Genetic Code as a Coherent System

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Abstract

The paper is a summarizing presentation of author's investigations of the genetic code, primarily in terms of its coherence. Thus, it is shown that within genetic code there are four times four types of entities: four types of coding, four types of degeneracy, four stereochemical types of canonical amino acids and four types of diversity of the same these amino acids. In addition, it is revealed some harmonic structures arising through the determination by the golden mean, enzymes aminoacyl-tRNA synthetases, Gaussian algorithm and so on.

Key Words: genetic code, harmony, golden mean, amino acids, amino bases, atom number balance, Gauss' algorithm, aminoacyl-tRNA synthetases

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1. Preliminaries

This paper represents a summarizing review of our investigations of the genetic code (GC), but only in terms of coherence, that means in terms of the proofs that within the genetic code all its constituents appear to be in harmonic interconnections. As the first, there is the connection between amino acids (AAs) and codons, then of both and related arithmetical and/or algebraic regularities and so on.

In order to show that the genetic code is a coherent system, we present, as the first, the fact that GC contains four times four entities: the four types of coding, four types of degeneracy, four stereochemical types of canonical AAs (Fig. 1) and four types of diversity of the same these AAs (Fig. 2). To understand how come the four types of coding one should start with the fact that GC works based on the connection between two alphabets, four-letter and twenty-letter, respectively. Those two cases appear to be optimal in terms of validity of the two principles, the principle of minimum change and continuity principle.

Moreover, regarding to the validity of these two principles the four-letter alphabet is not only optimal but also the one and only possible. Namely, from the four-letter alphabet follow three-letter words, each letter with two-letter root, and a single letter at the beginning. Altogether, we have the sequence of continuity: 4 - 3 - 2 – 1. If we would have a five-letter alphabet, from it generated words must be as four-letter, with the ambiguity in terms of the number of letters in the root - two or three letters? In six-letter alphabet the situation would be still more confused etc.

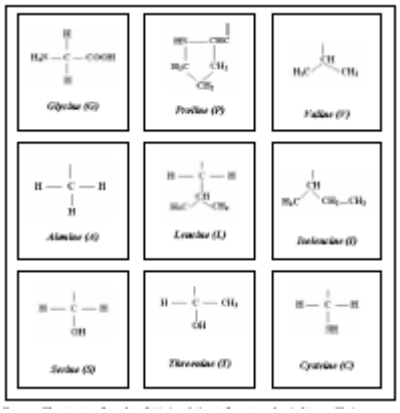

Figure 1. The structure formulae of AAs in relation to four stereochemical types: Glycine, one and only within glycine stereochemical type; proline in proline type; valine and isoleucine within valine type, and all other within alanine stereochemical type.

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As for the optimality of the number 20, there could be more reasons, but most important is this one which concerns to the generalization of the golden mean; such a generalization from which follows the so-called "metallic means family" (MMF) (Spinadel, 1999) as solutions of the Equation (1), for the various values of the parameters p and q:

$$x^2 \pm px - q = 0 \quad (1)$$

In fact, if p = q = 1, we have the square equation of golden mean. For p = 2 and q = 1 we obtain the silver mean; for p = 3 and q = 1, the bronze mean etc. On the other hand, if p = 1 and q = 2, we obtain the copper mean; for p = 1 and q = 3, we get the nickel mean and so on. Special cases are "the integer metallic means", for q = 2, 6, 12, 20, 30, ..., whose solutions (x_1, x_2), given by Equation (1), are positive integers: (1, 2), (2, 3), (3, 4), (4, 5), (5, 6) ... From these results "it is very easy to verify that ... the integer metallic means ... appear in quite a regular way" (Spinadel, 1999). What, however, is especially interesting, in connection with the said, is that Spinadel's integers (2, 6, 12, 20, 30, ...) appear in the diagonal of the very known Table of multiplication, with the number 20 in the central position (Table 1.1 in relation to Table 1.2). On the other hand, the number 20, together with all other essence GC-quantities (4, 16, 64, 81) can be found in relation to Plato's system of two progressions (Платων, 1970) (Tab. A.1 in Appendix); also in relation to the total number of atoms in 20 AAs (384) (Tab. A.2).

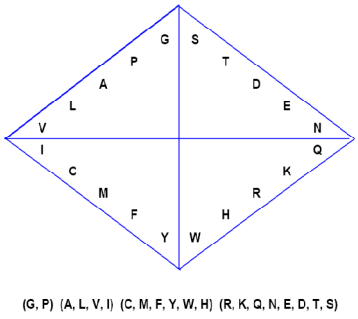

Figure 2. Four diversity types of protein amino acids in a linear arrangement in form of the sequence 2-4-6-8; then in a circular arrangement, in form of the sequence 5-5-5-5. From this last sequence it is possible a new arrangement in form of the sequence 4-4-4-4-4 as in system presented in Figure 3.

The following consequence of the validity of the two principles is that the coding must to be realized at the level of the quartet, quintet, sextet, etc., for the 4-letter, 5-letter, 6-letter alphabet, respectively. Hence, in the case of 4-letter alphabet inevitably there are four types of coding (codon → amino acid): I. (1 → 1), II. (2 → 1), III. (3 → 1), IV. (4 → 1), that means one word from the quartet codes for one amino acid; then - two, three, four words for one amino acid, respectively. [Of course, it is possible that, except one whole quartet, for one amino acid code the words from another quartet too.]

0	**0**	0	0	0	0	0	0	0	0
0	1	**2**	3	4	5	6	7	8	9
0	**2**	4	**6**	8	10	12	14	16	18
0	3	**6**	9	**12**	15	18	21	24	27
0	4	8	**12**	16	***20***	24	28	32	36
0	5	10	15	***20***	25	**30**	35	40	45
0	6	12	18	24	**30**	36	**42**	48	54
0	7	14	21	28	35	**42**	49	**56**	63
0	8	16	24	32	40	48	**56**	64	**72**
0	9	18	27	36	45	54	63	**72**	81

Table 1.1. The multiplication Table of decimal numbering system. The harmonic multiplication Table of decimal numbering system contains "the integer metallic means", for q = 0, 2, 6, 12, 20, 30, 42, 56 and 72 on the diagonal in the form of doublets (pairs): 0-0, 2-2, 6-6, 12-12, 20-20, 30-30, 42-42, 56-56 and 72-72.

$x^2 + x = z$		z
(0 x 0) + 0 = 00		0 x 1 = 00
(1 x 1) + 1 = 02		1 x 2 = 02
(2 x 2) + 2 = 06		2 x 3 = 06
(3 x 3) + 3 = 12		3 x 4 = 12
(4 x 4) + 4 = 20		**4 x 5 = 20**
(5 x 5) + 5 = 30		5 x 6 = 30
(6 x 6) + 6 = 42		6 x 7 = 42
(7 x 7) + 7 = 56		7 x 8 = 56
(8 x 8) + 8 = 72		8 x 9 = 72
(9 x 9) + 9 = 90		

Table 1.2. The key of the harmonic multiplication Table. This key is related to positive integers: (0, 1), (1, 2), (2, 3), (3, 4), (4, 5), (5, 6) which appear as solutions (x_1, x_2), given by Equation (1); as solutions for above given q (q = 0, 2, 6, 12, 20, 30, ...).

To understand that in the GC there are four types of degeneracy it is necessary the connection amino base - amino acid to be viewed from the aspect of the principle of donor – acceptor; from eight possible, four are implemented in the GC: I. (4), II. (3, 1), III. (2, 2), IV. (2, 1, 1); and four are not implemented: I. (1, 3), II. (1, 1, 2), III. (1, 2, 1), IV. (1, 1, 1, 1). Therefore, in the GC, it is not possible a coding option with only one codon ending with a pyrimidine (Py), while with the purine (Pu) is; or with two codons, of which one is ending with Py and the other with Pu; and also there is no possibility that all four of quartet-codons have to be coding for four different AAs.

2. Four stereochemical types of AAs

Regarding to the second alphabet of GC, the amino acid alphabet, it was shown that 20 AAs are classified into four stereochemical types (Popov, 1989; Rakočević and Jokić, 1996), as it is here presented in Figure 1 and Tables 2.1, 2.2 and Table 3.

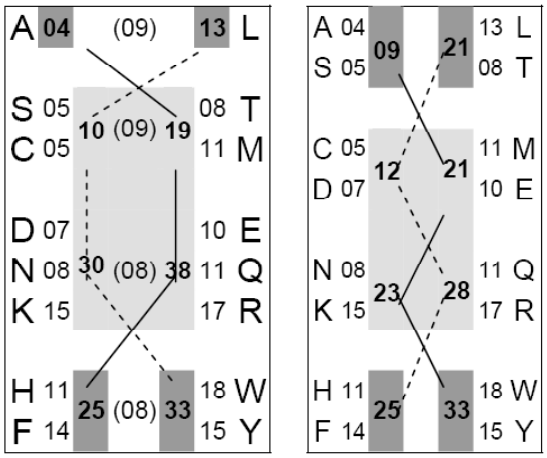

Table 2.1. The atom number within 8 pairs of alanine stereochemical type of AAs. On the full line, as well as on the dotted one, there are 86 atoms; the differences 8 and 9 (9 - 8 = 1) express ″the minimum change relation among the amino acids″ (Swanson, 1984, p 191). The order follows from the atom number hierarchy. For details see in Remark 2.2. By that notice that within outer class of AAs (AL + FY + HW) there are [(4 + 33 = 37) + (13 + 25 = 38) = 75] of atoms; and within inner class [(10 + 38 = 37 + 11) + (19 + 30 = 38 + 11) = 75 + 22 = 97]. For details, see the text.

