Genetic code as a semiotic system (Vers. 3)

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Abstract. In previous works (MMR, 2021a), 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 third 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

In the previous work (Rakočević, 2021a)[1] we presented a new type of mirror symmetry, expressed through the number of atoms in the set of 20 protein amino acids (AAs). Mirroring itself is created by crossing the last column of the periodic system of numbers (PSN) and the path of the largest change on the 6-bit binary tree (Table 1). That fact alone justifies the title of this paper. Another reason for title justification lies in the fact that in most of the illustrations of that previous paper (MMR, 2021a), the unity of chemism and semiosis is presented.

We take the notion of *semiosis* from Charles Sanders Peirce, through Charles W. Morris, in the sense that semiosis is "the process in which something functions as a sign" (Morris, 1938, Section II/2, p. 3). On the other hand, the notion of *sign* we take from Ferdinand de Saussure (1985) in the sense that "by sign we mean the total resulting from

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[1] Brief communication in: arXiv:2108.01563v4 [q-bio.BM]. Along with this quote, it should also be said that this is the third step on the way to the definitive version of the paper. The first two steps are listed in footnote 2. (Note: in further citations, instead of "Rakočević", only MMR.)

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

However, independently of the mentioned previous paper, we also presented the argumentation about the unity of chemism and semiosis in other papers, some of which were published before (MMR, 2018a, 2018b) and some after (MMR, 2021a, 2022) the cited work. [MMR, 2018a, pp. 31-32: "Rumer (1966) suggests that encoding (of amino acids) by dinucleotide aggregations is mediated by 'grammatical' formalism (the relation between words and the root of the word), semantics (one-meaning and multi-meaning codon families) and by semiology, i.e. semiotics (the classification of nucleotide doublets after the number of their hydrogen bonds which appear here as 'signifiant' and 'signifié' (signifier and signified) at the same time, that is as their unity (see: De Saussure, 1985, pp. 99-100).]

But what is most interesting is that the argumentation for the validity of the claim (attitude) contained in the title of this paper found already in the first results of genetic code researches. We cite examples. Codon AUG, as a chemical entity, encodes the amino acid methionine as a corresponded chemical entity; however, in parallel, it encodes a non-chemical entity, actually an event – the initiation of protein synthesis. And, second example: the codons AGA and AGG in the standard genetic code encode the amino acid arginine, while in the mitochondrial code, they encode an event: the termination i.e. the end of protein synthesis.

2. New elaboration[2]

In this paper, we continue to present new examples of the said new type of mirror symmetry in a set of 20 protein AAs. So, let us look at the PPAASS arrangement (Box 1) in Table 2, where we find something that cannot be expected from the aspect of everything that is known so far about causality in the natural sciences, primarily physics and chemistry. We find a strict mirror symmetry of quantities more than strangely obtained – by summing the ordinal number of each individual amino acid, the number of atoms in the amino acid molecule and the number of protons in those atoms (in the side chain of AA). It is strange and unbelievable, but at the same time it is also a serious fact. The essence – the chemical properties of similarity of AAs – is strict, but the form (semiosis) is also strict;[3] and in fact, the semiotic *sign* is also strictly constructed, as a

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[2] This elaboration is new just in relation to papers (MMR, 2021b, 2022), published after the above cited work (MMR, 2021a). On the other hand, the basis for writing this paper consists of two materials stored on my website (http://www.rakocevcode.rs). [Material I: "Genetic code as a semiotic system (Facts in support of the hypothesis)", 11. May 2023; and Material II: "Genetic code as a semiotic system (Materials for coming paper)", 6. August 2023.]

[3] MMR, 2004, p. 233: "The existence of such a harmonic structure with unity of a determination with physical–chemical characteristics and atom and nucleon number at the same time appealed to Aristotle and to his idea of unity of form and essence."

unity of the *signifier* through the mirror image and arbitrarily organized quantities and the *signified*, as the real chemical entities.[4]

Box 1. The PPAASS arrangement (Perfect Protein Amino Acid Similarity System)

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

The perfection of the PPAASS arrangement is also reflected in the fact that when moving from the 4:6 distinctions to the 5:5 distinctions (all five and five amino acids in both decades), symmetrically arranged quantities are obtained in a new way. Admittedly, not as a mirror image of the original, but a strict "quantization", a consistent change for the second-order unit in the quantity notation (Table 3). As a curiosity, or perhaps more than that, it should be noted that the first quantity is actually the sum of the first three perfect numbers (530 = 6 + 28 + 496).

In addition, there is at least an analogy (correspondence?) with the result of the distribution of AAs on four stereochemical types[5] (031, 041, 051, 061, 071), where "quantization" is with the same change for a second-order unit in the quantity notation (Table A1, on the right). With an insight into the fact that the quantities in the arrangement on Table A1 are literally "taken off" from the diagonal of PSN (Table A2), there can no longer be any doubt that semiotic arbitrariness is an essential feature of the Genetic Code; nor that the genetic code represents the unity of chemical and non-chemical entities; finally, there can be no doubt that GC itself represents a kind of semiotic system.

Because of those readers (because of that part of the scientific public) who will think that the views just presented were adopted too quickly, and that they are also too

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[4] 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."

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

optimistic, we believe that we should go a step further in testing the PPAASS arrangement. The best way to do this is for the test to be one possible (chemically justified) pairing of AAs. Can the resulting sequence of 10 AAs pairs also satisfy R. Swanson's requirement of ideality and perfection, but also our requirement to simultaneously express both the chemical properties and the semiotic essence of the amino acid code; in other words, to get: SSAAPP (Similarity System of Amino Acid Perfect Pairs). But then the question arises, whether the pairing that is contained in PPAASS, and which, obviously, has a chemical justification (GA, VP, IL, KR, QE, etc.), but does not take into account the distinctions of AAs into four stereochemical types, nor into four types of diversity; or so that these two distinctions are taken into account? The test showed that the latter is correct (Table 4).

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Table A4 shows how the sequence of 10 pairs is constituted in SSAAPP. When deciding on the order and position of the pairs, both classifications of amino acids had to be taken into account, in four stereochemical types, as well as in four types of diversity. Thus, at first there must come pairs from the set of 16 AAs of the alanine type, and, at the end their four chalcogen, 2 oxygenic and 2 sulfuric, because sulfur comes from the third group of the periodic system of chemical elements (PSE), while the previous pairs posses only elements from the first and second periods. Only after that come AAs from the remaining three stereochemical types. As we are dealing with pairs here, one would think that glycine and proline (GP) go together, since they are singlets, each in its stereochemical type, and as we find them in the basic setup of the four types of diversity (Figure 1). The valine-isoleucine (V-I) pair appears to be predetermined, as these are the only two AAs in the valine type. However, it is not so. The analysis showed that the third key must be included here, which is the key of classification of AAs into two classes handled by two classes of enzymes aminoacyl-tRNA synthetases (aaRS).[6] The same key had to be used when pairing ST and CM into SC and TM (MMR, 1998, Surv. 4, p. 290).

