Genetic code as a semiotic system (Vers. 2)

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Abstract. In previous works (MMR, 2019, 2021, 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. [This is the second version (on the way to the fourth), originally in the same form and content published here a few months ago.]

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

1. Introduction

The work we present is a direct continuation of some previous in which a completely new type of mirror symmetry was presented, expressed in a set of protein amino acids (Rakočević, 2019, 2021a,b; 2022).[1] The fact that protein amino acids are constituents of the genetic code, it is necessary to ask how this new type of mirror symmetry is expressed in the entirety of the genetic code. With this paper we provide an answer to that question. The essence of that answer is the idea that the genetic code itself is an entity of a semiotic nature.

The above two, a new type of mirror symmetry and the idea that the genetic code is an ontological entity, not a metaphor,[2] are the reason why this paper must inevitably be under the hypothesis.[3]

In order to find an answer to the fundamental question what in reality is the genetic code – an ontological entity or a metaphor – a special and full scientific discussion should

[1] In the following text, instead of Rakočević, MMR is cited.

[2] "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).

[3] The paper must be "under the hypothesis" because of the state in current science (as noted in footnote 2), not because of my position. My position is such as I presented above through three examples: bare scientific facts and strict scientific truth are at stake.

probably be organized. Instead, for this occasion, we choose to show three specific examples which, in our opinion, testify both to the bare facts and to the scientific truth.[4]

Example 1. On Figure 1.1 we see a system-arrangement of protein amino acids which, by the number of atoms in the molecules (within their side chains), through rows and columns, is in full accordance with one of the diagonals of the Periodic Number System (PSN) in the Decimal number system (Figure 2). It cannot be said that this "mirroring" is not a bare fact, and therefore a scientific truth. However, as we know (from the overall science so far) the indicated connection between the system-arrangement of molecules and the Periodic system of numbers cannot have any causal relationship, it follows that we have before us the bare fact that this connection, instead of being possibly causal, is actually of a semiotic nature, and this means that it is an arbitrary connection.[5]

The given example is even more significant, in terms of confirmation of semiological entities, more than above has been said. So, if the molecules of AAs are taken into account, once by rows, and secondly by columns (Figure 1.1), then the four number pairs from diagonal (11-91, 21-81, 31-71, 41-61) of PSN, in Figure 2, are fully represented in the system-arrangement given on Figure 1.1; there is no space for more or less atom quantities than 2 x 204. (The number 51 on the diagonal has no counterpart, and in the atom number sequences, that number does not exist.)

Example 2. On Tables 1.1 and 1.2 (in correspondence with Table 3.1) we have a system-arrangement of amino acid molecules, such that the number of atoms per row represents a mirror image of a specific unique crossing of a 6-bit binary tree and the last column of the PSN; those are the bare facts, which testify that it is so, and thus it is also the fact that it is a scientific truth. On the other hand, since this connection also is not causal than arbitrary, this example also confirms the semiotic nature of the genetic code.

And this example is even more significant, from the aspect of confirmation of semiological entities, than what was said above. Namely, from Table 1.2 (on the right side) we read that the presented crossing (binary tree with PSN) gives only one quantitative solution: 204, as atom number within 20 AAs. Bearing in mind this fact, and knowing the general law of the genetic code, we necessarily choose to search for the uniqueness of the quantity 204 within PSN. And that was what we find (Tables A1-A4 in

[4] Alexander Gottlieb Baumgarten, 1735: "Exemplum est repraesentatio magis determinati ad declarandam repraesentationem minus determinati suppeditata."

[5] Of course the shown diagonal sequence as a signifier is arbitrary in relation to the signified (atom number sequences by rows and columns), but not in the set of signifiers. [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."]

Appendix A). [**Remark 1.** The general law of the genetic code: unique chemical entities are accompanned by unique arithmetical and/or algebraic arrangement.][6]

Example 3. On Table 2.1 and Survey 1 (in correspondence with Surveys 2-4 and Tables A1, A3 and A4) we find the same quantities of number of atoms (60, 66, 78) in two different system-arrangements, each quantity with different amino acids. The starting quantity "60" in Table 2.1 appears as a semiotic signifier of five polar charged amino acids, while the starting quantity "60" in the arrangement of Survey 1 appears as the signifier of seven AAs, formally selected on the binary tree of the genetic code (formally, by determination of the golden mean) (MMR, 1998b).

We see that in Survey 1, in the follower of quantity "60" (in "66") there are AAs, which are chemical complements (counterparts) of AAs from "60", while this is not the case with the arrangement in Table 2.1. In the arrangement in Table 2.1, four of the five polar charged AAs have their counterparts within their subset (D-E and K-R), while the fifth amino acid (histidine) has yet to find a counterpart (to be H-W). And, here it seems that some kind of "intelligent design"[7] is on the scene. It was necessary to find such an amino acid (tryptophan) which, like histidine, would also be heterocyclic aromatic, and in addition to having exactly 18 atoms in the side chain, so that this "innovated" arrangement would pass from the state of the starting quantity "60" to the state of the final quantity "78". (The bottom, the last part of the arrangement in Survey 1.)

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When to the above illustrations are added from them derived illustrations (listed in the legend of Figure 2), then we have evidence not only that GC is of a semiotic nature, but also that PSN is a general determinant of GC; more precisely, from the aspect of semiotics, we have such a factual situation in which it is shown that PSN appears as the signifier and GC as the signified.

2. Generating of Genetic Code

In order to investigate the origin of the genetic code, from a chemical point of view it makes sense to put forward two working hypotheses: 1. Genetic code was originated by random chemical reactions that prevail in nature; 2. Genetic code was generated on the model of Periodic System of chemical Elements (PSE), via a possible analogy.

[6] There are two consequences of the validity of this law: 1. Minimum quantity – maximum quality. [Quality as properties of chemical substances and their system arrangements.]; 2. Minimum signifiers – maximum meanings (cf. MMR, 2022, Section 7).

[7] It makes sense to talk about "intelligent design", but only as such that is "handled" by the Periodic system of chemical elements, and as we explained in the previous work (The Spontaneous Intelligent Design, SPID) (MMR, 2018a, Box 4, p. 43).

If the first hypothesis is valid, it makes sense to assume that protolife started with only four amino acids corresponding to four Py-Pu bases within the RNA world.[8] Later, during the "evolution" of the genetic code, that number rose to 7–8, all the way to 16, and beyond 16, to finally stop at 20, and become the "frozen code".

We put the word evolution in quotation marks because, if the second working hypothesis were valid, then it makes no sense to talk about the evolution of the genetic code, but only about its generation, what implies that genetic code, from the aspect of the constituents (4 Py-Pu bases and 20 AAs was prebiotically complete.[9] So-called *deviant genetic codes*[10] are just variations within the degrees of freedom contained in the standard genetic code.

Box 1. *Generating of the life through a unique molecules aggregation*

MMR, 2004, p. 232: "Each of that aggregations [amino acid molecules] could (and must) have its own 'evolution', but only one could have been selected[11] – the one that gained the characteristic of self-reproduction (by which, through trial, error and success it became EVERYTHING); all other, not selected, could not have any chance (by which, through trial, error and unsuccess, from the aspect of code origin, and consequently life itself, they became NOTHING). Selfreproduction, in fact, could have indicated only that genetic code [as a set of its constituents] had been established and that it is the code that provides that reproduction. If there would not be this generated (not degenerated) genetic code afterwards or if it would have changed and became different, it would lose its characteristic of reproduction of already originated life."

But, we already have evidence for the validity of the second working hypothesis (MMR, 2018b, in Abstract: "... it appears a correspondence between the distribution of codons in the GC Table and the distribution of chemical elements in the PSE with respect to their even/odd parity and stability/instability of the isotopes."). In the mentioned paper it is shown (four Surveys on p. 296) that the system of the same two linear algebraic equations is a full accordance with the distribution of codons, coding for less complex and more complex AAs in GCT and with the distribution of stable and unstable chemical elements through periods and groups in PSE.

[8] MMR, 2004, p. 233: "Setting the problem in this manner could mean justification of the hypothesis on independent preceding existence of one 'RNA World' (Gilbert, 1986; Orgel, 1986) …"

[9] MMR, 2004, p. 231: "Hypothesis on a complete genetic code … By this hypothesis, derived from presented facts as we understand them, we support the stand point that genetic code is one and unique, universal, valid for everything living, in fact, it is the condition for origin and evolution of life." (Box 1.)

[10] Deviant codes, as we explained in: MMR, 2018a, Box 2, p. 41.

[11] This is not about Darwinian selection (which can only be valid from the moment when life was already generated), but about spontaneously occurring conditions that made it possible to find amino acids together in a set that, in itself, represents a perfect system. [Swanson, 1984, p. 201: "The actual amino acid code and the twenty amino acids it codes for suggest an idealized model coding system and idealized relationships among the amino acids. Using the idealized models, one could construct a 'perfect' genetic code … " (Cf. Figure 1.1 and Figure 5; Tables 1.2, 1.5, 1.6, 2.1, 4.1 and Survey 7; all in this paper).]

Admittedly, there is one missing "link" in the chain of proving the accordance of the two codes – genetic and chemical code. Complete accordance was shown for the distribution of less complex amino acids and, in parallel, for the distribution of unstable chemical elements. The solutions of the equations for both codes are the same (17 and 8). The missing link is where the distribution of codons encoding more complex amino acids is expected to agree with the distribution of stable chemical elements. The solutions of the equations for the chemical code are (23 and 13),[12] and for the genetic, therefore derivative code (10 and 26), which means that in the act of generating the GC, a change of ± 3 occurred (Box 2). But, in the meantime, the missing link was found, so we really have complete accordance (Figure 5 and Tables 5.1 and 5.2).

