Miloje M. Rakočević

GENETIC CODE AS A SEMIOTIC SYSTEM

(Versions I – IV)

Belgrade, 2024

Genetic code as a semiotic system (Vers. 1)

Miloje M. Rakočević

University of Niš, Faculty of Sciences and Mathematics
Department of Chemistry,
Višegradska 33, 18000 Niš, Serbia
(http://www.rakocevcode.rs)
(mirkovmiloje@gmail.com)

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 first 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 main paper of the scientific work, of which this paper is an accompanying part, was published last year (Rakočević, 2022).[1] The whole work is, by the way, in the status of a hypothesis, because in current science the term genetic code (GC) is not accepted as an ontological reality, but only as a metaphor; and, this is even more true for the concepts of semiotics and semiosis; in other words, current science does not accept that the genetic code could have a semiological nature (Slide 1).[2]

With such a state of affairs, the question arises as to the appropriateness of bringing such a large corpus of *bare facts* (as many as there are here) in support of the hypothesis about the semiological nature of GC; why is that, if the scientific truth itself is called into question in this matter.

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[1] The main paper was preceded by the Synopsis (Rakočević, 2021b), so the subject scientific paper (with a minimally varied title) consists of three parts. (*Note*: in further citations, instead of "Rakočević", only MMR.)

[2] n the case of my research, the situation is even more difficult. This is because the results of those researches, except for the term *genetic code*, require that the terms *Cipher of the genetic code* and *the code key* also be considered real ontological entities (MMR, 2018a, b).

But instead of opening a possible ontological and/or epistemological discussion, we opt for a very concrete matter: to show with two examples how we see the bare facts in this (semiological) matter, and, from our point of view, an undoubted scientific truth.

Example 1. On Slide 14 we see a system-arrangement of protein amino acids which, by the number of atoms in the molecules, by rows and columns, is in full accordance with one of the diagonals of the Periodic Number System (PSN: Slide 13) in the Decimal number system. It cannot be said that this 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.[3]

Example 2. On Slide 16 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; 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 is also non-causal (arbitrary), this example also confirms the semiotic nature of the genetic code.

*

In the same way that the two slides in the two given examples were commented on, all the remaining slides were also commented on, with as few words as possible, because the illustrations speak for themselves.

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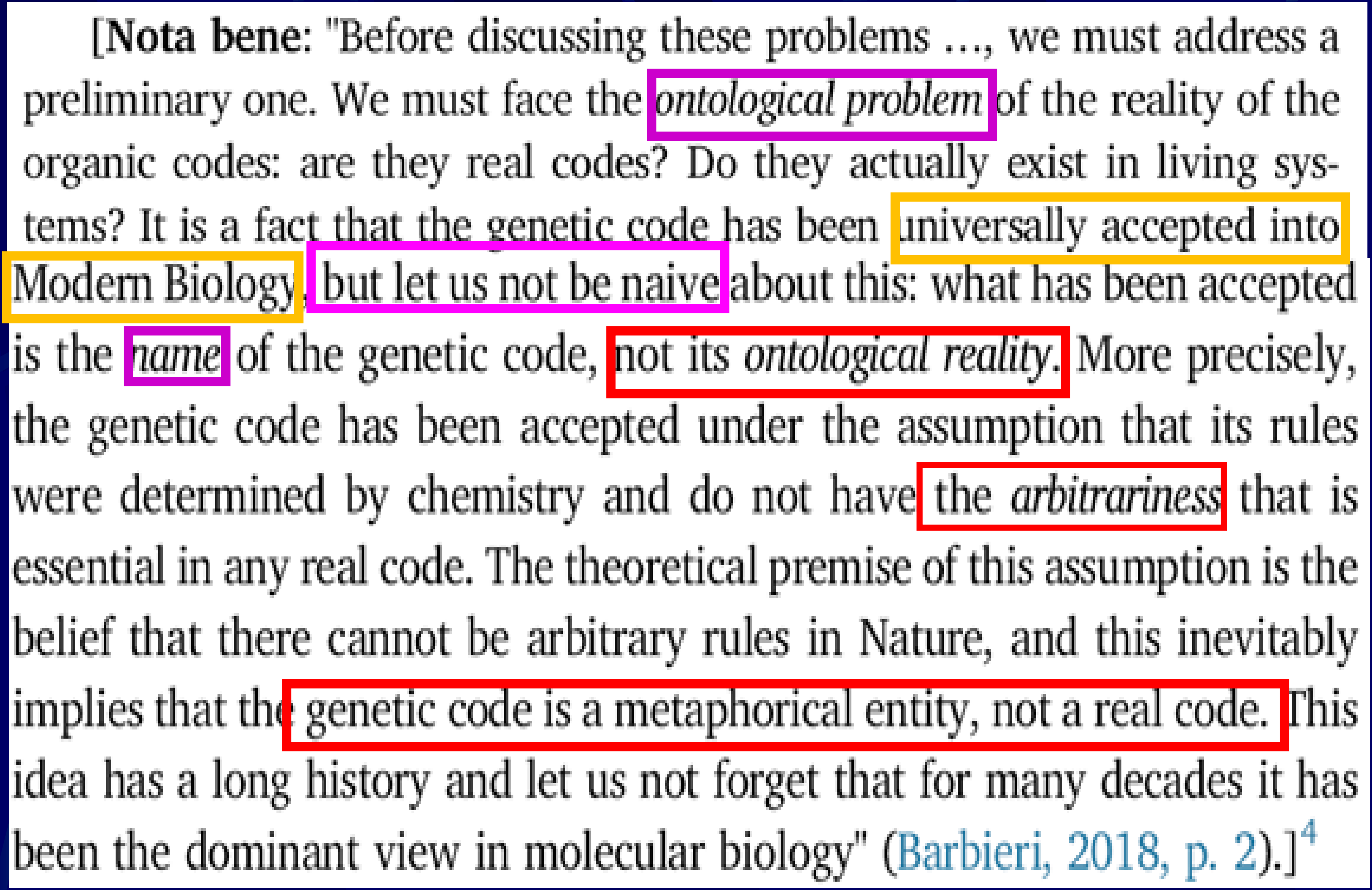
[3] Of course, as a signifier, it is arbitrary in relation to the signified, but not in the set of signifiers. [De Saussure, 1985, p. 100: "Le lien unissant le signifiant au signifié est arbitraire, ou encore, puique nous entendons par signe le total résultant de l'association d'un signifiant à un signifier 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."]

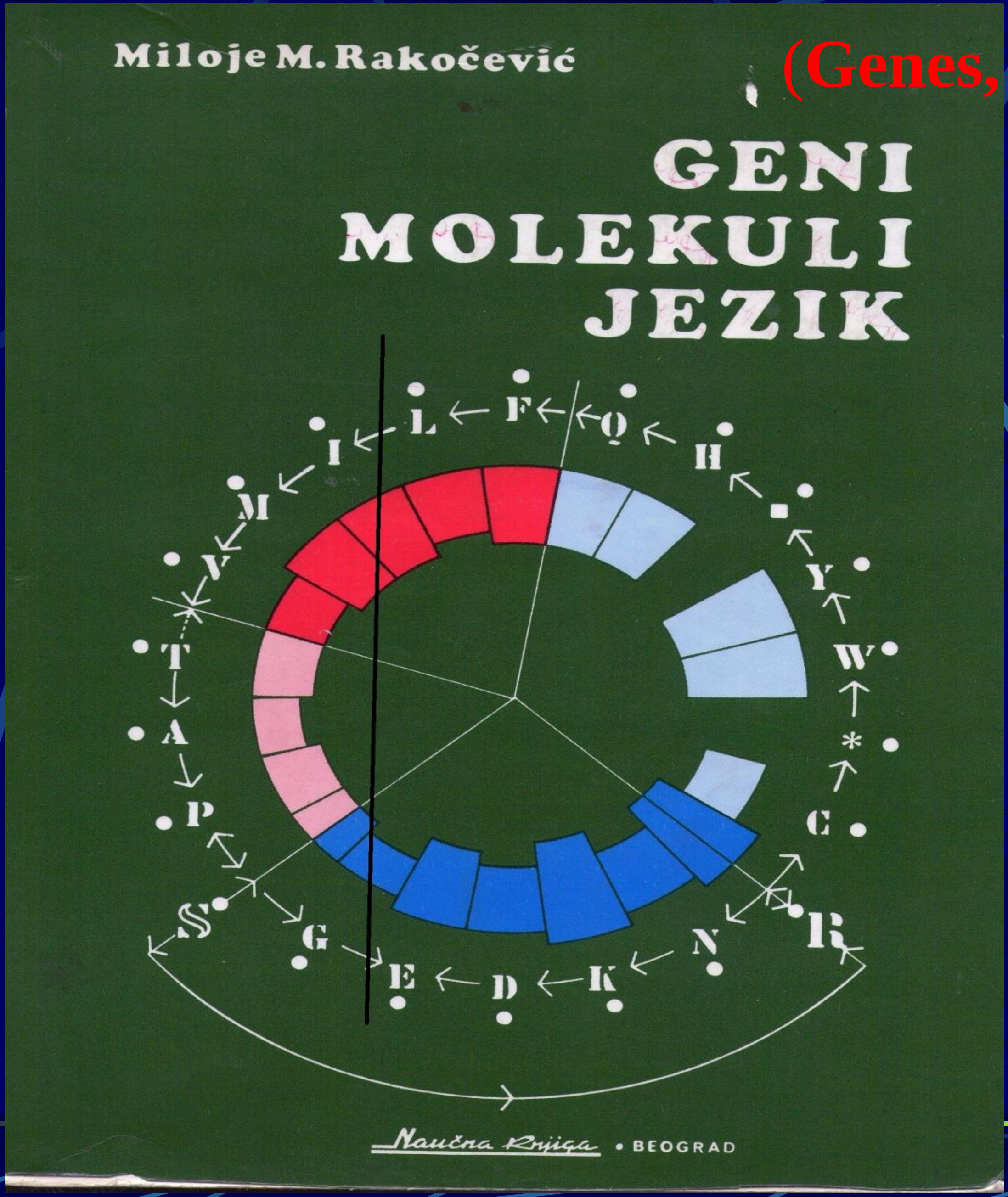
2. Basic slides: the presentation



[**Nota bene:** "Before discussing these problems …, we must address a preliminary one. We must face the *ontological problem* of the reality of the organic codes: are they real codes? Do they actually exist in living systems? 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*. More precisely, the genetic code has been accepted under the assumption that its rules were determined by chemistry and do not have the *arbitrariness* that is essential in any real code. The theoretical premise of this assumption is the belief that there cannot be arbitrary rules in Nature, and this inevitably implies that the genetic code is a metaphorical entity, not a real code. This idea has a long history and let us not forget that for many decades it has been the dominant view in molecular biology" (Barbieri, 2018, p. 2).][4]

4 “The very first model of the genetic code was the Stereochemical Theory, an idea proposed by George Gamow in 1954 … The second canonical model was the Coevolution ..” (Barbieri, 2018, p. 2)

(Genes, molecules, language)



Miloje M. Rakočević

GENI
MOLEKULI
JEZIK

Naučna Knjiga • BEOGRAD

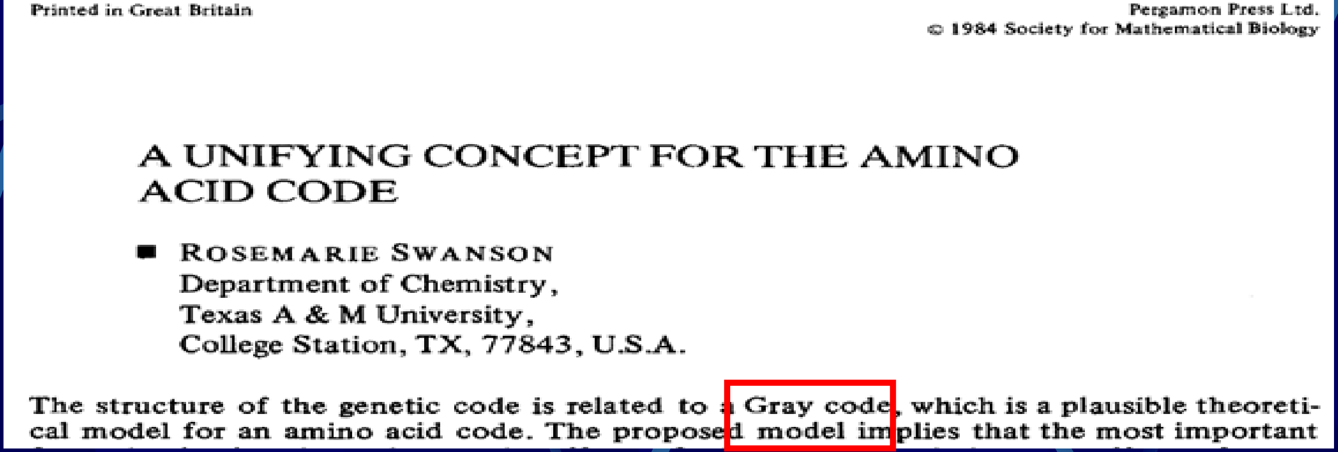
René Thom, 1979. *La Genèse de l'espace représentatif selon Piaget, in: Théories du language, théories de l'apprentissage. Le débat entre Jean Piaget et Noam Chomsky*. Éditions du Seuil, Paris:

"Sans doute, j'en suis profondément convaincu, les mathématiques ‘informent’ le monde comme elles ‘informent’ aussi notre propre structure. Mais ces mathématiques-là ne sont pas celles que nous connaissons, celles que les algébristes nous fabriquent dans l'élan têtu de l'itération indéfinie des opérations formelles. C'est au contraire dans l'étude des limitations naturelles des formalismes que réside la mathématique de demain."

Richard Dawkins, *River Out of Eden: A Darwinian View of Life*, Weidenfeld & Nicolson, London, 1995, p. 139:

"The minimal condition for true heredity would be the existence of at least two distinct kinds of H2O molecule, both of which give rise to (‘spawn’) copies of their own kind. Molecules sometimes come in two mirror varieties.

There are two kinds of glucose molecule, which contain identical atoms tinkertoyed together in an identical way except that the molecules are mirror images. The same is true of other sugar molecules, and lots of other molecules besides, including the all-important amino acids. Perhaps here is an opportunity for ‘like begets like’ – for chemical heredity."



Bulletin of Mathematical Biology Vol. 46, No. 2, pp. 187–203, 1984.
Printed in Great Britain

0092-8240/84$3.00+0.00
Pergamon Press Ltd.

A UNIFYING CONCEPT FOR THE AMINO ACID CODE

■ ROSEMARIE SWANSON
Department of Chemistry,
Texas A & M University,
College Station, TX, 77843, U.S.A.

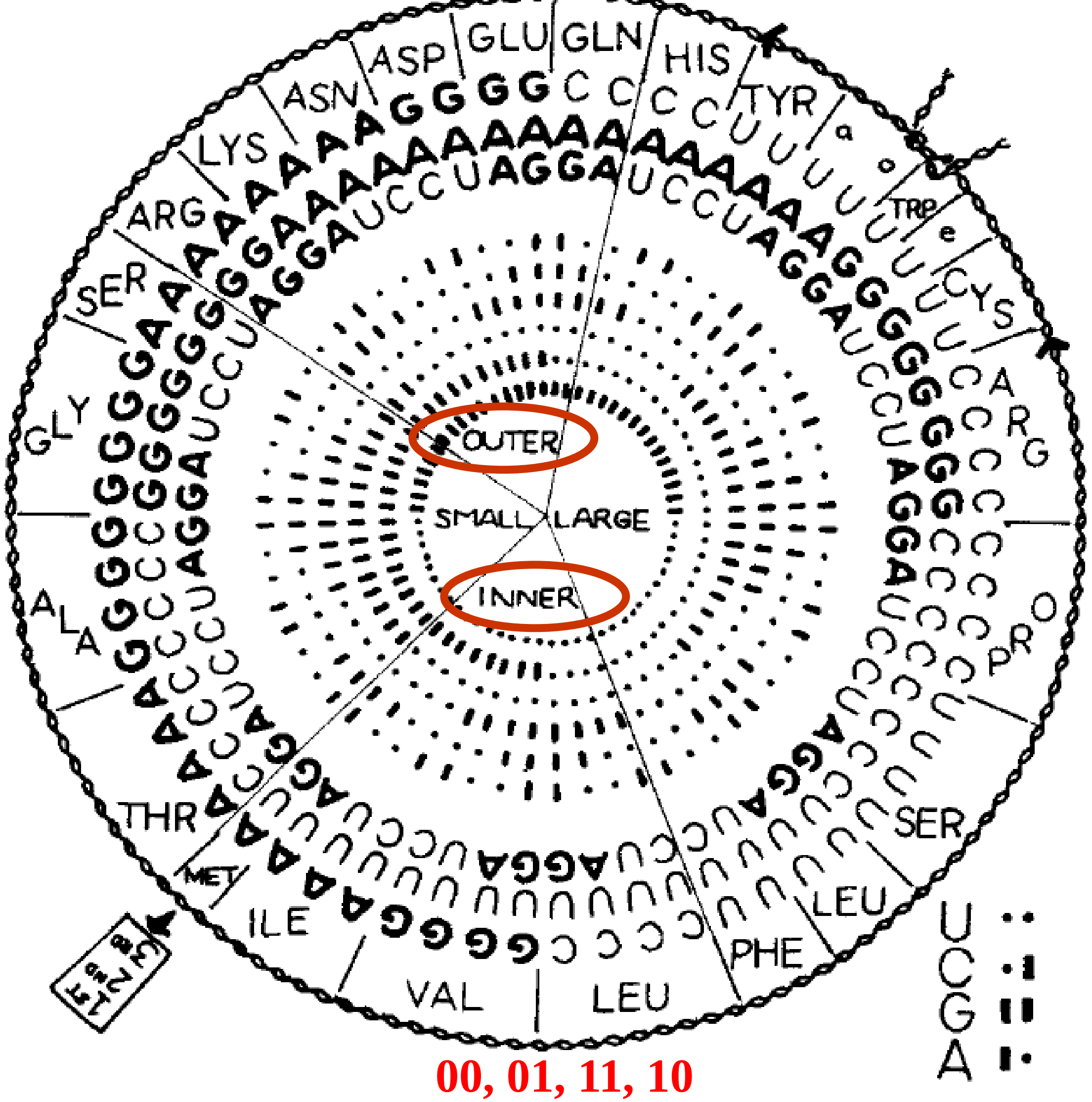
The structure of the genetic code is related to a Gray code, which is a plausible theoretical model for an amino acid code. The proposed model implies that the most important

Swanson, 1984, p. 201: "The actual amino acid code and the twenty amino acids it codes for suggest an idealized model coding system and idealized relationships among the amino acids. Using the idealized models, one could construct a 'perfect' genetic code and even choose a different set of amino acids to give a still more even distribution of their physical properties … The purpose of such an effort would be to make comparisons and gain insight into the actual code in use in organisms. … "

Gray code model of GC (Swanson, 1984)

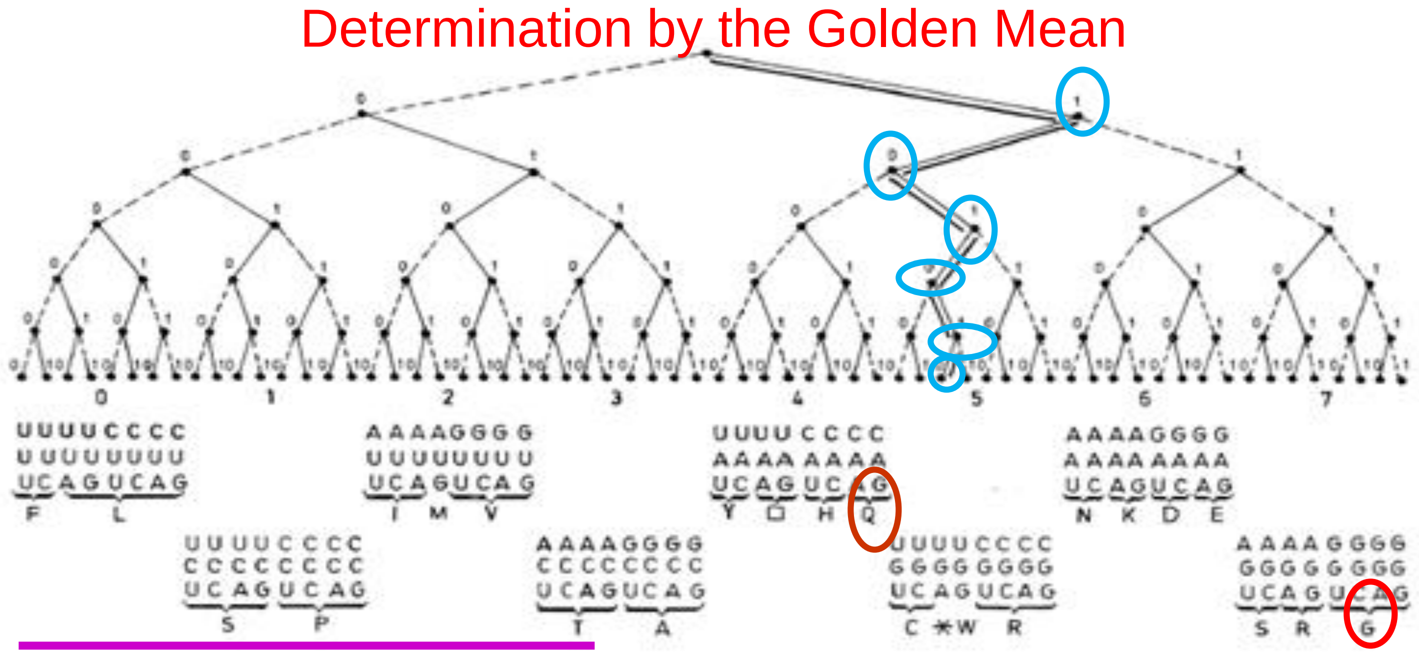
R. SWANSON

Codon ring. AAs as outter, inner / small, large



00, 01, 11, 10

Rakočević, BioSystems 46 (1998) 283–291



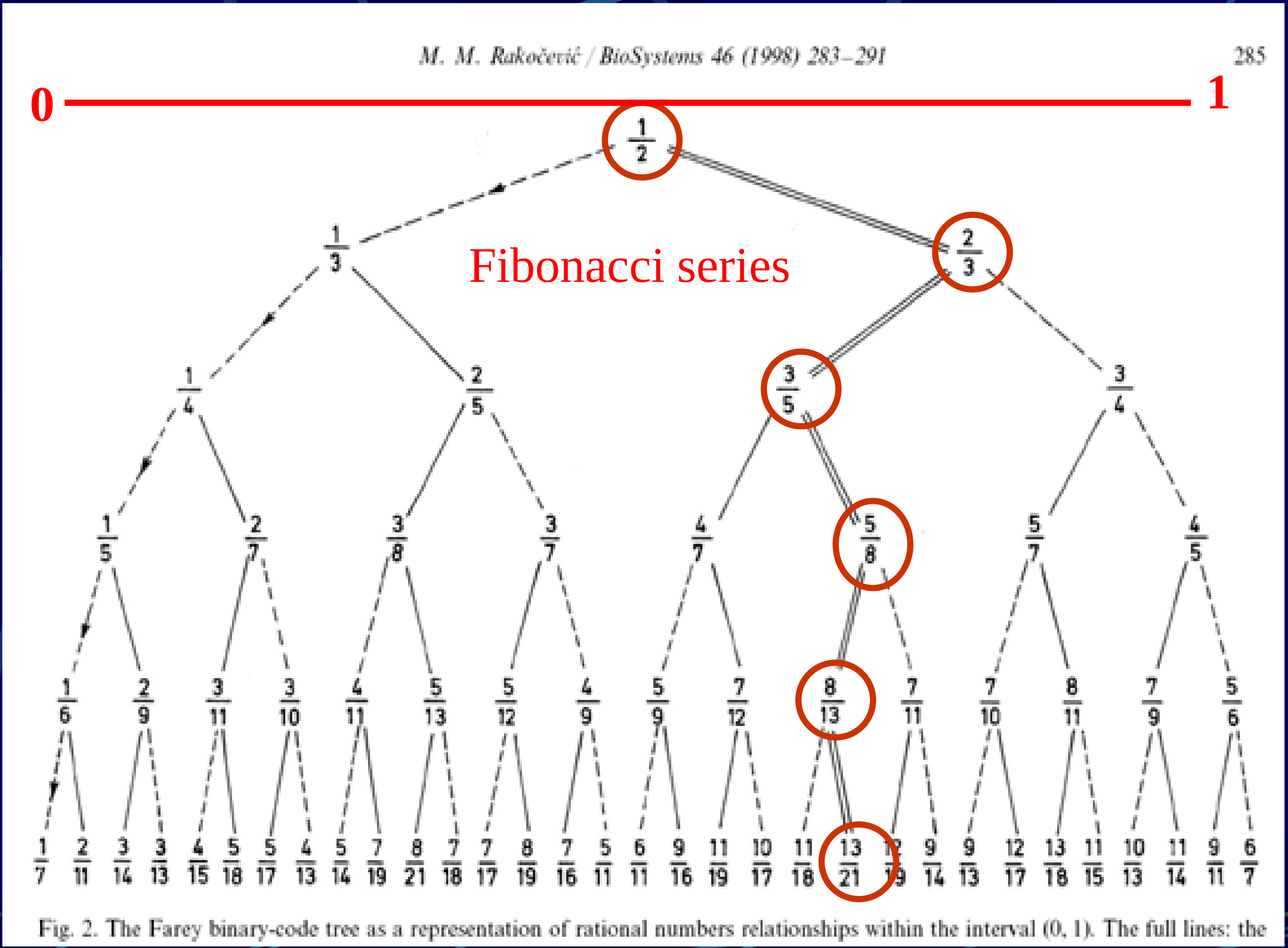
M. M. Rakočević / BioSystems 46 (1998) 283–291

Fig. 1. Genetic code as a binary-code tree. The full lines: the routes of the greater (faster) changes from pyrimidine to purine or from two to three hydrogen bonds and vice versa. The dotted lines: the routes of the less (slower) changes. The double full line: the route of the maximum possible (fastest) changes; the route corresponding to the 'Golden mean route' on the Farey tree (Fig. 2). Asterisks: 'stop' codon UGA. Quadrangles: 'stop' codons UAA and UAG.

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

(60, 66, 78) **[(10 x 6), 11 x 6), (13 x 6)]** **[(1 x 6), (2 x 6), (3 x 6)]**

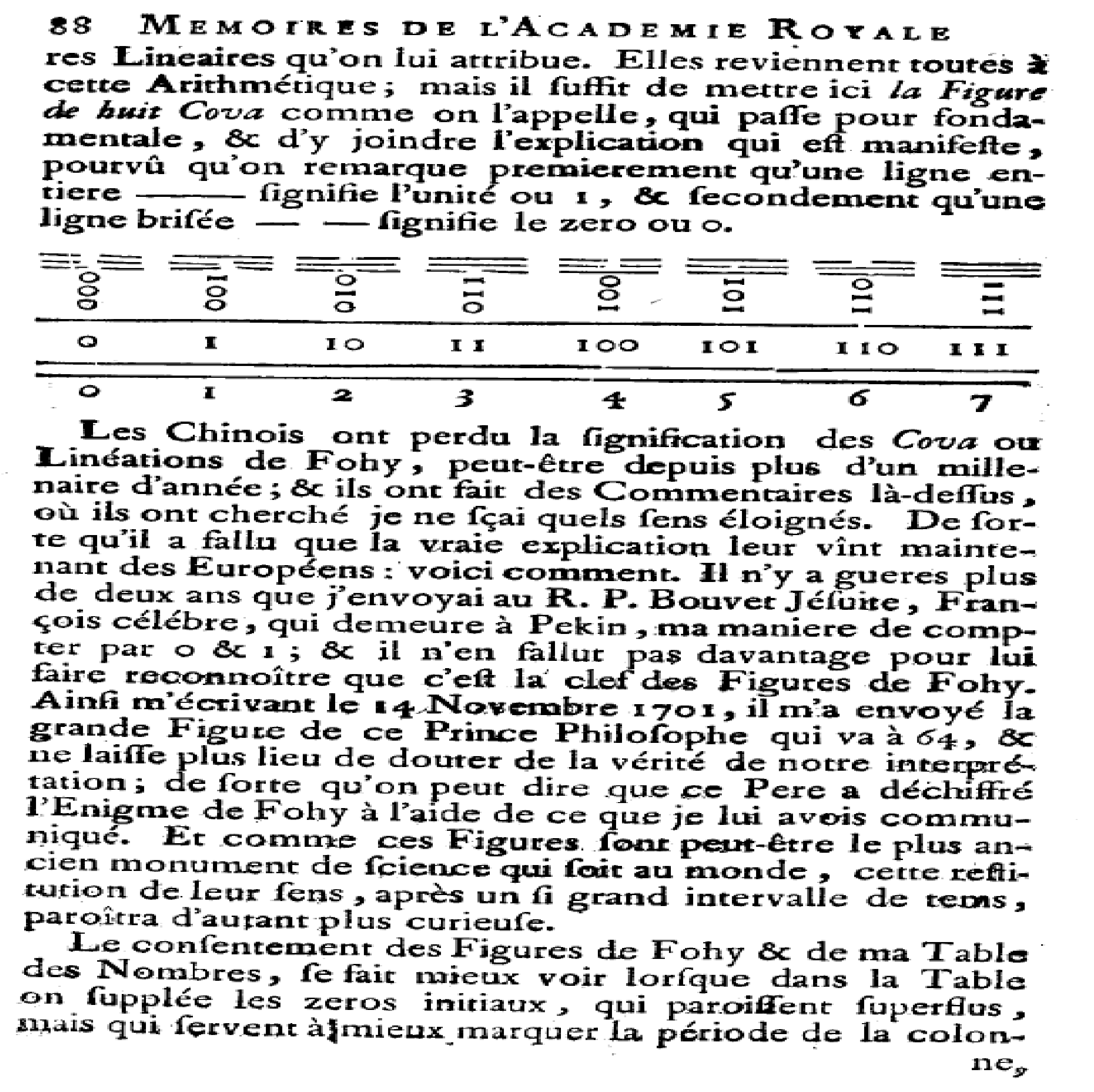
Physics of deterministic chaos: The Farey tree



M. M. Rakočević / BioSystems 46 (1998) 283–291 285

Fig. 2. The Farey binary-code tree as a representation of rational numbers relationships within the interval (0, 1). The full lines: the

Leibnitz’s interpretation of binary system



88 MEMOIRES DE L’ACADEMIE ROYALE

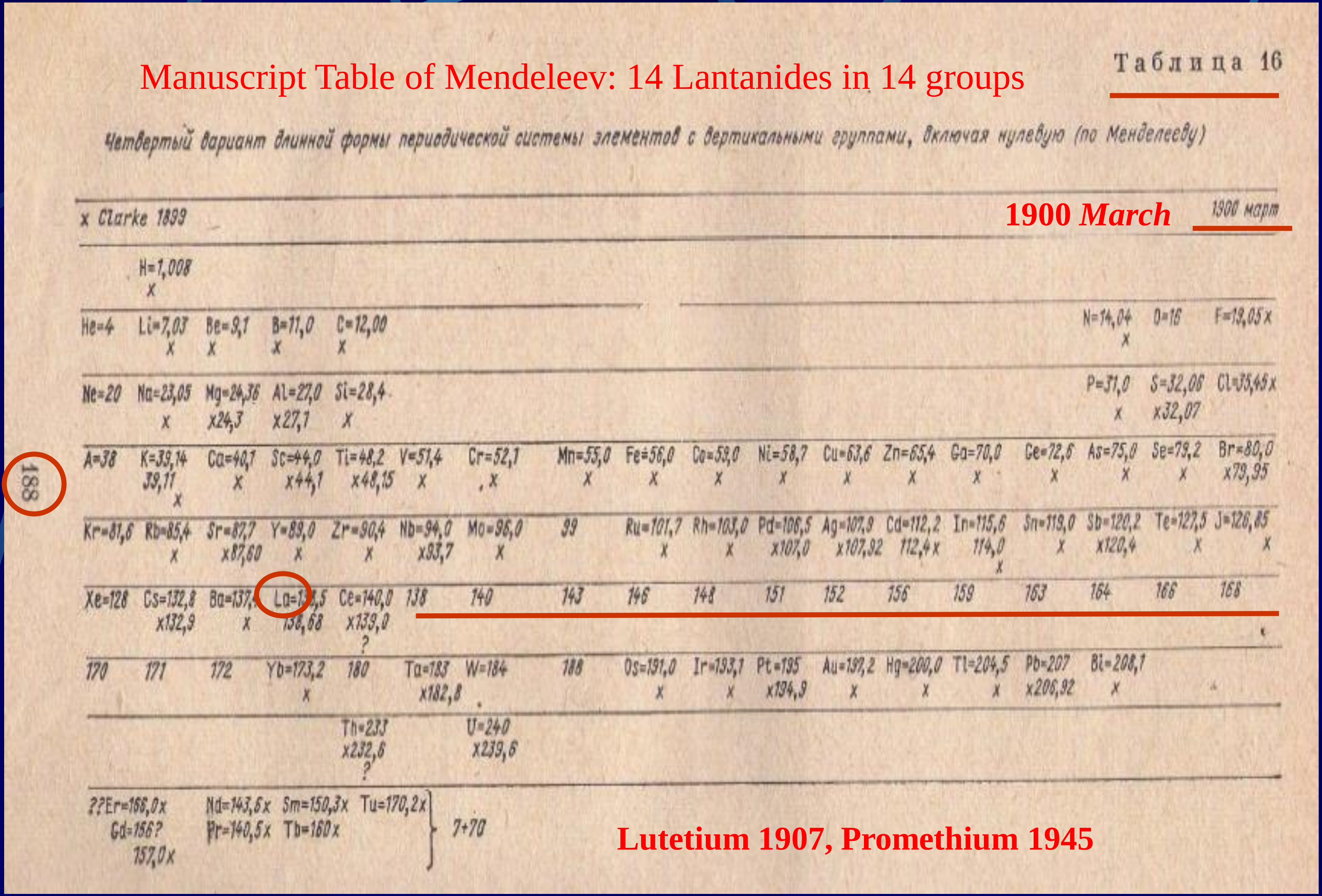
res Lineaires qu’on lui attribue. Elles reviennent toutes à cette Arithmétique; mais il ſuffit de mettre ici *la Figure de huit Cova* comme on l’appelle, qui paſſe pour fondamentale, & d’y joindre l’explication qui eſt manifeſte, pourvû qu’on remarque premierement qu’une ligne entiere ——— ſignifie l’unité ou 1, & ſecondement qu’une ligne briſée —— —— ſignifie le zero ou 0.

000	001	010	011	100	101	110	111
0	1	10	11	100	101	110	111
0	1	2	3	4	5	6	7

Les Chinois ont perdu la ſignification des *Cova* ou Linéations de Fohy, peut-être depuis plus d’un millenaire d’année; & ils ont fait des Commentaires là-deſſus, où ils ont cherché je ne ſçai quels ſens éloignés. De ſorte qu’il a fallu que la vraie explication leur vînt maintenant des Européens: voici comment. Il n’y a gueres plus de deux ans que j’envoyai au R. P. Bouvet Jéſuite, François célébre, qui demeure à Pekin, ma maniere de compter par 0 & 1; & il n’en fallut pas davantage pour lui faire reconnoître que c’eſt la clef des Figures de Fohy. Ainſi m’écrivant le 14 Novembre 1701, il m’a envoyé la grande Figure de ce Prince Philoſophe qui va à 64, & ne laiſſe plus lieu de douter de la vérité de notre interprétation; de ſorte qu’on peut dire que ce Pere a déchiffré l’Enigme de Fohy à l’aide de ce que je lui avois communiqué. Et comme ces Figures ſont peut-être le plus ancien monument de ſcience qui ſoit au monde, cette reſtitution de leur ſens, après un ſi grand intervalle de tems, paroîtra d’autant plus curieuſe.

Le conſentement des Figures de Fohy & de ma Table des Nombres, ſe fait mieux voir lorſque dans la Table on ſupplée les zeros initiaux, qui paroiſſent ſuperflus, mais qui ſervent à mieux marquer la période de la colonne,

"Fourth variant of long form PSE with vertical groups, including zeroth"



Manuscript Table of Mendeleev: 14 Lantanides in 14 groups

Таблица 16

188

Четвертый вариант длинной формы периодической системы элементов с вертикальными группами, включая нулевую (по Менделееву)

x Clarke 1899

1900 March

1900 март

	H=1,008 x																
He=4	Li=7,03 x	Be=9,1 x	B=11,0 x	C=12,00 x											N=14,04 x	O=16	F=19,05x
Ne=20	Na=23,05 x	Mg=24,36 x24,3	Al=27,0 x27,1	Si=28,4 x											P=31,0 x	S=32,06 x32,07	Cl=35,45x
A=38	K=39,14 39,11 x	Ca=40,1 x	Sc=44,0 x44,1	Ti=48,2 x48,15	V=51,4 x	Cr=52,1 x	Mn=55,0 x	Fe=56,0 x	Co=59,0 x	Ni=58,7 x	Cu=63,6 x	Zn=65,4 x	Ga=70,0 x	Ge=72,6 x	As=75,0 x	Se=79,2 x	Br=80,0 x79,95
Kr=81,6	Rb=85,4 x	Sr=87,7 x87,60	Y=89,0 x	Zr=90,4 x	Nb=94,0 x93,7	Mo=96,0 x	99	Ru=101,7 x	Rh=103,0 x	Pd=106,5 x107,0	Ag=107,9 x107,92	Cd=112,2 112,4x	In=115,6 114,0 x	Sn=119,0 x	Sb=120,2 x120,4	Te=127,5 x	J=126,85 x
Xe=128	Cs=132,8 x132,9	Ba=137,4 x	La=138,5 138,68	Ce=140,0 x139,0 ?	138	140	143	146	148	151	152	156	159	163	164	166	168
170	171	172	Yb=173,2 x	180	Ta=183 x182,8	W=184	188	Os=191,0 x	Ir=193,1 x	Pt=195 x194,9	Au=197,2 x	Hg=200,0 x	Tl=204,5 x	Pb=207 x206,92	Bi=208,1 x		
				Th=233 x232,6 ?		U=240 x239,6											

??Er=166,0x
Gd=156?
157,0x

Nd=143,6x Sm=150,3x Tu=170,2x
Pr=140,5x Tb=160x

7+70

Lutetium 1907, Promethium 1945

B.M. Kedrov, 1977, p. 188

Noble gases in the zeroth and VIII group

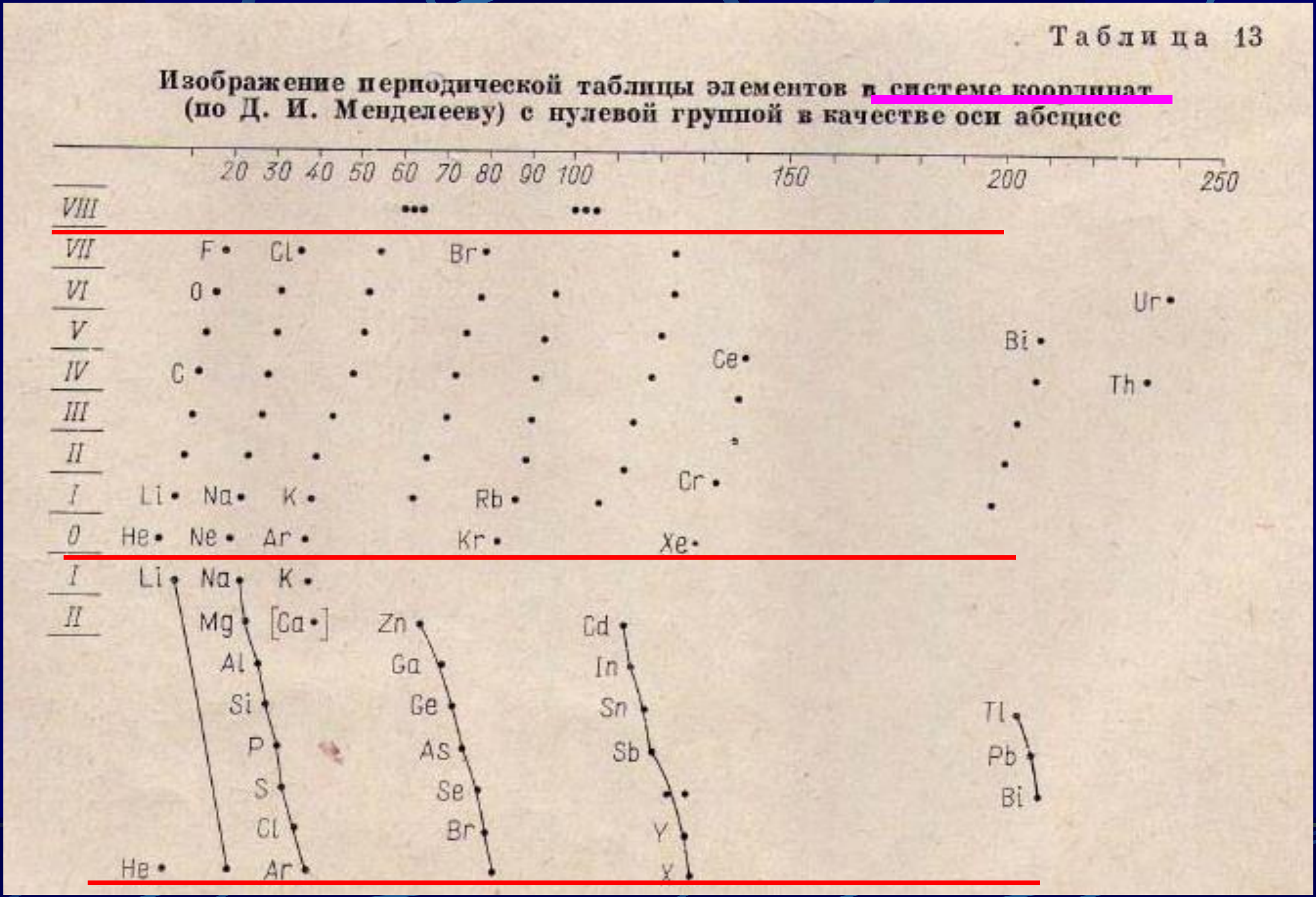
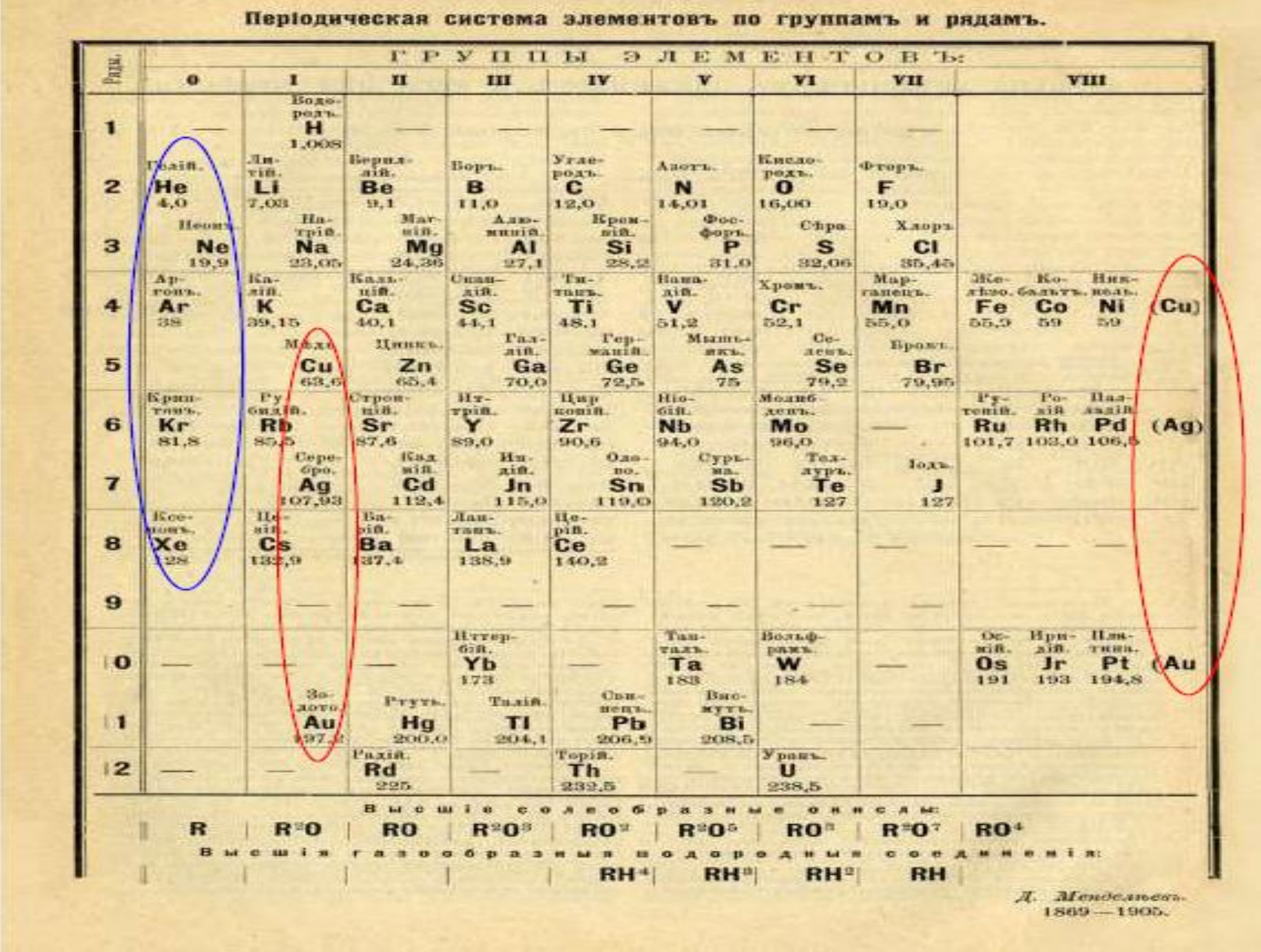


Таблица 13

Изображение периодической таблицы элементов в системе координат (по Д. И. Менделееву) с нулевой группой в качестве оси абсцисс

"Periodic system of elements by groups and rows"



Періодическая система элементовъ по группамъ и рядамъ.

Ряды	0	I	II	III	IV	V	VI	VII	VIII
	ГРУППЫ ЭЛЕМЕНТОВЪ:								
1	—	Водородъ. **H** 1,008	—	—	—	—	—	—	
2	Гелій. **He** 4,0	Литій. **Li** 7,03	Бериллій. **Be** 9,1	Боръ. **B** 11,0	Углеродъ. **C** 12,0	Азотъ. **N** 14,01	Кислородъ. **O** 16,00	Фторъ. **F** 19,0	
3	Неонъ. **Ne** 19,9	Натрій. **Na** 23,05	Магній. **Mg** 24,36	Алюминій. **Al** 27,1	Кремній. **Si** 28,2	Фосфоръ. **P** 31,0	Сѣра. **S** 32,06	Хлоръ. **Cl** 35,45	
4	Аргонъ. **Ar** 38	Калій. **K** 39,15	Кальцій. **Ca** 40,1	Скандій. **Sc** 44,1	Титанъ. **Ti** 48,1	Ванадій. **V** 51,2	Хромъ. **Cr** 52,1	Марганецъ. **Mn** 55,0	Желѣзо. **Fe** 55,9 Кобальтъ. **Co** 59 Никкель. **Ni** 59 **(Cu)**
5		Мѣдь. **Cu** 63,6	Цинкъ. **Zn** 65,4	Галлій. **Ga** 70,0	Германій. **Ge** 72,5	Мышьякъ. **As** 75	Селенъ. **Se** 79,2	Бромъ. **Br** 79,95	
6	Криптонъ. **Kr** 81,8	Рубидій. **Rb** 85,5	Стронцій. **Sr** 87,6	Иттрій. **Y** 89,0	Цирконій. **Zr** 90,6	Ніобій. **Nb** 94,0	Молибденъ. **Mo** 96,0	—	Рутеній. **Ru** 101,7 Родій **Rh** 103,0 Палладій. **Pd** 106,5 **(Ag)**
7		Серебро. **Ag** 107,93	Кадмій. **Cd** 112,4	Индій. **Jn** 115,0	Олово. **Sn** 119,0	Сурьма. **Sb** 120,2	Теллуръ. **Te** 127	Іодъ. **J** 127	
8	Ксенонъ. **Xe** 128	Цезій. **Cs** 132,9	Барій. **Ba** 137,4	Лантанъ. **La** 138,9	Церій. **Ce** 140,2	—	—	—	— — —
9		—	—	—	—	—	—	—	
10	—	—	—	Иттербій. **Yb** 173	—	Танталъ. **Ta** 183	Вольфрамъ. **W** 184	—	Осмій. **Os** 191 Иридій. **Jr** 193 Платина. **Pt** 194,8 **(Au)**
11		Золото. **Au** 197,2	Ртуть. **Hg** 200,0	Таллій. **Tl** 204,1	Свинецъ. **Pb** 206,9	Висмутъ. **Bi** 208,5	—	—	
12	—	—	Радій. **Rd** 225	—	Торій. **Th** 232,5	—	Уранъ. **U** 238,5		

Высшіе солеобразные окислы:

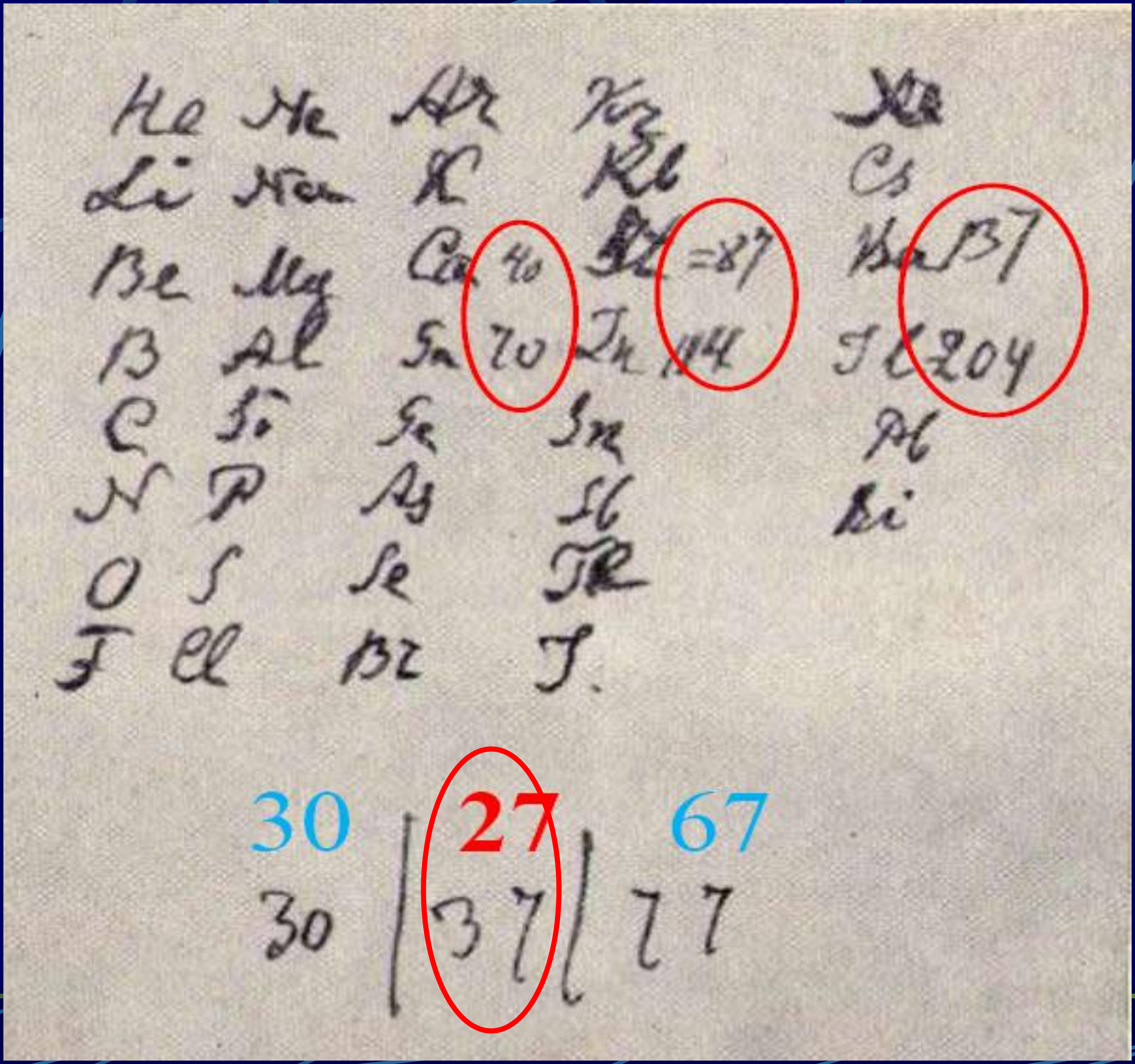
0	I	II	III	IV	V	VI	VII	VIII
R	R^2O	RO	R^2O^3	RO^2	R^2O^5	RO^3	R^2O^7	RO^4

Высшія газообразныя водородныя соединенія:

0	I	II	III	IV	V	VI	VII
				RH^4	RH^3	RH^2	RH

Д. Менделѣевъ.
1869 — 1905.

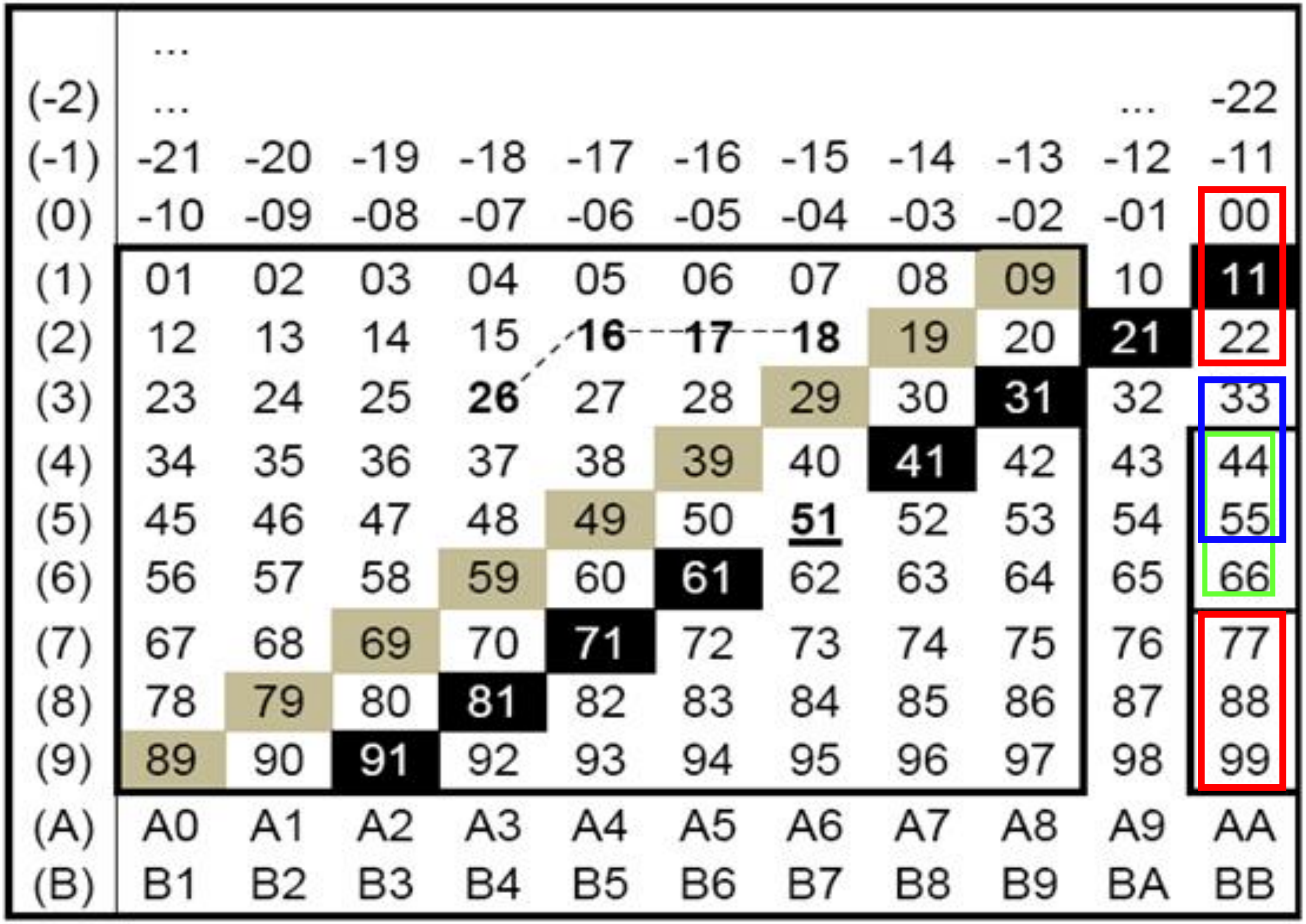
Mendeleev's „error", which it is not



He	Ne	Ar	Kr	Xe
Li	Na	K	Rb	Cs
Be	Mg	Ca 40	Sr =87	Ba 137
B	Al	Ga 70	In 114	Tl 204
C	Si	Ge	Sn	Pb
N	P	As	Sb	Bi
O	S	Se	Te	
F	Cl	Br	J.	

