Acid Similarity System)

The PPAASS arrangement was originally given as "The order of protein amino acids based on chemical similarity" (PAAS) (MMR, 2019, Table 2, p.14); but we have renamed it here in response to Rosemarie Swanson's appeal that "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" (Swanson, 1984, p. 201). Namely, we want to show that the real system of 20 existing protein AAs is actually the desired *Perfect system* and that there is no need to add new AAs. In addition, additional 2 AAs (selenocysteine and pyrrolysine) that can be incorporated by special translation mechanisms, we will consider as a change within the degree of freedom, which freedom applies to all exceptions to the standard GC, to all deviant Genetic codes (MMR, 2018a, Box 2, p. 41).

The perfection of the PPAASS arrangement is also reflected in the fact that when moving from the 4:6 distinctions to the 5:5 distinctions (all five and five amino acids in both decades), symmetrically arranged quantities are obtained in a new way. Admittedly, not as a mirror image of the original, but a strict "quantization", a consistent change for

[5] MMR, 2004, p. 233: "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."

[6] De Saussure, 1985, p. 100: "Le lien unissant le signifiant au signifié est arbitraire, ou encore, puique nous entendons par signe le total résultant de l'association d'un signifiant à un signifier nou pouvons dire plus simplement: le signe linguistique est arbitraire. … Le mot arbitraire appelle aussi une remarque. Il ne doit pas donné 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."

the second-order unit in the quantity notation (Table 5). As a curiosity, or perhaps more than that, it should be noted that the first quantity is actually the sum of the first three perfect numbers (530 = 6 + 28 + 496).[7]

In addition, there is at least an analogy (correspondence?) with the result of the distribution of AAs on four stereochemical types[8] (031, 041, 051, 061, 071), where "quantization" is with the same change for a second-order unit in the quantity notation (Table 6, on the right, in relation to Figure 3). With an insight into the fact that the quantities in the arrangement on Table 6 are literally "taken off" from the diagonal of PSN (Figure 2), there can no longer be any doubt that semiotic arbitrariness is an essential feature of the Genetic Code; nor that the genetic code represents the unity of chemical and non-chemical entities; finally, there can be no doubt that GC itself, in total, represents a kind of semiotic system.

*

Because of those readers (because of that part of the scientific public) who will think that the views just presented were adopted too quickly, and that they are also too optimistic, we believe that we should go a step further in testing the PPAASS arrangement. The best way to do this is for the test to be one possible (chemically justified) pairing of AAs. Can the resulting sequence of 10 AAs pairs also satisfy R. Swanson's requirement of ideality and perfection, but also our requirement to simultaneously express both the chemical properties and the semiotic essence of the amino acid code; in other words, to get: SSAAPP (Similarity System of Amino Acid Perfect Pairs). But then the question arises, whether the pairing that is contained in PPAASS, and which, obviously, has a chemical justification (GA, VP, IL, KR, QE, etc.) (Table 1), but does not take into account the distinctions of AAs into four stereochemical types (Rakočević and Jokić, 1996, Table 2, p. 347) nor into four types of diversity (Figure 4 and Table 7 in this paper); or so that these two distinctions are taken into account? The test showed that the latter (taking into account both: the four stereochemical types, as well as the four types of diversity of protein AAs) is correct (Tables 8 and 8.1).

*

Table 6.1 shows how the sequence of 10 pairs is constituted in SSAAPP (Table 8). When deciding on the order and position of the pairs, both classifications of amino acids had to be taken into account: classification into four stereochemical types, as well as in four types of diversity. Thus, at first there must come pairs from the set of 16 AAs of the

[7] With the change by 0 and 1 we have the number of nucleons (Table 5.1: 531/724 in two columns and 530/725 into two light and three dark "belts", respectively.

[8] Details about the four stereochemical types of AAs in (Popov, 1989) and in (Rakočević & Jokić, 1996).

alanine type, and, at the end their four chalcogen, 2 oxygenic and 2 sulfuric, because sulfur comes from the third group of the periodic system of chemical elements, while the previous pairs posses only elements from the first and second periods. Only after that come AAs from the remaining three stereochemical types. As we are dealing with pairs here, one would think that glycine and proline (GP) go together, since they are singlets, each in its stereochemical type, and as we find them in the basic setup of the four types of diversity (Figure 4). Also the valine-isoleucine pair (V-I) appears to be predetermined, as these are the only two AAs in the valine type. However, it is not so. The analysis showed that the third key must be included here, which is the key of classification of AAs into two classes handled by two classes of enzymes aminoacyl-tRNA synthetases (aaRS).[9] The same key had to be used when pairing ST and CM into SC and TM (MMR, 1998, Surv. 4, p. 290).

4. Discussion

If there were no other evidence that the genetic code itself has a semiotic nature, the mere fact that it represents the unity of chemical and non-chemical entities (as we have shown above, in the last paragraph of Section 2) would suffice. If it were not so, the synthesis of proteins would go on endlessly, or there would be a chaotic "breakdown" into larger and smaller sequences of proteins and peptides. On the other hand, if there was no a singlet codon-code determination of the initiation of protein synthesis (with the validity of the principles of similarity and self-similarity), a chaotic state would also occur, an orderly system-arrangement could not be obtained, as a pre-condition for the origin of life.[10]

However, despite the sufficiency of such an argumentation, within this discussion, we try to shed more light on the facts and arguments given in the previous Sections.

I

From the above facts and elaboration, a very important principle can be observed, valid in the genetic code, which could not be observed without a semiotic approach: with as few of the same quantities as possible (signifiers) to be designated as many different qualities as possible (signified). The next point is another important reference to De Saussure. The arbitrariness of signifiers has limitations (Box 3). We see this primarily in that, in all important cases, chemical distinctions are accompanied by changes in quantities for the unit of the first, second, and third order; for the unit in two or three

[9] Class I and II aminoacyl-tRNA synthetases attach amino acids to the 2′- and 3′-OH of the tRNA terminal adenosine, respectively. The only exception is phenylalanyl-tRNA synthetase (PheRS), which structurally belongs to Class II but attaches phenylalanine to the 2′-OH.)

[10] The same would be true for nucleotide sequences (Figure 5, in relation to Survey). We have elaborated the connection between amino acid and nucleotide components in GC in the Scenario, given in the previous work (MMR, 2018a, Section 2, p. 32).

positions of the quantity records.[11] We find such a situation in Tables 1– 8 and other illustrations in this as well as in my previous works.

Box 3. De Saussure's argumentation

De Saussure, 1985, pp. 182–183: "Tout ce qui a trait à la langue en tant que système demande, c'est notre conviction, a être abordé de ce point de vue, qui ne retient guère les linguistes: la limitation de l'arbitraire. C'est la meilleure base possible. En effet tout le système de la langue repose sur le principe irrationnel de l'arbitraire du signe qui, appliqué sans restriction, aboutirait à la complication suprême. … Si le mécanisme de la langue était entièrement rationnel, on pourrait l'étudier en lui-même; mais comme il n'est qu'une correction partielle d'un système naturellement chaotique, on adopte le point de vue imposé par la nature même de la langue, en étudiant ce mécanisme comme une limitation de l'arbitraire." [De Saussure, 1985, p. 33: "On peut donc concevoir *une science qui étudie la vie des signes* … Nous la nommerons *sémiologie* (du grec semeîon, "signe"). Elle nou apprendrait en quoi consistent les signes, quelles lois les régissent. Puisque'elle n'existe pas encore, on ne peut dire ce qu'elle cera; mais elle a droit à l'existence, sa place est déterminée d'avance. La linguistique n'est qu'une partie de cette science générale, les lois que découvrira la sémiologie seront applicables à la linguistique, et celle-ci se trouvera ainsi rattaché à un domaine bien défini dans l'ensemble de faits humains."]

II

With the facts and argumentation that we have presented in this paper, our hypothesis about a prebiotic complete genetic code is becoming now clearer (MMR, 2004, Section 7.1, p. 231). Only those aggregations of amino acid molecules that are prebiotic complete, in the sense of the PPAASS and SSAAPP system-arrangement, can be candidates for the generation of the genetic code.[12] This follows from the fact that the same Mendeleev principles apply to molecules in PPAASS as to pairs of molecules in SSAAPP, which we find to apply to chemical elements (atoms) in PSE (Remark 1).

Remark 1. Mendeleev's key principles are as follows: 1. Principle of continuity; 2. Principle of minimum change; 3. Principle of rows and columns; 4. Principle of cyclicity; 5. Principle of parity/oddity.[13] [The elements of the first group (Cu, Ag, Au) Mendeleev also placed at the end of the Table (Kedrov, 1977, pp. 128-129, Photocopy XII). In addition, he places the noble gases, both in zeroth and in the eighth group of PSE (Kedrov, 1977, Table 13, p. 183).]

III

Apart from the justification of the title of this work, given through chemistry and physics, the argumentation is also given through mathematics, specifically through

[11] In the chemical code (PSE), the minimum change manifests itself as a change for one proton in the atom of each successive element; in GC for a unit change in quantity (in the number of atoms and/or nucleons), namely: the change for the first-order unit, or for the second-order unit, or for third-order unit; or for two units, for three units etc. (MMR, 1994, p. 36: "Such strict regularity in a change (move) exactly for a unit shall be specified (and defined) as *the unit change law*.")

[12] Hence, GC cannot be degenerate, but only generated as it is.

[13] All photocopies from Kedrov's book are also on my website (January 18, 2014) [key words: Mendeleyev's Archive (http://www.rakocevcode.rs)

arithmetic and algebra. There are, however, hints that the unity of chemism and semiosis in GC can be proven through higher mathematics (Koruga, 1992; Raković, 2011; Negadi, 2014, 2023), and also through special mathematics, as is the case with p-adic mathematics. (Dragovich, Dragovich, 2009; Dragovich, Mišić, 2019; Dragovich et al, 2021).

Nevertheless, regardless of results of such a test of higher mathematics, as well as any special mathematics, the fact remains that the genetic code represents the unity of chemism and semiosis.

IV

A few words about significant and unique illustrations. Table 1 (and its derivative Tables from 2.1 to 2.5) presents the perfect amino acid system-arrangement (PPAASS), ordered by chemical similarity of individual molecules, while in Table 2.6, a system-arrangement, according to the similarity of molecular classes, arranged: in the penultimate row are AAs, which contain only carbon and hydrogen in the side sequence; in the last row are those AAs that, in addition to carbon and hydrogen, also contain nitrogen; in the first row are AAs, which, in addition to carbon and hydrogen, also contain oxygen; finally, in the second row are "combined" AAs: glycine, which contains only hydrogen in the side chain; along with it are two amides, which have nitrogen and oxygen added to the hydrocarbon base; finally, there are the only two sulfur AAs, cysteine and methionine.

The chemical connection of Table 2.6 and the following Table 3 is discussed in a previous work (MMR, 2004). It is also important to note that Table 3 directly corresponds with Table 6 through the quantities 60, 66, 78 and their determination by the Golden mean, in relation to the chemical properties of amino acids, as presented in Tables 6.1 and 6.2.

V

Table 6 contains a strictly ordered system-arrangement in which no AA can replace its place with another AA. It is the CIPS (Cyclic Invariant Periodic System): In position 1 there is a class of chalcogenous amino acids (containing either oxygen or sulfur in the side chain); at position 2 are four amino acids of non-alanine stereochemical type; in position 3 are two additionally acidic AAs (possessing a carboxyl group in the side chain also) and two of their amide derivatives; in position 4 there are two basic aliphatic AAs (alanine and leucine), and two amine derivatives (lysine and arginine); finally, at position 5 are four aromatic amino acids.

We singled out Table 6 in this discussion because it most directly shows the unity of chemism and semiosis. The system-arrangement given on the left follows from the golden section determination of seven positions on the genetic-coding binary tree. Thus, 7 "golden" AAs were "selected". Then they select 7 of their chemical counterparts. Finally, those 14 chosen ones are placed in a chemical relationship with the remaining 6.

On the right side, according to the number of atoms in the amino acid molecule (side row), they are classified into classes, so that at the same time they play a non-causal connection with the PSN diagonal, but at the same time based on strictly expressed chemical properties.