Box 2. *The relationship between codon distinctions in the genetic code and isotopic distinctions in the chemical code*

MMR, 2018b, Surveys 2a, 2b, 3a, 3b; pp. 196-197: "Tthe 25 codons encode the AAs of the less complexity (2AAs + 4AAs) [(GP) + (ALVI)] which have only carbon and hydrogen (glycine – only hydrogen!) in the side chain; and 36 codons encode the AAs of greater complexity which have, except C and H, some other elements (N, O or S). The number of codons for encoding less complex AAs corresponds to the solutions of the first linear equation ($x_1 = 8$ and $y_1 = 17$): two nonstandard hydrocarbon AAs (GP) are encoded with 8 codons, and four standard hydrocarbon AAs (ALVI) with 17 codons. On the other hand, the number of codons for encoding more complex AAs corresponds to the solutions of the second linear equation ($x_2 = 10$ and $y_2 = 26$): six AAs (CMFYWH) which do not have a 'mapping' of functional groups from the 'head' to the 'body' (side chain), are encoded with 10 codons, and the eight AAs (STDENQKR) which have a mapping of functional groups from the 'head' to the 'body', are encoded with 26 codons (Survey 2a).

Now we go to the PSE. The solutions of the system of two linear equations (in the shaded part of Survey 3a) are in an almost full accordance with the distribution of chemical elements (in terms of stability/instability and odd/even parity) into periods and groups. From a total of 61 multi-isotope elements, the 25, except stable isotopes, possess unstable primordial isotopes (light shaded tones in Survey 1); and 36 multi-isotope elements possess only stable isotopes (they do not have unstable primordial isotopes) (dark shaded tones in Survey 1).

Further distributions are carried out through distinctions into odd and even elements – the odd elements within the odd groups and the even elements within the even groups, in both cases are in accordance with the model (the shaded part in Survey 3a). In accordance with the solutions of the first linear equation (x1 = 8 and y1 = 17), the 8 unstable and odd elements are within the odd groups, and 17 unstable and even elements within the even groups. On the other hand, according to the solutions of the second linear equation ($x_2 = 13$ and $y_2 = 23$), the 13 stable and odd elements are in odd groups and 23 stable and even elements in even groups."

[12] MMR, 2018b, p. 296): "… the stable elements; a total of 36; the 13 odd in the odd groups and 23 even in the even groups…, the unstable elements, a total of 25; the 8 odd in odd groups and the 17 even in the even groups." ["Under 'unstable elements' we mean those elements, which in addition to the stable isotopes, also have unstable primordial isotopes, one or more."]

This is a new insight into the classification of AAs into four types of diversity, as shown in Figure 5. Namely, it is noted that chalcogen amino acids are found in the intersection of types III and IV. They are precisely coded with 13 codons (two oxygen, S-T, with 10 codons; and two sulfur, C-M, with 3 codons), and the remaining two types of diversity are coded with 23 codons (Figure 5.2).

With the finding of the missing "link" it no longer makes sense to talk only about the analogy of the genetic and chemical code, but about their unity. All the more so since we now additionally know that the two linear algebraic equations that appear as determinants of one and the other code are not ordinary linear equations, but also unique ones (Survey 8 and Box 3).

Box 3. *The unit change law*

When I defined the unit change law (MMR, 1994, p. 36; cf. footnote 15 in this paper), then that definition referred exclusively to the Gray code model of the genetic code, to a change of one bit. In the second phase of research, much later, I saw that this law also refers to the establishment of a balance between two parts of a given system-arrangement of the genetic code, based on different distinctions and/or classifications; change by ± 0, ±1 or, again, by some other small number; for example, ±2, ±3. However, without mentioning the position of the unit in the numerical notation, I also presented changes for ±10, ±11, not knowing then that it is necessary to introduce the position of the unit, as I now believe – that it is the essence of the law.

In recent times, however, I see that the unit change law has broader meanings. For example, in the Gray code model of the genetic code, it refers not only to a change of one bit (in binary notation), but also to a change of exactly one nucleotide in a codon, in each subsequent step of the *Codon ring*, presented by R. Swanson (1984). In addition, and as a change in the sequence of digits of the hierarchical record of corresponding significant quantities manifesting in the genetic code. So, now I also understand the determination of GC by the Pythagorean triple as that manner, as determination by a unit-hierarchical series of quantities: (3-4-5). The same is valid for a specific relation to Plato's four (3-4-5-6),[13] Mendel's quadruplet (1-2-3-4)[14] and Darwin's equation, combined with two equations valid for genetic as well as chemical code: all three together in relation to sequence of square numbers: (3-4-5-6). [Cf. Survey 8 and details in the (future) final version.]

[13] Négadi, 2014, p. 266: "Now, we return to Eq.(5), in connection with the '2 x 3456' pattern. This latter seems present in several works on the genetic code. It has been first mentioned by Rakočević (2011). He showed that there are 3456 atoms within the codons in two inner columns and 3456 atoms within the codons in two outer columns in his GCT (Genetic Code Table)."

[14] "Bezeichnet n die Anzahl der charakteristischen Unterschiede an den beiden Stammpflanzen so gibt 3^n die Gliederzahl der Kombinationsreihe, 4^n die anzahl der Individuen, welche in die Reihe gehören, und 2^n die Zahl der Verbindungen, welche konstant bleiben" [Mendel, 1866; MMR, 1994, p. 24). [MMR, 1994, p. 176: "… accoding to Mendel such system [of hybrid cross] is determined by the four entities: 1^n-2^n-3^n-4^n. … (Note that Mendel only use the term Stammarten, i.e. Stammpflanzen for the first entity but not the mathematical expression 1^n which we use for the explanation of the Mendelian idea)".]

3. Elaboration

The question arises as to how the system-arrangements presented in the above three discounted examples are arrived at. The first thing that is noticeable in the approach to the research of the genetic code is that it is immediately obvious that the constituents of the genetic code are chemical substances, molecules (in the act of generating of life – biomolecules), in this particular case amino acids. In such a state of affairs, and based on general knowledge about molecules, they should be analyzed from the aspect of their stereochemistry, diversity, chemical composition and chemical properties (presence of functional groups). Then make the first possible distinctions and classifications. That is exactly what we did in Example 1 (Figure 3 in relation to Figure 4). We analyze, at the first step, only amino acids of the alanine stereochemical type, their possible ordering from the aspect of respecting the three fundamental principles of Mendeleev: the principle of neighborhood, the principle of minimum change[15] and the principle of continuity.[16] In Figure 3 we see that two arrangements are possible from the aspect of chemical properties. We further see that Figure 1.1 is actually a "rewrite" of the right side of Figure 3. [We read the rows: in Figure 3 clockwise, and in the derivative Figure 1, in the opposite direction (ALTS, CMED, NQRK, HWYF).] Finally, we add amino acids from the remaining three non-stereochemical types, so that in that addition we also respect the hierarchy (G 01, P 08, V 10 and I 13).[17]

In Table 1.1 of Example 2, everything is already elaborated: we have the crossing of the zeroth Boolean triangle (00,11,22) from the beginning of the last column of the Periodic System of Numbers (PSN) with the path of the greatest change on the 6-bit binary tree "0-63", i.e. harmonic mean ("42")], where the harmonic mean appears to be semiotic signifier of the "stop" codon UGA, as signified entity (MMR, 1998b, Fig. 1).

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[15] 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*.") [Box 3.]

[16] The reason for respecting the mentioned three principles of Mendeleev came from the fact that molecules consist of atoms, which even within molecules "remember" their position in the Periodic System of Chemical Elements (PSE), and also "remember" the number of their isotopes (Tab. 1.3 and Surv. 5 and 6).

[17] About four stereochemical types of amino acids *see* in (Popov, 1988 and Rakočević & Jokić, 1996; also Figure 4 in this paper).

4. New insights

New insights primarily concern the distinction of protein amino acids into 05 polar charged and the remaining 15 – polar uncharged, semi-polar and nonpolar. On the illustrations within the main text (Figures, Tables and Surveys) and within the three appendices, these distinctions are indicated in red. … It is shown that balancing and nuancing are also realized within these two subsets.[18]

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5. Additional elaboration

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6. Concluding remarks

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[18] MMR, 2018a, p. 33: "**Definition 1**. The term (and notion) 'balancing' means the achieving a balance of the values of physical-chemical factors (measured by the appropriate parameters) between two subclasses of the constituents of genetic code, within the class as a whole … **Definition 2**. The term (and notion) 'nuancing' means a minimal change of values of the physical-chemical factors and quantities in establishing of the balances specified in Definition 1. [In the case of the balance of the number of atoms, and/or nucleons, that are the changes for ± 01, ± 10, ± 11 and the like. In the case of molecules polarity, that are the minimal changes in the series of negative and/or positive values …"

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FIGURES

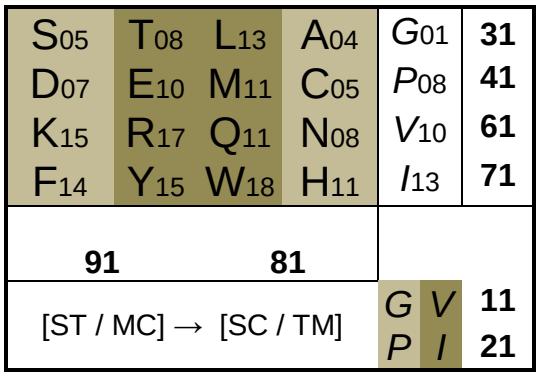


Figure 1.1. As in: MMR, 2019, Fig. 1, p. 6, and Box 2. [Here: Explanation in text (Introduction: Example 1.] Link: Fig. 3, where exists a cyclic arrangement of AAs [(ALTS), (CMED), (NQRK), (HWYF)] from which flows this linear here.