By this only one amino acid (G) belongs to the stereochemical type of glycine; also only one amino acid (P) belongs to the type of proline; the pair V-I belongs to the stereochemical type of valine; and, finally, to the stereochemical type of alanine belong all other, the 16 amino acids. The presented classification comes from the amino acid conformation states. However, the same four stereochemical types, two and two (G, A and V, P), following our idea, come also from the amino acid constitution structures, in the following manner. The side chain of glycine (- H) comes from the shortest possible hydrogen chain (H - H), and none of the other 19 amino acids has a hydrogen chain of this kind. The side chain of alanine (- CH_3), or, in relation to glycine, (- CH_2 - H), follows from the shortest possible noncyclic hydrocarbon chain (CH_4), and still 15 amino acids have the alanine – the same side chain in the form of (- CH_2 - R). The side chain of valine (H_3C-$\dot{C}$H-CH_3) follows from the shortest possible cyclic hydrocarbon, from cyclopropane, with a permanent openness and with a linkage to the ″head″ of amino acid through only one vertex of cyclopropane ″triangle″; still only one amino acid, isoleucine, belongs to this type with the side chain H_3C-$\dot{C}$H-CH_2-CH_3. The proline type (only with proline) follows from the same source (cyclopropane), but with a permanent non-openness and with a linkage to the ″head″ through two vertices of cyclopropane ″triangle″.

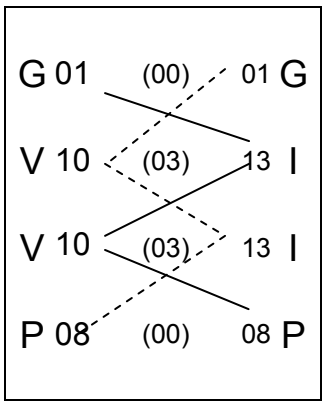

Table 2.2. The atom number within four pairs of non-alanine type of AAs. The two lines have 32 atoms each. The number of amino acids must be doubled through the pairs G-G and P-P; the amino acid order comes from the atom number hierarchy.

Four stereochemical types can be further classified into two classes, the class of “non-contact” AAs, all from alanine stereochemical type, and the class of “contact” AAs where are AAs of the other three types (G, P, V-I) (Tabs 2.1 & 2.2 and Box 2.1).

Box 2.1. *Molecule pairs hierarchy in relation to natural numbers series (The generating of the Table 2. 1)*

1. Aliphatic AAs (simpler than aromatic)

1.1. Hydrocarbon AAs (start: 04 atoms);

1.2. First possible OH derivatives (start: 05 atoms);

1.3. Sulfur OH analogs, i.e. SH derivatives (S > O);

1.4. Carboxyl group derivatives (start: 07 atoms);

1.5. Amide derivatives (start: 08 atoms);

1.6. Amino derivatives (start: 15 atoms);

2.2. Heteroatom derivatives (start: 11 atoms);

2.1. Aromatic hydrocarbon and its OH derivative (start: 15 atoms);

2. Aromatic AAs (more complex than aliphatic)

[*Remark* 2.1. "Contact" AAs are AAs in which there is a direct contact between the "body" and the "head", i.e. between the side chain and the amino acid functional group. On the other side, in "non-contact" AAs such a possible contact is mediated by a CH_2 group (only within threonine that group is methyl-substituted: H – C – CH_3).]

Viewing that valine type is arranged into the pairs (although only with one pair) we researched the alanine type following the same concept. The result was as it is shown in Table 2.1. There are eight pairs of alanine type, classified into two subclasses. The three amino acid pairs belong to the first (outer) subclass: 1. with hydrocarbon noncyclic aliphatic chain (A-L), 2. with aromatic chain, without hetero atom (F-Y) and 3. with aromatic chain, with hetero atom (H-W). The five other and different pairs belong to the second (inner) subclass, with the presence of oxygen, nitrogen or sulfur atoms within a noncyclic side chain, in the form of a functional group: 1. with hydroxy group (S-T), 2. with sulfur atom (C-M), 3. with carboxylic group (D-E), 4. with amide group (N-Q) and 5. with amino group (K-R). This classification into two subclasses is accompanied by specific balances of number of atoms within amino acids molecules (within their side chains).

CE	HP					HP	CE
-0.16	-0.4	G	01	15 (12) 27	01	G	-0.4	-0.16
-0.09	+1.8	A	04		13	L	+3.8	-0.54
-0.52	+4.2	V	10		13	I	+4.5	-0.56
+0.24	-0.8	S	05	20 (12) 32	08	T	-0.7	+0.27
-0.73	+2.5	C	05		11	M	+1.9	-0.57
-0.52	+4.2	V	10		13	I	+4.5	-0.56
+0.69	-3.5	D	07	30 (08) 38	10	E	-3.5	+0.71
+0.52	-3.5	N	08		11	Q	-3.5	+0.91
+1.46	-3.9	K	15		17	R	-4.5	+0.87
+0.46	-1.6	P	08	33 (08) 41	08	P	-1.6	+0.46
±0.00	-3.2	H	11		18	W	-0.9	-0.25
-0.56	+2.8	F	14		15	Y	-1.3	+0.42

Table 3. Atom Number within 12 doublets and 8 triplets of "24" Amino Acids. On the full line, as well as on the dotted one, there are 118 atoms; HP: hydropathy index (Kyte and Doolittle, 1982) on a number unnamed scale; CE: cloister energy (a form of the free thermodynamical energy) in kcal/mol (Swanson, 1984). For details see the text.

[*Remark* 2.2. (*a*) In five pairs of AAs within inner subclass, in Table 2.1, there are 97 atoms, that means 11 atoms more than in a half of total atom number within whole system of eight pairs (172 : 2 = 86; 86 + 11 = 97). (*b*) Within three pairs in outer subclass there are 75 atoms, what means 11 atoms less in relation to the same half (86 – 11 = 75). The arithmetical pattern (75-86-97) we will also find in the system presented in Figure 4, which follows from Figure 3 and Table 6, but not for the atom number than for the nucleotide number within the codons. On the other hand, the half of half (Table 2.1) stands in the same relation to atom number within four contact AAs (86:2 = 43; 43 – 32 = 11). (*c*) The 97 atoms within inner subclass in Table 2.1. plus 32 atoms within contact AAs in Table 2.2 equals 129 atoms; then, 129 atoms plus 75 (43 + 32) atoms within outer subclass equals, in total, 204 atoms within 20 amino acid molecules, in their side chains. Cf. this arithmetical pattern, 129-75-43-32, with the same one in Figure 10 and Remark 4.4. (*d*) The arithmetical sense of the balances through number 11 one can see in "Table of minimal adding" (adding for 01 in one digit position and for 11 in two digit position), presented here as Table 4.]

One must notice that the amino acid order placed on the left side in Table 2.1 reflects two things at the same time – the grading continuity of pairs and cycling: 1-2-3-2-1 (AL – HW – FY – AL). But there is a chemical justification for the sequencing of

the pairs – all times two in each step – as given on the right. The S in relation to A as its first possible OH derivative; NQ – KR as nitrogen AAs; HF – WY as aromatic AAs. If so, then there remains only one, albeit chemically "impossible" situation, but the system has no choice but to be so as it is (CD – ME). In some way unexpected, but also this different chemical classification is also accompanied by arithmetical regularities. First, there is a diagonal connection of pairs, as shown in Equations (2). The second arithmetical regularity follows from the four amino acid sequences, to which have been attached the contact amino acids in the order of molecule size; in such a new arrangement follow very specific arithmetical regularities valid within Gauss' algorithm.

CD 12 + QR 28 = 40
AS 09 + WY 33 = 42 (Eq.2)
ME 21 + NK 23 = 44
LT 21 + HF 25 = 46

[*Remark* 2.3. (*a*) The balance of atom number within the class of alanine stereochemical type: 40 + 46 = 42 + 44 = 86 (86 x 2 = 172; 172 + 32 = 204);[2] (*b*) The correspondence with the Gauss' algorithm (Section 4.3): (STLA-G 31), (DEMC-P 41), ... (51) ... , (KRQN-V 61), (FYWH-I 71); (LA-MC-QN-WH 81), (ST-DE-KR-FY 91)[3] (Figure 9 & 10).]

If two separate systems, presented in Tables 2.1 and 2.2, are viewed as subsystems, we can then integrate them into a single system, as it is presented in Table 3, composed of doublets and triplets[4]. If even just one amino acid, in the system in Table 2.2, appears twice, then all others must be represented twice. Then, in the integrated system (Table 3) the ratio of the number of contact and non-contact AAs is 8:16 = 1:2, corresponding to the symmetry in the simplest case (Marcus, 1989) and to the zeroth case of generalized golden mean (Stakhov, 1989; Rakočević, 2004b). On the other hand, the ratio of the differences of the number of atoms in the integrated system is 8:12 = 2:3. If we add to all those relationships still the relationship between the differences of atoms in the system of Table 2.1 (which is 8:9) we reach the Platonic-Pythagorean system of harmonic musical scale, where also is "hidden" the total number of atoms within 20 whole molecules of canonical AAs (384) (Table A.2 in Appendix).