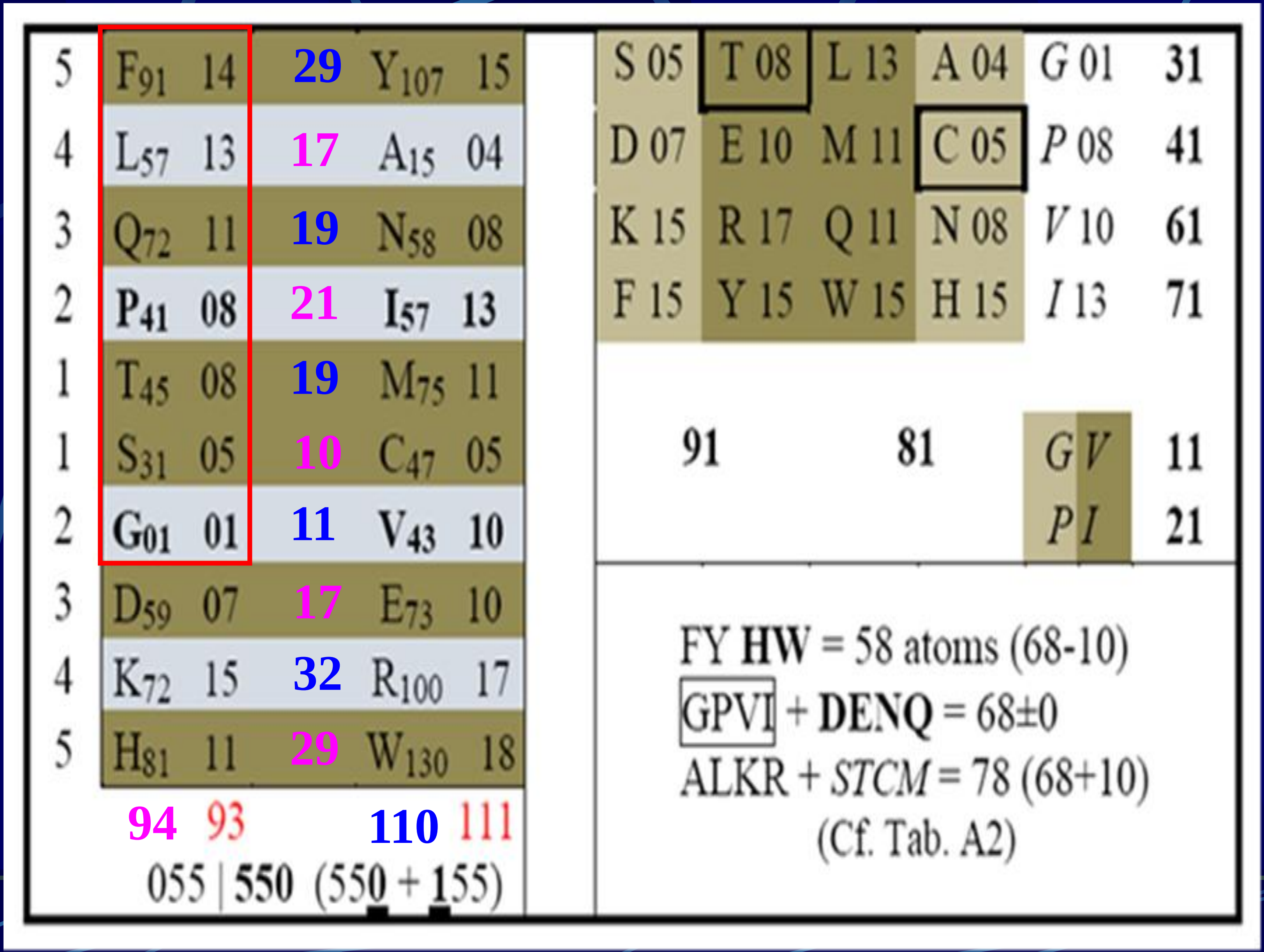
30	27	67
30	37	77

Periodic System of Numbers (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
(A)	A0	A1	A2	A3	A4	A5	A6	A7	A8	A9	AA
(B)	B1	B2	B3	B4	B5	B6	B7	B8	B9	BA	BB

Determination by Golden Mean and PSN (CIPS) [MMR, 2019, Fig. 1)



5	F_{91}	14	29	Y_{107}	15
4	L_{57}	13	17	A_{15}	04
3	Q_{72}	11	19	N_{58}	08
2	**P_{41}**	**08**	21	**I_{57}**	**13**
1	T_{45}	08	19	M_{75}	11
1	S_{31}	05	10	C_{47}	05
2	**G_{01}**	**01**	11	**V_{43}**	**10**
3	D_{59}	07	17	E_{73}	10
4	K_{72}	15	32	R_{100}	17
5	H_{81}	11	29	W_{130}	18
	94	93		110	111

055 | **550** (550 + 155)

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 15	Y 15	W 15	H 15	*I* 13	71
	91		81	*G V*	11
				P I	21

FY **HW** = 58 atoms (68-10)

$\boxed{\text{GPVI}}$ + **DENQ** = 68±0

ALKR + *STCM* = 78 (68+10)

(Cf. Tab. A2)

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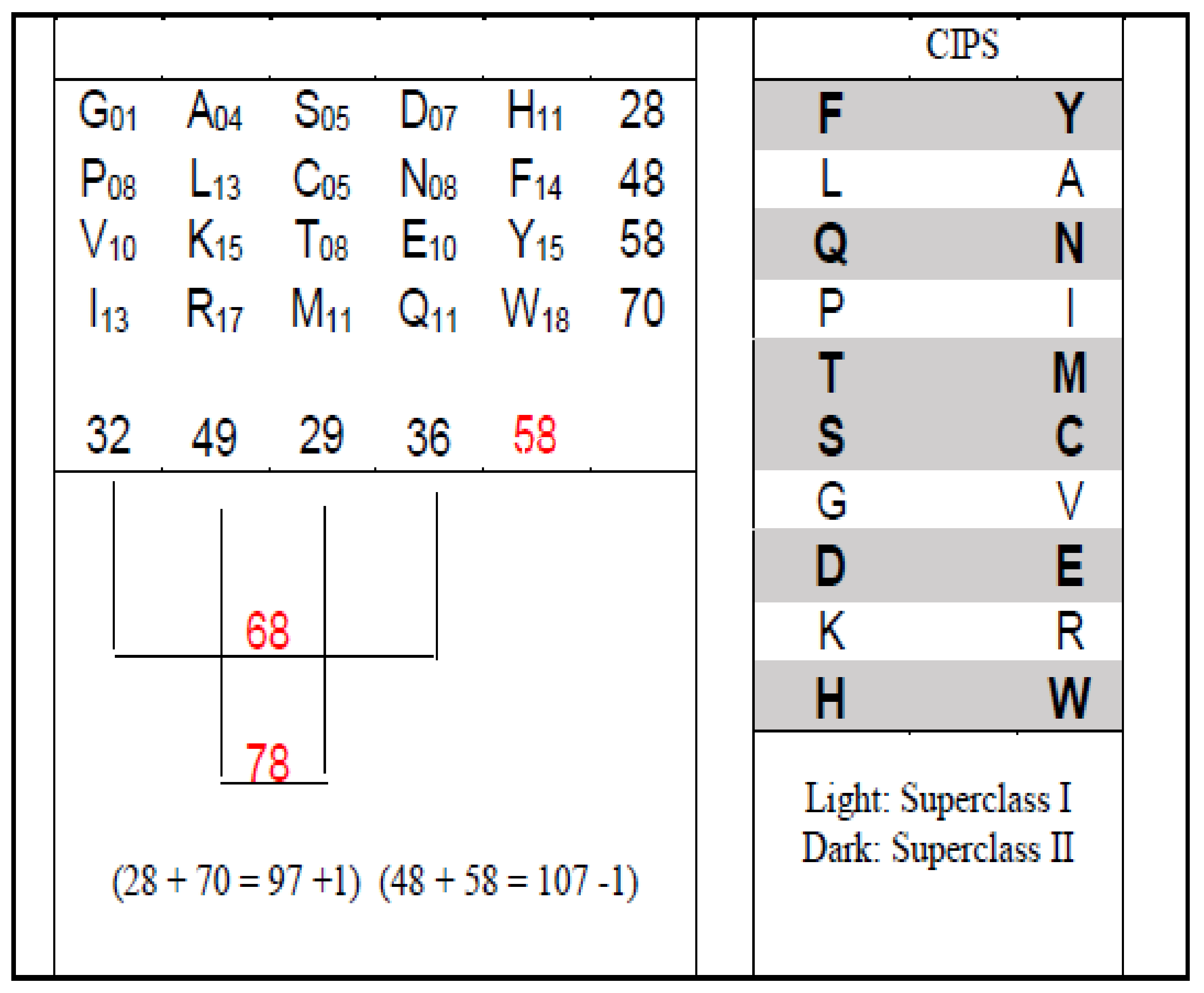
CIPS: Cyclic Invariant Periodic System of AAs (MMR, 2019, Fig. 1))



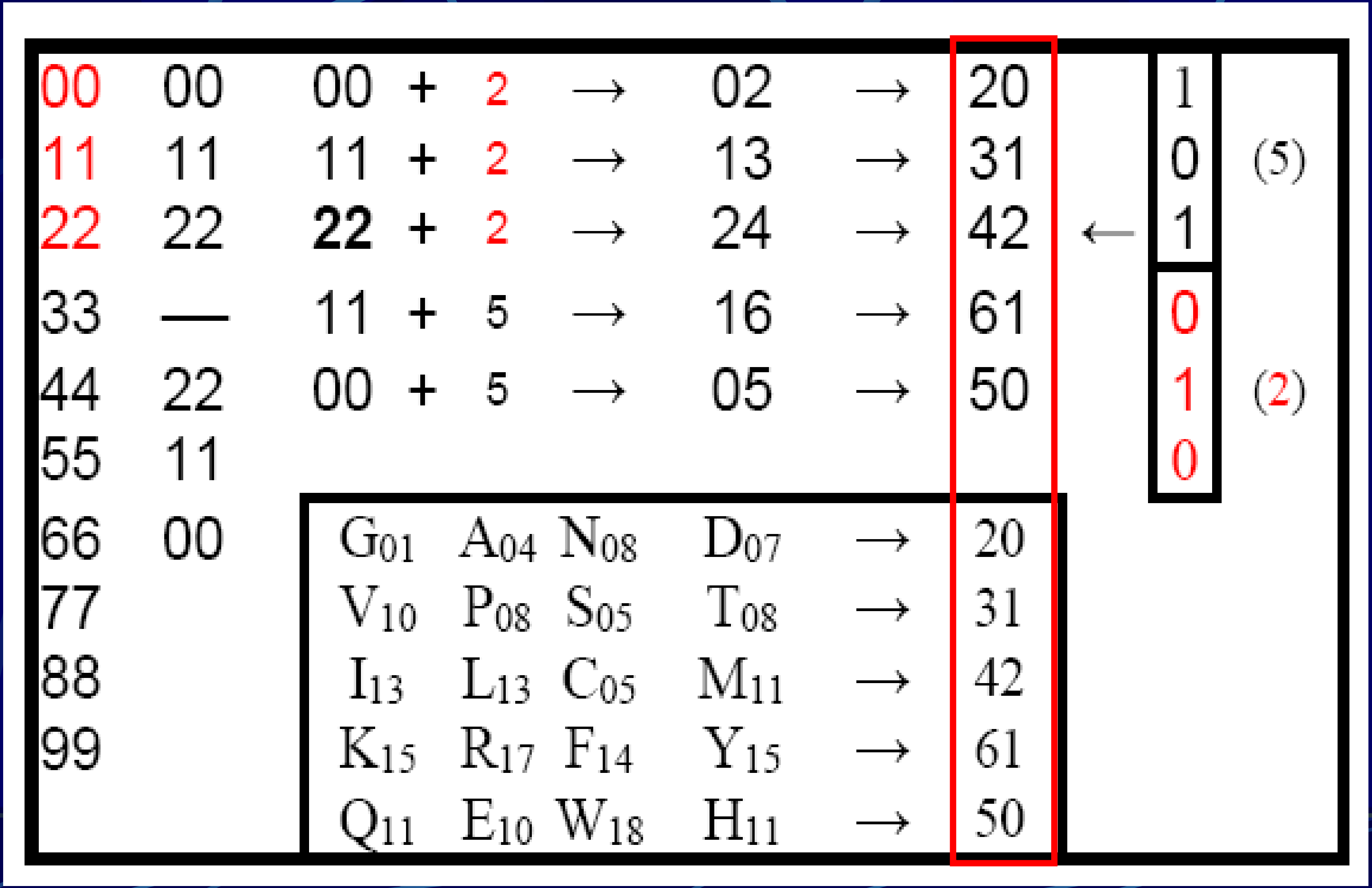
G_{01}	A_{04}	S_{05}	D_{07}	H_{11}	28
P_{08}	L_{13}	C_{05}	N_{08}	F_{14}	48
V_{10}	K_{15}	T_{08}	E_{10}	Y_{15}	58
I_{13}	R_{17}	M_{11}	Q_{11}	W_{18}	70
32	49	29	36	58	

(28 + 70 = 97 +1) (48 + 58 = 107 -1)

CIPS	
F	**Y**
L	A
Q	**N**
P	I
T	**M**
S	**C**
G	V
D	**E**
K	R
H	**W**

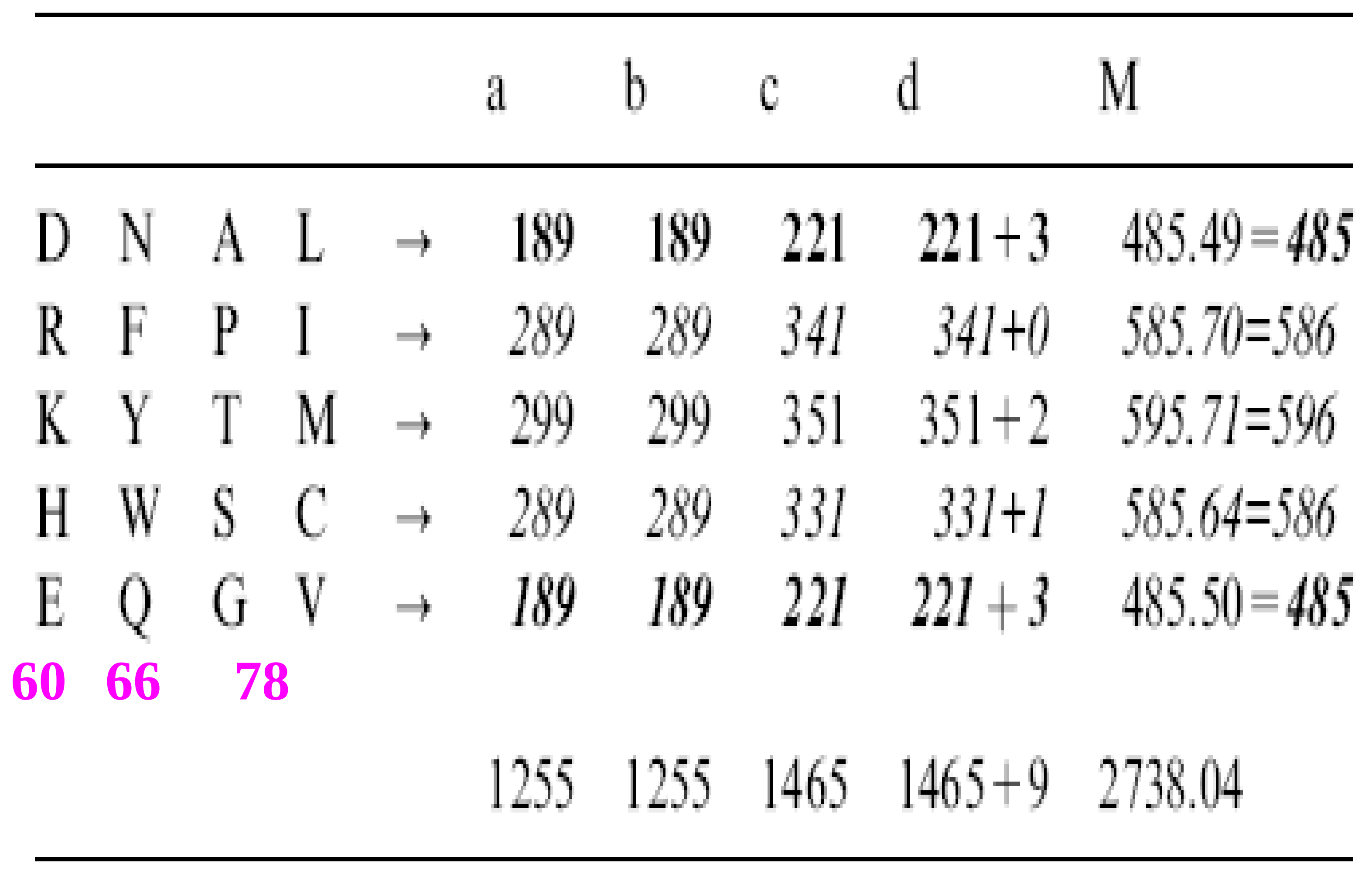
Light: Superclass I
Dark: Superclass II

The crossing of the Periodic System of numbers (of the last column) and the 6-bit binary tree (of the path of the greatest change)



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			
88		I_{13} L_{13} C_{05}		M_{11}	→	42			
99		K_{15} R_{17} F_{14}		Y_{15}	→	61			
		Q_{11} E_{10} W_{18}		H_{11}	→	50			

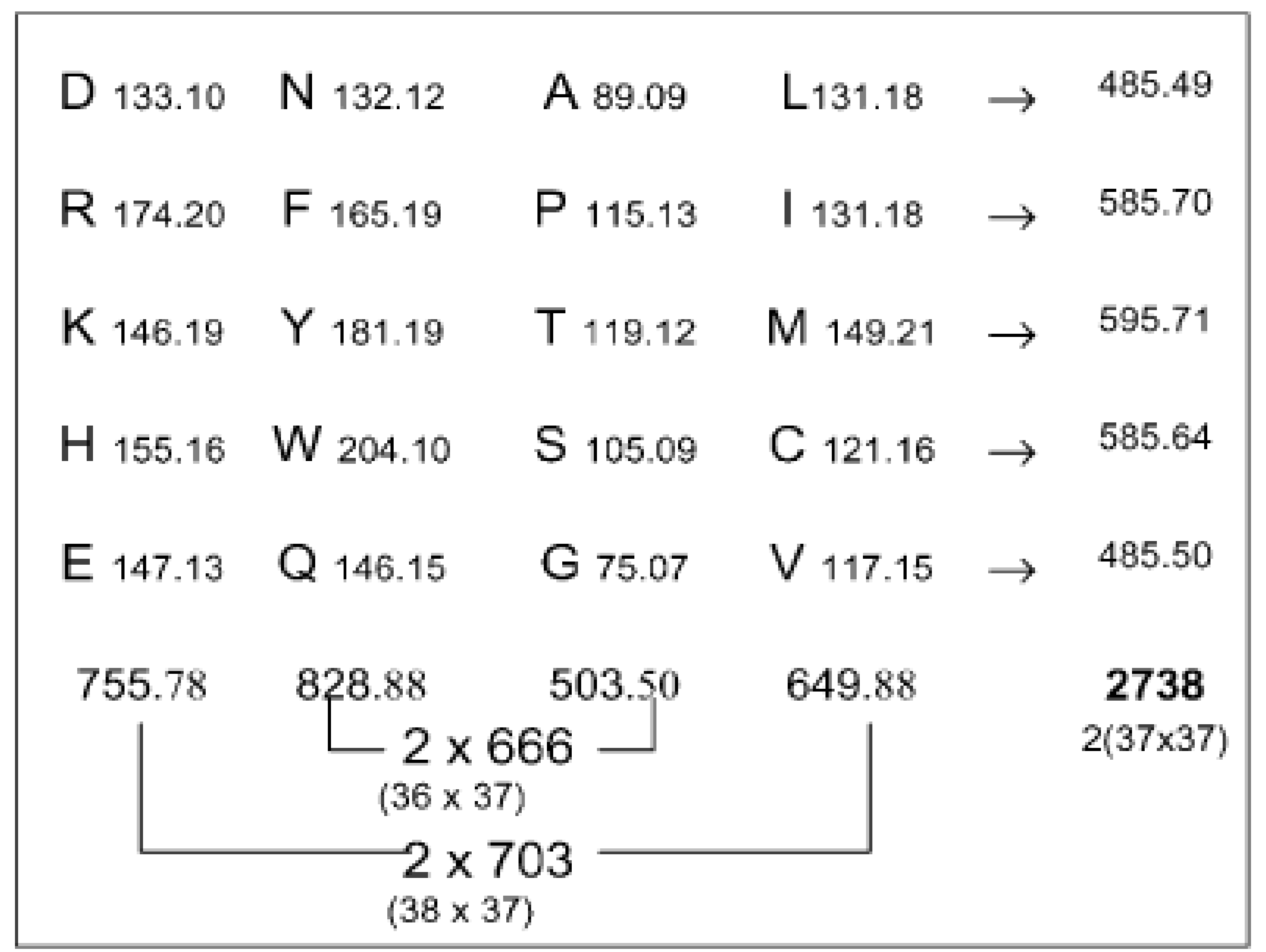
A harmonic structure of the genetic code (MMR, 2004a)



					a	b	c	d	M
D	N	A	L	→	189	189	221	221+3	485.49=485
R	F	P	I	→	289	289	341	341+0	585.70=586
K	Y	T	M	→	299	299	351	351+2	595.71=596
H	W	S	C	→	289	289	331	331+1	585.64=586
E	Q	G	V	→	189	189	221	221+3	485.50=485
60	66	78							
					1255	1255	1465	1465+9	2738.04

Molecules mass in harmonic structure of GC

[MMR, 2004a, Tab. 2, p. 223]

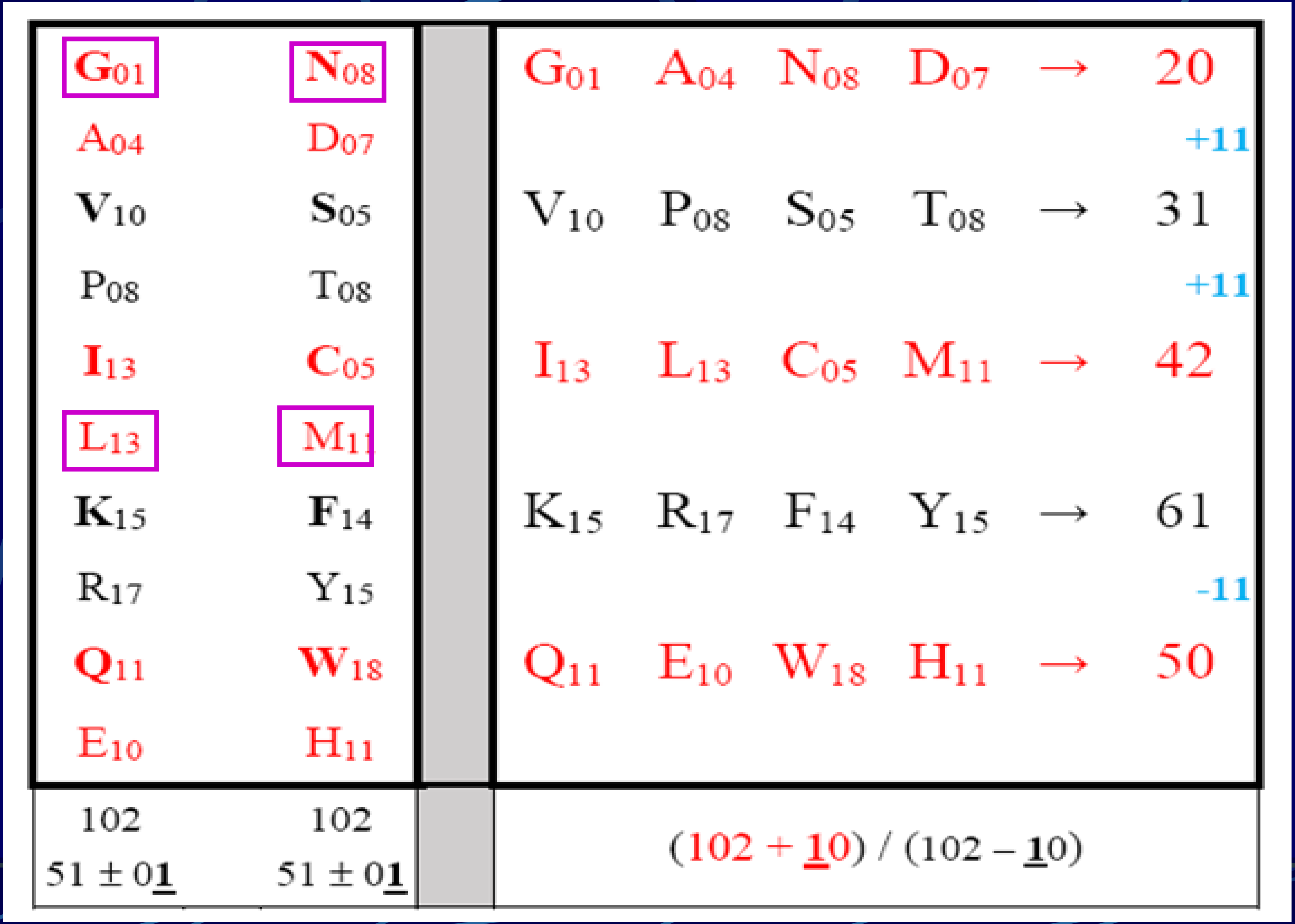


D 133.10	N 132.12	A 89.09	L131.18	→	485.49
R 174.20	F 165.19	P 115.13	I 131.18	→	585.70
K 146.19	Y 181.19	T 119.12	M 149.21	→	595.71
H 155.16	W 204.10	S 105.09	C 121.16	→	585.64
E 147.13	Q 146.15	G 75.07	V 117.15	→	485.50
755.78	828.88	503.50	649.88		**2738** 2(37x37)

2 x 666
(36 x 37)

2 x 703
(38 x 37)

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

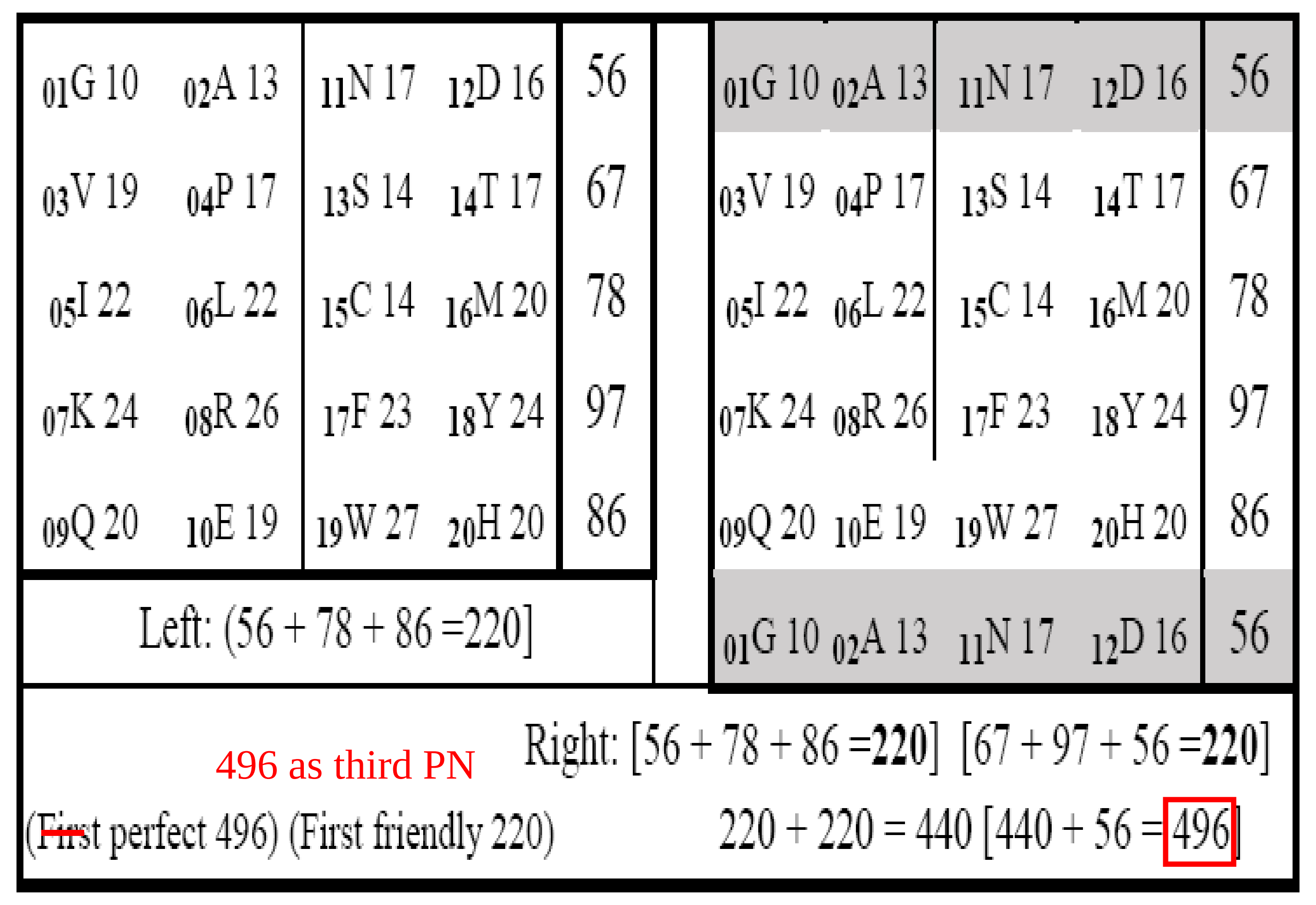


G_{01}	N_{08}
A_{04}	D_{07}
V_{10}	S_{05}
P_{08}	T_{08}
I_{13}	C_{05}
L_{13}	M_{11}
K_{15}	F_{14}
R_{17}	Y_{15}
Q_{11}	W_{18}
E_{10}	H_{11}
102 51 ± 0$\underline{1}$	102 51 ± 0$\underline{1}$

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
K_{15}	R_{17}	F_{14}	Y_{15}	→	61
					-11
Q_{11}	E_{10}	W_{18}	H_{11}	→	50

$(102 + \underline{1}0) / (102 - \underline{1}0)$

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



$_{01}$G 10	$_{02}$A 13	$_{11}$N 17	$_{12}$D 16	56
$_{03}$V 19	$_{04}$P 17	$_{13}$S 14	$_{14}$T 17	67
$_{05}$I 22	$_{06}$L 22	$_{15}$C 14	$_{16}$M 20	78
$_{07}$K 24	$_{08}$R 26	$_{17}$F 23	$_{18}$Y 24	97
$_{09}$Q 20	$_{10}$E 19	$_{19}$W 27	$_{20}$H 20	86

Left: (56 + 78 + 86 =220]

$_{01}$G 10	$_{02}$A 13	$_{11}$N 17	$_{12}$D 16	56
$_{03}$V 19	$_{04}$P 17	$_{13}$S 14	$_{14}$T 17	67
$_{05}$I 22	$_{06}$L 22	$_{15}$C 14	$_{16}$M 20	78
$_{07}$K 24	$_{08}$R 26	$_{17}$F 23	$_{18}$Y 24	97
$_{09}$Q 20	$_{10}$E 19	$_{19}$W 27	$_{20}$H 20	86
$_{01}$G 10	$_{02}$A 13	$_{11}$N 17	$_{12}$D 16	56

496 as third PN

Right: [56 + 78 + 86 =**220**] [67 + 97 + 56 =**220**]

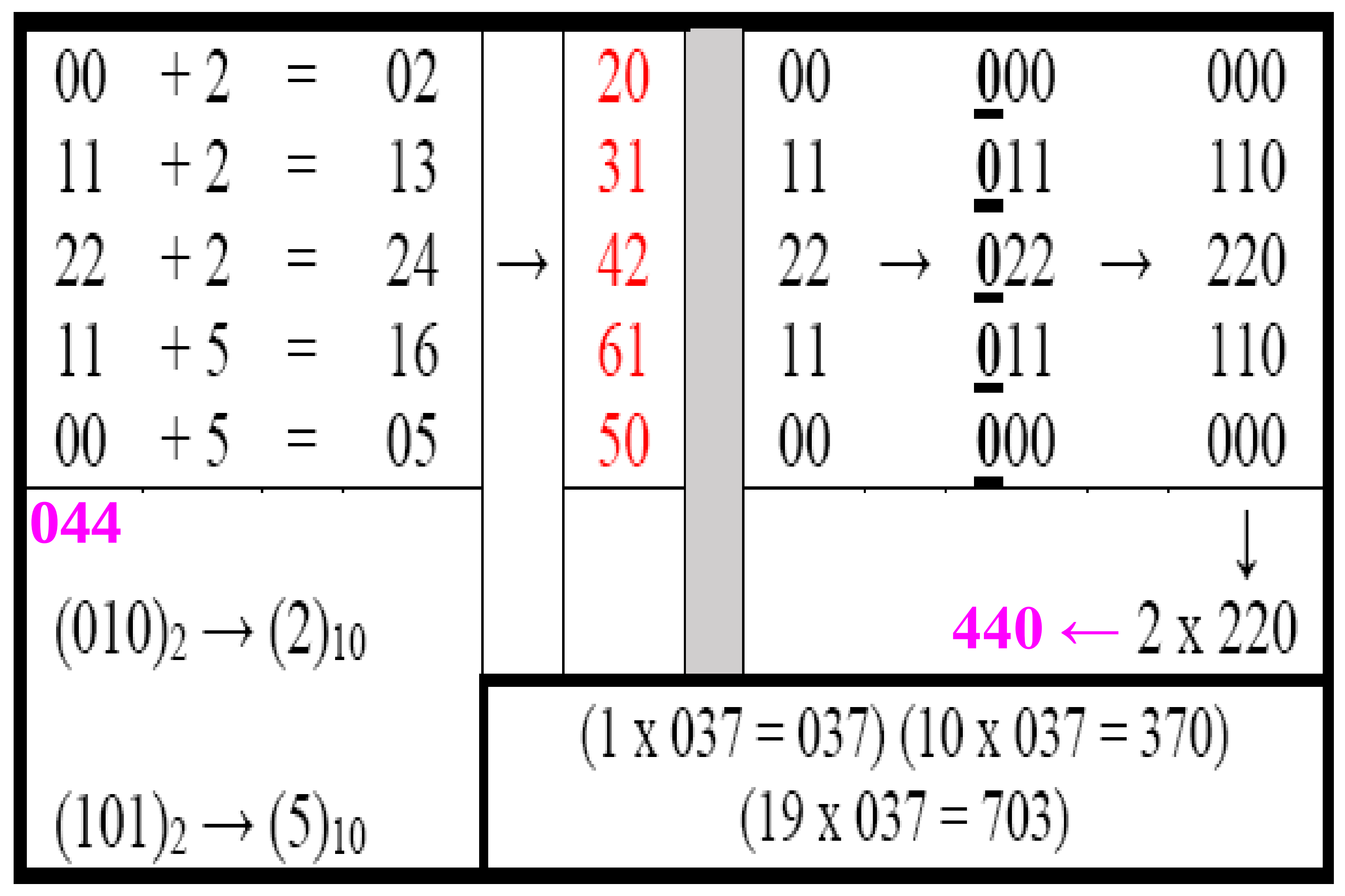
(~~First~~ perfect 496) (First friendly 220)

220 + 220 = 440 [440 + 56 = 496]

Inversion:

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

Two-digit numbers understood as three-digit, analogous to Shcherbak's Prime-quantum 037



00 + 2 = 02		20	00		$\underline{0}00$		000
11 + 2 = 13		31	11		$\underline{0}11$		110
22 + 2 = 24	→	42	22	→	$\underline{0}22$	→	220
11 + 5 = 16		61	11		$\underline{0}11$		110
00 + 5 = 05		50	00		$\underline{0}00$		000

044

$(010)_2 \rightarrow (2)_{10}$

$(101)_2 \rightarrow (5)_{10}$

↓

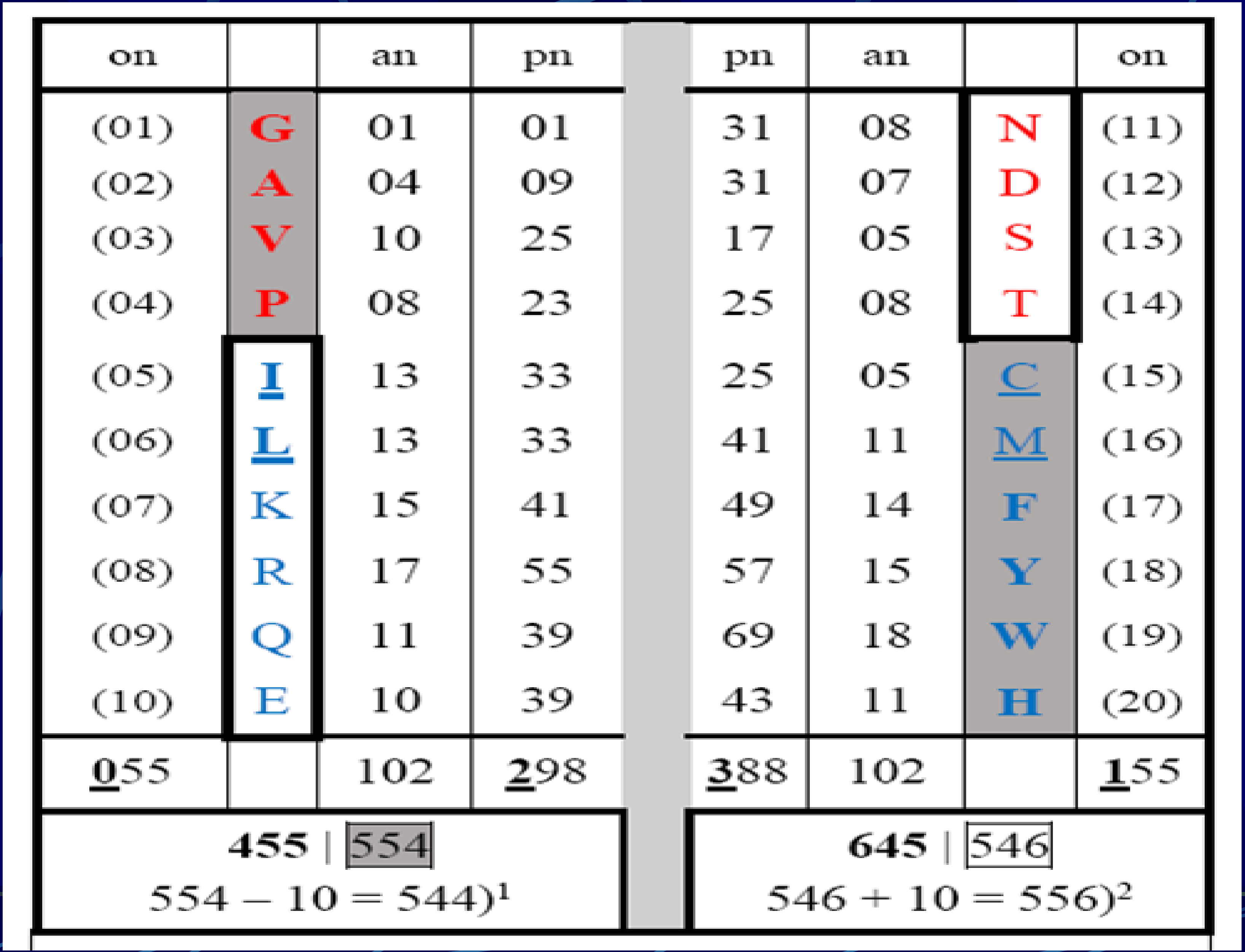
440 ← 2 x 220

(1 x 037 = 037) (10 x 037 = 370)

(19 x 037 = 703)

044 + 440 = 44 x 11

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



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	298		388	102		155

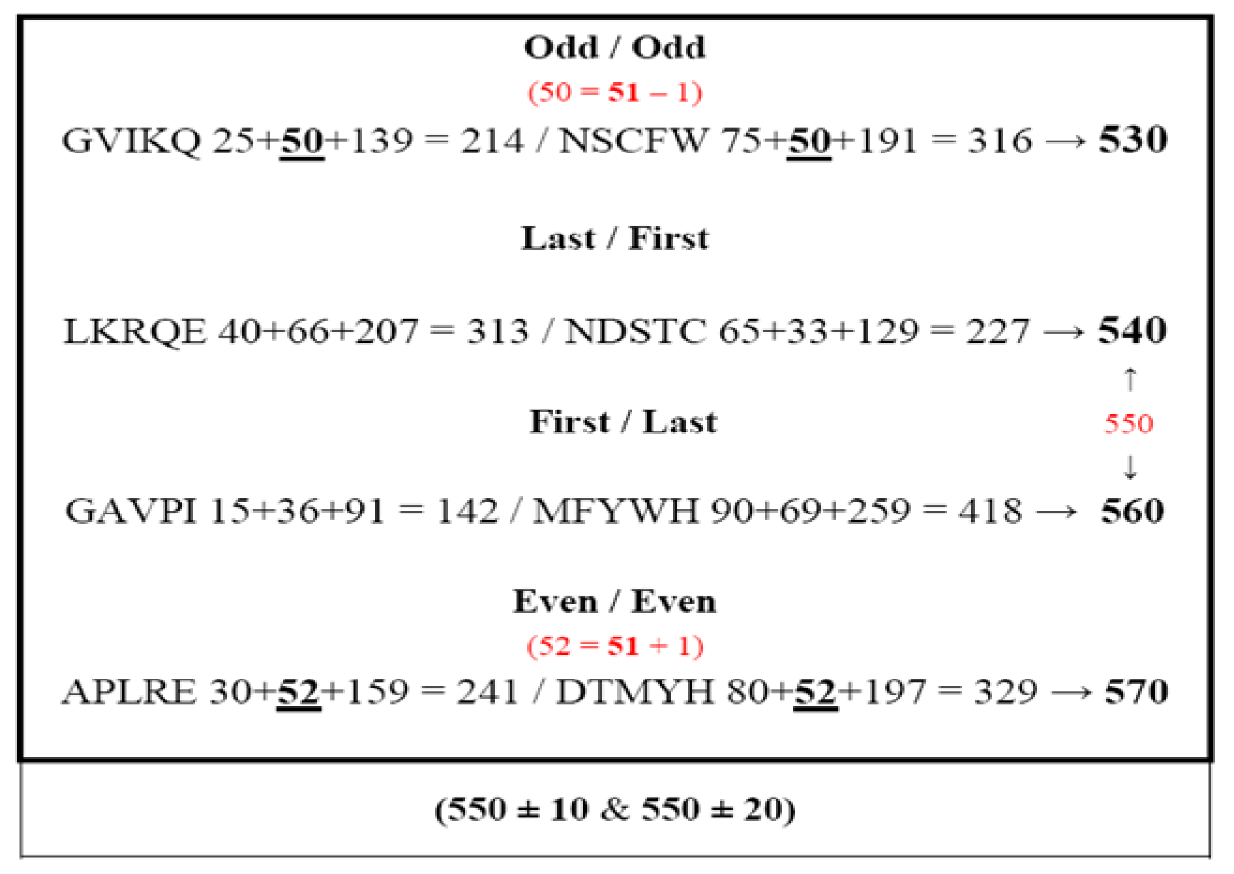
455 | 554

554 – 10 = 544)[1]

645 | 546

546 + 10 = 556)[2]

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



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**

↑

550

↓

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**

(550 ± 10 & 550 ± 20)

[530 + 540 + 560 + 570 = 2200]

[035 + 045 + 065 + 075 = 220]

[530 + 570 = 1100]

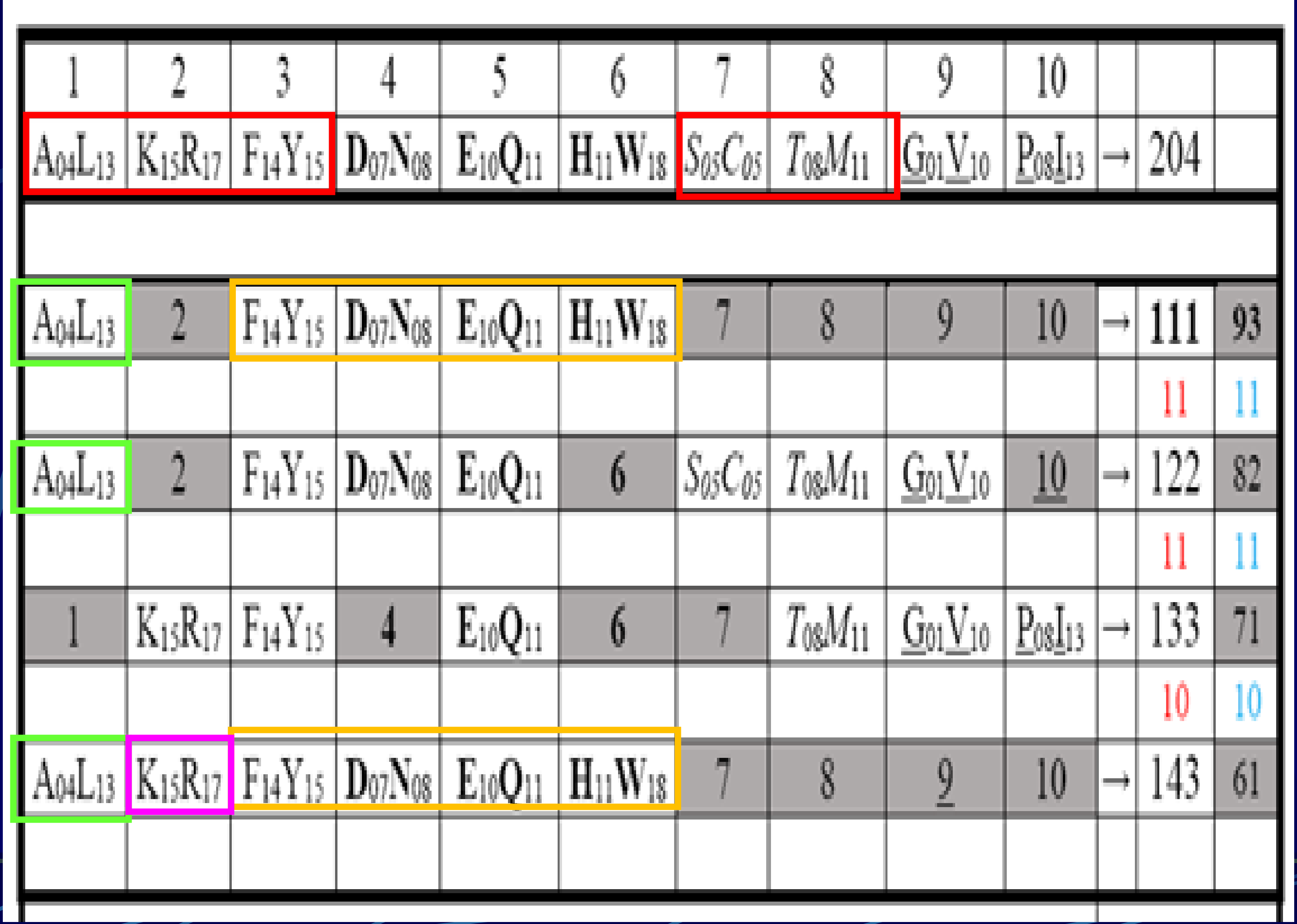
[540 + 560 = 1100]

[1100 = 5 x 220
110 = 5 x 022]

[035 + 075 = 110]

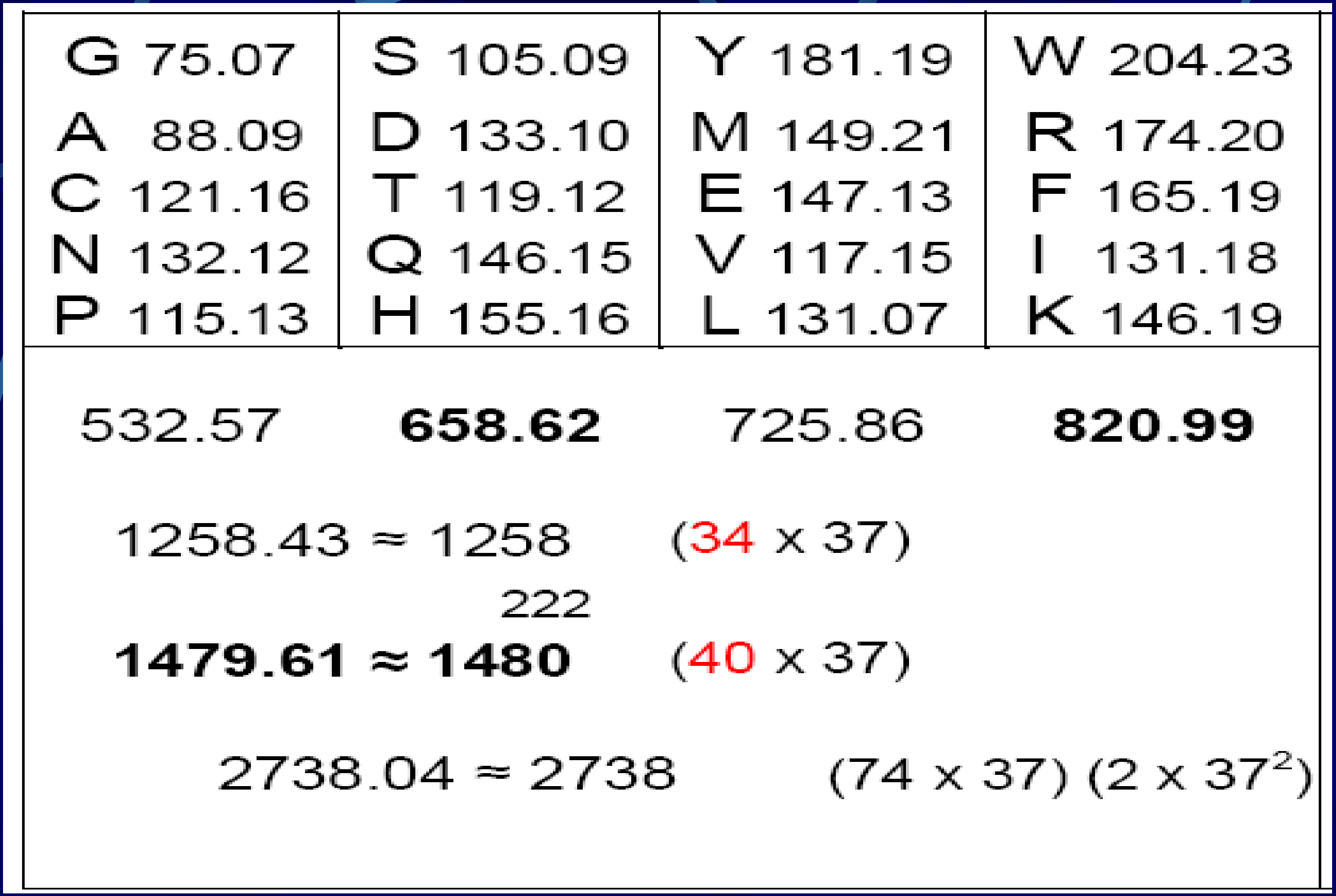
[045 + 065 = 110]

Similarity System of Amino Acid Perfect Pairs (SSAAPP)



1	2	3	4	5	6	7	8	9	10			
$A_{04}L_{13}$	$K_{15}R_{17}$	$F_{14}Y_{15}$	$D_{07}N_{08}$	$E_{10}Q_{11}$	$H_{11}W_{18}$	$S_{05}C_{05}$	$T_{08}M_{11}$	$\underline{G}_{01}\underline{V}_{10}$	$\underline{P}_{08}\underline{I}_{13}$	→	204	
$A_{04}L_{13}$	2	$F_{14}Y_{15}$	$D_{07}N_{08}$	$E_{10}Q_{11}$	$H_{11}W_{18}$	7	8	9	10	→	111	93
											11	11
$A_{04}L_{13}$	2	$F_{14}Y_{15}$	$D_{07}N_{08}$	$E_{10}Q_{11}$	6	$S_{05}C_{05}$	$T_{08}M_{11}$	$\underline{G}_{01}\underline{V}_{10}$	$\underline{10}$	→	122	82
											11	11
1	$K_{15}R_{17}$	$F_{14}Y_{15}$	4	$E_{10}Q_{11}$	6	7	$T_{08}M_{11}$	$\underline{G}_{01}\underline{V}_{10}$	$\underline{P}_{08}\underline{I}_{13}$	→	133	71
											10	10
$A_{04}L_{13}$	$K_{15}R_{17}$	$F_{14}Y_{15}$	$D_{07}N_{08}$	$E_{10}Q_{11}$	$H_{11}W_{18}$	7	8	$\underline{9}$	10	→	143	61

The result of crossing of four types of diversity of AAs and PSN (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
532.57	**658.62**	725.86	**820.99**

1258.43 ≈ 1258 (34 x 37)

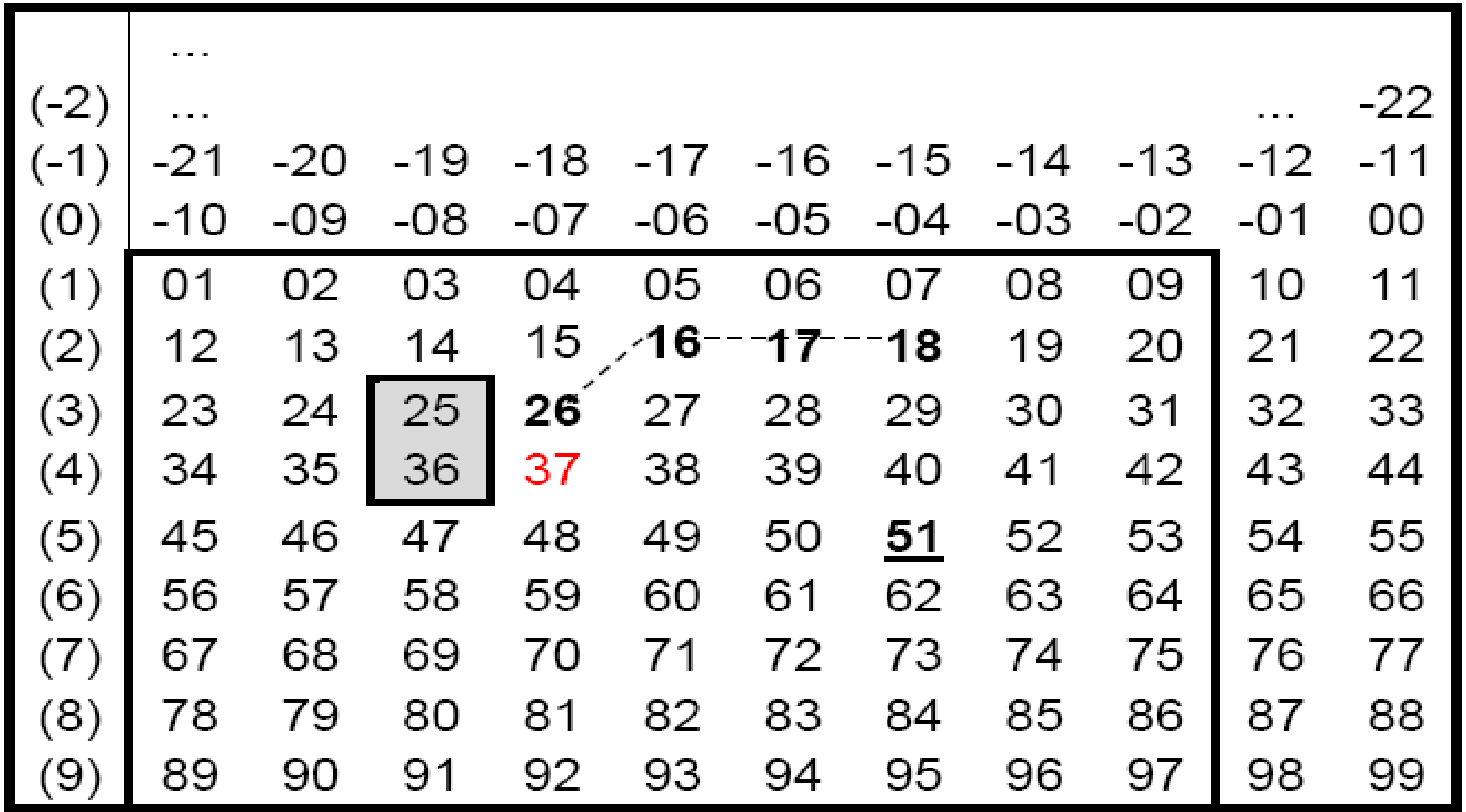
222

1479.61 ≈ 1480 (40 x 37)

2738.04 ≈ 2738 (74 x 37) (2 x 37^2)

Molecules mass in four types of diversity of AAs (MMR, 2013b, Tab. 7)

Quantitative relations in PSN (I)



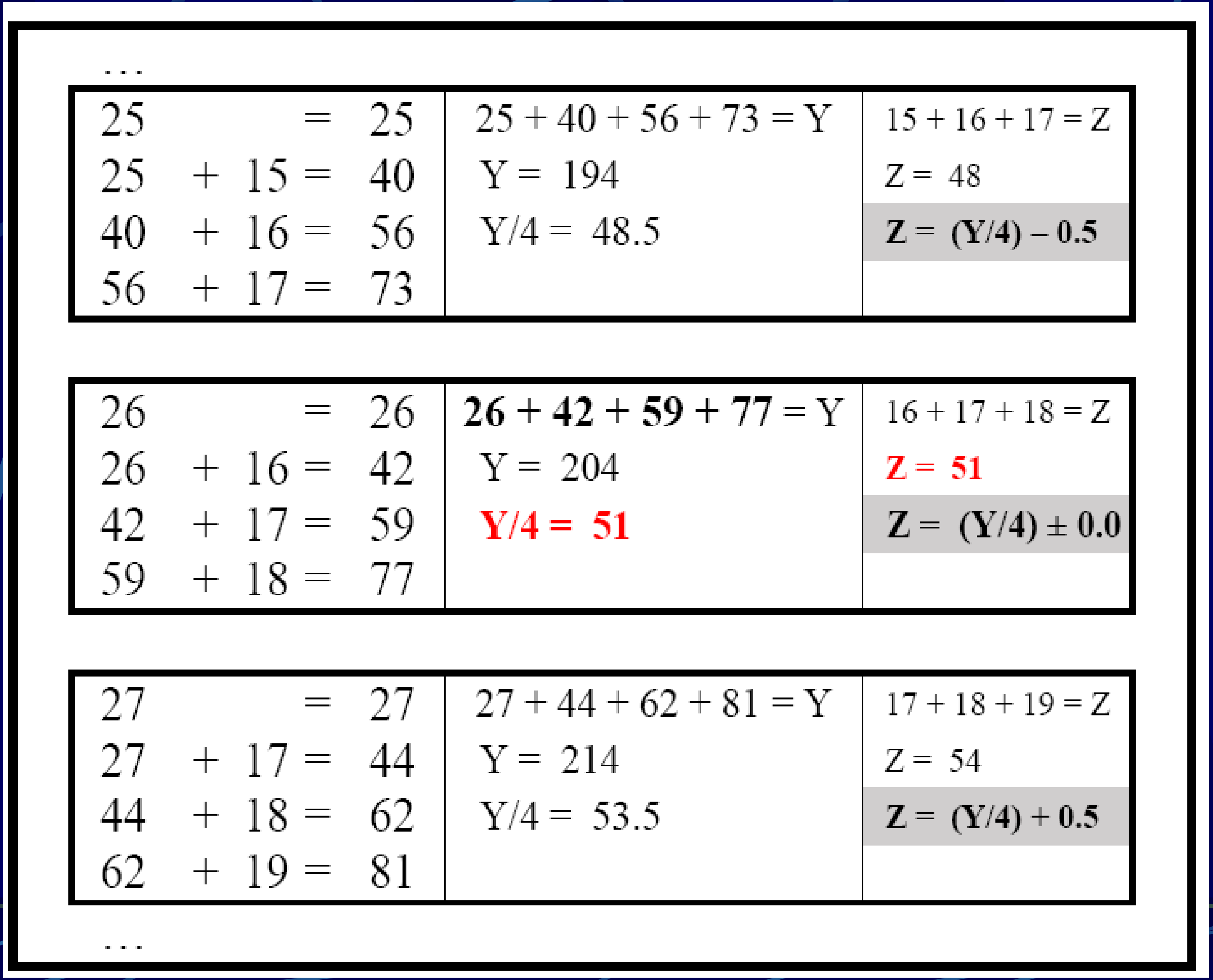
	...										
(-2)	...									...	-22
(-1)	-21	-20	-19	-18	-17	-16	-15	-14	-13	-12	-11
(0)	-10	-09	-08	-07	-06	-05	-04	-03	-02	-01	00
(1)	01	02	03	04	05	06	07	08	09	10	11
(2)	12	13	14	15	**16**	**17**	**18**	19	20	21	22
(3)	23	24	25	**26**	27	28	29	30	31	32	33
(4)	34	35	36	37	38	39	40	41	42	43	44
(5)	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

15 = 15
15 + 05 = 20
20 + 06 = 26
26 + 07 = 33

26 = 26
26 + 16 = 42
42 + 17 = 59
59 + 18 = 77

37 = 37
37 + 27 = 64
64 + 28 = 92
92 + 29 = 121

Quantitative relations in PSN (II)



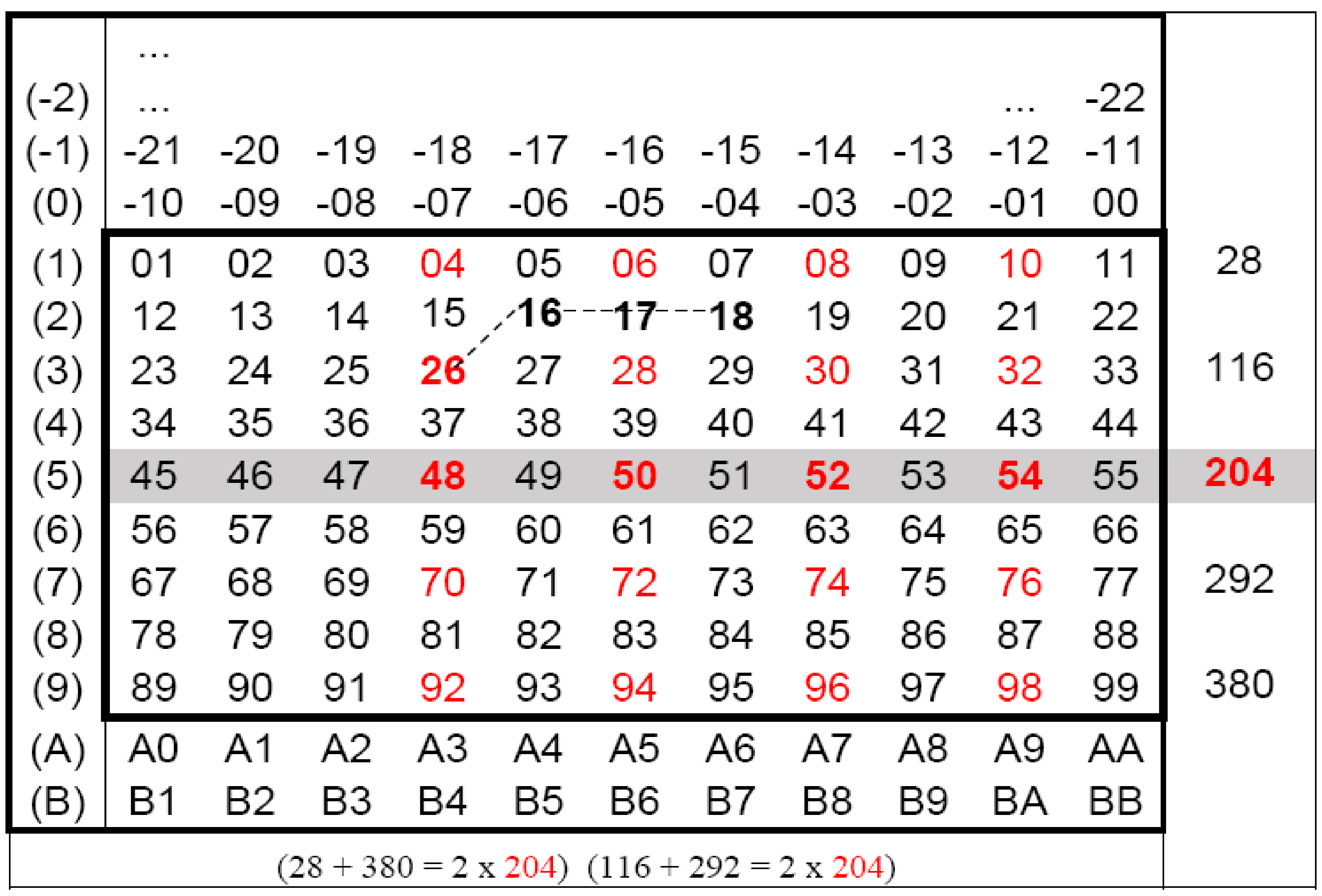
…

25 = 25	25 + 40 + 56 + 73 = Y	15 + 16 + 17 = Z
25 + 15 = 40	Y = 194	Z = 48
40 + 16 = 56	Y/4 = 48.5	**Z = (Y/4) – 0.5**
56 + 17 = 73		

26 = 26	**26 + 42 + 59 + 77** = Y	16 + 17 + 18 = Z
26 + 16 = 42	Y = 204	**Z = 51**
42 + 17 = 59	**Y/4 = 51**	**Z = (Y/4) ± 0.0**
59 + 18 = 77		

27 = 27	27 + 44 + 62 + 81 = Y	17 + 18 + 19 = Z
27 + 17 = 44	Y = 214	Z = 54
44 + 18 = 62	Y/4 = 53.5	**Z = (Y/4) + 0.5**
62 + 19 = 81		

…

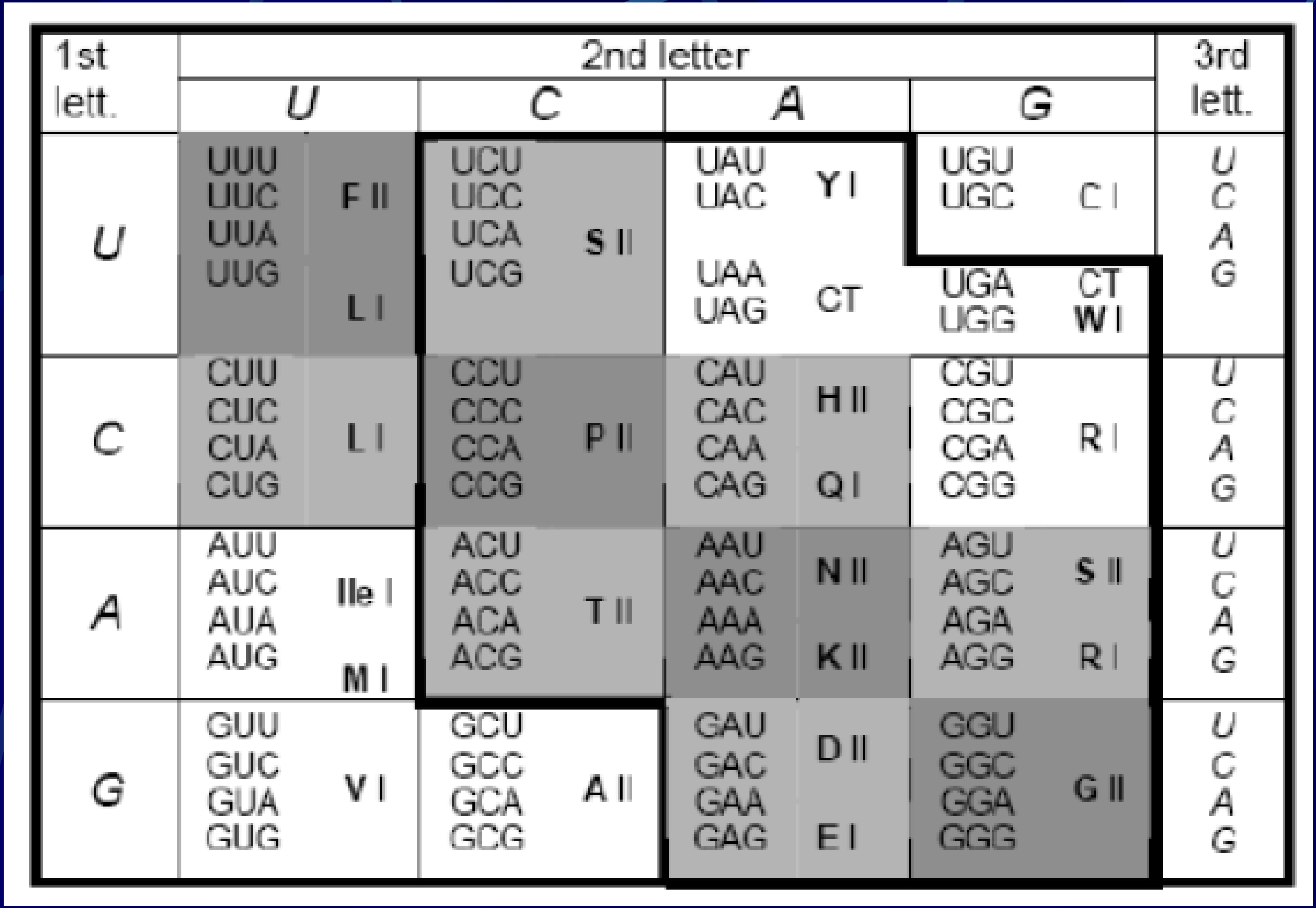


	...											
(-2)	...									...	-22	
(-1)	-21	-20	-19	-18	-17	-16	-15	-14	-13	-12	-11	
(0)	-10	-09	-08	-07	-06	-05	-04	-03	-02	-01	00	
(1)	01	02	03	04	05	06	07	08	09	10	11	28
(2)	12	13	14	15	**16**	**17**	**18**	19	20	21	22	
(3)	23	24	25	**26**	27	28	29	30	31	32	33	116
(4)	34	35	36	37	38	39	40	41	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
(A)	A0	A1	A2	A3	A4	A5	A6	A7	A8	A9	AA	
(B)	B1	B2	B3	B4	B5	B6	B7	B8	B9	BA	BB	

(28 + 380 = 2 x 204) (116 + 292 = 2 x 204)

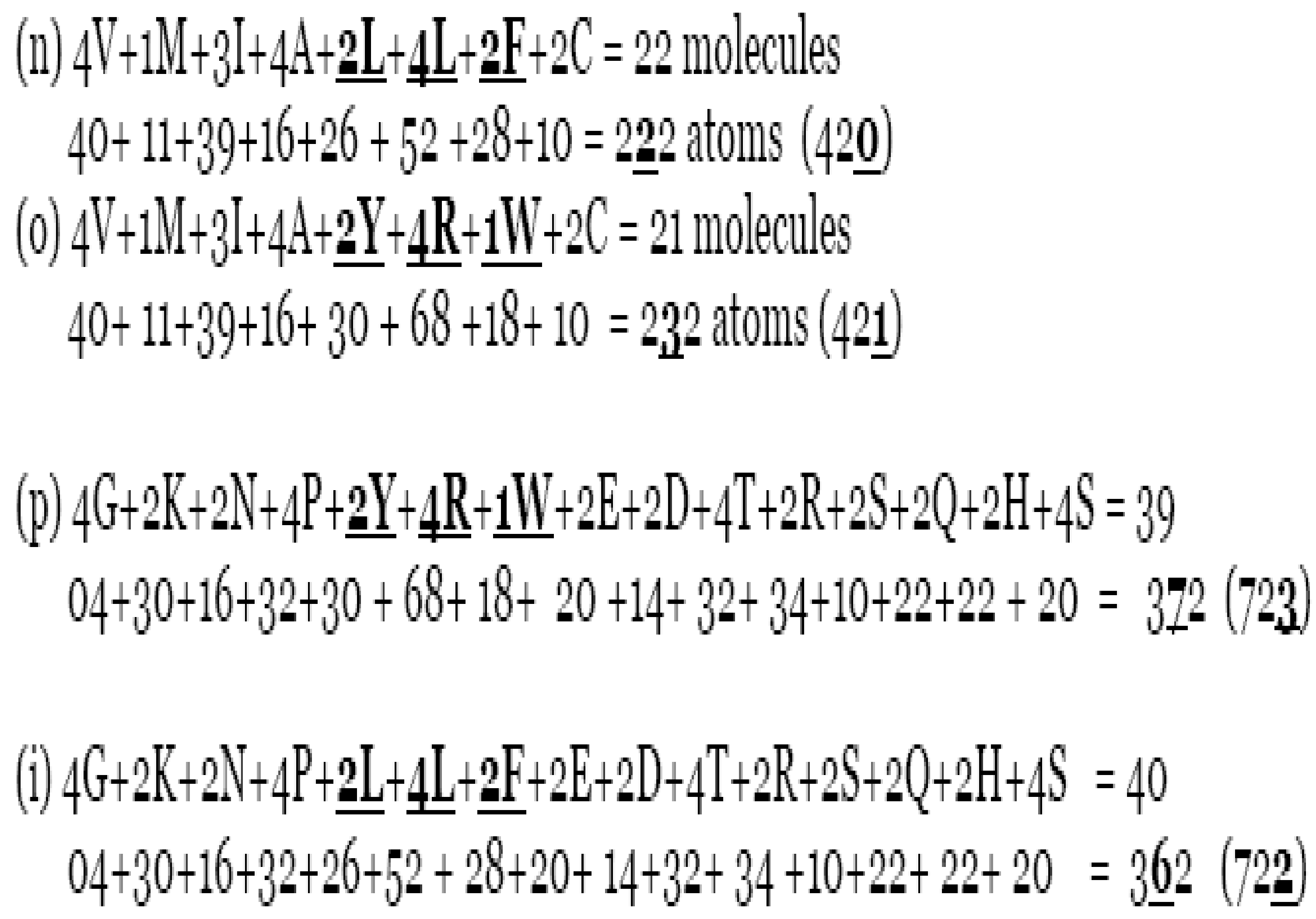
	...											
(-2)	...									...	-22	
(-1)	-21	-20	-19	-18	-17	-16	-15	-14	-13	-12	-11	
(0)	-10	-09	-08	-07	-06	-05	-04	-03	-02	-01	00	
(1)	01	02	03	04	05	06	07	08	09	10	11	
(2)	12	13	14	15	**16**	**17**	**18**	19	20	21	22	30
(3)	23	24	25	**26**	27	28	29	30	31	32	33	
(4)	**34**	35	**36**	37	**38**	39	**40**	41	42	43	44	**74 x 2**
(5)	45	46	47	48	49	50	51	52	53	54	55	
(6)	56	57	58	59	60	61	62	63	64	65	66	118
(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	
(A)	A0	A1	A2	A3	A4	A5	A6	A7	A8	A9	AA	
(B)	B1	B2	B3	B4	B5	B6	B7	B8	B9	BA	BB	

(30 + 118 = 74 x 2)



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

“The relations of amino acids positions within GCT and their polarity” (II)



(n) 4V+1M+3I+4A+$\underline{\mathbf{2L}}$+$\underline{\mathbf{4L}}$+$\underline{\mathbf{2F}}$+2C = 22 molecules