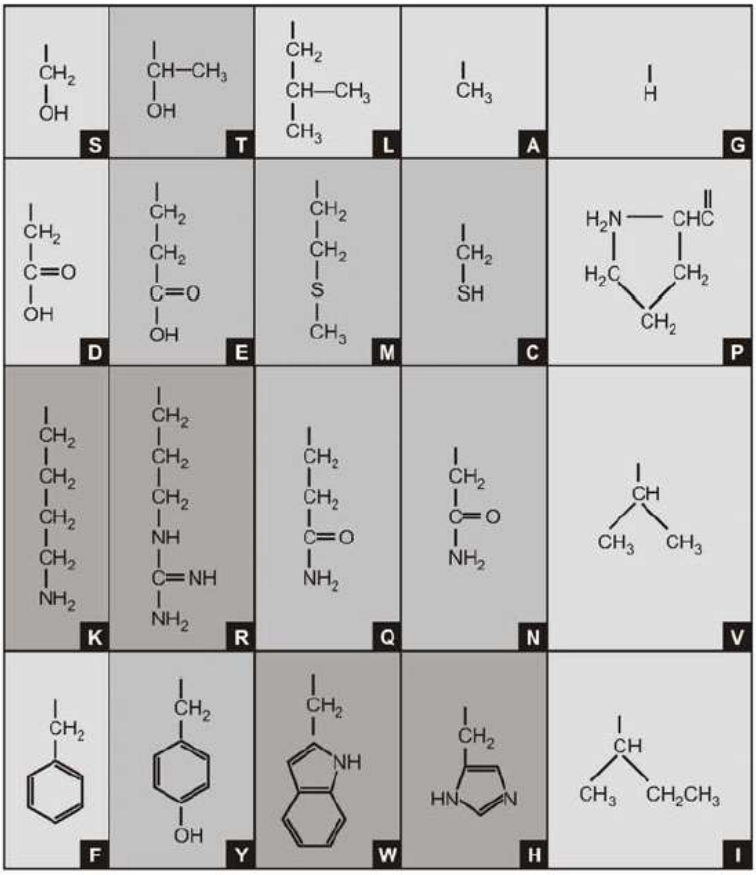


Figure 1.2. MMR, 2006, Fig. 1.2, p. 6: "The structure of amino acid molecules. The simplest amino acid is glycine (G) whose side chain is only one atom of hydrogen. It is followed by alanine (A) whose side chain is only one CH3 group, which is the smallest hydrocarbon group. There are total of 16 amino acids of alanine stereochemical type. …The glycine type contains glycine (G) only; valine type contains valine and isoleucine (V, I); … The proline type, proline only (P) [Popov, 1989; Rakočević & Jokić, 1996).] … Light tones (G, P, V, I & A, L, S, D, F): invariant AAs; most dark tones (K, R, W, H): most variant AAs; less dark tones (T, E, Y, M, Q, C, N,): less variant AAs."

[*Note 2023*: four amino acids (AAs) of non-alanine stereochemical type as invariant AAs: GPVI 32; then five AAs of alanine type as invariant: ALSDF 43. The remaining 11 AAs are of the alanine type and all are variant (they are not the only and/or the first possible cases). Of those 11, first come five less variant amino acids: TEYMQCN 68, and then four most variant AAs: KRWH 61. (68 + 61 = 129 = 3 x 43); (Cf. Survey 8: Darwin's diagram).]

<table>
<tr>
<td>S05 T08 L13 A04
D07 E10 M11 C05
K15 R17 Q11 N08
F14 Y15 W18 H11</td>
<td>G01
P08
V10
I13</td>
<td>31 (00)
24 (17)
29 (32)
60 (11)</td>
<td>31 + 29 = 60

24 + 60 = 84</td>
</tr>
<tr>
<td colspan="2">1922 /2327 /5300 / 4911

19 + 53 = 72

23 + 49 = 72</td>
<td>144
60
↓
204</td>
<td>00 + 32 = 32
17 + 11 = 28

22 + 00 = 22
27 + 11 = 38</td>
</tr>
<tr>
<td>66 = 11 x 6
78 = 13 x 6</td>
<td colspan="2">60 = 10 x 6
72 = 12 x 6
84 = 14 x 6</td>
<td>31/29 vs 32/28

32/28 vs 22/38</td>
</tr>
</table>

Figure 1.3. AAs: DE KR H as polar charged. Multiples [(10 x 6), (11 x 6), (13 x 6)], except here, also in Survs 1, 3 and 4; then in Tab. 2.1, Tab. A3, Tabs C1 and C5. [(31-32-22) (29-28-38) → Change for the unit of the first order, and then for the unit of both the first and the second order.] (Additional detailed explanations in: Additional elaboration.)

		...										
	(-2)	...									...	-22
	(-1)	-21	-20	-19	-18	-17	-16	-15	-14	-13	-12	-11
1	(0)	-10	-09	-08	-07	-06	-05	-04	-03	-02	-01	00
2	(1)	01	02	03	04	05	06	07	08	09	10	11
3	(2)	12	13	14	15	**16**	**17**	**18**	19	20	21	22
4	(3)	23	24	25	**26**	27	28	29	30	31	32	33
5	(4)	**34**	35	**36**	37	**38**	39	**40**	41	42	43	44
5	(5)	45	46	47	**48**	49	**50**	**51**	**52**	53	**54**	55
4	(6)	56	57	58	59	60	61	62	63	64	65	66
3	(7)	67	68	69	70	71	72	73	74	75	76	77
2	(8)	78	79	80	81	82	83	84	85	86	87	88
1	(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

Figure 2. Periodic System on Numbers (PSN) according to: (MMR, 2011b, Table 4, p. 826) and (MMR, 2019, Figure A1, p. 28). Distinctions: the splitting of the sequence 34, 36, 38, 40 into 34, 40 and 36, 38. Quantities 36, 38 in Table 2.4, and quantities 34, 40 in Tab. 4.3. The sequence 40, 42, 44, 46 in Tab B1 and the sequence 48, 50, 52, 54 in Tables 6.2 and in Tables B2 and B4.

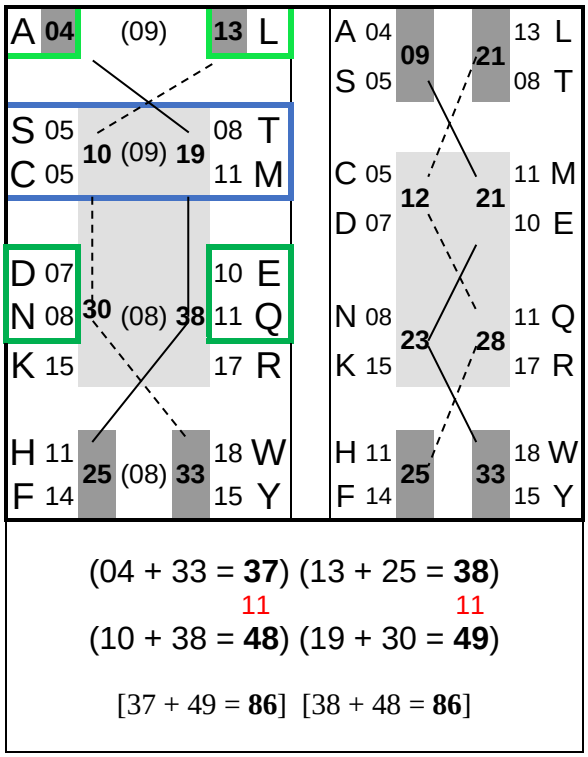


Figure 3. As in (MMR, 2011b, Tab. 2.1, p. 623): "The atom number within 8 pairs of alanine stereochemical type of AAs. On the full line, as well as on the dotted one, there are 86 atoms; the differences 8 and 9 (9 - 8 = 1) express 'the minimum change relation among the amino acids' (Swanson, 1984, p 191). The order follows from the atom number hierarchy. …" Link: Surv. 4, where the sequence DNKHF has the same position: here in the hierarchy of the number of atoms, and there in the hierarchy of two classes of synthetases; Link: Fig. 1.1, where the linear arrangement of AAs follows from the cyclic one, given here: [(ALTS), (CMED), (NQRK), (HWYF)].