Immediately it is obvious that in this new system (Table 3) the proline (P) as a heterocyclic molecule, has to go together with histidine and tryptophan. This leads to two triplets. Valine, which must be twice represented, from chemical reasons best fits in the set of serine and cysteine (S, C, V), and still once with alanine. However, with alanine also fit well glycine, and by this all possible triplets have been completed; eight of them, at the same time arranged in 12 doublets (pairs).

As we can see the pairing process is realized through a full accordance with the parameters for the polarity, the hydropathy index, HP (Kyte and Doolittle, 1982)[5] and the cloister energy, CE, as a form of thermodynamycal free energy (Swanson, 1984); in all but one cases (phenylalanine is an exception: although non-polar, it pairs up with polar tyrosine; for further exceptions of phenylalanine see Footnote 10 and Remark 4.3); also through a strict atom number balance (118/118 atoms in both zigzag lines). By this, the order of doublets and triplets is established with a strict atom number increasing from one to another next amino acid in correspondence with the involvement of the biosynthetic precursors one after another: first, the less complex and then the more complex precursors (cf. Table 1 in Rakočević & Jokić, 1996).

[2] The 32 atoms within four contact AAs: G, P, V, I; cf. the quartet 40-42-44-46 valid for 16 AAs of alanine stereoch. type with this one 48-50-52-54 valid for the whole amino acid system in Tab. 9.

[3] Two missing members to the full Gaussian algorithm are "hidden" within the two pairs of contact amino acids (GV-11 and PI-21). Notice that these two pairs we can find in Table 2.2 and they also appear to be pairs in an enzyme determination (Figure 8).

[4] "Notice that out of all doublet-triplet systems, this is the only one with two possible distinctions for doublets (i.e. six and six, and then, three and three doublets) and three possible distinctions for triplets (i.e. four and four, then two and two, and, finally, one and one triplet)" (Rakočević & Jokić, 1996).

[5] It appears that amino acid arrangement within Genetic Code Table (GCT) stays in a strict balanced relation to the polarity, expressed through hydropathy (Table A.3 in Appendix).

3. Four diversity types of AAs

Shcherbak (1994) pointed out that the number of nucleons within two classes of AAs (the four-codon and non-four-codon amino acids), appears to be equal with multiples of the number 037, a very specific and unique number. But among the arithmetical regularities valid for number 037 in the decimal numbering system, Shcherbak has shown that such a unique number is also present in the system of numbers which are analogs of 037 in some other numbering systems; their values for *q* (numbering system basis), going from one to another, differ by three units. Written together without specifying the numbering basis, these numbers-analogs (Shcherbaks' "Prime Quantums", PQ) are as follows: 13, 25, 37, 49, ... As we can see, the first digit belongs to the series of natural numbers, and the second to the series of odd integers.

***Remark* 3.1.** The uniqueness of number 037 is because the multiplication through the module (q - 1) preserves all three digits: (1 x 037 = 037; 10 x 037 = 370; 19 x 037 = 703), (2 x 037 = 074; 11 x 037 = 407; 20 x 037 = 740) etc.

***Remark* 3.2.** The Shcherbak's numbers by himself personally: "In the close vicinity of the decimal system, for example, some number systems with the bases 4 (Quantum 13_4 = 7), 7 (25_7 = 19), 10 (37), 13 (49_{13} = 61), etc, have the same periodic features for three-digit numbers" (Shcherbak, 1994).

Knowing this, it is easy to see the possibility of a specific presentation of a series of natural numbers, in the form of a matrix scheme (n x 11_q) (Tables 4 - 5)[6]; such a scheme (TMA) along whose first diagonal appear numbers in the form of Shcherbak's numbers, analogs of number 37 (N = 13, 25, 37, 49, 5B, ...). But as a noteworthy is the fact that in TMA specific and unique arithmetical regularities characterize not only number 37 but also its neighbors, numbers 26 and 48, each in its own way.

3.1. The uniqueness of the number 26

If the first diagonal neighbor of the number 26, the number 16 is added to the number 26 and its two followers (17 and 18) are successively added to the obtained result, we get the results as in Equations-solutions (3):

$$\begin{array}{l} 26 = 26 \\ 26 + \mathbf{16} = 42 \\ 42 + \mathbf{17} = 59 \\ 59 + \mathbf{18} = 77 \end{array} \qquad \begin{array}{l} 26 + 42 + 59 + 77 = Y \\ Y = 204 \\ Y/4 = 51 \end{array} \qquad \begin{array}{l} \mathbf{16} + \mathbf{17} + \mathbf{18} = Z \\ Z = 51 \\ Z = Y/4 \end{array} \qquad \text{(Eq.3)}$$

With three adding (16 +17 +18 = 51 = Z) we obtained three new results, and with the inclusion of the initial number 26 – four results. Their sum is 204 (26 + 42 + 59 + 77 = 204 = Y = 4Z), exactly four times greater than the sum of the three adding (16+17+18 = 51 = Z). But this connection of two equalities is a single and unique case in the entire system of numbers within Table 4, in other words within the set of natural numbers.[7]

	...										
(-2)	...									...	-22
(-1)	-21	-20	-19	-18	-17	-16	-15	-14	-13	-12	-11
(0)	-10	-09	-08	-07	-06	-05	-04	-03	-02	-01	00
(1)	01	02	03	04	05	06	07	08	09	10	11
(2)	12	13	14	15	16	17	18	19	20	21	22
(3)	23	24	25	26	27	28	29	30	31	32	33
(4)	34	35	36	37	38	39	40	41	42	43	44
(5)	45	46	47	48	49	50	51	52	53	54	55
(6)	56	57	58	59	60	5B	62	63	64	65	66
(7)	67	68	69	70	71	72	6D	74	75	76	77
(8)	78	79	80	81	82	83	84	7F	86	87	88
(9)	89	90	91	92	93	94	95	96	97	98	99
(A)	A0	A1	A2	A3	A4	A5	A6	A7	A8	A9	AA
(B)	B1	B2	B3	B4	B5	B6	B7	B8	B9	BA	BB

Table 4. The Table of minimal adding in decimal numbering system. A specific arrangement of natural numbers in decimal numbering system, going from 01 to 11 and so on, with Shcherbak's "simulation" analogs (13, 25, 37, 49 ...) within the first diagonal. For details see the text.

The uniqueness of the number 26 is expressed not only through the difference 26 - 10 = 16, but also through the sum 26 + 10 = 36, where number 36, as the second diagonal neighbor of the number 26, appears to be the member of a unique pair 25-36; unique case in the entire system of numbers within Table 4, and that means within the set

[6] In both cases the word is on the "Table of minimal adding" (TMA), the adding for 01 in one digit position and for 11 in two digit position, as it is said in Remark 2.2 d.

[7] Moreover, it appears that this is the zeroth case in the 4th column of Table 4 in the decimal numbering system, and also the zeroth case within all Shcherbak's numbering systems (q = 4, 7, **10**, 13, 16, ...); in all other cases, discrepancies arise (Tables C1 and C2 in Rakočević, 2011a).

of natural numbers. Namely, the numbers 25 and 36 are neighbors in third column of Table 4 with a difference of 11 as in all other cases, in all columns.

(1)	01	02	03	04	05	06	07	08	09	0A	0B	0C	0D	0E	0F	10	11
(2)	12	13	14	15	16	17	18	19	1A	1B	1C	1D	1E	1F	20	21	22
(3)	23	24	25	26	27	28	29	2A	2B	2C	2D	2E	2F	30	31	32	33
(4)	34	35	36	37	38	39	3A	3B	3C	3D	3E	3F	40	41	42	43	44
(5)	45	46	47	48	49	4A	4B	4C	4D	4E	4F	50	51	52	53	54	55
(6)	56	57	58	59	5A	5B	5C	5D	5E	5F	60	61	62	63	64	65	66
(7)	67	68	69	6A	6B	6C	6D	6E	6F	70	71	72	73	74	75	76	77
(8)	78	79	7A	7B	7C	7D	7E	7F	80	81	82	83	84	85	86	87	88
(9)	89	8A	8B	8C	8D	8E	8F	90	91	92	93	94	95	96	97	98	99
(A)	9A	9B	9C	9D	9E	9F	A0	A1	A2	A3	A4	A5	A6	A7	A8	A9	AA
(B)	AB	AC	AD	AE	AF	B0	B1	B2	B3	B4	B5	B6	B7	B8	B9	BA	BB

Table 5. The Table of minimal adding in hexadecimal numbering system. A specific arrangement of natural numbers in hexadecimal numbering system, going from 01 to 11 and so on, with Shcherbak's "simulation" analogs (13, 25, 37, 49 ...) within first diagonal. For details see the text.