VI

Table 6.1 is essentially the same as Table 6, with the focus here on molecular weight. On the other hand, Table 3.2 highlights the relationship between polar charged amino acids, polar non-charged and non-polar amino acids. There are 5, 8 and 7, respectively. The system-arangement, presented in Survey 8, shows that the 5-7-8 sequence is generated from a specific genetic mathematical sequence (like the ubiquitous genetic sequences, Fibonacci and Lucas).

The key characteristic of genetic sequences is the following: the follower contains within itself the predecessor, analogous to the events in biological systems, where the descendant, mutatis mutandis, contains within itself the parent.

5. Conclusion

The regularities, presented through previous four sections provide evidence to support the hypothesis, given in the title of this paper, that in reality Genetic code exists as a specific semiotic system; more exactly, Genetic code represents the unity of chemism and semiosis.

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TABLES

Table 1. Perfect Protein Amino Acid Similarity System (PPAASS)

on		an	pn		pn	an		on
01	**G**	01	01		31	08	N	11
02	**A**	04	09		31	07	D	12
03	**V**	10	25		17	05	S	13
04	**P**	08	23		25	08	T	14
05	I	13	33		25	05	**C**	15
06	L	13	33		41	11	**M**	16
07	K	15	41		49	14	**F**	17
08	R	17	55		57	15	**Y**	18
09	Q	11	39		69	18	**W**	19
10	E	10	39		43	11	**H**	20
055		102	**2**98		**3**88	102		**1**55
455 | **554**					645 | 546			
(455 | 554) + (645 | 546) → (1100 + 1100) → 10 x 220								

on – Ordinal number; an – Atom number; pn – Proton number

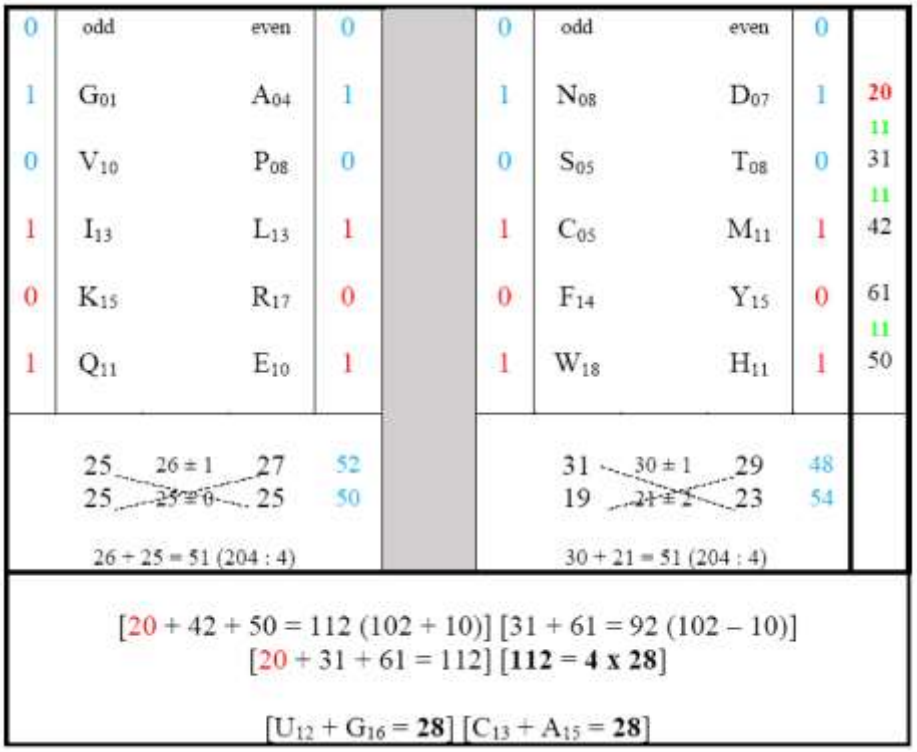
Table 2. Mirror symmetry through the number of atoms in AAs

00	00	00	+	2	→	02	→	20		**1**	
11	11	11	+	2	→	13	→	31	←	**0**	(5)
22	**22**	**22**	+	2	→	24	→	42		**1**	
33	—	11	+	5	→	16	→	61		**0**	
44	**22**	00	+	5	→	05	→	50		**1**	(2)
55	11	**(044)**								**0**	
66	00	G **01**	A **04**	N **08**	D **07**	→	20				
77		V **10**	P **08**	S **05**	T **08**	→	31			**022**	
88		I **13**	L **13**	C **05**	M **11**	→	42			—	
99		K **15**	R **17**	F **14**	Y **15**	→	61			**022**	
		Q **11**	E **10**	W **18**	H **11**	→	50				

(Quantity 044 see as zeroth one in MMR, 2019, Tab. A3; and in MMR, 2021a, Fig. 2.)

Taken from: arXiv:2108.01563v4 [q-bio.BM], (Box 1), modified and refined. The first and third columns are AAs from odd positions within PPAASS in Table 1, while the second and fourth columns are from even positions.

Table 2.1. Odd and even quintets, taken from Table 2 (I)



Atom number in amino acid side chain. Again even / odd by column, for "bodies". We note that the quantities 48, 50, 52 and 54 are also in the central area of the Periodic System of Numbers (PSN: Figure 2).

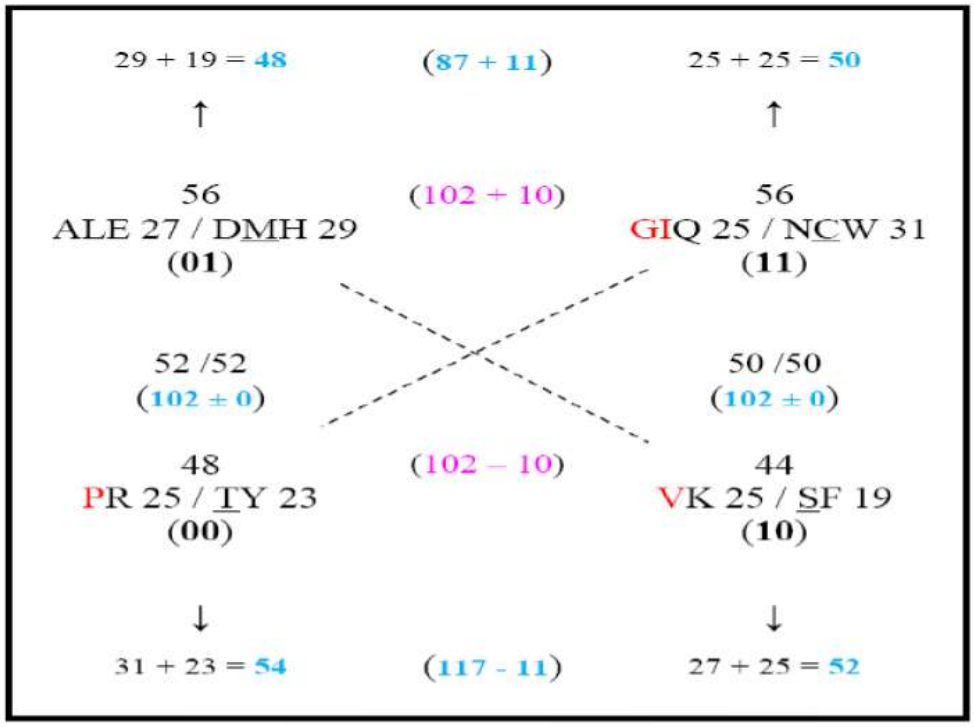
Table 2.2. Odd and even quintets, taken from Table 2 (II)

0	odd	even	0		0	odd	even	0	
1	G_{10}	A_{13}	1		1	N_{17}	D_{16}	1	**56** 11
0	V_{19}	P_{17}	0		0	S_{14}	T_{17}	0	67 11
1	I_{22}	L_{22}	1		1	C_{14}	M_{20}	1	78
0	K_{24}	R_{26}	0		0	F_{23}	Y_{24}	0	97 11
1	Q_{20}	E_{19}	1		1	W_{27}	H_{20}	1	86
	52 53 ± 1 54		97			58 57 ± 1 56		93	
	43 ~~43 ± 0~~ 43		95			37 ~~39 ± 2~~ 41		99	
[53 + 43 = 97 – 1] [57 + 39 = 97 – 1] [97 = 87 + 10 & 117 – 20]									
[56 + 78 + 86 = 220] [56 + 67 + 97 = 220]									
[65 + 87 + 68 = 220] [65 + 76 + 79 = 220]									

[(78 – 67 = 11) / (97 – 86 = 11)] [(87 – 76 = 11) / (79 – 68 = 11)]

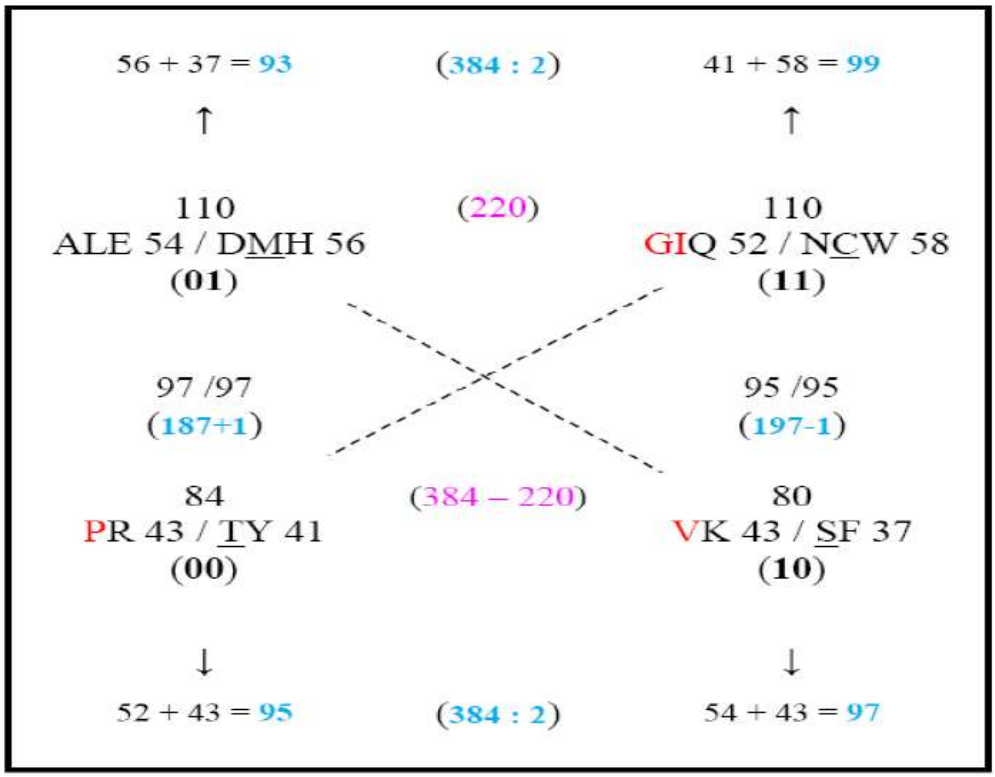
Atom number in amino acid whole molecule. Again even/odd by column, for whole molecule. We note that the quantities 93, 95, 97 and 99 are four last two-digit numbers of the decimal system, as we also find in PSN, in Figure 2.

Table 2.3. Distribution of quintets from Table 2 by even and odd positions (I)



Atom number in amino acid side chain. Even vs odd and vice versa for "body". We note that the quantities 48, 50, 52 and 54 are also in the central area of the Periodic System of Numbers (PSN: Figure 2).