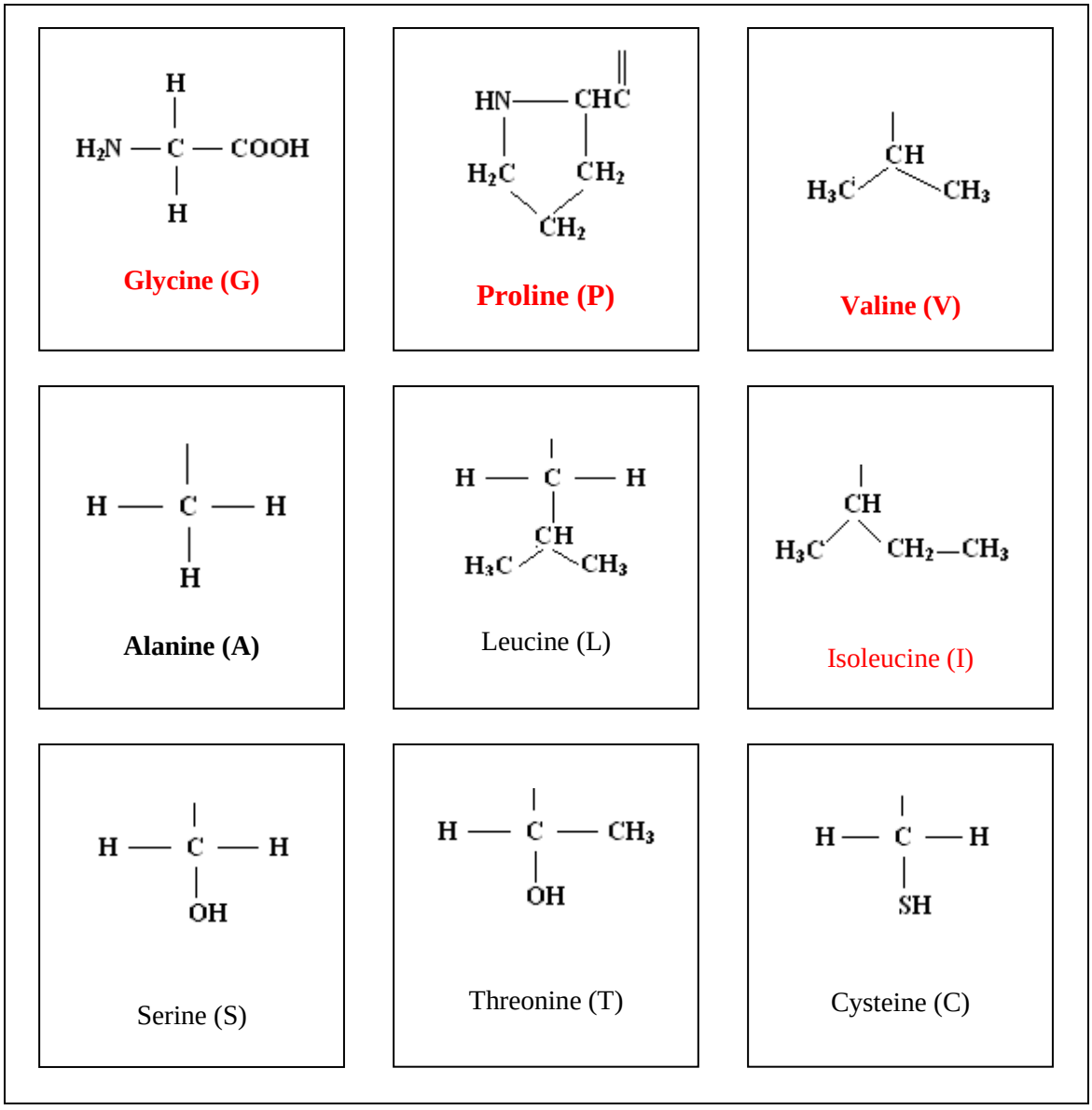


Figure 4. As in MMR, 2011b, Tab. 2.1, p. 823: "The structure formulae of AAs in relation to four stereochemical types: Glycine, one and only within glycine stereochemical type; proline in proline type; valine and isoleucine within valine type, and all other within alanine stereochemical type."

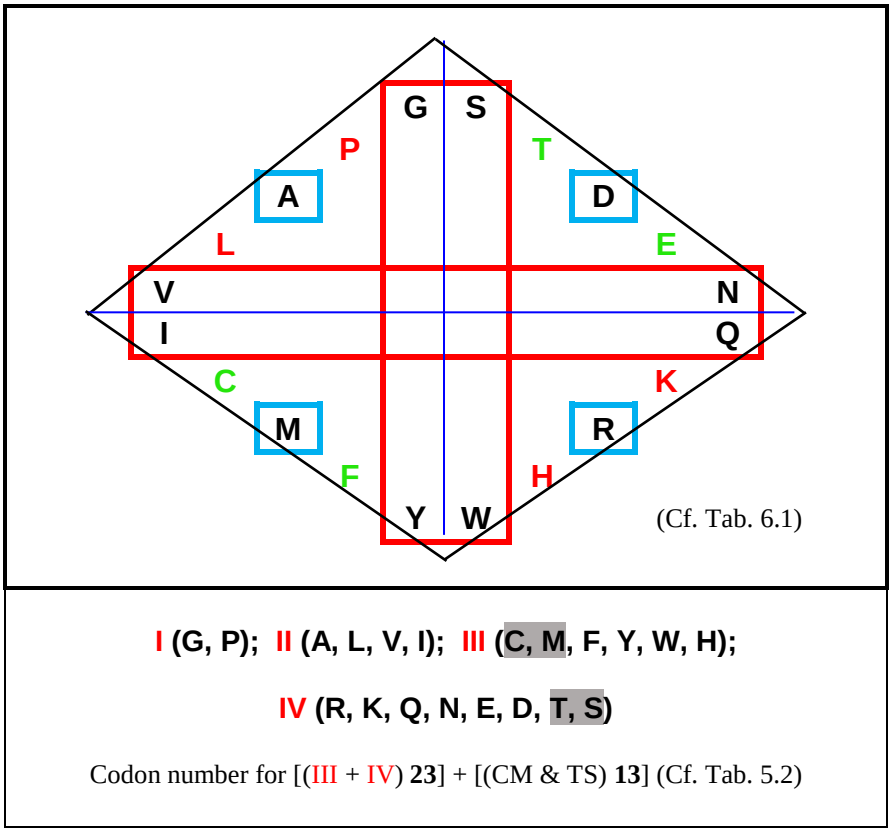


Figure 5. From MMR, 2011b, Fig. 2, p. 822: "Four diversity types of protein amino acids in a linear arrangement in form of the sequence 2-4-6-8; then in a circular arrangement, in form of the sequence 5-5-5-5. From this last sequence it is possible a new arrangement in form of the sequence 4-4-4-4-4 as in system presented in Figure 3" [here: Tabs 4.1 and 4.2.]

TABLES

Table 1.1. Perfect Protein Amino Acid Similarity System (PPAASS) [I]

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									**0**	
66	00										
77											
88											
99											

G **01**	A **04**	N **08**	D **07**	→	20
V **10**	P **08**	S **05**	T **08**	→	31
I **13**	L **13**	C **05**	M **11**	→	42
K **15**	R **17**	F **14**	Y **15**	→	61
Q **11**	E **10**	W **18**	H **11**	→	50

Explanation in text (Introduction: Example 2)

Table 1.2. Perfect Protein Amino Acid Similarity System (PPAASS) [II]

G 01	**N 08**	**G 01**	**A 04**	**N 08**	**D 07**	→	**20**
A 04	D 07						11
V 10	**S 05**	V 10	P 08	S 05	T 08	→	31
P 08	T 08						11
I 13	**C 05**	**I 13**	**L 13**	**C 05**	**M 11**	→	**42**
L 13	**M 11**						
K 15	**F 14**	K 15	R 17	F 14	Y 15	→	61
R 17	Y 15						11
Q 11	**W 18**	**Q 11**	**E 10**	**W 18**	**H 11**	→	**50**
E 10	H 11						
102	102	**(102 + <u>10</u>)** / (102 - <u>10</u>)					
51 ± <u>01</u>	51 ± <u>01</u>						

Left side as in: MMR, 2019, Tab. 2, p. 14; right side as in: MMR, 2021a: Graphical abstract and Box 1. Link: Tables 1.3, 1.4 and 3.2. Note: Change for first-order unit, change for second-order unit; and the unit change of both, the first and second orders.

Table 1.3. Perfect Protein Amino Acid Similarity System (PPAASS) [VIII]

		119			
G 01	**N 08**	**L 13**	**M 11**	**(33)**	120
A 04	D 07	K 15	F 14	(40)	
V 10	**S 05**	**R 17**	**Y 15**	**(47)**	
P 08	T 08	Q 11	W 18	(45)	117
I 13	**C 05**	**E 10**	**H 11**	**(39)**	
G 01	N 08	L 13	M 11	(33)	
24/13	**18**/23	**40**/39	**37**/43	118/**119**	
(37)	**(41)**	**(79)**	(80)	117/**120**	
78		79	80	(237)	
		118			

MMR, 2021a, Figure 3: "The unity of chemism and semiosis (III): 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). [Note: The unity of chemism and semiosis, as found here, is analogous to the such unity in arrangement within Rumer's system of nucleotide doublets. …]" Link: Tables 1.1 and 1.2.

Table 1.4. Perfect Protein Amino Acid Similarity System (PPAASS) [IX]

		[**80** /39]			
G 01	**N 08**	**L 13**	**M 11**	**(33) 00**	
A 04	D 07	K 15	F 14	(18) 22	**81** 39
V 10	**S 05**	**R 17**	**Y 15**	**(30) 17**	
P 08	T 08	Q 11	W 18	(45) 00	
I 13	**C 05**	**E 10**	**H 11**	**(18) 21**	**96** 21
G 01	N 08	L 13	M 11	(33) 00	
37 00	34 07	37 42	69 11	177/60	
78		79	80	237	
[odd / even: 81 / 96]		[**97** /21]	[odd / even: **38** / 22]		
(**33 + 30 +33 = 81**) (18 + 45 + 33 = 96) [78, 79, 80, 81]					

In relation to the previous Table 1.3, a distinction was made into 05 polar charged, and all other, the 15 AAs; balancing and nuancing are established in a new way, in both classes of AAs. (Additional detailed explanations in: Additional elaboration.)

Table 1.5. Perfect Protein Amino Acid Similarity System (PPAASS) [III]

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			

[GAVP (10+23+58) 91] + [VMFYWH (105+74+284) **463**]
(91 + 463 = 554)

[NDST (50+28+104) 182] + [ILKRQE (45+79+240) **364**]
(182 + 364 = 546) [182 = 91 + 91]

(455 | 554) + (645 | 546) → (1100 + 1100) → 10 x 220

on – Ordinal number; an – Atom number; pn – Proton. The quantities 298-288 in Table 6.1 as nucleon number.

Table 1.6. Perfect Protein Amino Acid Similarity System (PPAASS) [IV]

	Odd / Odd (**50** = 51 -1)		
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 (**52** = 51 +1)		
APLRE 30+**52**+159 = 241	DTMYH 80+**52**+197 = 329	→	**570**

Table 2.1. "The harmonic structure with two ‘acidic’ and three ‘basic’ amino acid quartets" (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**
					1255	1255	1465	1465+9	2738.04
60	**66**	**78**							
									2 (37 x 37)

Mirroring in "d" (binary): 11 – **0**0 ← 10 → 0**1** – 11

Link: Surv. 4: the same hierarchy of the pairs: G-V, S-C, T-M, P-I, A-L;

Table 2.2. "The harmonic structure with two ‘acidic’ and three ‘basic’ amino acid quartets" (II)

D 07	N 08	A 04	L 13	→	**32**	84
R 17	**P 08**	**F 14**	I 13	→	52	
K 15	Y 15	T 08	M 11	→	**49**	120
H 11	W 18	S 05	C 05	→	39	
E 10	Q 11	G 01	V 10	→	**32**	
↓ 60	↓ 60	↓ 32	↓ 52	→		↓ **204**
120		84		**32+49+32 = 123-10** 52+39 = 81+10		

(Rakočević, 2004, Tab. 1, p. 223)

Table 2.3. "The harmonic structure with two 'acidic' and three 'basic' amino acid quartets" (IV)

D 07	N 08	A 04	L 13	→	**07 / 08 / 17**
R 17	~~P 08~~	**F 14**	I 13	→	17 / 08 / 27
K 15	Y 15	T 08	M 11	→	**15 / 23 / 11**
H 11	W 18	S 05	C 05	→	11 / 23 / 05
E 10	Q 11	~~G 01~~	V 10	→	**10 / 12 / 10**
↓	↓	↓	↓	GP	**32 / 43 / 38**
60	65		70	09	28 / 31 / 32

(60)$_5$, (65)$_6$, (70)$_7$

32 **43** **38** → 123 - 10
28 31 32 → 81 + 10

o / e → 102 ± 1

60 + 70 = 130) [65 x 2]

660 + 770 = 1430 [(650 + 65) x 2]

6660 + 7770 = 14430 [(6500 + 650 + 65) x 2]

(Additional detailed explanations in: Additional elaboration.)