40+ 11+39+16+26 + 52 +28+10 = $2\underline{2}2$ atoms ($42\underline{\mathbf{0}}$)

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

40+ 11+39+16+ 30 + 68 +18+ 10 = $2\underline{3}2$ atoms ($42\underline{1}$)

(p) 4G+2K+2N+4P+$\underline{\mathbf{2Y}}$+$\underline{\mathbf{4R}}$+$\underline{\mathbf{1W}}$+2E+2D+4T+2R+2S+2Q+2H+4S = 39

04+30+16+32+30 + 68+ 18+ 20 +14+ 32+ 34+10+22+22 + 20 = $3\underline{7}2$ ($72\underline{3}$)

(i) 4G+2K+2N+4P+$\underline{\mathbf{2L}}$+$\underline{\mathbf{4L}}$+$\underline{\mathbf{2F}}$+2E+2D+4T+2R+2S+2Q+2H+4S = 40

04+30+16+32+26+52 + 28+20+ 14+32+ 34 +10+22+ 22+ 20 = $3\underline{6}2$ ($72\underline{2}$)

“The relations of amino acids positions within GCT and their polarity” (III)

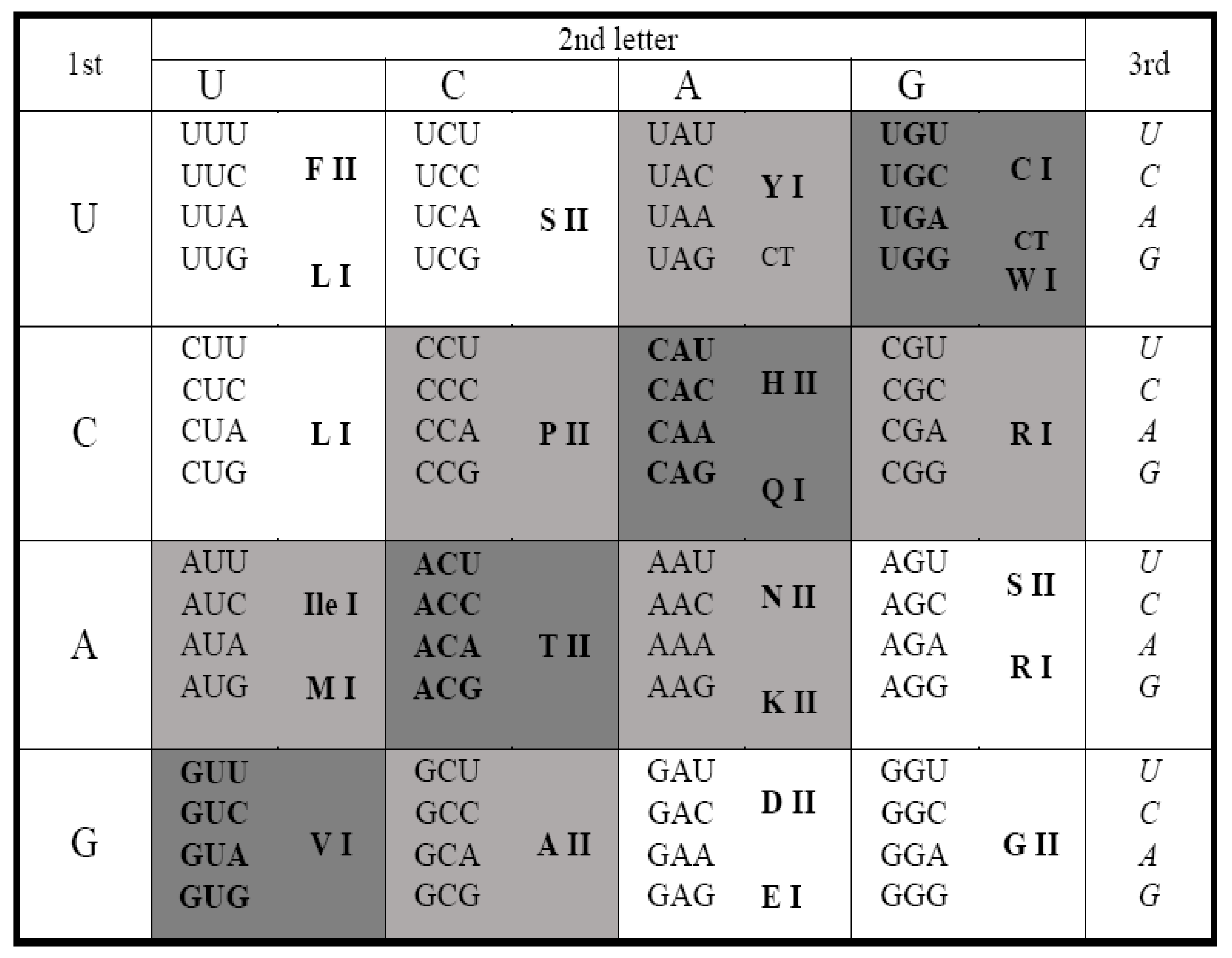
$$(n)\ F_{14}+L_{13}+L_{13}+I_{13}+M_{11}+V_{10}+A_{04}+C_{05}=8\ (\underline{8}3)\ [1\underline{5}5]$$ 22

$$(o)\ I_{13}+M_{11}+V_{10}+A_{04}+Y_{15}+C_{05}+W_{18}+R_{17}=8\ (\underline{9}3)\ [1\underline{6}5]$$ 21

$$(p)\ S_{05}+P_{08}+T_{08}+Y_{15}+H_{11}+Q_{11}+N_{08}+K_{15}+D_{07}+E_{10}+W_{18}+R_{17}+S_{05}+R_{17}+G_{01}=15\ (1\underline{5}6)\ [2\underline{9}1]$$ 39

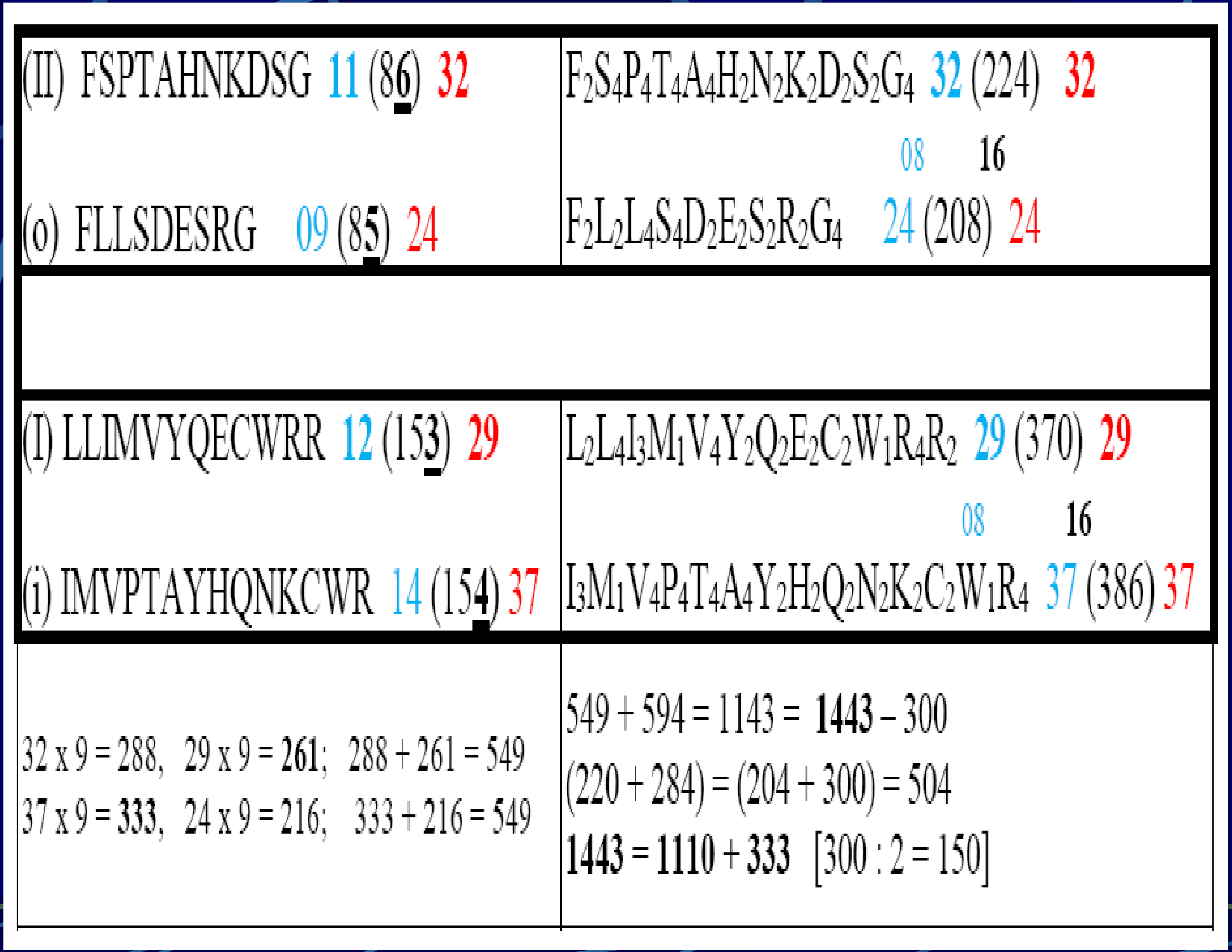
$$(i)\ F_{14}+L_{13}+L_{13}+S_{05}+P_{08}+T_{08}+H_{11}+Q_{11}+N_{08}+K_{15}+D_{07}+E_{10}+S_{05}+R_{17}+G_{01}=15\ (1\underline{4}6)\ [2\underline{8}1]$$ 40

Two distinctions: two AAs classes and two spaces



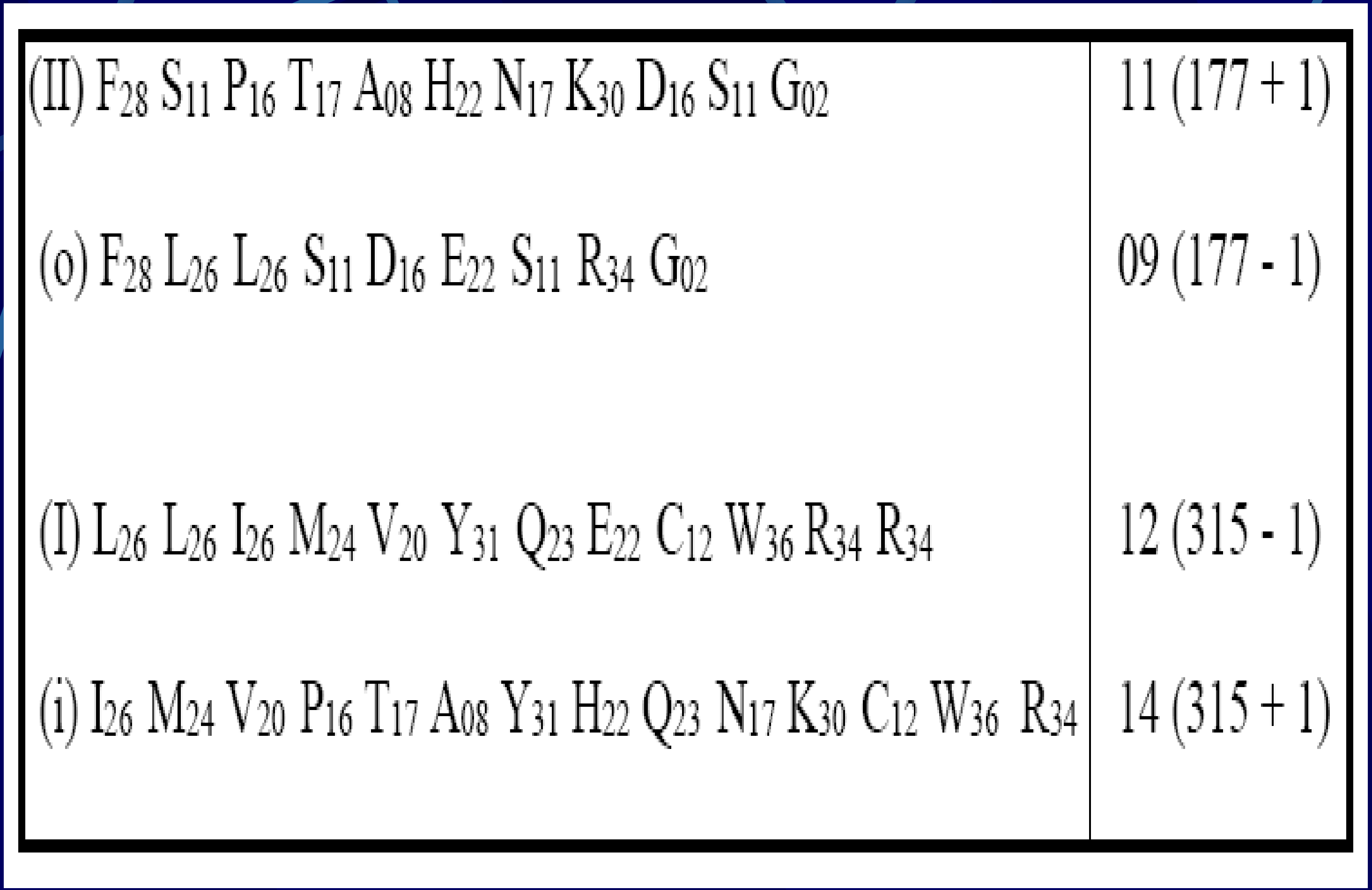
1st	2nd letter								3rd
	U		C		A		G		
U	UUU		UCU		UAU		UGU		U
	UUC	F II	UCC		UAC	Y I	UGC	C I	C
	UUA		UCA	S II	UAA		UGA	CT	A
	UUG	L I	UCG		UAG	CT	UGG	W I	G
C	CUU		CCU		CAU		CGU		U
	CUC		CCC		CAC	H II	CGC		C
	CUA	L I	CCA	P II	CAA		CGA	R I	A
	CUG		CCG		CAG	Q I	CGG		G
A	AUU		ACU		AAU		AGU		U
	AUC	Ile I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

The relations of AAs positions within GCT and their atom number within two classes



(II) FSPTAHNKDSG 11 (8**6**) **32** (o) FLLSDESRG 09 (8**5**) 24	$F_2S_4P_4T_4A_4H_2N_2K_2D_2S_2G_4$ **32** (224) **32** 08 16 $F_2L_2L_4S_4D_2E_2S_2R_2G_4$ 24 (208) 24
(I) LLIMVYQECWRR **12** (15**3**) **29** (i) IMVPTAYHQNKCWR 14 (15**4**) 37	$L_2L_4I_3M_1V_4Y_2Q_2E_2C_2W_1R_4R_2$ **29** (370) **29** 08 16 $I_3M_1V_4P_4T_4A_4Y_2H_2Q_2N_2K_2C_2W_1R_4$ 37 (386) 37
32 x 9 = 288, 29 x 9 = **261**; 288 + 261 = 549 37 x 9 = **333**, 24 x 9 = 216; 333 + 216 = 549	549 + 594 = 1143 = **1443** – 300 (220 + 284) = (204 + 300) = 504 **1443 = 1110 + 333** [300 : 2 = 150]

The relations of AAs positions within GCT and their isotope number within two classes (I)

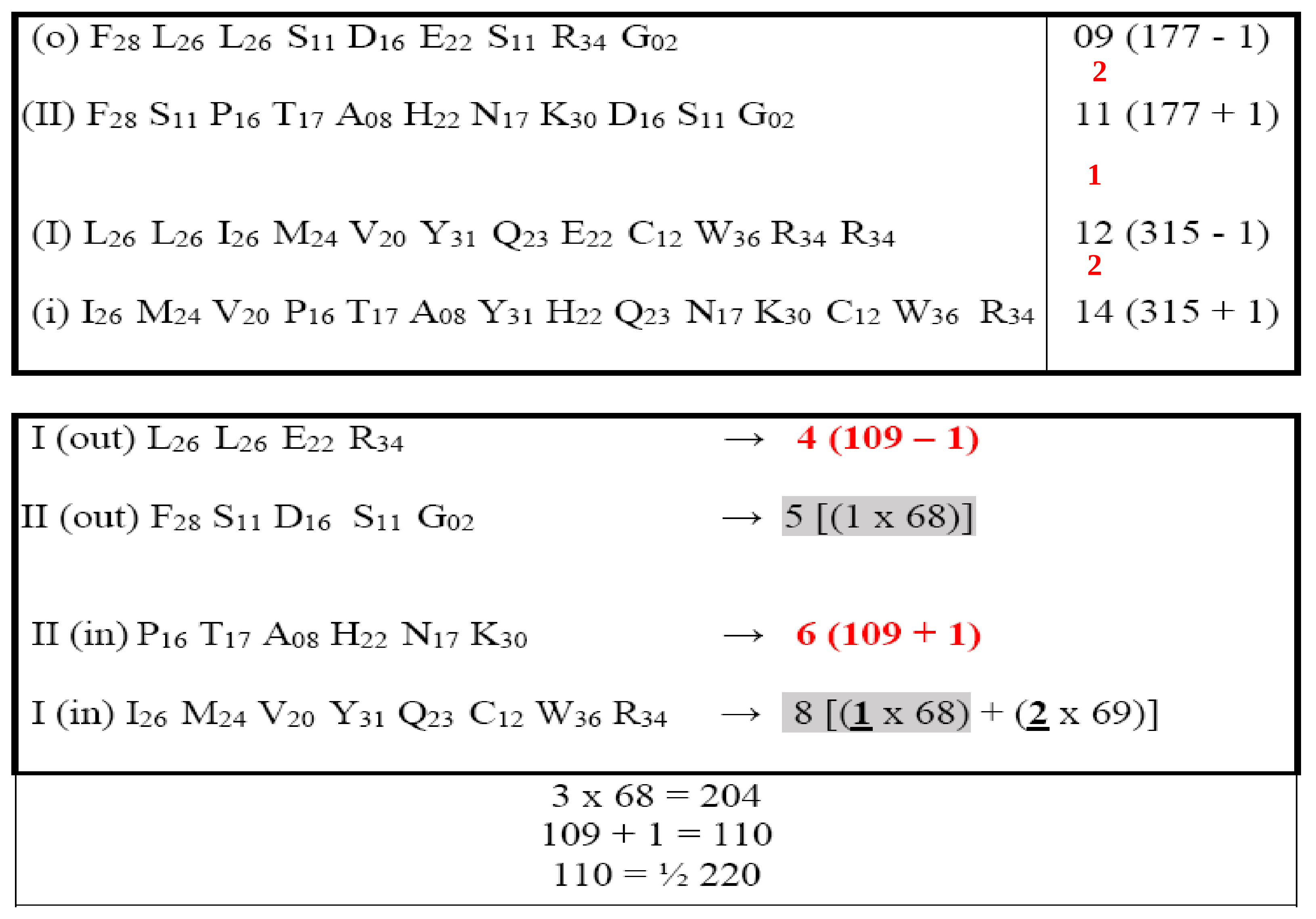


(II) F_{28} S_{11} P_{16} T_{17} A_{08} H_{22} N_{17} K_{30} D_{16} S_{11} G_{02}	11 (177 + 1)
(o) F_{28} L_{26} L_{26} S_{11} D_{16} E_{22} S_{11} R_{34} G_{02}	09 (177 - 1)
(I) L_{26} L_{26} I_{26} M_{24} V_{20} Y_{31} Q_{23} E_{22} C_{12} W_{36} R_{34} R_{34}	12 (315 - 1)
(i) I_{26} M_{24} V_{20} P_{16} T_{17} A_{08} Y_{31} H_{22} Q_{23} N_{17} K_{30} C_{12} W_{36} R_{34}	14 (315 + 1)

[**178** + (314 – 71) = 421] [S 11 + L 26 + R 34 = 71]

[314 – 71 = **243**]

The relations of AAs positions within GCT and their isotope number within two classes (II)

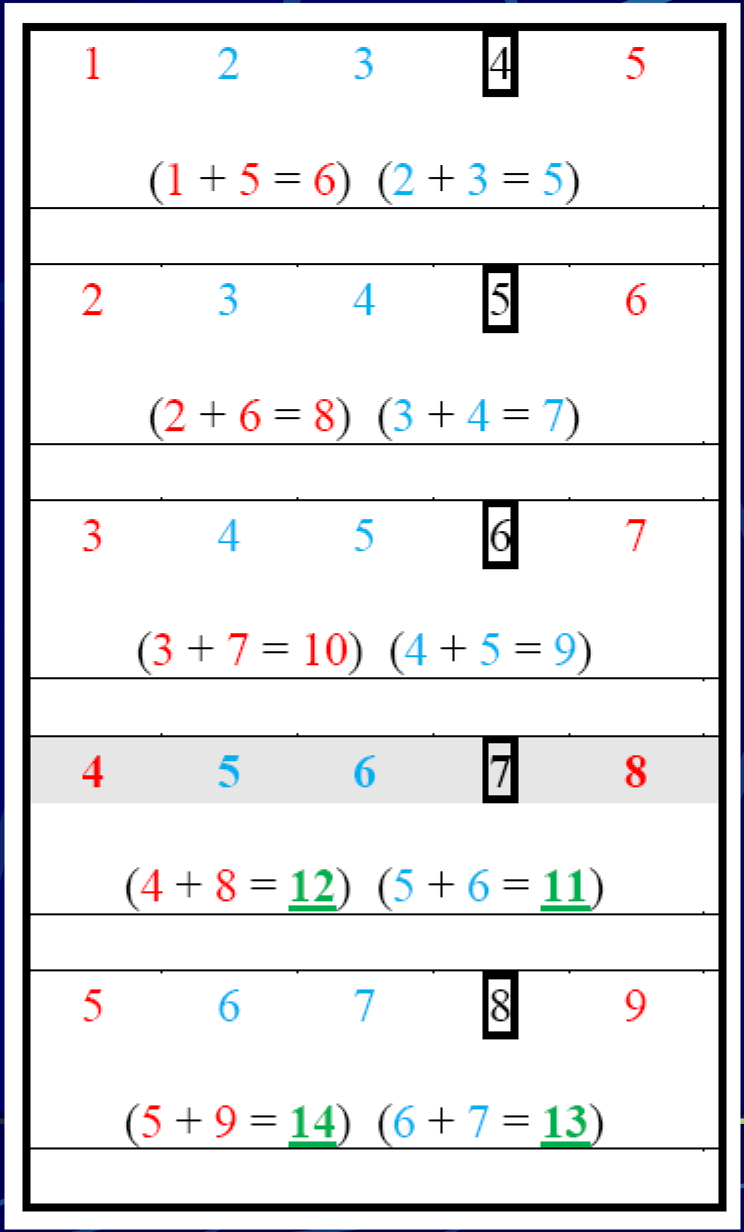


(o) F_{28} L_{26} L_{26} S_{11} D_{16} E_{22} S_{11} R_{34} G_{02}	09 (177 - 1)
	2
(II) F_{28} S_{11} P_{16} T_{17} A_{08} H_{22} N_{17} K_{30} D_{16} S_{11} G_{02}	11 (177 + 1)
	1
(I) L_{26} L_{26} I_{26} M_{24} V_{20} Y_{31} Q_{23} E_{22} C_{12} W_{36} R_{34} R_{34}	12 (315 - 1)
	2
(i) I_{26} M_{24} V_{20} P_{16} T_{17} A_{08} Y_{31} H_{22} Q_{23} N_{17} K_{30} C_{12} W_{36} R_{34}	14 (315 + 1)

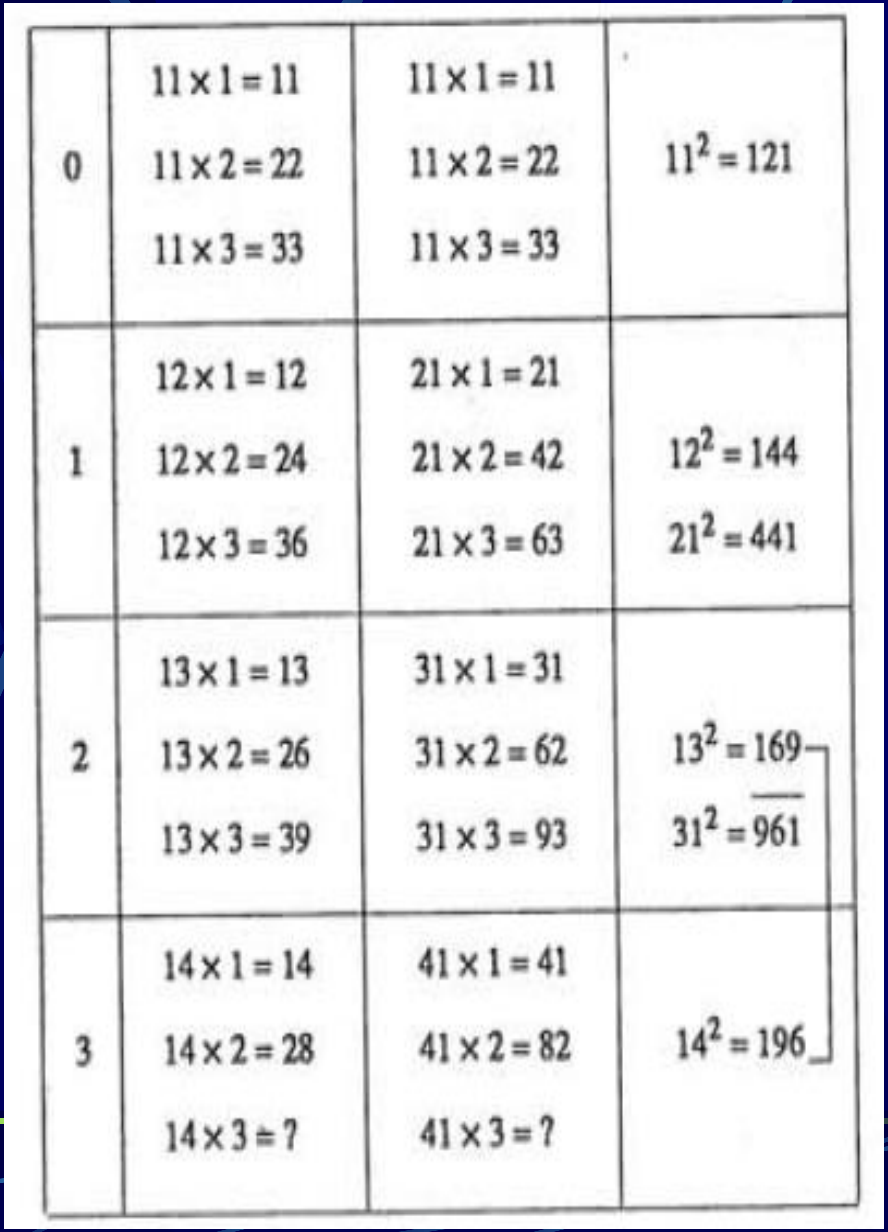
I (out) L_{26} L_{26} E_{22} R_{34}	→	**4 (109 – 1)**
II (out) F_{28} S_{11} D_{16} S_{11} G_{02}	→	5 [(1 x 68)]
II (in) P_{16} T_{17} A_{08} H_{22} N_{17} K_{30}	→	**6 (109 + 1)**
I (in) I_{26} M_{24} V_{20} Y_{31} Q_{23} C_{12} W_{36} R_{34}	→	8 [($\underline{\mathbf{1}}$ x 68) + ($\underline{\mathbf{2}}$ x 69)]

3 x 68 = 204
109 + 1 = 110
110 = ½ 220

The relations of AAs positions within GCT and their isotope number within two classes (III)

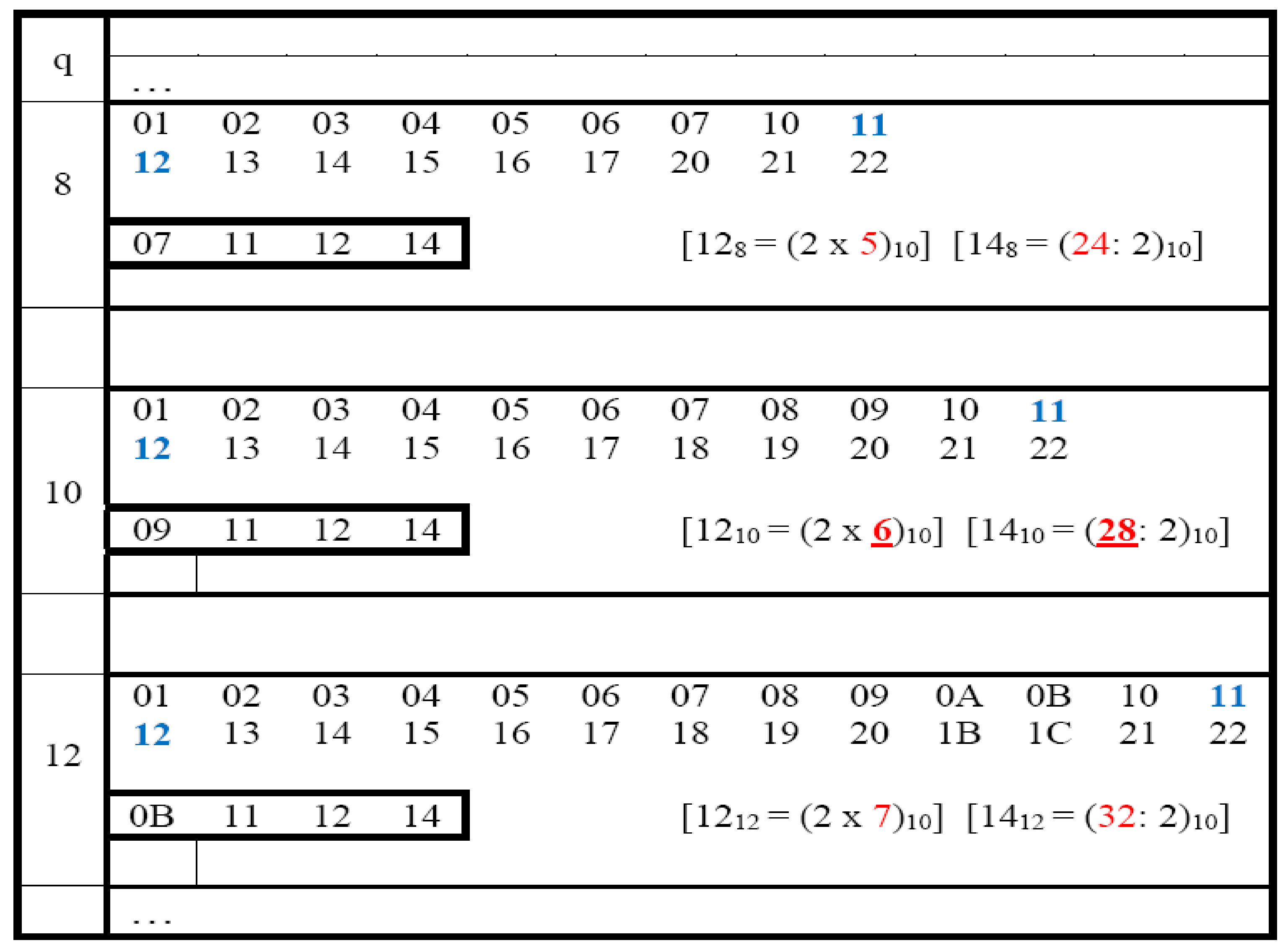


1	2	3	$\boxed{4}$	5
(1 + 5 = 6) (2 + 3 = 5)				
2	3	4	$\boxed{5}$	6
(2 + 6 = 8) (3 + 4 = 7)				
3	4	5	$\boxed{6}$	7
(3 + 7 = 10) (4 + 5 = 9)				
4	**5**	**6**	$\boxed{7}$	**8**
(4 + 8 = $\underline{12}$) (5 + 6 = $\underline{11}$)				
5	6	7	$\boxed{8}$	9
(5 + 9 = $\underline{14}$) (6 + 7 = $\underline{13}$)				



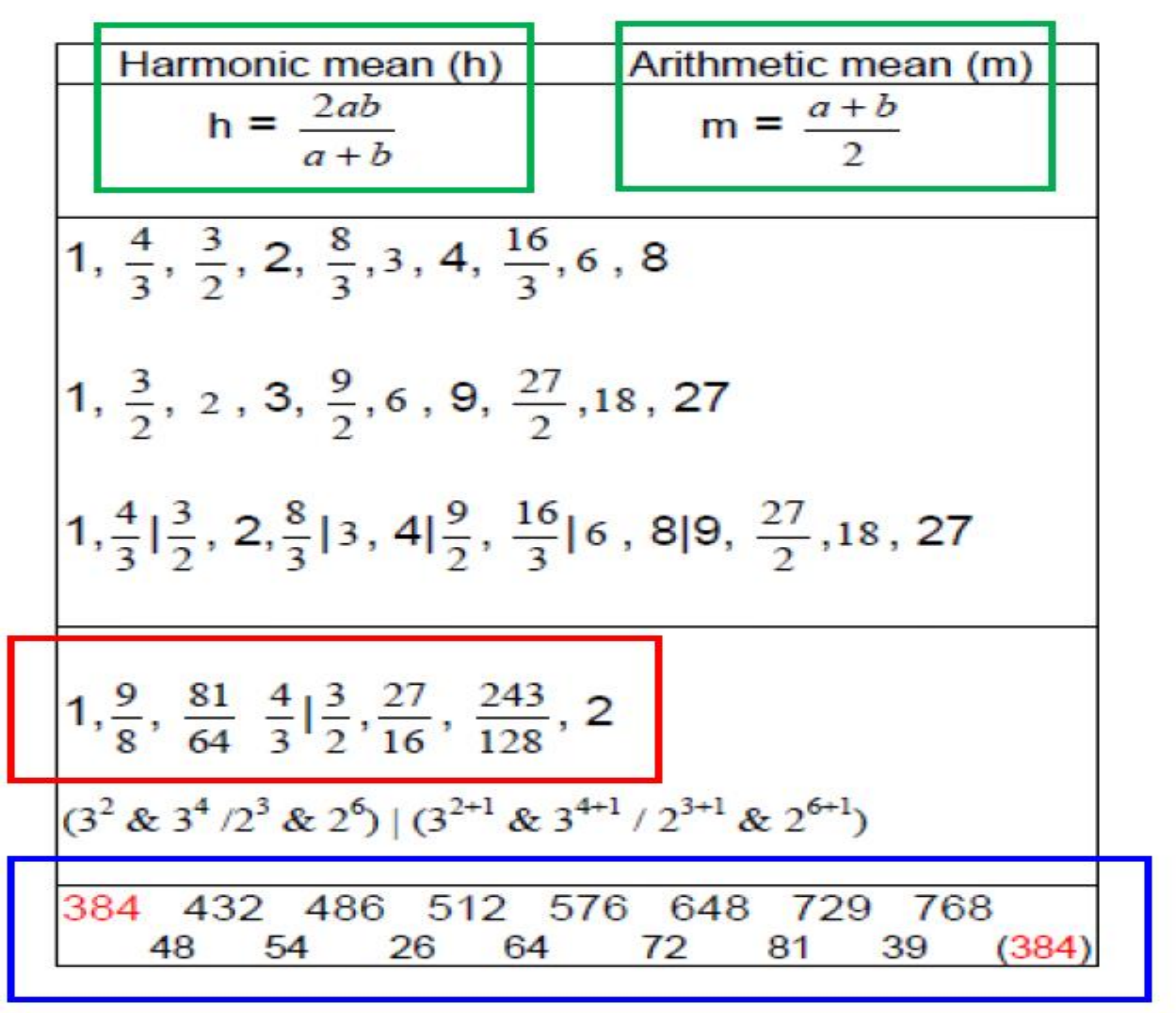
0	$11 \times 1 = 11$ $11 \times 2 = 22$ $11 \times 3 = 33$	$11 \times 1 = 11$ $11 \times 2 = 22$ $11 \times 3 = 33$	$11^2 = 121$
1	$12 \times 1 = 12$ $12 \times 2 = 24$ $12 \times 3 = 36$	$21 \times 1 = 21$ $21 \times 2 = 42$ $21 \times 3 = 63$	$12^2 = 144$ $21^2 = 441$
2	$13 \times 1 = 13$ $13 \times 2 = 26$ $13 \times 3 = 39$	$31 \times 1 = 31$ $31 \times 2 = 62$ $31 \times 3 = 93$	$13^2 = 169$ $31^2 = 961$
3	$14 \times 1 = 14$ $14 \times 2 = 28$ $14 \times 3 = ?$	$41 \times 1 = 41$ $41 \times 2 = 82$ $41 \times 3 = ?$	$14^2 = 196$

The correspondence of the distribution of the number of AAs molecules and decimal number system



q													
	...												
8	01	02	03	04	05	06	07	10	**11**				
	12	13	14	15	16	17	20	21	22				
	07	11	12	14				$[12_8 = (2 \text{ x } 5)_{10}]$			$[14_8 = (24 : 2)_{10}]$		
10	01	02	03	04	05	06	07	08	09	10	**11**		
	12	13	14	15	16	17	18	19	20	21	22		
	09	11	12	14				$[12_{10} = (2 \text{ x } \underline{6})_{10}]$			$[14_{10} = (\underline{28} : 2)_{10}]$		
12	01	02	03	04	05	06	07	08	09	0A	0B	10	**11**
	12	13	14	15	16	17	18	19	20	1B	1C	21	22
	0B	11	12	14				$[12_{12} = (2 \text{ x } 7)_{10}]$			$[14_{12} = (32 : 2)_{10}]$		
	...												

Plato's unique arithmetic existing in the genetic code



Harmonic mean (h)

$$h = \frac{2ab}{a+b}$$

Arithmetic mean (m)

$$m = \frac{a+b}{2}$$

$$1, \frac{4}{3}, \frac{3}{2}, 2, \frac{8}{3}, 3, 4, \frac{16}{3}, 6, 8$$

$$1, \frac{3}{2}, 2, 3, \frac{9}{2}, 6, 9, \frac{27}{2}, 18, 27$$

$$1, \frac{4}{3} \mid \frac{3}{2}, 2, \frac{8}{3} \mid 3, 4 \mid \frac{9}{2}, \frac{16}{3} \mid 6, 8 \mid 9, \frac{27}{2}, 18, 27$$

$$1, \frac{9}{8}, \frac{81}{64}\ \frac{4}{3} \mid \frac{3}{2}, \frac{27}{16}, \frac{243}{128}, 2$$

$$(3^2 \;\&\; 3^4 / 2^3 \;\&\; 2^6) \mid (3^{2+1} \;\&\; 3^{4+1} / 2^{3+1} \;\&\; 2^{6+1})$$

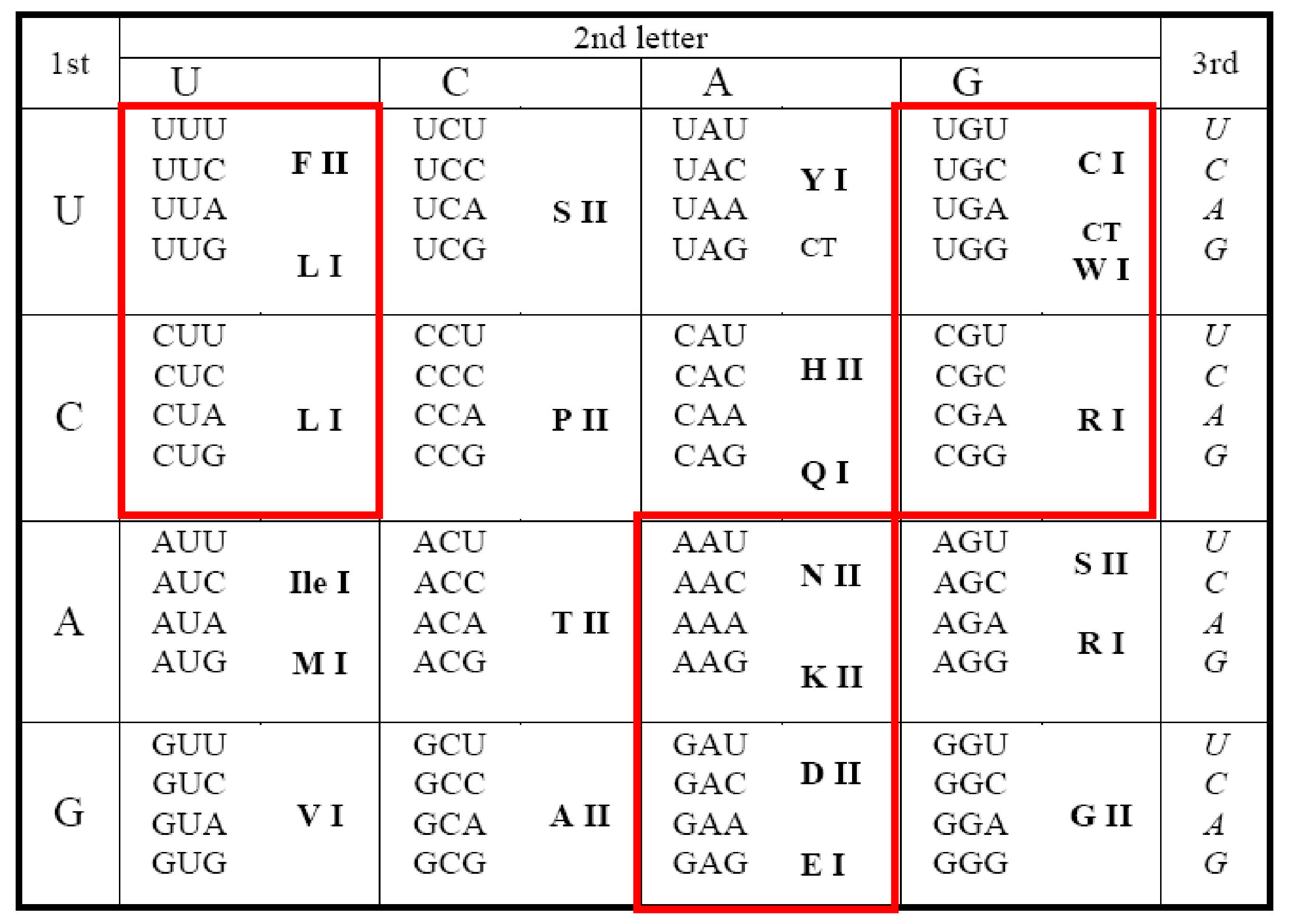
384 432 486 512 576 648 729 768

48 54 26 64 72 81 39 (384)

The unity of chemistry type and the position

Py-Py
Py-Py

Py-Pu
Py-Pu



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

Pu-Py
Pu-Py

Pu-Pu
Pu-Pu

(FLL 40) +[(NKDE 40 + CWR 40) = 80] = 120

[(IMV + SPTA = 60-1)] + [(YHQ + SRG = 60)] = 120-1

(50±10) [(40:80 = 1:2) (60:120 = 1:2)]

1. *Nota bene*. From: MMR, 2018a, p. 33: I added this *Nota bene* at the beginning of my paper on the Cipher of the genetic code (MMR, 2018a). This meant that the state of affairs in understanding the genetic code is as it is seen and described by M. Barbieri. [In my case it is even more difficult. It is claimed that both the concepts of the Cipher of the genetic code and the Key of the Cipher are also ontological realities.] On the other hand, I also wanted to say that everything that M. Barbieri says corresponds (directly or indirectly) to the key contents of my book *Genes, molecules, language*, published 35 years ago (Slide 2).

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

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

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

'... On ne pourrait concevoir un tel changement [lors de l'introduction de normes dans la langue] que par l’intervention de spécialistes, grammairiens, logiciens, etc.; mais l’expérience montre que jusqu’ici les ingérences de cette nature n’ont eu aucun succès' (De Saussure, 1985, p. 107).

‘How poor will his (of man) products be, compared with those accumulated by nature during whole geological periods.’ (Darwin, 1859, p. 66) [*Origin of Species*: second British edition (1860), page 84.]

Many more such, almost identical statements, can be found in *The origin of species* and *Cours de linguistique general*, with Darwin talking about organisms and Saussure about language."

On p. 65: "This universality in language, which can also be revealed in other phenomena, was emphasized by linguists even after De Saussure, especially Louis Hjelmslev. In his famous monograph, a scientific study, *Prolegomena to the Theory of Language*, he says: ‘In a new sense, it seems that it is as fruitful as it is necessary to establish a certain common point of view for a whole range of sciences, from literature science, through the science of art, musicology and general history, to logic and mathematics, wouldn't they all, from such a common platform, focus on the problem defined by linguistics. Each of them will be able to contribute to the general science of language in their own way if they try to investigate to what extent and in what way their subject can be subjected to an analysis that would be in accordance with the requirements of language theory, so perhaps new light could be shed on these disciplines, encourage them to do their own self-reflection. In this way, through all-round fruitful cooperation, it would be possible to arrive at a kind of general encyclopedia of sign structures’ (Hjelmslev, 1980, p. 101)".[4]

*

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

For the next few years, new and different studies began and continued for me. I searched for chemistry in non-chemical sciences and again tried to see in chemistry the non-chemical – what is common to molecules and individuals of any other species in the living and non-living world. Thermodynamics was now to be studied again, but not without of information theory; genetics and theory of evolution, but not without cybernetics and systems theory; biochemical and genetic language, but not without structural linguistics and semiology…."

3. *Rene Thom:* "… in the study of the natural limitations of the formalism reside the mathematics of tomorrow"*; Richard Dawkins:* "Perhaps here is an opportunity for ‘like begets like’ – for chemical heredity."

4. *Rosemarie Swanson:* "The actual amino acid code and the twenty amino acids it codes for suggest an idealized model coding system … a 'perfect' genetic code."

5. *Gray code model of GC (Swanson, 1984).* This Gray code model of Genetic code (Codon ring), in itself, is proof that the genetic code is determined by Boolean spaces. (Cf. Mutation ring on App-Slide 1.) [How is it possible that after several million years of evolution of organisms, evolution of protein macromolecules, after many random

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[4] I took the advice of L. Hjelmslev and took the steps listed below, under the asterisk. [Of course, I read L. Hjelmslev's book in the early seventies of the 20th century.] But, in addition to the above, I also studied the structure and composition of works of literary classics, in parallel with the study of the structure of natural codes. Some of these results have been published in OSF preprints (for example here: MMR, 2021c, Box 13.1 – 13.4; Tables B6 and B7; Displays B6 and B7; but also elsewhere, a few books, too). I have published several papers (in Serbian and/or English) at: ECPD, European Center for Peace and Development of the United Nations University for Peace, Belgrade.

mutations, the *Mutation ring* retains, *mutatis mutandis*, all the relationships that we also find in the *Codon ring*?! The answer to this question cannot be given from the aspect of current science. The missing "hoop" in the possible explanation is that it does not take into account the *space* in which the atoms are; the space in which the molecules are.[5] Atoms, in the Periodic System of chemical elements (PSE), "carry" their space with them; molecules, in some autonomous system-arrangement, like the Genetic Code System, carry their space with them. (*Proof-example*: It makes no sense to "cram" 14 lanthanides into a unit space, together with lanthanum, but 14 elements should be arranged in 14 groups, as Mendeleev arranged them) (MMR, 2018b; Slide 9 in relation to Slides 10, 11 and 12; also in relation with App-Slides 5, 6, 7 and 8).]

Swanson, 1984, Legend to Fig. 1, p. 188: "Codon ring. The central part of the figure is an example of minimum change binary code. Note that the inner two rings are split into a dotted half and a dashed half. Successive rings split into quarters, eighths, sixteenths, etc. The two split inner circles correspond to identical splittings of the middle and first base rings of the nucleotide circles into pyrimidine and purine halves. The codons are arranged so that the middle base changes most slowly, the first base more often and the third base most frequently."[6]

6. *Determination of GC by the Golden Mean.* Determination on the binary-code tree (developed from the Gray code model of GC). MMR, 1998a, Fig. 1, p. 284: "The full lines: the routes of the greater (faster) changes from pyrimidine to purine or from two to three hydrogen bonds and vice versa. The dotted lines: the routes of the less (slower) changes. The double full line: the route of the maximum possible (fastest) changes; the route corresponding to the ‘Golden mean route’ on the Farey tree [Slide 7]. Asterisks: ‘stop’ codon UGA. Quadrangles: ‘stop’ codons UAA and UAG."

Amino acids in Golden mean positions: FLSPTQG with 60 atoms in their side chain; their chemical complements: YACIMNV with 66, and non-complements: DE KR HW with 78 atoms (cf. Slide 14). Quantities 60, 66, 78 appear in many system-arrangements of the 20 protein amino acids. Same quantities for different qualities (*Principle of the sameness*). MMR, 2018a: Observation on the determination with the Golden mean, as it is cited in Main paper (MMR, 2022, Box 1, p. 2: second paragraph).

7. *The Farey binary tree.* MMR, 1998a: Fig. 2. "The Farey binary-code tree as a representation of rational numbers relationships within the interval (0, 1). The full lines: the routes of the greater fractions of the rational numbers, i.e. of the faster changes (for example: the faster routes into deterministic chaos). The dotted lines: the routes of the

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[5] If Einstein's theory about the unity of space and time "drinks water", and it is surely certain that it "drinks", then here too, whenever we talk about *space*, we mean Einstein's *space-time*.

[6] This and such a Boolean type Gray code represents, per se, a Boolean space (the Boolean space of the genetic code), from which a series of natural numbers can be generated. [Carbo-Dorca and Perelman (2022, p. 80): "Using simple arguments derived from the Boolean hypercube configuration, the structure of natural spaces, and the recursive exponential generation of the set of natural numbers, a linear classification of the natural numbers is presented".]

smaller fractions of the rational numbers, i.e. of the slower changes. The double full line: the route with the greatest rational numbers (greatest or fastest changes) whose numerators and denominators are given by the Fibonacci numbers sequence – the ‘Golden route’. Notice that ‘each rational number between 0 and 1 occur exactly once somewhere in the infinite Farey tree’ (Schroeder, 1991 p. 336). [The figure is made after: Belić (1990), Schroeder (1991).]"

8. *Leibniz's binary system, taken from the ancient Chinese.* The famous German philosopher and great mathematician Gottfried Wilhelm Leibniz published (in 1703) an article on the *Binary Arithmetic* ("*Explication de l’atithmetique binaire*") in the French Academy of Sciences. In the article, on only five pages, he presented the binary number system, and nowadays there are more and more researchers who consider that article, in itself, to be a prophecy of the future, from the aspect of the emergence of universal binarity and digitality. The 6-bit binary tree, which the ancient and modern Chinese have been dealing with for a total of several thousand years, proves to be unique on several grounds. Only in the case of such a binarity both Mendeleev's principles are satisfied: the Principle of continuity and the Principle of minimum change. Three-letter words from the four-letter alphabet, with two-letter word root, and one-letter on the start. Only in the case of this binary tree is there no ambiguity about the root of the word. (See Rumer's presentation of nucleotide doublets on App-Slides 9 and 10).[7]

Symmetry in the reading of individual hexagrams (codons in GC) and their families: 3 bits for the position of the family and 6 bits for the position of the individual hexagram, i.e. the codon. Such symmetry, apart from being shown as symmetry in the simplest case (Markus 1989), also contains mirror symmetry of the Dirac type (111 | 000); (101 | 010) etc. [Cf. Slide 8 with Slides 6 and 7.]

9. *Slide explanation ....*

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[7] Ю. Б. Румер, 1966, 1393: „Рассмотрение группы кодонов, относящихся к одной и той же аминокислоте, показывает, что в каждом кодоне (xy | z) целесобразно отделить двухбуквенный ‘корень’ (xy |) от ‘окончания’ (| z). Тогда каждой аминокислоте, в общем случае, будет соотвествовать один определенный корень ...“ [Y. B. Rumer, 1966, p. 1393: “Consideration of a group of codons referring to the same amino acid shows that in each codon (xy | z) it is useful to separate the two-letter 'root' (xy |) from the 'end' (| z). Then each amino acid, in the general case, will correspond to one specific root ...“

4. Concluding remark

It is expected that the presented facts testify sufficiently convincingly that the genetic code is indeed a semiotic system. ...

Acknowledgements

I am grateful to Branko Dragovich, Djuro Koruga and Dejan Raković for helpful, stimulating discussions and benevolent critique over a long period of years.

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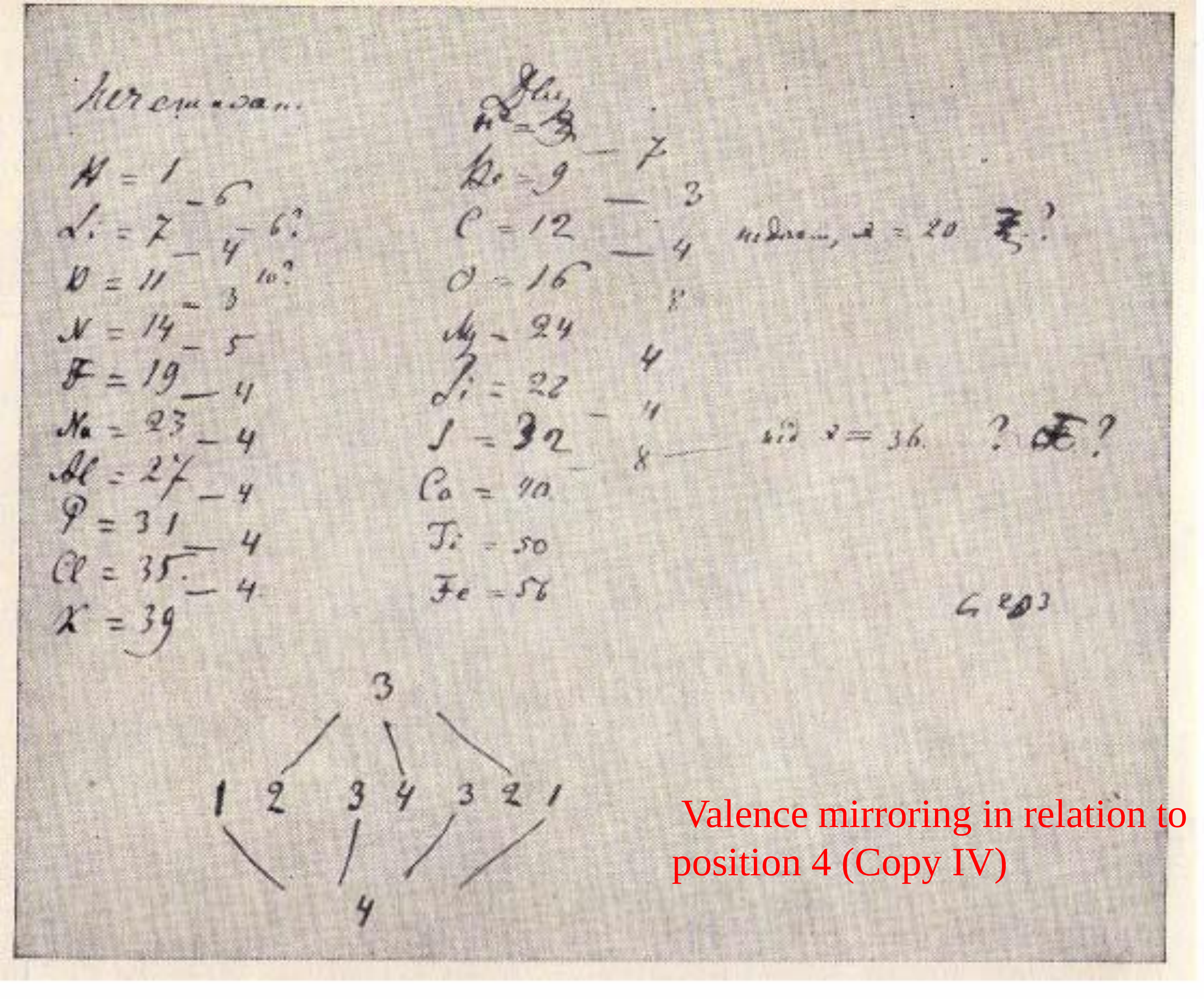
APPENDIX

1. Appendix Slides presentation

Distances between atomic masses: Principle of continuity and Principle of minimum change



[illegible]

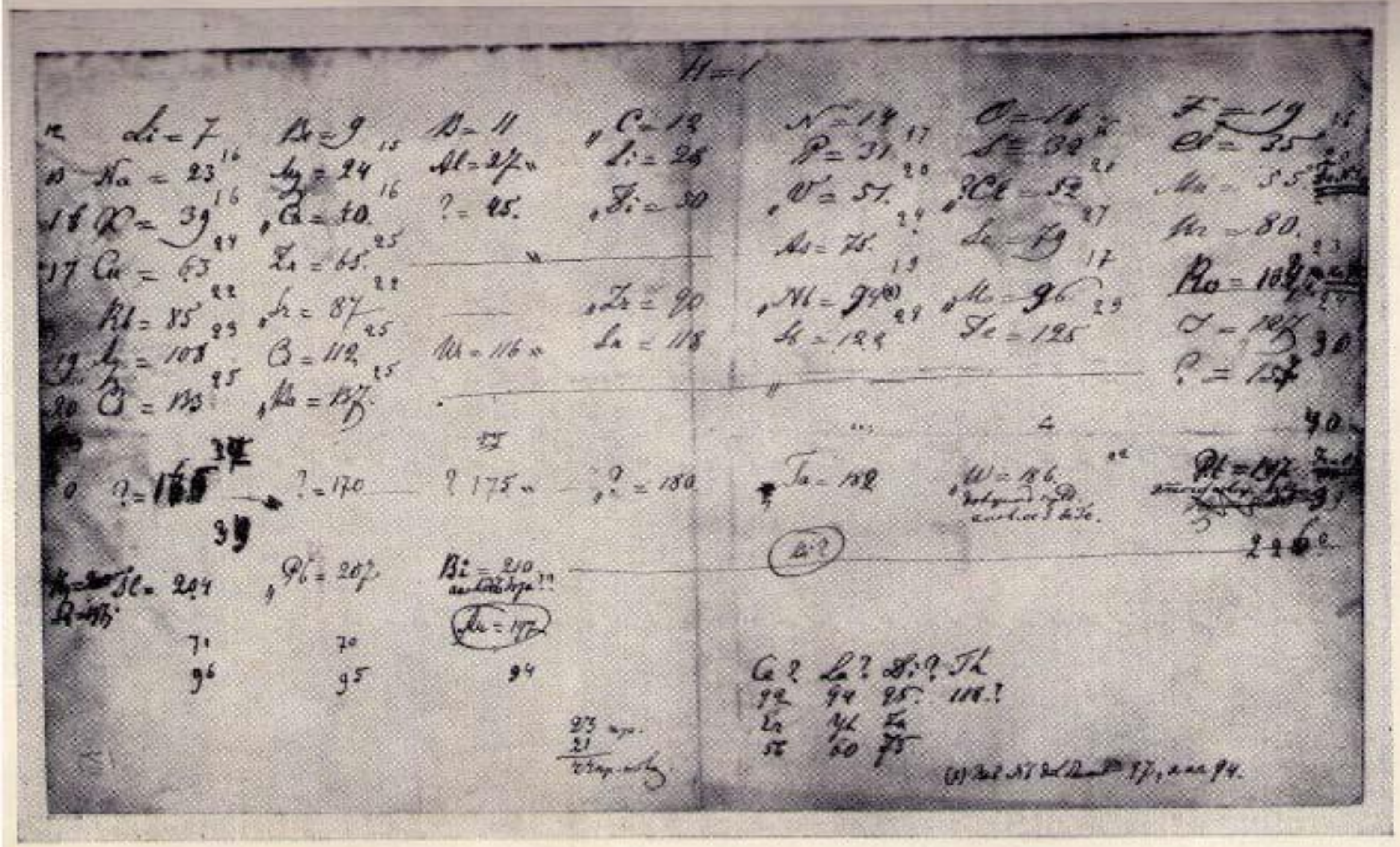
H = 1
Li = 7
B = 11
N = 14
F = 19
Na = 23
Al = 27
P = 31
Cl = 35
K = 39

[illegible]
Be = 9
C = 12
O = 16
Mg = 24
Si = 28
S = 32
Ca = 40
Ti = 50
Fe = 56

[illegible] = 20 ?
[illegible] = 36 ? ?

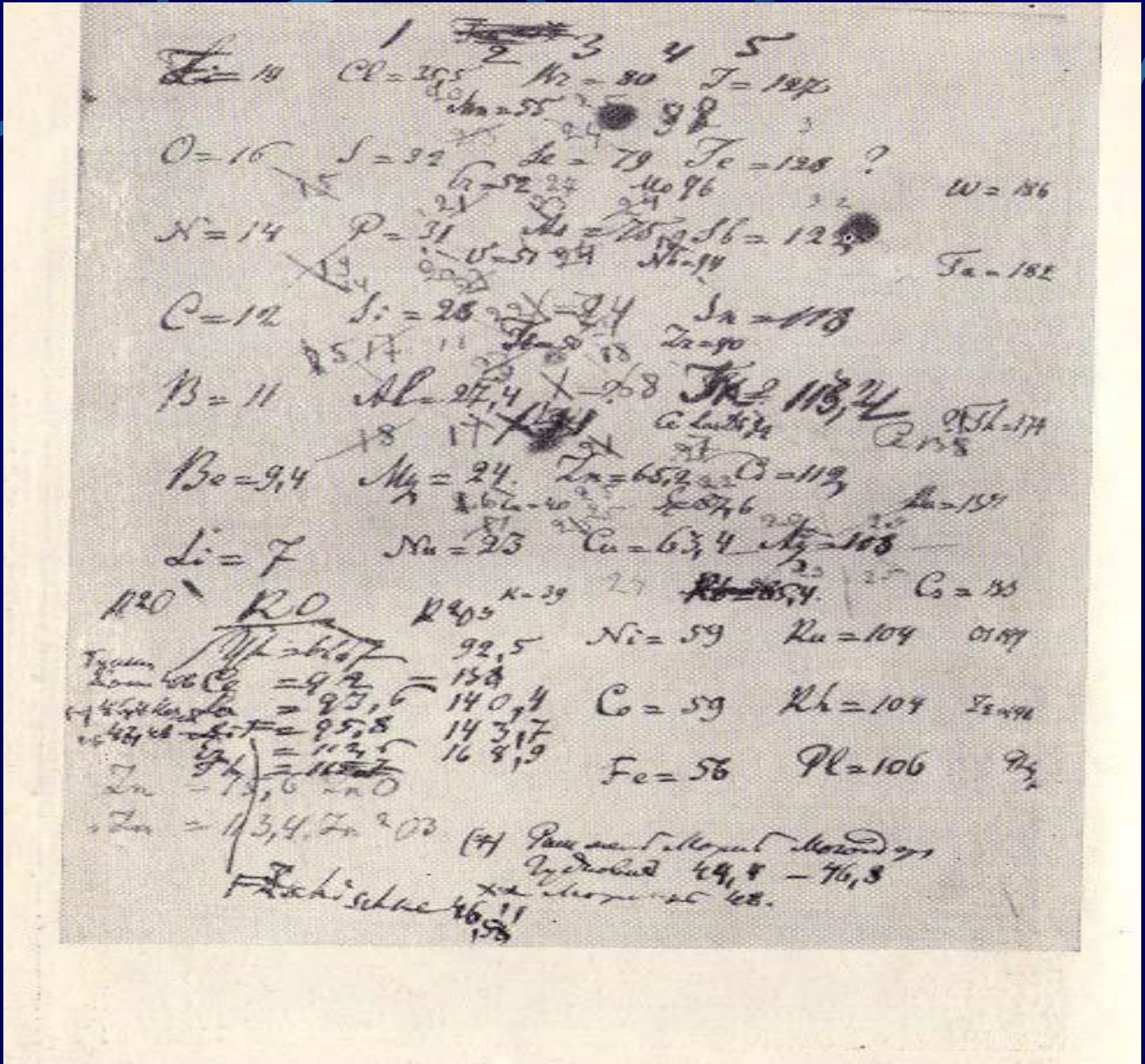
Valence mirroring in relation to position 4 (Copy IV)

Hydrogen on the right side of the Periodic System



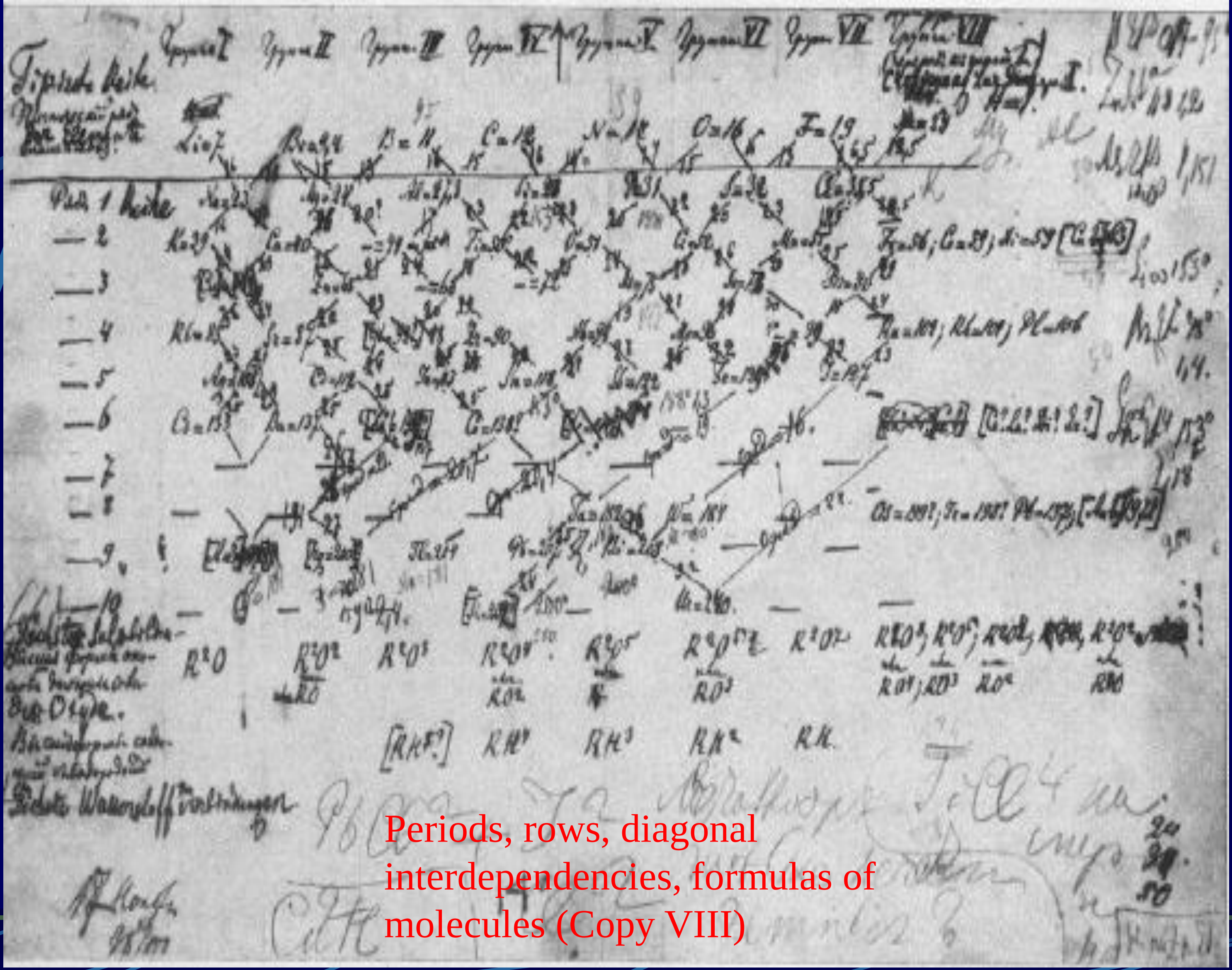
Фотокопия V. Первый вариант короткой таблицы элементов с подразделением рядов на четные и нечетные. Февраль/март 1869 г.