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

3. Discussion

We have a few more important things to discuss when the definitive version of this paper comes up. First of all, we see that one of the main principles that apply to the genetic code is this: as few of the same quantities appear as the signifiers for as many different qualities as possible, as signified. The next point is another important reference to De Saussure. The arbitrariness of signifiers has limitations.[7] We see this primarily in that, in all important cases, chemical distinctions are accompanied by changes in quantities for the unit of the first, second, and third order; for the unit in two or three positions of the quantity records.[8] We find such a situation in Tables 1, 2 and 3; Tables 3.1, 3.2 and 3.3; and also in Displays 1 and 2. Of course, in many other situations throughout this work, as well as in my previous works.

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4. Conclusion

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

[8] 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*.")

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[Also available at: https://doi.org/10.48550/arXiv.q-bio/0607018]

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ILLUSTRATIONS FOR THE MAIN TEXT

Table 1. Mirror symmetry through the number of atoms in AAs

00	00	00	+	2	→	02	→	20		**1**	
11	11	11	+	2	→	13	→	31	←	**0**	(5)
22	**22**	**22**	+	2	→	24	→	42		**1**	
33	—	11	+	5	→	16	→	61		**0**	
44	**22**	00	+	5	→	05	→	50		**1**	(2)
55	11									**0**	
66	00	G_{01}	A_{04}	N_{08}	D_{07}		→	20			
77		V_{10}	P_{08}	S_{05}	T_{08}		→	31		**022**	
88		I_{13}	L_{13}	C_{05}	M_{11}		→	42		—	
99		K_{15}	R_{17}	F_{14}	Y_{15}		→	61		**022**	
		Q_{11}	E_{10}	W_{18}	H_{11}		→	50			

According to the original, modified and refined:
arXiv:2108.01563v4 [q-bio.BM]: (Box 1)

Survey 1. A "hidden" mirroring

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

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

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

440 + 56 = 496 [440 | 044]

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

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

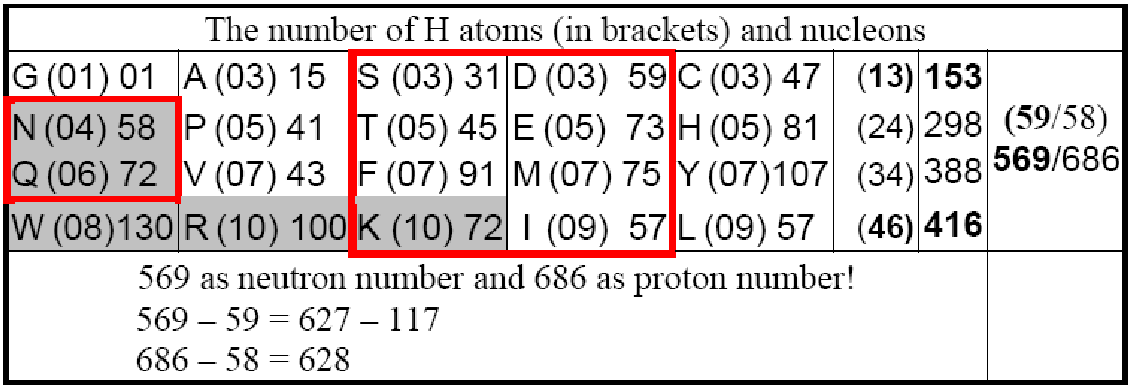
The establishing of cyclicity through the first order of AAs

Table 2. Perfect Protein Amino Acid Similarity System (PPAASS) [I]

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

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

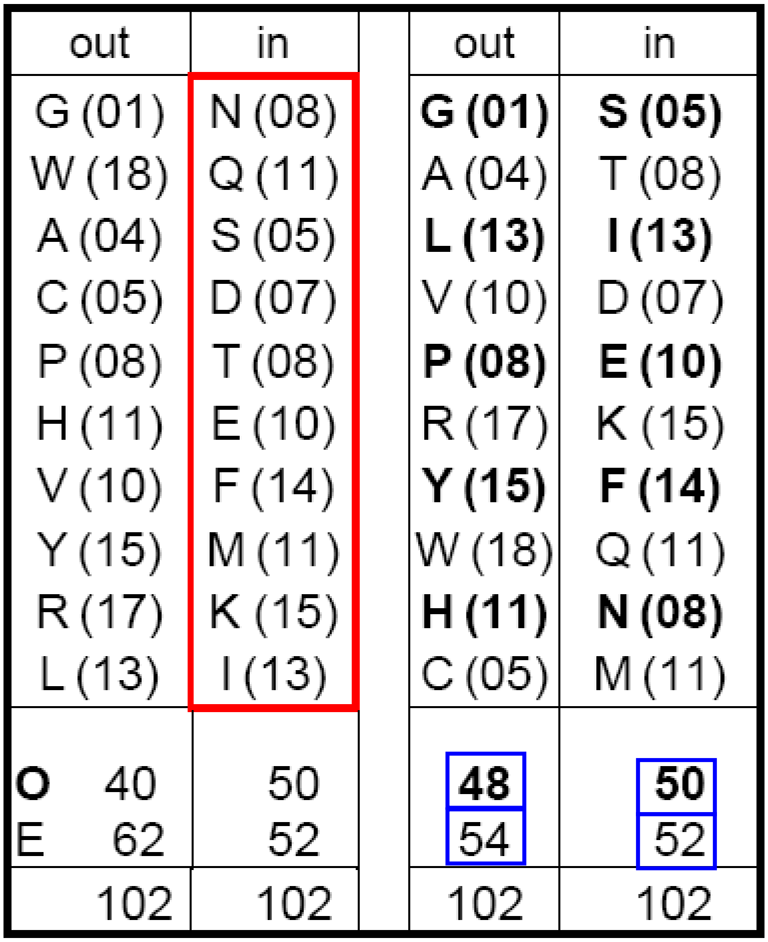
Survey 2. Distribution of AAs according to the number of hydrogen atoms (I)



The number of H atoms (in brackets) and nucleons							
G (01) 01	A (03) 15	S (03) 31	D (03) 59	C (03) 47	**(13)**	**153**	
N (04) 58	P (05) 41	T (05) 45	E (05) 73	H (05) 81	(24)	298	(**59**/58) **569**/686
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							

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

Survey 3. 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, 2011, Tab. 9, p. 830