Table 2.4. Distribution of quintets from Table 2 by even and odd positions (II)



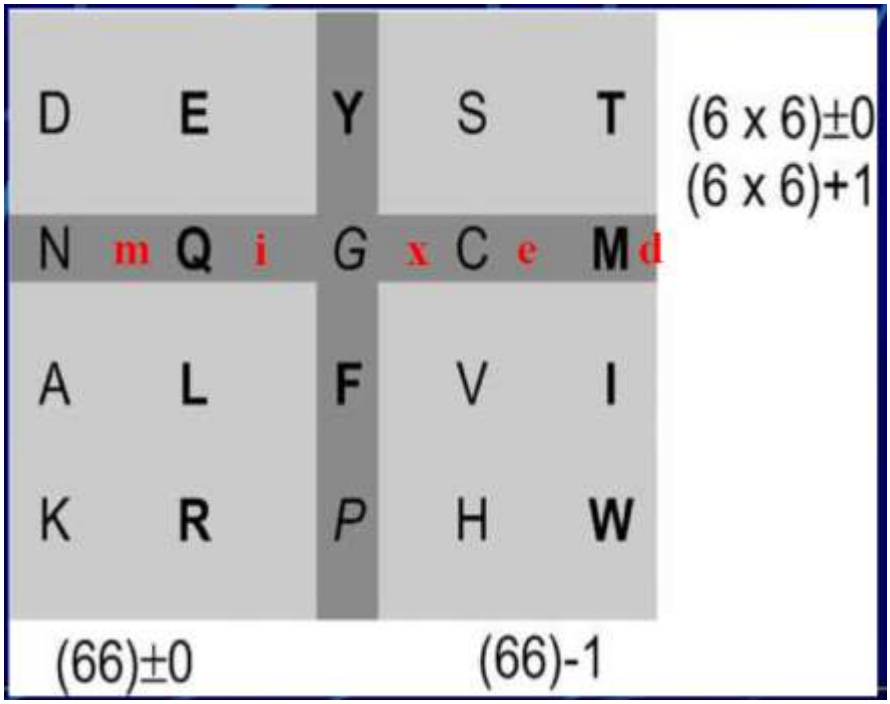
Atom number in amino acid side chain. Even vs odd and vice versa for whole molecule. Atom number in amino acid whole molecule. Again even/odd by column, for whole molecule. We note that the quantities 93, 95, 97 and 99 are four last two-digit numbers of the decimal system, as we also find in PSN, in Figure 2.

Table 2.5. Significant quantities "6 x 6" and "66" in the Genetic Code (I)

2 x (6 x 6) ± 00				
G 01	A 04	N 08	D 07	**20**
				11
V 10	P 08	S 05	T 08	31
				11
I 13	L 13	C 05	M 11	**42**
K15	R 17	F 14	Y 15	61
				11
Q11	E 10	W 18	H 11	**50**
51-1	51+1	51-1	51+1	**102 + 10**
(2 x 66) ± 00				102 - 10

Correspondences: Table 2 and Survey 1–5. Uniqueness of quantity 66 and 36 in the mentioned Surveys.

Table 2.6. Significant quantities "6 x 6" and "66" in the Genetic Code (II)



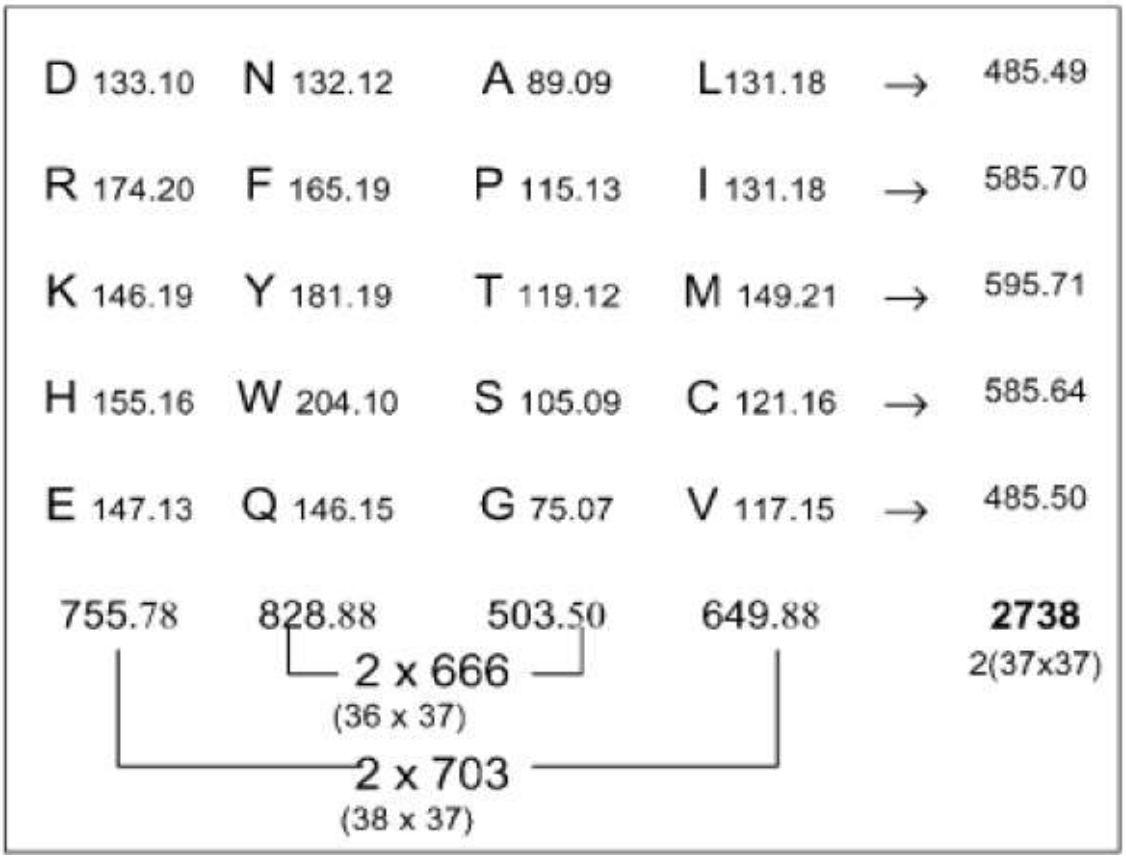
Classification of amino acids according to similarity/dissimilarity of molecules classes. From (MMR, 2004, Tab. 9, p. 229): "First row (down): N-ended AAs. Second row: solely C-ended AAs. Last row (up): O-ended AAs. First to last row: remaining five AAs (one solely H-ended, two S-ended and two N-, O-ended, 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 x 6) ± 0 of atoms, and within vertical leg (without glycine), there are (6 x 6) ±1. Without cross: on the left there are (66) ± 0 and (66)–1 on the right." The significance and uniqueness of the quantities 36 and 66 can be seen in Surveys 1–5.

Table 3. A harmonic structure of Genetic code (I)

					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
60	66		78						
					1255	1255	1465	1465+9	2738.04

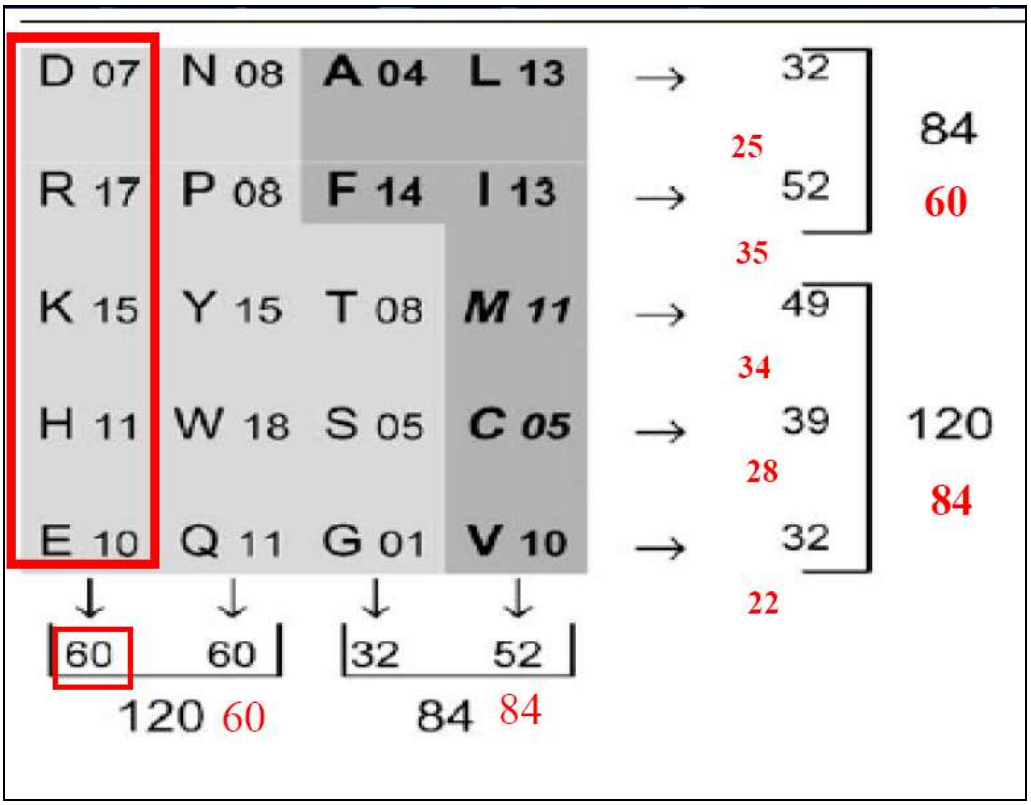
From (MMR, 2004, Table 1, p. 233). "Four choices after four types of isotopes: (a) The number of nucleons within 20 AAs side chains, calculated from the first, the lightest nuclide (H-1, C-12, N-14, O-16, S-32). (b) The number of nucleons within 20 AAs side chains, calculated from the nuclide with the 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 x (37 x 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."

Table 3.1. A harmonic structure of Genetic code (II)



Explanation in the text, in: (MMR, 2004, Table 1, p. 233). It can be noticed that the quantities 36 and 38 form a common sequence with the quantities 34 and 40, in Table 7. And this sequence we also find in the central area of the system-arrangement presented in Figure 2, that is, in the central area of PSN.

Table 3.2. A harmonic structure of Genetic code (III)



The splitting of AAs into polar (light ton) and non-polar (bold, dark ton). The polarity as hydropathy (Kyte and Doolittle, 1982, Table 2, 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 other three rows in relation to first two columns (120 atoms). In the red frame are the polar charged AAs. The numbers marked in red represent the number of atoms in polar uncharged and nonpolar amino acids. As we can see, the balances apply both ways: in the set of all 20 amino acid molecules, as well as in the subset of polar charged and subset of all the others. (Note: The classification of amino acids into 5 polar charged, 7 non-polar and 8 polar non-charged corresponds to a unique situation in the series of natural numbers; with a series determined by the law of genetic nature (the follower contains the predecessor) (Survey 8). [*Note*: Here one can notice a *vice-versa* change in the positions of phenylalanine and proline: from F-P in Tables 3 and 3.1, to P-F in this Table. Just such a change (balancing and nuancing, according to the definitions given in: MMR, 2018a, p. 33) creates the conditions for the distinction (classification) of amino acids into 5 polar charged, 7 non-polar and 8 polar non-charged, corresponding to a unique genetic mathematical series (Survey 8).]

Table 4. The four quintets of amino acids within PPAASS in Table 1 (I)

36	36 - 3	66	66 +3		
G 01	**N 08**	**L 13**	**M 11**	**(33)**	
A 04	D 07	K 15	14	(40)	**120**
V 10	**S 05**	**R 17**	**Y 15**	**(47)**	
P 08	T 08	Q 11	W 18	(45)	
I 13	**C 05**	**E 10**	**H 11**	**(39)**	84
(a) **24**/12	**18**/15	**40**/26	**37**/32	85/**119**	
(b) (36)	**(33)**	(66)	**(69)**	102/**102**	84 33 ↓
[(85 = 87 – 2) (**119** = **117** + 2)] [(85 + 102 = 87 +100] [001 + 220 = **119** + **102**					**119**

The first and third quintet are taken from the first decade of Table 1, and the second and fourth from the second decade. The quantities 117 and 87 respectively refer to the number of hydrogen and non-hydrogen atoms in the set of 20 amino acids.