Zigzag connection and interdependence as a "start" to diagonal connection

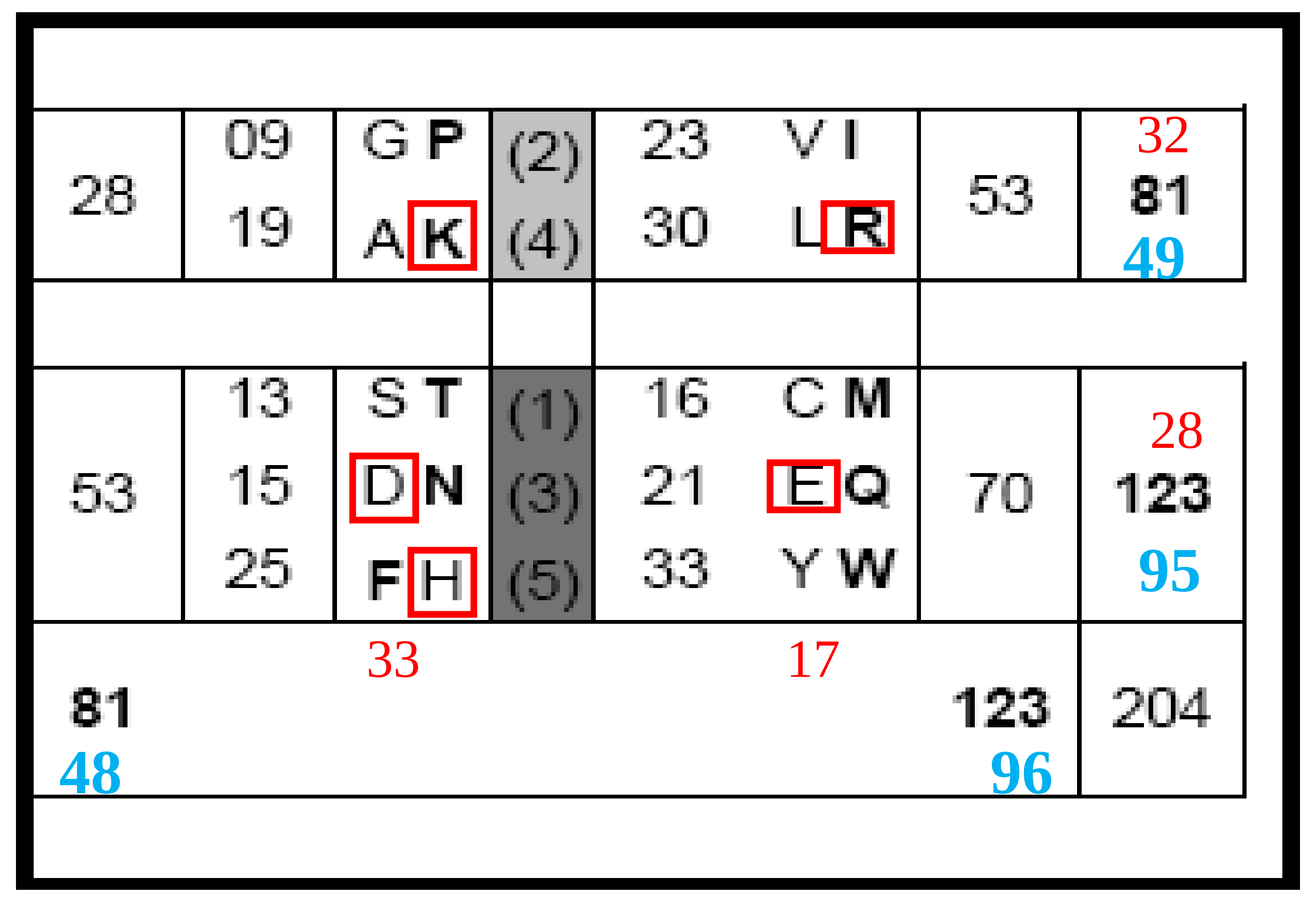


Фотокопия VI. Набросок короткой таблицы элементов с выявленным диагональным направлением. Лето или осень 1870 г.

The law of diagonal interdependence

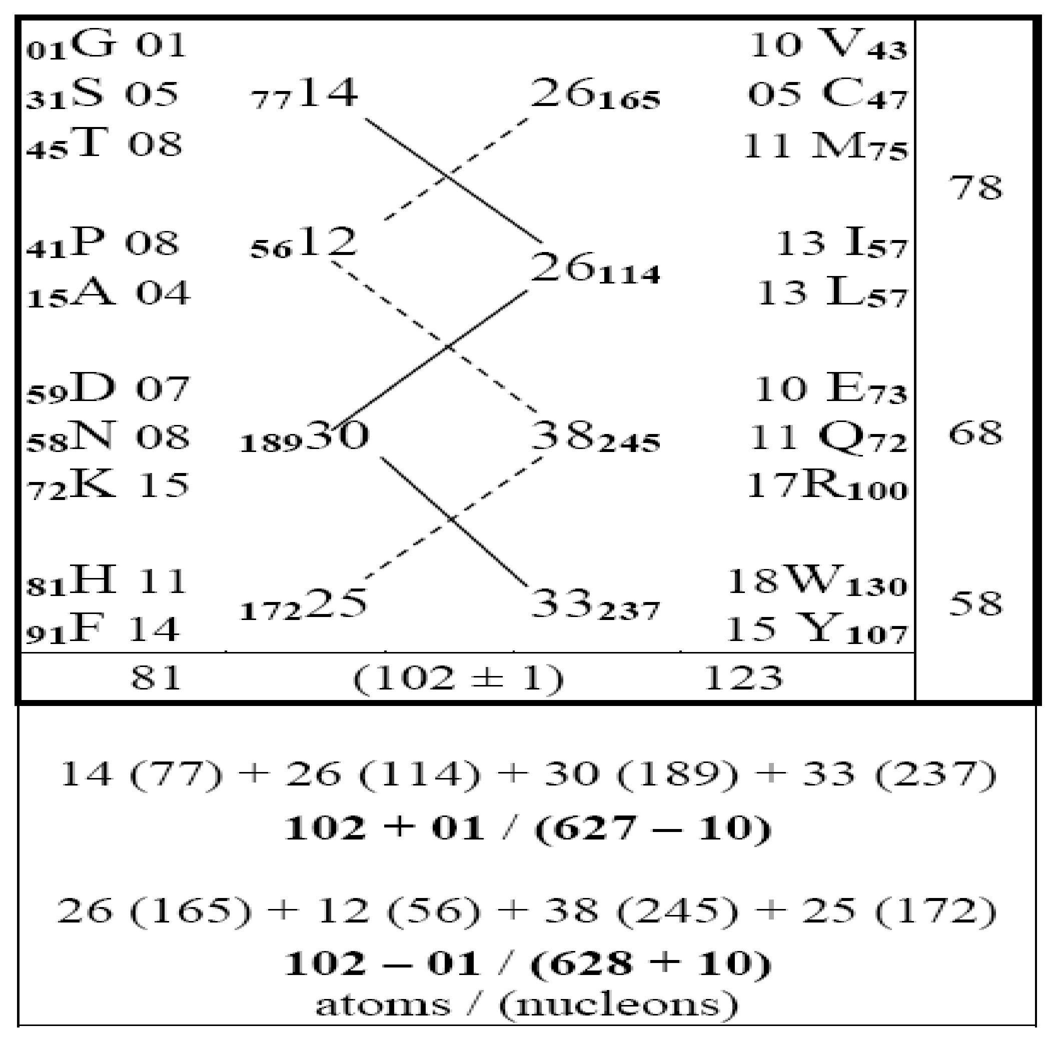


Periods, rows, diagonal interdependencies, formulas of molecules (Copy VIII)



28	09 19	G P A K	(2) (4)	23 30	V I L R	53	32 81 49
53	13 15 25	S T D N F H	(1) (3) (5)	16 21 33	C M E Q Y W	70	28 123 95
81 48		33			17	123 96	204

Two classes of amino acids related to two classes of synthetases



${}_{01}$G 01 — 10 V_{43}

${}_{31}$S 05 — ${}_{77}14$ — 26_{165} — 05 C_{47}

${}_{45}$T 08 — 11 M_{75}

78

${}_{41}$P 08 — ${}_{56}12$ — 13 I_{57}

${}_{15}$A 04 — 26_{114} — 13 L_{57}

${}_{59}$D 07 — 10 E_{73}

${}_{58}$N 08 — ${}_{189}30$ — 38_{245} — 11 Q_{72} — 68

${}_{72}$K 15 — 17R_{100}

${}_{81}$H 11 — 18W_{130}

${}_{91}$F 14 — ${}_{172}25$ — 33_{237} — 15 Y_{107} — 58

81 (102 ± 1) 123

14 (77) + 26 (114) + 30 (189) + 33 (237)

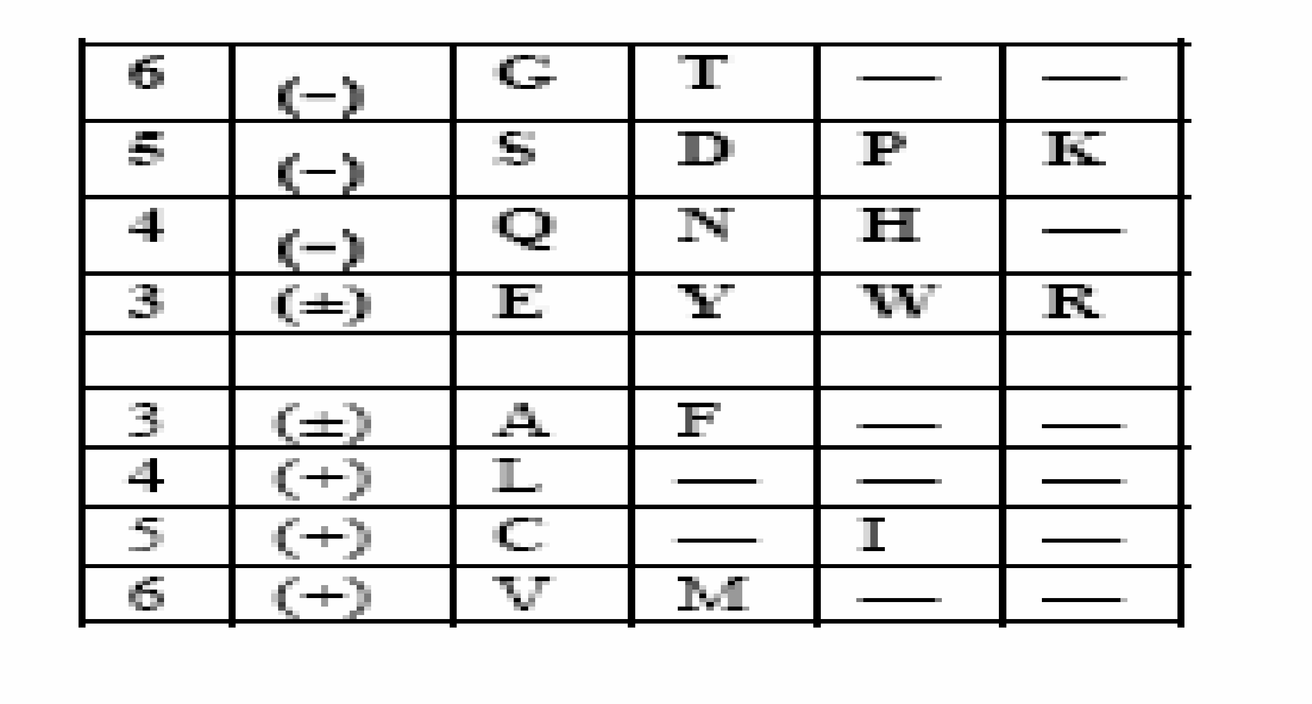
102 + 01 / (627 – 10)

26 (165) + 12 (56) + 38 (245) + 25 (172)

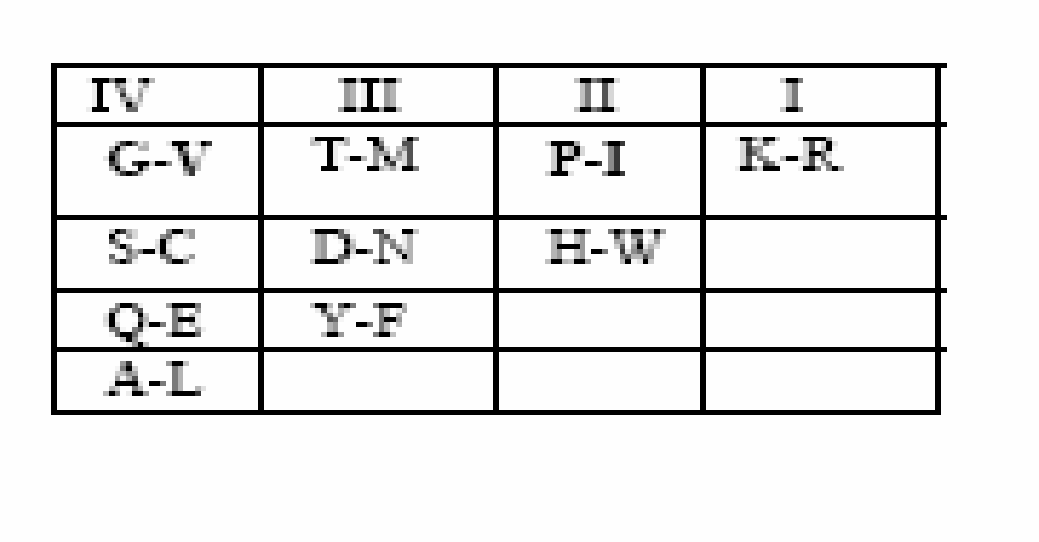
102 – 01 / (628 + 10)

atoms / (nucleons)

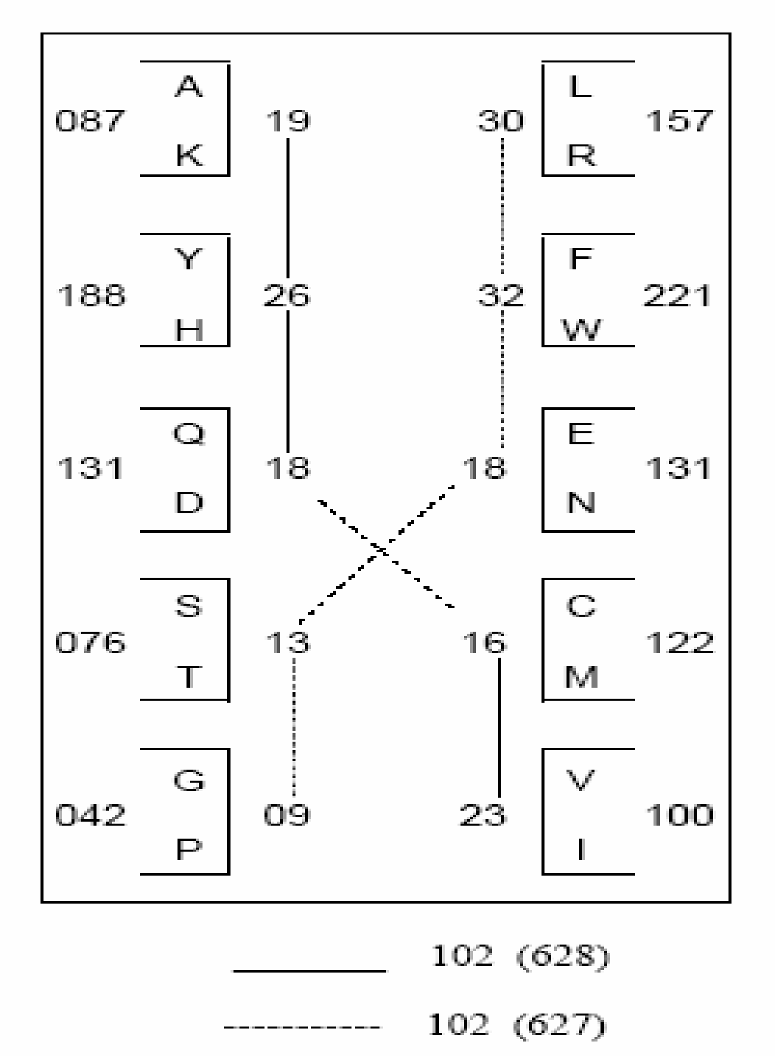
Rakočević, 1998a, Surv. 4, p. 290

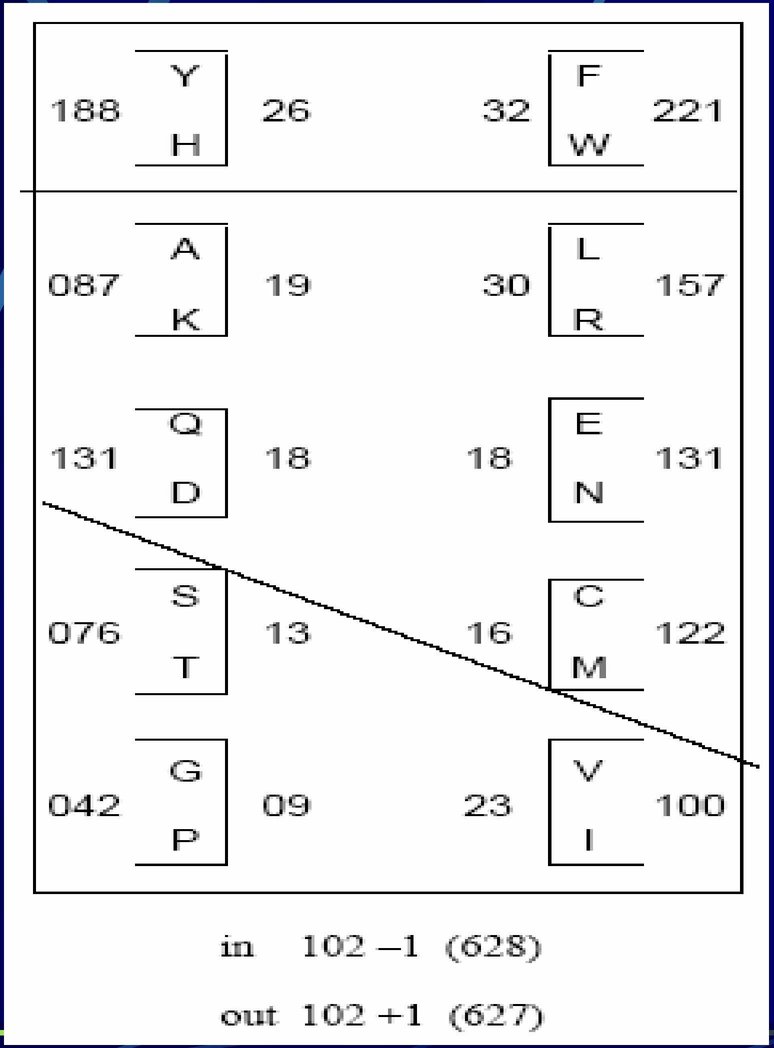


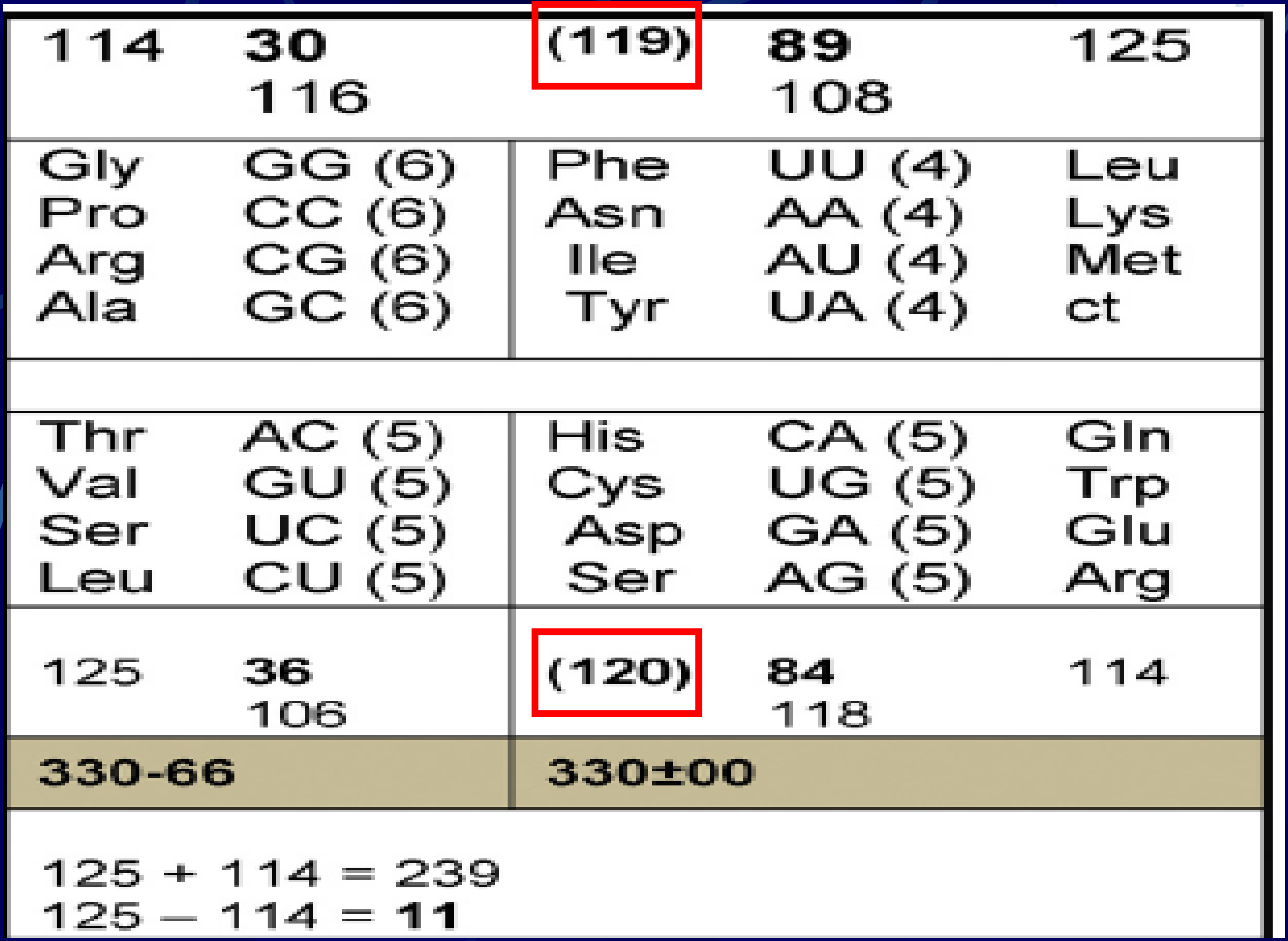
6	(−)	G	T	—	—
5	(−)	S	D	P	K
4	(−)	Q	N	H	—
3	(±)	E	Y	W	R
3	(±)	A	F	—	—
4	(+)	L	—	—	—
5	(+)	C	—	I	—
6	(+)	V	M	—	—



IV	III	II	I
G-V	T-M	P-I	K-R
S-C	D-N	H-W	
Q-E	Y-F		
A-L			


087
A
K
19
30
L
R
157
188
Y
H
26
32
F
W
221
131
Q
D
18
18
E
N
131
076
S
T
13
16
C
M
122
042
G
P
09
23
V
I
100
102 (628)
102 (627)


188
Y
H
26
32
F
W
221
087
A
K
19
30
L
R
157
131
Q
D
18
18
E
N
131
076
S
T
13
16
C
M
122
042
G
P
09
23
V
I
100
in 102 −1 (628)
out 102 +1 (627)

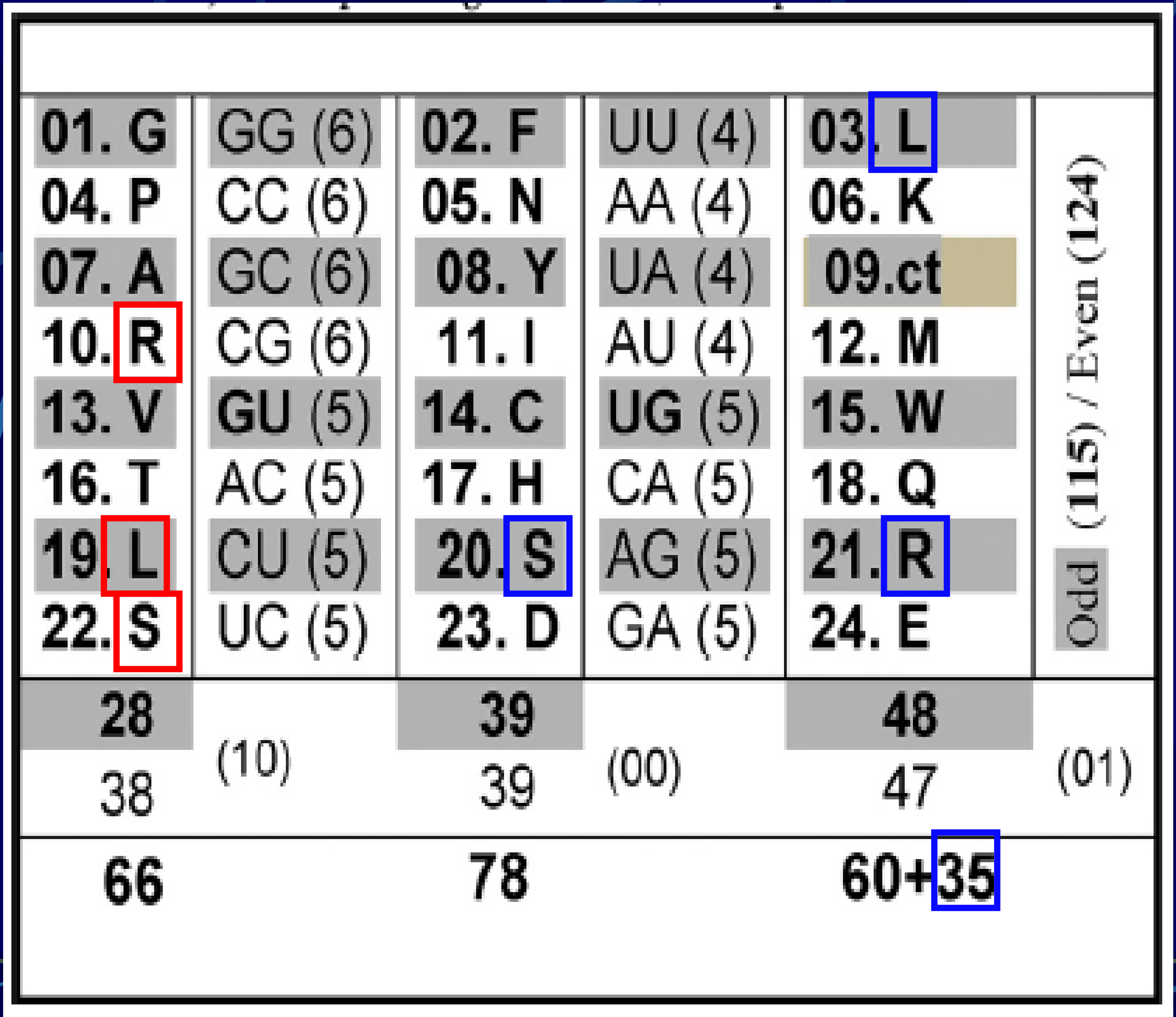


114	30 116	(119)	89 108	125
Gly	GG (6)	Phe	UU (4)	Leu
Pro	CC (6)	Asn	AA (4)	Lys
Arg	CG (6)	Ile	AU (4)	Met
Ala	GC (6)	Tyr	UA (4)	ct
Thr	AC (5)	His	CA (5)	Gln
Val	GU (5)	Cys	UG (5)	Trp
Ser	UC (5)	Asp	GA (5)	Glu
Leu	CU (5)	Ser	AG (5)	Arg
125	36 106	(120)	84 118	114
330-66		330±00		

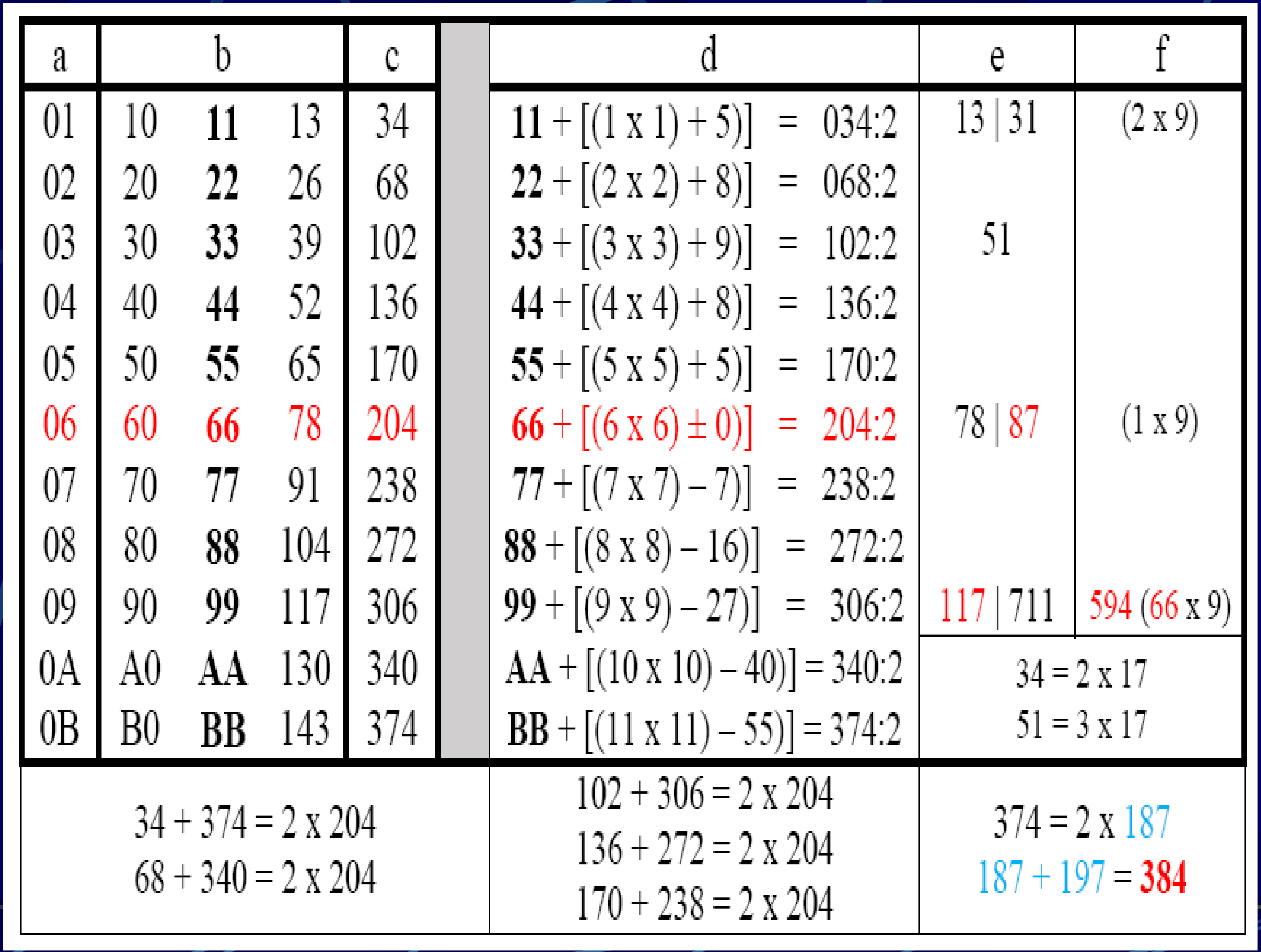
125 + 114 = 239
125 — 114 = 11

(FLL 40) +[(NKDE 40 + CWR 40) = 80] = 120

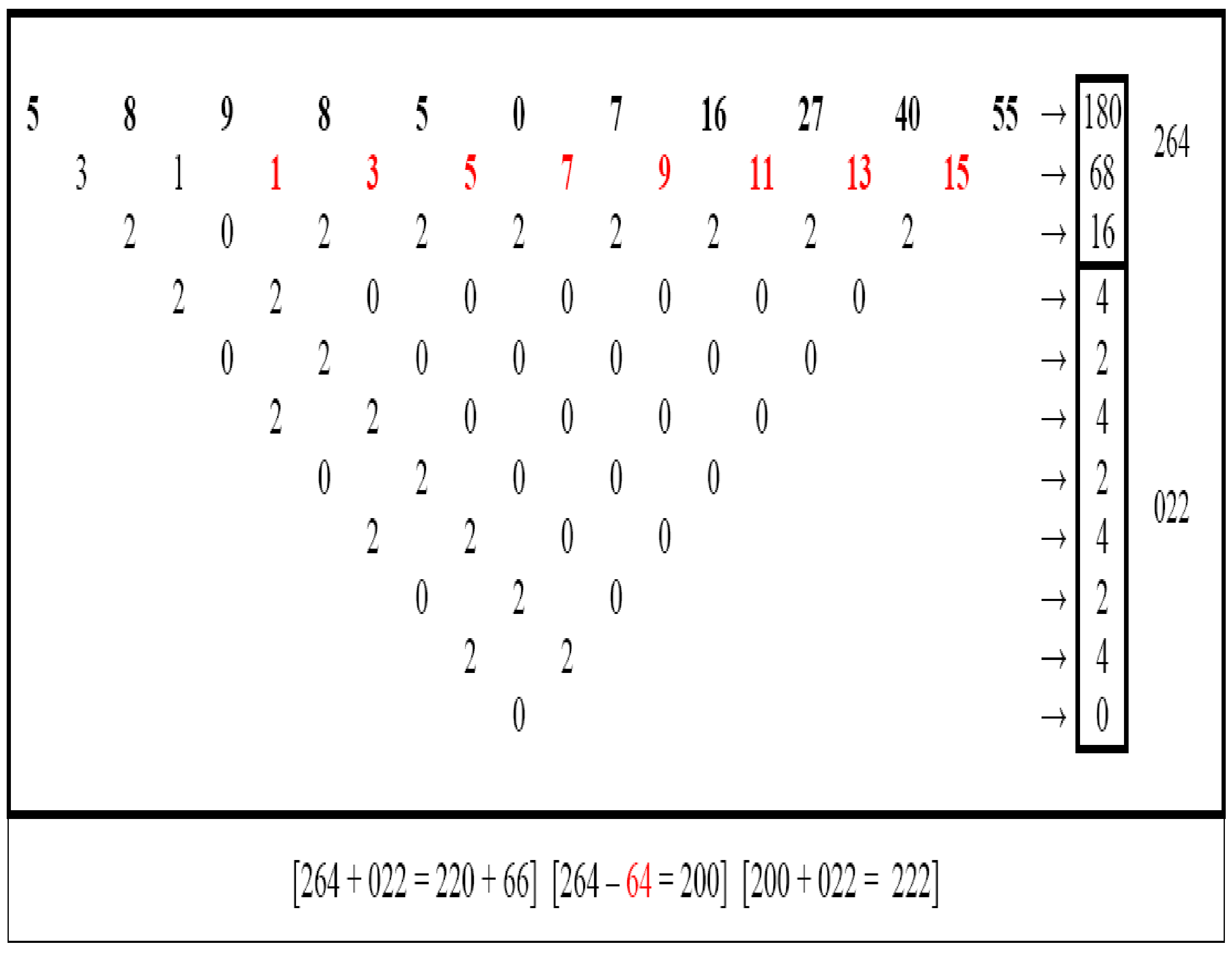
[(TVSL 36 + HCDS 28 + QWER 56 = 120



01. G	GG (6)	02. F	UU (4)	03. L	Odd (115) / Even (124)
04. P	CC (6)	05. N	AA (4)	06. K	
07. A	GC (6)	08. Y	UA (4)	09.ct	
10. R	CG (6)	11. I	AU (4)	12. M	
13. V	GU (5)	14. C	UG (5)	15. W	
16. T	AC (5)	17. H	CA (5)	18. Q	
19. L	CU (5)	20. S	AG (5)	21. R	
22. S	UC (5)	23. D	GA (5)	24. E	
28 38	(10)	39 39	(00)	48 47	(01)
66		78		60+35	



a	b			c		d	e	f
01	10	**11**	13	34		**11** + [(1 x 1) + 5)] = 034:2	13 | 31	(2 x 9)
02	20	**22**	26	68		**22** + [(2 x 2) + 8)] = 068:2		
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	594 (66 x 9)
0A	A0	**AA**	130	340		**AA** + [(10 x 10) – 40)] = 340:2	34 = 2 x 17 51 = 3 x 17	
0B	B0	**BB**	143	374		**BB** + [(11 x 11) – 55)] = 374:2		
34 + 374 = 2 x 204 68 + 340 = 2 x 204						102 + 306 = 2 x 204 136 + 272 = 2 x 204 170 + 238 = 2 x 204	374 = 2 x 187 187 + 197 = **384**	



5 8 9 8 5 0 7 16 27 40 55 → 180

3 1 1 3 5 7 9 11 13 15 → 68

2 0 2 2 2 2 2 2 2 → 16

2 2 0 0 0 0 0 0 → 4

0 2 0 0 0 0 0 → 2

2 2 0 0 0 0 → 4

0 2 0 0 0 → 2

2 2 0 0 → 4

0 2 0 → 2

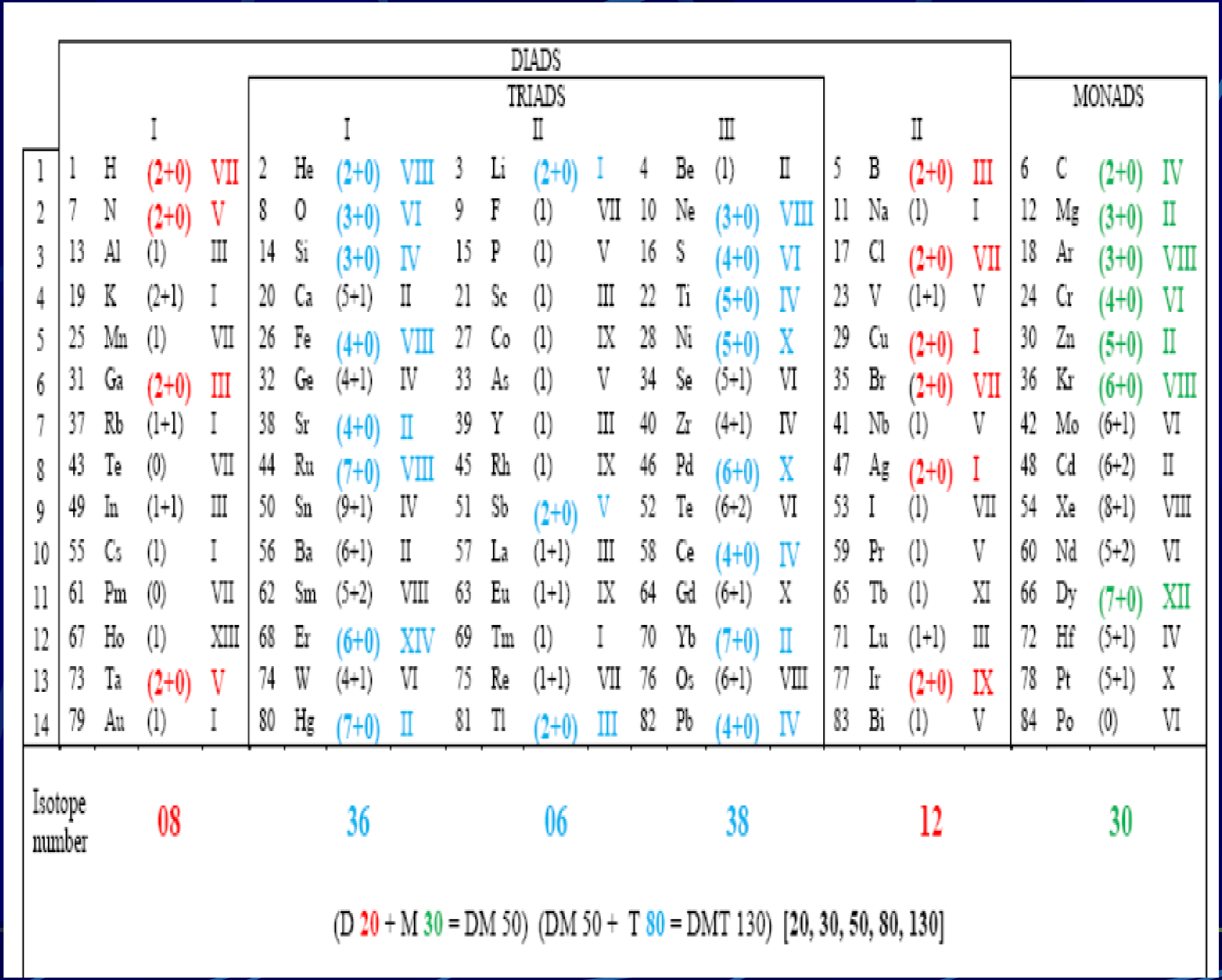
2 2 → 4

0 → 0

264

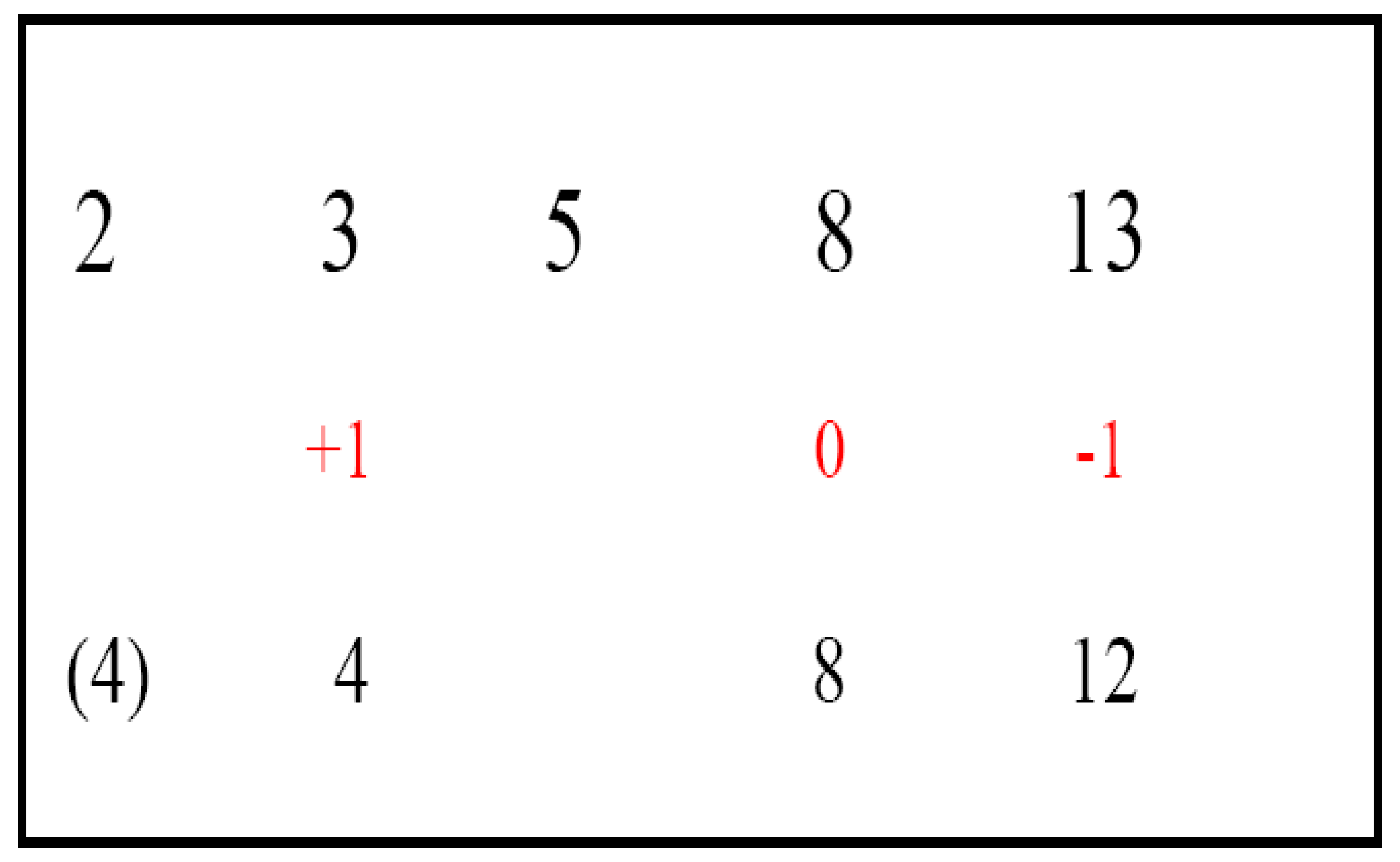
022

[264 + 022 = 220 + 66] [264 – 64 = 200] [200 + 022 = 222]



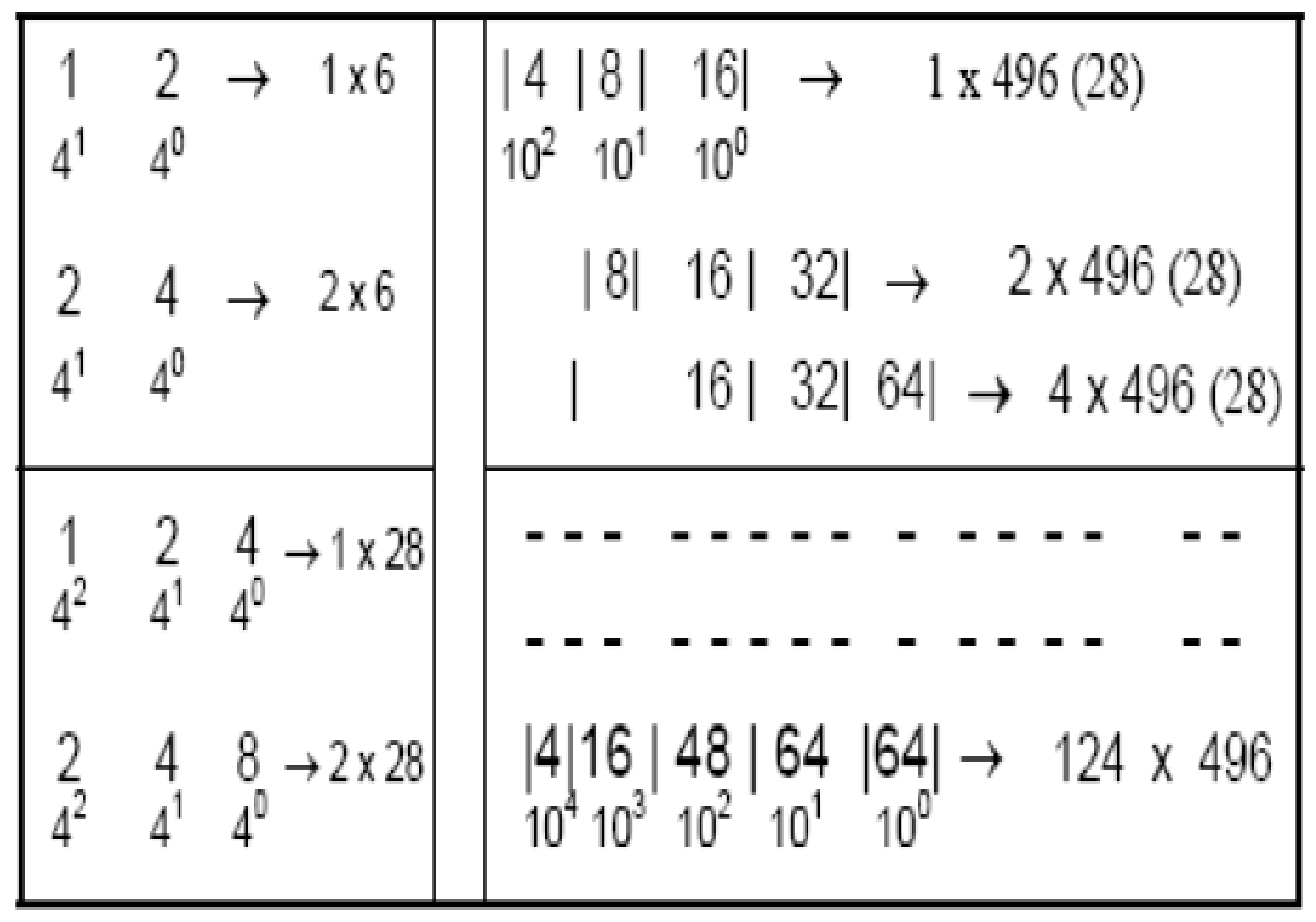
	DIADS																							MONADS			
					TRIADS																						
		I				I				II				III				II							
1	1	H	(2+0)	VII	2	He	(2+0)	VIII	3	Li	(2+0)	I	4	Be	(1)	II	5	B	(2+0)	III	6	C	(2+0)	IV
2	7	N	(2+0)	V	8	O	(3+0)	VI	9	F	(1)	VII	10	Ne	(3+0)	VIII	11	Na	(1)	I	12	Mg	(3+0)	II
3	13	Al	(1)	III	14	Si	(3+0)	IV	15	P	(1)	V	16	S	(4+0)	VI	17	Cl	(2+0)	VII	18	Ar	(3+0)	VIII
4	19	K	(2+1)	I	20	Ca	(5+1)	II	21	Sc	(1)	III	22	Ti	(5+0)	IV	23	V	(1+1)	V	24	Cr	(4+0)	VI
5	25	Mn	(1)	VII	26	Fe	(4+0)	VIII	27	Co	(1)	IX	28	Ni	(5+0)	X	29	Cu	(2+0)	I	30	Zn	(5+0)	II
6	31	Ga	(2+0)	III	32	Ge	(4+1)	IV	33	As	(1)	V	34	Se	(5+1)	VI	35	Br	(2+0)	VII	36	Kr	(6+0)	VIII
7	37	Rb	(1+1)	I	38	Sr	(4+0)	II	39	Y	(1)	III	40	Zr	(4+1)	IV	41	Nb	(1)	V	42	Mo	(6+1)	VI
8	43	Te	(0)	VII	44	Ru	(7+0)	VIII	45	Rh	(1)	IX	46	Pd	(6+0)	X	47	Ag	(2+0)	I	48	Cd	(6+2)	II
9	49	In	(1+1)	III	50	Sn	(9+1)	IV	51	Sb	(2+0)	V	52	Te	(6+2)	VI	53	I	(1)	VII	54	Xe	(8+1)	VIII
10	55	Cs	(1)	I	56	Ba	(6+1)	II	57	La	(1+1)	III	58	Ce	(4+0)	IV	59	Pr	(1)	V	60	Nd	(5+2)	VI
11	61	Pm	(0)	VII	62	Sm	(5+2)	VIII	63	Eu	(1+1)	IX	64	Gd	(6+1)	X	65	Tb	(1)	XI	66	Dy	(7+0)	XII
12	67	Ho	(1)	XIII	68	Er	(6+0)	XIV	69	Tm	(1)	I	70	Yb	(7+0)	II	71	Lu	(1+1)	III	72	Hf	(5+1)	IV
13	73	Ta	(2+0)	V	74	W	(4+1)	VI	75	Re	(1+1)	VII	76	Os	(6+1)	VIII	77	Ir	(2+0)	IX	78	Pt	(5+1)	X
14	79	Au	(1)	I	80	Hg	(7+0)	II	81	Tl	(2+0)	III	82	Pb	(4+0)	IV	83	Bi	(1)	V	84	Po	(0)	VI
Isotope number			08				36				06				38				12				30	

(D 20 + M 30 = DM 50) (DM 50 + T 80 = DMT 130) [20, 30, 50, 80, 130]



2	3	5	8	13
	+1		0	-1
(4)	4		8	12

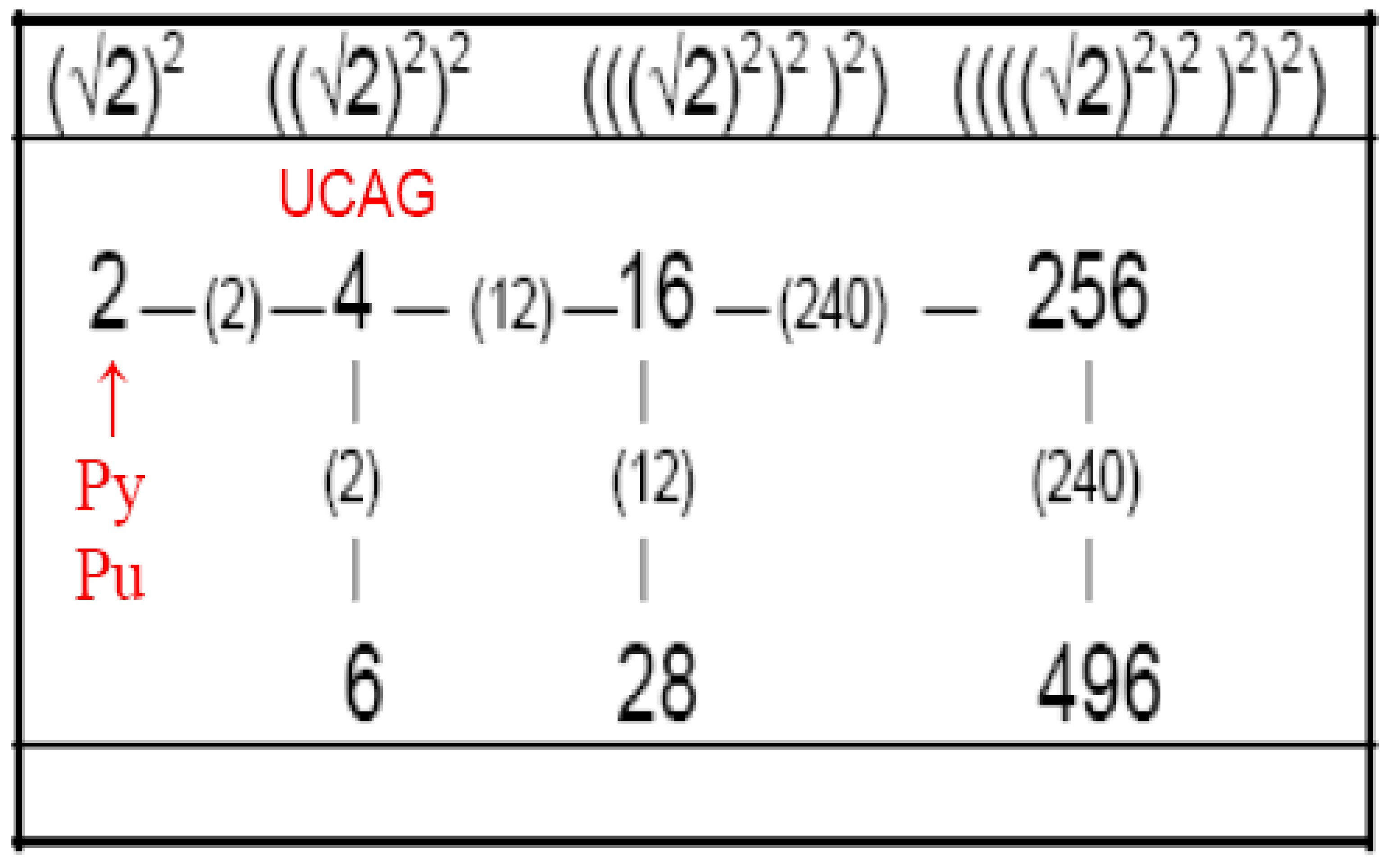
Generating binary sequences of perfect numbers in Boolean spaces



<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>

Rakočević, 2007a, Tab. 12, p. 96.

Binary multiplication of the number 2 in relation to perfect numbers



$(\sqrt{2})^2$ $((\sqrt{2})^2)^2$ $(((\sqrt{2})^2)^2)^2)$ $((((\sqrt{2})^2)^2)^2)^2)$

UCAG

2 — (2) — 4 — (12) — 16 — (240) — 256

↑

Py

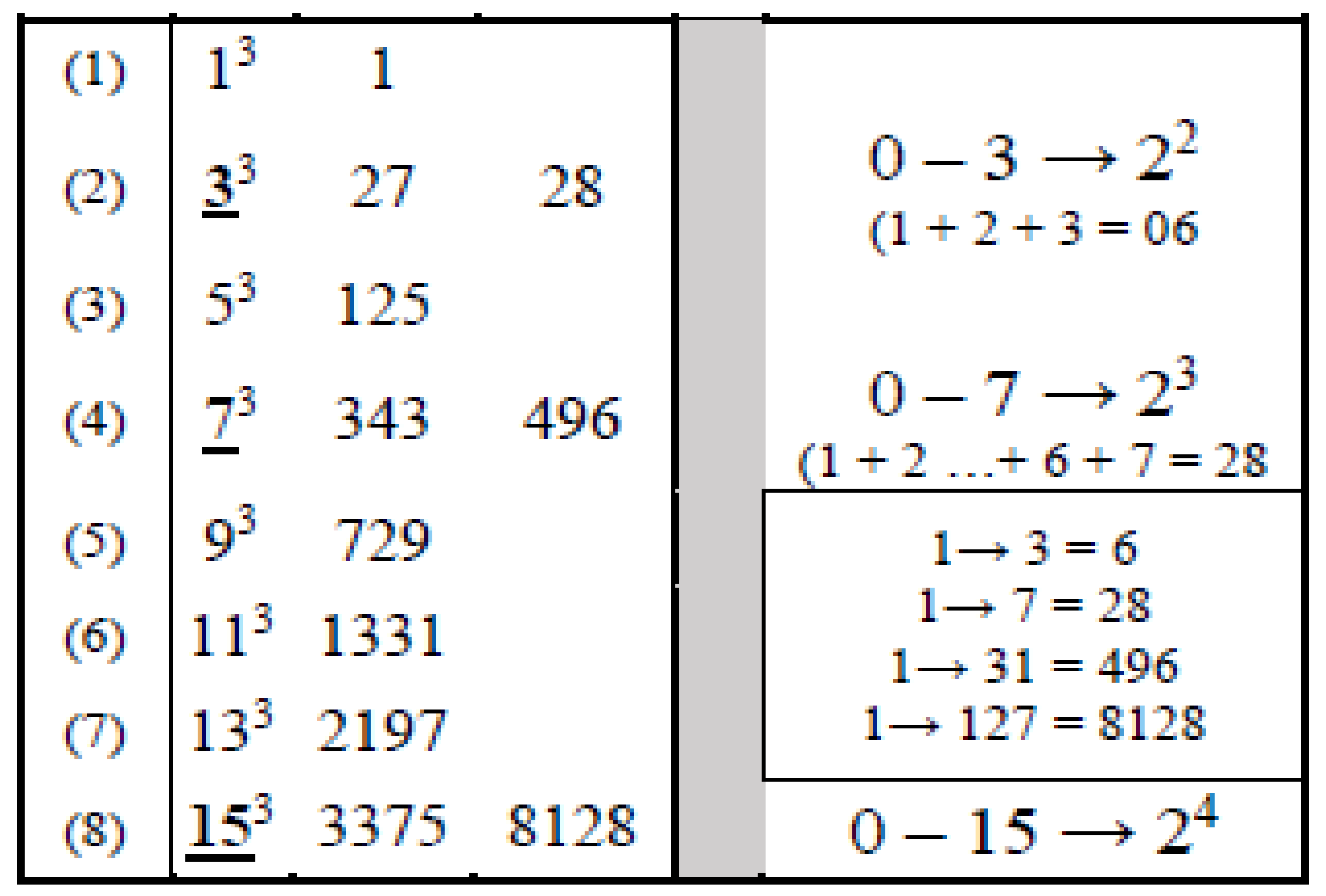
Pu

(2) (12) (240)

6 28 496

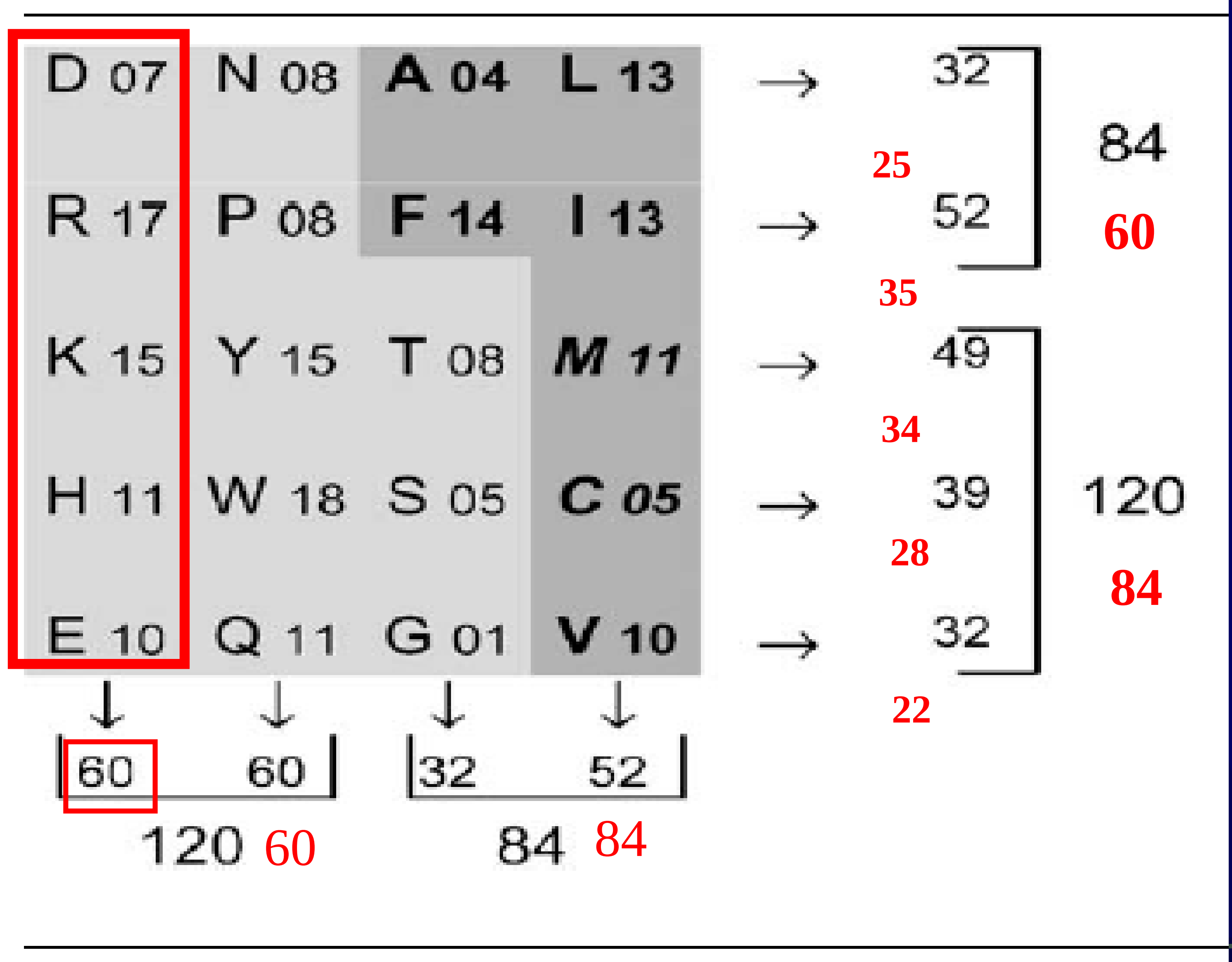
Rakočević, 2007a, Tab. 5, p. 82.