But their square roots, as integers, appear to be also neighbors, and that is the said uniqueness (Equations-solutions (4):

$$x_1 + y_1 = 36 = \mathbf{6^2} \quad (x_1 = 26; y_1 = 10)$$
$$x_2 + y_2 = 25 = \mathbf{5^2} \quad (x_2 = 17; y_2 = 08) \qquad \text{(Eq.4)}$$
$$x_1 - y_1 = 16 = \mathbf{4^2}$$
$$x_2 - y_2 = 09 = \mathbf{3^2}$$

3.2. The unity of two realities – chemical and mathematical

Through a purely chemical analysis it is possible to find such an arrangement of protein amino acids that fully corresponds to the observed arithmetical regularities, related to the uniqueness of number 26. Namely, Figure 3 shows an arrangement of AAs (in the 4 x 5 system), with the number of atoms as in Equations (3). This arrangement follows from a classification and systematization of 20 protein AAs into four diversity types[8], as it is shown in Figure 2: first row in Figure 3 comes from the vertical line of the circular model in Figure 2; fourth row from the horizontal line; second row from four middle points of circular model; third row make two left and two right AAs in relation to two middle points (M & D); finally, fifth row make two left and two right AAs in relation to two middle points (A & R). By this, each sequence in Figure 3 is arranged by the size of molecules, i.e. by the number of atoms in the side chains,[9] going from left to right; and the order of sequences is determined by the size of the first amino acid molecule in the sequence.[10] Only with such a precise and strictly regulated system can we get the desired result, the sequence 26-42-59-77, signifying the number of atoms in the four columns of AAs, in their side chains (cf. Table 4, Equations (3) and Figures 2 & 3).

Bearing in mind that an arithmetical law, presented in Equation (3), is fully confirmed, it makes sense to set up a *working hypothesis*, related to an algebraic law, presented in Equations (4): it must be that the quantities, given in Equation (4), $x_1 = 26$, $y_1 = 10$ as well as $x_2 = 17$, $y_2 = 08$, in a way also have been contained in the genetic code. Table 6 is an obvious and direct evidence for this. The first diversity type of AAs (P, G) and corresponding 08 codons appear to be diagonally on the right within Genetic Code Table (GCT), designated in Table 6 in light tones; the second one (L, I, V, A) with 17 codons diagonally on the left (in dark tones); altogether, in both diversity types of chemically low-level-functions (possessing only carbon and hydrogen within side chain) there are 25 codons.

The third diversity type of AAs and corresponding 10 codons follows, within GCT (Table 6), in the next order (light blue tones): in column "U" *up* and *down*, and in columns "A" and "G" only *up*. The fourth type, with 26 codons (the dark blue tones), in column "C" *up* and *down*, and in columns "A" and "G" only *down*; altogether, in two diversity types of chemically high-level-

[8] More details on the four diversity types of AAs (2 + 4 + 6 + 8) as it is presented in linear model of Figure 2, about a strict chemical hierarchy within and between them, the reader can see in (Rakočević, 2011a).

[9] The only exception is valine, which is understandable enough when we know that valine and isoleucine belong to the same stereochemical type, the valine type. That sequence should, therefore, be understood as follows: two AAs of the alanine stereochemical type (N, Q) are followed by two AAs of the valine stereochemical type (V, I).

[10] The dilemma whether before N or P is resolved by the following pairs: N is followed by a smaller pair V(10) – I(13), while P by a larger one L(13) – K(15).

functions (except C and H, possessing still O, and/or N, and/or S)[11] there are 36 codons.

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	
					13	**102**
N 08	Q 11	V 10	I 13	**42**	**89**	
P 08	H 11	L 13	K 15	**47**		
26	42	59	77			
	16	**17**	**18**			
	(1 x 68)		(2 x 68)			

Figure 3. 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.

The positioning of codons within the system of GCT (Table 6) in the terms "up" and "down" at first glance seem to be arbitrary and optional. However, if such a classification is viewed from the aspect of key qualificatives – the first half of the GCT (of pyrimidine kind) is of lower rank, and the second half of a higher rank (of purine kind) – then we get here also to the very strict quantitative relations (Figure 4). The Figure 4, in fact, shows that the principle of self-similarity (through the alignment into 25/36 codons) achieved in a way. First, if a series of I-II-III-IV types is taken as splitting into two classes, then in the first class belong two types from odd positions, and in the second one two types from even positions. And then "enters" at the scene the validity of the following regularity: the number of low-ranking codons in two types at the odd positions, plus the number of higher-ranking codons in the two types at the even positions is the same as the number of all codons in the first two diversity types (25). The reverse is true for the reverse situation: the number of low-ranking codons in the two types placed at the even positions, plus the number of higher-ranking codons in two types placed at the odd positions is the same as the number of all codons in the second two diversity types, the third and fourth, just 36. (From Figure 4 it follows that this zigzag regularity is valid also for the number of nucleotides).

It goes without saying that here is a case of coherence between codons and AAs, and also between AAs and an arithmetical system (Equations (3) as well as codons and an algebraic system (Equations (4).

That the presented coherence, except all the said, even more is stylized and sophisticated, shows the order of the AAs (related by codons) in GCT (Table 6) which is also followed by atom number balance as it is presented in Remark 3.3.

***Remark* 3.3.** Two halves of amino acid molecules, connected through a base-acidic loop in position K-D[12] within GCT: (1.F-14, 2.L-13, 3.I-13, 4.M11, 5.V-10, 6.Y-15, 7.H-11, 8.Q-11, 9.N-8, 10.K-15) + (1.S-5, 2.P-8, 3.T-8, 4.A-4, 5.C-5, 6.W-18, 7.R-17, 8.G-1, 9.E-10, 10.D-7) = (Odd/Even 56/65 = 76-11) + (Odd/Even 56 - 11/76:2) = Odd/Even 102±1 as a balance – the tab on the Libra (cf. Tab. 7 in Rakočević, 2004a).

3.3. The uniqueness of the number 48

Now we will demonstrate the uniqueness of number 48 within the system of numbers in Table 4 with one exercise: Find a number in this system, in series of odd or even numbers, which with its three followers gives the same result (204) which we obtained with number 26, as it is shown above. It is

[11] The only one exception is phenylalanine (F) which possesses within side chain the benzene with only carbon and hydrogen atoms. But the aromatic function is more complex than aliphatic one within the first two types of diversity. It is interesting (as we said in last paragraph in Section 2) that phenylalanine is also an exception in the pairing process in the integrated system in Table 3: although non-polar, it pairs up with polar tyrosine. In addition, phenylalanine is also an exception in the determination by two classes of enzymes aminoacyl-tRNA-synthetases (see Remark 4.3.).

[12] This chemically valid loop appears to be also a formal loop adequate and fit to the Gauss' algorithm as a splitting between second and third row in Figure 9 (in relation to Remark 2.3b).

immediately obvious that this number is 48, as it is shown in Equation (5):

48+50+52+54 = 204 (Eq.5)

	a	b			U,C	A,G		U,G	C,A
I	04	04	**25**		12	12		12	12
II	17	00			31	20		31	20
III	03	07	**36**		**20**	*10*		**19**	*11*
IV	08	18			**30**	*48*		**29**	*49*
	25		o/e →		100	83		100	83
	36				(93)	(90)		(91)	(92)

	U	C	A	G			U,A	C,G		75	
I	02	10	02	10			04	20			11
II	19	12	08	12	**75**		27	24		86	
III	14	06	05	05			19	11			11
IV	10	20	29	19	**108**		39	39		97	
					183						11
				o/e →			**86**	**97**		108	
			183 + 9 = 192				(89)	(94)			
					89-90-91-92-93-94						

Figure 4. This Figure follows from Figure 3 and Table 6. The designations I-IV: Four diversity types of amino acids. In first quadrant there is the number of three-letter words, i.e. codons within GCT (in total 61), while in other three quadrants – the number of letters (nucleotides). The regularity valid for zigzag line is given in the forth paragraphs of Section 3.2. (a) The first half of Table 6. (b) The second half of Table 6. In column "a" there are codons of pyrimidine kind, regarding at the middle position in codon, whereas in column "b" of purine. The validity of two principle (continuity and minimum change) is self-evident; also the changes for 01, 10 and 11. Besides the obvious, there are some "hidden" regularities as, for example, the redistribution of 75/108 letters through the doublets. Thus, in the first two types (I, II), which possess chemical properties of lower rank, we have: UC43 - AG32 = 11 and CA43 - CA32 = 11. (Cf. with the same pattern, 43-32 in Remark 2.2b and in Table A.4.1.) On the other hand, the doublets AG32 and CA32 appear to be in a unit change relation with UA31; then, the doublets UC43 and UG43 with CG44. Similarly is in doublets of two other types (III, IV), which possess chemical properties of higher rank: CA60 - UC50 = 10 and AG58 - UG 48 = 10. On the other hand, the doublets AG58 and UC50 appear to be in a zeroth change relation with the doublets UA58 and CG50.

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

Table 6. The standard Genetic Code Table. This Table represents the relationships within the so cold "standard Genetic code" with designation of four diversity types of protein amino acids and corresponding codons: first and second type without color (in light and dark tones, respectively), but third and forth in color. The codon number: for first type 08, second 17, third 10 and fourth 26, just as in algebraic system in Equations (4). The roman numbers designate two classes of AAs, handled by class I and class II of aminoacyl-tRNA synthetases.

It is also immediately obvious that this is the middle row in the system of numbers (in decimal numbering system) of TMA in Table 4. Thus, it is inevitable that every two rows at the same distance from the middle row (in analogous positions) yield twice the value of number 204 [Example: (37+39+41+43) + (59+61+63+65) = 2 x 204).] In addition, in relation to the two ends, and the two central numbers of the sequence 48-50-52-54, there is a symmetrical and cross-regularity (cf. Table C4 in Rakočević, 2011a).