Table 2.4. "The harmonic structure with two ‘acidic’ and three ‘basic’ amino acid quartets" (V)

D 133.10	N 132.12	A 089.09	L 131.18	→	485.49
R 174.20	F 165.19	P 115.13	I 131.18	→	585.70
K 146.19	Y 181.19	T 119.12	M 149.21	→	595.71
H 155.16	W 204.10	S 105.09	C 121.16	→	585.64
E 147.13	Q 146.15	G 075.07	V 117.15	→	485.50
755.78	**828.88**	**503.50**	649.88		2738 2 (37 x 37)
	[2 x 666 (36 x 37)] [2 x 703 (38 x 37)]				

Molecules mass of 20 As (cf. sequence 34, 36, 38, 40 in Fig 2.)

Table 3.1. Perfect Protein Amino Acid Similarity System (PPAASS) [VII]

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

The unique entity-arrangement, ordered by the chemical similarity of AAs (entity, as "signified"), possesses a unique "signifier" – a unique connection of two mathematical operations: multiplication in relation to the "packaging" of quantities by positions (6 x 6 vs 66). Almost the same happens with the entity-arrangement ordered by the chemical composition of amino acid molecules (cf. Table 3.2).

Table 3.2. Distribution of AAs according to chemical composition (MMR, 2004, Tab. 9, p. 229)

D_{07}	E_{10}	Y_{15}	S_{05}	T_{08}	(6 x 6) + 01
N_{08}	**Q_{11}**	**G_{01}**	**C_{05}**	**M_{11}**	**(6 x 6) ± 00**
A_{04}	L_{13}	F_{14}	V_{10}	I_{13}	
K_{15}	R_{17}	P_{08}	H_{11}	W_{18}	
66 ± 00			66 – 01		

Distinction of amino acids. In second row: AAs only of hydrocarbon; the first row with added nitrogen; fourth row with added oxygen; third row combined.

Table 4.1. Distribution of four types of diversity of AAs according to Fig. 5 (II)

G 01	S 05	Y 15	W 18	**39**	78	102 ± 00
A 04	D 07	M 11	R 17	39		
C 05	T 08	E 10	F 14	**37**	24	
					13	102 ± 00
N 08	Q 11	V 10	I 13	42	89	
P 08	H 11	L 13	K 15	**47**		
26	**42**	**59**	**77**			
	16 (1 x 68)	17	18 (2 x 68)			

Additional explanation of Tabs 4.1 and 4.2: Quantities distinction 3-5-5-7 as in Table 4.1; the distinction of the quantities 4-5-5-6 as the number of hydrogen bonds in Rumer's Table of nucleotide doublets (MMR, 2018a, Tab. 2A, p. 34).

Table 4.2. Distribution of four types of diversity of AAs according to Fig. 5 (I)

G 01	**S 05**	**Y 15**	**W 18**	**39**	78	102 -11
A 04	D 07	M 11	R 17	39		
C 05	**T 08**	**E 10**	**F 14**	**37**	13	
					24	102 +11
N 08	Q 11	V 10	I 13	42	89	
P 08	**H 11**	**L 13**	**K 15**	**47**		
26	**42**	**59**	**77**	26 + 77 = 102 + 01 42 + 59 = 102 – 01		
16 (1 x 68)		17 (2 x 68)	18	68 = 4 x 17) 136 = 8 x 17		

3–5–5–7 vs 4–5–5–6
4556 – 3557 = 999 (Cf. Table C6)
4556 + 3557 = 8658 – 545

YWCEL 61 / GSTFPHK 62 (5, 7)
39 + 37 + 47 = 123 (as Class I)
39 + 42 = 81 (as Class II)
ADN 19 / MRQVI 62 (3, 5)

Symmetrical distinctions in even and odd rows. Balancing and nuancing at "work": All AAs in odd rows from both classes (I + II) possess as many atoms as AAs of class I (123). In even rows, as many as class II itself (81). [Class I red and class II black. Classification into two classes according to two classes of catalyzing enzymes amino-acyl tRNA synthetases. Class I has two highly conserved sequence motifs. while Class II has three highly conserved sequence motifs.] (Additional detailed explanations in: Additional elaboration.)

Table 4.3. Distribution of four types of diversity according to Fig. 5 (III)

G 75.07	S 105.09	Y 181.19	W 204.23
A 88.09	D 133.10	M 149.21	R 174.20
C 121.16	T 119.12	E 147.13	F 165.19
N 132.12	Q 146.15	V 117.15	I 131.18
P 115.13	H 155.16	L 131.07	K 146.19
26	**42**	**59**	**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)

Table 5.1. "The standard genetic code with new distinctions"
(MMR, 2018b, Table 5, p. 295)

1st	2nd letter								3rd
	U		C		A		G		
U	UUU	**F**	UCU	**S**	UAU	**Y**	UGU	**C**	*U*
	UUC		UCC		UAC		UGC		*C*
	uua	**L**	UCA		~~UAA~~	CT	~~UGA~~	CT	*A*
	uug		UCG		~~UAG~~		UGG	**W**	*G*
C	**cuu**	**L**	ccu	**P**	CAU	**H**	CGU	**R**	*U*
	cuc		ccc		CAC		CGC		*C*
	cua		cca		CAA	**Q**	CGA		*A*
	cug		ccg		CAG		CGG		*G*
A	**auu**	**I**	ACU	**T**	AAU	**N**	AGU	**S**	*U*
	auc		ACC		AAC		AGC		*C*
	aua		ACA		AAA	**K**	AGA	**R**	*A*
	AUG	**M**	ACG		AAG		AGG		*G*
G	**guu**	**V**	**gcu**	**A**	GAU	**D**	ggu	**G**	*U*
	guc		**gcc**		GAC		ggc		*C*
	gua		**gca**		GAA	**E**	gga		*A*
	gug		**gcg**		GAG		ggg		*G*

MMR, 2018b: Polyhedron, Table 5: "The design responds to the classification of protein AAs into four classes, correspondently with four diversity types. The first diversity type (GP): the 8 codons in small non-bolding letters; second type (ALVI), the 17 codons in small bolding letters; third type (CMFYWH), the 10 codons in large letters and light shadow tones; fourth type (STDENQKR): the 26 codons in large letters and dark shadow tones. The three codons which are cross out, are the 'stop' codons. …"

Distribution through codon number: 1st diversity type GP 8; 2nd LIVA 17; 3rd **FYHW**CM 10; 4th diversity type ST**DENQKR** 26. [STCM 13; (**DENQKR** + **FYHW**) 23] (Cf. four Surveys in: MMR, 2018b, p. 296.)

Table 5.2. The solution to the missing "link"

1st	2nd letter								3rd
	U		C		A		G		
U	UUU UUC	**F**	UCU UCC	**S**	UAU UAC	**Y**	**UGU** **UGC**	**C**	*U* *C*
	uua **uug**	**L**	UCA UCG		~~UAA~~ ~~UAG~~	CT	~~UGA~~ UGG	CT **W**	*A* *G*
C	**cuu** **cuc** **cua** **cug**	**L**	ccu ccc cca ccg	**P**	CAU CAC CAA CAG	**H** **Q**	CGU CGC CGA CGG	**R**	*U* *C* *A* *G*
A	**auu** **auc** **aua** **AUG**	**I** **M**	ACU ACC ACA ACG	**T**	AAU AAC AAA AAG	**N** **K**	AGU AGC AGA AGG	**S** **R**	*U* *C* *A* *G*
G	**guu** **guc** **gua** **gug**	**V**	**gcu** **gcc** **gca** **gcg**	**A**	GAU GAC GAA GAG	**D** **E**	ggu ggc gga ggg	**G**	*U* *C* *A* *G*

Intersection of sets of 3rd and 4th diversity types STCM 13 codons decode; the two remaining parts (DENQKR + FYHW) 23 codons decode. (Cf. four Surveys in: MMR, 2018b, p. 296.)

Table 6.1. 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**	(**59**/58) **569**/686
N (04) 58	P (05) 41	T (05) 45	E (05) 73	H (05) 81	(24)	298	
Q (06) 72	V (07) 43	F (07) 91	M (07) 75	Y (07)107	(34)	388	
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							

MMR, 2011b, Tab. 7 p. 830. The quantities 298-388 given here as number of nucleons, appear in Table 1.5 as number of protons.