Table 4.1. The four quintets of amino acids within PPAASS in Table 1 (II)

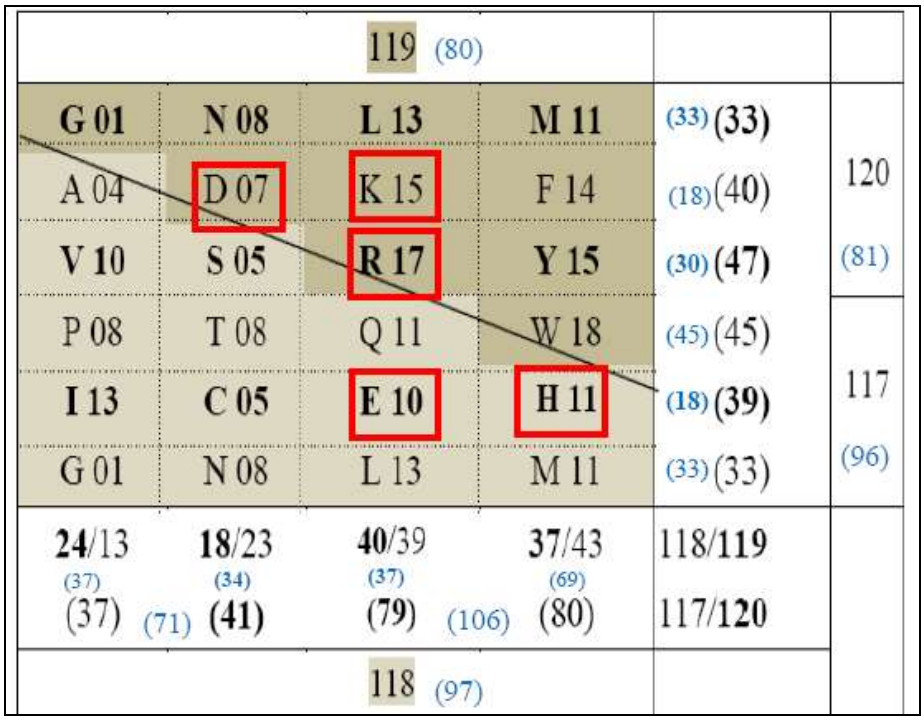
36	36 - 3	66	66 +3		
G 01	**N 08**	**L 13**	**M 11**	**(33)** 33 / 00	81
A 04	D 07	K 15	F 14	(40) 18 / 22	120
V 10	**S 05**	**R 17**	**Y 15**	**(47)** 30 / 17	39
P 08	T 08	Q 11	W 18	(45) 45 / 00	63
I 13	**C 05**	**E 10**	**H 11**	**(39) 18** / 21	84
36 / 00	26 / 07	24 / 42	58 / 11		21
62 /42		82 / 18		144 / 60	

[(81 vs 82) and (63 vs 62)] / [(39 vs 42) and (21 vs 18)]

[(82 - 81 = 1) and (63 – 62 = 1)] / [(42 – 39 = 3) and (21 – 18 = 3)]

Everything is the same as in the previous Table 4, with the fact that here distinctions (in the number of atoms) are given in the subset of polar-charged AAs and subset of all others. Considered so separately, through columns and rows, changes are for ± 1 and ± 3. On the other hand, the quintet changes are for ± 3. All together can be compared to the system-arrangement (ordered by similarity within molecules classes) in Table 2.6, where the changes are for ± 1.

Table 4.2. Diagonal distinction of the quintets given in the previous Table 4.1



(Rows in red: 32 / 17 / 21) / (Columns in red: 07 / 42 / 11)
[32 vs 42; 17 vs 07 and 21 vs 11)]
Correspondences in blue:
(80 vs 81), (96 vs 97); (96 vs 106), (81 vs 71)

Everything is the same as in the Table given in the previous paper (MMR., 2021a, Fig. 3, p. 13) (arXiv:2108.01563v4 [q-bio.BM]) with the fact that here, along with the diagonal, a distinction has been added to the subsets of polar-charged and all other AAs: "A specific protein amino acids arrangement: The first row is repeated at the bottom, and thus one cyclic system is obtained. There are 117 atoms in two outer columns; at even positions 118, at odd 119; in two inner columns 120 atoms. On the other hand, in the lower half of the Table there are 117 atoms ones more; in the lower diagonally 'wrapped' area 118, and in the upper 119; in the upper half of Table 120 atoms. The repeated four AAs at the bottom of the Table make to achieve a diagonal balance with a difference of only one atom; moreover, to establish a sequence from the series of natural numbers: 117, 118, 119, 120" (MMR, 2017, Table 4, p. 13).

Table 5. Further distinctions in PPAASS (Table 1)

Odd / Odd		
GVIKQ 25+**50**+139 = 214	NSCFW 75+**50**+191 = 316	→ **530**
Last / First		
LKRQE 40+66+207 = 313	NDSTC 65+33+129 = 227	→ **540**
First / Last		
GAVPI 15+36+91 = 142	MFYWH 90+69+259 = 418	→ **560**
Even / Even		
APLRE 30+**52**+159 = 241	DTMYH 80+**52**+197 = 329	→ **570**

Order of quantities according to Table 2: ordinal number, number of atoms, number of protons. [For example: ordinal number: (G_{01}+V_{03}+I_{05}+K_{07}+Q_{09}=25); number of atoms: (1+10+13+15+11=50); number of protons: (1+25+33+41+39=139).]

Table 5.1. Nucleon number in PPAASS (Table 1)

(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)	
			724			**725**
		531				530

The change of ±1 [(725 – 724 = 1) and (531 – 530 = 1)], compared to the change for ±2, as we find in Table 5.3.

Table 5.2. Neutron number in PPAASS (Table 1)

(1)	G	00	27	N	(11)	**61**
(2)	A	06	28	D	(12)	
(3)	V	18	14	S	(13)	70
(4)	P	18	20	T	(14)	
(5)	I	24	22	C	(15)	**104**
(6)	L	24	34	M	(16)	
(7)	K	31	42	F	(17)	168
(8)	R	45	50	Y	(18)	
(9)	Q	33	61	W	(19)	**166**
(10)	E	34	38	H	(20)	
		233			(5**6**4)	**331**
			336		(5**7**4)	238

The uniqueness of the quantities 233 and 336 is found in the relationships within the 3-bit binary tree (number 2 as 010; number 3 as 011 and number 6 as 110) (Survey 9).

Table 5.3. Neutron number in PPAASS:
Further distinctions

(1)	G	00	27	N	(11)	**61**
(2)	A	06	28	D	(12)	
(3)	V	18	14	S	(13)	**70**
(4)	P	18	20	T	(14)	
(5)	I	24	22	C	(15)	**104**
(6)	L	24	34	M	(16)	
(7)	K	31	42	F	(17)	168
(8)	R	45	50	Y	(18)	
(9)	Q	33	61	W	(19)	166
(10)	E	34	38	H	(20)	
		233				**235**
			336			334
(234 ± 1) (335 ± 1) [335 – 234 = 101]						

The change of ±2 [(235 – 233 = 2) and (336 – 334 = 2)], compared to the change for ±1, as we find in Table 5.1. The uniqueness of the quantities 233 and 336 is found in the relationships within the 3-bit binary tree (Survey 9).

Table 5.4. Isotope number in PPAASS (Table 1)

(1)	G	02	17	N	(11)	**43**
(2)	A	08	16	D	(12)	
(3)	V	20	11	S	(13)	64
(4)	P	16	17	T	(14)	
(5)	I	26	12	C	(15)	**88**
(6)	L	26	24	M	(16)	
(7)	K	31	28	F	(17)	124
(8)	R	34	31	Y	(18)	
(9)	Q	22	36	W	(19)	**102**
(10)	E	22	22	H	(20)	
		207			(440)	**233**
			214		(**402**)	188

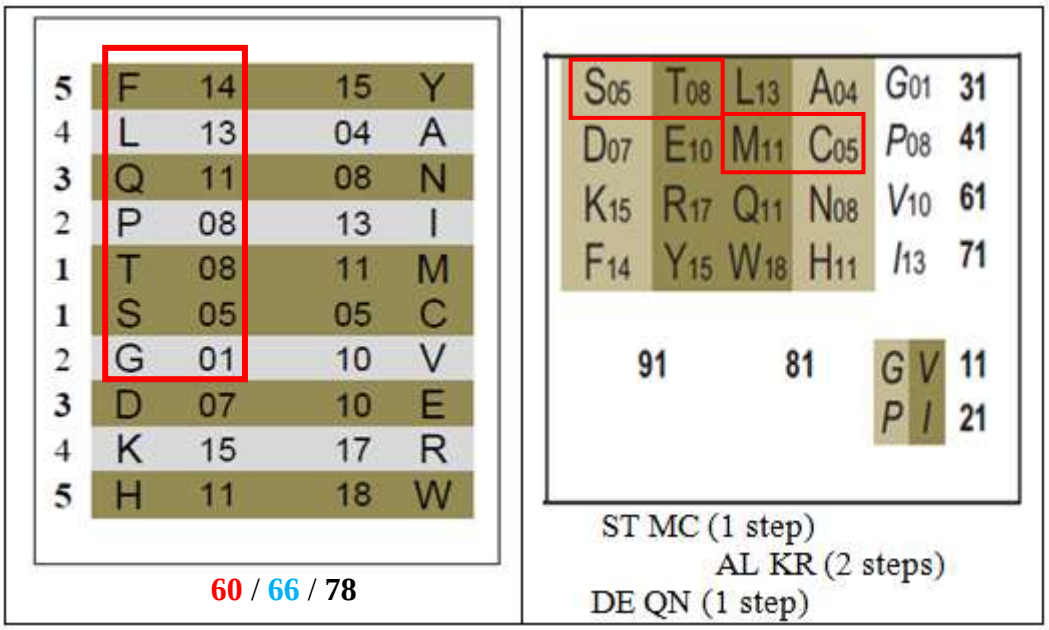
Isotope number as in (MMR, 2004, Table 7). The result 440 / 402 is the reverse case in relation to the result in Tab. 5.5.

Table 5.5. Isotope number in PPAASS:
Further distinctions

(1)	G	02	17	N	(11)	**43**
(2)	A	08	16	D	(12)	
(3)	V	20	11	S	(13)	**64**
(4)	P	16	17	T	(14)	
(5)	I	26	12	C	(15)	**88**
(6)	L	26	24	M	(16)	
(7)	K	31	28	F	(17)	124
(8)	R	34	31	Y	(18)	
(9)	Q	22	36	W	(19)	102
(10)	E	22	22	H	(20)	
		207			(**402**)	**195**
(440 | 044			214		(440)	226
842 | 248 (248 x 2 = 496)			402 | 204			

Isotope number as in (MMR, 2004, Table 7). The 044 as in Tab. 2. The number 496 is the third perfect number, and the number 204 corresponds to the number of atoms in 20 amino acids (side chains). The result 402 / 440 is the reverse case in relation to the result in Tab. 5.4.

Table 6. Two amino acid systems: CIPS on the left and SCAS on the right



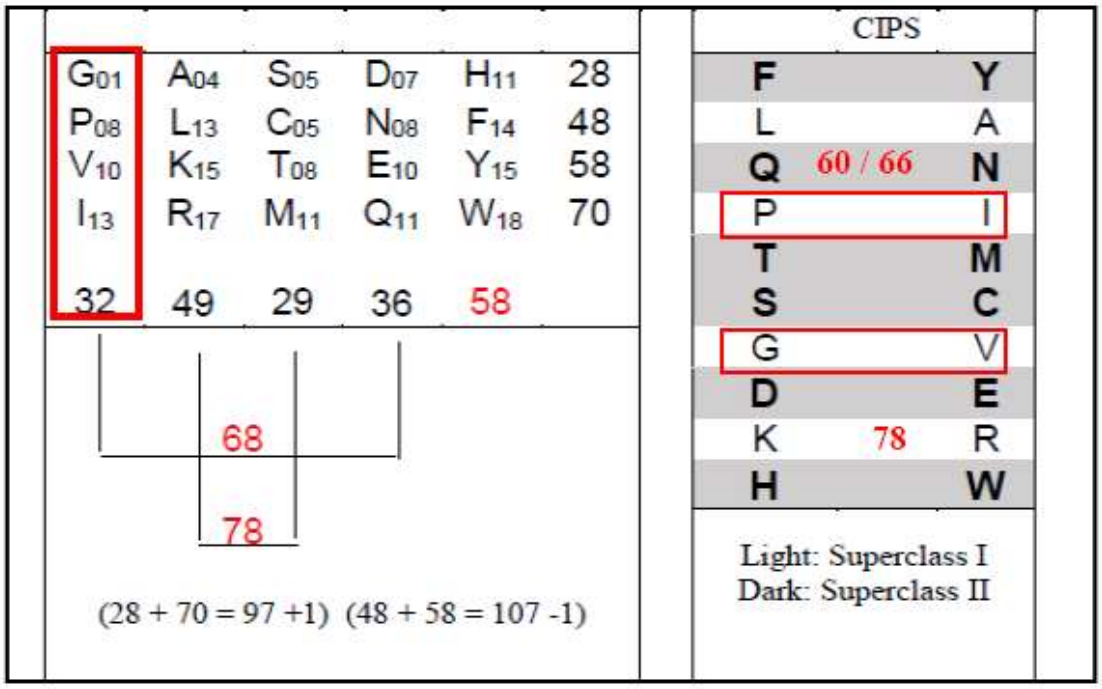
CIPS: Cyclic Invariant Periodic System from: MMR, 2011, Fig 6, p. 832; SCAS: Stereo-Chemically Arranged System. From: MMR, 2019, Fig 1, p. 6. In both cases, the number of atoms in the molecule (in the side chain) is attached to the amino acid designation in normal and index notation, respectively. MMR, 2011: The Cyclic Invariant Periodic System (CIPS) of canonical AAs. … 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. Notice, that each amino acid position in this CIPS is strictly determined and none can be changed. MMR, 2019: The right picture: Dark tones: Class I of amino acids handled by class I of enzymes aminoacyl-tRNA synthetases [except T]; light tones: Class II [except C]."