Through an exact chemical analysis it is also possible to find such an arrangement of protein amino acids that fully corresponds to the observed arithmetical regularities, related to the uniqueness of number 48. By this we start from an elegant hydrogen atom number determined system given by V. Sukhodolets (1985) (Table 7 in relation to Table 8). The system in Table 7 consists of two subsystems; the first subsystem: the left (small) subsystem consisting of four AAs (G, N, Q, W) in the form of four singlet sequences [(G), (N), (Q), (W)]; the second subsystem: the right (large) subsystem of 16 AAs, in the form of four quaternary sequences [(ASDC), (PTEH), (VFMY),

(RKIL)]; in the subsystem with 4 AAs, the outer are G and W; the inner ones N and Q; in the subsystem with 16 AAs, alanine (A) and cysteine (C) are the outer; serine (S) and aspartic acid (D) the inner ones, and so on.

After this analysis we can generate the left subsystem of Table 9: within the first column ("out") are the outer, and within the second one ("in") the inner AAs, given in the same order as in Sukhodolets' system in Table 7. Now the next question makes sense: is it possible to sort AAs in both columns in accordance with their fundamental chemical nature? The answer is affirmative, as it is demonstrated in the right subsystem of Table 9. (For details see Section 4.2.1. in Rakočević, 2011a.)

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						

Table 7. 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: number of hydrogen atoms and out of brackets 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).

G P	A L V I	C M F Y W H	R K Q N E D T S
01 08	04 13 10 13	05 11 14 15 18 11	17 15 11 08 10 07 08 05
9+18=27	40+36 =76	74 + 54 = 128	81+ 72 = 153
(27+153 = **180**) (76+128 =**204**)			

Table 8. Four types of diversity of protein amino acids. The relationships between four diversity types of protein amino acids (2+4+6+8). In second row there is the number of atoms within side chains of amino acids. The calculations: within 10 AAs of two inner types there are 180 atoms, just as within 20 amino acid "heads", i.e. 20 amino acid functional groups (20 x 9 = 180). On the other hand, within 10 AAs of two outer types there are 204 atoms, just as within 20 amino acid side chains. This specific "simulation" is analogue to the "simulation", valid for the number of protons and neutrons in Table 7.

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

Table 9. Atom number within 20 side chains of AAs as a quartet of even numbers. The outer/inner amino acid pairs which follow from Sukhodolets' Table (Table 7). On the left: the original order as in Table 7; on the right: the chemical order of AAs as it is explained in Section 3.3.

4. Harmonic structures

A proof more that genetic code is a coherent system is the fact that there are some harmonic structures within it, which are presented in several previous works (Rakočević, 1997, 1998, 2004a, 2006, 2009, 2011). By this the term (and concept) "harmonic" is not used as a metaphor but as concrete mathematical expression, such as golden mean, harmonic mean, arithmetic mean etc.

4.1. Determination by Golden mean

First, we showed (Rakočević, 1998) that it makes sense GCT, given in the form as in Table 6, developed into a binary-code tree (0-63), exactly in the order specified here: first, codon octets with both pyrimidines, and then with both purines (F, L, L), (S, P), (I, M, V), (T, A), (Y, CT, H, Q), (C, CT, W, R), (N, K, D, E), (S, R, G). Such a tree appears to be in a strict correspondence to the Farey tree, including the correspondence between the route of most change (at each step turns

the zeros and ones: 0101010) and the "golden route" with Fibonacci numbers in fractions, both numerators and denominators: 1/2, 2/3, 3/5, 5/8, 8/13, 13/21, 21/34. (Notice that Fibonacci numbers are in a strict relation to golden mean.) By this, in the case of six-bit binary tree and the adequate Farey tree last fraction point (21/34) stays in relation to number 0101010 (42) which number represents the harmonic mean of the interval 0-63 and its half. In this point stays the codon with most diversity – the stop codon UGA; its neighbor is the codon UGG which codes for the most complex amino acid, tryptophan(W), only and one with two aromatic rings. As we see, the sense is clear: to balance the great diversity with maximum of harmony! (Cf. Fig. 1 and Fig. 2 in Rakočević, 1998)

Bearing in mind above presented harmonic relations it makes sense to determine (calculate!) the golden mean for interval 0-63, in the form of the generalized golden mean, ϕ^n (n = 0, 1, 2, 3, … , 9) (Stakhov, 1989, Rakočević, 2004b), as in Table 10. Then exactly seven AAs are on the positions of the golden mean.[13] They are G, Q, T, P, S, L, F with 60 atoms. Across from them must be seven of their chemically pairing "partners" as the complements: V, N, M, I, C, A, Y with 60 + (1 x 6) atoms; and the six remaining AAs, the three pairs of the non-complements: D-E, K-R, H-W with [60 + (1 x 6)] + (2 x 6) atoms; for them it makes sense that aliphatic AAs come first (D-E/K-R), followed by aromatic ones (H-W) (Figure 5).

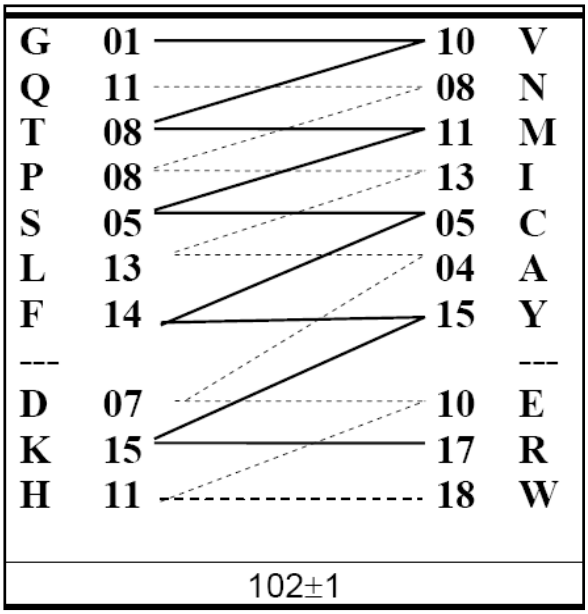

Figure 5. Atom number balance directed by Golden mean on the binary-code tree (presented in Figure 1 in Rakočević, 1998). First seven amino acids on the left are 'golden' amino acids; the arrangement-ordering follows from the ordering given in Table 10. On the right are their complements; below are three amino acid pairs as non-complements. The atom number balance: On the zigzag lines there are 102±1 of atoms. Within three classes of AAs there are 60, 66 and 78 atoms (with the differences for 1 x 6, 2 x 6 and 3 x 6), respectively.

[***Remark* 4.1.** The differences between three groups of amino acids, through the number of atoms (60, 66, 78), are 1 x 6, 2 x 6 and 3 x 6 respectively.]

In next step it makes sense the amino acid order, presented in Figure 5, to be rearranged by the size of the molecules: first glycine with one atom in the side chain, then serine with 5, threonine with 8 atoms, follows proline (the pair T-08/M-11 before the pair of P-08/I-13) etc. If this new sequence of the seven "golden" AAs was turned through 180 degrees, we actually got a strict system that we called CIPS (Cyclic Invariant Periodic System) (Figure 6).[14]

[***Remark* 4.2.** The presented order of codons in Table 6 is based on the codon octets, but for a better viewing how the system, presented in Figure 6, follows from GCT (Table 6), it is also necessarily to have an order based on the codon quartets, such as it is presented in Table 11 (Négadi, 2009).

[13] It is self-evident that only at the six-bit binary tree the determination with the generalized golden mean is going through module 9, that is through the decimal numbering system. On the other hand, because two golden mean values are calculated from the quadratic equation by square root of the number five (which represents half of the decimal scale of 10 digits) it is reason why decimal numbering system is - the only "golden" numbering system.

[14] Cyclicity and periodicity through the positions of two and two amino acids – up/down – in relation to middle chalcogene AAs, on the position "3".

Also to have a very symmetric form of GCT, valid for mitochondrial genetic code (Dragovich & Dragovich, 2010).

The further analysis shows that the order of five amino acid classes makes an adequate chemical sense: on the middle position (the position "1") came non-contact, the chalcogene AAs (S, T & C, M); follow (on the position "2") contact AAs G-P and V-I; then came (on the position "3") next class of non-contact AAs, two very polar, double acidic AAs with two their amide derivatives (D, E & N, Q); follow (on the position "4") the source aliphatic AAs of the alanine stereochemical type (A-L and K-R), two of which are amine derivatives (K-R), with a lower degree of polarity (nitrogen is less polar then oxygen!); finally came four aromatic AAs (F,Y & H, W) on the position "5".

5	073	F	14	15	Y	079
4	235	L	13	04	A	172
3	087	Q	11	08	N	085
2	160	P	08	13	I	121
1	168	T	08	11	M	043
1	243	S	05	05	C	081
2	184	G	01	10	V	168
3	087	D	07	10	E	093
4	091	K	15	17	R	265
5	081	H	11	18	W	044

Figure 6. The Cyclic Invariant Periodic System (CIPS) of canonical AAs. At the outer side, left and right, it is designated the number of atoms within coding codons; more exactly, in the Py-Pu bases (U = 12, C = 13, A = 15 and G = 16); at the inner side – the atom number within amino acid side chains. In the middle position there are chalcogene AAs (S, T & C, M); follow - in next „cycle" - the AAs of non-alaninic 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 (Rakočević, 2009).

From pure chemical reasons it makes sense to say that two classes (light tones in Figure 6) belong to *a primary superclass*, with original aliphatic AAs (and/or derivatives of lower level), whereas the three remaining classes (dark tones) to *a secondary superclass*, with the derivatives of a higher level.