Table 3. Perfect Protein Amino Acid Similarity System (PPAASS) [II]

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

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

Table 3.1. Nucleon number in PPAASS

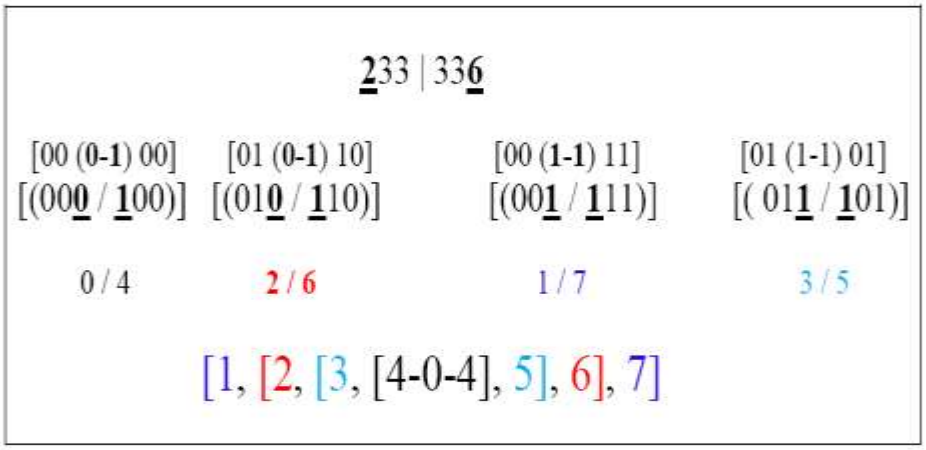
(1)	G	01	58	N	(11)	**133**
(2)	A	15	59	D	(12)	
(3)	V	43	31	S	(13)	160
(4)	P	41	45	T	(14)	
(5)	I	57	47	C	(15)	**236**
(6)	L	57	75	M	(16)	
(7)	K	72	91	F	(17)	370
(8)	R	100	107	Y	(18)	
(9)	Q	72	130	W	(19)	**356**
(10)	E	73	81	H	(20)	
			724			**725**
		531				530

The change of ±1, compared to the change for ±2, as we find in Table 3.3.

Table 3.2. Neutron number in PPAASS (I)

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

Display 1. Mirroring of neutron number in PPAASS



233 | 33**6**

[00 (**0**-**1**) 00]	[01 (**0**-**1**) 10]	[00 (**1**-**1**) 11]	[01 (1-1) 01]
[(00**0** / **1**00)]	[(01**0** / **1**10)]	[(00**1** / **1**11)]	[(01**1** / **1**01)]
0 / 4	**2 / 6**	1 / 7	3 / 5

[1, [2, [3, [4-0-4], 5], 6], 7]

Display 2. "The Number System of Multiples, NSM III"

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

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

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

Table 3.3. Neutron number in PPAASS (II)

(1)	G	00	27	N	(11)	**61**
(2)	A	06	28	D	(12)	
(3)	V	18	14	S	(13)	**70**
(4)	P	18	20	T	(14)	
(5)	I	24	22	C	(15)	**104**
(6)	L	24	34	M	(16)	
(7)	K	31	42	F	(17)	168
(8)	R	45	50	Y	(18)	
(9)	Q	33	61	W	(19)	166
(10)	E	34	38	H	(20)	
		$23\underline{3}$				$\mathbf{23\underline{5}}$
			$33\underline{6}$			$33\underline{4}$

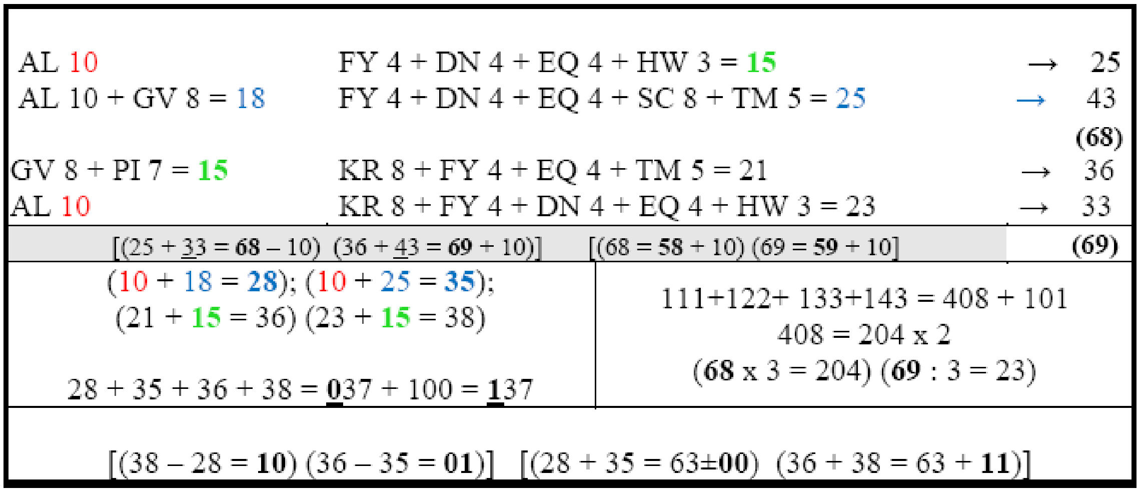
The change of ±2, compared to the change for ±1, as we find in Table 3.1.

Table 4. 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. … Quantity 143 as in Survey A5 (66 + 77 = 143). A critical point of distinction.

Survey 4. The number of amino acid coding codons within Table 4



AL 10	FY 4 + DN 4 + EQ 4 + HW 3 = **15**	→	25
AL 10 + GV 8 = 18	FY 4 + DN 4 + EQ 4 + SC 8 + TM 5 = 25	→	43
			(68)
GV 8 + PI 7 = **15**	KR 8 + FY 4 + EQ 4 + TM 5 = 21	→	36
AL 10	KR 8 + FY 4 + DN 4 + EQ 4 + HW 3 = 23	→	33
[(25 + 33 = **68** – 10) (36 + 43 = **69** + 10)]	[(68 = **58** + 10) (69 = **59** + 10]		**(69)**
(10 + 18 = **28**); (10 + 25 = **35**); (21 + **15** = 36) (23 + **15** = 38) 28 + 35 + 36 + 38 = 037 + 100 = 137	111+122+ 133+143 = 408 + 101 408 = 204 x 2 (**68** x 3 = 204) (**69** : 3 = 23)		
[(38 – 28 = **10**) (36 – 35 = **01**)] [(28 + 35 = 63±**00**) (36 + 38 = 63 + **11**)]			

Survey 5. Natural numbers series in a relation to Plato's four

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

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

Quantities 28 and 35 are found in Survey 4, and 21 and 42 as the harmonic mean on the 6-binary tree, in reading from one side and the other. Quantities 28 and 35 are found in Survey 4, and 21 and 42 as the harmonic mean on the 6-binary tree, in reading from one side and the other.