Generating of perfect numbers in relation to the series of odd natural numbers



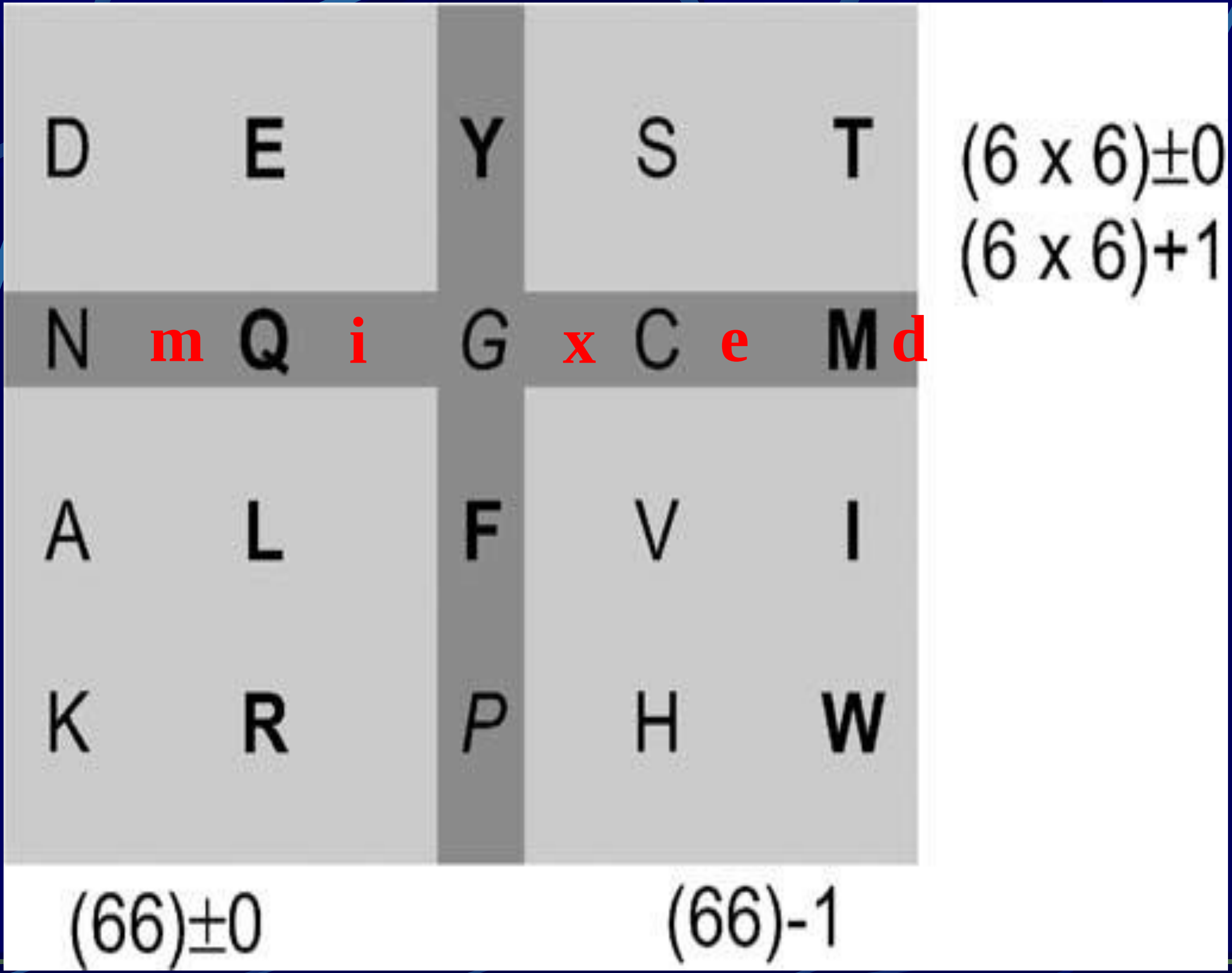
(1)	1^3	1			
(2)	$\underline{3}^3$	27	28		$0 - 3 \rightarrow 2^2$ $(1 + 2 + 3 = 06$
(3)	5^3	125			
(4)	$\underline{7}^3$	343	496		$0 - 7 \rightarrow 2^3$ $(1 + 2 \ldots + 6 + 7 = 28$
(5)	9^3	729			$1 \rightarrow 3 = 6$ $1 \rightarrow 7 = 28$ $1 \rightarrow 31 = 496$ $1 \rightarrow 127 = 8128$
(6)	11^3	1331			
(7)	13^3	2197			
(8)	$\underline{15}^3$	3375	8128		$0 - 15 \rightarrow 2^4$

Rakočević, 2007a, Tab. 4, p. 82.



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

mixed



O D E Y S T

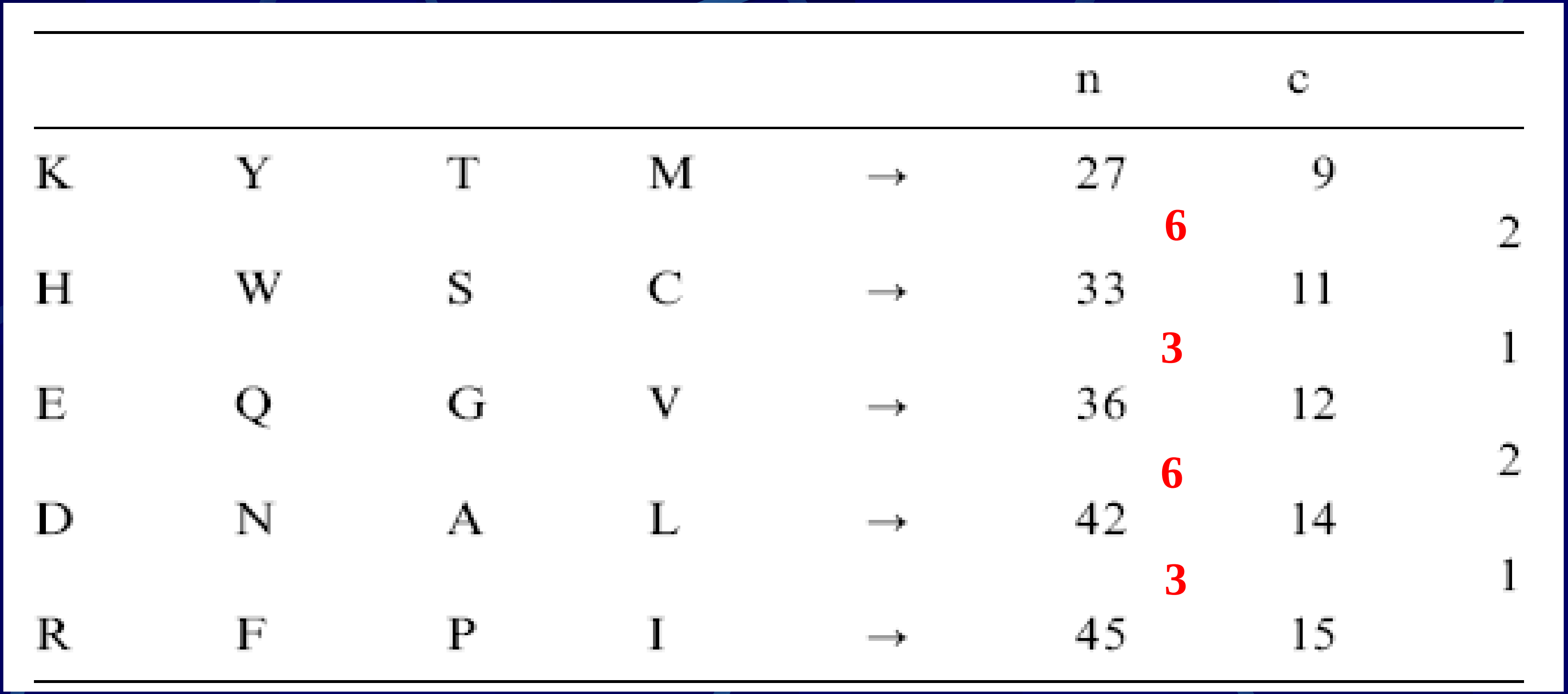
N m Q i G x C e M d

C A L F V I

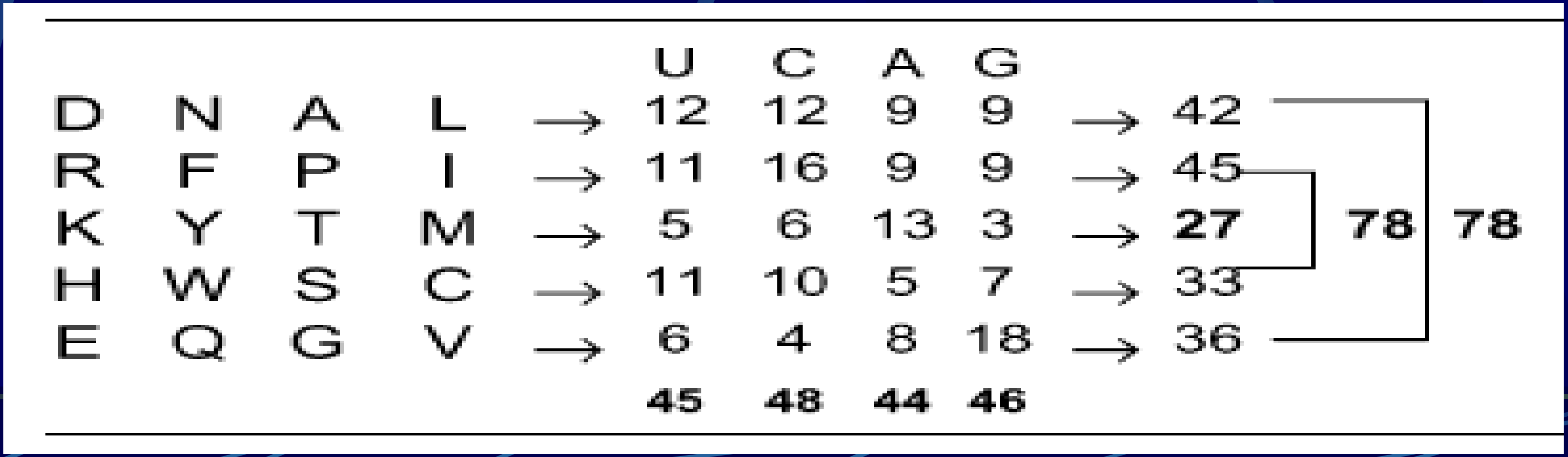
N K R P H W

(6 x 6)±0
(6 x 6)+1

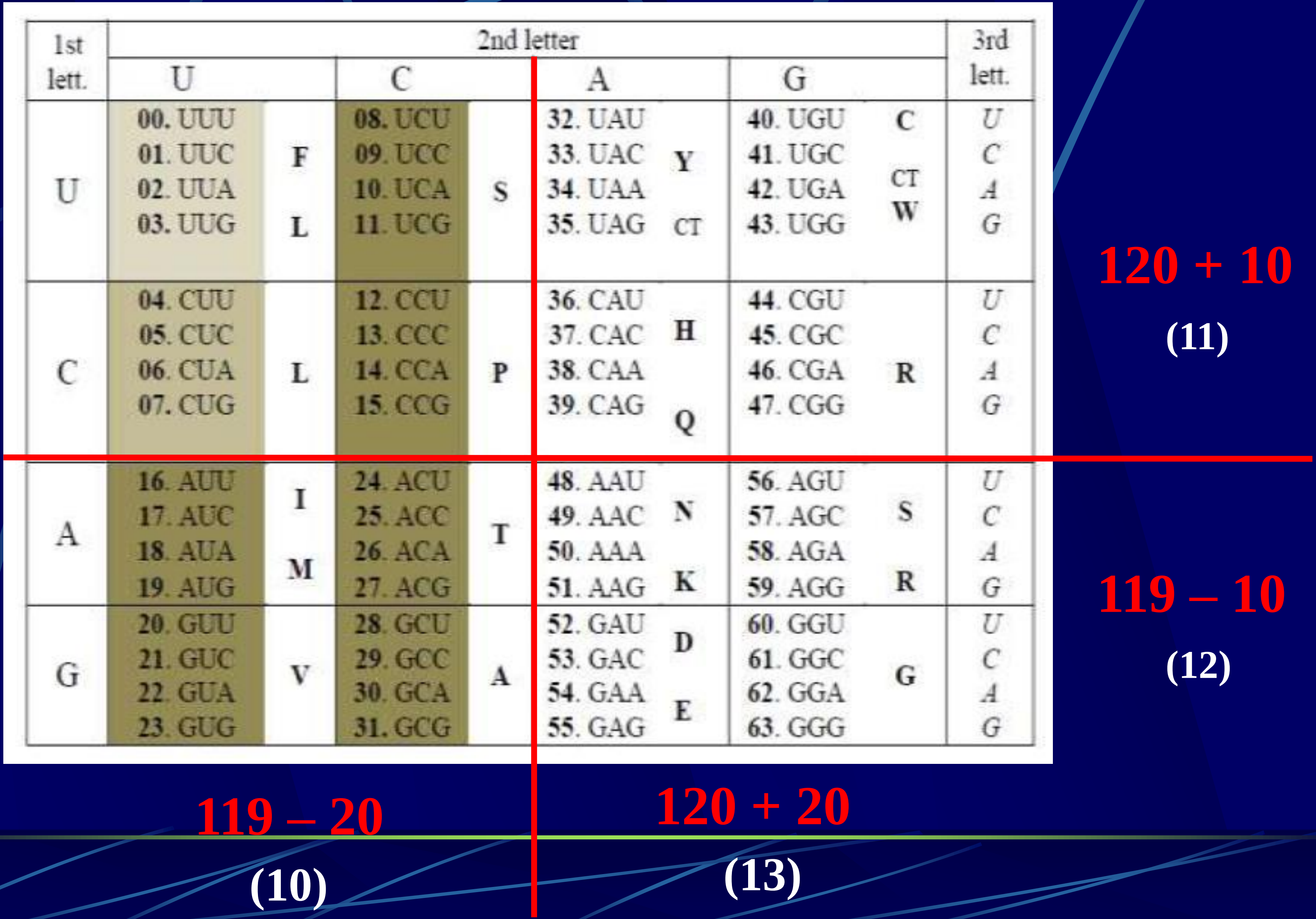
(66)±0
(66)-1



					n		c	
K	Y	T	M	→	27		9	
						6		2
H	W	S	C	→	33		11	
						3		1
E	Q	G	V	→	36		12	
						6		2
D	N	A	L	→	42		14	
						3		1
R	F	P	I	→	45		15	



					U	C	A	G				
D	N	A	L	→	12	12	9	9	→	42		
R	F	P	I	→	11	16	9	9	→	45		
K	Y	T	M	→	5	6	13	3	→	27	**78**	**78**
H	W	S	C	→	11	10	5	7	→	33		
E	Q	G	V	→	6	4	8	18	→	36		
					45	**48**	**44**	**46**				



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

120 + 10

(11)

119 – 10

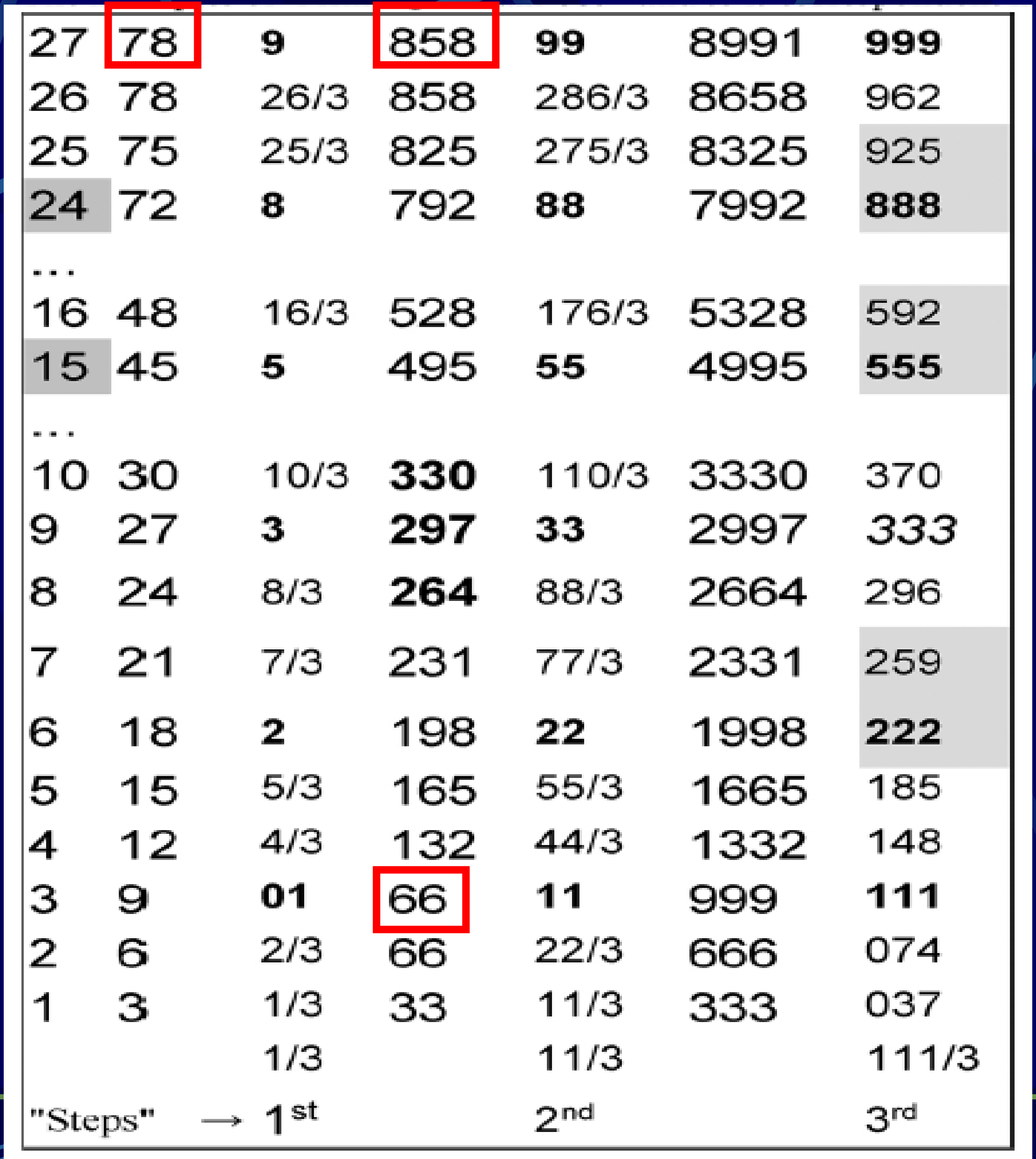
(12)

119 – 20

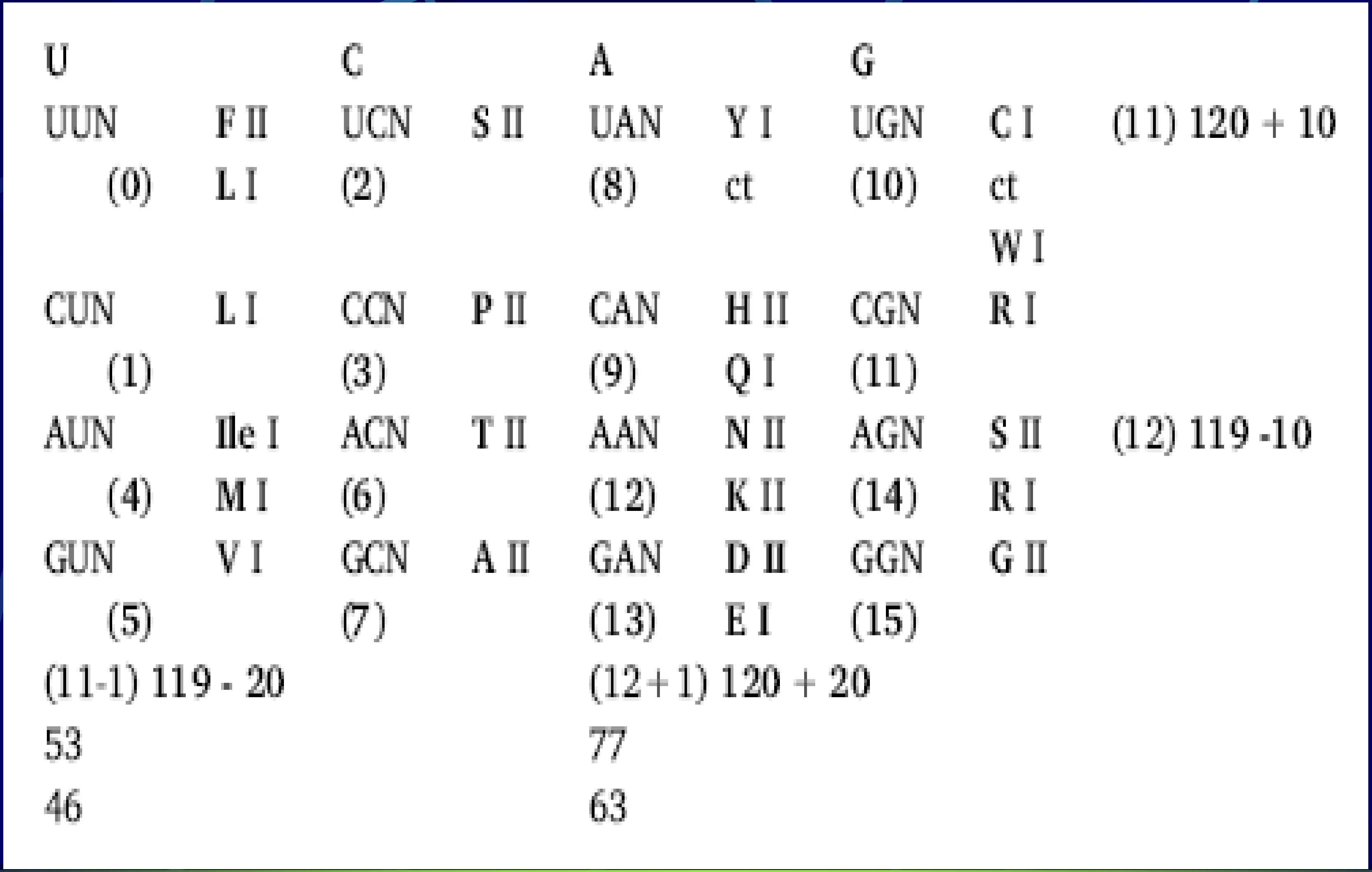
(10)

120 + 20

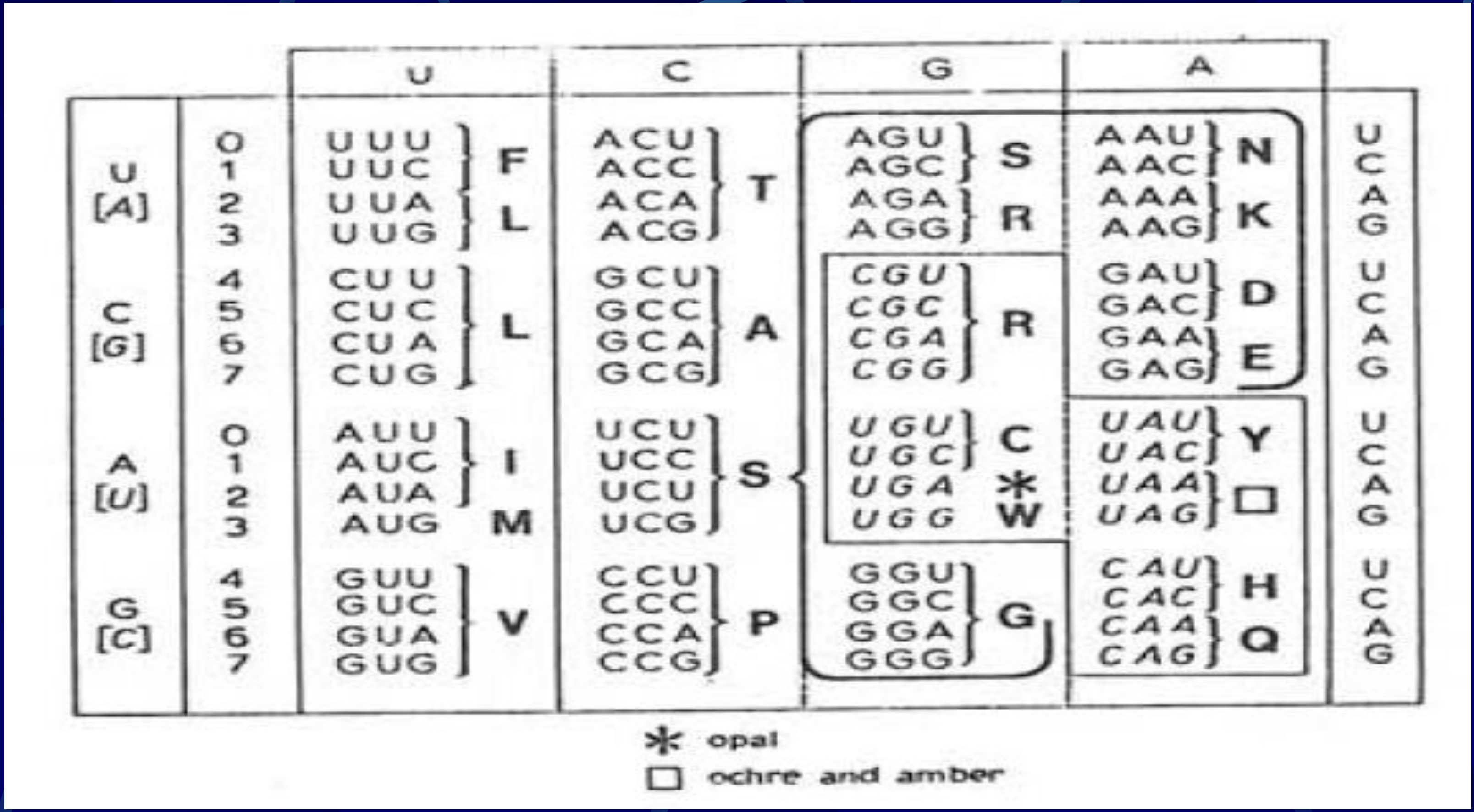
(13)



27	78	**9**	858	**99**	8991	**999**
26	78	26/3	858	286/3	8658	962
25	75	25/3	825	275/3	8325	925
24	72	**8**	792	**88**	7992	**888**
...						
16	48	16/3	528	176/3	5328	592
15	45	**5**	495	**55**	4995	**555**
...						
10	30	10/3	**330**	110/3	3330	370
9	27	**3**	**297**	**33**	2997	*333*
8	24	8/3	**264**	88/3	2664	296
7	21	7/3	231	77/3	2331	259
6	18	**2**	198	**22**	1998	**222**
5	15	5/3	165	55/3	1665	185
4	12	4/3	132	44/3	1332	148
3	9	**01**	66	**11**	999	**111**
2	6	2/3	66	22/3	666	074
1	3	1/3	33	11/3	333	037
		1/3		11/3		111/3
"Steps"	→	1st		2nd		3rd



U		C		A		G		
UUN	F II	UCN	S II	UAN	Y I	UGN	C I	(11) 120 + 10
(0)	L I	(2)		(8)	ct	(10)	ct	
							W I	
CUN	L I	CCN	P II	CAN	H II	CGN	R I	
(1)		(3)		(9)	Q I	(11)		
AUN	Ile I	ACN	T II	AAN	N II	AGN	S II	(12) 119 -10
(4)	M I	(6)		(12)	K II	(14)	R I	
GUN	V I	GCN	A II	GAN	D II	GGN	G II	
(5)		(7)		(13)	E I	(15)		
(11-1) 119 - 20				(12+1) 120 + 20				
53				77				
46				63				



		U		C		G		A		
U [A]	0	UUU	F	ACU	T	AGU	S	AAU	N	U
	1	UUC		ACC		AGC		AAC		C
	2	UUA	L	ACA		AGA	R	AAA	K	A
	3	UUG		ACG		AGG		AAG		G
C [G]	4	CUU	L	GCU	A	CGU	R	GAU	D	U
	5	CUC		GCC		CGC		GAC		C
	6	CUA		GCA		CGA		GAA	E	A
	7	CUG		GCG		CGG		GAG		G
A [U]	0	AUU	I	UCU	S	UGU	C	UAU	Y	U
	1	AUC		UCC		UGC		UAC		C
	2	AUA		UCU		UGA	*	UAA	□	A
	3	AUG	M	UCG		UGG	W	UAG		G
G [C]	4	GUU	V	CCU	P	GGU	G	CAU	H	U
	5	GUC		CCC		GGC		CAC		C
	6	GUA		CCA		GGA		CAA	Q	A
	7	GUG		CCG		GGG		CAG		G

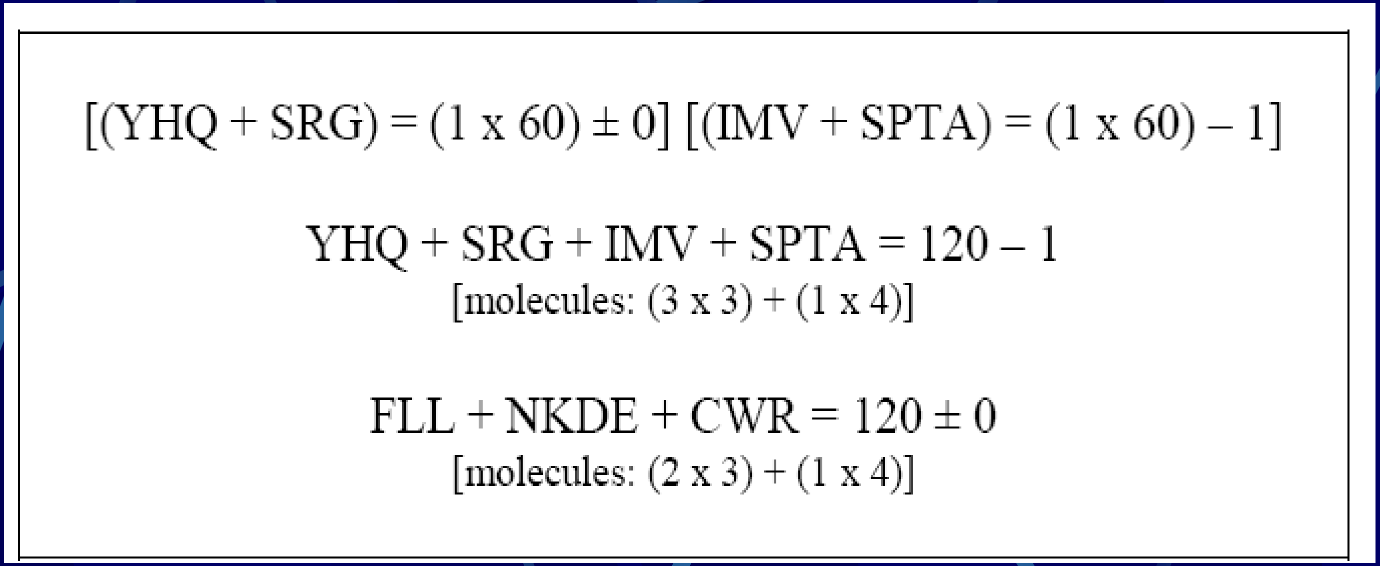
* opal

□ ochre and amber

[(YHQ + SRG) = (1 x 60) ± 0] [(IMV + SPTA) = (1 x 60) – 1]

YHQ + SRG + IMV + SPTA = 120 – 1
[molecules: (3 x 3) + (1 x 4)]

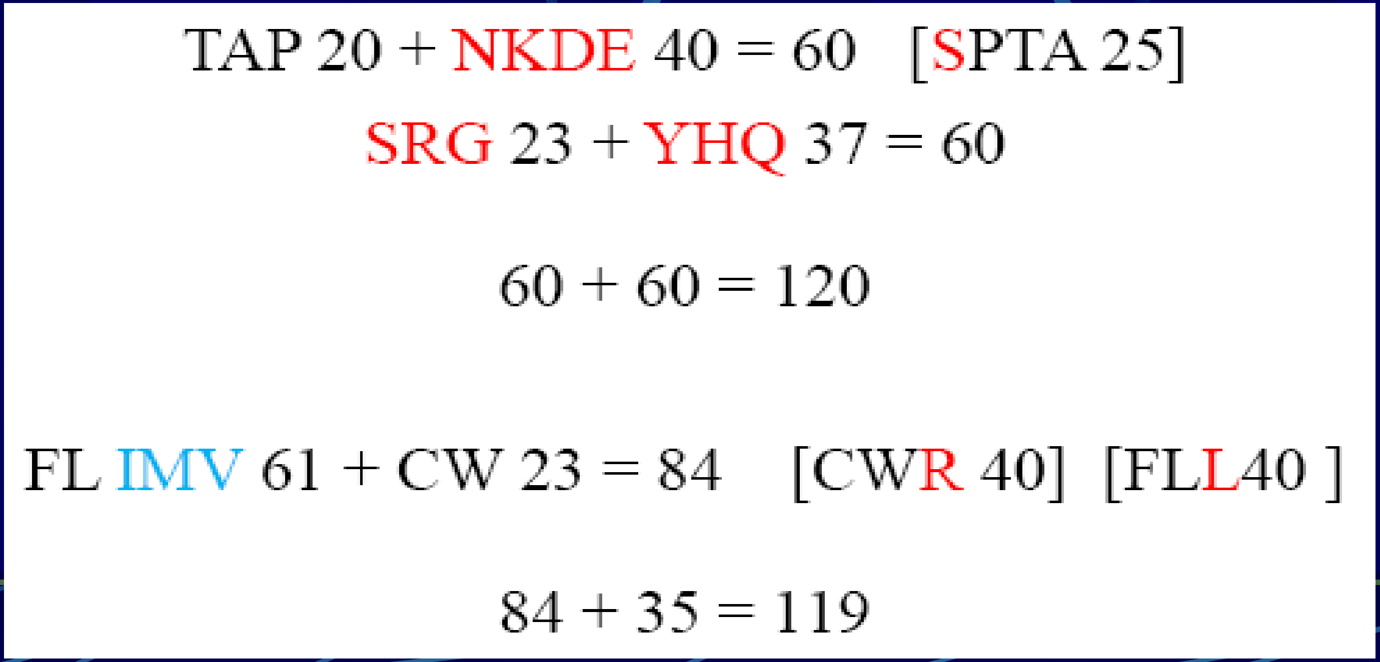
FLL + NKDE + CWR = 120 ± 0
[molecules: (2 x 3) + (1 x 4)]



[(YHQ + SRG) = (1 x 60) ± 0] [(IMV + SPTA) = (1 x 60) – 1]

YHQ + SRG + IMV + SPTA = 120 – 1
[molecules: (3 x 3) + (1 x 4)]

FLL + NKDE + CWR = 120 ± 0
[molecules: (2 x 3) + (1 x 4)]

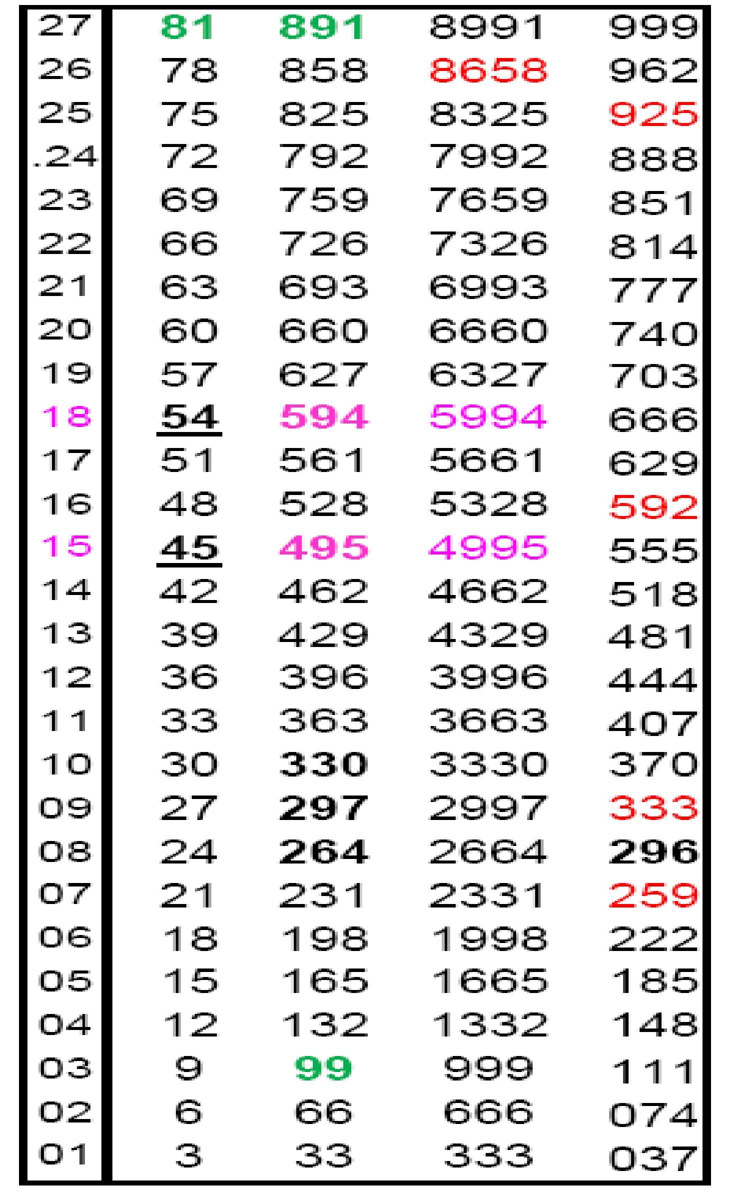


TAP 20 + NKDE 40 = 60 [SPTA 25]
SRG 23 + YHQ 37 = 60

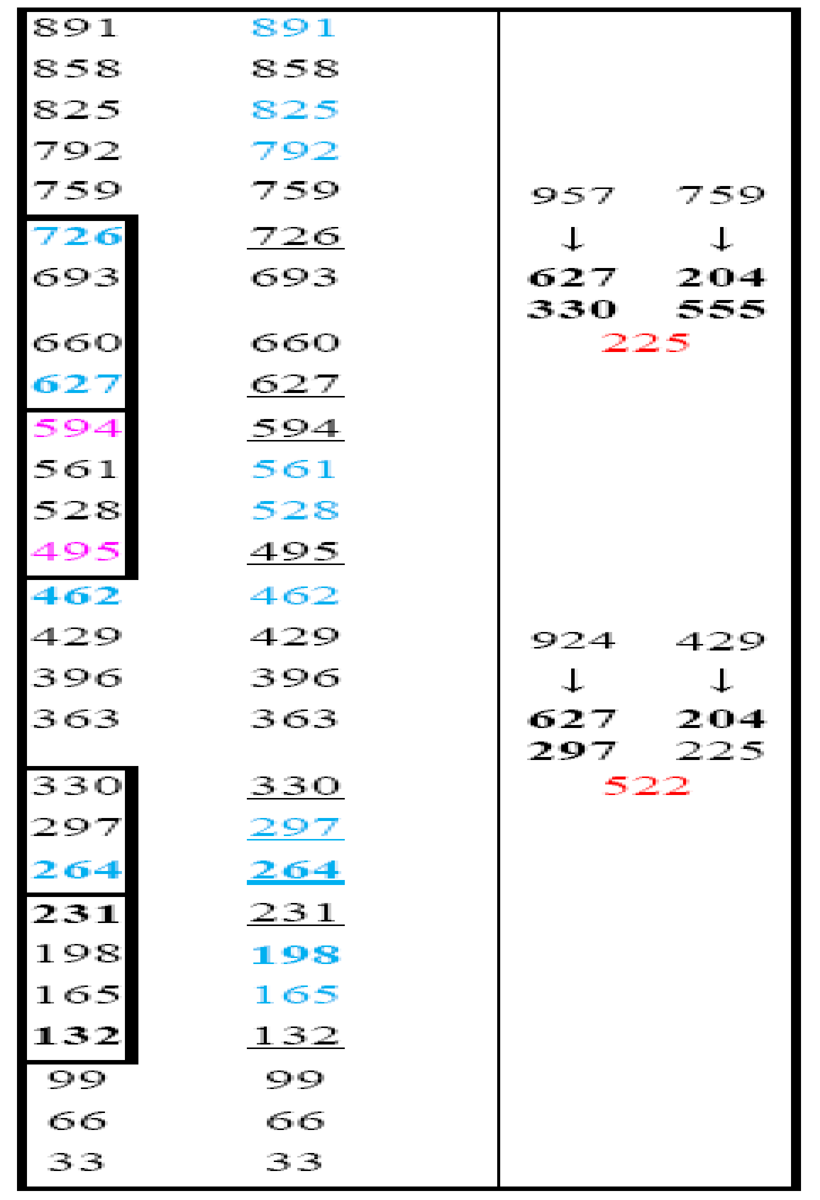
60 + 60 = 120

FL IMV 61 + CW 23 = 84 [CWR 40] [FLL40]

84 + 35 = 119



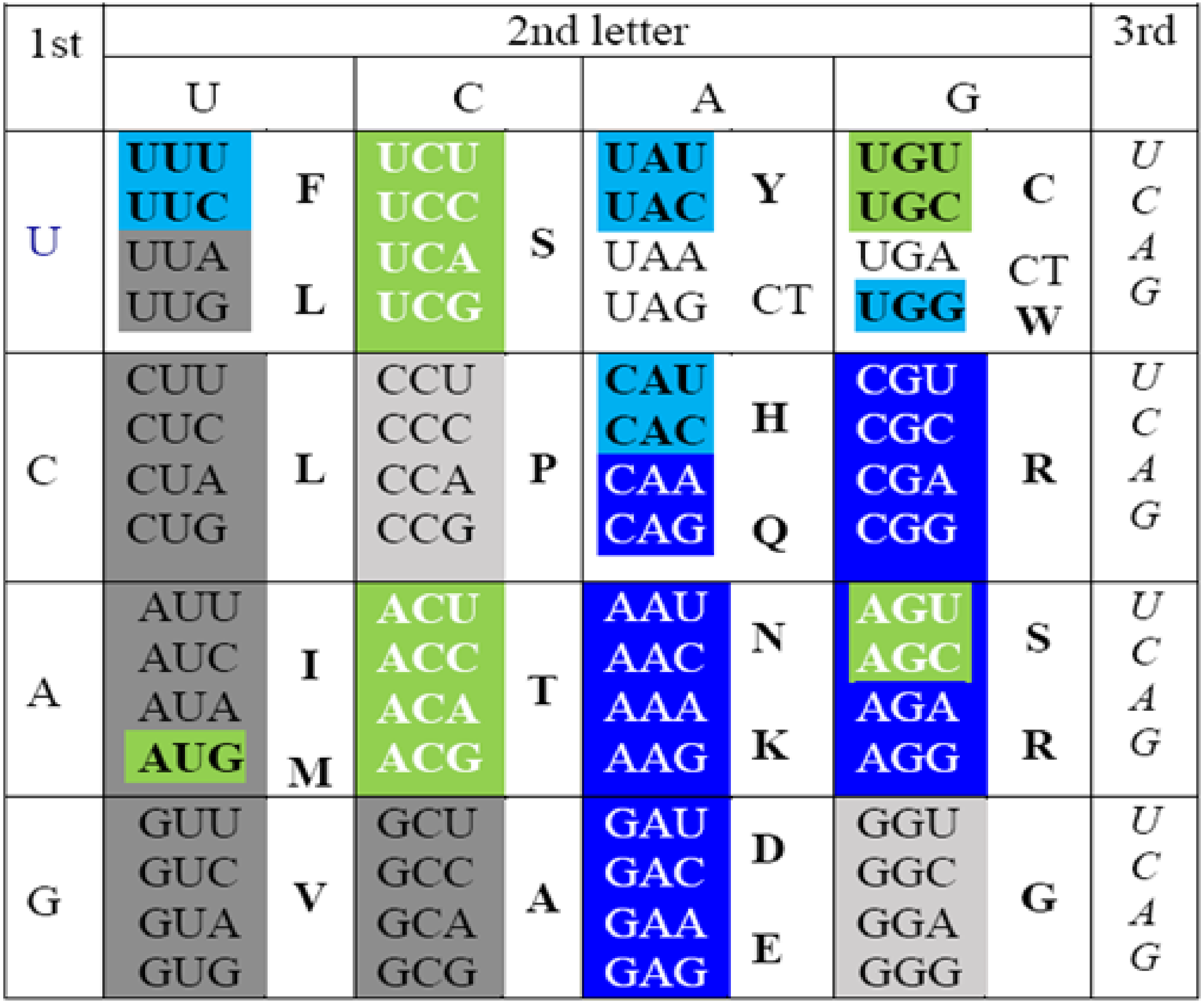
27	81	891	8991	999
26	78	858	8658	962
25	75	825	8325	925
.24	72	792	7992	888
23	69	759	7659	851
22	66	726	7326	814
21	63	693	6993	777
20	60	660	6660	740
19	57	627	6327	703
18	**54**	594	5994	666
17	51	561	5661	629
16	48	528	5328	592
15	**45**	495	4995	555
14	42	462	4662	518
13	39	429	4329	481
12	36	396	3996	444
11	33	363	3663	407
10	30	**330**	3330	370
09	27	**297**	2997	333
08	24	**264**	2664	**296**
07	21	231	2331	259
06	18	198	1998	222
05	15	165	1665	185
04	12	132	1332	148
03	9	99	999	111
02	6	66	666	074
01	3	33	333	037



891	891
858	858
825	825
792	792
759	759
726	726
693	693
660	660
627	627
594	594
561	561
528	528
495	495
462	462
429	429
396	396
363	363
330	330
297	297
264	**264**
231	231
198	**198**
165	165
132	132
99	99
66	66
33	33

957 759
↓ ↓
627 **204**
330 **555**
225

924 429
↓ ↓
627 **204**
297 225
522



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

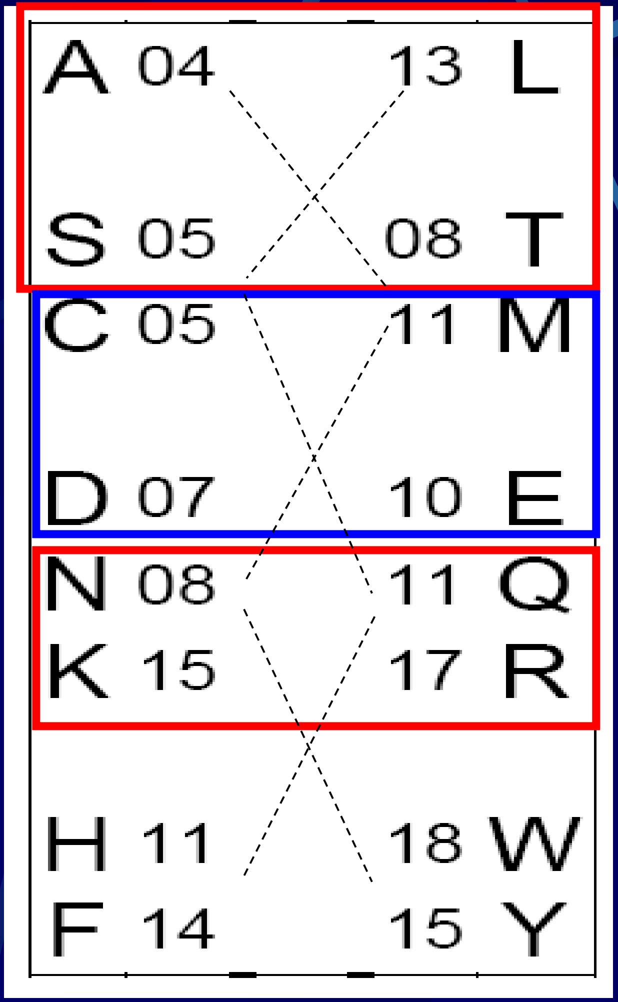
2. Appendix Slides explanations

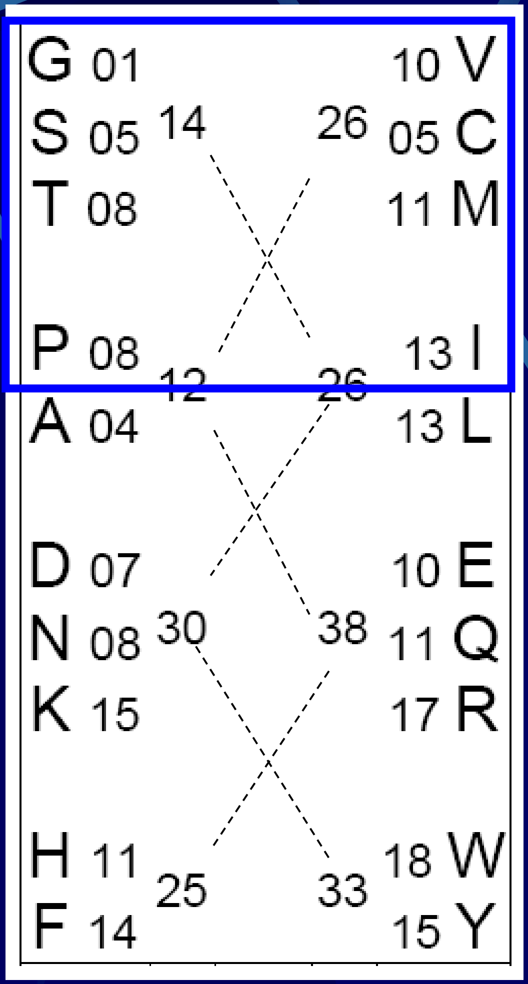
3. *Explanation* ... :
4. *Explanation* ... :
5. *Explanation* ... :
6. *Explanation* ... :
7. *Explanation* ... :

3. Slides explanations

Materials (Slides) for future Supplements

Amino acid system-arrangements (Sis-ars)


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


G 01 10 V
S 05 14 26 05 C
T 08 11 M
P 08 13 I
12 26
A 04 13 L
D 07 10 E
N 08 30 38 11 Q
K 15 17 R
H 11 18 W
25 33
F 14 15 Y

D−E−R−K−H/W−Y−F
N−Q−F−Y−W

D−R−K−H−E
N−F−Y−W−Q

A − P − T − S − G
L − I − M − C − V

D	N	A	L
R	F	P	I
K	Y	T	M
H	W	S	C
E	Q	G	V

86 / 86 **102 ± 1** **60 66 78**

(Atom number within amino acid side chains)

[124 / 421] [299 / 992]

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ELSEVIER

"A harmonic structure of the genetic code"

Journal of Theoretical Biology 229 (2004) 221–234

Journal of Theoretical Biology

www.elsevier.com/locate/jtbi

Isotope number (124 + 54 = 178) [135 + 108 = (1 x 243)]

124	124	54	54		a	b	c	d	M
	+11		x 2			nucleon number			
D	N	A	L	→	189	189	221	221 + 3	485.49 = 485
R	F	P	I	→	289	289	341	341+0	585.70=586
K	Y	T	M	→	299	299	351	351 + 2	595.71=596
H	W	S	C	→	289	289	331	331+1	585.64=586
E	Q	G	V	→	189	189	221	221 + 3	485.50 = 485

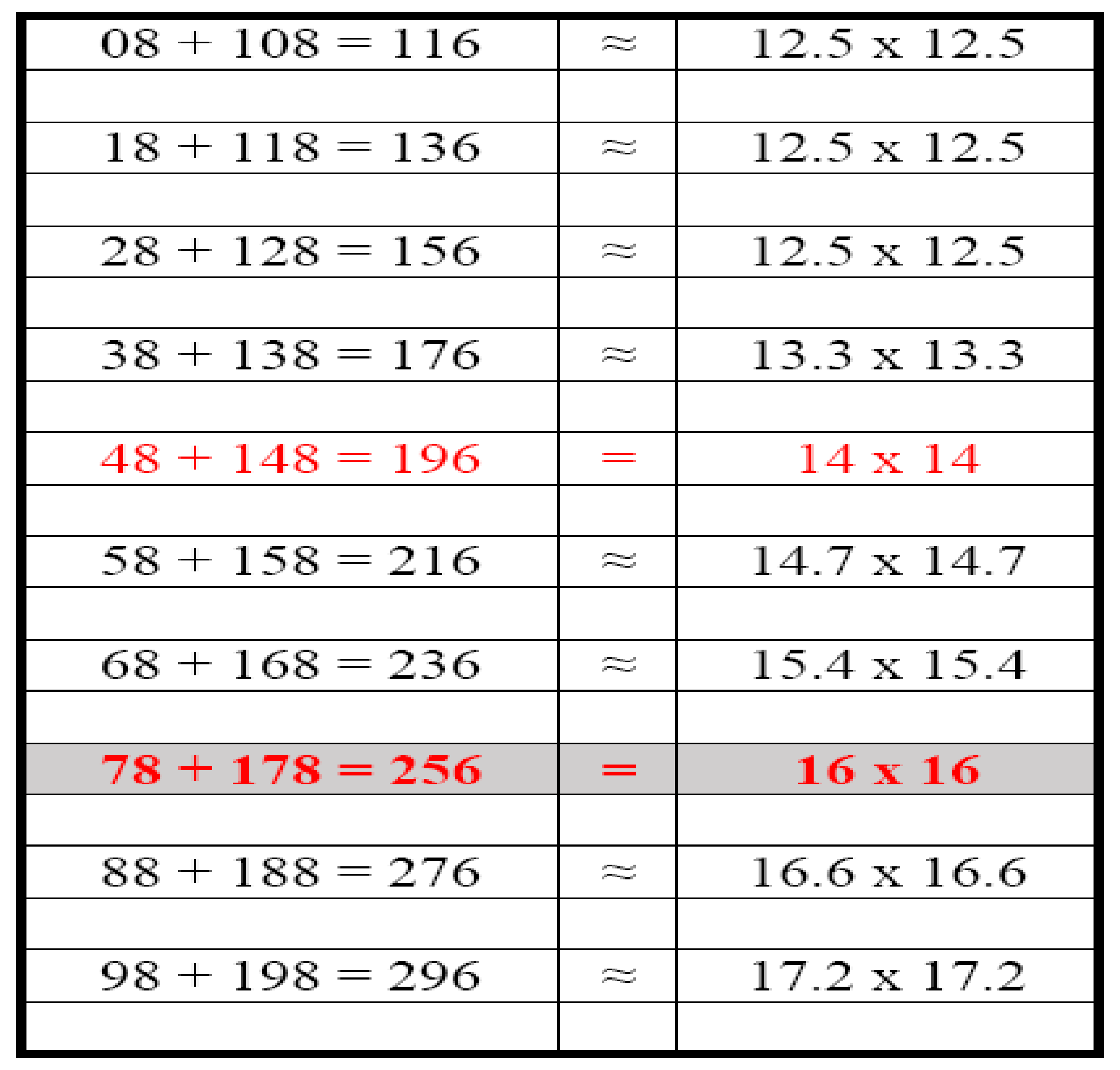
60 66 78

70 = 124 – 54; 30 =108 – **0**78 [60 + 66 = (2 x **0**63)]

1255 1255 1465 1465+9 2738.04

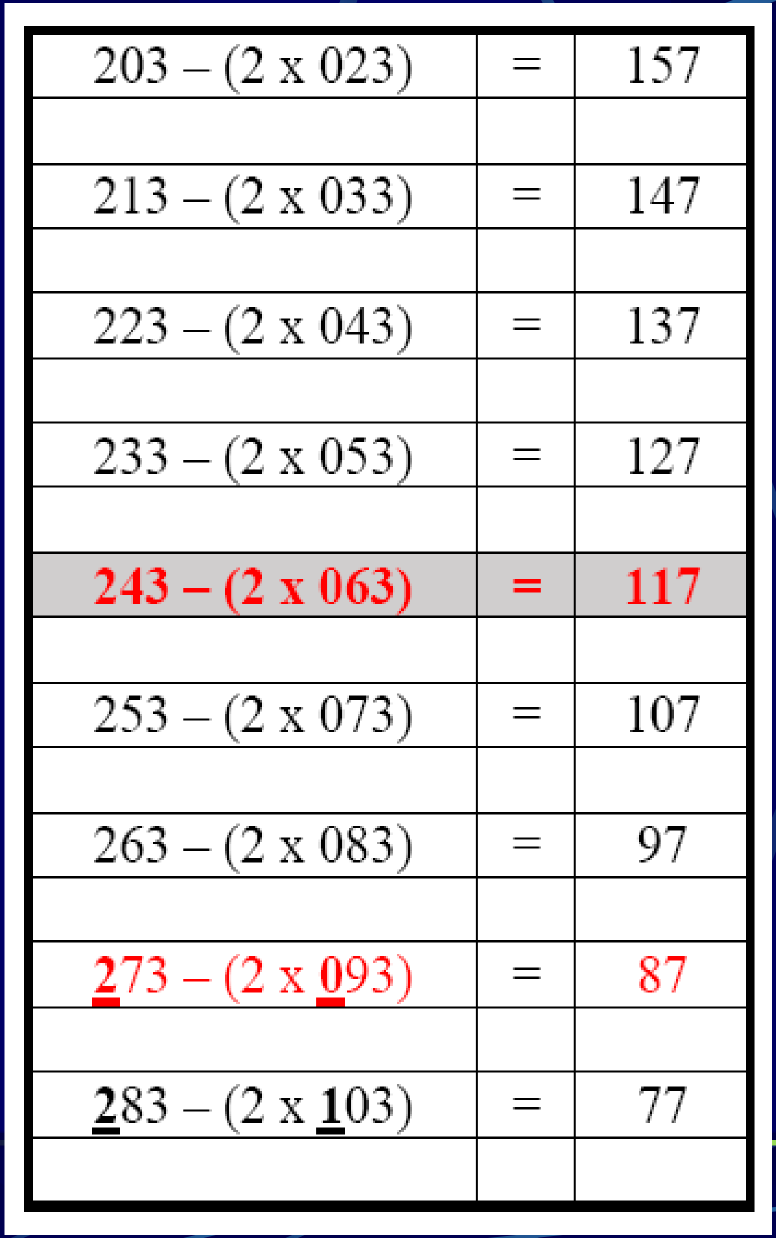
10 – 20 30 40 – 50 – 60 70 80 – 90

Relations with isotope number (I)

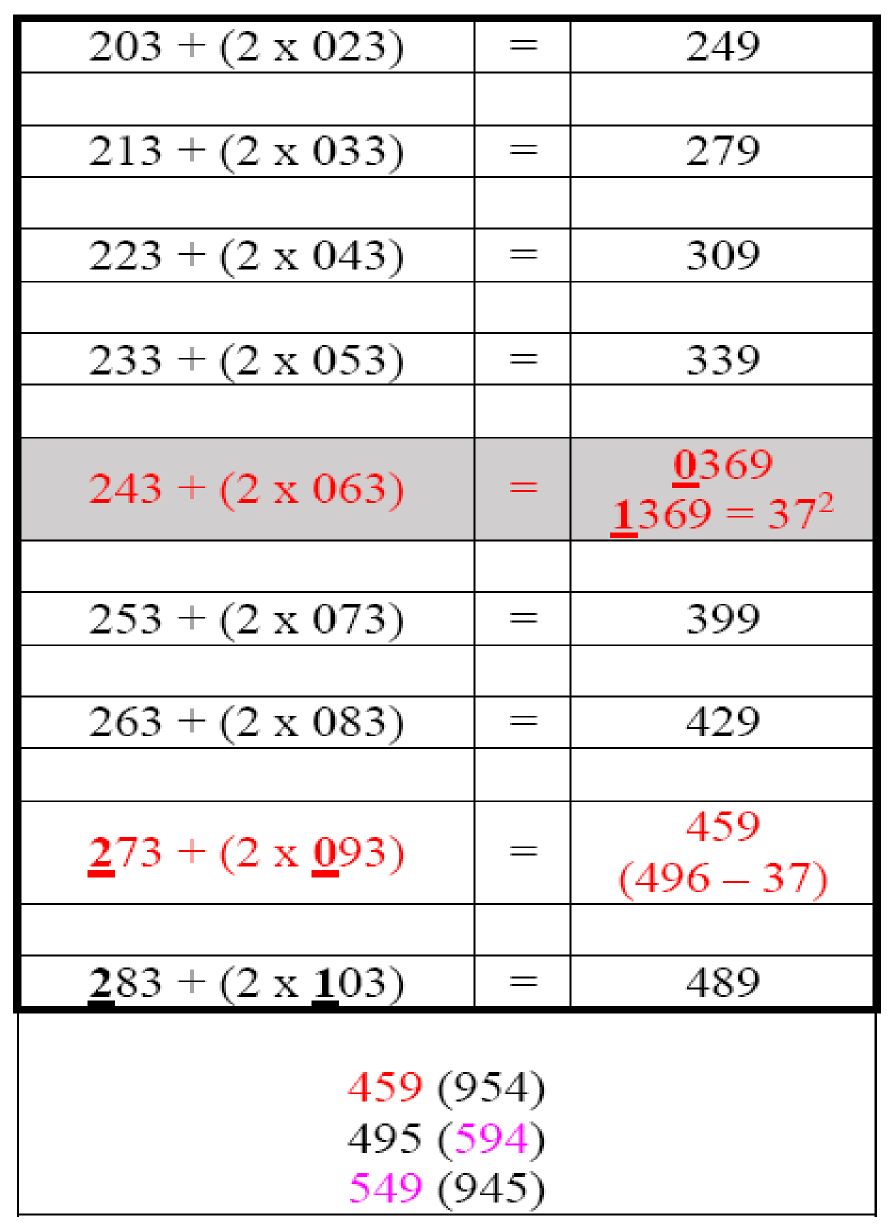


08 + 108 = 116	≈	12.5 x 12.5
18 + 118 = 136	≈	12.5 x 12.5
28 + 128 = 156	≈	12.5 x 12.5
38 + 138 = 176	≈	13.3 x 13.3
48 + 148 = 196	=	14 x 14
58 + 158 = 216	≈	14.7 x 14.7
68 + 168 = 236	≈	15.4 x 15.4
78 + 178 = 256	**=**	**16 x 16**
88 + 188 = 276	≈	16.6 x 16.6
98 + 198 = 296	≈	17.2 x 17.2

Relations with isotope number (II)



203 – (2 x 023)	=	157
213 – (2 x 033)	=	147
223 – (2 x 043)	=	137
233 – (2 x 053)	=	127
243 – (2 x 063)	**=**	**117**
253 – (2 x 073)	=	107
263 – (2 x 083)	=	97
273 – (2 x 093)	=	87
283 – (2 x 103)	=	77



203 + (2 x 023)	=	249
213 + (2 x 033)	=	279
223 + (2 x 043)	=	309
233 + (2 x 053)	=	339
243 + (2 x 063)	=	0369 1369 = 37^2
253 + (2 x 073)	=	399
263 + (2 x 083)	=	429
273 + (2 x 093)	=	459 (496 – 37)
283 + (2 x 103)	=	489

459 (954)
495 (594)
549 (945)

Relations with isotope number (III)

…

$(1 \longrightarrow 36 = 666)\ (072 = 36 + 36)$

$(1 \longrightarrow 37 = 703)\ (074 = 37 + 37)$

$(1 \longrightarrow 38 = 741)\ (076 = 38 + 38)$

$(1 \longrightarrow 39 = 780)\ (078 = 39 + 39)$

$(1 \longrightarrow 40 = 820)\ (080 = 40 + 40)$

$(1 \longrightarrow 41 = 861)\ (082 = 41 + 41)$

$(1 \longrightarrow 42 = 903)\ (084 = 42 + 42)$

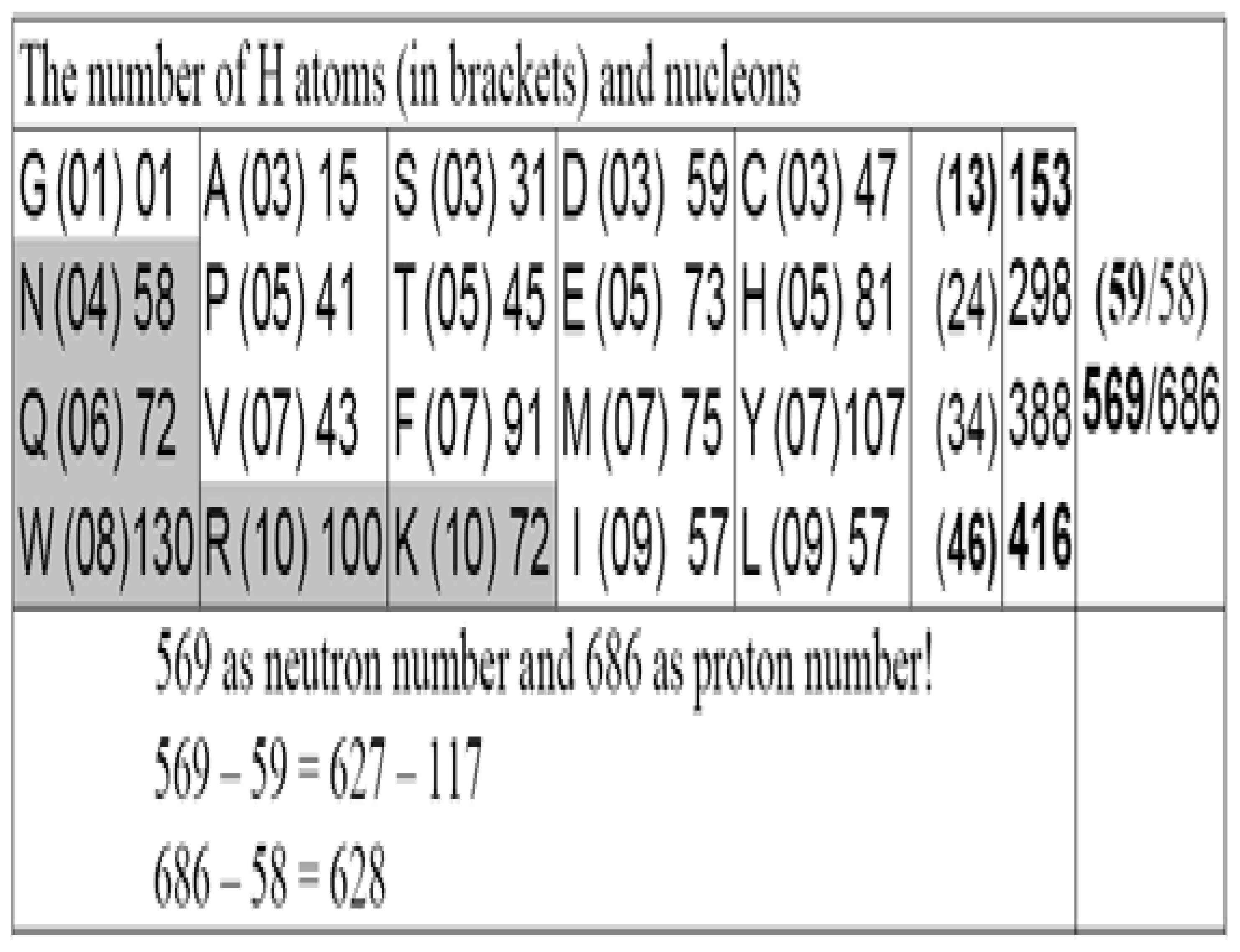
…

780 - 078 = 6 x 117
(780 | 087)

001
110

02	24	1		021, 023, 025, 027	241, 243, 245, 247
04	26	3		041, 043, 045, 047	261, 263, 265, 267
06		5		061, 063, 065, 067	
		7		(2 x 063) + (1 x 243) = 0369 [1369 = 37 x 37]	

System-arrangement of AAs thtough the number of hydrogen atoms (I)



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

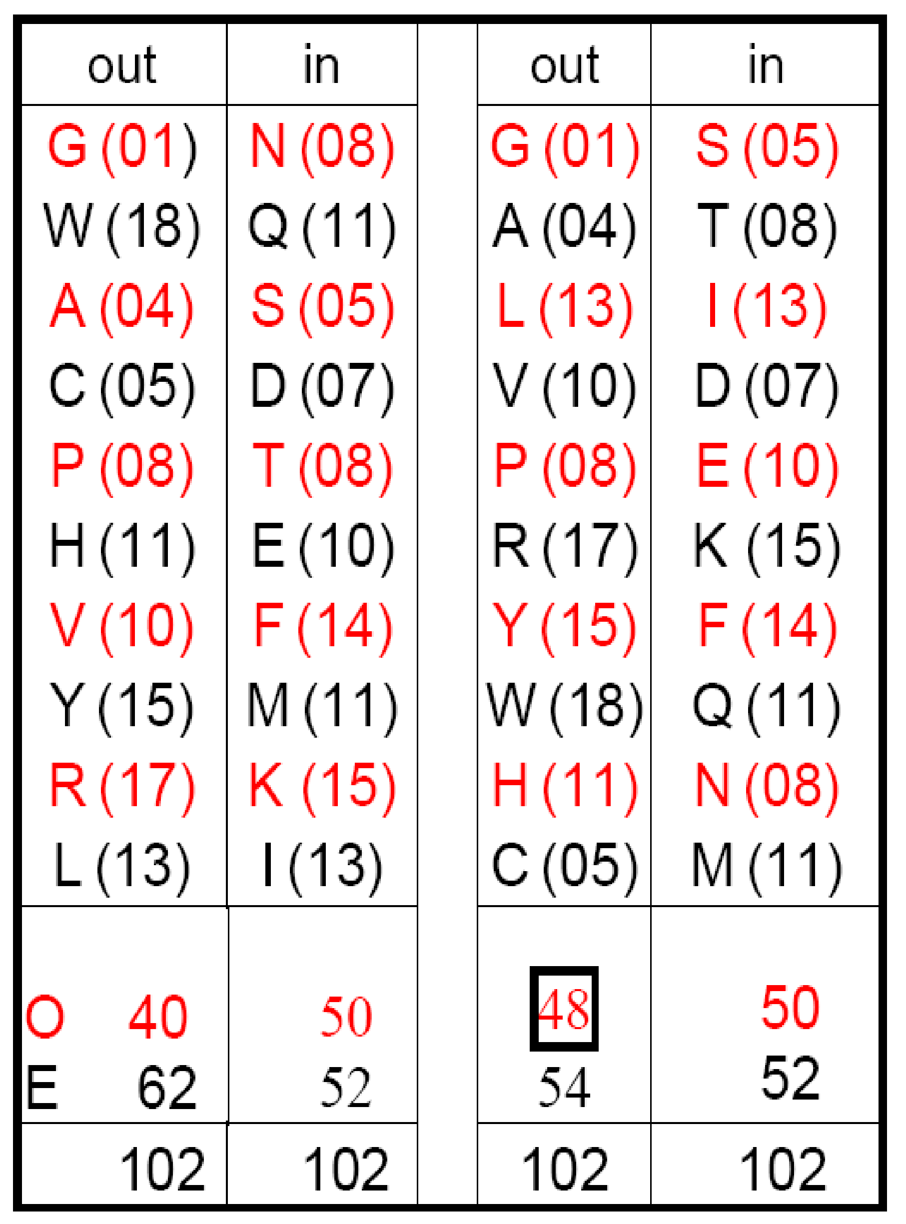
569 as neutron number and 686 as proton number!