Table 6.2. 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

MMR, 2011b, Tab. 9, p. 830

SURVEYS

Survey 1. Cyclic Invariant Periodic System (CIPS)

AAs classes / CIPS					
G	A	S	D	**H**	28
P	L	C	N	**F**	48
V	K	T	E	**Y**	58
I	R	M	Q	**W**	70
32	49	29	*36*	**58**	
78 / *68* / **58**					
28 + 70 = 87 + 11 48 + 58 = 117 – 11					

60 / 66 / 78		
5	F_{14}	Y_{15}
4	L_{13}	A_{04}
3	Q_{11}	N_{08}
2	P_{08}	I_{13}
1	T_{08}	M_{11}
1	S_{05}	C_{95}
2	G_{01}	V_{10}
3	D_{07}	E_{10}
4	K_{15}	R_{17}
5	H_{11}	W_{18}

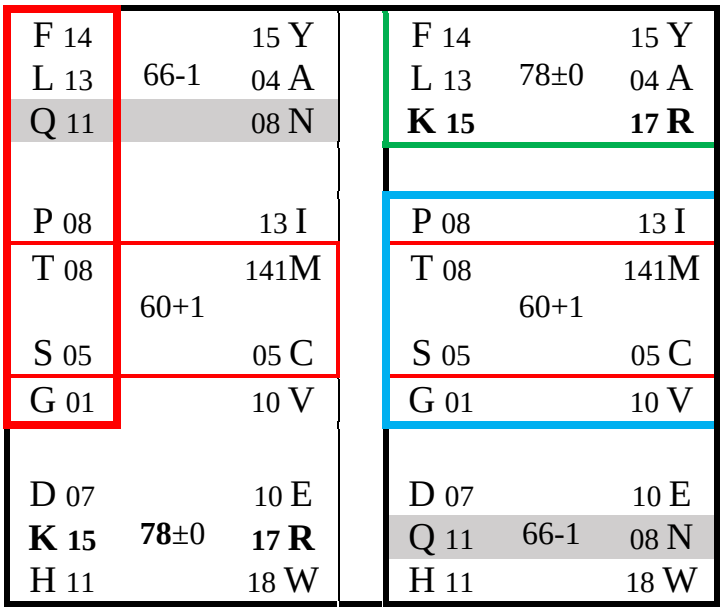
MMR (2011b, Fig. 6, p. 832) and MMR (2019, Fig. 1, p. 6; Box 2). Relations: 58, 68, 78 versus 60, 66, 78 (the change for ± 2 and ±0). The 117 is number of hydrogen atoms in set of 20 protein AAs (in their side chains); and 87, the number of non-hydrogen atoms. The sequ. GSTPQLF 60 as "golden" AAs (MMR, 1998b, Tab. 2, p. 288; Link: Surv. 3)

Survey 2. The CIPS in relation to two classes of AAs handled by two classes of the amino acyl-tRNA synthetases

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

MMR (2011b, Fig. 7, p. 833) and MMR (2019, Fig. 1, p. 6; Box 2)

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



(MMR, 2018a, Surv. 3. p. 39). Link: Survey 1.

Survey 4. "Atom number balance directed by two classes of enzymes aminoacyl-tRNA synthetases" (MMR, 1998b, Surv. 4, p. 290)

G	01			10	V	G	01			43	V	
S	05	**14**	**26**	05	C	S	31	**77**	**165**	47	C	
T	08			11	M	T	45			75	M	
												78
P	08	12	26	13	I	P	41	56	114	57	I	
A	04			13	L	A	15			57	L	
D	07			10	E	D	59			73	E	
N	08	**30**	**38**	11	Q	N	58	**189**	**245**	72	Q	**68**
K	15			17	R	K	72			100	R	
H	11	25	33	18	W	H	81	172	237	130	W	
F	14			15	Y	F	91			107	Y	**58**
Odd		**44**	**64**					**266**	**410**			
Even		37	59					228	351			
		81	123					494	761			

44 + **64** = 107 + 01
37 + 59 = 97 – 01

107 = 117 - 10
97 = 87 + 10

44 + 59 = 102 + 01
64 + 37 = 102 - 01

266 + **410** = 686 – 10
228 + 351 = 569 + 10

266 + 351 = 627 – 10
410 + 228 = 628 + 10

686 + 569 = 1255
628 + 627 = 1255

Link: Tab. 2.1, with the same hierarchy of the pairs: G-V, S-C, T-M, P-I, A-L; Link: Figure 3, where the sequence DNKHF has the same position: there in the hierarchy of the number of atoms, and here in the hierarchy of two classes of synthetases;

Survey 5. Perfect Protein Amino Acid Similarity System (PPAASS) [V]

	in		in	
G	02		17	N
A	08		16	D
V	20	46 061	11	S
P	16	**1**07	17	T
I	26		12	C
L	26		24	M
K	30		28	F
R	34	161 153	31	Y
Q	23	**3**07+07	36	W
E	22		22	H
		207	**2**07+07	

153 = 061 + (46 x 2)
161 + 061 = 211 + 11
153 + 046 = 210 – 11

211 + 210 = 421

Number of isotopes (I)

Survey 6. Perfect Protein Amino Acid Similarity System (PPAASS) [VI]

	in		in	
G	02		17	N
A	08		16	D
V	20	72 73	11	S
P	16	145	17	T
I	26		12	C
L	26		24	M
K	30		28	F
R	34	135 141	31	Y
Q	23	276	36	W
E	22		22	H
		207 214		
276 - 145 = 131 73 + 135 = 208 72 + 141 = 213			208 - 207 = 01 214 - 213 = 01	
208 + 213 = 421 207 + 214 = 421				

Number of isotopes (II)

Survey 7. 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	2	FY	DN	EQ	HW	7	8	9	10	→	111
											11
AL	2	FY	DN	EQ	6	SC	TM	GV	10	→	122
											11
1	KR	FY	4	EQ	6	7	TM	GV	PI	→	133
											10
AL	KR	FY	DN	EQ	HW	7	8	9	10	→	143

Twice the change for the first-order unit and the second-order unit; one time change for the unit of the second order.

Survey 8. Darwin's equation in unity with equations of genetic and chemical code

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**

Darwin's equation in GC

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:
$1^n - 2^n - 3^n - 4^n$

26 + 10 = 36	$1^2 - 0^2 = 01$	$5^2 - 4^2 = 09$
16 + 09 = 25	$2^2 - 1^2 = 03$	$6^2 - 5^2 = 11$
17 + 08 = 25	$3^2 - 2^2 = 05$	$7^2 - 6^2 = 13$
09 + 07 = **16**	$4^2 - 3^2 = 07$	…
43 | 34		

(MMR, 2015, Tab. 5, p. 47) (MMR, 2019, Tabs. C1, C2 and C3, pp. 38-40). Mendel's result in Box 3.

Appendix A

Table A1. Unique position of the number 204 in PSN (I)

	...										
(-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	28
(2)	12	13	14	15	16	17	18	19	20	21	22	
(3)	23	24	25	26	27	28	29	30	31	32	33	116
(4)	34	35	36	37	38	39	40	41	42	43	44	
(**5**)	45	46	47	**48**	49	**50**	51	**52**	53	**54**	55	**204**
(6)	56	57	58	59	60	61	62	63	64	65	66	
(7)	67	68	69	70	71	72	73	74	75	76	77	292
(8)	78	79	80	81	82	83	84	85	86	87	88	
(9)	89	90	91	92	93	94	95	96	97	98	99	380
	(28 + 380 = 2 x 204) (116 + 292 = 2 x 204)											

Unique position of the number 204 in Periodic System of Numbers (PSN) in decimal number system

Table A2. Unique position of the number 204 in PSN (II)

25	=	x	=	25	25 + 40 + 56 + 73 = y y = 194 y/4 = 48.5	15 + 16 + 17 = z z = 48 z = (y/4) - 0.5
25	+	15	=	40		
40	+	16	=	56		
56	+	17	=	73		
26	=	x	=	26	26 + 42 + 59 + 77 = y **y = 204** y/4 = 51	16 + 17 + 18 = z z = 51 **z = (y/4) ± 0.0**
26	+	16	=	42		
42	+	17	=	59		
59	+	18	=	77		
27	=	x	=	27	27 + 44 + 62 + 81 = y y = 214 y/4 = 53.5	17 + 18 + 19 = z z = 54 z = (y/4) + 0.5
27	+	17	=	44		
44	+	18	=	62		
62	+	19	=	81		

Quantities 26, 42, 59 and 77 are found in four types of diversity of 20 protein AAs (in their side chains) (Figure 5 and Tabs 4.1, 4.2 and 4.3).

Table A3. Unique position of the number 204 in natural numbers series

a	b			c		d	e	f
01	10	11	13	34		11 + [(1 x 1) + 5] = 34:2	13/31	2 x 9
02	20	22	26	68		22 + [(2 x 2) + 8] = 68:2		
03	30	33	39	102		33 + [(3 x 3) + 9] = 102:2	51	
04	40	44	52	136		44 + [(4 x 4) + 8] = 136:2		
05	50	55	65	170		55 + [(5 x 5) + 5] = 170:2		
06	60	66	78	204		66 + [(6 x 6) ± 0] = 204:2	78 / 87	1 x 9
07	70	77	91	238		77 + [(7 x 7) – 7] = 238:2		
08	80	88	104	272		88 + [(8 x 8) – 16] = 272:2		
09	90	99	117	306		99 + [(9 x 9) – 27] = 306:2	117/711	66 x 9
0A	A0	AA	13	340		AA+[(10 x 10) – 40] = 340:2	594	
0B	B0	BB	13	374		BB +[(11 x 11) – 55] = 374:2	(atoms in 61 molec.)	