Table 5. Distribution of AAs within four types of diversity according to Fig. 1

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

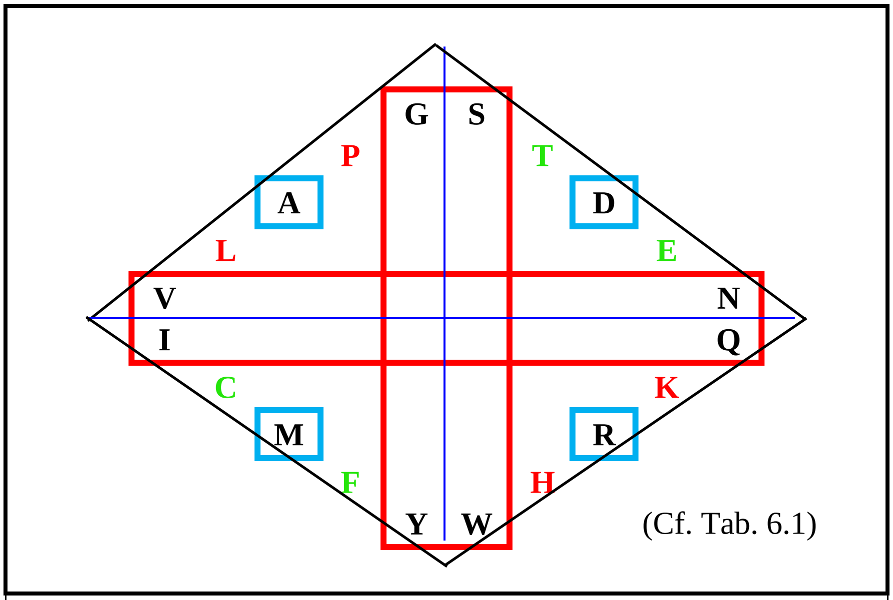
532.57+ 725.86 = 1258.43 ≈ 1258 → 34 x 37

222

658.62 + 820.99 = 1479.61 ≈ 1480 → 40 x 37

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

From [DOI 10.31219/osf.io/fzgjp], Table 7, p. 5.



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

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

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

Figure 1. 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 it is 4 x 5 AAs and in Table 5 there are 5 x 4 ones.

Appendix A

Cyclic Invariant Periodic system of AAs (CIPS: Table A1, on the left) is created as follows. First, the Gray code model of Genetic code of R. Swanson (1984) is developed into a 6-bit binary tree (MMR, 1998). Then AAs whose positions are determined by the Golden mean are "taken off" from it (MMR, 1998, Table 2, p. 288; and MMR, 2022, Surv. 2.1, p. 53). Finally, they are arranged hierarchically in compliance with Mendeleev's two principles (continuity and minimum change); that is according to the number of atoms in their molecules, taking into account their chemical counterparts, i.e. complements. Three pairs of non-complements remain at the bottom of the system-arrangement.

Altogether, chemically strictly determined classes of molecules are obtained. So, in the middle position there are chalcogen AAs (S, T & C, M); follow - in next ‘cycle’ – the AAs of non-alanine stereochemical types (G, P & V, I); then two double acidic AAs with two their amide derivatives (D, E & N, Q); after them come two aliphatic hydrocarbon AAs, with their nitrogen (amine) derivatives (A, L & K, R); and, finally, four aromatic ones (F, Y & H, W) – two up and two down. The mentioned five classes belong to two superclasses: primary superclass in light areas and secondary one in dark areas. Notice that each amino acid position in this CIPS is strictly determined, and none can be changed. Within ‘2-3-4-5’ rows above plus CM from ‘1’ there are 102 and within ‘2-3-4-5’ down plus ST from ‘1’ also 102 atoms.

The system-arrangement on the right illustration of Table A1 is reached in the following way. First, the 16 amino acids of the alanine stereochemical type are arranged according to two Mendeleev principles: the principle of continuity and minimum change, that is, by the number of atoms in the side chain of the amino acid molecule. It goes without saying that aliphatic amino acids come first, as less complex, and then aromatic amino acids, as more complex. Chemical similarity of AAs dictates grouping by: 1, 2 and 3 AAs in both columns, with chemical pairing: AL, ST, CM, DE, NQ, KR; plus two pairs of aromatic AAs, HW and FY (Rakočević and Jokić, 1996, Survey 1.1, p. 346) 346) (Solution 1).[9]

{(A) (SC) (DNK) / (L) (TM) (EQR)}+ {(HF) (WY)} → [86 / 86] ………...……… (1)

{(AS) (CD) (NK) / (LT) (ME) (QR)}+ {(HF) (WY)} → [86 / 86] …………………. (2)

(ALTS, CMED, NQRK, HWYF) → [86 / 86] ………………………….………… (3)

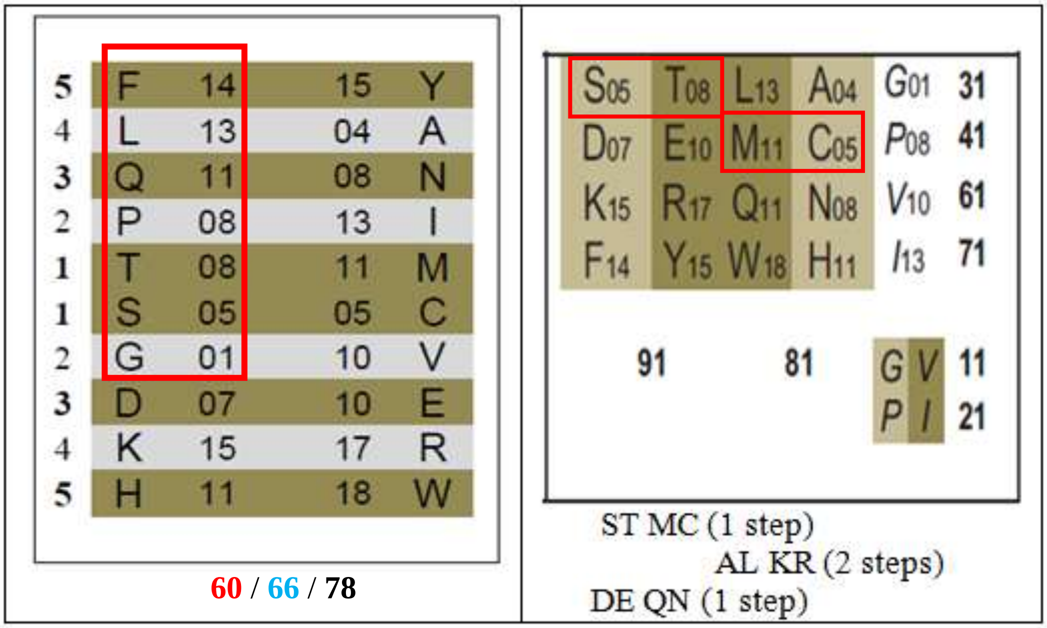
---

[9] Note that due to the fact that the histidine molecule has fewer atoms than the phenylalanine molecule (11 vs 14), the HW pair in this system-arrangement is first to last; while in the system-arrangement in Table 2 it is the last. The principle of minimum change applies both here and there, but here the size of the molecule is taken into account, and there it is not.