Table 6.1. "Golden" amino acids, their complements and non-complements

F 14		15 Y		F 14	15 Y
L 13	66-1	04 A		L 13	78±0 04 A
Q 11		08 N		**K 15**	**17 R**
P 08		13 I		P 08	13 I
T 08		11M		T 08	11M
	60+1			60+1	
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	**78**±0	**17 R**		Q 11	66-1 08 N
H 11		18 W		H 11	18 W

The left side is taken from (MMR, 2018a, Surv. 3, p. 39). That is the natural state of GC on a 6-bit binary tree, from the aspect of Golden mean determination. [The effect of the Golden mean: to balance less complex and more complex amino acid molecules.] The right side is the expectation from the chemistry perspective: in one subset less complex and in a second subset more complex molecules.

Table 6.2. Four "cycles" of AAs in CIPS (I)



From (MMR, 2011, Figure 6, p. 832), refined and adapted. Significant quantitative relationships: [(97 = 87 + 10) (107 = 117 - 10)] [117 as the number of H atoms within 20 AAs (side chains); 87 as the number of non-H atoms. [CIPS: Cyclic Invariant Periodic System.]

Table 6.3. Four "cycles" of AAs in CIPS (II)

H 11	W 18	→	29	78
K 15	R 17	→	32	
D 07	E 10	→	17	
N 08	Q 11	→	19	68
P 08	I 13	→	21	
A 04	L 13	→	17	
G 01	V 10	→	11	
S 05	C 05	→	10	58
T 08	M 11	→	19	
F 14	Y 15	→	29	
Odd 35	62		097	4 x 34
11	01		10	2 x 34
Even 46	61		107	

[CIPS: Cyclic Invariant Periodic System.] The classes are marked with colors as in Table 6. The new arrangement of amino acid pairs (chemically also meaningful) shows that the quantities 58, 68, 78 are obtained again, as we find in the original arrangement (Table 6.2). [Revalidation of the principle: "with as few of the same quantities as possible (signifiers) to be designated as many different qualities as possible (signified)" (Discussion, I).]

Table 6.4. Two classes and two superclasses of amino acids

28	09 19	G **P** A **K**	(2) (4)	23 30	V **I** L **R**	53	**81**	32 / 49
53	13 15 25	S **T** D **N** **F** H	(1) (3) (5)	16 21 33	C **M** E **Q** Y **W**	70	**123**	28 / 95
81		33 / 48			27 / 96	**123**	204	60 / 144

Primary superclass vs Secondary class: (32 vs 33 and 49 vs 48)
Secondary Superclass vs Primary class: (28 vs 27 and 95 vs 96)
[96 = 48 x 2]

(KR 32 vs DEH 28); and in Tab C3: (DKE 32 vs RH 28)
[Primary superclass KR vs Secondary superclass DEH]
Table C3: [Odd DKE vs even RH]

Everything is the same as in: (MMR, 2011, Fig 7, p. 833) with the fact that here distinctions (in the number of atoms) are given in the subset of polar-charged AAs (red) and subset of all others. Legend from the mentioned work: "… on the left there are AAs (81 atoms) from the left side of Figure 8 (class II, with smaller molecules within the pairs); and on the right there are AAs (123 atoms) from the right side of Figure 8 (class I, with larger molecules within the pairs). At the same time very up there are AAs from primary superclass (81 atoms), just aliphatic and nonpolar (A, V, L, I) and "a little" polar (G, P, K, R) (hydrogen and nitrogen are less polar then oxygen!); in the other hand, except aromatic and sulfur AAs, down are AAs from secondary superclass (the row with 123 atoms), also aliphatic, but 'full' polar."

Table 6.5. Relationships among two classes and two superclasses of AAs through non-H atoms

09	03 06	*G*$_{00}$ **P**$_{03}$ *A*$_{01}$ **K**$_{05}$	(2) (4)	07 11	*V*$_{03}$ **I**$_{04}$ *L*$_{04}$ **R**$_{07}$	*18*	27
26	05 08 13	*S*$_{02}$ **T**$_{03}$ *D*$_{04}$ **N**$_{04}$ *H*$_{06}$ **F**$_{07}$	(1) (3) (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* [35]

P$_{03}$+ **K**$_{05}$+ **T**$_{03}$+ **N**$_{04}$+ **F**$_{07}$ = **22**
I$_{04}$+ **R**$_{07}$+ **M**$_{04}$+ **Q**$_{05}$+ **W**$_{10}$ = **30** [52]

(*13* + **30** = 43) (*22* + **22** = 44)

(30 as ½ 60) (27 as ½ 54) (54 = 44 + 10)

Taken from (MMR, 2022, Table C3, p. 80). Two inner rows vs two outer ones. There is also Table C1 for the total number of atoms in the side chains of amino acids, as well as Table C2 for the number of hydrogen atoms. To the left of the shaded column are amino acids of the second class, handled by the second class of aaRS. On the right are AAs of the first class. The first two rows (above) make up the amino acids of the primary superclass of CIPS (Table 6 on the left). The bottom three rows belong to the secondary superclass. Non-bold and italicized amino acids are of lower rank, less complexity; while the bold ones are of a higher rank, that is, of greater complexity. The exception is phenylalanine because as a member of the FY pair it is of lower rank. However, given the fact that PheRS attaches phenylalanine to the 2′-OH of the tRNA terminal adenosine, it is considered to be of higher rank in this constellation. [Class I and II aminoacyl-tRNA synthetases attach amino acids to the 2′- and 3′-OH of the tRNA terminal adenosine, respectively. The only exception is phenylalanyl-tRNA synthetase (PheRS), which structurally belongs to Class II but attaches phenylalanine to the 2′-OH.)]

Table 6.6. Quantitative relationships in Table 6.5

ST+DN+FH = 26 (GP, AK) 9 + (VI, LR) 18 = **27** CM+EQ+YW = 34 (GP, AK) 9 + (ST DN FH) 26 = **35**	26 + 9 = **35** [35+35 = 70] 18 + 34 = 52 27 + 35 = 52 + 10 26 + 34 = 70 - 10
[(2S, 2T, 2D, 2N, 2 F, 2H) (26 x 2 = 52)] (2G, 2P, 2A, 2K) (9 x 2 = 18) **52 + 18 = 70**	(V, I, L, R) 18 (C, M, E, Q, Y, W) 34 18 + 34 = 52
(5 AAs → if two times, then **52**)	(10 AAs → if once, then **52**)

Table 7. Distribution of AAs within four types of diversity according to Fig. 4

$_{01}$G 75.07	$_{05}$S 105.09	$_{15}$Y 181.19	$_{18}$W 204.23
$_{04}$A 88.09	$_{07}$D 133.10	$_{11}$M 149.21	$_{17}$R 174.20
$_{05}$C 121.16	$_{08}$T 119.12	$_{10}$E 147.13	$_{14}$F 165.19
$_{08}$N 132.12	$_{11}$Q 146.15	$_{10}$V 117.15	$_{13}$I 131.18
$_{08}$P 115.13	$_{11}$H 155.16	$_{13}$L 131.07	$_{15}$K 146.19
26 (16)	**42** (17)	**59** (18)	**77**
532.57	**658.62**	725.86	**820.99**

532.57+ 725.86 = 1258.43 ≈ 1258 → 34 x 37

222

658.62 + 820.99 = 1479.61 ≈ 1480 → 40 x 37

[2738.04 ≈ 2738 = 2 x (37 x 37)] [(36 x 37 = 1332) (38 x 37 = 1406)]

From [DOI 10.31219/osf.io/fzgjp] (Table 7, p. 5). Hierarchy of rows and columns taken from Figure 4. It can be noticed that the quantities 34 and 40 form a common sequence with the quantities 36 and 38, in Table 3.1. And this sequence we also find in the central area of the system-arrangement presented in Figure 2, that is, in the central area of PSN.

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

1	2	3	4	5	6	7	8	9	10		
A_4L_{13}	$K_{15}R_{17}$	$F_{14}Y_{15}$	D_7N_8	$E_{10}Q_{11}$	$H_{11}W_{18}$	S_5C_5	T_8M_{11}	G_1V_{10}	P_8I_{13}	→	204
17	+ 32	+ 29	+ 15	+ 21	+ 29	+ 10	+ 19	+ 11	+ 21	=	204
AL_{10}	2	FY_4	DN_4	EQ_4	HW_3	7	8	9	10	$\|_{25}$	111
											11
AL_{10}	2	FY_4	DN_4	EQ_4	6	$\mathbf{SC}_8$	TM_5	GV_8	10	$\|_{43}$	122
											11
1	$\mathbf{KR}_8$	FY_4	4	EQ_4	6	7	TM_5	GV_8	$\mathbf{PI}_7$	$\|_{36}$	133
											10
AL_{10}	$\mathbf{KR}_8$	FY_4	DN_4	EQ_4	HW_3	7	8	9	10	$\|_{33}$	143

Twice the change (in atom number) for the first-order unit and the second-order unit (red color); one time change for the unit of the second order: from quantity 133 to quantity 143 as in Table B6 (66 + 77 = 143). Black indices indicate the number of atoms, and blue indices indicate the number of codons.

Table 8.1. The number of amino acid coding codons (I)

AL 10	FY 4 + DN 4 + EQ 4 + HW 3 = 15	→	25
AL 10 + GV 8 = 18	FY 4 + DN 4 + EQ 4 + SC 8 + TM 5 = 25	→	43
			(68)
GV 8 + PI 7 = 15	KR 8 + FY 4 + EQ 4 + TM 5 = 21	→	36
AL 10	KR 8 + FY 4 + DN 4 + EQ 4 + HW 3 = 23	→	33
[(25 + 33 = **68** – 10) (36 + 43 = **69** + 10)]	[(68 = **58** + 10) (69 = **59** + 10]		**(69)**
(10 + 18 = **28**); (10 + 25 = **35**); (21 + 15 = 36) (23 + 15 = 38) 28 + 35 + 36 + 38 = **0**37 + 100 = **1**37	111+122+ 133+143 = 408 + 101 408 = 204 x 2 (**68** x 3 = 204) (**69** : 3 = 23)		
[(38 – 28 = **10**) (36 – 35 = **01**)]	[(28 + 35 = 63±**00**) (36 + 38 = 63 + **11**)]		

Codon number relationships within Table 8. Quantities 28 and 35, together with quantities 21 and 42 (Survey 7) correspond to the harmonic mean of a 6-bit binary tree (MMR, 1998, Fig. 1). In the final outcome, the whole system-arrangement is determined by the quantities 25 and 36, which we find as unique situations (unique states) in the Periodic system of numbers (Figure 2), and also in two algebraic equations that determine both the chemical and the genetic code (MMR, 2018b, Surveys, 2a and 3a). The uniqueness of the quantities, i.e. the numbers 25 and 36, concerns the fact that there are only two adjacent numbers in the series of natural numbers (they differ by the unit of the first order) whose squares are neighbors, as they differ by the unit of the first order and the unit of the second order. This applies only in the Periodic System of Numbers (PSN) of the Decimal number system, while it does not apply to the other Periodic systems of numbers (Survey 7.2). [*Note:* The two aforementioned algebraic equations, changed for a first-order and/or second-order unit, are found in a mathematical program printed in Darwin's Diagram, the only illustration in his book *On the Origin of Species*. (Table A3 in this paper; then in: MMR, 2019, Tab. C1, Fig. C1; MMR, 2015.]