569 – 59 = 627 – 117

686 – 58 = 628

Sukhodolets, 1985; MMR, 2011, Tab. 7.

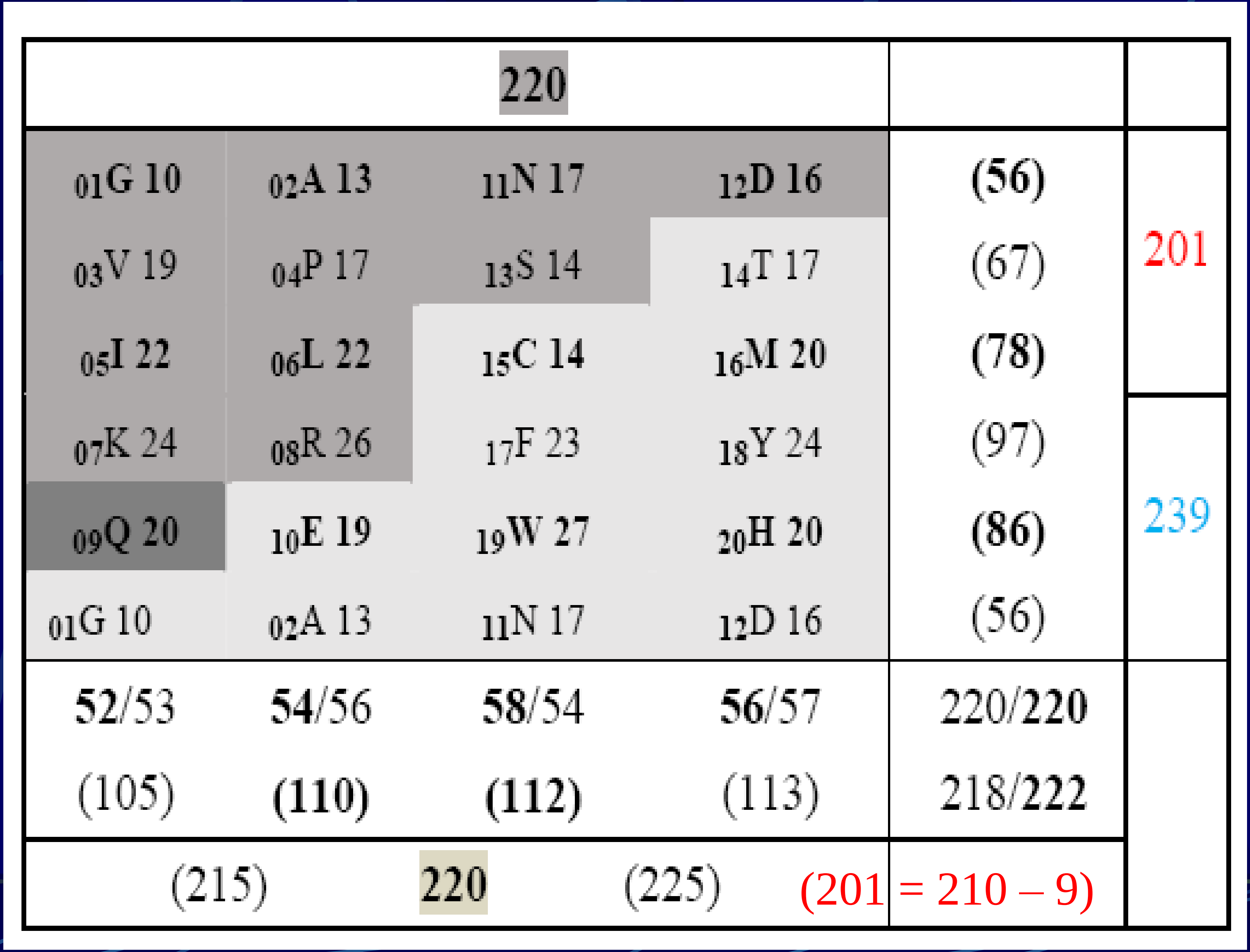
System-arrangement of AAs through the number of hydrogen atoms (II)



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 E 62	50 52		$\boxed{48}$ 54	50 52
102	102		102	102

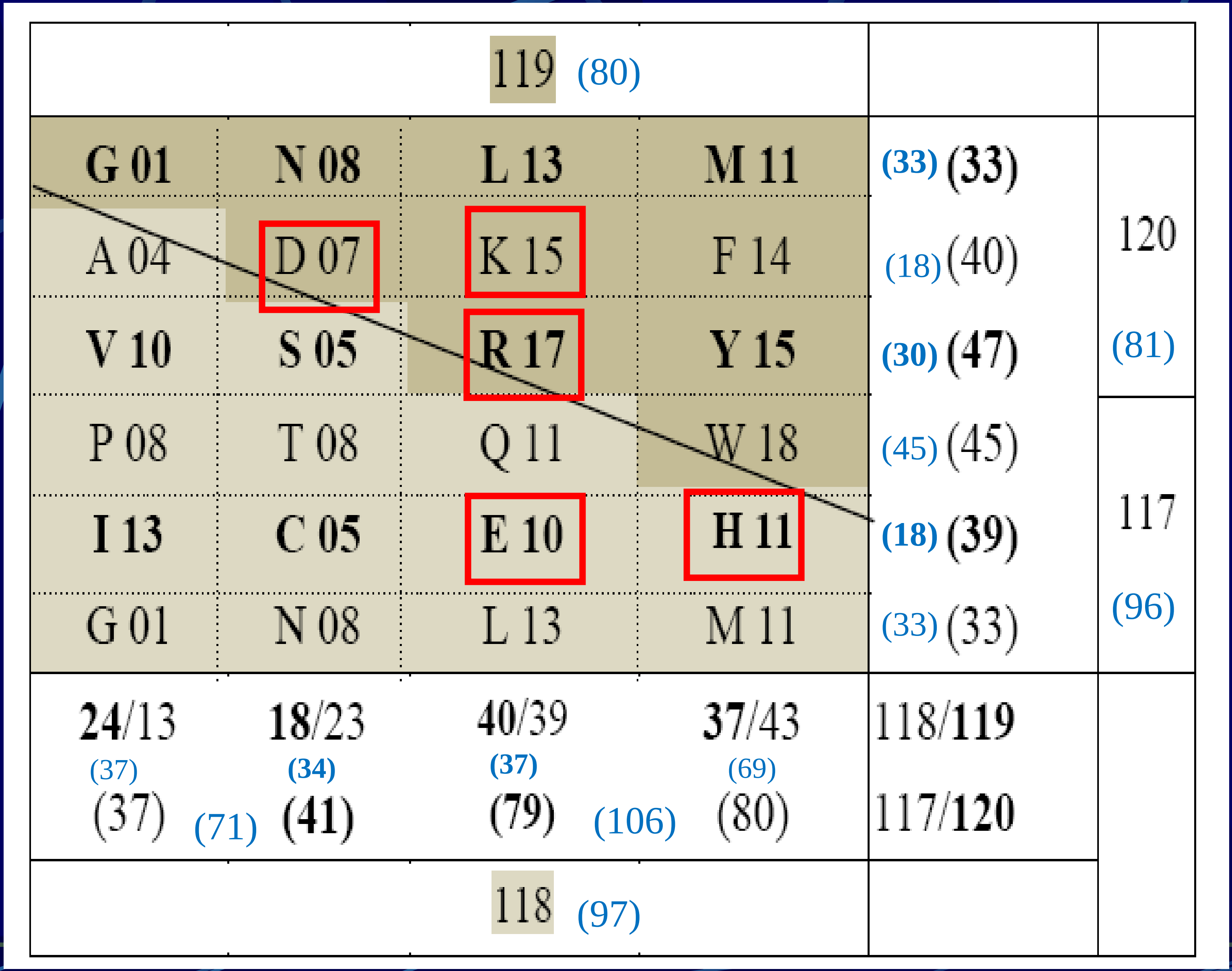
Sukhodolets, 1985; MMR, 2011, Tab. 9.

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



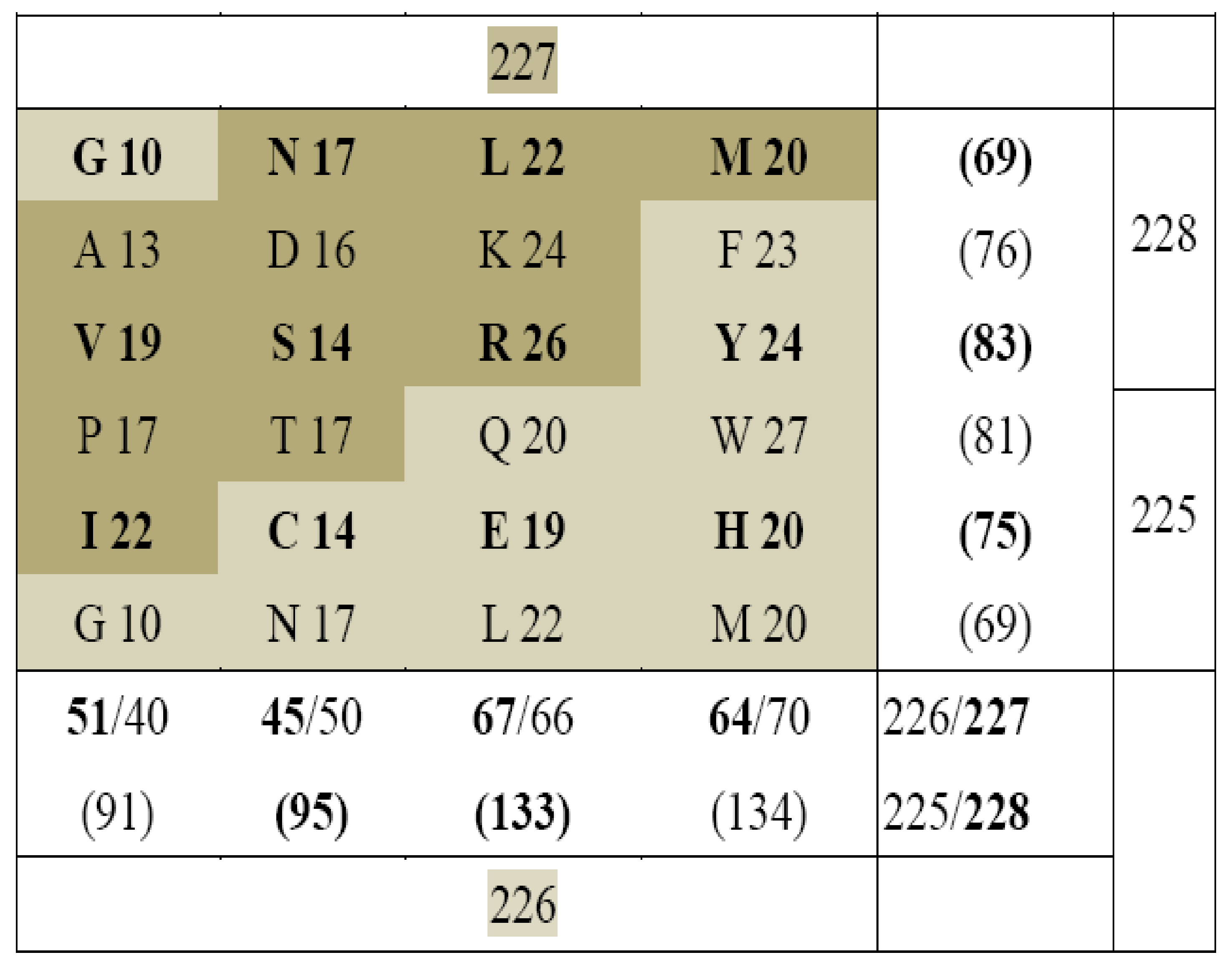
220					
$_{01}$G 10	$_{02}$A 13	$_{11}$N 17	$_{12}$D 16	(56)	201
$_{03}$V 19	$_{04}$P 17	$_{13}$S 14	$_{14}$T 17	(67)	
$_{05}$I 22	$_{06}$L 22	$_{15}$C 14	$_{16}$M 20	(78)	
$_{07}$K 24	$_{08}$R 26	$_{17}$F 23	$_{18}$Y 24	(97)	239
$_{09}$Q 20	$_{10}$E 19	$_{19}$W 27	$_{20}$H 20	(86)	
$_{01}$G 10	$_{02}$A 13	$_{11}$N 17	$_{12}$D 16	(56)	
52/53	54/56	58/54	56/57	220/220	
(105)	(110)	(112)	(113)	218/222	
(215)	220	(225)		(201 = 210 – 9)	

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



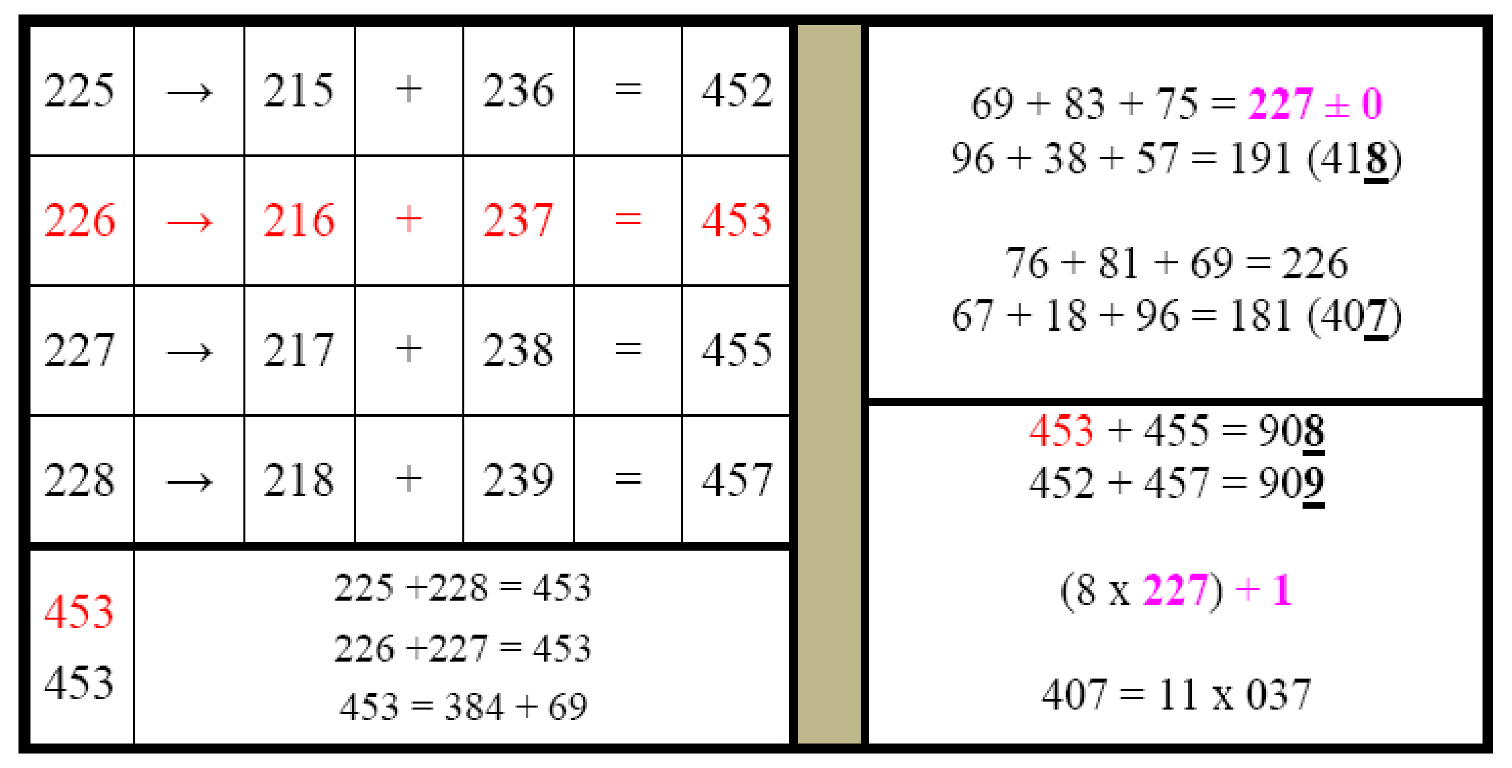
		119 (80)			
G 01	**N 08**	**L 13**	**M 11**	**(33) (33)**	120 (81)
A 04	D 07	K 15	F 14	(18) (40)	
V 10	**S 05**	**R 17**	**Y 15**	**(30) (47)**	
P 08	T 08	Q 11	W 18	(45) (45)	117 (96)
I 13	**C 05**	**E 10**	**H 11**	**(18) (39)**	
G 01	N 08	L 13	M 11	(33) (33)	
24/13 (37) (37) (71)	**18/23** **(34)** **(41)**	40/39 **(37)** (79) (106)	**37**/43 (69) (80)	118/**119** 117/**120**	
		118 (97)			

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



		227			
G 10	**N 17**	**L 22**	**M 20**	**(69)**	228
A 13	D 16	K 24	F 23	(76)	
V 19	**S 14**	**R 26**	**Y 24**	**(83)**	
P 17	T 17	Q 20	W 27	(81)	225
I 22	**C 14**	**E 19**	**H 20**	**(75)**	
G 10	N 17	L 22	M 20	(69)	
51/40	**45**/50	**67**/66	**64**/70	226/**227**	
(91)	**(95)**	**(133)**	(134)	225/**228**	
		226			

Quantity relationships in (PPAASS) [V]



225	→	215	+	236	=	452
226	→	216	+	237	=	453
227	→	217	+	238	=	455
228	→	218	+	239	=	457
453 453	225 +228 = 453 226 +227 = 453 453 = 384 + 69					

69 + 83 + 75 = **227 ± 0**
96 + 38 + 57 = 191 (41**8**)

76 + 81 + 69 = 226
67 + 18 + 96 = 181 (40**7**)

453 + 455 = 90**8**
452 + 457 = 90**9**

(8 x **227**) **+ 1**

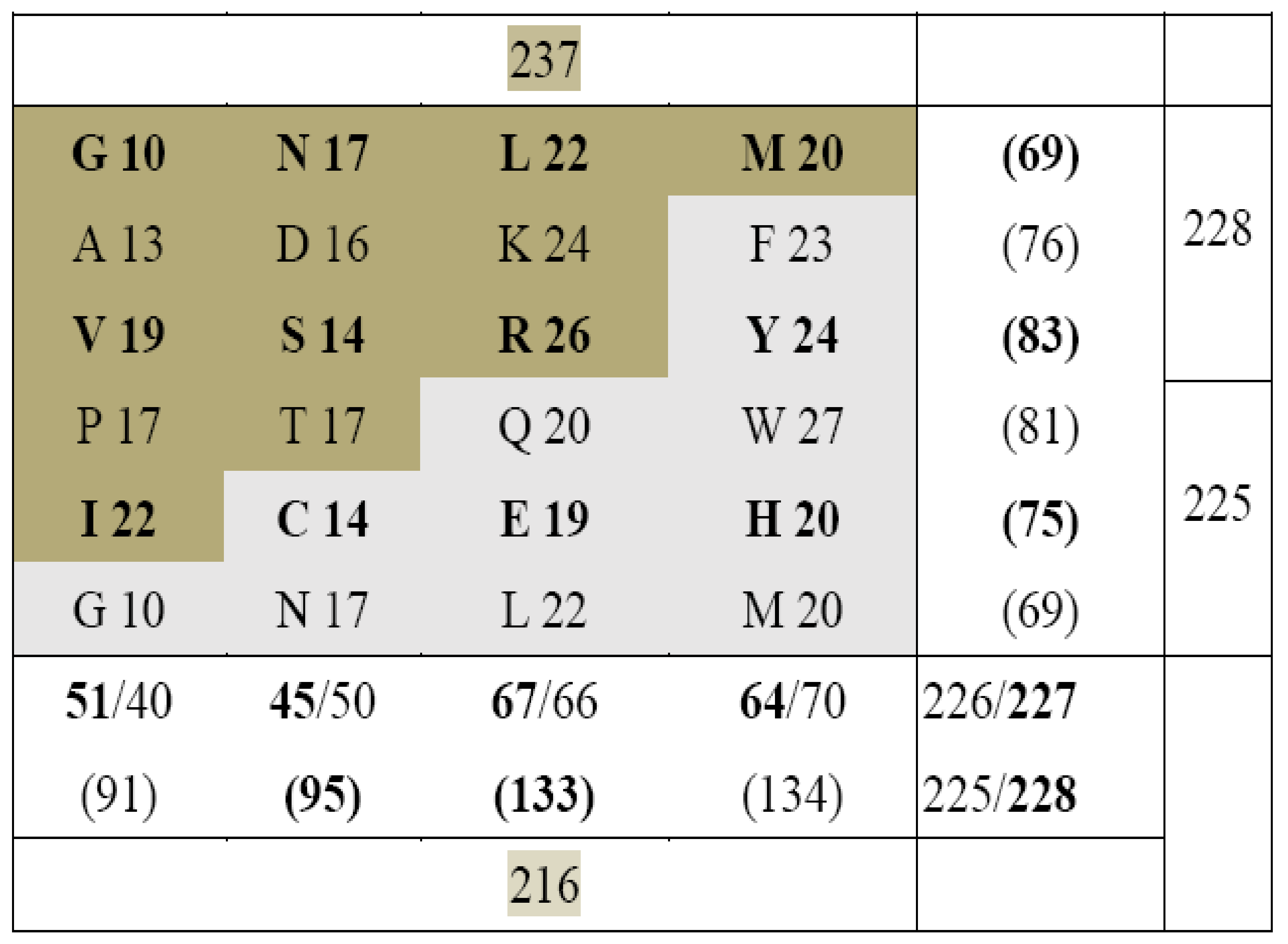
407 = 11 x 037

11**7** + 10**8** = 225
118 + 108 = 226

(108 = 12 x 9)

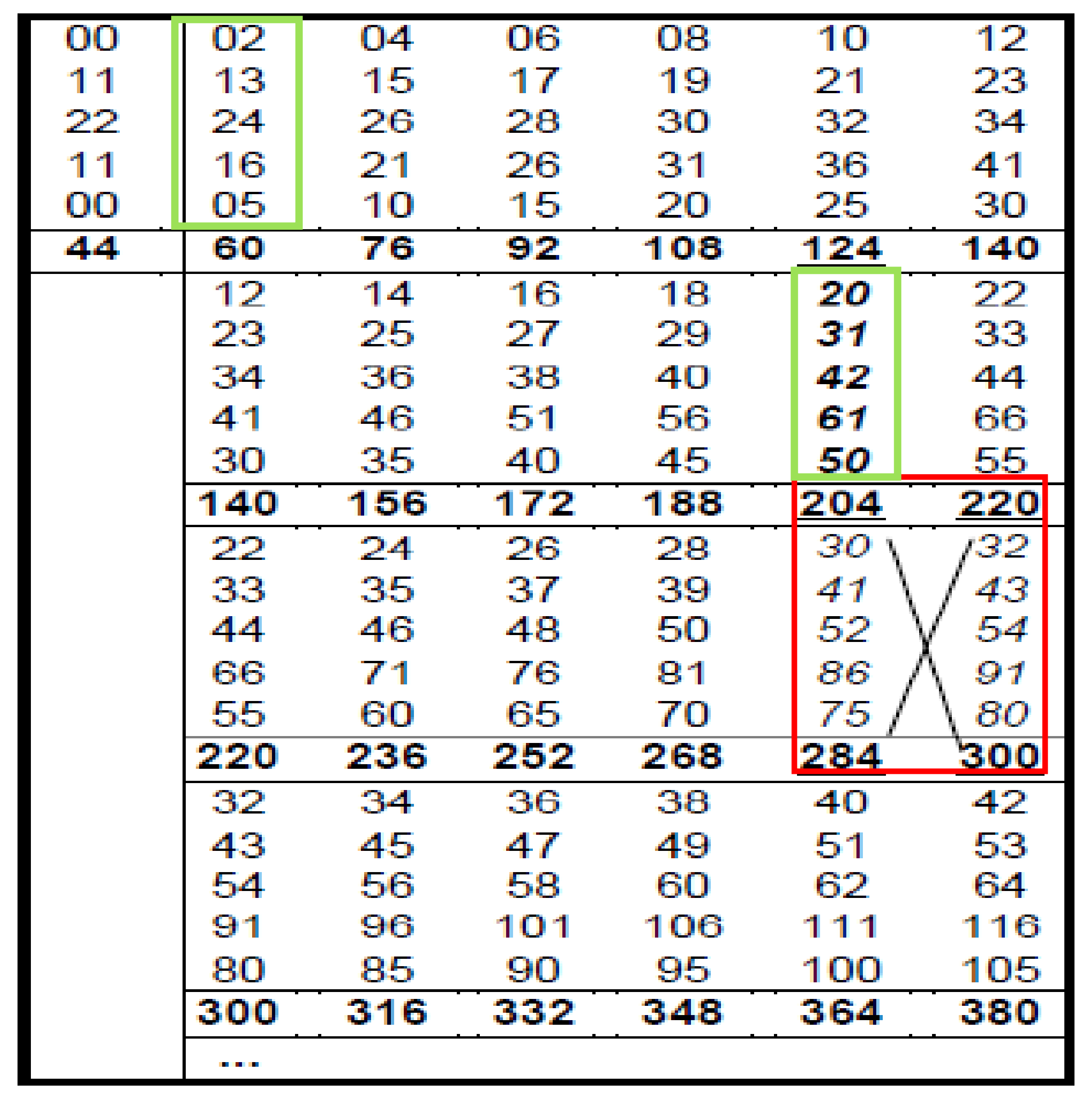
11**9** + 10**8** = 227
120 + 108 = 228

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



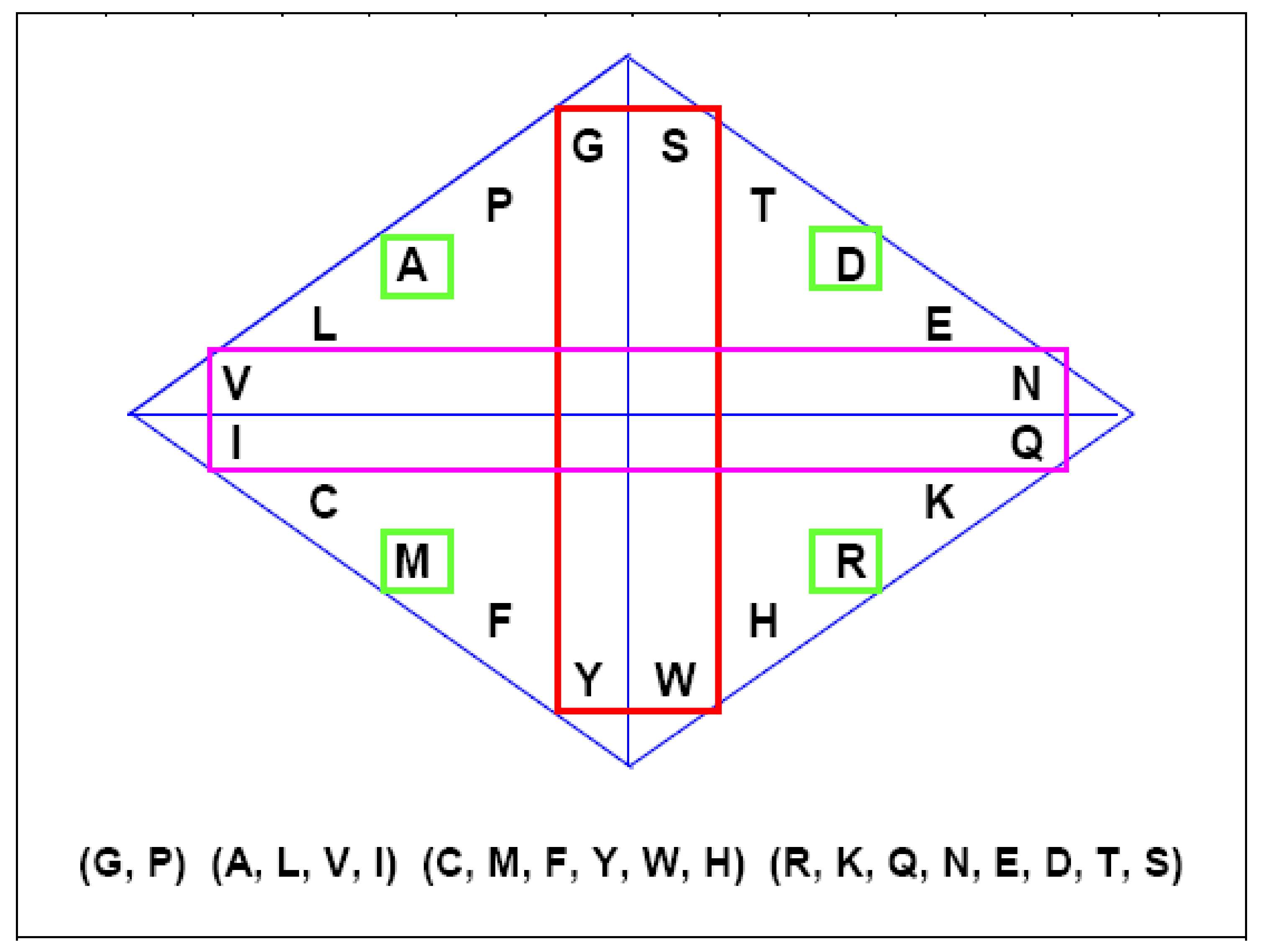
		237			
G 10	**N 17**	**L 22**	**M 20**	**(69)**	228
A 13	D 16	K 24	F 23	(76)	
V 19	**S 14**	**R 26**	**Y 24**	**(83)**	
P 17	T 17	Q 20	W 27	(81)	225
I 22	**C 14**	**E 19**	**H 20**	**(75)**	
G 10	N 17	L 22	M 20	(69)	
51/40	**45**/50	**67**/66	**64**/70	226/**227**	
(91)	**(95)**	**(133)**	(134)	225/**228**	
		216			

The source of atom number quantities in PAASS

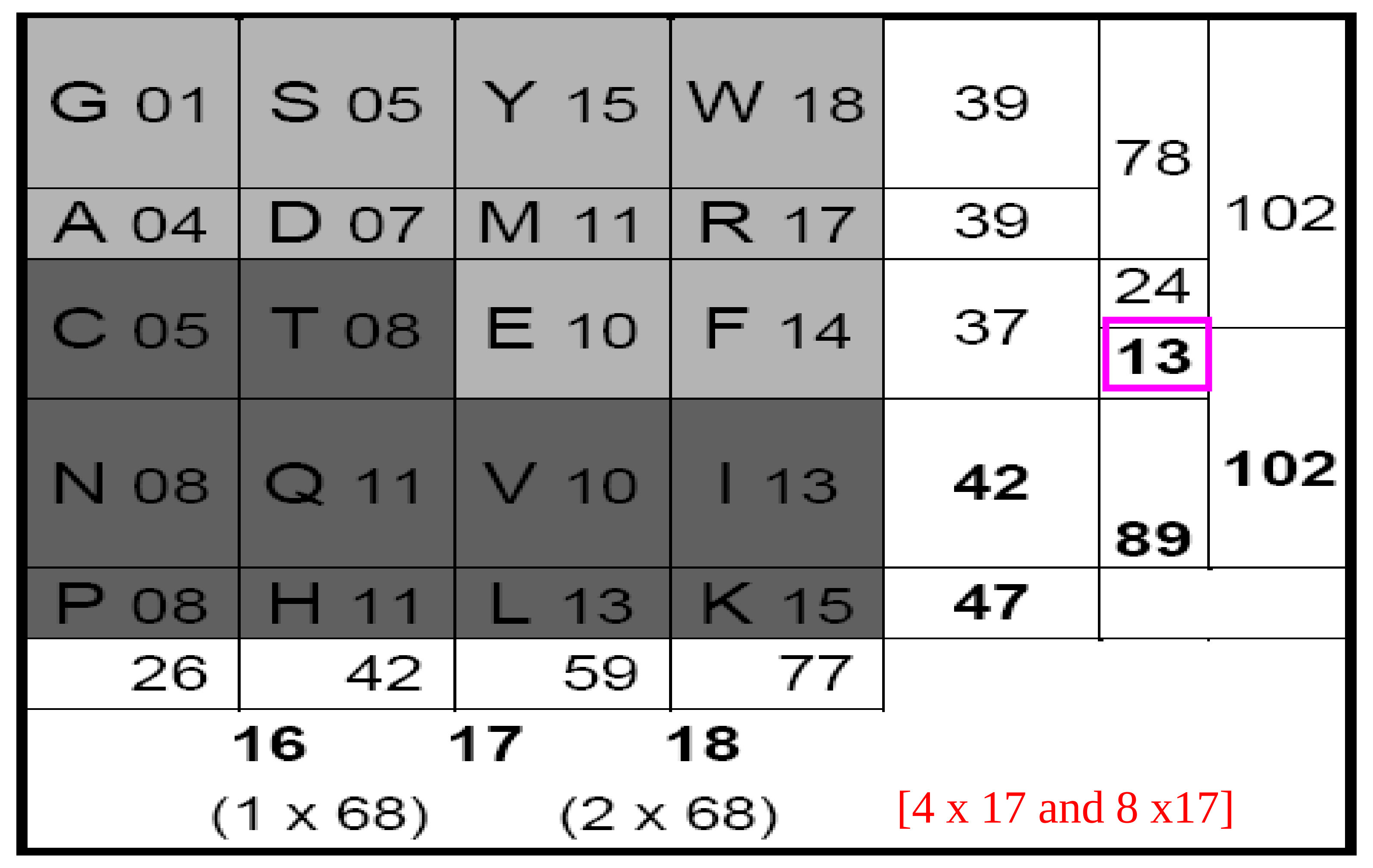


00	02	04	06	08	10	12
11	13	15	17	19	21	23
22	24	26	28	30	32	34
11	16	21	26	31	36	41
00	05	10	15	20	25	30
44	**60**	**76**	**92**	**108**	**124**	**140**
	12	14	16	18	***20***	22
	23	25	27	29	***31***	33
	34	36	38	40	***42***	44
	41	46	51	56	***61***	66
	30	35	40	45	***50***	55
	140	**156**	**172**	**188**	**204**	**220**
	22	24	26	28	*30*	*32*
	33	35	37	39	*41*	*43*
	44	46	48	50	*52*	*54*
	66	71	76	81	*86*	*91*
	55	60	65	70	*75*	*80*
	220	**236**	**252**	**268**	**284**	**300**
	32	34	36	38	40	42
	43	45	47	49	51	53
	54	56	58	60	62	64
	91	96	101	106	111	116
	80	85	90	95	100	105
	300	**316**	**332**	**348**	**364**	**380**
	...					

The starting position of generating four types of diversity of AAs



The result of crossing of four types of diversity of AAs and PSN (I)



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

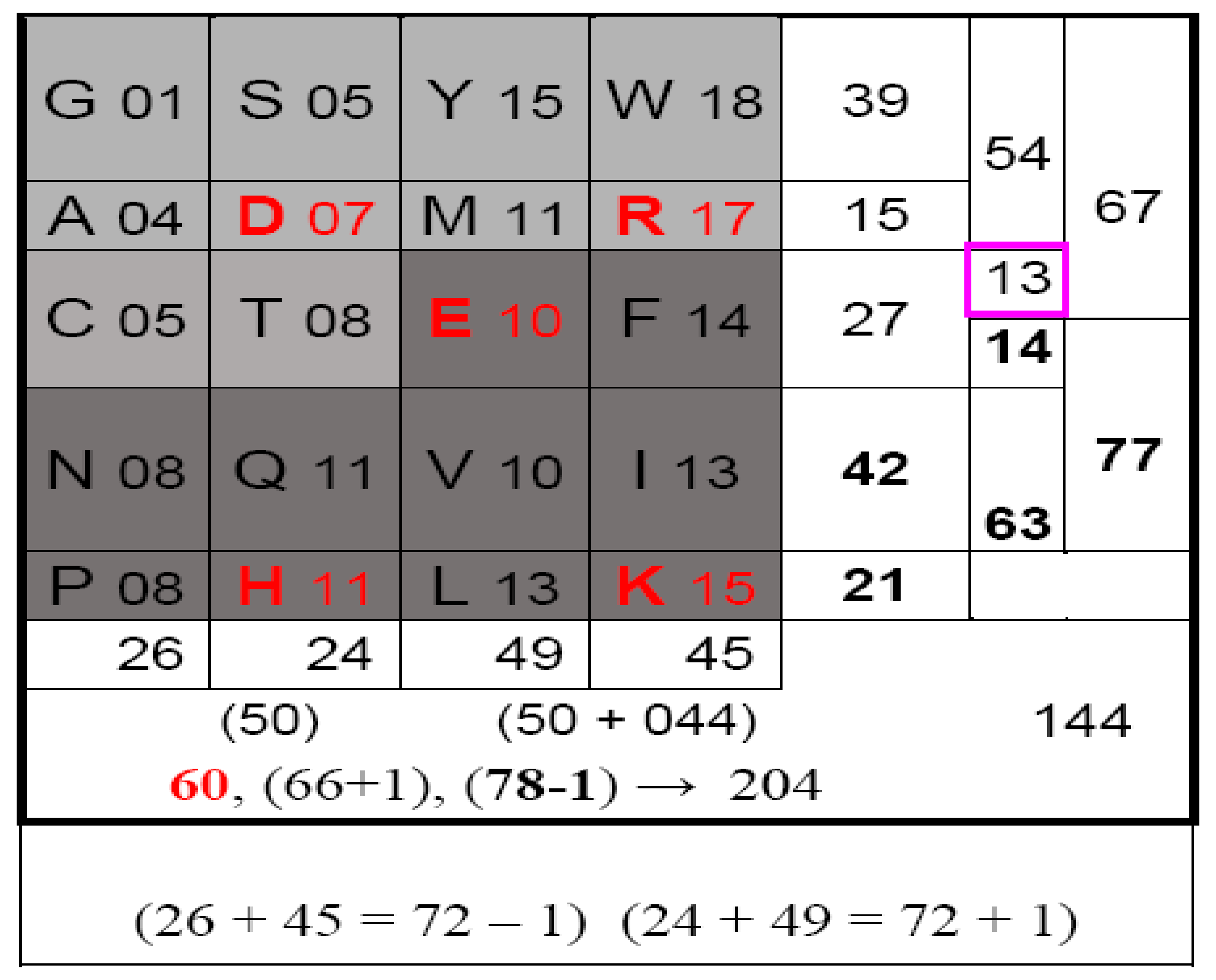
16 **17** **18**

(1 x 68) (2 x 68)

[4 x 17 and 8 x17]

[26 + 77 = 102 + 1] [42 + 59 = 102 – 1]

The result of crossing of four types of diversity of AAs and PSN (II)



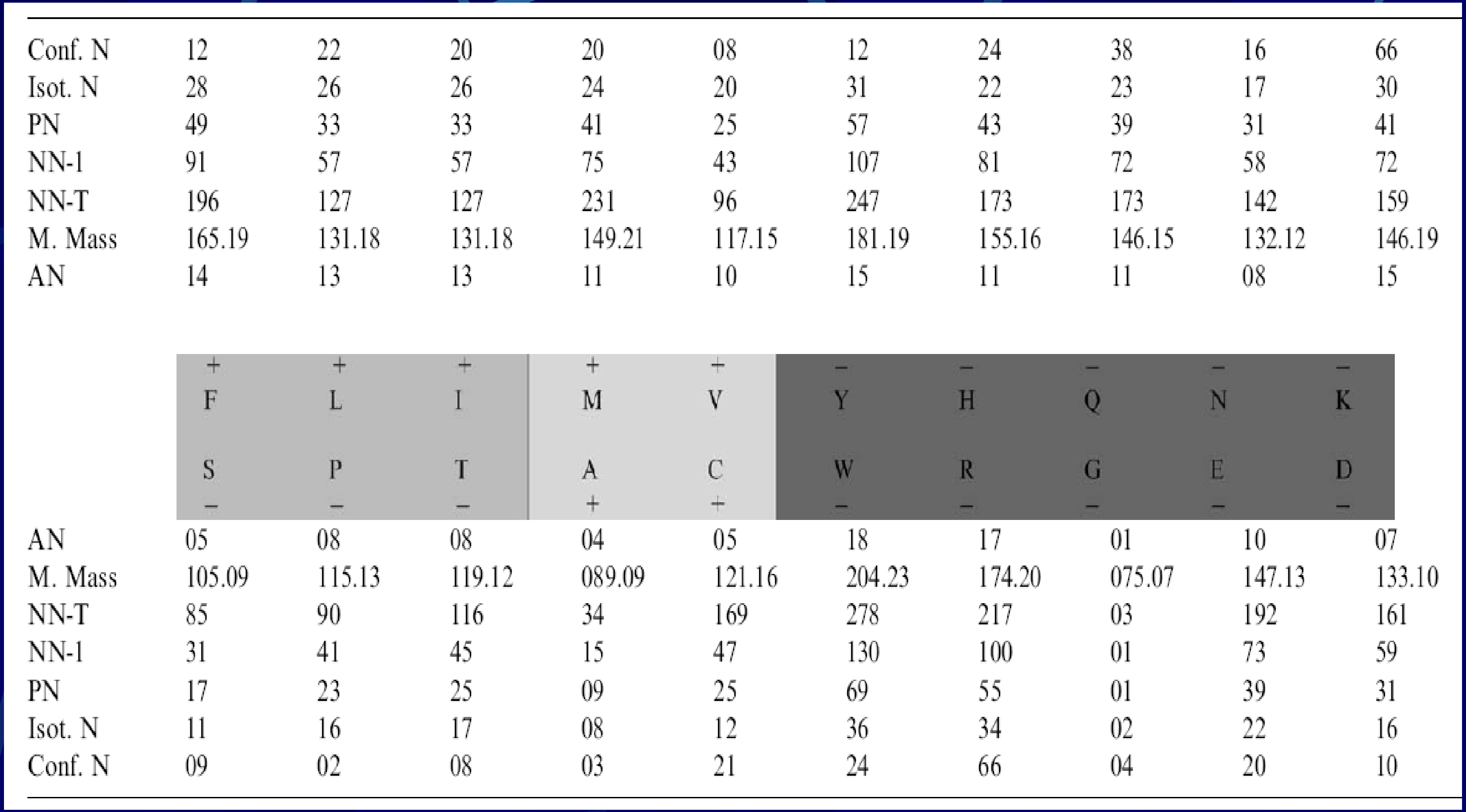
G 01	S 05	Y 15	W 18	39	54	67
A 04	**D 07**	M 11	**R 17**	15		
C 05	T 08	**E 10**	F 14	27	13 **14**	
N 08	Q 11	V 10	I 13	**42**	**63**	**77**
P 08	**H 11**	L 13	**K 15**	**21**		
26	24	49	45			

(50) (50 + 044) 144

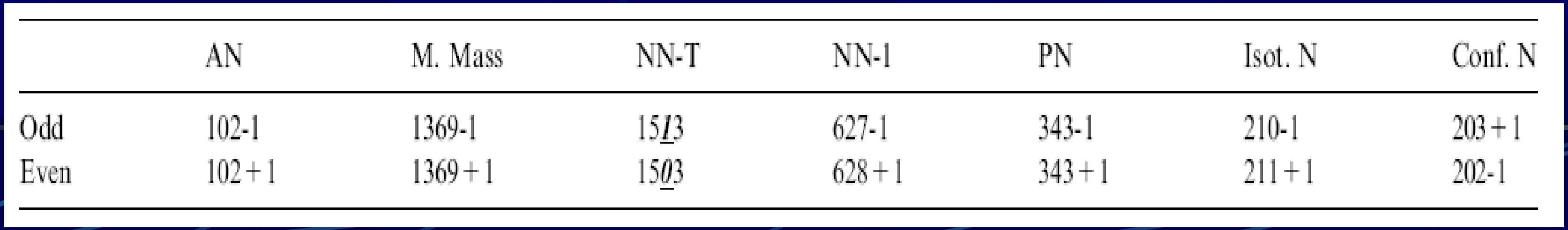
60, (66+1), (**78**-**1**) ⟶ 204

(26 + 45 = 72 – 1) (24 + 49 = 72 + 1)

Seeing the set of 20 amino acids in GCT with quantities of essential parameters

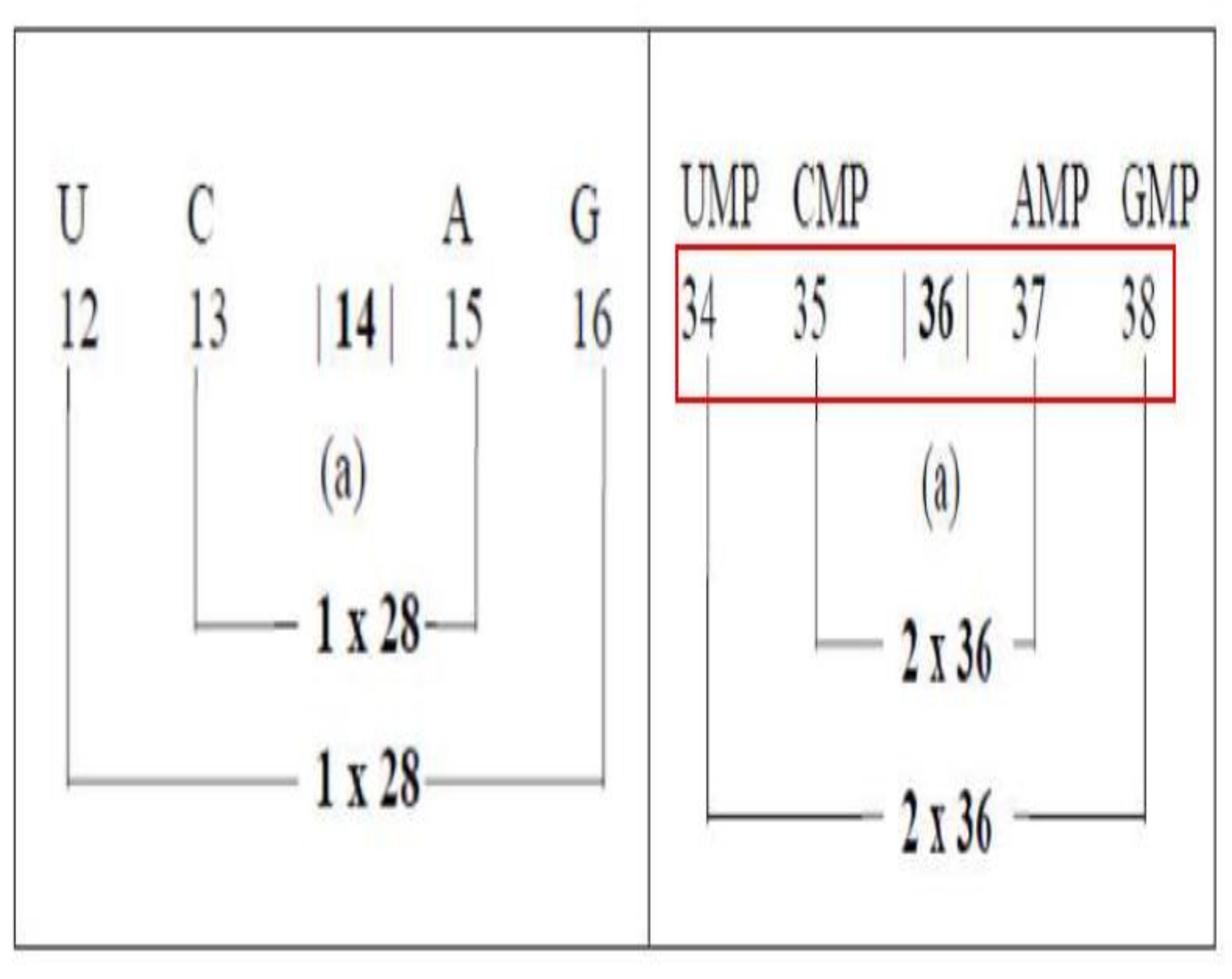


Conf. N	12	22	20	20	08	12	24	38	16	66
Isot. N	28	26	26	24	20	31	22	23	17	30
PN	49	33	33	41	25	57	43	39	31	41
NN-1	91	57	57	75	43	107	81	72	58	72
NN-T	196	127	127	231	96	247	173	173	142	159
M. Mass	165.19	131.18	131.18	149.21	117.15	181.19	155.16	146.15	132.12	146.19
AN	14	13	13	11	10	15	11	11	08	15
	+	+	+	+	+	−	−	−	−	−
	F	L	I	M	V	Y	H	Q	N	K
	S	P	T	A	C	W	R	G	E	D
	−	−	−	+	+	−	−	−	−	−
AN	05	08	08	04	05	18	17	01	10	07
M. Mass	105.09	115.13	119.12	089.09	121.16	204.23	174.20	075.07	147.13	133.10
NN-T	85	90	116	34	169	278	217	03	192	161
NN-1	31	41	45	15	47	130	100	01	73	59
PN	17	23	25	09	25	69	55	01	39	31
Isot. N	11	16	17	08	12	36	34	02	22	16
Conf. N	09	02	08	03	21	24	66	04	20	10

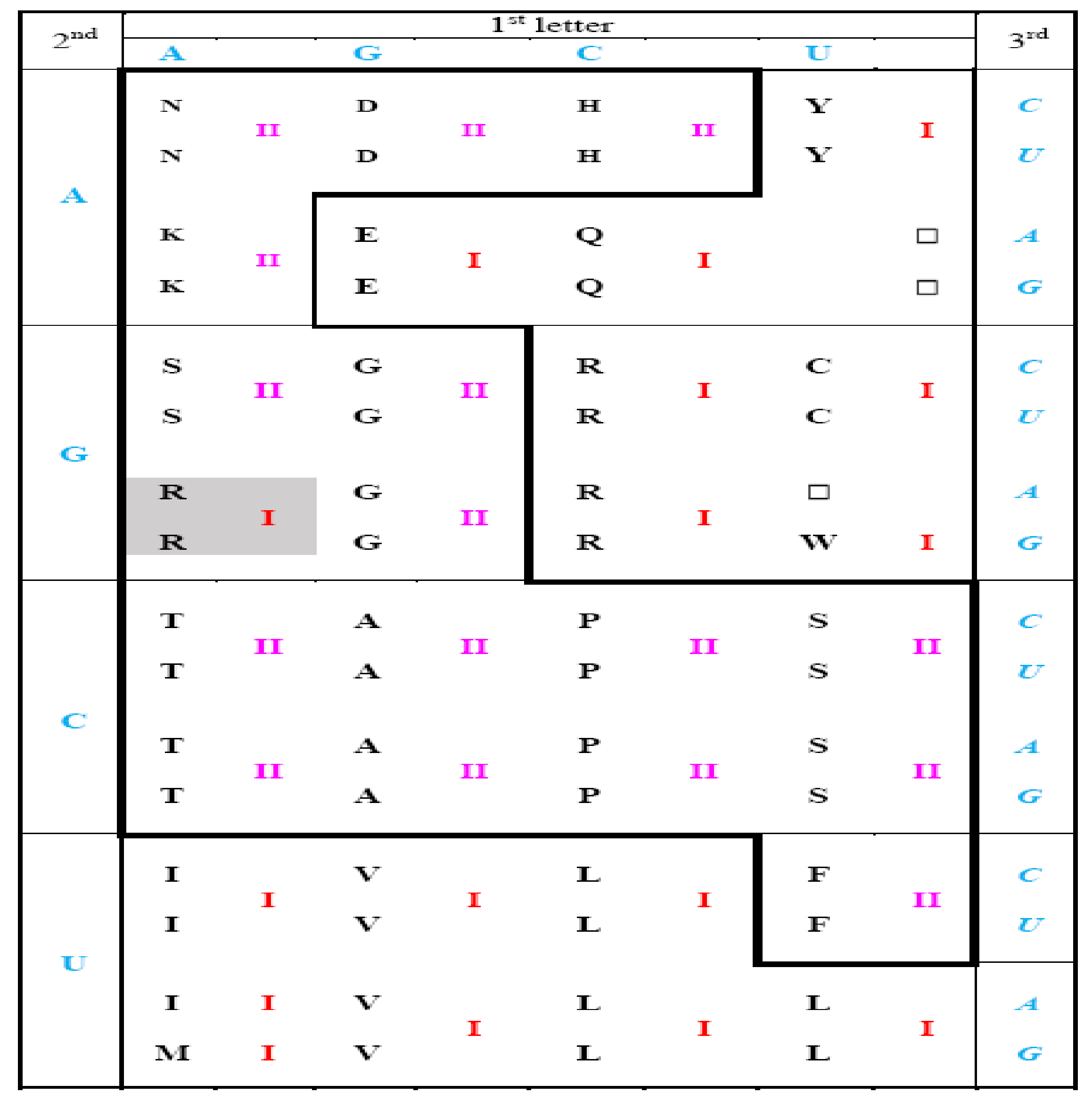


	AN	M. Mass	NN-T	NN-1	PN	Isot. N	Conf. N
Odd	102-1	1369-1	15*1*3	627-1	343-1	210-1	203 + 1
Even	102 + 1	1369 + 1	15*0*3	628 + 1	343 + 1	211 + 1	202-1

The number of atoms in bases and nucleotides in relation to the first and second perfect number

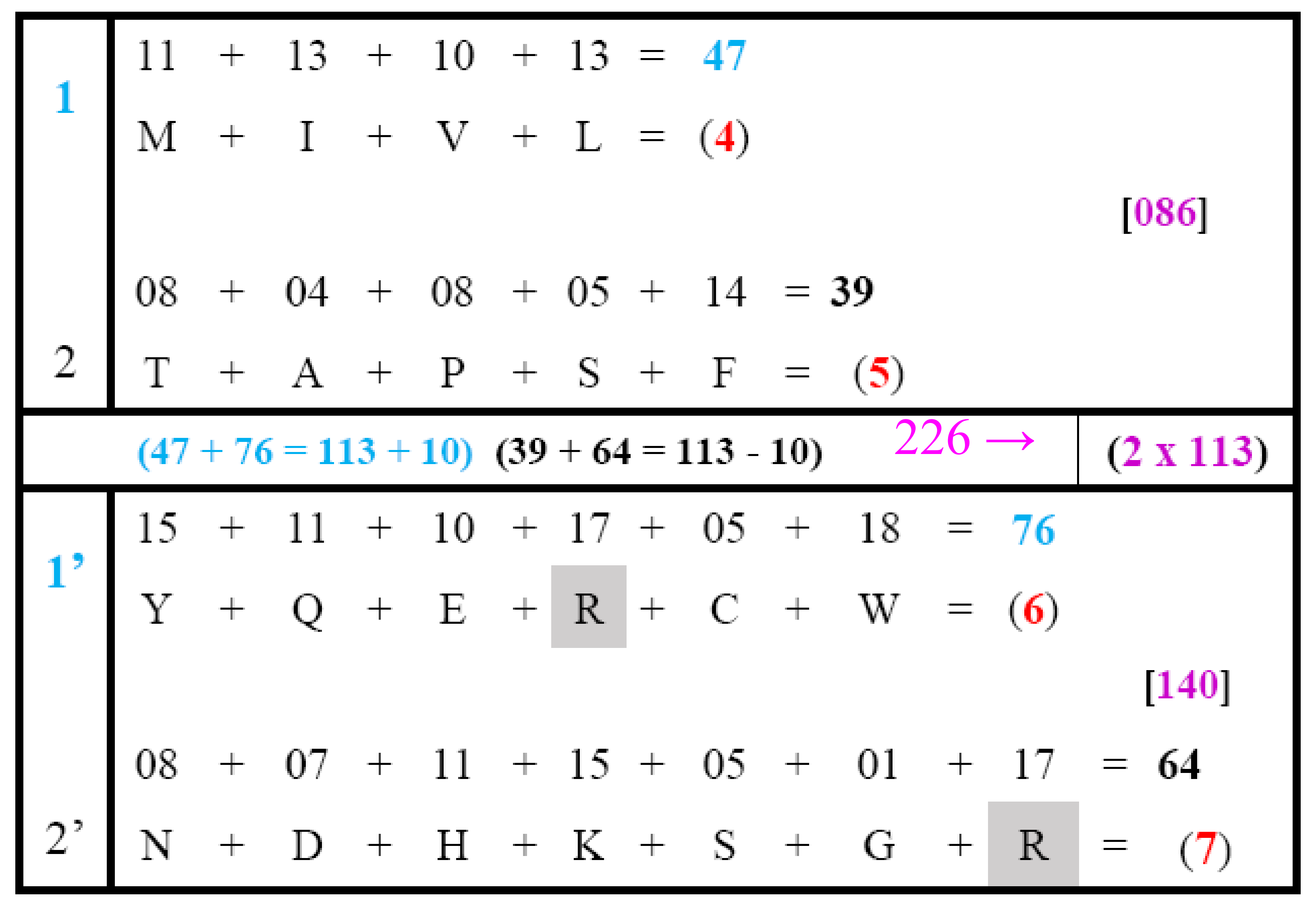


Codon path cube: two classes of amino acids in relation to two classes of aminoacyl-tRNA synthetases (I) (MMR, 1997a)



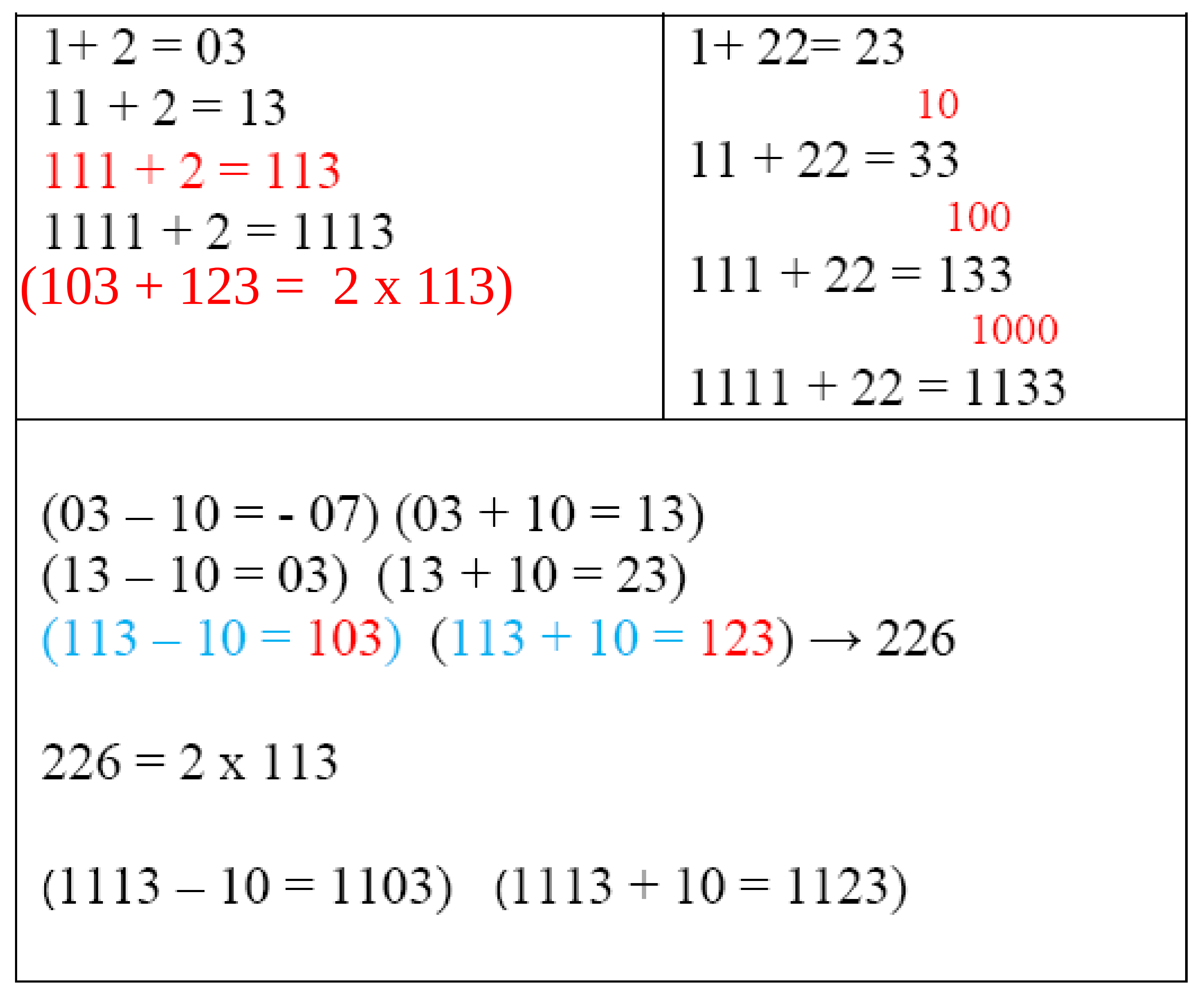
2nd	1st letter								3rd
	A		G		C		U		
A	N	II	D	II	H	II	Y	I	C
	N		D		H		Y		U
	K	II	E	I	Q	I	□		A
	K		E		Q		□		G
G	S	II	G	II	R	I	C	I	C
	S		G		R		C		U
	R	I	G	II	R	I	□		A
	R		G		R		W	I	G
C	T	II	A	II	P	II	S	II	C
	T		A		P		S		U
	T	II	A	II	P	II	S	II	A
	T		A		P		S		G
U	I	I	V	I	L	I	F	II	C
	I		V		L		F		U
	I	I	V	I	L	I	L	I	A
	M	I	V		L		L		G

Codon path cube: two classes of amino acids in relation to two classes of aminoacyl-tRNA synthetases (II) (MMR, 1997a)



1	11 + 13 + 10 + 13 = 47 M + I + V + L = (4)	
		[086]
2	08 + 04 + 08 + 05 + 14 = 39 T + A + P + S + F = (5)	
	(47 + 76 = 113 + 10) (39 + 64 = 113 - 10) 226 →	(2 x 113)
1’	15 + 11 + 10 + 17 + 05 + 18 = 76 Y + Q + E + R + C + W = (6)	
		[140]
2’	08 + 07 + 11 + 15 + 05 + 01 + 17 = 64 N + D + H + K + S + G + R = (7)	

Unique arithmetic existing in the genetic code (I)



1+ 2 = 03
11 + 2 = 13
111 + 2 = 113
1111 + 2 = 1113
(103 + 123 = 2 x 113)

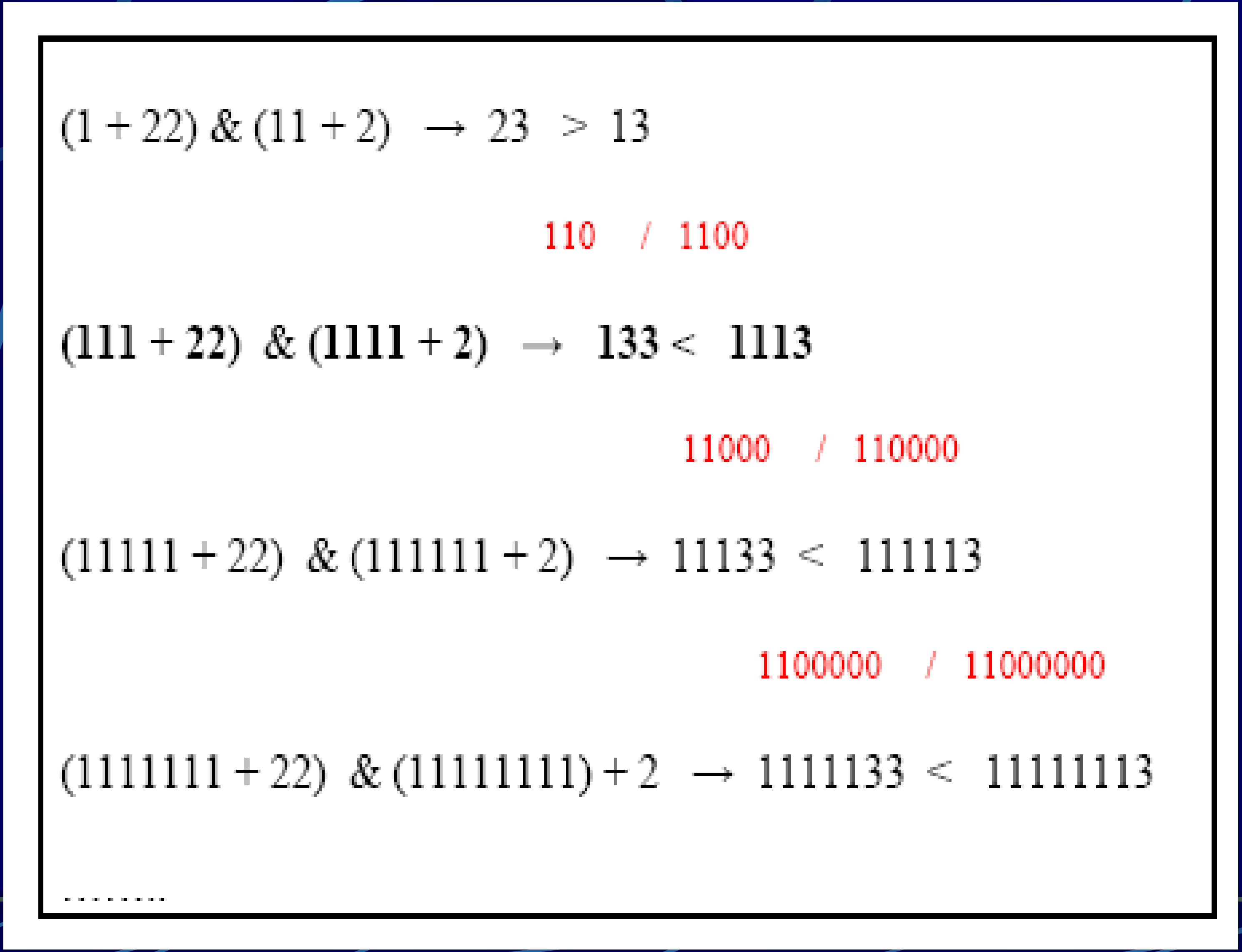
1+ 22= 23
10
11 + 22 = 33
100
111 + 22 = 133
1000
1111 + 22 = 1133

(03 – 10 = - 07) (03 + 10 = 13)
(13 – 10 = 03) (13 + 10 = 23)
(113 – 10 = 103) (113 + 10 = 123) → 226

226 = 2 x 113

(1113 – 10 = 1103) (1113 + 10 = 1123)

Unique arithmetic existing in the genetic code (II)



$(1+22)\ \&\ (11+2)\ \rightarrow\ 23\ >\ 13$

110 / 1100

$(111+22)\ \&\ (1111+2)\ \rightarrow\ 133 <\ 1113$

11000 / 110000

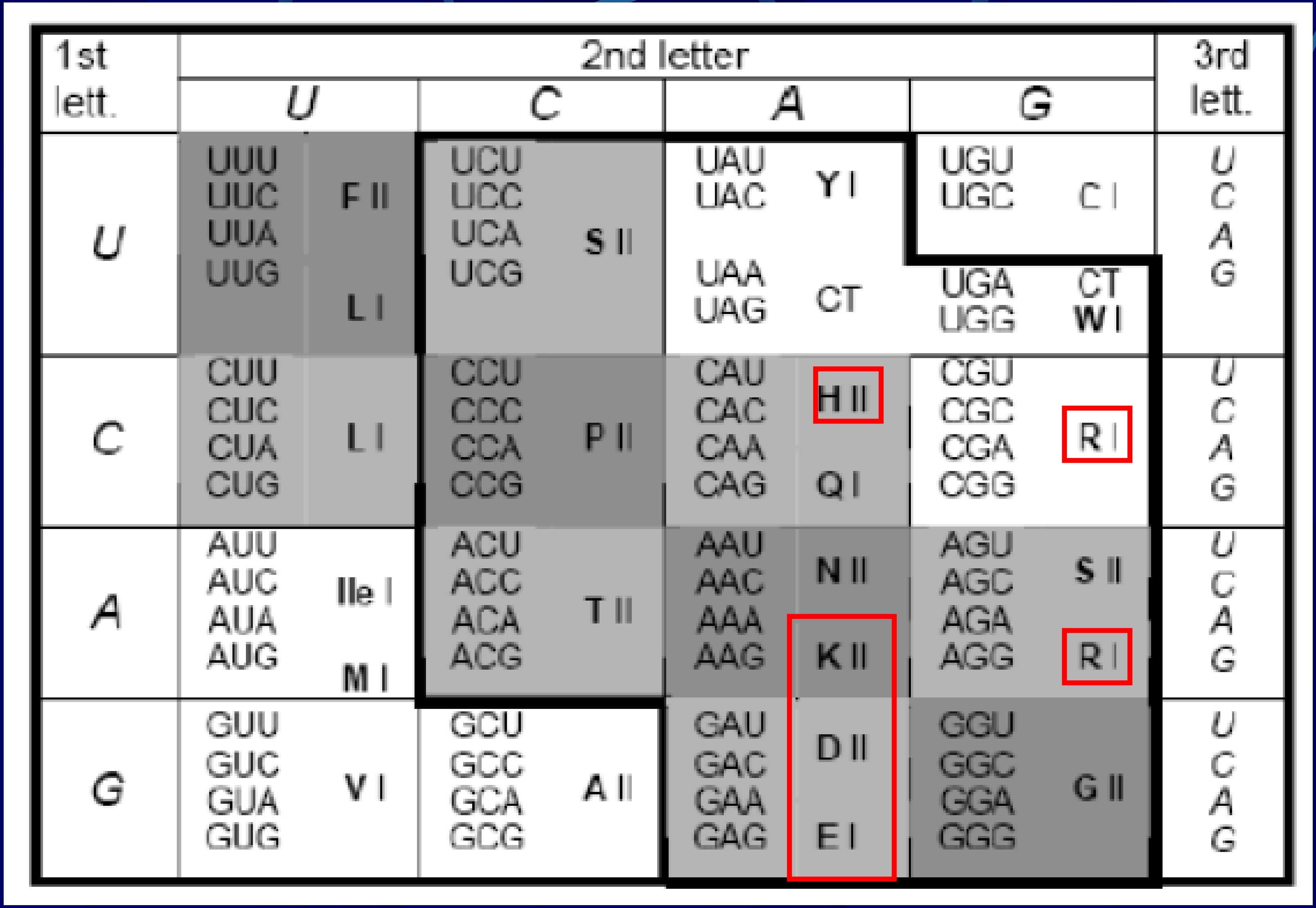
$(11111+22)\ \&\ (111111+2)\ \rightarrow\ 11133\ <\ 111113$

1100000 / 11000000

$(1111111+22)\ \&\ (11111111)+2\ \rightarrow\ 1111133\ <\ 11111113$

……..