ϕ^0	ϕ^1	ϕ^2	ϕ^3	ϕ^4	$\phi^{5\text{-}7}$	ϕ^8	ϕ^9
G	Q	T	P	S	L	L-F	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

Table 10. The determination of the amino acid positions through the golden mean. The distribution of AAs by the generalized Golden mean (through power values) within the sequence 0–63 on the binary-code tree (as in Fig. 1 in Rakočević, 1998). 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. Fourth row: the values of the Golden mean powers within the interval 0–63. The calculations: 0.618033 x 63 = 38.94; 0.618033 x 0.618033 x 63 = 24.06 etc.

U-U-X	U-C-X	C-U-X	C-C-X
U-A-X	U-G-X	C-A-X	C-G-X
A-U-X	A-C-X	G-U-X	G-C-X
A-A-X	A-G-X	G-A-X	G-G-X

Table 11. A model for codon distribution in Genetic Code Table. The codon order in Genetic Code Table, based on the codon quartets in first and second half of the Table, as in Table 1 in (Négadi, 2009), here simplified and generalized.

4.2. Golden mean – enzyme determination

The splitting into two above presented superclasses exists in a strict correspondence to the splitting into two enzyme-directed classes (amino acids handled by class I and by class II of aminoacyl-tRNA synthetases), as it is shown in Figure 7 and Figure 8, in relation to Box 4.1.

[***Remark* 4.3.** There are two classes of aminoacyl-tRNA synthetases: Class I has two highly conserved sequence motifs. It aminoacylates at the 2'-OH of an adenosine nucleotide, and is usually monomeric or dimeric (one or two subunits, respectively). Class II has three highly conserved sequence motifs. It aminoacylates at the 3'-OH of the same adenosine, and is usually dimeric or tetrameric (two or four subunits, respectively). Although phenylalanine-tRNA synthetase is class II, it aminoacylates at the

2'-OH. The amino acids are attached to the hydroxyl (-OH) group of the adenosine via the carboxyl (-COOH) group.]

Box 4.1. Molecule pairs hierarchy in relation to natural numbers series (going from Tables 2. 1 & 2.2 to Figure 8)[15]

1. Vertical pairs in SubS1 (Tab. 2.1) and SubS2 (Tab. 2.2)

1.1. Glycine as the simplest (G-V) (start: 01 atom);
1.2. Serine as next (S-C) (start: 05 atoms);
1.3. Threonine as next (T-M) (start: 08 atoms);
1.4. Proline as next (P-I) (start: 08 atoms; M < I);

2. Horizontal pairs in SubS1 (Tab. 2.1) and SubS2 (Tab. 2.2)

2.1. Hydrocarbons (A-L) (start: 04 atoms);
2.2. Carboxyl group derivatives (D-E) (start: 07 atoms);
2.3. Amide derivatives (N-Q) (start: 08 atoms);
2.4. Amino derivatives (K-R) (start: 15 atoms);

3.2. Heteroatom derivatives (H-W) (start: 11 atoms);
3.1. Aromatic hydrocarbon and its OH derivative (F-Y) (start: 15 atoms);
3. Aromatic AAs (more complex than aliphatic)

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

Figure 7. The amino acid arrangement in accordance to the principle: "a little" and "full" in relation to "small" and "large". So, 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.

From the correspondence between two superclasses, two classes and four subclasses as it is presented in Figure 7, can follow *a prediction* (Prediction 1) for further researches: the demonstrated crossing of two superclasses, two classes and four subclasses must be reflected, in some way, in the protein structures and functions. [Additional texts about amino acid handling by two classes of enzymes see in: (Rakočević, 1997, 2009)].

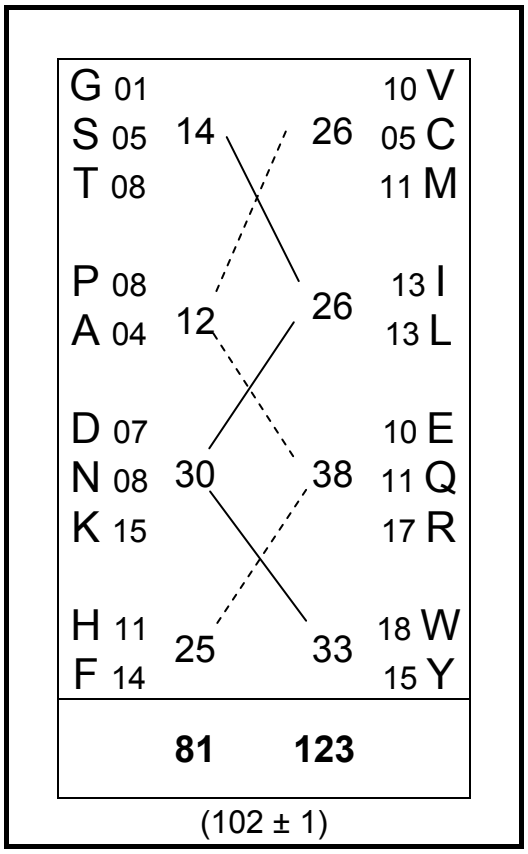

Figure 8. Atom number balance directed by two classes of enzymes aminoacyl -tRNA synthetases. This system follows from the systems given in Figure 5 in relation to Tables 2.1 and 2.2 (cf. Box 4.1). As in the system given in Figure 5, on the zigzag lines there is a balance of 102±1 of atoms. Class II handles the smaller amino acids within the pairs (on the left), whereas the larger (on the right) are handled by class I aminoacyl-tRNA synthetases.

4.3. The Little Gauss' algorithm

There are several anecdotes about Gauss as a little boy and his understanding of mathematics at his earliest age. One of them say that the teacher gave an exercise to a class of young pupils (only nine years of age) to add all the numbers from 1 to 100, thinking he would have enough time to get on with some other things, while the pupils did the very long addition. However, the teacher was surprised when one pupil produced the correct answer in less than 3 minutes. The answer was 5050. Asked how calculated it, the young student explained

[15] For details about first subsystem, presented in Table 2.1 (SubS1) and second subsystem, presented in Table 2.2 (SubS2) as well as theirs "translation" into system presented in Figure 8, see in: (Rakočević, 1998).

that he added the first and last numbers (1 + 100 = 101), then the following and the first preceding one (2 + 99 = 101) and so on. Since there are 50 such pairs, he multiplied 50 x 101 and obtained the requested result. The young pupil was named Gauss, and the algorithm he used to get the answer has become known as Gauss' Algorithm.

Now, let us consider what would happen if the teacher had asked the students to sum all the numbers from 1 to 101, distributing results in a Table with 10 columns. The following Table would be obtained where are 50 pairs plus a single unpaired number, the 51 (Equations-solutions (6) :

(01 + 101), **(11 + 91), (21 + 81), (31 + 71), (41 + 61)**
(02 +100), (12 + 90), (22 + 80), (32 + 70), (42 + 60)
(10 + 92), (20 + 82), (30 + 72), (40 + 62), (50 + 52)
(Eq.6)

And now the reader is asked to look at the first row in Equation 6. We see that the particularly designated quantities (bold) are the same as the number of atoms within molecule side chains of AAs found in patterns which are "downloaded" from the right side of Table 2.1, as shown in Remark 2.3b and Figure 9 in relation to Figure 10.

[*Remark* 4.4. Notice that the pattern (129-75-43-32) of atoms is the same as in Remark 2.2c. Arithmetical regularities background of this pattern as well as of the pattern 129 = 61 + 68 one can find in Table A.4.1 and A.4.2, in Appendix.]

In Figure 10 are given formulae of 20 canonical AAs in order as in Figure 9. From those formulae, i.e. from the chemical structures it is easy to see that the four contact AAs (GPVI), with 32 atoms within their side chains, can be classified together with five other AAs (ALSDF), possessing 43 atoms, into the class of *invariant* AAs (light tones). The remaining 11 AAs constitute a class of *variant* AAs with a total of 129 atoms in their side chains. Furthermore it makes sense to break this class into two subclasses: the subclass of *less variant* AAs (TEMCQNY) with 68 atoms and the subclass of *more variant* AAs (KRWH) with 61 atoms.

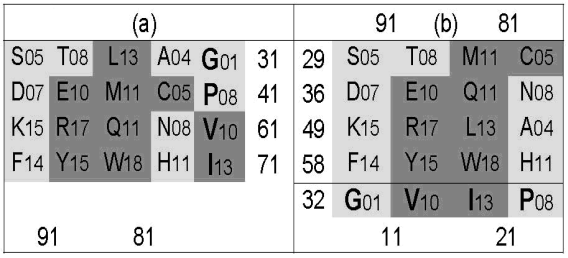

Figure 9. The distribution of amino acids according to Gauss' algorithm; (a) the distribution of amino acids has been derived from right side of Table 2.1, by presenting two pairs here in one row as the "pair of pairs". In the beginning of each row obtained in this way one "contact" amino acid has been associated, by the increasing molecule mass. (About "contact" and "non-contact" amino acids see in Remark 2.1.). Atom number (in amino acid side chains) in the rows and columns generated in this way corresponds, one hundred per cent, to the quantums from the first row of Gauss' algorithm of adding numbers from 1 to 101 (Equations-solutions (6). Dark tones: Class I of amino acids handled by class I of enzymes aminoacyl-tRNA synthetases; light tones: Class II. Going from (a) to (b) it is obviously that chemically related groups of AAs have been "taken off" by 0, 1 and 2 steps, respectively. By zero "steps" in aromatics; by one step in chalcogenic AAs (M, C in relation to S, T) and carboxylic (carboxylic AAs D & E in relation with their amides N & Q); by two steps in source aliphatic AAs: A, L & K, R. The distribution in (b) is the same as in (a) but "leveling" has been conducted here according to the chemical properties of molecules, so there is no more taking off. The class of contact AAs has been added to the beginning of columns, instead of to the beginning of rows. Shading is the same as in (a).