0B = 11 1st row in PSN (Fig. 2): 1 → 11	34 = 2 x 17 51 = 3 x 17	374 = 2 x 187 187 + 197 = 384

If (10, 11, 12), then 1, 1, 2
If (10, 11, 13), then 1, 2, 3
(as differences)
	68 = 2 x 34 [1 → 34 = 595]
	78 = 2 x 39 [1 → 39 = **78**0]
	88 = 2 x 44 [1 → 44 = 990]
		H atoms: 1**9**7
		non-H atoms: 1**8**7
		
		117 + (20 x 4) = 197
		87 + (20 x 5) = 187

Table A4. Unique position of the number 204 in the set of even natural numbers

…		
198	(14 + 184 = 198); [13 + 14 + 15 = ¼ (198 – 30)	[114 + 84 = 198]
200	(15 + 185 = 200); [14 + 15 + 16 = ¼ (200 – 20)	[115 + 85 = 200]
202	(16 + 186 = 202); [15 + 16 + 17 = ¼ (202 – 10)	[116 + 86 = 202]
204	**(17 + 187 = 204); [16 + 17 + 18 = ¼ (204 ± 00)**	**[117 + 87 = 204]**
206	(18 + 188 = 206); [17 + 18 + 19 = ¼ (206 + 10)	[118 + 88 = 206]
208	(19 + 189 = 208); [18 + 19 + 20 = ¼ (208 + 20)	[119 + 89 = 208]
210	(20 + 190 = 210); [19 + 20 + 21 = ¼ (210 + 30)	[120 + 90 = 210]
…		

Table A5. The uniqueness of decimal number system

q					q	$(17)_{10}$
2	0 x 1 = 00	0 + 1 = 01	00 + 01 = 01		2	10001
4	2 x 3 = 12	2 + 3 = 11	12 + 11 = 23		4	101
6	4 x 5 = 32	4 + 5 = 13	32 + 13 = 45		6	25
8	6 x 7 = 52	6 + 7 = 15	52 + 15 = 67		8	021 / 165
10	8 x 9 = 72	8 + 9 = 17	72 + 17 = 89		10	017 / 117
12	Ax B = 92	A+ B = 19	92+ 19 = AB		12	
14	C x D = B2	C + D = 1B	B2 + 1B = CD		14	
16	E x F = D2	E + F = 1D	D2 + 1D = EF		16	11 / 75
…						

Table A6. Unique position of Shcherbak's quantum 74 in PSN

	...										
(-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	61	62	63	64	65	66
(7)	67	68	69	70	71	72	73	74	75	76	77
(8)	78	79	80	81	82	83	84	85	86	87	88
(9)	89	90	91	92	93	94	95	96	97	98	99

- 28
30
74 x 2
118
324

(324 - 28 = 2 x 74) (118 + 30 = 2 x 74)

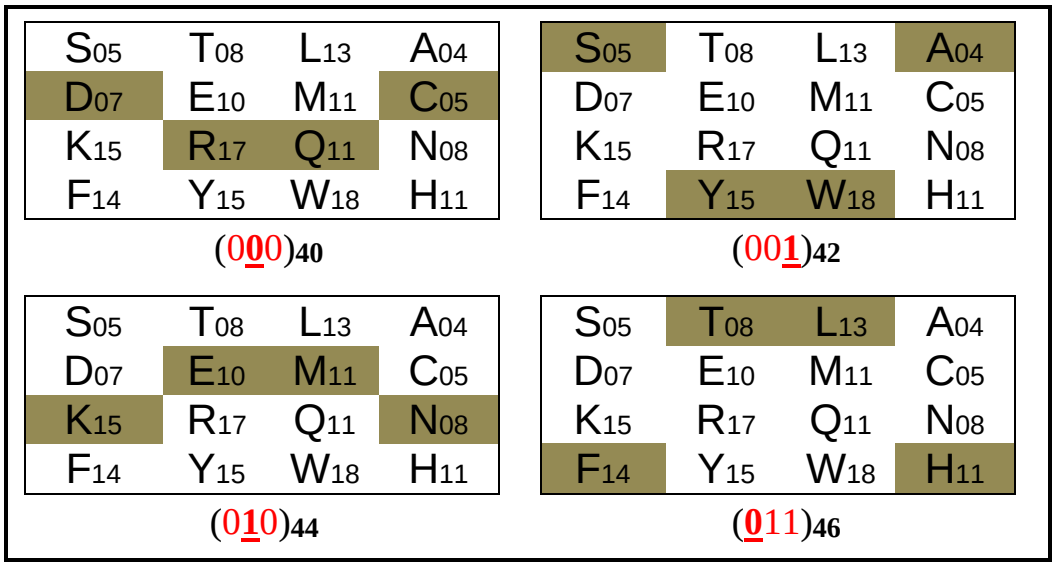
Tab A7. The uniqueness of the pair "(6+7)" and the sum 8658

0 + 1 = 1 00 + 11 = 11 000 + 111 = 111	2 + 3 = 5 22 + 33 = 55 222 + 333 = 555	4 + 5 = 9 44 + 55 = 99 444 + 555 = 999
6 + 7 = 13 66 + 77 = 143 666 + 777 = **1443**	8 + 9 = 17 88 + 99 = 187 888 + 999 = 1887	A + B = 21 AA + BB = 231 AAA + BBB = 2331
four-codon AAs + non-four-codon AAs = 333 + 1110 = **1443** nucleons		
C + D = 25 CC + DD = 275 CCC + DDD = 2775 …	E + F = 29 EE + FF = 319 EEE + FFF = 3219	…
13 x 666 ↓ **8658** (7770 + 0888)		
[6 + 28 + 496 + 8128 = **8658**]	[13 X 777 = 010101 (**010** / **101**)]	
6 x 111 = 666 [8658 – (12 x 666)] 6 x 555 = 3330 [8658 – (8 x 666)] 6 x 999 = 5994 [8658 – (4 x 666)] 6 x 1443 =8658 [8658 ± (0 x 666)]	6 x 1887 = 11322 [8658 + (4 x 666)] 6 x 2331 = 13986 [8658 + (8 x 666)] 6 x 2775 = 16650 [8658 + (12 x 666)] 6 x 3219 = 19314 [8658 + (16 x 666)] …	

The sum of the first four perfect numbers: 6 + 28 + 496 + 8128 = 8658 (7770 + 0888)
8658 = 1443 x 6

Appendix B

Table B1. Logical square in the set of 16 AAs of alanine stereochemical type, taken from Figure 1.1.



Two inner rows vs 2 outer rows. Link Fig 3

Tab. B2. Odd and even quintets, taken from Table 1.5 (I)

0	odd	even	0		0	odd	even	0	
1	G_{01}	A_{04}	1		1	N_{08}	D_{07}	1	**20** **11**
0	V_{10}	P_{08}	0		0	S_{05}	T_{08}	0	31 **11**
1	I_{13}	L_{13}	1		1	C_{05}	M_{11}	1	42
0	K_{15}	R_{17}	0		0	F_{14}	Y_{15}	0	61 **11**
1	Q_{11}	E_{10}	1		1	W_{18}	H_{11}	1	50
	25 26 ± 1 27		52			31 30 ± 1 29		48	
	25 25 ± 0 25		50			19 21 ± 2 23		54	
	26 + 25 = 51 (204 : 4)					30 + 21 = 51 (204 : 4)			

[20 + 42 + 50 = 112 (102 + 10)] [31 + 61 = 92 (102 – 10)]
[20 + 31 + 61 = 112] [**112 = 4 x 28**]

[U_{12} + G_{16} = **28**] [C_{13} + A_{15} = **28**]

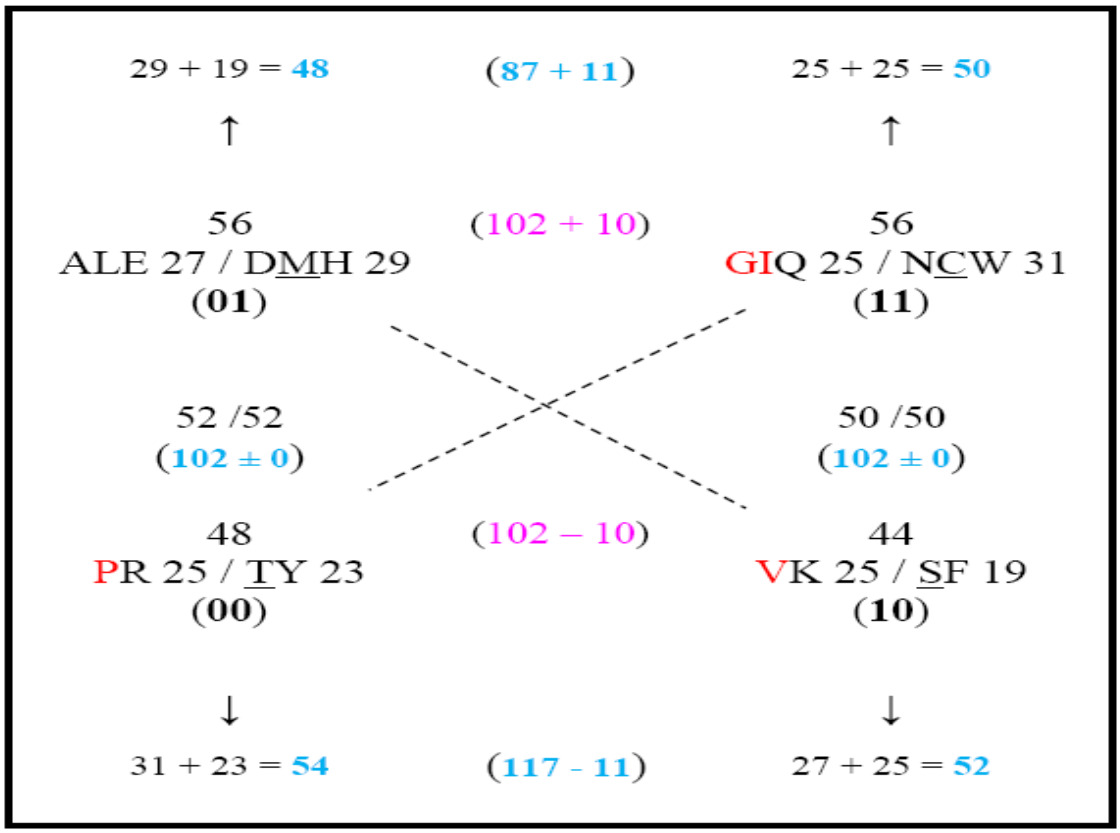
Atom number in amino acid side chain

Tab. B3. Odd and even quintets, taken from Table 1.5 (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]									