“The relations of amino acids positions within GCT and their polarity” (I)



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

.70

.32 / 28

.45 / 32

.15 / 17

.74 .25 .34 / 43 .29 / 34

Genetic code as a semiotic system (Vers. 2)

Miloje M. Rakočević
University of Niš, Faculty of Sciences and Mathematics
Department of Chemistry,
Višegradska 33, 18000 Niš, Serbia
(http://www.rakocevcode.rs)
(mirkovmiloje@gmail.com)

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

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[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

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[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.)

*

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.

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[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.

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[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."

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[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.]

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[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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Acknowledgements

I am grateful to Branko Dragovich, Djuro Koruga, Dejan Raković, Tidjani Négadi and Aleksandar Petrović for helpful, stimulating discussions and benevolent critique over a long period of years.

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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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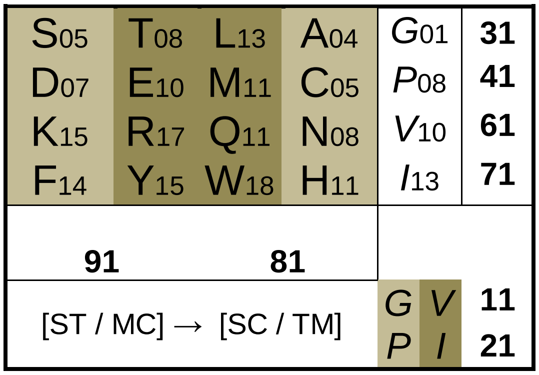
FIGURES



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**			
[ST / MC] → [SC / TM]				*G* *V*	**11**
				P *I*	**21**

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.

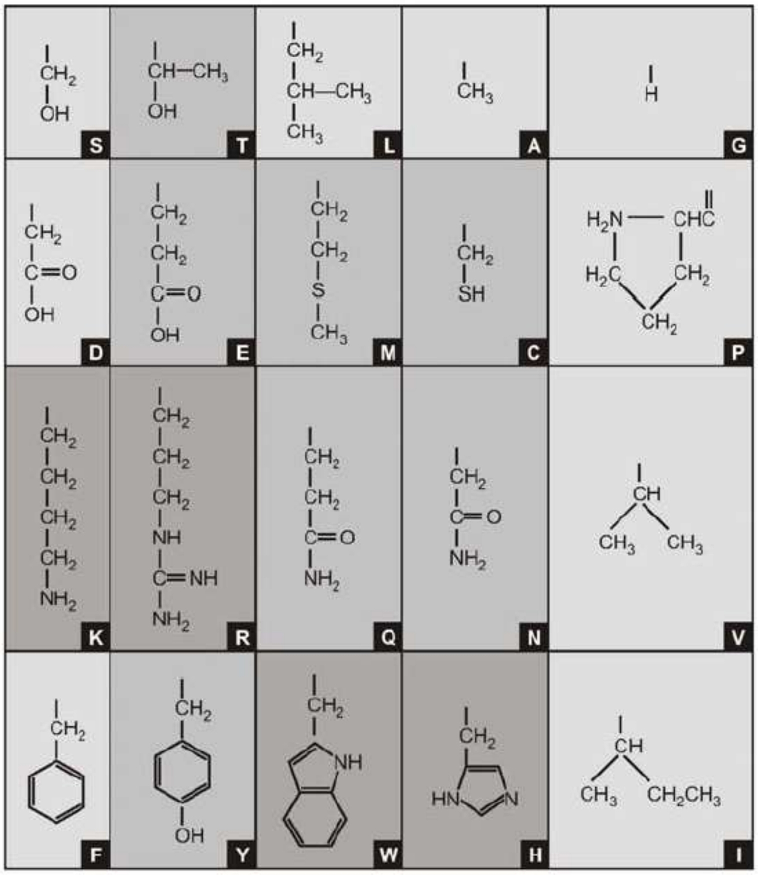
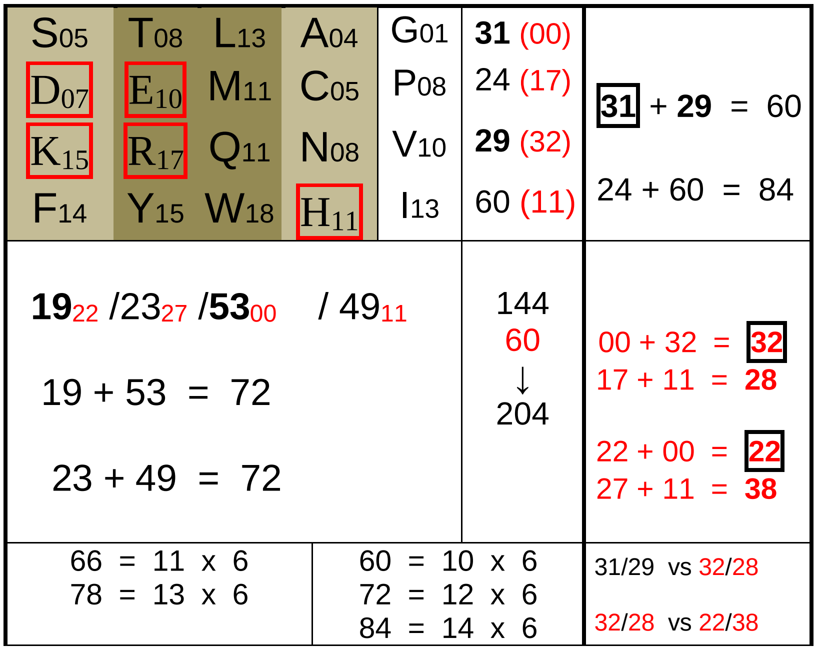


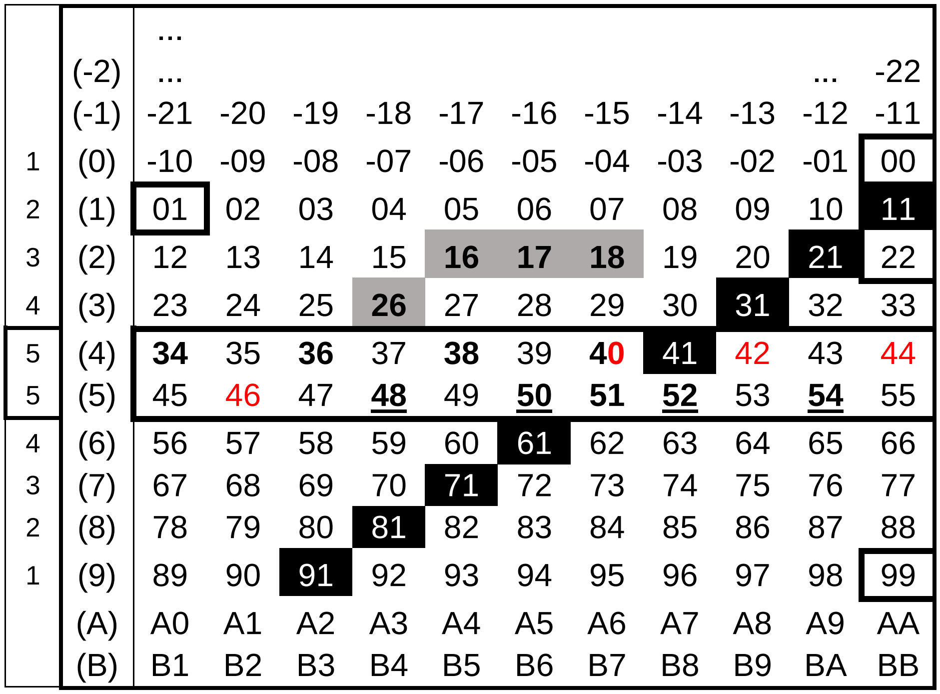
Figure 1.2. MMR, 2006, Fig. 1.2, p. 6: "The structure of amino acid molecules. The simplest amino acid is glycine (G) whose side chain is only one atom of hydrogen. It is followed by alanine (A) whose side chain is only one CH3 group, which is the smallest hydrocarbon group. There are total of 16 amino 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).]



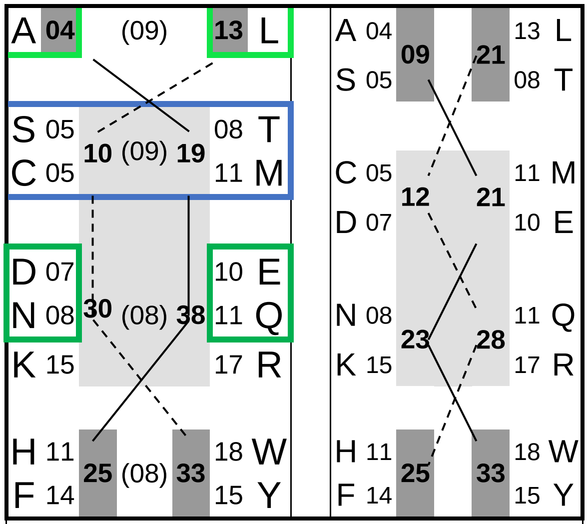
S$_{05}$	T$_{08}$	L$_{13}$	A$_{04}$	G$_{01}$	**31** (00)	$\boxed{\mathbf{31}}$ + **29** = 60
$\boxed{\text{D}_{07}}$	$\boxed{\text{E}_{10}}$	M$_{11}$	C$_{05}$	P$_{08}$	24 (17)	24 + 60 = 84
$\boxed{\text{K}_{15}}$	$\boxed{\text{R}_{17}}$	Q$_{11}$	N$_{08}$	V$_{10}$	**29** (32)	
F$_{14}$	Y$_{15}$	W$_{18}$	$\boxed{\text{H}_{11}}$	I$_{13}$	60 (11)	
19$_{22}$ /23$_{27}$ /**53**$_{00}$ / 49$_{11}$ 19 + 53 = 72 23 + 49 = 72					144 60 ↓ 204	00 + 32 = $\boxed{\mathbf{32}}$ 17 + 11 = **28** 22 + 00 = $\boxed{\mathbf{22}}$ 27 + 11 = **38**
66 = 11 x 6 78 = 13 x 6			60 = 10 x 6 72 = 12 x 6 84 = 14 x 6			31/29 vs 32/28 32/28 vs 22/38

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

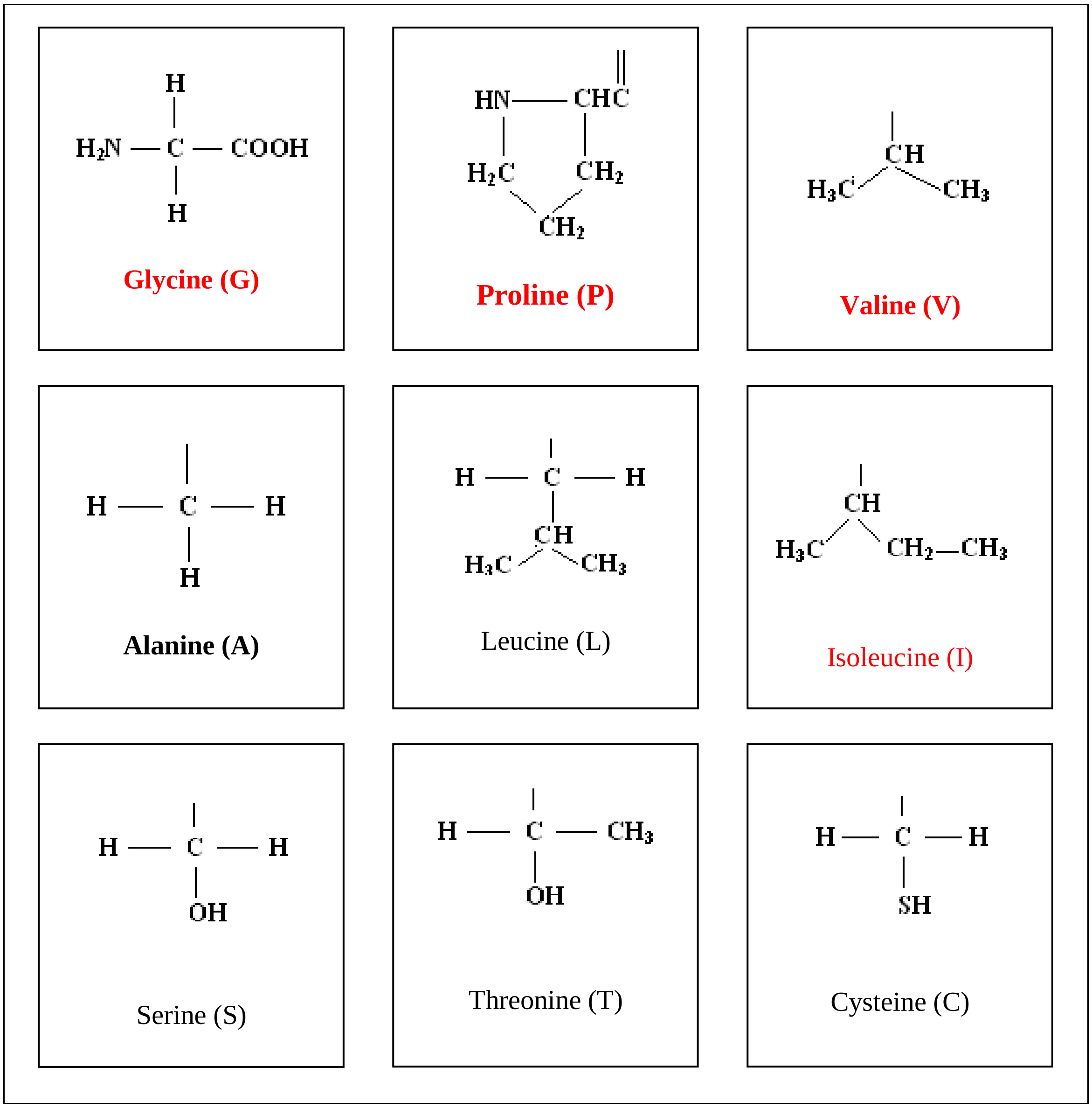
Figure 2. Periodic System on Numbers (PSN) according to: (MMR, 2011b, Table 4, p. 826) and (MMR, 2019, Figure A1, p. 28). Distinctions: the splitting of the sequence 34, 36, 38, 40 into 34, 40 and 36, 38. Quantities 36, 38 in Table 2.4, and quantities 34, 40 in Tab. 4.3. The sequence 40, 42, 44, 46 in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



(04 + 33 = **37**) (13 + 25 = **38**)
11 11
(10 + 38 = **48**) (19 + 30 = **49**)

[37 + 49 = **86**] [38 + 48 = **86**]

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)].



Glycine (G)

Proline (P)

Valine (V)

Alanine (A)

Leucine (L)

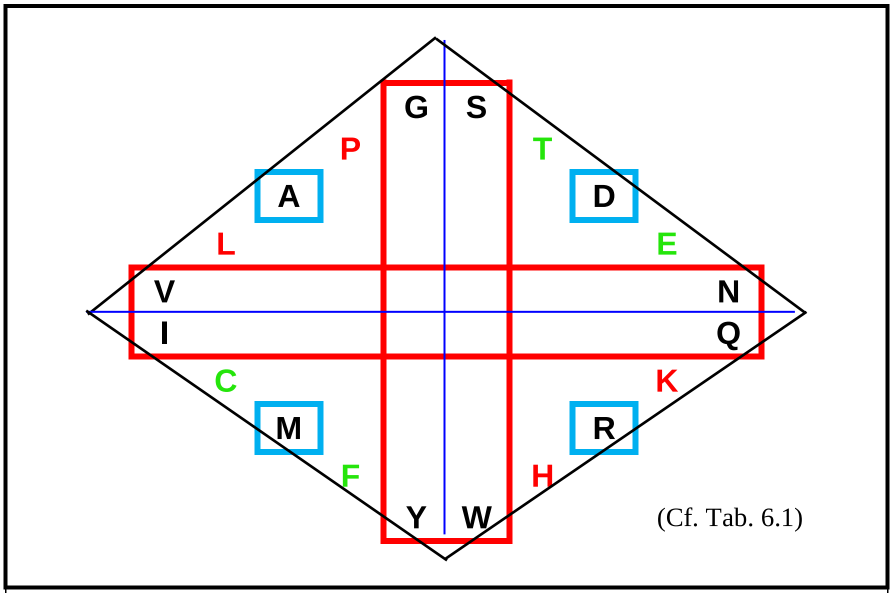
Isoleucine (I)

Serine (S)

Threonine (T)

Cysteine (C)

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."



(Cf. Tab. 6.1)

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**] (Cf. Tab. 5.2)

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**$_{08}$
A$_{04}$	D$_{07}$
V$_{10}$	**S**$_{05}$
P$_{08}$	T$_{08}$
I$_{13}$	**C**$_{05}$
L$_{13}$	**M**$_{11}$
K$_{15}$	**F**$_{14}$
R$_{17}$	Y$_{15}$
Q$_{11}$	**W**$_{18}$
E$_{10}$	H$_{11}$
102 51 ± 01	102 51 ± 01

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**
K$_{15}$	R$_{17}$	F$_{14}$	Y$_{15}$	→	61
					11
Q$_{11}$	**E**$_{10}$	**W**$_{18}$	**H**$_{11}$	→	**50**
(102 + 10) / (102 - 10)					

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**	**81** 39
A 04	D 07	K 15	F 14	(18) 22	
V 10	**S 05**	**R 17**	**Y 15**	**(30) 17**	
P 08	T 08	Q 11	W 18	(45) 00	**96** 21
I 13	**C 05**	**E 10**	**H 11**	**(18) 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*	*3**4**1*	*341+0*	*585.70 ≈586*
K	Y	T	M	→	299	299	351	351+ 2	595.71 ≈ 596
H	W	S	C	→	*289*	*289*	*3**3**1*	*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**
↓ 60	↓ 65	↓	↓ 70	GP 09	**32 / 43 / 38** 28 / 31 / 32
$(60)_{5}$, $(65)_{6}$, $(70)_{7}$					**32** $\boxed{\textbf{43}}$ **38** → 123 - 10 $\boxed{28}$ 31 $\boxed{32}$ → 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 **(6 x 6) ± 00**
N_{08}	**Q_{11}**	**G_{01}**	**C_{05}**	**M_{11}**	
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)

<table>
<tr><td>G 01</td><td>S 05</td><td>Y 15</td><td>W 18</td><td>39</td><td rowspan="2">78</td><td rowspan="3">102 ± 00</td></tr>
<tr><td>A 04</td><td>D 07</td><td>M 11</td><td>R 17</td><td>39</td></tr>
<tr><td rowspan="2">C 05</td><td rowspan="2">T 08</td><td rowspan="2">E 10</td><td rowspan="2">F 14</td><td rowspan="2">37</td><td>24</td></tr>
<tr><td>13</td><td rowspan="2">102 ± 00</td></tr>
<tr><td>N 08</td><td>Q 11</td><td>V 10</td><td>I 13</td><td>42</td><td>89</td></tr>
<tr><td>P 08</td><td>H 11</td><td>L 13</td><td>K 15</td><td>47</td><td colspan="2"></td></tr>
<tr><td>26</td><td>42</td><td>59</td><td>77</td><td colspan="3" rowspan="2"></td></tr>
<tr><td colspan="4">16 17 18
(1 x 68) (2 x 68)</td></tr>
</table>

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**

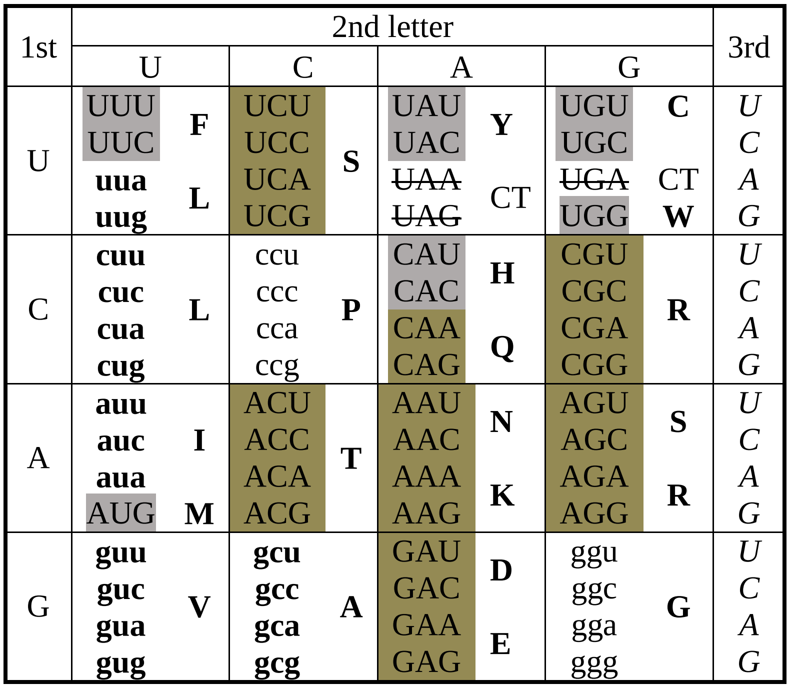
532.57+ 725.86 = 1258.43 ≈ 1258 → 34 x 37

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	**F**	UCU	**S**	UAU	**Y**	**UGU**		*U*
	UUC		UCC		UAC		**UGC**	**C**	*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**		ACU	**T**	AAU	**N**	AGU	**S**	*U*
	auc	**I**	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*

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**

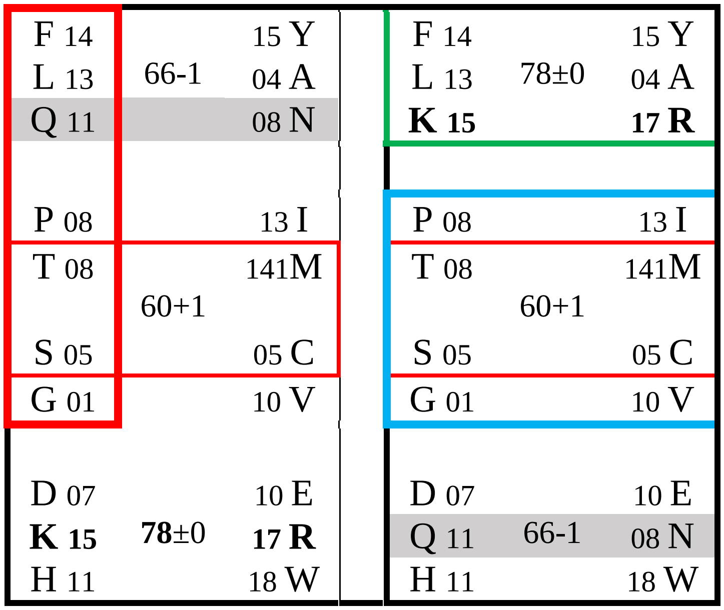
MMR (2011b, Fig. 6, p. 832) and MMR (2019, Fig. 1, p. 6; Box 2). Relations: 58, 68, 78 versus 60, 66, 78 (the change for ± 2 and ±0). The 117 is number of hydrogen atoms in set of 20 protein AAs (in their side chains); and 87, the number of non-hydrogen atoms. The sequ. GSTPQLF 60 as "golden" AAs (MMR,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



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		141M	T 08		141M
	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). 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	**58**
F	14			15	Y	F	91			107	Y	
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	7**2**	7**3**	11	S
P	16	1**4**5		17	T
I	26			12	C
L	26			24	M
K	30			28	F
R	34	1**3**5	1**4**1	31	Y
Q	23	276		36	W
E	22			22	H
		20**7**	21**4**		

276 - 145 = 1**3**1
73 + 135 = 20**8**
72 + 141 = 21**3**

20**8** - 207 = 01
214 - 213 = 01

208 + 213 = 421
207 + 214 = 421

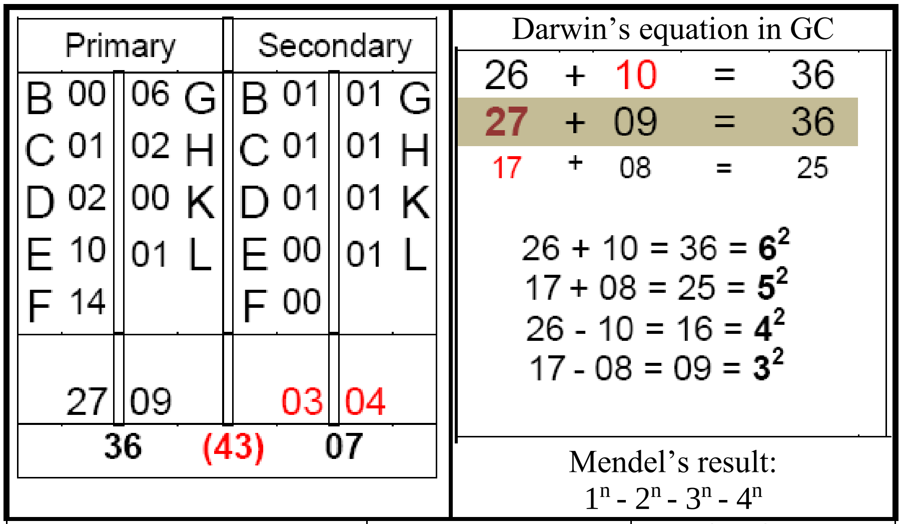
Number of isotopes (II)

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 **<u>16</u>** + 09 = 25 17 + 08 = 25	$1^2 - 0^2 = 01$ $2^2 - 1^2 = 03$ $3^2 - 2^2 = 05$ $4^2 - 3^2 = 07$	$5^2 - 4^2 = 09$ $6^2 - 5^2 = 11$ $7^2 - 6^2 = 13$ …
09 + 07 = **<u>16</u>** 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	- 28
(1)	01	02	03	04	05	06	07	08	09	10	11	
(2)	12	13	14	15	16	17	18	19	20	21	22	30
(3)	23	24	25	26	27	28	29	30	31	32	33	
(4)	**34**	35	**36**	37	**38**	39	**40**	41	42	43	44	74 x 2
(5)	45	46	47	48	49	50	51	52	53	54	55	
(6)	56	57	58	59	60	61	62	63	64	65	66	118
(7)	67	68	69	70	71	72	73	74	75	76	77	
(8)	78	79	80	81	82	83	84	85	86	87	88	324
(9)	89	90	91	92	93	94	95	96	97	98	99	

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

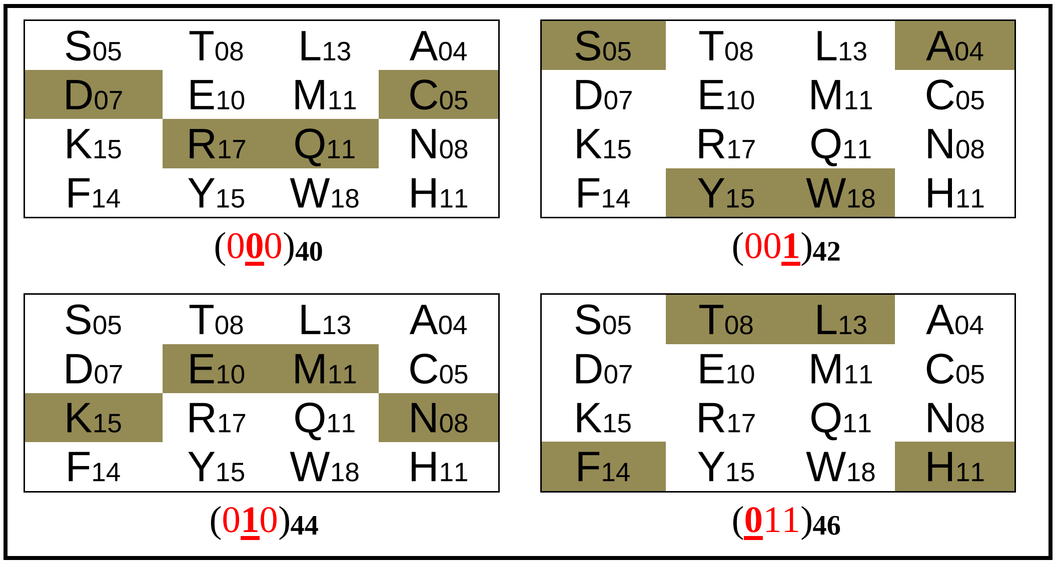
Tab A7. The uniqueness of the pair "(6+7)" and the sum 8658

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.



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

(0**0**0)**40**

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

(00**1**)**42**

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

(0**1**0)**44**

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

(**0**11)**46**

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**
0	V$_{10}$	P$_{08}$	0		0	S$_{05}$	T$_{08}$	0	**11** 31
1	I$_{13}$	L$_{13}$	1		1	C$_{05}$	M$_{11}$	1	**11** 42
0	K$_{15}$	R$_{17}$	0		0	F$_{14}$	Y$_{15}$	0	61
1	Q$_{11}$	E$_{10}$	1		1	W$_{18}$	H$_{11}$	1	**11** 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**
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	

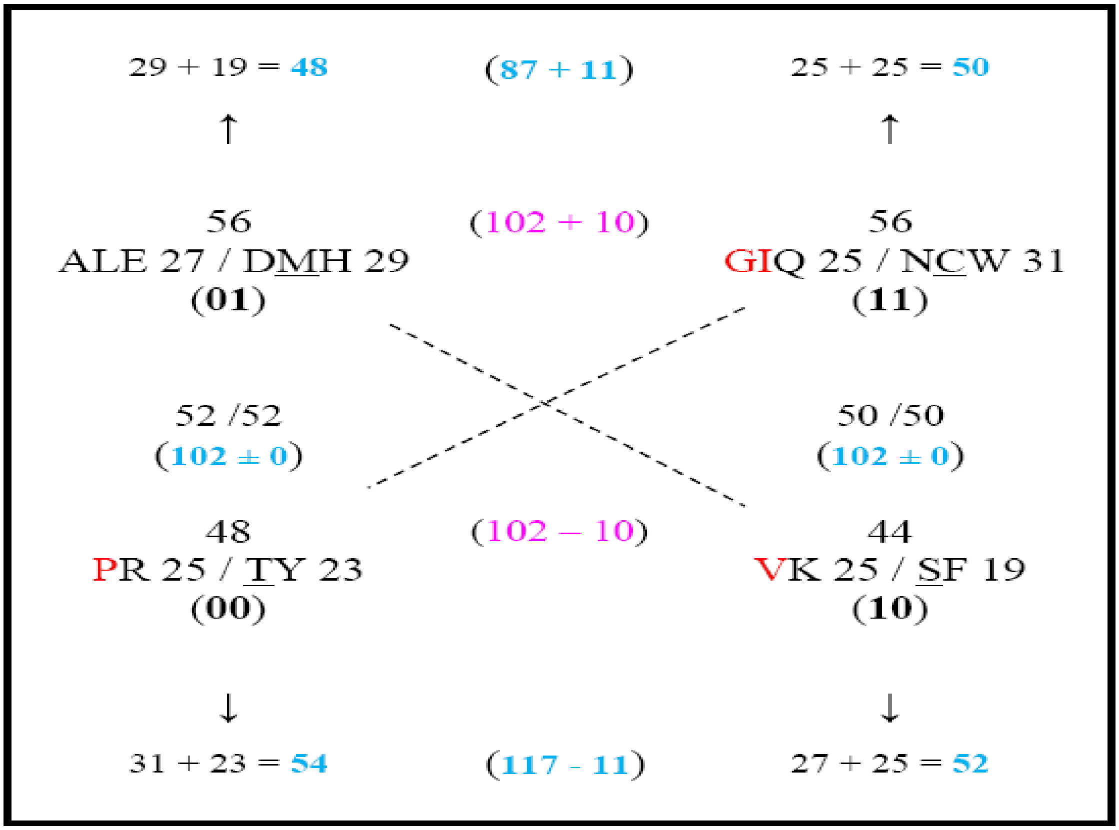
[53 + 43 = 97 – 1] [57 + 39 = 97 – 1] [97 = 87 + 10 & 117 – 20]

[56 + 78 + 86 = 220] [56 + 67 + 97 = 220]

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

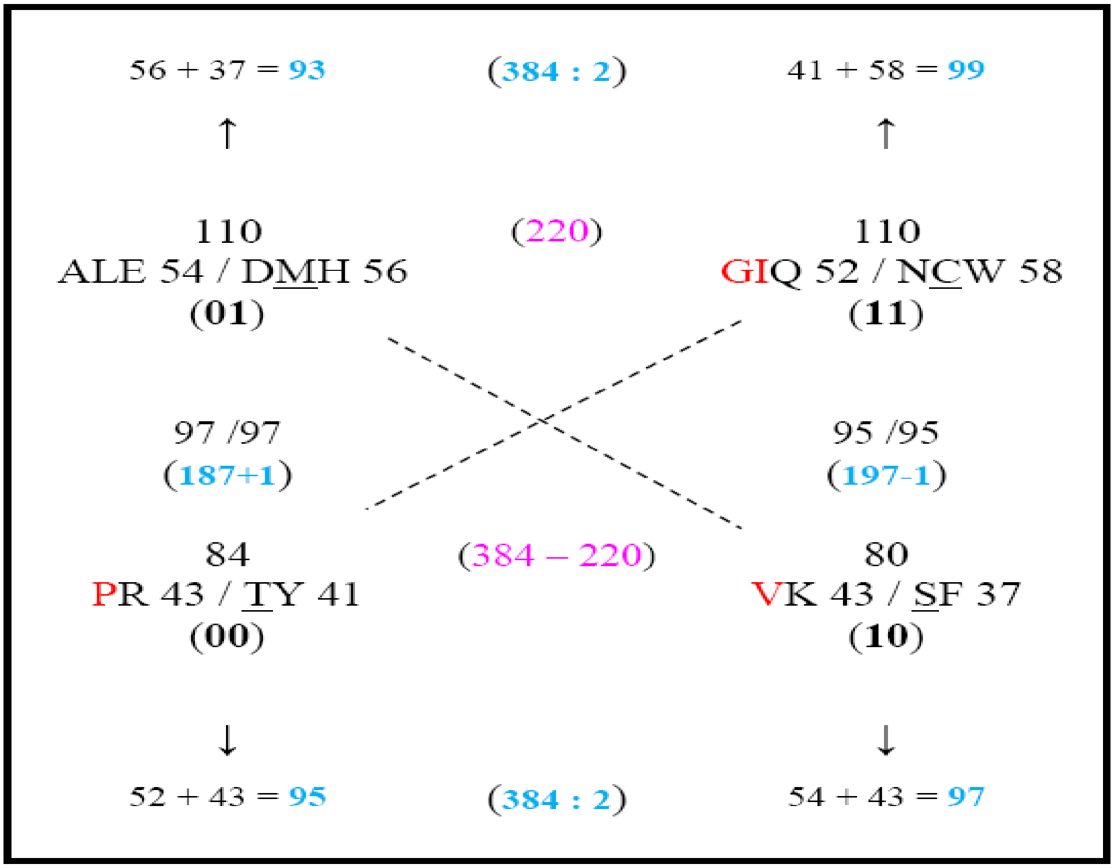
Atom number in amino acid whole molecule

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	N 08	A 04	L 13	→	**25 (07)**	60 (24) **84**
R 17	**P 08**	**F 14**	I 13	→	35 (17)	
K 15	Y 15	T 08	M 11	→	**34 (15)**	84 (36) **120**
H 11	W 18	S 05	C 05	→	28 (11)	
E 10	Q 11	G 01	V 10	→	**22 (10)**	
↓ 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 **36** / 24
C 05	T 08	E 10	F 14	**27** **10**	
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	17	18		
	(1 x 68)		(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**	→	$\boxed{\mathbf{5\ x\ 220}}$
			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)

. . .

<table>
<tr><td colspan="7"></td></tr>
<tr><td rowspan="6">440
044
↓
496 - 100</td><td>0|00</td><td>→</td><td>000</td><td>→</td><td>000 / 000</td><td rowspan="6">440
044
↓
4 x 121
121 = 11 x 11</td></tr>
<tr><td>0|11</td><td>→</td><td>011</td><td>→</td><td>011 / 110</td></tr>
<tr><td>0|22</td><td>→</td><td>022</td><td>→</td><td>022 / 220</td></tr>
<tr><td>0|11</td><td>→</td><td>011</td><td>→</td><td>011 / 110</td></tr>
<tr><td>0|00</td><td>→</td><td>000</td><td>→</td><td>000 / 000</td></tr>
<tr><td></td><td></td><td>↓</td><td></td><td>↓</td></tr>
<tr><td colspan="7">044 (2 x 022) 440 $\boxed{\mathbf{220}\ \text{x}\ \mathbf{2}}$</td></tr>
</table>

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

$\mathbf{G_{10}}$	$\mathbf{A_{13}}$	$\mathbf{N_{17}}$	$\mathbf{D_{16}}$	→	**56**
					11
V_{19}	P_{17}	S_{14}	T_{17}	→	67
					11
$\mathbf{I_{22}}$	$\mathbf{L_{22}}$	$\mathbf{C_{14}}$	$\mathbf{M_{20}}$	→	**78**
K_{24}	R_{26}	F_{23}	Y_{24}	→	97
					11
$\mathbf{Q_{20}}$	$\mathbf{E_{19}}$	$\mathbf{W_{27}}$	$\mathbf{H_{20}}$	→	**86**
G_{10}	A_{13}	N_{17}	D_{16}	→	56
105	110	112	113		
2$\underline{1}$5		2$\underline{2}$5			
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 (-887)	=	999	04 / 04	
						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).

Genetic code as a semiotic system (Vers. 3)

Miloje M. Rakočević

University of Niš, Faculty of Sciences and Mathematics
Department of Chemistry,
Višegradska 33, 18000 Niš, Serbia
(http://www.rakocevcode.rs)
(mirkovmiloje@gmail.com)

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).

*

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*.")

Acknowledgements

I am grateful to Branko Dragovich, Djuro Koruga, Dejan Raković and Tidjani Négadi for helpful, stimulating discussions and benevolent critique over a long period of years.

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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$_{\mathbf{01}}$	A$_{\mathbf{04}}$	N$_{\mathbf{08}}$		D$_{\mathbf{07}}$	→	20			
77		V$_{\mathbf{10}}$	P$_{\mathbf{08}}$	S$_{\mathbf{05}}$		T$_{\mathbf{08}}$	→	31		**022**	
88		I$_{\mathbf{13}}$	L$_{\mathbf{13}}$	C$_{\mathbf{05}}$		M$_{\mathbf{11}}$	→	42		—	
99		K$_{\mathbf{15}}$	R$_{\mathbf{17}}$	F$_{\mathbf{14}}$		Y$_{\mathbf{15}}$	→	61		**022**	
		Q$_{\mathbf{11}}$	E$_{\mathbf{10}}$	W$_{\mathbf{18}}$		H$_{\mathbf{11}}$	→	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]

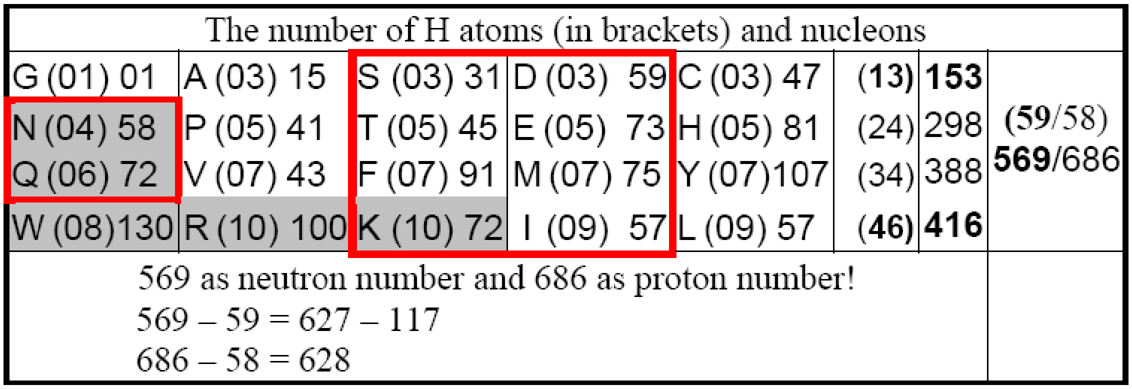
The establishing of cyclicity through the first order of AAs

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	298		388	102		155
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)

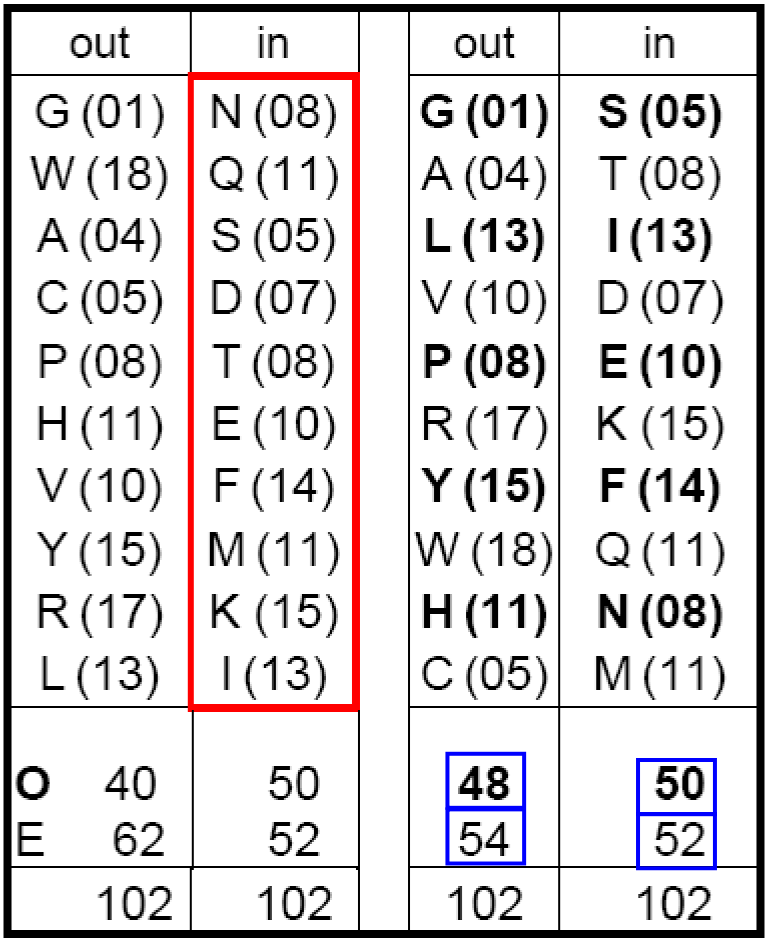


The number of H atoms (in brackets) and nucleons							
G (01) 01	A (03) 15	S (03) 31	D (03) 59	C (03) 47	**(13)**	**153**	(59/58) **569**/686
N (04) 58	P (05) 41	T (05) 45	E (05) 73	H (05) 81	(24)	298	
Q (06) 72	V (07) 43	F (07) 91	M (07) 75	Y (07)107	(34)	388	
W (08)130	R (10) 100	K (10) 72	I (09)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

569 as neutron number and 686 as proton number!
569 – 59 = 627 – 117
686 – 58 = 628

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+**$\underline{50}$**+139 = 214	NSCFW 75+**$\underline{50}$**+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+**$\underline{52}$**+159 = 241	DTMYH 80+**$\underline{52}$**+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

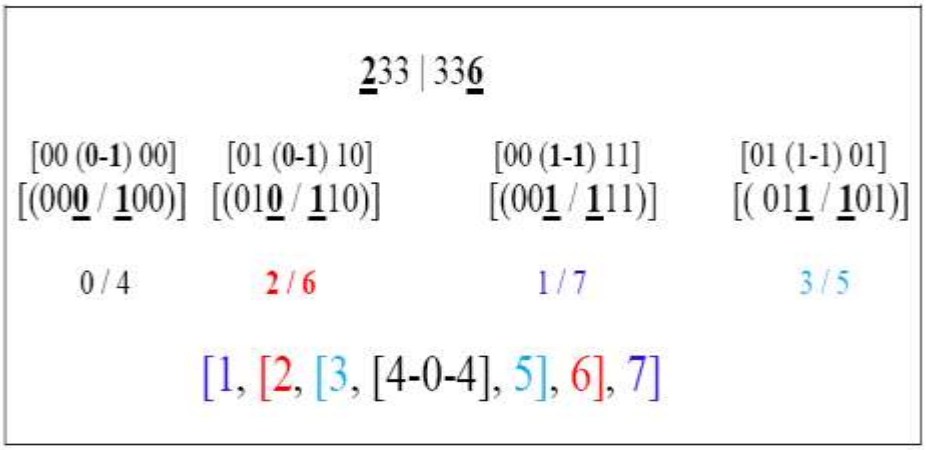
(1)	G	01	58	N	(11)	**133**
(2)	A	15	59	D	(12)	
(3)	V	43	31	S	(13)	160
(4)	P	41	45	T	(14)	
(5)	I	57	47	C	(15)	**236**
(6)	L	57	75	M	(16)	
(7)	K	72	91	F	(17)	370
(8)	R	100	107	Y	(18)	
(9)	Q	72	130	W	(19)	**356**
(10)	E	73	81	H	(20)	
			72$\underline{4}$			**72$\underline{5}$**
		53$\underline{1}$				53$\underline{0}$

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 = **0**37 + 100 = **1**37	111+122+ 133+143 = 408 + 101 408 = 204 x 2 (**68** x 3 = 204) (**69** : 3 = 23)		
[(38 – 28 = **10**) (36 – 35 = **01**)]	[(28 + 35 = 63±**00**) (36 + 38 = 63 + **11**)]		

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**

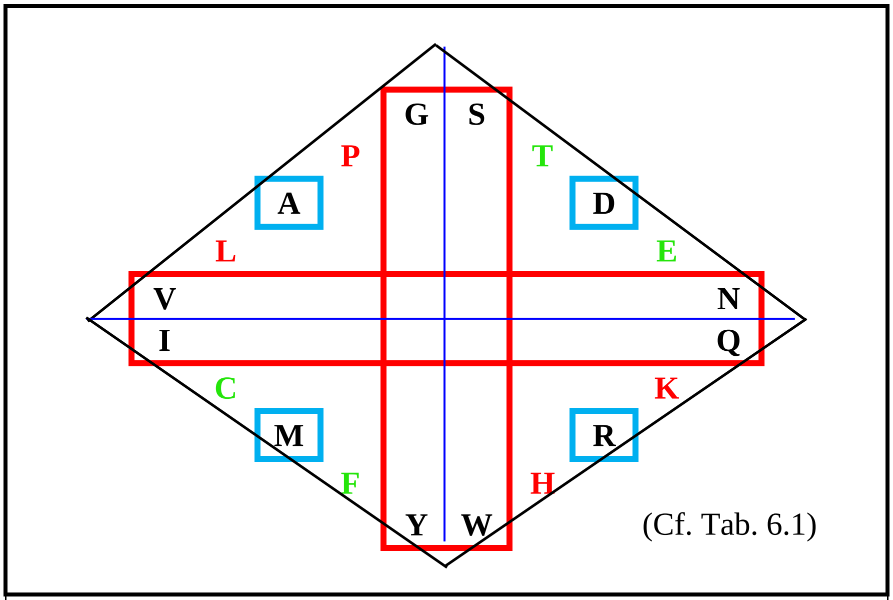
532.57+ 725.86 = 1258.43 ≈ 1258 → 34 x 37

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)

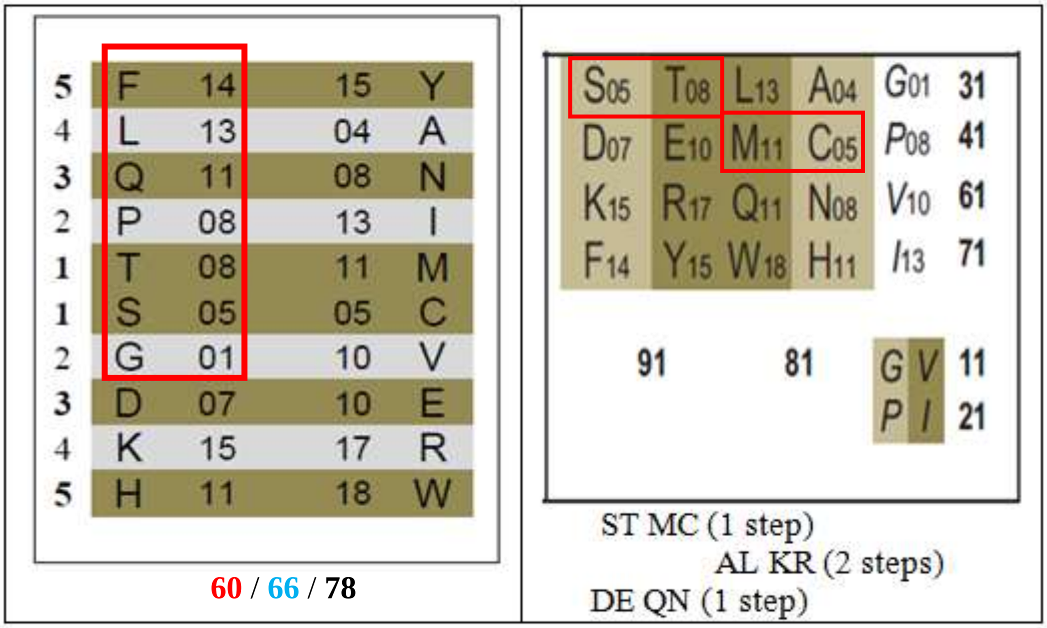
---

[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

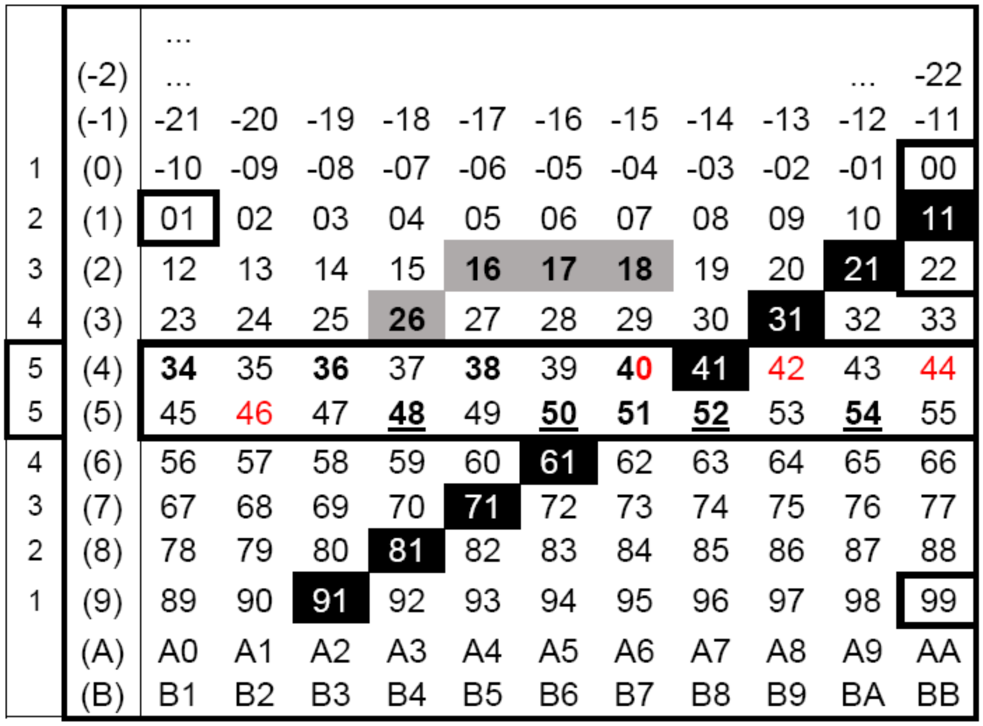
ST MC (1 step)

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.

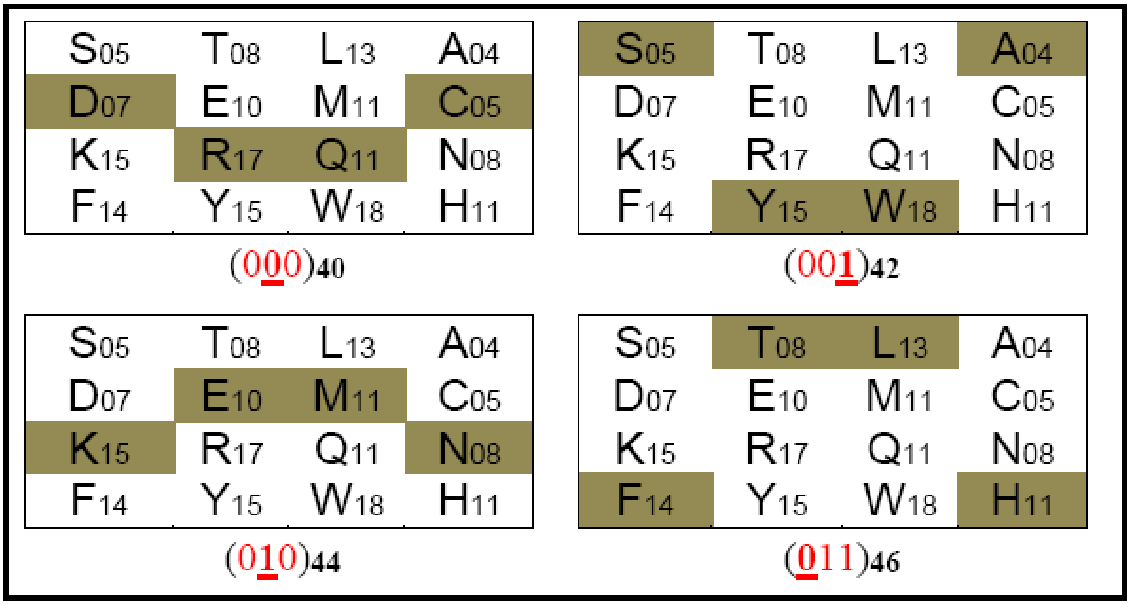
Table A2. Periodic system of the numbers in decimal number system



		...										
	(-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

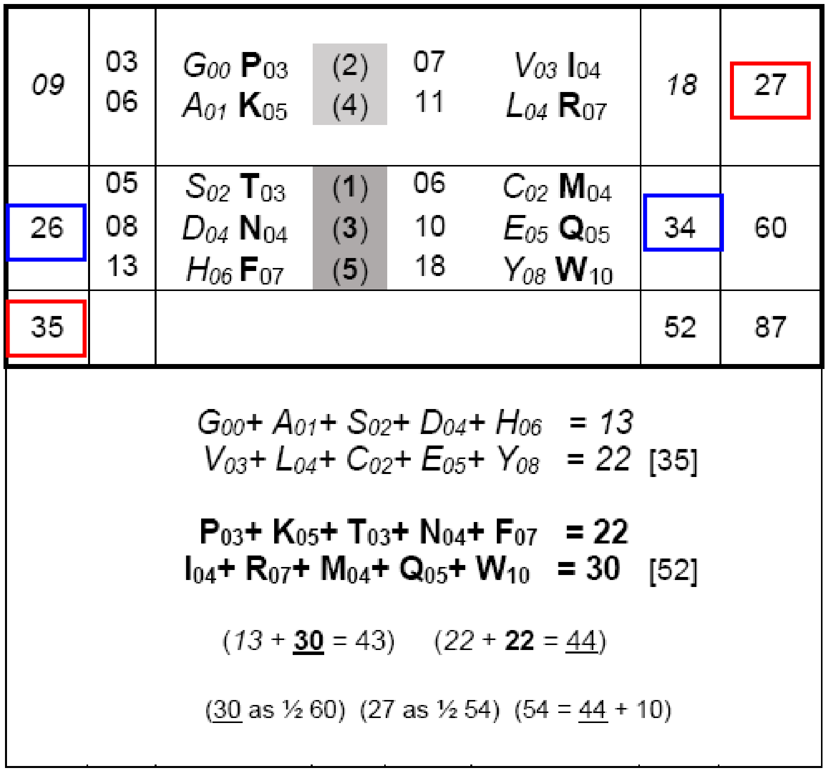
(010)**44**

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.