This is followed by the view that it makes chemical sense to transform the hierarchy from Solution 1 into a hierarchy of "everything by 2" (MMR, 2011, Fig. 7) (Solution 2). The following is the association "everything by 4", which we find here in Table A1, with quadruplets increased by one AA of non-alanine stereochemical types, from a hierarchically strictly ordered sequence (G 01, P 08, V 10, I 13). Finally, we are surprised to find that the final result looks like it was "taken off the diagonal from Periodic System of Numbers (PSN) (Table2).

Illustrations for Appendix A

Table A1. Two amino acid systems: CIPS on the left and SCAS on the right



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

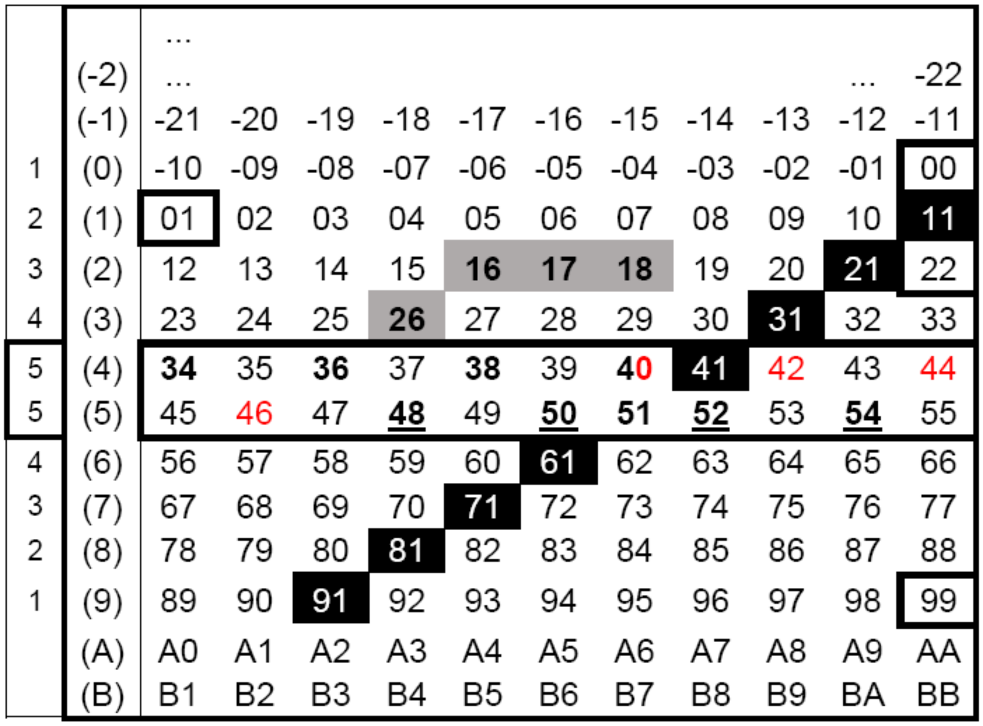
60 / 66 / 78

S_{05}	T_{08}	L_{13}	A_{04}	G_{01}	31
D_{07}	E_{10}	M_{11}	C_{05}	P_{08}	41
K_{15}	R_{17}	Q_{11}	N_{08}	V_{10}	61
F_{14}	Y_{15}	W_{18}	H_{11}	I_{13}	71
91		81		G V	11
				P I	21

ST MC (1 step)
AL KR (2 steps)
DE QN (1 step)

CIPS: Cyclic Invariant Periodic System from: MMR, 2011, Fig 6, p. 832; SCAS: Stereo-Chemically Arranged System. From: MMR, 2019, Fig 1, p. 6. In both cases, the number of atoms in the molecule (in the side chain) is attached to the amino acid designation in normal and index notation, respectively.

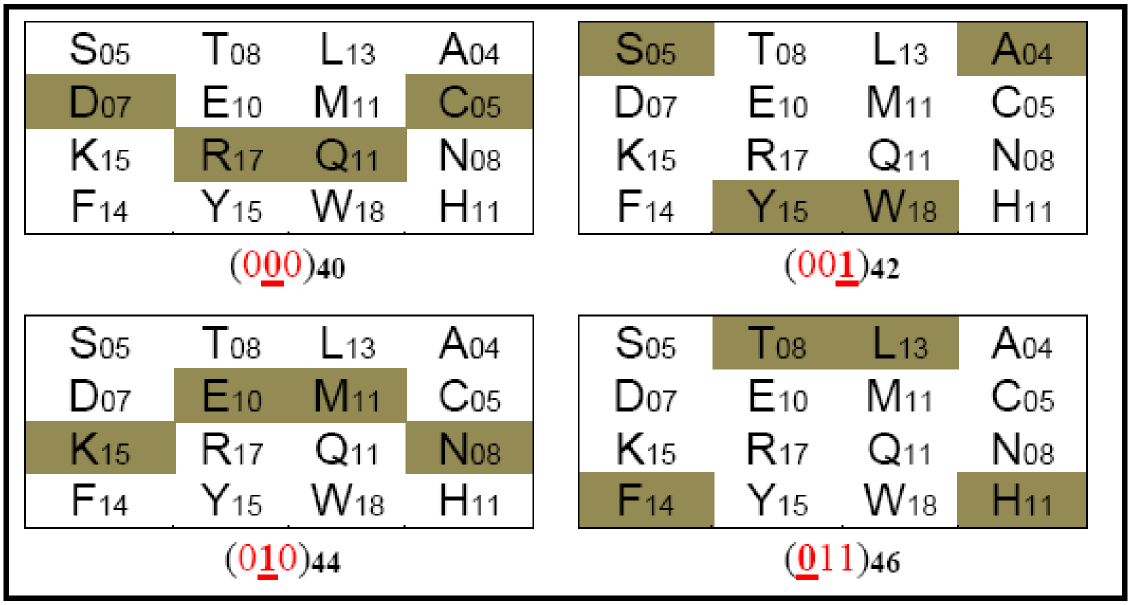
Table A2. Periodic system of the numbers in decimal number system



		...										
	(-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

The illustration is taken from (MMR, 2019, Figure A1, p. 28) with a few added indications of essentially significant areas.