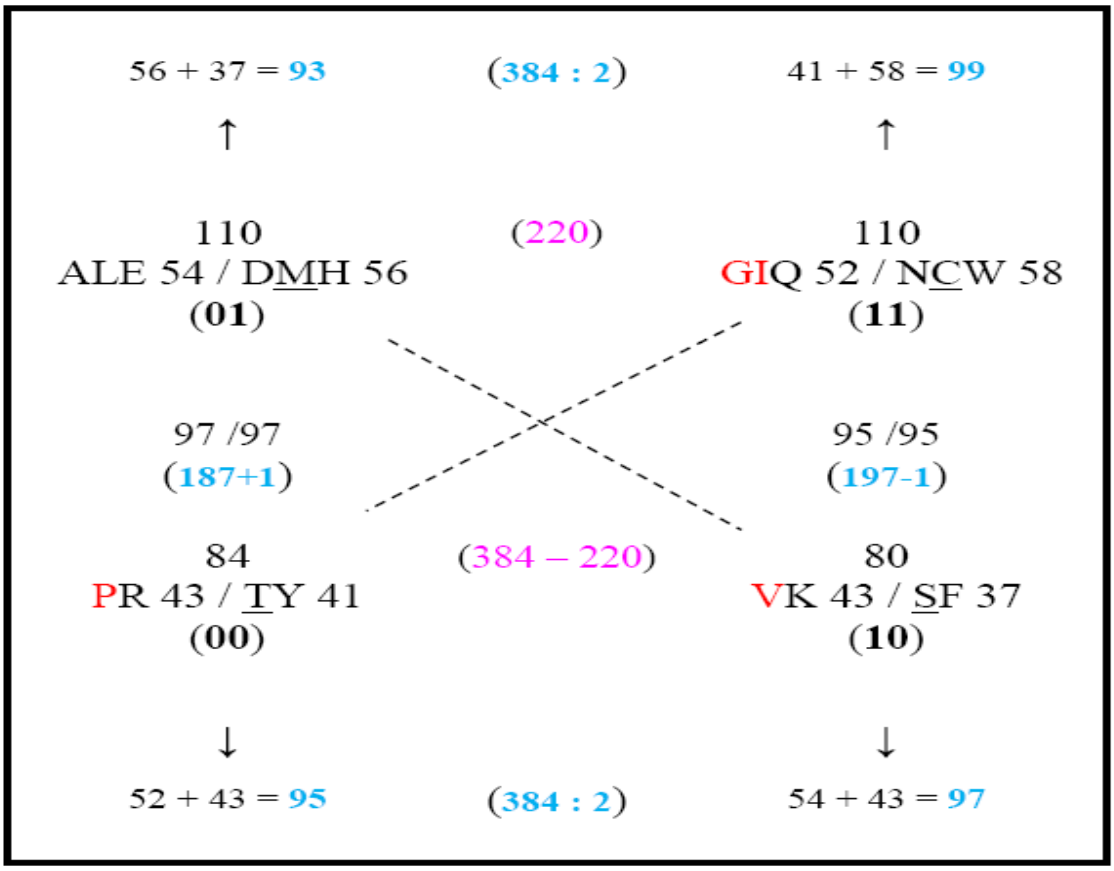
Atom number in amino acid whole molecule

Tab. B4. Distribution of quintets from Table B3 by even and odd positions (I)



Atom number in amino acid side chain

Tab. B5. Distribution of quintets from Table B3 by even and odd positions (II)



Atom number in amino acid whole molecule

Appendix C

Table C1. "The harmonic structure with two ‘acidic’ and three ‘basic’ amino acid quartets"

D 07 R 17	N 08 **P 08**	A 04 **F 14**	L 13 I 13	→ →	**25 (07)** 35 (17)	60 (24) **84**
K 15 H 11 E 10	Y 15 W 18 Q 11	T 08 S 05 G 01	M 11 C 05 V 10	→ → →	**34 (15)** 28 (11) **22 (10)**	84 (36) **120**
↓ 60	↓ 60	↓ 32	↓ 52	[(10 + 4 = **14**)] x 6 = 84 [(**14** + 6= **20**)]) x 6 = 120		
120		**84**		(60 = 66 – 6) (84 = 78 + 6)		

25 (**07**) + **34** (**15**) **22** (**10**) = **81** (**32**) → 123 - 10
35 (17) + 28 (11) = 63 (28) → 81 + 10

(Additional detailed explanations in: Additional elaboration.)

Table C2. Distribution of four types of diversity according to Fig. 5 (IV)

G 01	S 05	Y 15	W 18	**39** **00**	67 - 10
A 04	D 07	M 11	R 17	15 24	**87**/57
C 05	T 08	E 10	F 14	**27** **10**	**36** / 24
N 08	Q 11	V 10	I 13	42 00	77+10
P 08	H 11	L 13	K 15	**21** **26**	6 x 6 = 36 6 x 4 = 24
26	42	59	77	As Class I 87+36 = 123 57+24 = 81 As Class II	
16 (1 x 68)		17	18 (2 x 68) →		

(Additional detailed explanations in: Additional elaboration.)

Table C3. The uniqueness of number 144

0	x	6	=	**00**		[00 + 21 = 21]		21 + (31 + 41) + 51	→	**72**
					12		12			
2	x	6	=	12		[12 + 21 = 33]		33 + (43 + 53) + 63	→	**96**
					12		12			
4	x	6	=	24		[24 + 21 = 45]		45 + (55 + 65) + 75	→	**120**
					12		12			
6	x	6	=	36		[36 + **21** = **57**]		**57** + (67 + 77) + **87**	→	**144**
					12		12			
8	x	6	=	48		[48 + 21 = 69]		69 + (79 + 89) + 99	→	**168**
					12		12			
10	x	6	=	**60**		[60 + 21 = 81]		81 + (91 + 101) + 121	→	**192**
							12			
12	x	6	=	72		[72 + 21 = 93]		93 + (103 + 113) + 123	→	**216**

72 + 216 = 2 x 144 96 + 192 = 2 x 144 120 + 168 = 2 x 144	00 + 12 = 24 - 12 12 + 24 = 36 ± 0 24 + 36 = 48 +12 36 + 48 = 60 +24 48 + 60 = 72 +36	–12 + 72 = 60 **00 +60 = 60** 12 +48 = 60 24 + 36 = 60	**57 + 60 = 117** **87 + 117 = 204**

The 05 polar charged AAs with 60 atoms; the remaining 15 with 144 atoms.

Table C4. The uniqueness of numbers 57 and 87 (I)

07	+	87	=	94		67	+	87	=	154
17	+	87	=	104		77	+	87	=	164
27	+	87	=	114		87	+	87	=	174
37	+	87	=	124		97	+	87	=	184
47	+	87	=	134		107	+	87	=	194
57	**+**	**87**	**=**	**144**		**117**	**+**	**87**	**=**	**204**

(07+17+27+37 = 88), (07+17+27+37+47 = 135), (07+17+27+37+47 + **57** = 192), (07+17+27+37+47 +57 + 67= 259), (07+17+27+37+47 +57 + 77 = 336).

(Cf. next Table C5)

Table C5. The uniqueness of numbers 57 and 87 (II)

88	(540)	628	135	(**60**0)	735	192	(660)	852
47		107	57		117	67		127
↓		↓	↓		↓	↓		↓
135	(600)	735	192	(**66**0)	852	259	(720)	979
57		117	67		127	77		137
↓		↓	↓		↓	↓		↓
192	(660)	852	259	(**72**0)	979	336	(780)	1116
67		127	77		137	87		147
↓		↓	↓		↓	↓		↓
259	(720)	979	336	(**78**0)	1116	423	(840)	1263
77		137	87		147	97		157
↓		↓	↓		↓	↓		↓
336	(780)	1116	423	(**84**0)	1263	520	(900)	1420

(57-87-117) vs (60-66-72-78-84)

Table C6. Cantor's triadic set within decimal number system

999 = 545 + 454

| 123 | **456** | 789 |

5 x 220	←	644	456 / 654	446	→	5 x 220
5 x 220	←	635	465 / 564	536	→	5 x 220
5 x 220	←	**554**	**546 / 645**	**455**	→	**5 x 220**

545

. . .

AAA → 3 x 10 = 30; [30 x 40 ≠ AAA]

999 → 3 x 9 = 27; [27 x 37 = 999]

888 → 3 x 8 = 24; [24 x 34 ≠ 888)

. . .

440 044 ↓ 496 - 100	0|00	→	000	→	000 / 000	440 044 ↓ 4 x 121 121 = 11 x 11
	0|11	→	011	→	011 / 110	
	0|22	→	022	→	022 / 220	
	0|11	→	011	→	011 / 110	
	0|00	→	000	→	000 / 000	
			↓		↓	
	044 (2 x 022)			440	**220** x 2	

Table C7. System-arrangement from Table 1.2 in cyclic form

G 10	**A** 13	**N** 17	**D** 16	→	**56**
					11
V 19	P 17	S 14	T 17	→	67
					11
I 22	**L** 22	**C** 14	**M** 20	→	**78**
K 24	R 26	F 23	Y 24	→	97
					11
Q 20	**E** 19	**W** 27	**H** 20	→	**86**
G 10	A 13	N 17	D 16	→	56
105	110	112	113		
215		225			

56 + 78 + 86 = 220
65 + 87 + 68 = 220

67 + 97 + 56 = 220
76 + 79 + 65 = 220

880

880
112
↓
992

First row two times

204 + 20 = 224 (224 : 2 = 112)
384 + 56 = 440 (440 : 2 = 220)

Table C8. The uniqueness of sequences 4556 and 3557

Duodecimal					
…					…
2334	–	1335	=	BBB	10 / 10
					8
4556	–	3557	=	BBB	18 / 18
					8
6778	–	5779	=	BBB	24 / 24
					8
899A	–	799B	=	BBB	30 / 30
…					…
[B – 8 = +3]					

Decimal					
0112	–	-1 1 1 3	=	999	04 / 04
		(-887)			8
2334	–	1335	=	999	12 / 12
					8
4556	**–**	**3557**	**=**	**999**	**20 / 20**
					8
6778	–	5779	=	999	28 / 28
					8
899A	–	799B	=	999	36 / 36

(04 +36 = 12+28 = **2 x 20**) [9 – 8 = +1]
(4556 +3557 = 8658 – **545**)

Octal					
…					…
2334	–	1335	=	777	14 / 14
					10
4556	–	3557	=	777	24 / 24
					10
6|7|7|10	–	5|7|7|11	=	777	34 / 28
…					…
[7 – 10 = -1]					

The sequence 4556 as number of hydrogen bonds in Rumer's Table (MMR, 2018a, Table 2A, p. 34) Link: Tab. 1.3; Tabs 6.1 and 6.2; Tab. A4; the sequence 3557 in relations to two classes of the amino acyl-tRNA synthetases (Table 4.2).