Table 8.2. The number of amino acid coding codons (II)

					n	c	
K	Y	T	M	→	27	9	
							2
H	W	S	C	→	33	11	
							1
E	Q	G	V	→	36	12	
							2
D	N	A	L	→	42	14	
							1
R	F	P	I	→	45	15	

From (MMR, 2004, Tab. 6, p. 225): Relationships of the number of codons in a harmonic structure of GC (Table 3); c. Codon number; n. Number of nucleotides in codons. There are 25 codons within the even rows, and 36 in the odd rows, which respectively correspond to the number of coding codons for the first two and the second two types of amino acid diversity (MMR, 2018b, Tab. 5 and Section 2.2); in the first three rows 32 codons, and in the last two rows 29 codons, all together as in the first and second half of the Genetic Code Table (not counting STOP codons).

FIGURES

G 10	A 13	N 17	D 16	→	**56**
V 19	P 17	S 14	T 17	→	67
I 22	L 22	C 14	M 20	→	**78**
K 24	R 26	F 23	Y 24	→	97
Q 20	E 19	W 27	H 20	→	**86**
G 10	A 13	N 17	D 16	→	56

(56 + 78 + 86 = 220) (67 + 97 + 56 = 220)

(65 + 87 + 68 = 220) (76 + 79 + 65 = 220)

440 + 56 = 496 [440 | 044]

056 + 067 + **078** + 097 + **086** + 056 → **220** + 220
650 + 760 + **870** + 790 + **680** + 650 → **2200** + 2200

220 + 2200 = 1210 x 2 [220 x 011]

Figure 1. A "hidden" mirroring. The establishing of cyclicity through the first order of AAs.

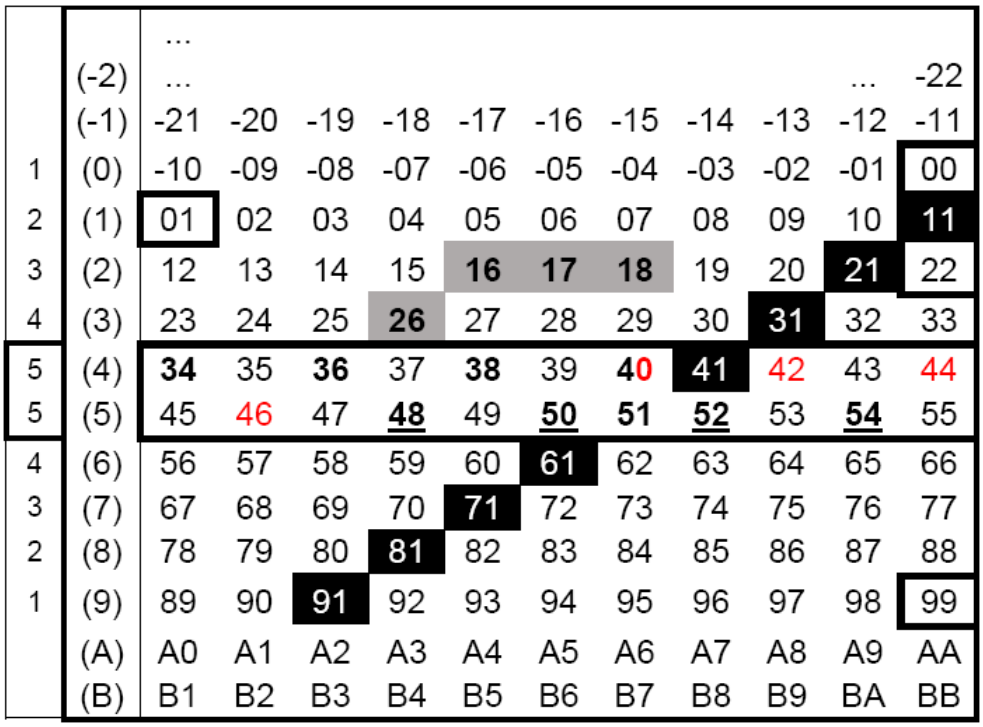


Figure 2. Periodic system of the numbers in decimal number system. Taken from (MMR, 2019, Figure A1, p. 28) with a few added indications of essentially significant areas.

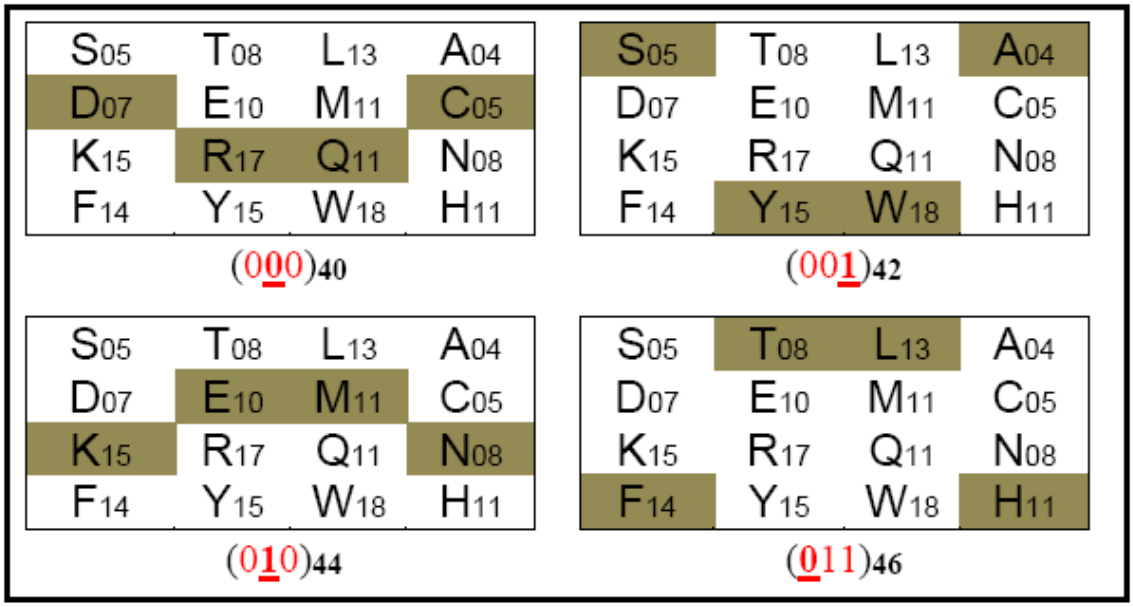
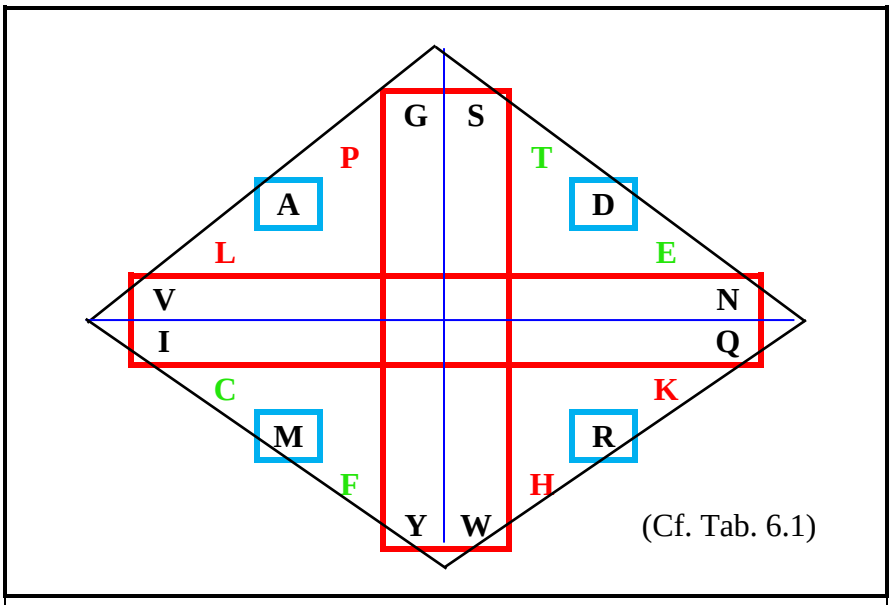


Figure 3. Logical square in the set of 16 AAs of alanine stereochemical type. System-arrangement of 16 AAs of the alanine stereochemical type, viewed as a logical square (Table 6, right). Taken from Material II (quoted here in footnote 2): Table B1, p. 54. Two inner rows vs two outer ones. One can notice that the quantities 40, 42, 44, 46 are "taken off" from the central area of the Periodic Table of Numbers in the decimal number system (PSN: Figure 2).



I (G, P); II (A, L, V, I); III (C, M, F, Y, W, H);

IV (R, K, Q, N, E, D, T, S)

Codon number for (III + IV): [**23**] + [(CM & TS) **13**] = 36

Figure 4. From MMR, 2011, Fig. 2, p. 822: "Four diversity types of protein amino acids in a linear arrangement in form of the sequence 2-4-6-8; then in a circular arrangement, in form of the sequence 5-5-5-5. From this last sequence it is possible a new arrangement in form of the sequence 4-4-4-4-4 as in system presented in [Table 7]." Here it is 4 x 5 AAs and in Table 7 there are 5 x 4 ones. [*Note 2023*: The number of codons for coding chalcogen AAs (shaded: STCM) is 13, and for the rest AAs in III and IV diversity types 23. This resolves the issue of the "missing link" in relation to the chemical code. The form is therefore completely identical in both codes – chemical and genetic one (Cf. MMR, 2018b, Survey 3a, p. 296).]

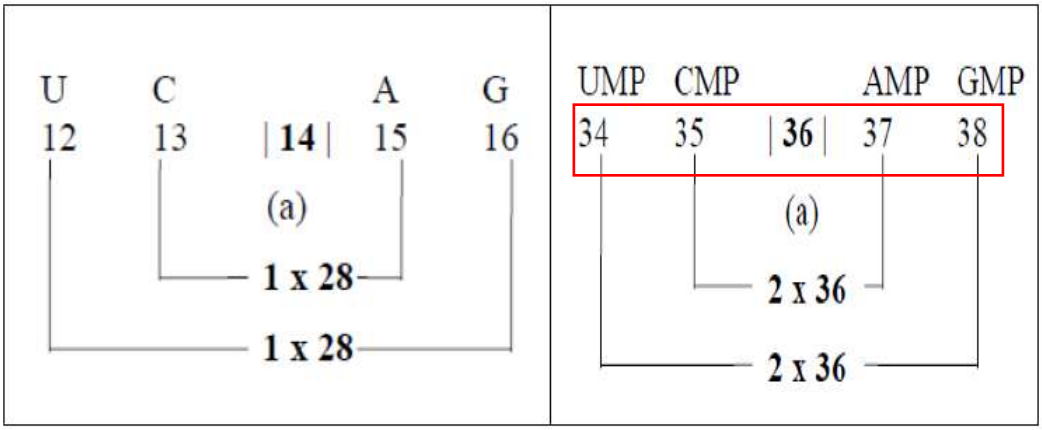


Figure 5. From (MMR, 1997b, pp. 62-63, Equ. 25-29). Distinctions as [(1 x 28) : (2 x 36)]. Quantities 12, 13, [14], 15, 16, as well as quantities 34, 35, [36], 37 38 are also found in one unique series of natural numbers (Survey 8).