Survey A1. Logical square in the set of 16 AAs of alanine stereochemical type, corresponded with right illustration in Table A1.



S05	T08	L13	A04
D07	E10	M11	C05
K15	R17	Q11	N08
F14	Y15	W18	H11

(000)40

S05	T08	L13	A04
D07	E10	M11	C05
K15	R17	Q11	N08
F14	Y15	W18	H11

(001)42

S05	T08	L13	A04
D07	E10	M11	C05
K15	R17	Q11	N08
F14	Y15	W18	H11

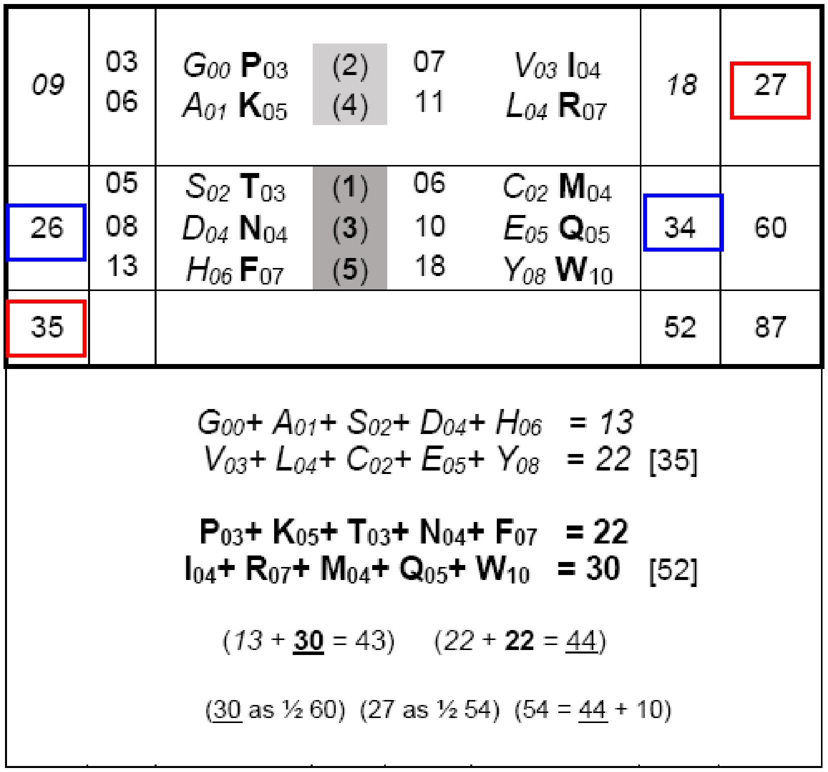
(010)44

S05	T08	L13	A04
D07	E10	M11	C05
K15	R17	Q11	N08
F14	Y15	W18	H11

(011)46

Taken from Material II (quoted here in footnote 2): Table B1, p. 54. Two inner rows vs two outer ones.

Table A3. Relationships among two classes and two superclasses of AAs through non-H atoms



09	03 06	G_{00} $\mathbf{P}_{03}$ A_{01} $\mathbf{K}_{05}$	(2) (4)	07 11	V_{03} $\mathbf{I}_{04}$ L_{04} $\mathbf{R}_{07}$	*18*	27
26	05 08 13	S_{02} $\mathbf{T}_{03}$ D_{04} $\mathbf{N}_{04}$ H_{06} $\mathbf{F}_{07}$	**(1)** **(3)** **(5)**	06 10 18	C_{02} $\mathbf{M}_{04}$ E_{05} $\mathbf{Q}_{05}$ Y_{08} $\mathbf{W}_{10}$	34	60
35						52	87

$G_{00} + A_{01} + S_{02} + D_{04} + H_{06} = 13$
$V_{03} + L_{04} + C_{02} + E_{05} + Y_{08} = 22$ [35]

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

$(13 + \underline{\mathbf{30}} = 43)$ $(22 + \mathbf{22} = \underline{44})$

$(\underline{30}$ as ½ 60) (27 as ½ 54) $(54 = \underline{44} + 10)$

Taken from Material II (quoted here in footnote 2): Table C3, p. 54. Two inner rows vs two outer ones. There is also Table C1 for the total number of atoms in the side chains of amino acids, as well as Table C2 for the number of hydrogen atoms.

To the left of the shaded column are amino acids of the second class, handled by the second class of aaRS. On the right are AAs of the first class. The first two rows (above) make up the amino acids of the primary superclass of CIPS (Table A1 on the left). The bottom three rows belong to the secondary superclass. Non-bold and italicized amino acids are of lower rank, less complexity; while the bold ones are of a higher rank, that is, of greater complexity. The exception is phenylalanine because as a member of the FY pair it is of lower rank. However, given the fact that PheRS attaches phenylalanine to the 2′-OH of the tRNA terminal adenosine, it is considered to be of higher rank in this constellation. [Class I and II aminoacyl-tRNA synthetases attach amino acids to the 2′- and 3′-OH of the tRNA terminal adenosine, respectively. The only exception is phenylalanyl-tRNA synthetase (PheRS), which structurally belongs to Class II but attaches phenylalanine to the 2′-OH.)]

Survey A2. Quantitative relationships in Table 3

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

Table A4. "Golden" amino acids, their complements and non-complements

F 14		15 Y	F 14		15 Y
L 13	66-1	04 A	L 13	78±0	04 A
Q 11		08 N	**K 15**		**17 R**
P 08		13 I	P 08		13 I
T 08		11M	T 08		11M
	60+1			60+1	
S 05		05 C	S 05		05 C
G 01		10 V	G 01		10 V
D 07		10 E	D 07		10 E
K 15	**78±0**	**17 R**	Q 11	66-1	08 N
H 11		18 W	H 11		18 W

(MMR, 2018a, Surv. 3. p. 39) [Cf. left side in Tab. A1] in MMR, 2022, Display 1 – 6 H and non-H, pp. 63–68. This Table corresponds to that Display 1, p. 63, with additional important chemical distinctions indicated here.