Now the question what is the meaning of the concepts (notions) of "invariant" or "variant". It is easy to understand why, for example, the glycine and alanine are invariant molecules; a molecule (G) with the smallest possible non-hydrocarbon side chain, and a molecule (A) with the smallest possible hydrocarbon side chain. But, it is harder to understand why valine with a propyl group as its side chain is also invariant if there is (in the nature) simpler ethyl group. The explanation is contained in Figure 1. Here we see the sense, meaning and meaningfulness (logic?) of choice: after the first possible case of non-hydrocarbonicity come possible cases of hydrocarbonicity; the first possible case of openness, then of half-cyclicity, cyclicity and branching (hence the meaning of four stereochemical types of AAs). In such a choice it has to be so as it is (and so must be anywhere in the universe). If, however, could be possible second, third etc. cases, then the invariant AAs outlined here would not be

invariant. Hence it makes sense to talk not only about more or less variant, but also of more or less invariant (Figure 11).

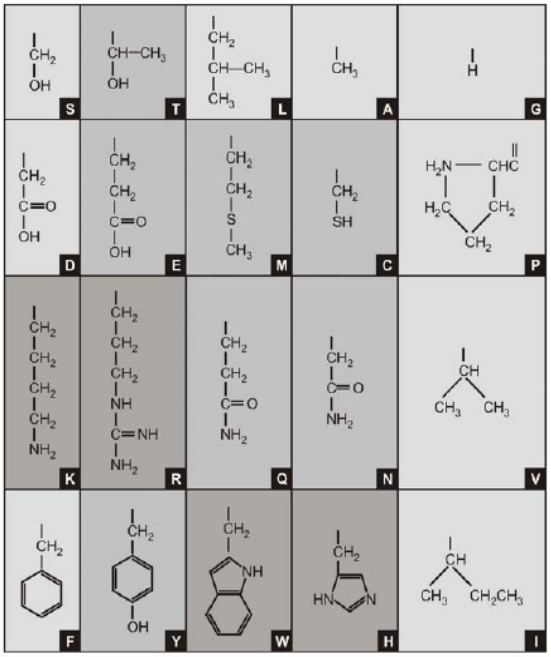

Figure 10. The structure of amino acid molecules. The simplest amino acid is glycine (G) whose side chain is only one atom of hydrogen. It is followed by alanine (A) whose side chain is only one CH_3 group, which is the smallest hydrocarbon group. There are total of 16 amino acids of alaninic stereochemical type ("non-contact" amino acids) with one CH_2 group, each between the "body" and the "head". The glycine type contains glycine (G) only; valine type contains valine and isoleucine (V, I). The last stereochemical type is proline type with proline (P) which represents the inversion of valine in the sense that the "triangle" of three CH_2 groups for the "head" is not bound by the basis, therefore not only with one but with two CH_2 groups (Popov, 1989; Rakočević & Jokić, 1996). Light tones [(G, P, V, I)(32 atoms)] & [(A, L, S, D, F)(43 atoms)]: invariant AAs; most dark tones [(K, R, W, H)(61 atoms]: most variant AAs; less dark tones [(T, E, M, C, Q, N, Y)(68 atoms)]: less variant AAs. Notice a further possibility for splitting: 1. two aliphatic AAs [(K, R)(32 atoms)], 2. two aromatic AAs [(W, H) (29 atoms)], 3. chalcogene AAs plus aromatic hydroxide derivative [(MC, TY)(39 atoms), and 4. dicarboxilic amino acid plus two amides [(E, QN)(29 atoms) (Cf. Section 4.3.). A specific calculation: less variant AAs, all aliphatic but one (Y), plus two more variant (aromatic: W, H), equals 68 + 29 = 97 atoms; invariant AAs, all aliphatic but one (F) plus two more variant (aliphatic: K, R), equals 75 + 32 = 107 atoms; if so, then: 107 – 97 = 10; 107 + 97 = 204. [Additional calculations: 32 + 43 = 75; 61+68 = 129 (cf. Remark 2.2).]

Figure 11 shows that the splitting of AAs into two classes – variant and invariant – is not only a formality (the result of Gauss' algorithm)[16], or just a matter of chemical structure of molecules, but also the matter of amino acid functions (polarity). In column "more" (more variant and more invariant) there are six AAs, two polar (KR) and four semi-polar (GP and HW).[17] In column "less" (less variant and less invariant) there are 14 AAs, seven polar and seven non-polar. If, however, do not look at the number of molecules than at the number of atomic associations then they are seven polar and six non-polar. [The AAs leucine (L) and isoleucine (I) are one and the same atom association through the structural isomery.] Altogether, the amino acid molecule pattern expressed in Figure 11 appears to be 4-9-6, what means: 4 semi-polar, 9 polar and 6 non-polar.[18] [About relations between polarity of AAs and their positions within GCT see Table A.3 in Appendix]

more	less		
G P	V I A L F S D	invariant	66
H W K R	T E Y N Q C M	variant	68
60 + 10	68 = 78 - 10		

Figure 11. The variability of AAs with respect to their polarity; explanation in the text (cf. two last paragraphs in Section 4.3).

From the showed distinctions into invariant and variant AAs can follow *a prediction* (Prediction 2) and from distinctions into semi-polar, polar and non-

[16] The matter of formality is also the atom number pattern: (60 + 10), 66, (78 – 10) in relation to the pattern which follows from the golden mean determination: 60, 66, 78 as it is presented in Remark 5.1.

[17] From the Table 3 we se that lysine (K) and arginine (R) are polar in both parameters: hydropathy and cloister energy. On the other hand glycine (G) and triptophan (W) are polar in hydtropathy and non-polar in cloister energy. The histidine (H) is polar in hydropathy, but neutral in cloister energy. The P is special case: it is polar from the aspect of hydropathy, and non-polar from the aspect of polar requirement (Woese et al., 1966; Konopel'chenko and Rumer, 1975; Rakočević, 2004a).

[18] As a noteworthy is the fact that the pattern 4-9-6 corresponds to the third perfect number 496 (cf. Table A.4.1 and 4.2 in Appendix).

polar AAs also *a prediction* (Prediction 3) both for further researches: the demonstrated distinctions have to be reflected, in some way, in the protein structures and functions in healthy as well as sick states.

4.4. A specific harmonic structure

From the system presented in Figure 8 follows a new very specific harmonic structure within a system of 5 x 4 of AAs as it is presented in Table 12 (the same as Table 1 in Rakočević, 2004a). The five rows within the system start with one polar charged amino acid each, making first column, consisting from five polar charged AAs (D, R, K, H, E).

In Figure 8 the molecule pair D-E make the only two charged acidic molecules (dicarboxilic AAs). In their neighborhood are two their amide derivatives (N-Q). The following six molecules, in a strict order, appear to be two triplets; the first (three basic molecules) RKH and the second one (three neither acidic nor basic molecules), the triplet FYW. Actually, the first triplet ends with the sole aromatic amino acid, which is basic charged (H), and continue with three aromatic non-electrified; and then: between the first two amino acids (D-E) comes the first triplet, and between the second two (N-Q) comes the second triplet. Thus, in such a manner is generated the left half of the system in Table 12; then comes the right half taking two sequences in a vice versa position from the upper part of the system in Figure 8.

					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 2 (37 x 37)

Table 12. The harmonic structure with two "acidic" and three "basic" amino acid quartets. The two "acidic" AAs because D & E are acidic and the three "basic" AAs because R, K & H are basic. 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 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 (Rakočević, 2004a).

Within the first two columns in Table 12 [(a) and (b)] is given the number of nucleons within twenty amino acid molecules (side chains), calculated after the first i.e. the lightest nuclides (a), also the nuclides with the maximal abundance (b)[19] (H = 1, C = 12, N = 14, O = 16, S = 32). In third column (c) is the number of nucleons, calculated according to the nuclides with lowest abundance in nature (H = 2, C = 13, N = 15, O = 17, S = 36); fourth column (d): the number of nucleons, calculated according to the latest, i.e. heaviest nuclides (H = 2, C = 13, N = 15, O = 18, S = 36); finely, in last column (M) is the calculated molecular mass.

It should be noted that for nucleon number (within all nuclides) as well as for molecule mass, two principles are valid: the principle of continuity and unit change principle (Equations (7-9). That means that other possible balances of nucleon number as well as molecule mass, in accordance with a-b-c-b-a pattern, can not save neither the neighborhood of pair-members nor the validity of these two principles. By this, in the system in Table 12 the pairs are as in

[19] The "a" and "b" are the same because the matter is about one and the same nuclide: the first nuclide (isotope) appears to be with the maximal abundance.

upper row of Equation-solution (10). In the bottom row there are the pairs as in the linear arrangement of the system consisting of four diversity types, shown in Figure 2.