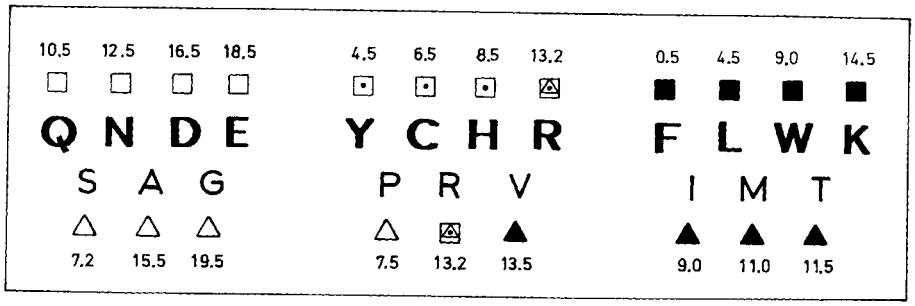


Figure 6. Taken from (MMR, 1997b, Figure 5, pp. 26-27 and from MMR, 2021b, Fig. A1): "Here are given the amino acids from Space-3 (triangles) and Space-4 (squares) [of Boolean space] depending on the binary value (strict order per rising values in each group) …The mean binary values are given in Figure according to Rakočević, 1994, p.72..." [*Note 2023*: Boolean Space-3 in Boolean cube, B^3, corresponding with 6-bit binary tree: 011-001, 011-010, 011-111; Space-4: 100-000, 100-101, 100-110. As 'signified' entities amino acid molecules appear here; and as 'signifiers' appear Boolean spaces-3 and Boolean spaces-4, also the binary value of each of the molecules. The essentiality (dark squares and triangles), however, appears in both roles. The classification of amino acids into essential, semi-essential ("quasi-essential") and non-essential, as in (Van Nostrand, 1983, p. 119, Table 2).]

SURVEYS

Survey 1. The significance and uniqueness of the quantities 36 and 66 (I)

n	n + n	n x n	nn		nn – (n x n)	
01	1 + 1 = 2	1 x 1 = 1	11		11 – 1 = 10	
						8
2	2 + 2 = 4	2 x 2 = 4	22		22 – 4 = 18	
						6
3	3 + 3 = 6	3 x 3 = 9	33		33 – 9 = 24	
						4
4	4 + 4 = 8	4 x 4 = 16	44		44 – 16 = 28	
						2
5	5 + 5 = 10	5 x 5 = 25	55		55 – **25** = 30	
					mirroring: ↓↑	0
6	6 + 6 = 12	6 x 6 = 36	66		66 – **36** = 30	
						2
7	7 + 7 = 14	7 x 7 = 49	77		77 – 49 = 28	
						4
8	8 + 8 = 16	8 x 8 = 64	88		88 – 64 = 24	
						6
9	9 + 9 = 18	9 x 9 = 81	99		99 – 81 = 18	
						8
10	10 + 10 = 20	10 x 10 = 100	110		110 – 100 = 10	

Survey 2. The significance and uniqueness of the quantities 36 and 66 (II)

n	n + n	nn		nn – (n + n)	mirror. diff.	
01	1 + 1 = 2	11		11 – 2 = 09	(9 x 9)	1 + 2 + 3 1 x 2 x 3 ↓ 6
2	2 + 2 = 4	22		22 – 4 = 18	(7 x 9)	
3	3 + 3 = 6	33		33 – 6 = 27	(5 x 9)	
4	4 + 4 = 8	44		44 – 8 = 36	(3 x 9)	(6 x 6)
5	5 + 5 = 10	55		55 – 10 = 45	**(1 x 9)**	
						0110
6	6 + 6 = 12	66		66 – 12 = 54	**(1 x 9)**	1001
7	7 + 7 = 14	77		77 – 14 = 63	(3 x 9)	
8	8 + 8 = 16	88		88 – 16 = 72	(5 x 9)	
9	9 + 9 = 18	99		99 – 18 = 81	(7 x 9)	(9 x 9)
10	10 + 10 = 20	110		110 – 20 = 90	(9 x 9)	

Further variations of the numbers 1, 2, 3 in the act of determination the genetic and chemical code can be seen in the previous work (MMR, 2018b, Equ. 1, p. 293 and Tab. 4, p. 295).

Survey 3. The significance and uniqueness of the quantities 36 and 66 (III)

n	nn		nn – (n + n)	mirror. diff.
01	11		11 – 2 = 09	(9 x 9)
			(1 x 9)	
2	22		22 – 4 = 18	(7 x 9)
			(**2** x 9), (3 x 6)	
3	33		33 – 6 = 27	(5 x 9)
			(3 x 9)	
4	44		44 – 8 = 36	(3 x 9)
			(**4** x 9), (6 x 6)	
5	55		55 – 10 = 45	**(1 x 9)**
			(5 x 9)	
6	66		66 – 12 = 54	**(1 x 9)**
			(**6** x 9), (9 x 6)	
7	77		77 – 14 = .63	(3 x 9)
			(7 x 9)	
8	88		88 – 16 = 72	(5 x 9)
			(**8** x 9), (12 x 6)	
9	99		99 – 18 = 81	(7 x 9)
			(9 x 9)	
10	110		110 – 20 = 90	(9 x 9)
			(**10** x 9), (15 x 6)	

Survey 4. The significance and uniqueness of the quantities 36 and 66 (IV)

n	n x n	nn		nn + (n x n)	
01	1 x 1 = 1	11		11 + 1 = 12	
					14
2	2 x 2 = 4	22		22 + 4 = 26	
					16
3	3 x 3 = 9	33		33 + 9 = 42	
					18
4	4 x 4 = 16	44		44 + 16 = 60	
					20
5	5 x 5 = 25	55		55 + 25 = 80	
				(220 | 022)	**022**
6	6 x 6 = 36	66		66 + 36 = 102	
					24
7	7 x 7 = 49	77		77 + 49 = 126	
					26
8	8 x 8 = 64	88		88 + 64 = 152	
					28
9	9 x 9 = 81	99		99 + 81 = 180	
					30
10	10 x 10 = 100	110		110 + 100 = 210	

12 + 210 = 222 = 6 x 37

Survey 5. The significance and uniqueness of the quantities 36 and 66 (V)

n	nn			
				102 + 102 = 204 34 + 170 = 204 68 + 136 = 204 ↓ 10 x 51
2	22	22 + 12 = 34		
			34	
4	44	44 + 24 = 68		
			34	
6	66	66 + 36 = 102		
			34	
8	88	88 + 48 = 136		
			34	
A	AA	AA + 5A = 170		

Survey 6. Relations of quantities 51 and 66

	n	1n + n1
1	0	10 + 01 = 11
2	1	11 + 11 = 22
3	2	12 + 21 = 33
4	3	12 + 21 = 33
5	4	12 + 21 = 33
6	5	15 x 51 = 66
5	6	16 + 61 = 77
4	7	17 + 71 = 88
3	8	18 + 81 = 99
2	9	19 + 91 = AA
1	A	1A + A1 = BB

Missing quantity 51 in Table 6 (on the right) and
existing quantity in Table 2.6.

Survey 7. Natural numbers series in a relation to Plato's four

1	1, 2, **(**3, 4, 5, 6**)**, **7**, 8, **9**	
2	2, 4, **(**6, 8, 10, 12**)**, **14**, 16, **18**	
3	3, 6, **(**9, 12, 15, 18**)**, **21**, 24, **27**	**21**
4	4, 8, **(**12, 16, 20, 24**)**, **28**, 32, **36**	**28**
5	5, 10, **(**15, 20, **25**, 30**)**, **35**, 40, **45**	**35**
6	6, 12, **(**18, 24, 30, **36**)**, **42**, 48, **54**	**42**
7	7, 14, **(**21, 28, 35, 42**)**, **49**, 56, **63**	
8	8, 16, **(**24, 32, 40, 48**)**, **56**, 64, **72**	
9	9, 18, **(**27, 36, 45, 54**)**, **63**, 72, **81**	

0 → 1, 3, 7, 15, 31, 63, 127, …
Bits → 1, 2, 3, 4, 5, 6, 7, …

Quantities 28 and 35 are found as realities of the genetic code (Table 8.1); quantities 21 and 42 as the harmonic mean on the 6-binary tree, in reading from one side and the other (MMR, 1998, Fig. 1). [Cf. Table 8.1.)

Survey 7.1. Mirroring the neighborhood via powers with exponents "1"

(**1** x 3) + (3 x **2**) = 9	[9 x 3 = 27]	$\underline{\mathbf{1}}^1$ ------ $\underline{\mathbf{2}}^1$
6	18	
(**2** x 3) + (3 x **3**) = 15	[15 x 3 = 45]	$\underline{\mathbf{2}}^1$ ------ $\underline{\mathbf{3}}^1$
6	18	
(**3** x 3) + (3 x **4**) = 21	[21 x 3 = **63**]	$\underline{\mathbf{3}}^1$ ------ $\underline{\mathbf{4}}^1$
6	18	
(**4** x 3) + (3 x **5**) = 27	[27 x 3 = **81**]	$\underline{\mathbf{4}}^1$ ------ $\underline{\mathbf{5}}^1$
6	18	
(**5** x 3) + (3 x **6**) = 33	[33 x 3 = 99]	$\underline{\mathbf{5}}^1$ ------ $\underline{\mathbf{6}}^1$
. . .	Pythagorean triple: 3-4-5	

This neighborhood mirroring corresponds to the analogous neighborhood mirroring we find in the formula, both for the chemical and for the genetic code (MMR, 2018b, Eq. 2 on p. 293). In the third row, we find a pattern that corresponds to the distinction and distribution of amino acids from the aspect of essentiality, as well as from the aspect of their positions in Boolean spaces (Figure 6). On the other hand, in the third and fourth rows we find quantities, which also correspond to the quantities in GC: 63 as the end point on the 6-bit binary tree (MMR, 1998, Fig. 1); 81 as 61 amino acid codons plus 20 AAs.

Survey 7.2. Mirroring the neighborhood via powers with exponents "2"

q	*q*/2	squares	addends	diff.
2	1	$1^2 + 2^2$	$(01 + 100)_2$	$(11)_2$
4	2	$2^2 + 3^2$	$(10 + 21)_4$	$(11)_4$
6	3	$3^2 + 4^2$	$(13 + 24)_6$	$(11)_6$
8	4	$4^2 + 5^2$	$(20 + 31)_8$	$(11)_8$
10	5	$5^2 + 6^2$	$(25 + 36)_{10}$	$(11)_{10}$
12	6	$6^2 + 7^2$	$(30 + 41)_{12}$	$(11)_{12}$
14	7	$7^2 + 8^2$	$(37 + 48)_{14}$	$(11)_{14}$
16	8	$8^2 + 9^2$	$(40 + 51)_{16}$	$(11)_{16}$
...				

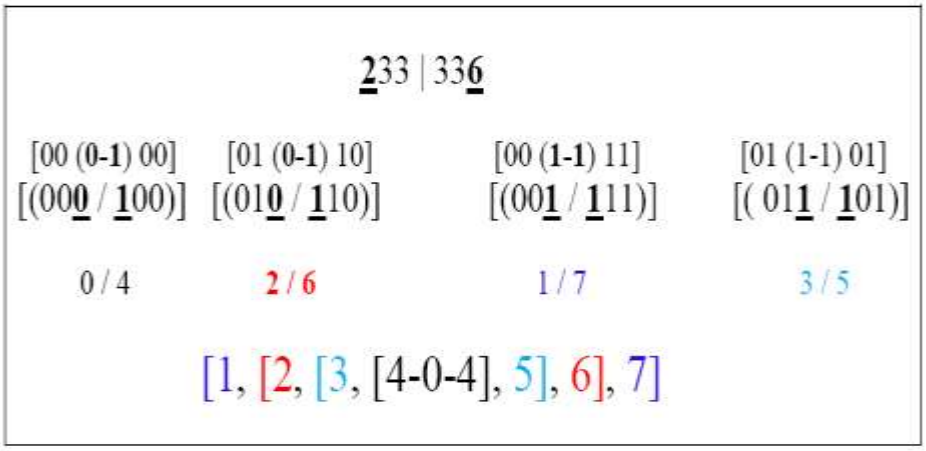
From MMR, 2019, Table A1, p. 29: “The row "10" in this Table follows from PSN presented in Table A1; all other rows follow from analog number systems. From the fact that pattern 25-36-1, valid both in genetic and chemical codes, follows the conclusion that in the case of the existence of biomolecules, only decimal number system has "passed" through Darwin's selective sieve. What is surprising, however, is the fact that Darwin's sieve is matched with the "pulse" of Bing Bang.” (*Note 2023*: This neighborhood mirroring corresponds to the analogous neighborhood mirroring we find in the formula for the chemical code (MMR, 2018b, Eq. 1 on p. 293).