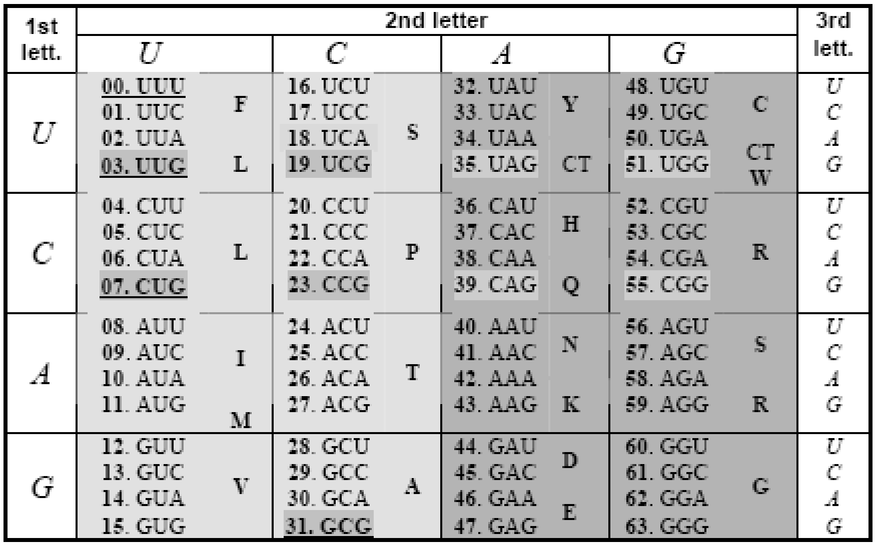
Table A5. Adjacency relations of pairs in the series of natural numbers

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

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

fc = four-codon; nfc = non-four-codon

Table A6. System-arrangement of codons in relation to perfect numbers

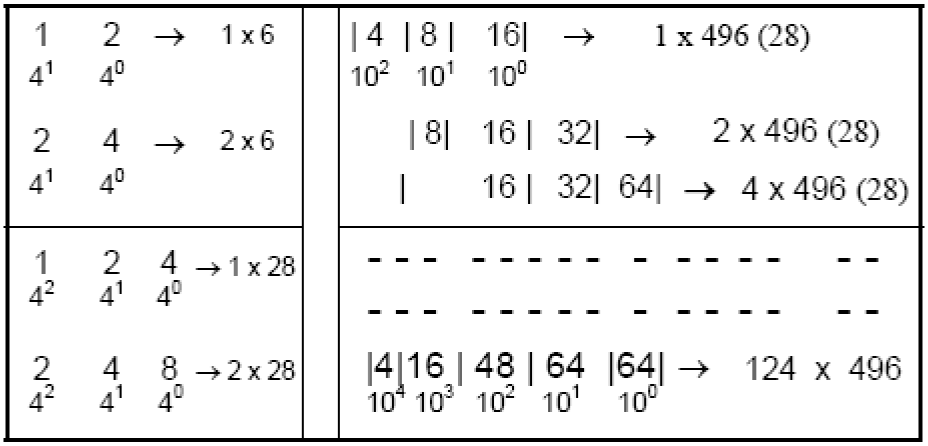


1st lett.	2nd letter								3rd lett.
	U		*C*		*A*		*G*		
U	00. UUU	F	16. UCU	S	32. UAU	Y	48. UGU	C	*U*
	01. UUC		17. UCC		33. UAC		49. UGC		*C*
	02. UUA		18. UCA		34. UAA		50. UGA	CT	*A*
	03. UUG	L	19. UCG		35. UAG	CT	51. UGG	W	*G*
C	04. CUU	L	20. CCU	P	36. CAU	H	52. CGU	R	*U*
	05. CUC		21. CCC		37.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

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

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

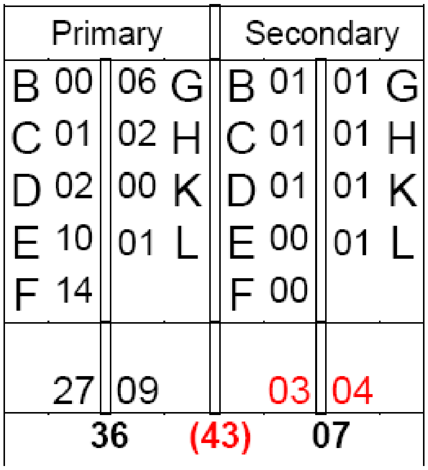
Table A7. Binary "travel" of the second and third perfect numbers through the space



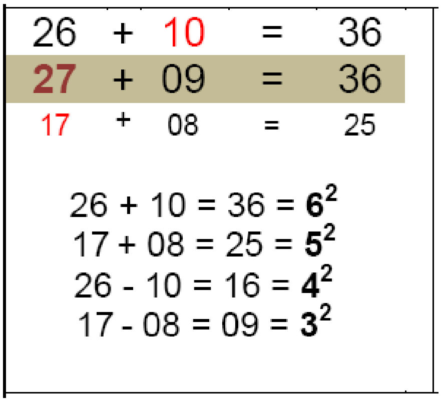
<table>
<tr><td>1 2 → 1 x 6
4^1 4^0
2 4 → 2 x 6
4^1 4^0</td><td></td><td>| 4 | 8 | 16| → 1 x 496 (28)
10^2 10^1 10^0
| 8| 16 | 32| → 2 x 496 (28)
| 16 | 32| 64| → 4 x 496 (28)</td></tr>
<tr><td>1 2 4 → 1 x 28
4^2 4^1 4^0
2 4 8 → 2 x 28
4^2 4^1 4^0</td><td></td><td>- - - - - - - - - - - - - - - - -
-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

(Taken from MMR, 2007, Tab. 12, p. 96)

Table A8. The key of Darwin's Diagram



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



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

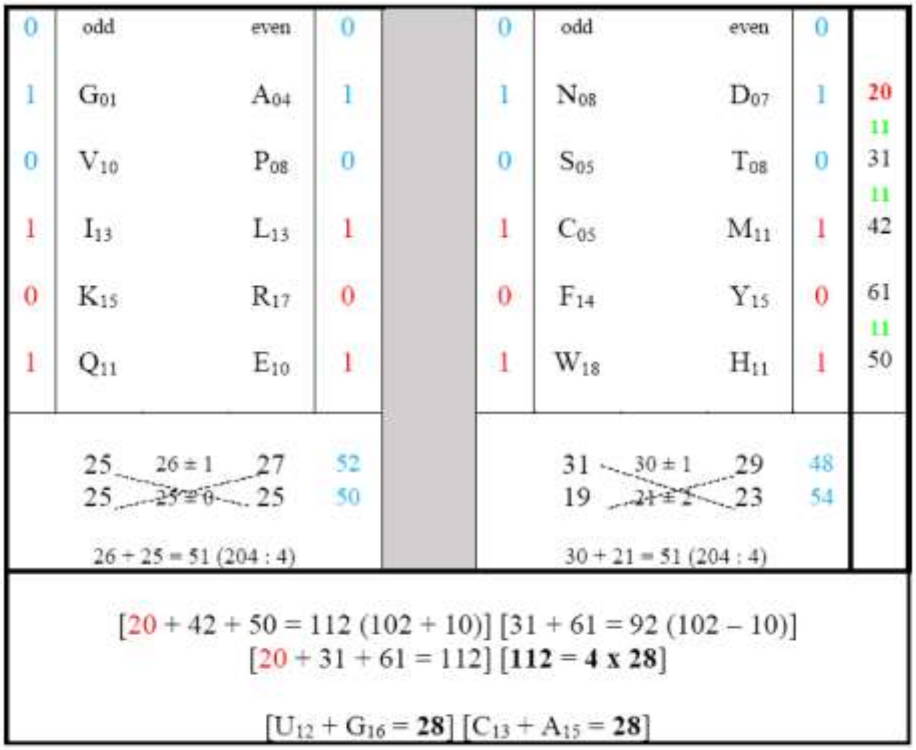
(Taken from MMR, 2019, Tab. C1, p. 38)