189 – 100 – **289** – 10 – **299** – 10 – **289** – 100 – **189** (Eq.7)

221 – 110 – **331** – 10 – **341** – 10 – **351** (Eq.8)

485 – 101 – **586** – 10 – **596** – 101 – **586** – 101 – **485** (Eq.9)

(GV, PI); (SC, TM, AL, DE [DN, EQ], NQ, KR, HW, FY)

(GV, PI), (AL, CM, FY / WH, RK, QN, ED, TS) (Eq.10)

As we see from Table 12 the number of nucleons within 20 side chains of 20 amino acid molecules is 1255. Adding to this result the number of nucleons within amino acid functional group, 20 times (20 x 74 = 1480), we get a total of 2735; that means for three units less than molecule mass (2738 – 2735 = 3). But these three units enabled that the molecular mass appears to be determined by the Shcherbak's key parameter, the number 37, very unique and very specific. More than all that, despite all the other isotopes, all except the first, participate with a minimum percentage, the balance of the total number of nucleons in these isotopes is complete (columns c and d), as if they participate in the full amount.[20]

5. Concluding remark

The presented coherent and harmonic structures support the hypothesis of Sukhodolets (1985), as well as our own (Rakočević, 2004a), that the genetic code still in prebiotic conditions was complete, consisting of four amino bases and twenty amino acids. It remains, however, an open question of relationships between the standard genetic code (which we analyze here) and the so-called deviant codes. For example, the Table of mammalian mitochondrial code is more symmetrical than the Table of the standard one, because it does not possess asymmetric degeneracy (3-1), or (2-1-1), but only symmetrical (4) and (2-2). However, it fits only with the arithmetical system, given in Equation-solutions (3), but not with the algebraic, given in Equation-solutions (4). From this follows a new question: what is older - and who is here the chicken, and who the egg - the mitochondrial code which is determined with only one, or the standard one, determined with both mathematical systems? It is our hope that the answer to this question will be given in the future researches.

Acknowledgement
I am very grateful to Editor-in-chief Sultan Tarlacı and the Editor Tidjani Négadi for the invitation to participate in this Special issue of the NeuroQuantology. I also thank to my friends and colleagues Branko Dragovich, Dragiša Janković, Djuro Koruga and Dejan Raković for stimulating discussions and benevolent critique. And last, but not the least, I would like to thank to my chemistry-colleague Ruža Halaši for a wholehearted support and friendship through many years.

[20] "We can see that, in some unknown way to us, the unity of 'Real and Possible' was realized." (Rakočević, 2004a).

Appendix
Some source harmonic structures

The Table A.1 represents the Plato's system of two progressions, the first with the quotient 2, and second one with the quotient 3, both in relations to natural numbers series, their squares and the sum (first to last and the last column) of both. Notice that from two middle rows, 4th and 5th, the 4th appears to be in relation to genetic code entities. For example, the 4 & 16 as four contact and 16 noncontact AAs or 4 x 16 codons within GCT; the 81 as 61 amino acid codons plus 20 AAs; the 64 as 64 codons; the 20 as 20 AAs in a 4 x 5 arrangement.

The Table A.2 represents the Plato's viewing how from two progressions (the third and fourth columns in Table A.1) follows a Pythagorean musicale tone scale. The order of four blocks as follows: 1. the formulas for harmonic and arithmetical means; 2. two progressions extended with harmonic and arithmetical means between two members in all steps, then combined; 3. first two members of progression with the quotient 2, the 1-2 interval, extended with harmonic and arithmetical means and then with additional two members through the rule given in row below in order to become a whole musicale tone scale (the quotient of all two neighbor numbers is 9/8, corresponding to a whole tone, except in two cases where it is 256/243, corresponding to a half-tone; 4. the reducing of fractions in the previous interval 1-2 in a common denominator, the number 384, wich number we can also find as a total number of atoms within 20 amino acid molecules.

The Table A.3 shows that strictly arranged positions of AAs within GCT appear to be in a strong correspondence with the polarity of amino acid molecule and its size (atom number) through the validity of the principle of minimum change as follows, in the designations: (n) non-polar, (p) polar, (o) outer, (i) inner (Rakočević, 2000):

(n) 4V+1M+3I+4A+**2L**+**4L**+**2F**+2C = 22 molecules
40+ 11+39+16+26 + 52 +28+10 = 2**2**2 atoms (42**0**) (Eq.11)
(o) 4V+1M+3I+4A+**2Y**+**4R**+**1W**+2C = 21 molecules
40+ 11+39+16+ 30 + 68 +18+ 10 = 2**3**2 atoms (42**1**) (Eq.12)

(p) 4G+2K+2N+4P+**2Y**+**4R**+**1W**+2E+2D+4T+2R+2S+2Q+2H+4S = 39
04+30+16+32+30 + 68+ 18+ 20 +14+ 32+ 34+10+22+22 + 20 = 3**7**2 (72**3**) (Eq.13)

(i) 4G+2K+2N+4P+**2L**+**4L**+**2F**+2E+2D+4T+2R+2S+2Q+2H+4S = 40
04+30+16+32+26+52 + 28+20+ 14+32+ 34 +10+22+ 22+ 20 = 3**6**2 (72**2**) (Eq.14)

From the above presented equations follows that in 22 molecules of non-polar AAs there are 222 of atoms within their side chains, and 420 of atoms within the whole molecules; in outer space, however: 01 molecule less, 10 of atoms more within side chains and 01 atom more within the whole molecules. On the other hand, in 39 molecules of polar AAs there are 372 of atoms within their side chains and 723 of atoms within the whole molecules; in inner space, however: 01 molecule more, 10 of atoms less within side chains and 01 atom less within the whole molecules.

The Table A.4.1. shows the changes through the application of the two principles (of minimum change and of the continuity), starting from the first possible two-digit number in decimal numbering system (from the number 10 in column *a1* in correspondence to the first perfect number, the number 6, in column *d*). In this Table one can find the background of arithmetical patterns (32+43 = 75) and (61+ 68 = 129), given in Remark 2.2 and Figure 10.

The Table A.4.2. shows that all relations in Table A.4.1, ultimately are determined by the third perfect number, the number 496.

x^1	x^2=y	2^x	3^x	xy=x^3	x+y=z	z
0	0	1	1	0	0	0 x 1
1	1	2	3	1	2	1 x 2
2	4	4	9	8	6	2 x 3
3	9	8	27	27	12	3 x 4
4	**16**	16	81	**64**	**20**	**4 x 5**
5	25	32	243	125	30	5 x 6
6	36	**64**	729	216	42	6 x 7
7	49	128	2187	343	56	7 x 8
8	**64**	256	6561	512	72	8 x 9
9	81	512	19683	729	90	9 x 10

Table A.1. Two Plato's progressions in relations to natural numbers series

Harmonic mean (h)	Arithmetic mean (m)
$h = \frac{2ab}{a+b}$	$m = \frac{a+b}{2}$
$1, \frac{4}{3}, \frac{3}{2}, 2, \frac{8}{3}, 3, 4, \frac{16}{3}, 6, 8$	
$1, \frac{3}{2}, 2, 3, \frac{9}{2}, 6, 9, \frac{27}{2}, 18, 27$	
$1, \frac{4}{3} \mid \frac{3}{2}, 2, \frac{8}{3} \mid 3, 4 \mid \frac{9}{2}, \frac{16}{3} \mid 6, 8 \mid 9, \frac{27}{2}, 18, 27$	
$1, \frac{9}{8}, \frac{81}{64}\ \frac{4}{3} \mid \frac{3}{2}, \frac{27}{16}, \frac{243}{128}, 2$	
$(3^2 \,\&\, 3^4 / 2^3 \,\&\, 2^6) \mid (3^{2+1} \,\&\, 3^{4+1} / 2^{3+1} \,\&\, 2^{6+1})$	
384 432 486 512 576 648 729 768	
48 54 26 64 72 81 39 (384)	

Table A.2. The relations of two Plato's progressions with Pythagorean musical note scale

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

Table A.3. The relations of amino acids positions within GCT and their polarity; the polarity after (Kyte and Doolittle, 1982)

e	a_1	b	a_2	c	d
160	10	31	20	10 + B9 = **129**	06 + 123 = **129**
	21		31	21 + A8 = **129**	17 + 112 = **129**
(44)		**(44)**			
204	32		42	32 + 97 = **129**	28 + 101 = **129**
	43	**75**	53	43 + 86 = **129**	39 + 90 = **129**
(44)		**(44)**			
248	54		64	54 + 75 = **129**	50 + 79 = **129**
	65	119	75	65 + 64 = **129**	61 + 68 = **129**
(44)		**(44)**			
292	76	163	86	76 + 53 = **129**	72 + 57 = **129**
	87		97	87 + 42 = **129**	83 + 46 = **129**
(44)		**(44)**			
336	98		A8	98 + 31 = **129**	94 + 35 = **129**
	A9	207	B9	A9 + 20 = **129**	A5 + 24 = **129**

Table A 4.1. The first two-digit number in "moving" for 11 in all steps (cf. column a_1 with first to last column in Table 4)

<table>
<tr><td>160 + 336 = 496
204 + 292 = 496
248 + 248 = 496</td><td>31+ 207 = 248 – 10
75+ 163 = 248 – 10
119 + 119 = 248 - 10</td><td rowspan="2">31 – 31 = 00; 31 – 20 = 11
75 – 53 = 22; 75 – 42 = 33
119 – 75 = 44; 119 – 64 = 55
163 – 97 = 66; 163 – 86 = 77
207 – 119 = 88; 207 – 108 = 99</td></tr>
<tr><td colspan="2">496 – 238 = 2 x 129</td></tr>
</table>

Table A.4.2. The determinations by the third perfect number, the number 496

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