Survey 8. The source of the key AAs distinction in the Genetic Code

1, (2), 3, 4 → 1, 7,	8	
	6	
3, (4), 5, 6 → 3, 11,	14	
	6	1 x 5 3 x 5 4 x 5
5, (**6**), 7, 8 → 5, 15,	**<u>20</u>**	
	6	
7, (8), 9, 10 → 7, 19,	26	
. . .		
2, 3, (4), 5, 6 → (8 x 2)		
	8	
4, 5, (6), 7, 8 → (12 x 2)		
	8	
6, 7, (8), 9, 10 → (16 x 2)		
	8	
8, 9, (10), 11, 12 → (20 x 2)		
	8	
10, 11, (12), 13, 14 → (24 x 2)		
	8	
12, 13, (**14**), 15, 16 → (**28** x 2)		
	8	
14, 15, (16), 17, 18 → (32 x 2)		
. . .		
32, 33, (34), 35, 36 → (68 x 2)		
	8	
34, 35, (**36**), 37, 38 → (72 x 2)		
. . .		

Correspondences: Table 3,2 and Figure 5.

Survey 9. Mirroring of neutron number in PPAASS



Correspondences: Table 5.2 and 5.3

Appendix A. *Genetic code in relation to Periodic system of numbers*

Table A1. Distribution of AAs according to the number of hydrogen atoms (I)

The number of H atoms (in brackets) and nucleons							
G (01) 01	A (03) 15	S (03) 31	D (03) 59	C (03) 47	**(13)**	**153**	
N (04) 58	P (05) 41	T (05) 45	E (05) 73	H (05) 81	(24)	298	(**59**/58)
Q (06) 72	V (07) 43	F (07) 91	M (07) 75	Y (07)107	(34)	388	**569**/686
W (08)130	R (10) 100	K (10) 72	I (09) 57	L (09) 57	**(46)**	**416**	
569 as neutron number and 686 as proton number! 569 – 59 = 627 – 117 686 – 58 = 628							

Sukhodolets' system-arrangement of AAs according to the number of hydrogen atoms. From (MMR, 2011, Tab. 7 p. 830). The quantities 298 and 388 given here as number of nucleons, within two inner rows, appear in Table 1 as number of protons (298+388 = 686); within two outer rows as number of neutrons in the set of 20 AAs (in their side chains). The hydrogen atom number quantities 58 and 59 appear in the Standard GC Table as the number of all atoms in the side chain of each individual AA: [{(LI M A DE) 58}, {(SY R S R) 59}, {(FL V CW G) 61}, {(PT HQ NK) 61}] (Cf. MMR, 2017, DOI 10.31219/osf.io/2pfe7, Figs 3 and 4; also: Shcherbak, 2008, Fig. 10b, p. 173).

Table A2. Distribution of AAs according to the number of hydrogen atoms (II)

out	in		out	in
G (01)	N (08)		**G (01)**	**S (05)**
W (18)	Q (11)		A (04)	T (08)
A (04)	S (05)		**L (13)**	**I (13)**
C (05)	D (07)		V (10)	D (07)
P (08)	T (08)		**P (08)**	**E (10)**
H (11)	E (10)		R (17)	K (15)
V (10)	F (14)		**Y (15)**	**F (14)**
Y (15)	M (11)		W (18)	Q (11)
R (17)	K (15)		**H (11)**	**N (08)**
L (13)	I (13)		C (05)	M (11)
O 40	50		**48**	**50**
E 62	52		54	52
102	102		102	102

From (MMR, 2011, Tab. 9, p. 830)

Table A3. The key of Darwin's Diagram

Primary		Secondary	
B 00	06 G	B 01	01 G
C 01	02 H	C 01	01 H
D 02	00 K	D 01	01 K
E 10	01 L	E 00	01 L
F 14		F 00	
27	09	03	04
36		**(43)**	**07**

26 + 10 = 36		
16 + 09 = 25		
17 + 08 = 25		
09 + 07 = **16**		
	$1^2 - 0^2 = 01$	$5^2 - 4^2 = 09$
	$2^2 - 1^2 = 03$	$6^2 - 5^2 = 11$
	$3^2 - 2^2 = 05$	$7^2 - 62 = 13$
	$4^2 - 3^2 = 07$	…

26 + 10 = 36		
27 + 09 = 36		
17 + 08 = 25		
$26 + 10 = 36 = \mathbf{6^2}$		
$17 + 08 = 25 = \mathbf{5^2}$		
$26 - 10 = 16 = \mathbf{4^2}$		
$17 - 08 = 09 = \mathbf{3^2}$		

Mendel's result:
$1^n - 2^n - 3^n - 4^n$

Taken from (MMR, 2015, Table 5, p. 47). Also from (MMR, 2019, Tab. C1, p. 38). Two equations which we find both in the chemical and in the genetic code (MMR, 2018b, Surveys 2a and 3a, p. 296), we also find in the Darwin's Diagram, changed for the first-order unit and/or the second-order unit: (27 + 9 = 36) and (16 + 9 = 25) (Cf. *Note* in Legend of Table 8.1.) [The nth power of the number 1 refers to the parent pair, and the remaining three cases are found in Mendel's original work.]

Appendix B. *Genetic code in relation to binary spaces of perfect numbers*

Table B1. System-arrangement of codons in relation to *first four* perfect numbers

1st lett.	2nd letter								3rd lett.
	U		*C*		*A*		*G*		
U	00. UUU	F	16. UCU	S	32. UAU	Y	48. UGU	C	*U*
	01. UUC		17. UCC		33. UAC		49. UGC		*C*
	02. UUA		18. UCA		34. UAA		50. UGA	CT W	*A*
	03. UUG	L	19. UCG		35. UAG	CT	51. UGG		*G*
C	04. CUU	L	20. CCU	P	36. CAU	H	52. CGU	R	*U*
	05. CUC		21. CCC		37. CAC		53. CGC		*C*
	06. CUA		22. CCA		38. CAA		54. CGA		*A*
	07. CUG		23. CCG		39. CAG	Q	55. CGG		*G*
A	08. AUU	I	24. ACU	T	40. AAU	N	56. AGU	S	*U*
	09. AUC		25. ACC		41. AAC		57. AGC		*C*
	10. AUA		26. ACA		42. AAA		58. AGA		*A*
	11. AUG	M	27. ACG		43. AAG	K	59. AGG	R	*G*
G	12. GUU	V	28. GCU	A	44. GAU	D	60. GGU	G	*U*
	13. GUC		29. GCC		45. GAC		61. GGC		*C*
	14. GUA		30. GCA		46. GAA	E	62. GGA		*A*
	15. GUG		31. GCG		47. GAG		63. GGG		*G*

Quantitative-qualitative distinctions:
[(0 – 3) (UUU – UUG) → 6], [(0 – 7) (UUU – CUG) → 28], [(0 – 31) (UUU – GCG) → 496],
{[(0 – 63) (UUU – GGG)] + [(64 – 127) (GGG – UUU) → 8128]}
6 + 28 + 496 + 8128 = 8658 = 7770 + 088 = 6 x 1443

(Taken from MMR, 2007, Tab. 11, p. 96)

Table B2. Generating the second, third and fourth perfect number in the series of cubes of odd natural numbers.

$0 - 3 \rightarrow 6$		1^3	1	
$0 - 7 \rightarrow 28$		**3^3**	**27**	**28**
$0 - 31 \rightarrow 496$		5^3	125	
$0 - 127 \rightarrow 8128$		**7^3**	**343**	**496**
		9^3	729	
$2^1 \times 3 = 6$		11^3	1331	
$2^2 \times 7 = 28$		13^3	2197	
$2^4 \times 31 = 496$		**15^3**	**3375**	**8128**
$2^6 \times 127 = 8128$				
(0 – 63) + (64 – 127) = 8128 (63 as 64) & (0 as 127)				

Table B3. Generating the first, second and third perfect number in the series of squares of root of number 2

$(\sqrt{2})^2$	$((\sqrt{2})^2)^2$	$(((\sqrt{2})^2)^2)^2$	$((((\sqrt{2})^2)^2)^2)^2$
	UCAG		
2 — (2) —	4 —	(12) —	16 — (240) — 256
↑	|	|	|
Py	(2)	(12)	(240)
Pu	|	|	|
	6	28	496

(Taken from MMR, 2007, Tab. 5, p. 82)

Table B4. Binary "travel" of the first, second and third perfect numbers through the space

<table>
<tr><td>1 2 → 1 x 6
4^1 4^0
2 4 → 2 x 6
4^1 4^0</td><td></td><td>| 4 | 8 | 16| → 1 x 496 (28)
10^2 10^1 10^0
| 8| 16 | 32| → 2 x 496 (28)
| 16 | 32| 64| → 4 x 496 (28)</td></tr>
<tr><td>1 2 4 → 1 x 28
4^2 4^1 4^0
2 4 8 → 2 x 28
4^2 4^1 4^0</td><td></td><td>- - - - - - - - - - - - - - - - -
- - - - - - - - - - - - - - - - -
|4|16 | 48 | 64 |64| → 124 x 496
10^4 10^3 10^2 10^1 10^0</td></tr>
</table>

Taken from MMR, 2007, Tab. 12, p. 96). Binary "travel" of the second and third perfect numbers through the space.

Table B5. "The Number System of Multiples, NSM III"

a	*b*	*c*	*d*	*e*
14	27	20979	17982	999
13	26	20202	17316	962
12	25	19425	16650	925
11	24	18648	15984	888
10	23	17871	15318	851
09	22	17094	14652	814
08	21	16317	13986	777
07	20	15540	13320	740
06	19	14763	12654	703
05	18	13986	11988	666
04	17	13209	11322	629
03	16	12432	10656	592
02	15	11655	09990	555
01	14	10878	09324	518
00	13	**010101**	**8658**	481
01	12	09324	07992	444
02	11	08547	07326	407
03	10	07770	06660	370
04	09	06993	05994	333
05	08	06216	05328	296
06	07	05439	04662	259
07	06	04662	03996	222
08	05	03885	03330	185
09	04	03108	02664	148
10	03	02331	01998	111
11	02	01554	01332	074
12	01	00777	00666	037
13	00	00000	00000	000

a. The original number, countdown starting from the middle row;
b. The original number, countdown starting from starting (zero) point;
c. The multiples of the number 777; c = 21 x e;
d. The multiples of the number 666; d = 18 x e;
e. The multiples of the number 037; they are existing only in NSM III

[Additional Note 1, 2023: All given here comes from (MMR, 1997b, p. 61. The system-arrangements: MSM I, the multiples of 6; II, of 66; and III of 666. Note 2: The result 010101 in row 13th shows the connection between the binary and decimal number systems, and also the connection with the sum of the first four perfect numbers (8658). Note 3: The result 010101 actually represents the mirror image of the path of the largest change in the 6-bit binary tree (Table 2).]

Table B6. Adjacency relations of pairs in the series of natural numbers

0 + 1 = 1	2 + 3 = 5	4 + 5 = 9
00 + 11 = 11	22 + 33 = 55	44 + 55 = 99
000 + 111 = 111	222 + 333 = 555	444 + 555 = 999
6 + 7 = 13	8 + 9 = 17	A + B = 21
66 + 77 = 143	88 + 99 = 187	AA + BB = 231
666 + 777 = **1443**	888 + 999 = 1887	AAA + BBB = 2331

fc AAs + nfc AAs = 333+1110 = **1443** nucleons
6 x 1443 = **8658** = 7770 + 0888
[6 + 28 + 496 + 8128 = **8658**]

fc = four-codon; nfc = non-four-codon. Number 1443 was also found as number of nucleons in the set of 23 AAs (side chains) (Shcherbak, 1994, Fig. 1, p. 475). Number 8658 as the sum of first four perfect numbers. (See its position in the system-arrangement in Display 2.)