Appendix B

Appendix B is taken in its entirety from Appendix B in Material II (cited in footnote 2); in everything except that the Table B1 from there is missing here.

Illustrations for Appendix B

Tab. B1. Odd and even quintets, taken from Table 2 (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. B2. Odd and even quintets, taken from Table 2 (II)

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

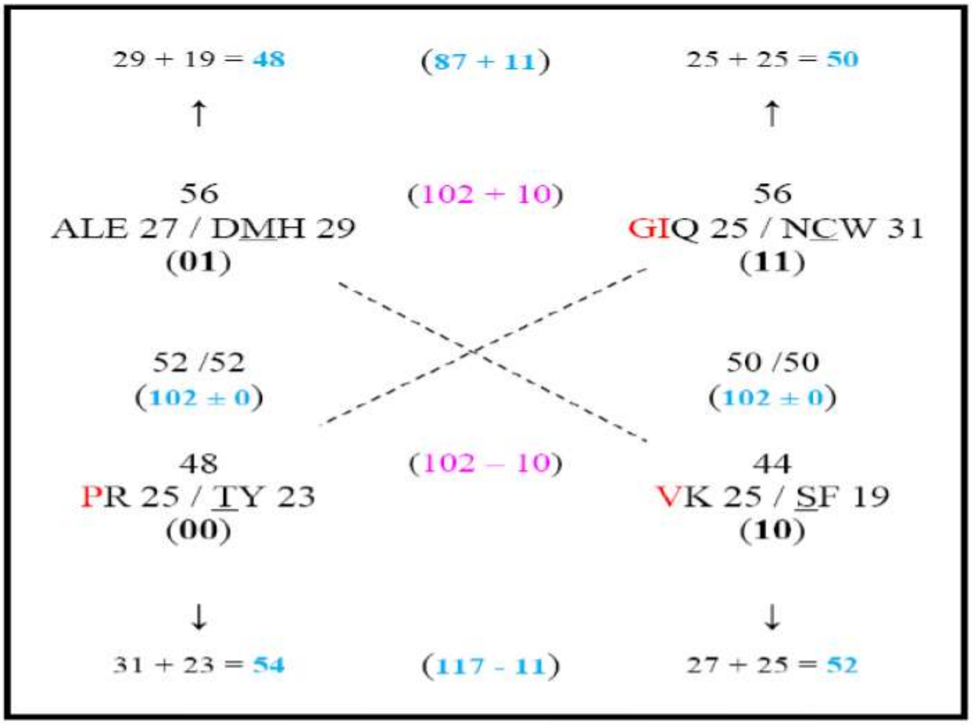
[53 + 43 = 97 – 1] [57 + 39 = 97 – 1] [97 = 87 + 10 & 117 – 20]

[56 + 78 + 86 = 220] $\boxed{[56 + 67 + 97}$ = 220]

[65 + 87 + 68 = 220] [65 + 76 + 79 = 220]

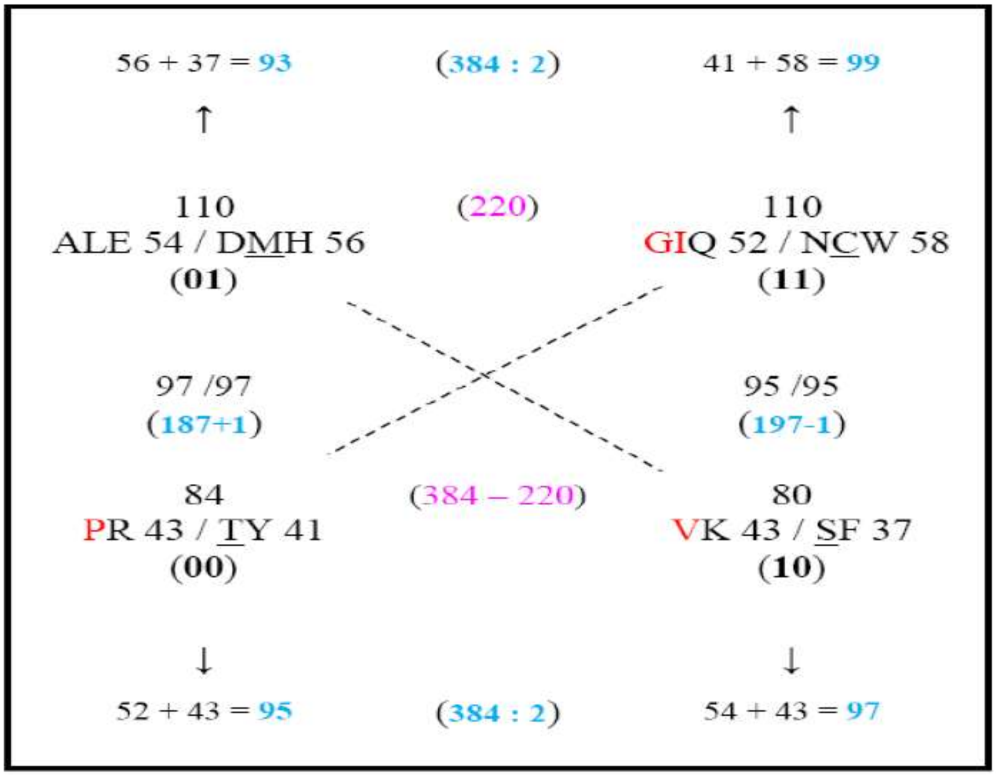
Atom number in amino acid whole molecule

Tab. B3. Distribution of quintets from Table B2 by even and odd positions (I)



Atom number in amino acid side chain

Tab. B4. Distribution of quintets from Table B2 by even and odd positions (II)



Atom number in amino acid whole molecule