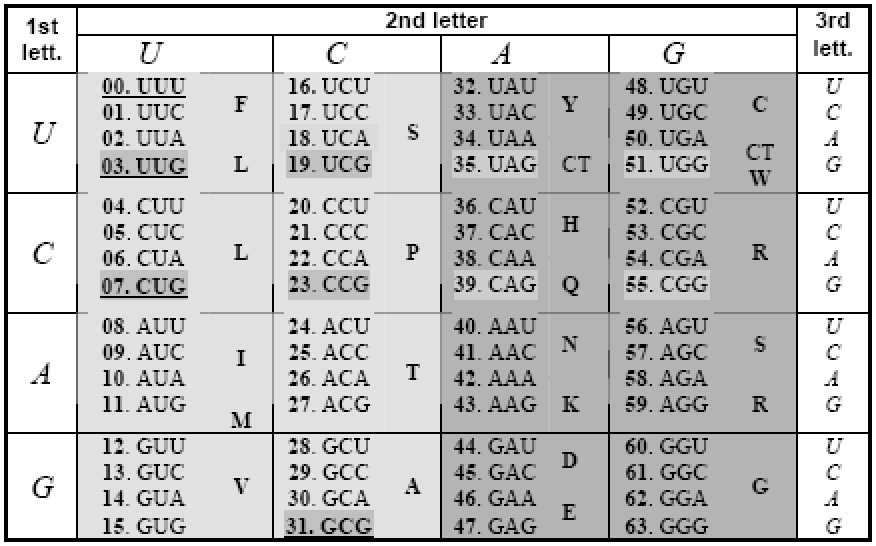
Table A5. Adjacency relations of pairs in the series of natural numbers

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

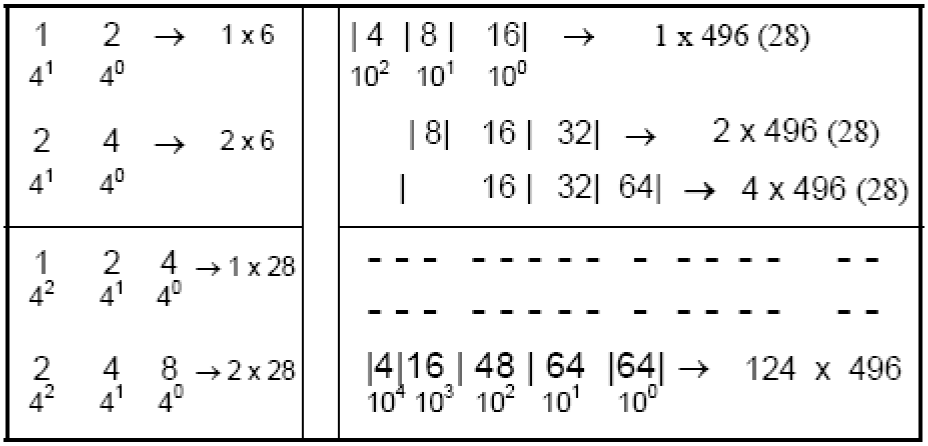


1st lett.	2nd letter U		C		A		G		3rd lett.
U	00. UUU	F	16. UCU	S	32. UAU	Y	48. UGU	C	U
	01. UUC		17. UCC		33. UAC		49. UGC		C
	02. UUA		18. UCA		34. UAA		50. UGA		A
	03. UUG	L	19. UCG		35. UAG	CT	51. UGG	CT W	G
C	04. CUU	L	20. CCU	P	36. CAU	H	52. CGU	R	U
	05. CUC		21. CCC		37. CAC		53. CGC		C
	06. CUA		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)

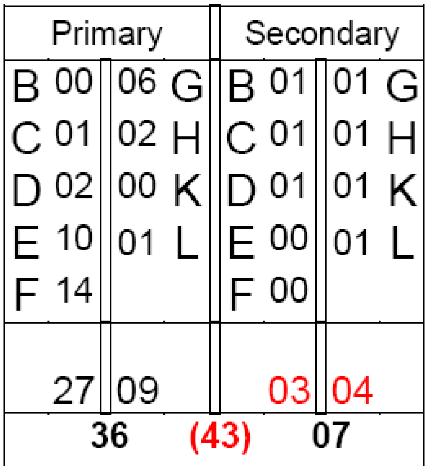
Table A7. Binary "travel" of the second and third perfect numbers through the space



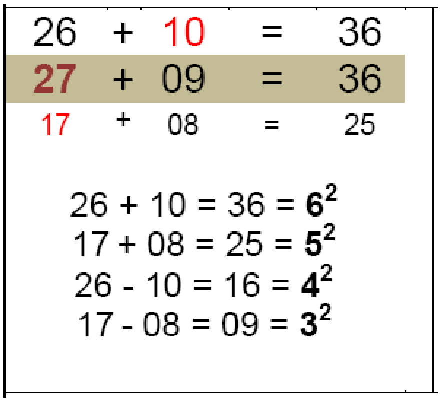
<table>
<tr><td>1 2 → 1 x 6
4^1 4^0
2 4 → 2 x 6
4^1 4^0</td><td></td><td>| 4 | 8 | 16| → 1 x 496 (28)
10^2 10^1 10^0
| 8| 16 | 32| → 2 x 496 (28)
| 16 | 32| 64| → 4 x 496 (28)</td></tr>
<tr><td>1 2 4 → 1 x 28
4^2 4^1 4^0
2 4 8 → 2 x 28
4^2 4^1 4^0</td><td></td><td>- - - - - - - - - - - - - - - - -
-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

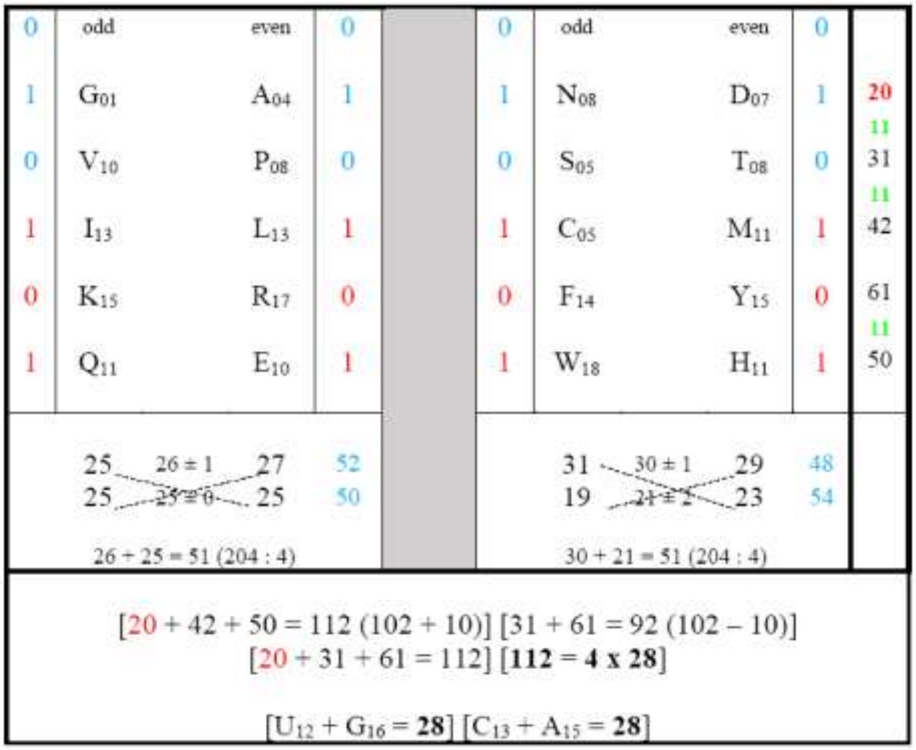
(Taken from MMR, 2019, Tab. C1, p. 38)

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 25 25 ± 0 25		52 50			31 30 ± 1 29 19 21 ± 2 23		48 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**]

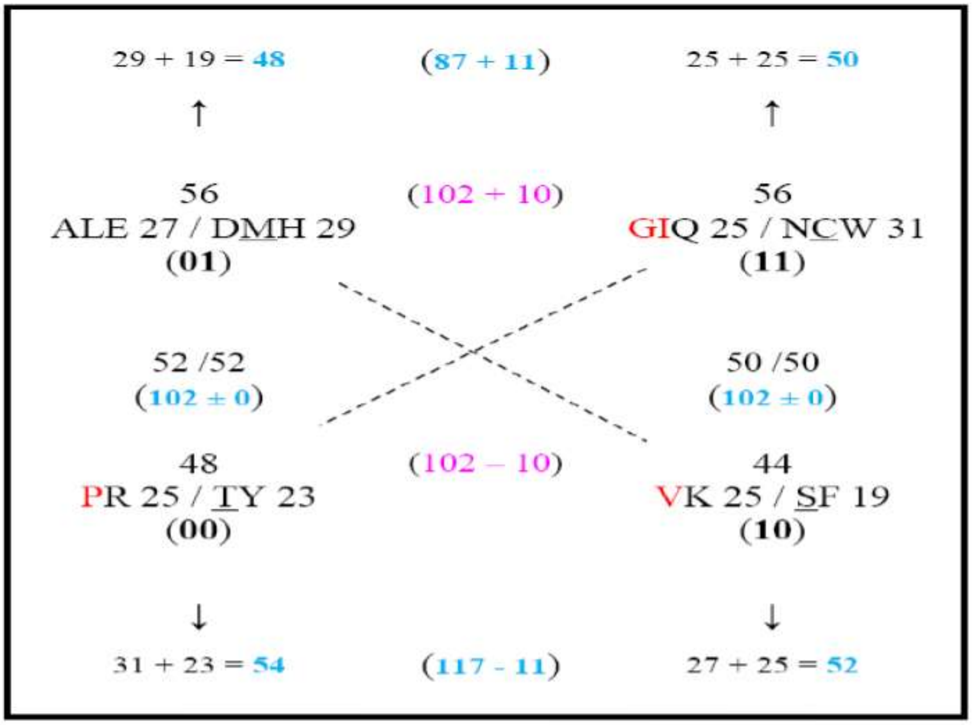
Atom number in amino acid side chain

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
											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] $\boxed{[56 + 67 + 97}$ = 220]											
[65 + 87 + 68 = 220] [65 + 76 + 79 = 220]											

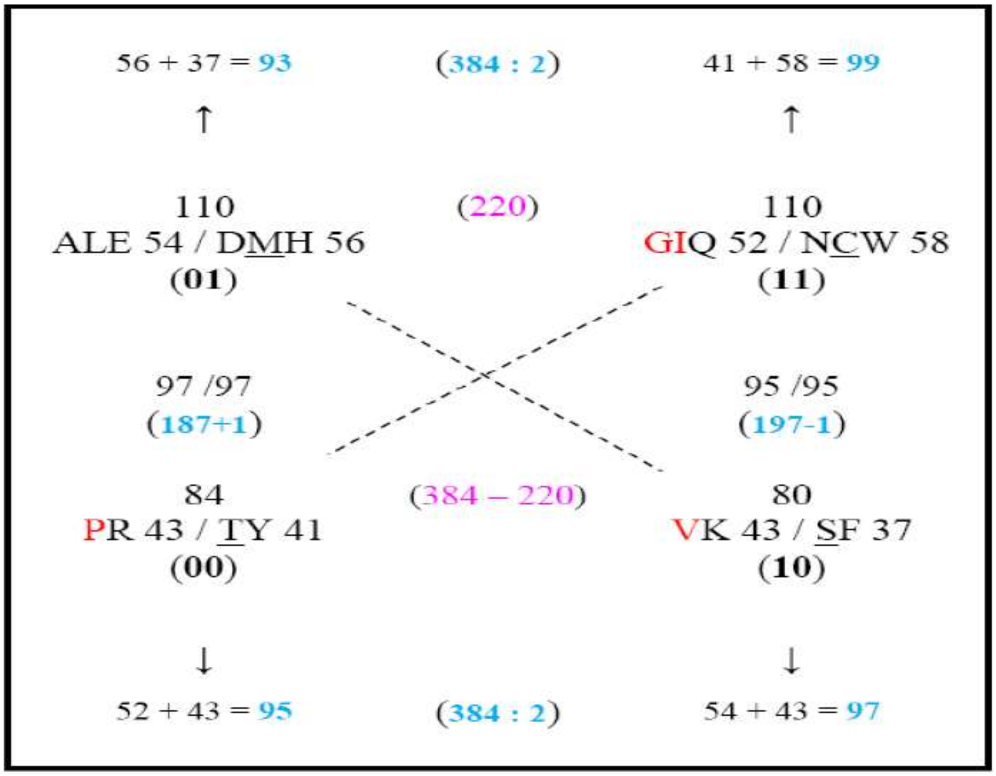
Atom number in amino acid whole molecule

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)



56 + 37 = 93 (384 : 2) 41 + 58 = 99

↑ ↑

110 (220) 110

ALE 54 / DMH 56 GIQ 52 / NCW 58

(01) (11)

97 /97 95 /95

(187+1) (197-1)

84 (384 – 220) 80

PR 43 / TY 41 VK 43 / SF 37

(00) (10)

↓ ↓

52 + 43 = 95 (384 : 2) 54 + 43 = 97

Atom number in amino acid whole molecule

Genetic code as a semiotic system (Vers. 4)

Miloje M. Rakočević
University of Niš, Faculty of Sciences and Mathematics
Department of Chemistry,
Višegradska 33, 18000 Niš, Serbia
(http://www.rakocevcode.rs)
(mirkovmiloje@gmail.com)

Abstract. In previous work (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.

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

1. Introduction

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

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

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

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

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

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

MMR, 1988, on page 4: “The way in which [Mendel] arrived at scientific conclusions is closer to the methodology of scientific reasoning in information theory and systems theory than to the methodology of reasoning in classical biology. Darwin's entire work also has a systemic character. ... The founder of structural linguistics, Ferdinand de Saussure, already in 1908 said everything about the universal in language, either natural speech or the language of other sign systems; even about the interdependence of language units ... By genetic language we mean the system of nucleotide sequences in nucleic acids and a system of amino acid sequences in proteins.”

On p. 64: “From De Saussure's point of view, language (observed in its phylogeny) is a system of words with all the connections and relations between them, and all the changes that have befallen them on the evolutionary path; that is, from an other side, it is a system of macromolecules (nucleic acids or proteins), also with all the connections and relationships between them and changes in the evolutionary path”] “Therefore, it is not about any norms that are prescribed, but the laws of language, the laws of synchrony and diachrony, independent of "agreements about language, from the norms prepared by experts and specialists"... "The laws of synchrony and diachrony have a universal character". Saussure well observed the universal character of phenomena in language, in the same way as Darwin, when it comes to the laws of evolution of organisms.

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

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

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

2. A new elaboration

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

We take the notion of *semiosis* from Charles Sanders Peirce, through Charles W. Morris, in the sense that semiosis is "the process in which something functions as a sign" (Morris, 1938, Section II/2, p. 3). On the other hand, the notion of *sign* we take from Ferdinand de Saussure (1985) in the sense that "by sign we mean the total resulting from the association of a signifier with a signified." (De Saussure, 1985, pp. 99–100: "Nous entendons par signe le total résultant de l'association d'un signifiant à un signifié".) By chemism we mean the chemical affinity and chemical reactivity of substances.

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

[MMR, 2018a, pp. 31-32: "Rumer (1966) suggests that encoding (of amino acids) by dinucleotide aggregations is mediated by ‘grammatical’ formalism (the relation between words and the root of the word), semantics (one-meaning and multi-meaning codon families) and by semiology, i.e. semiotics (the classification of nucleotide doublets after the <u>number</u> of their hydrogen bonds which appear here as ‘signifiant’ and ‘signifié’ (signifier and signified) at the same time, that is as their unity (De Saussure, 1985, pp. 99-100)".]

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

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

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

3. New insights

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

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

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

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

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

[6] De Saussure, 1985, p. 100: "Le lien unissant le signifiant au signifié est arbitraire, ou encore, puique nous entendons par signe le total résultant de l'association d'un signifiant à un signifier nou pouvons dire plus simplement: le signe linguistique est arbitraire. … Le mot arbitraire appelle aussi une remarque. Il ne doit pas donné l'idée que le signifiant dépend du libre choix … Nous voulons dire qu'il est immotivé, c'est-à-dire arbitraire par rapport au signifié, avec lequel il n'a aucune attache naturelle dans la réalité."

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

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

*

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

*

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

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

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

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

4. Discussion

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

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

I

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

---

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

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

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

Box 3. De Saussure's argumentation

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

II

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

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

III

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

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

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

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

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

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

IV

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

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

V

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

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

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

VI

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

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

5. Conclusion

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

Acknowledgements

I am grateful to Branko Dragović, Djuro Koruga, Dejan Raković and Tidjani Négadi for helpful, stimulating discussions and benevolent critique over a long period of years.

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TABLES

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

on		an	pn		pn	an		on
01	**G**	01	01		31	08	N	11
02	**A**	04	09		31	07	D	12
03	**V**	10	25		17	05	S	13
04	**P**	08	23		25	08	T	14
05	I	13	33		25	05	**C**	15
06	L	13	33		41	11	**M**	16
07	K	15	41		49	14	**F**	17
08	R	17	55		57	15	**Y**	18
09	Q	11	39		69	18	**W**	19
10	E	10	39		43	11	**H**	20
055		102	298		388	102		155
455 | **554**					645 | 546			
(455 | 554) + (645 | 546) → (1100 + 1100) → 10 x 220								

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

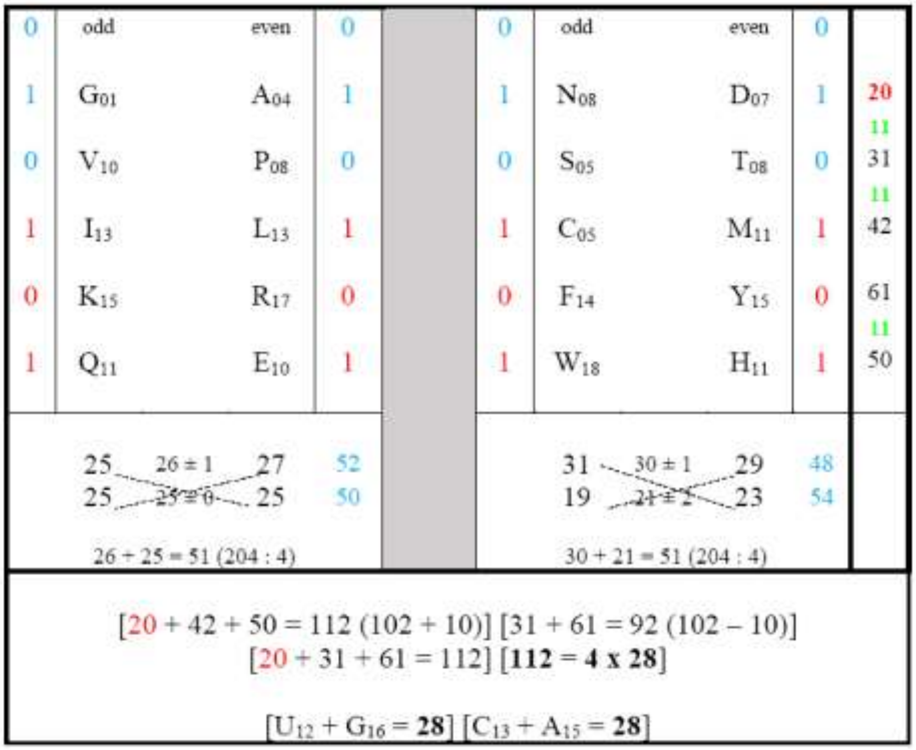
Table 2. Mirror symmetry through the number of atoms in AAs

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

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

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

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



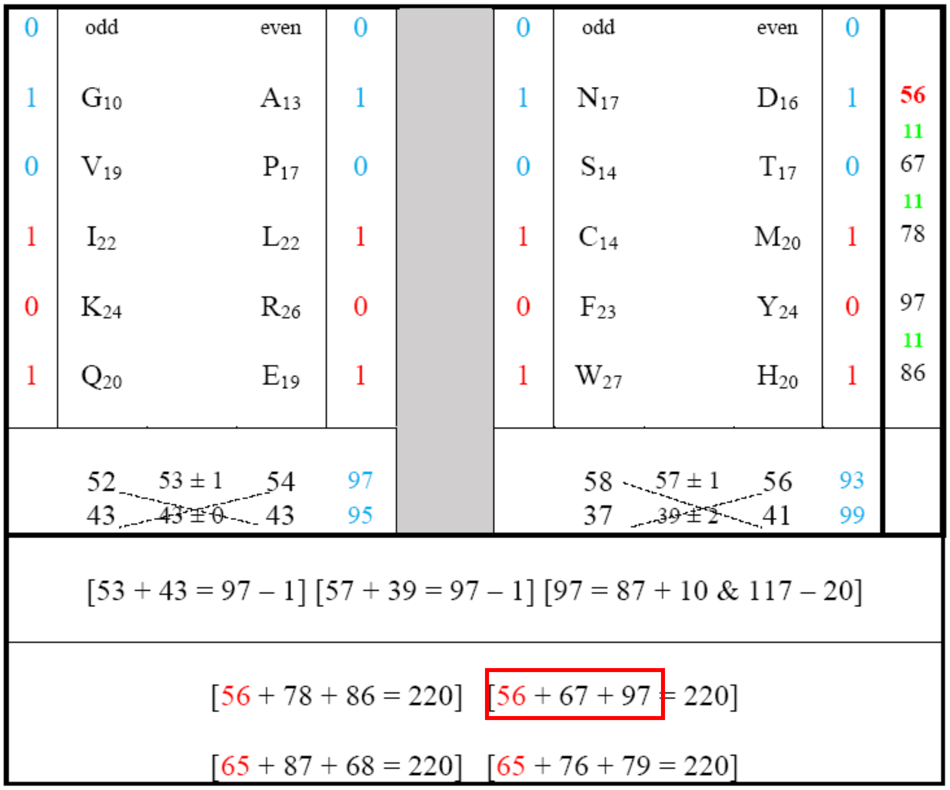
0	odd	even	0		0	odd	even	0	
1	G_{01}	A_{04}	1		1	N_{08}	D_{07}	1	20 11
0	V_{10}	P_{08}	0		0	S_{05}	T_{08}	0	31 11
1	I_{13}	L_{13}	1		1	C_{05}	M_{11}	1	42
0	K_{15}	R_{17}	0		0	F_{14}	Y_{15}	0	61 11
1	Q_{11}	E_{10}	1		1	W_{18}	H_{11}	1	50
	25 25	26 ± 1 25 ± 0	27 25		31 19	30 ± 1 21 ± 2	29 23	48 54	
	26 + 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. Again even / odd by column, for "bodies". We note that the quantities 48, 50, 52 and 54 are also in the central area of the Periodic System of Numbers (PSN: Figure 2).

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



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

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

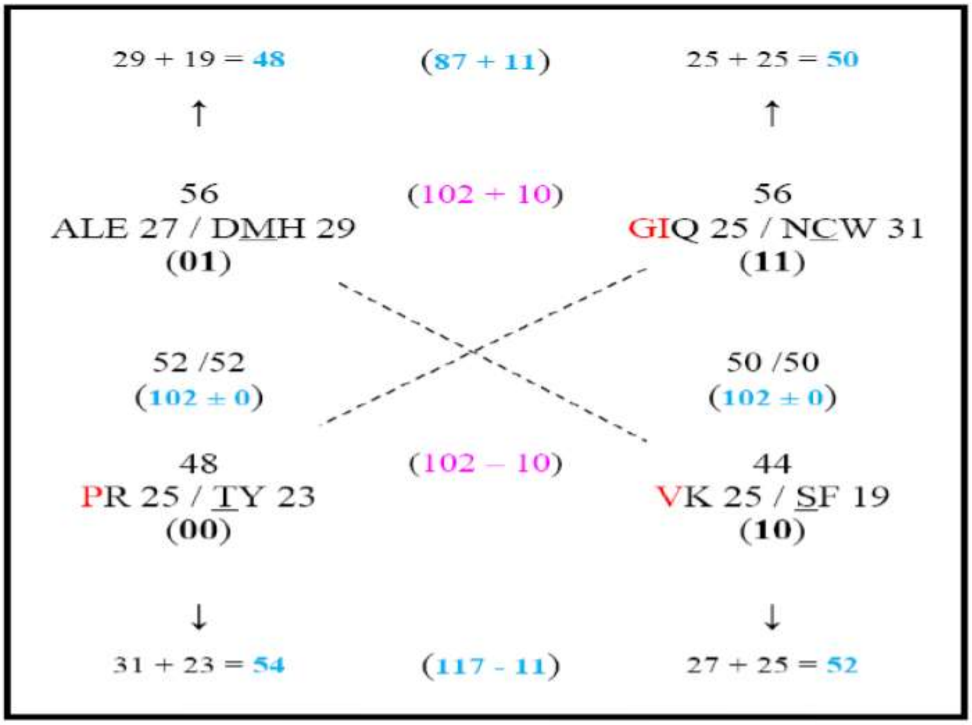
[56 + 78 + 86 = 220] [56 + 67 + 97 = 220]

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

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

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

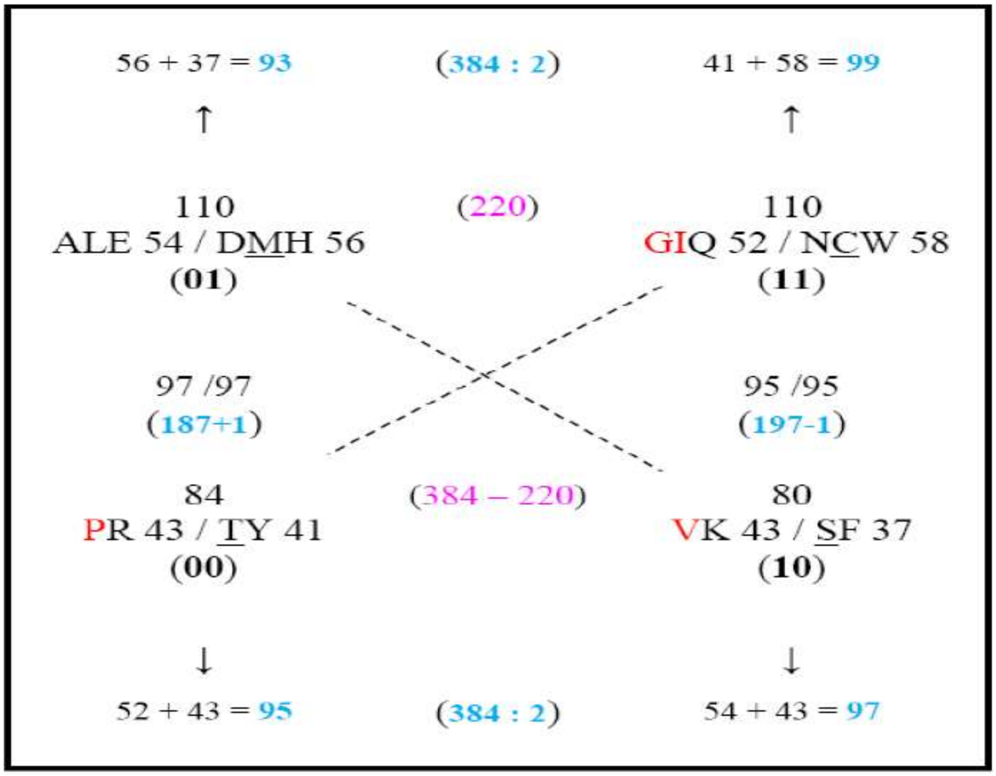
Table 2.3. Distribution of quintets from Table 2 by even and odd positions (I)



29 + 19 = 48	(87 + 11)	25 + 25 = 50
↑		↑
56 ALE 27 / DMH 29 **(01)**	(102 + 10)	56 GIQ 25 / NCW 31 **(11)**
52 /52 (102 ± 0)		50 /50 (102 ± 0)
48 PR 25 / TY 23 **(00)**	(102 – 10)	44 VK 25 / SF 19 **(10)**
↓		↓
31 + 23 = 54	(117 - 11)	27 + 25 = 52

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

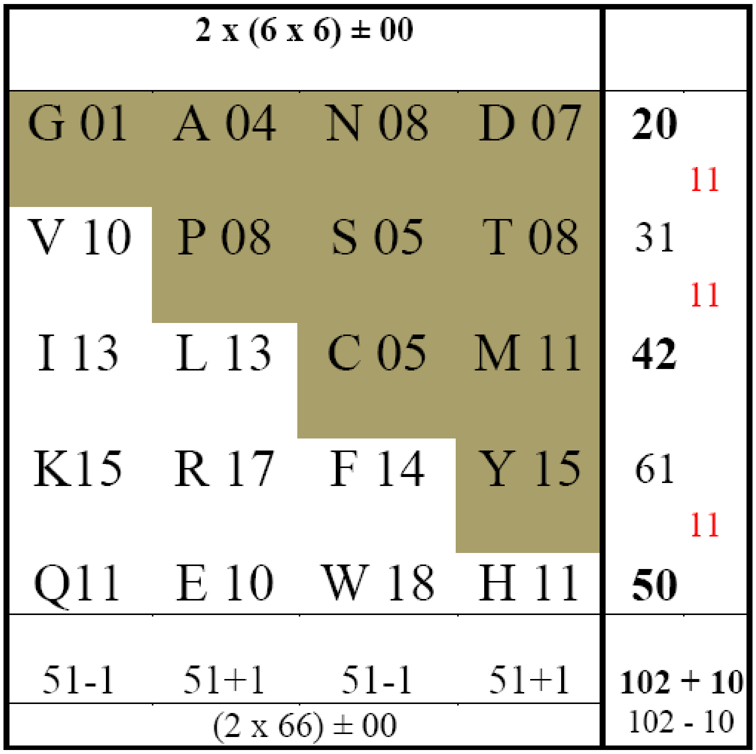
Table 2.4. Distribution of quintets from Table 2 by even and odd positions (II)



56 + 37 = 93	(384 : 2)	41 + 58 = 99
↑		↑
110 ALE 54 / DMH 56 **(01)**	(220)	110 GIQ 52 / NCW 58 **(11)**
97 /97 (187+1)		95 /95 (197-1)
84 PR 43 / TY 41 **(00)**	(384 – 220)	80 VK 43 / SF 37 **(10)**
↓		↓
52 + 43 = 95	(384 : 2)	54 + 43 = 97

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

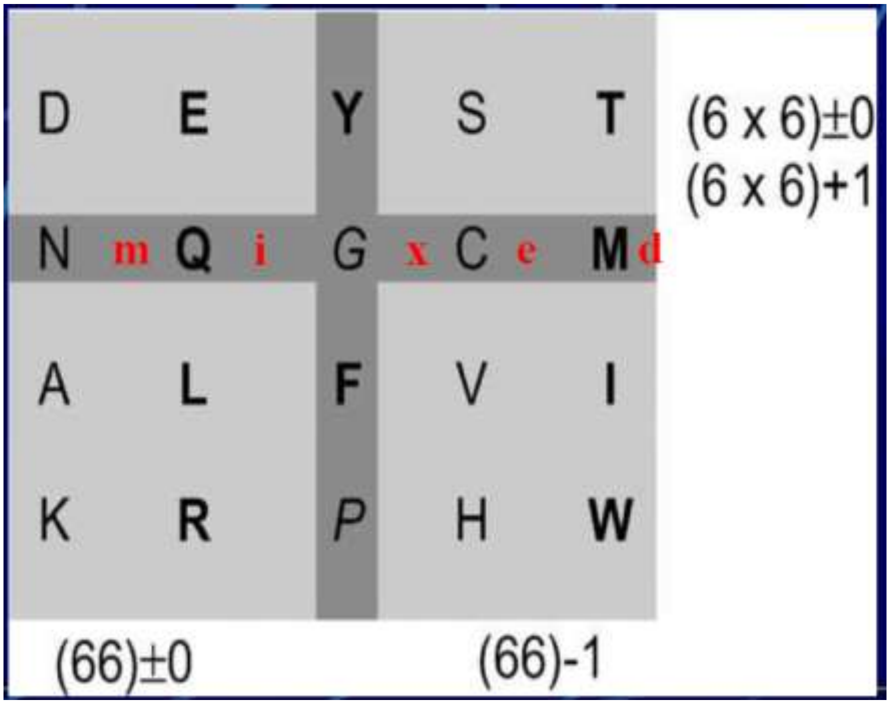
Table 2.5. Significant quantities "6 x 6" and "66" in the Genetic Code (I)



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

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

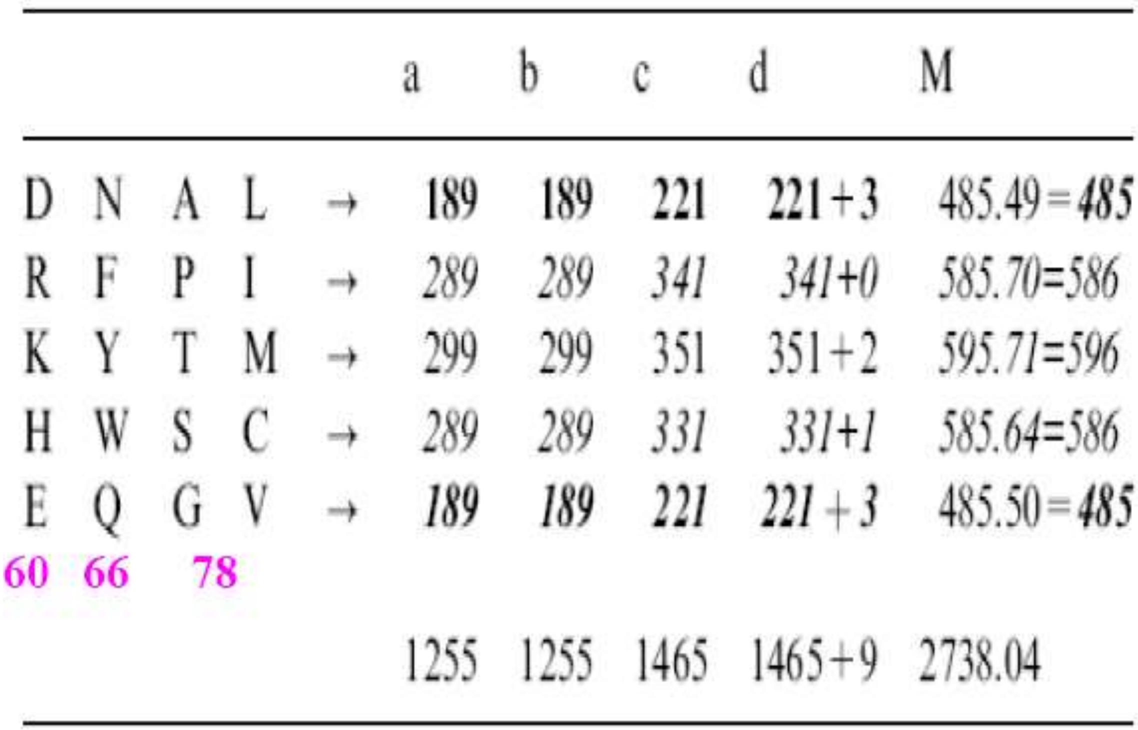
Table 2.6. Significant quantities "6 x 6" and "66" in the Genetic Code (II)



D	E	Y	S	T	(6 x 6)±0
N m	Q i	G x	C e	M d	(6 x 6)+1
A	L	F	V	I	
K	R	*P*	H	W	
(66)±0			(66)-1		

Classification of amino acids according to similarity/dissimilarity of molecules classes. From (MMR, 2004, Tab. 9, p. 229): "First row (down): N-ended AAs. Second row: solely C-ended AAs. Last row (up): O-ended AAs. First to last row: remaining five AAs (one solely H-ended, two S-ended and two N-, O-ended, all five as a ‘combination’. Within the cross there are only the exceptions: horizontally five the mentioned combining AAs; vertically: Y as aromatic within aliphatic AAs; G without carbon; F as aromatic within aliphatic AAs; and, finally, P as cyclic aliphatic amino acid. In the system there is a balanced proportionality as follows: within horizontal leg of the cross there are (6 x 6) ± 0 of atoms, and within vertical leg (without glycine), there are (6 x 6) ±1. Without cross: on the left there are (66) ± 0 and (66)–1 on the right." The significance and uniqueness of the quantities 36 and 66 can be seen in Surveys 1–5.

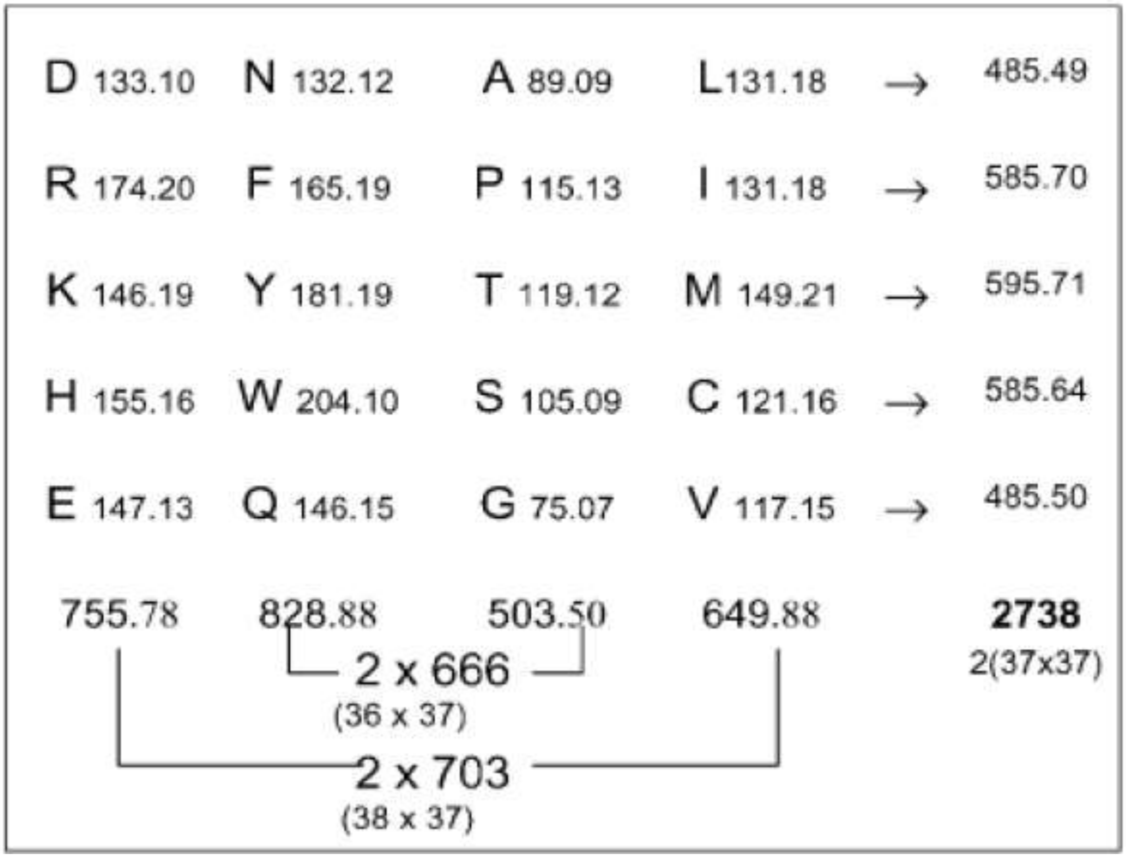
Table 3. A harmonic structure of Genetic code (I)



					a	b	c	d	M
D	N	A	L	→	**189**	**189**	**221**	**221+3**	485.49=***485***
R	F	P	I	→	*289*	*289*	*341*	*341+0*	*585.70=586*
K	Y	T	M	→	299	299	351	351+2	*595.71=596*
H	W	S	C	→	*289*	*289*	*331*	*331+1*	*585.64=586*
E	Q	G	V	→	***189***	***189***	***221***	***221+3***	485.50=***485***
60	66	78							
					1255	1255	1465	1465+9	2738.04

From (MMR, 2004, Table 1, p. 233). "Four choices after four types of isotopes: (a) The number of nucleons within 20 AAs side chains, calculated from the first, the lightest nuclide (H-1, C-12, N-14, O-16, S-32). (b) The number of nucleons within 20 AAs side chains, calculated from the nuclide with the most abundance in the nature [the same patterns as in (a): H-1, C-12, N-14, O-16, S-32; at heavier nuclides of other bioelements the data by (a) and (b) are not the same]. (c) The number of nucleons within 20 AAs side chains, calculated from the nuclide with the less abundance in the nature (H-2, C-13, N-15, O-17, S-36); (d) The number of nucleons within 20 AAs side chains, calculated from the last, the heaviest nuclide (H-2, C-13, N-15, O-18, S-36). (M) The AAs molecule mass. Notice that (d) is greater from (c) for exactly one modular cycle (in module 9) and that total molecules mass is equal to 2 x (37 x 37). Notice also that molecule mass within five rows is realized through the same logic-patterns of notations as the first nuclide, i.e. isotope."

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



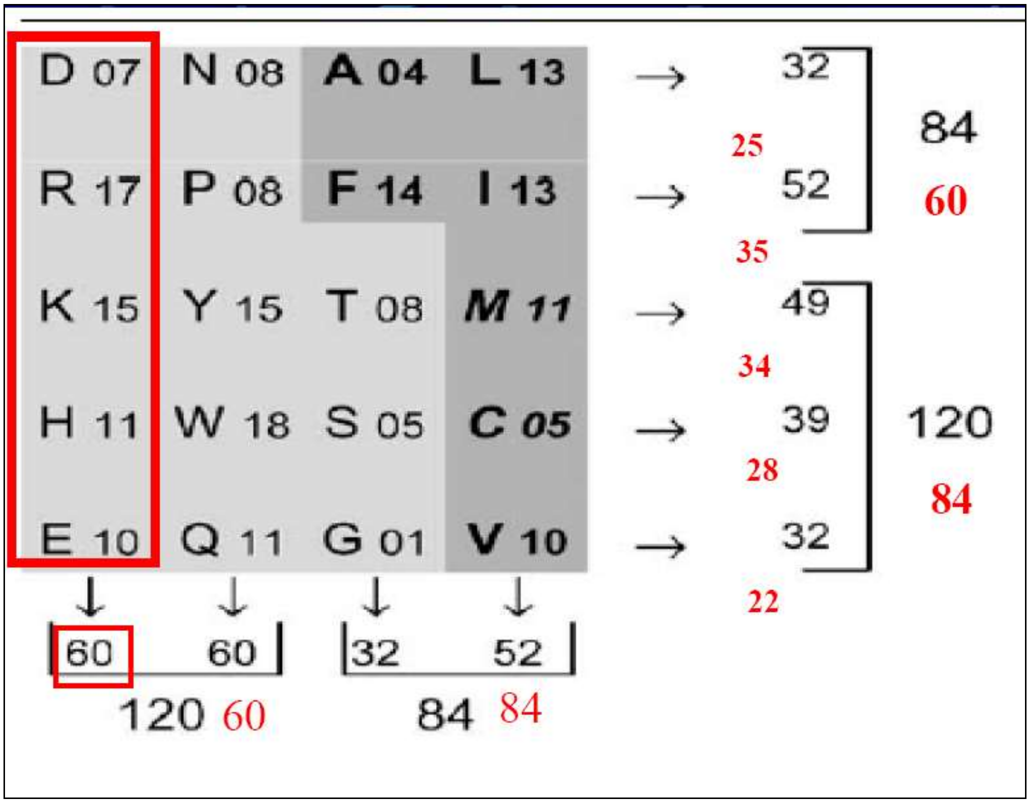
D 133.10	N 132.12	A 89.09	L131.18	→	485.49
R 174.20	F 165.19	P 115.13	I 131.18	→	585.70
K 146.19	Y 181.19	T 119.12	M 149.21	→	595.71
H 155.16	W 204.10	S 105.09	C 121.16	→	585.64
E 147.13	Q 146.15	G 75.07	V 117.15	→	485.50
755.78	828.88	503.50	649.88		**2738** 2(37x37)

2 x 666
(36 x 37)

2 x 703
(38 x 37)

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

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



D 07	N 08	**A 04**	**L 13**	→		32	
					25		84
R 17	P 08	**F 14**	**I 13**	→		52	60
					35		
K 15	Y 15	T 08	***M 11***	→		49	
					34		
H 11	W 18	S 05	***C 05***	→		39	120
					28		84
E 10	Q 11	G 01	**V 10**	→		32	
					22		
↓	↓	↓	↓				
60	60	32	52				
120 60		84 84					

The splitting of AAs into polar (light ton) and non-polar (bold, dark ton). The polarity as hydropathy (Kyte and Doolittle, 1982, Table 2, p. 110). The number of atoms within AAs molecules (side chains) in first two rows as well as in second two columns is identical (84 atoms). The same is valid for other three rows in relation to first two columns (120 atoms). In the red frame are the polar charged AAs. The numbers marked in red represent the number of atoms in polar uncharged and nonpolar amino acids. As we can see, the balances apply both ways: in the set of all 20 amino acid molecules, as well as in the subset of polar charged and subset of all the others. (Note: The classification of amino acids into 5 polar charged, 7 non-polar and 8 polar non-charged corresponds to a unique situation in the series of natural numbers; with a series determined by the law of genetic nature (the follower contains the predecessor) (Survey 8). [*Note*: Here one can notice a *vice-versa* change in the positions of phenylalanine and proline: from F-P in Tables 3 and 3.1, to P-F in this Table. Just such a change (balancing and nuancing, according to the definitions given in: MMR, 2018a, p. 33) creates the conditions for the distinction (classification) of amino acids into 5 polar charged, 7 non-polar and 8 polar non-charged, corresponding to a unique genetic mathematical series (Survey 8).]

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

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

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

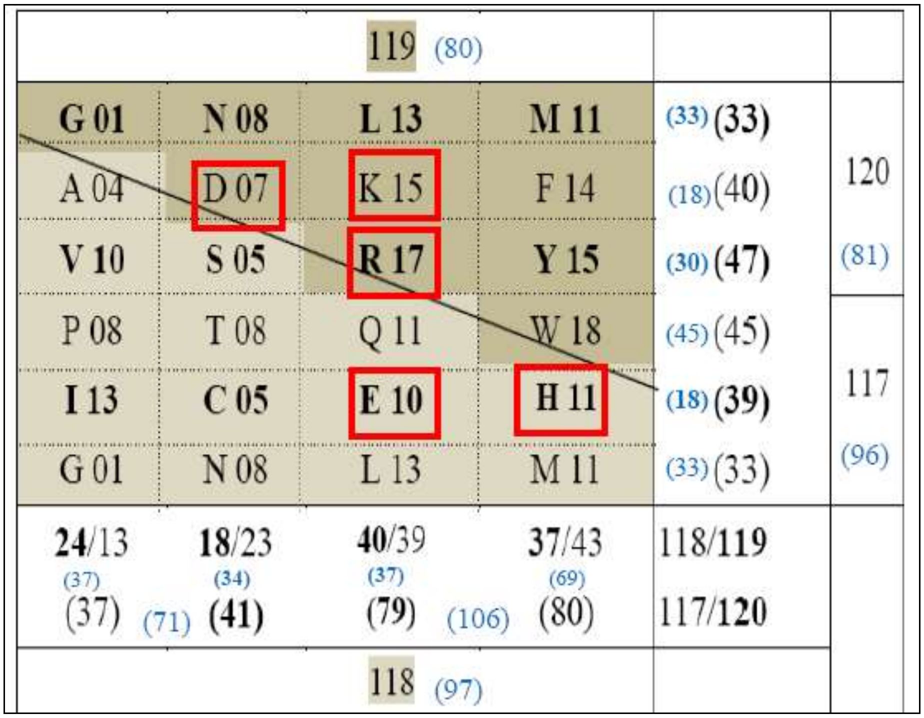
Table 4.1. The four quintets of amino acids within PPAASS in Table 1 (II)

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

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

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

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



		119 (80)			
G 01	N 08	L 13	M 11	(33) (33)	120 (81)
A 04	D 07	K 15	F 14	(18) (40)	
V 10	S 05	R 17	Y 15	(30) (47)	
P 08	T 08	Q 11	W 18	(45) (45)	117 (96)
I 13	C 05	E 10	H 11	(18) (39)	
G 01	N 08	L 13	M 11	(33) (33)	
24/13 (37) (37) (71)	18/23 (34) (41)	40/39 (37) (79) (106)	37/43 (69) (80)	118/119 117/120	
		118 (97)			

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

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

Table 5.1. Nucleon number in PPAASS (Table 1)

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

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

Table 5.2. Neutron number in PPAASS (Table 1)

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

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

Table 5.3. Neutron number in PPAASS:
Further distinctions

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

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

Table 5.4. Isotope number in PPAASS (Table 1)

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

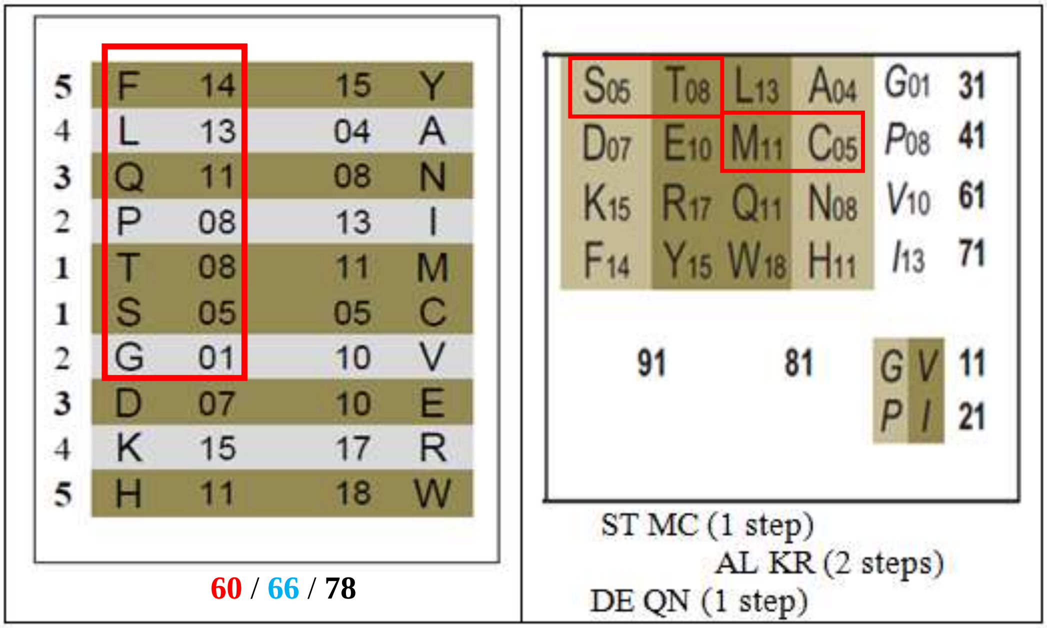
Isotope number as in (MMR, 2004, Table 7). The result 440 / 402 is the reverse case in relation to the result in Tab. 5.5.

Table 5.5. Isotope number in PPAASS:
Further distinctions

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

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

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



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)

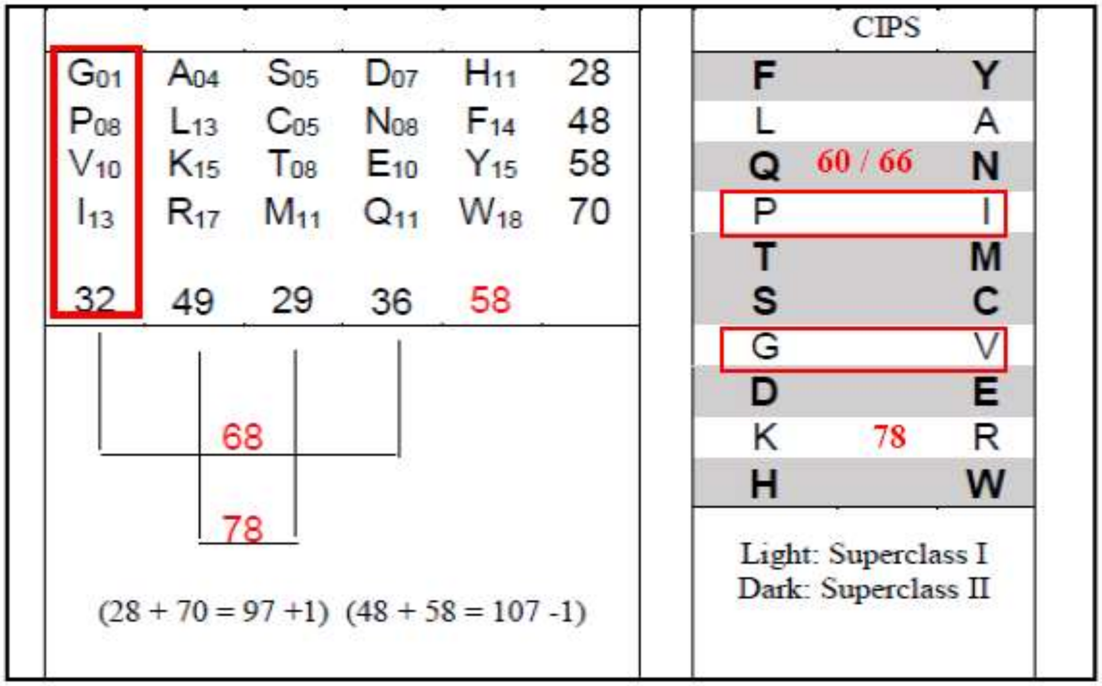
CIPS: Cyclic Invariant Periodic System from: MMR, 2011, Fig 6, p. 832; SCAS: Stereo-Chemically Arranged System. From: MMR, 2019, Fig 1, p. 6. In both cases, the number of atoms in the molecule (in the side chain) is attached to the amino acid designation in normal and index notation, respectively. MMR, 2011: The Cyclic Invariant Periodic System (CIPS) of canonical AAs. … In the middle position there are chalcogen AAs (S, T & C, M); follow - in next "cycle" – the AAs of non-alanine stereochemical types (G, P & V, I), then two double acidic AAs with two their amide derivatives (D, E & N, Q), the two original aliphatic AAs with two amine derivatives (A, L & K, R); and, finely, four aromatic AAs (F, Y & H, W) – two up and two down. The said five classes belong to two superclasses: primary superclass in light areas and secondary superclass in dark areas. Notice, that each amino acid position in this CIPS is strictly determined and none can be changed. MMR, 2019: The right picture: Dark tones: Class I of amino acids handled by class I of enzymes aminoacyl-tRNA synthetases [except T]; light tones: Class II [except C]."

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

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

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

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



G_{01}	A_{04}	S_{05}	D_{07}	H_{11}	28
P_{08}	L_{13}	C_{05}	N_{08}	F_{14}	48
V_{10}	K_{15}	T_{08}	E_{10}	Y_{15}	58
I_{13}	R_{17}	M_{11}	Q_{11}	W_{18}	70
32	49	29	36	58	

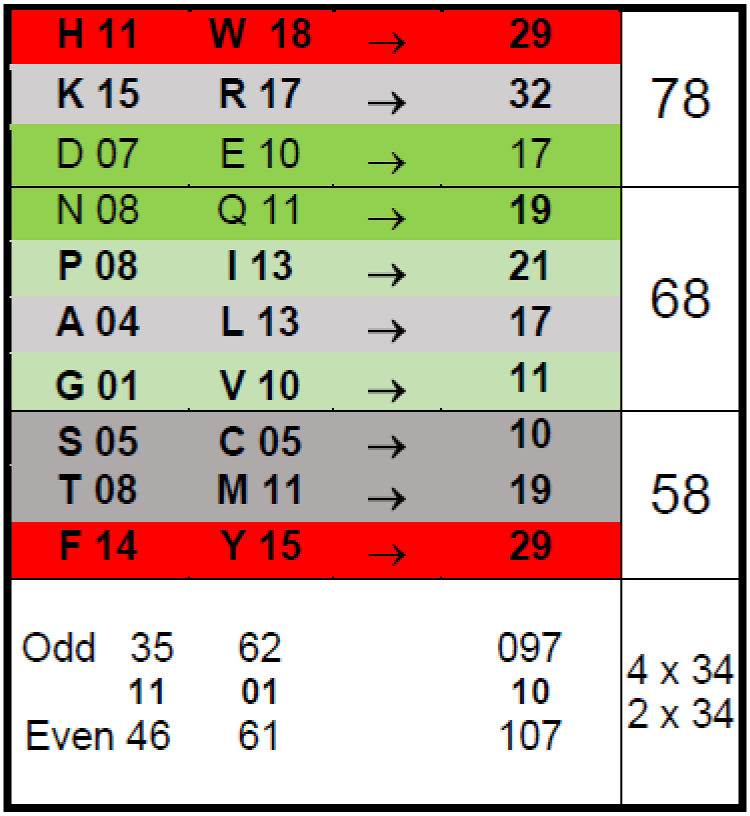
(28 + 70 = 97 +1) (48 + 58 = 107 -1)

CIPS		
F		**Y**
L		A
Q	60 / 66	**N**
P		I
T		**M**
S		**C**
G		V
D		**E**
K	78	R
H		**W**

Light: Superclass I
Dark: Superclass II

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

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



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

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

Table 6.4. Two classes and two superclasses of amino acids

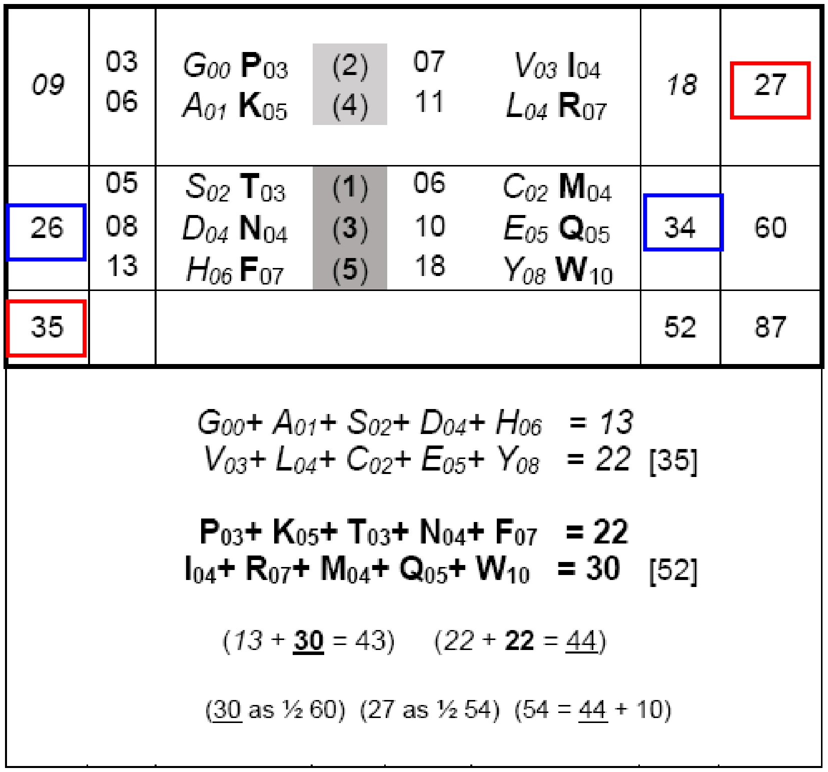
28	09 19	G **P** A **K**	(2) (4)	23 30	V **I** L **R**	53	**81**	32 / 49
53	13 15 25	S **T** D **N** **F** H	(1) (3) (5)	16 21 33	C **M** E **Q** Y **W**	70	**123**	28 / 95
81		33 / 48			27 / 96	**123**	204	60 / 144

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

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

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

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



09	03 06	G_{00} $\mathbf{P}_{03}$ 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 (MMR, 2022, Table C3, p. 80). Two inner rows vs two outer ones. There is also Table C1 for the total number of atoms in the side chains of amino acids, as well as Table C2 for the number of hydrogen atoms. To the left of the shaded column are amino acids of the second class, handled by the second class of aaRS. On the right are AAs of the first class. The first two rows (above) make up the amino acids of the primary superclass of CIPS (Table 6 on the left). The bottom three rows belong to the secondary superclass. Non-bold and italicized amino acids are of lower rank, less complexity; while the bold ones are of a higher rank, that is, of greater complexity. The exception is phenylalanine because as a member of the FY pair it is of lower rank. However, given the fact that PheRS attaches phenylalanine to the 2′-OH of the tRNA terminal adenosine, it is considered to be of higher rank in this constellation. [Class I and II aminoacyl-tRNA synthetases attach amino acids to the 2′- and 3′-OH of the tRNA terminal adenosine, respectively. The only exception is phenylalanyl-tRNA synthetase (PheRS), which structurally belongs to Class II but attaches phenylalanine to the 2′-OH.)]

Table 6.6. Quantitative relationships in Table 6.5

ST+DN+FH = 26 (GP, AK) 9 + (VI, LR) 18 = **27** CM+EQ+YW = 34 (GP, AK) 9 + (ST DN FH) 26 = **35**	26 + 9 = **35** [35+35 = 70] 18 + 34 = 52 27 + 35 = 52 + 10 26 + 34 = 70 - 10
[(2S, 2T, 2D, 2N, 2 F, 2H) (26 x 2 = $\boxed{\mathbf{52}}$)] (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 7. Distribution of AAs within four types of diversity according to Fig. 4

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

532.57+ 725.86 = 1258.43 ≈ 1258 → 34 x 37

222

658.62 + 820.99 = 1479.61 ≈ 1480 → 40 x 37

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

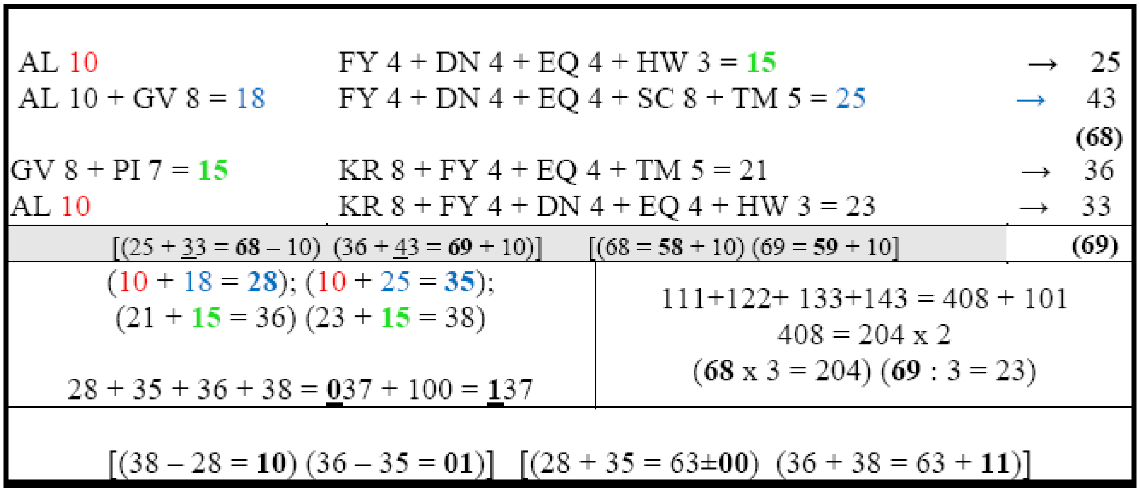
From [DOI 10.31219/osf.io/fzgjp] (Table 7, p. 5). Hierarchy of rows and columns taken from Figure 4. It can be noticed that the quantities 34 and 40 form a common sequence with the quantities 36 and 38, in Table 3.1. And this sequence we also find in the central area of the system-arrangement presented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

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

1	2	3	4	5	6	7	8	9	10		
A$_4$L$_{13}$	K$_{15}$R$_{17}$	F$_{14}$Y$_{15}$	D$_7$N$_8$	E$_{10}$Q$_{11}$	H$_{11}$W$_{18}$	S$_5$C$_5$	T$_8$M$_{11}$	G$_1$V$_{10}$	P$_8$I$_{13}$	→	204
17	+ 32	+ 29	+ 15	+ 21	+ 29	+ 10	+ 19	+ 11	+ 21	=	204
AL$_{10}$	2	FY$_4$	DN$_4$	EQ$_4$	HW$_3$	7	8	9	10	|$_{25}$	111
											11
AL$_{10}$	2	FY$_4$	DN$_4$	EQ$_4$	6	**SC**$_8$	TM$_5$	GV$_8$	10	|$_{43}$	122
											11
1	**KR**$_8$	FY$_4$	4	EQ$_4$	6	7	TM$_5$	GV$_8$	**PI**$_7$	|$_{36}$	133
											10
AL$_{10}$	**KR**$_8$	FY$_4$	*DN*$_4$	EQ$_4$	HW$_3$	7	8	9	10	|$_{33}$	143

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

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



AL 10	FY 4 + DN 4 + EQ 4 + HW 3 = **15**	→	25
AL 10 + GV 8 = 18	FY 4 + DN 4 + EQ 4 + SC 8 + TM 5 = 25	→	43
			(68)
GV 8 + PI 7 = **15**	KR 8 + FY 4 + EQ 4 + TM 5 = 21	→	36
AL 10	KR 8 + FY 4 + DN 4 + EQ 4 + HW 3 = 23	→	33
[(25 + 33 = **68** – 10) (36 + 43 = **69** + 10)]	[(68 = **58** + 10) (69 = **59** + 10]		**(69)**

(10 + 18 = **28**); (10 + 25 = **35**);
(21 + **15** = 36) (23 + **15** = 38)

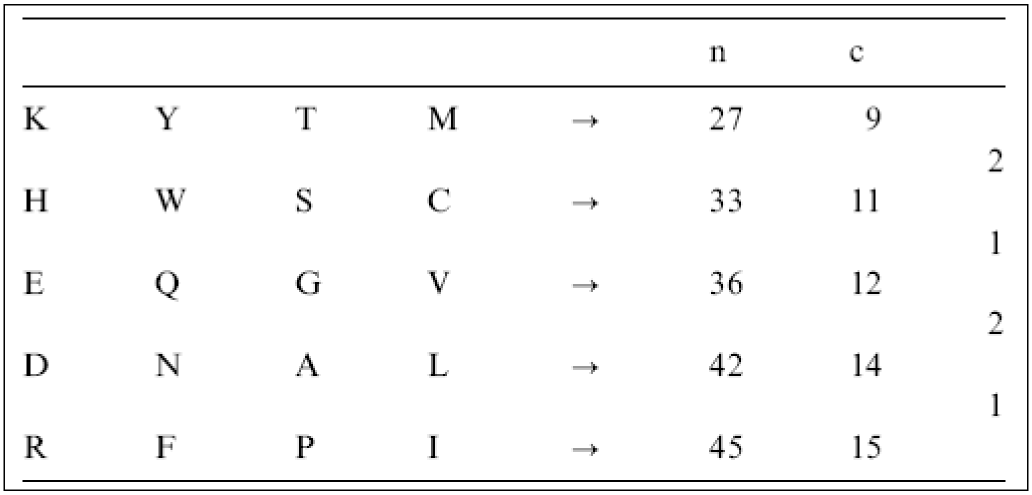
28 + 35 + 36 + 38 = **0**37 + 100 = **1**37

111+122+ 133+143 = 408 + 101
408 = 204 x 2
(**68** x 3 = 204) (**69** : 3 = 23)

[(38 – 28 = **10**) (36 – 35 = **01**)] [(28 + 35 = 63±**00**) (36 + 38 = 63 + **11**)]

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

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



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

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

FIGURES

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

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

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

440 + 56 = 496 [440 | 044]

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

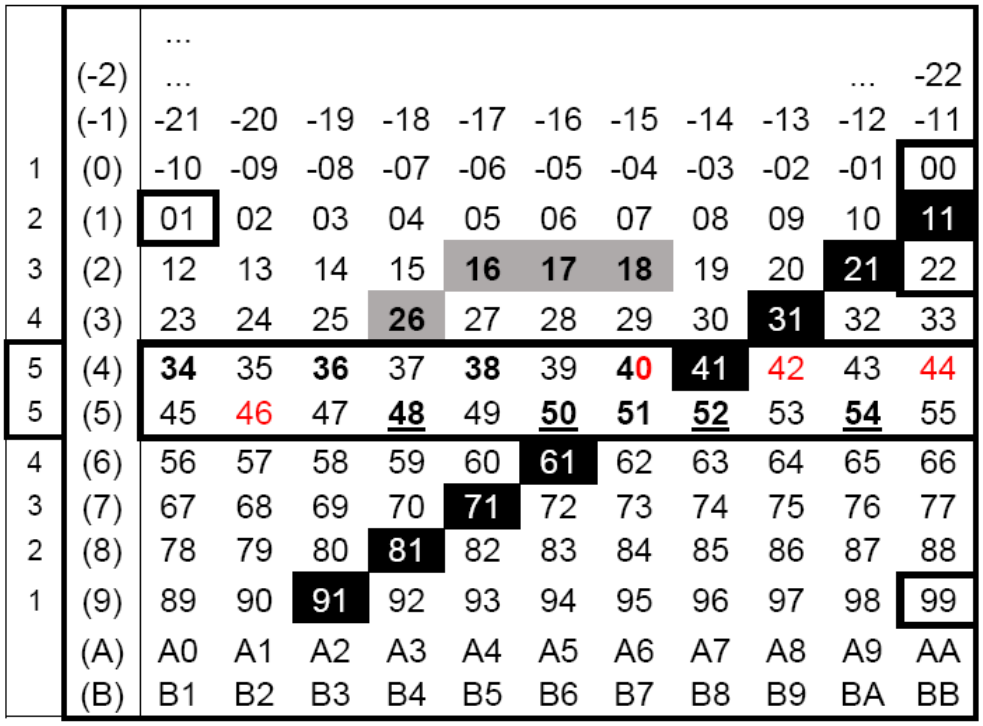
220 + 2200 = 1210 x 2 [220 x 011]

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

Table 5. Further distinctions in PPAASS (Table 1)

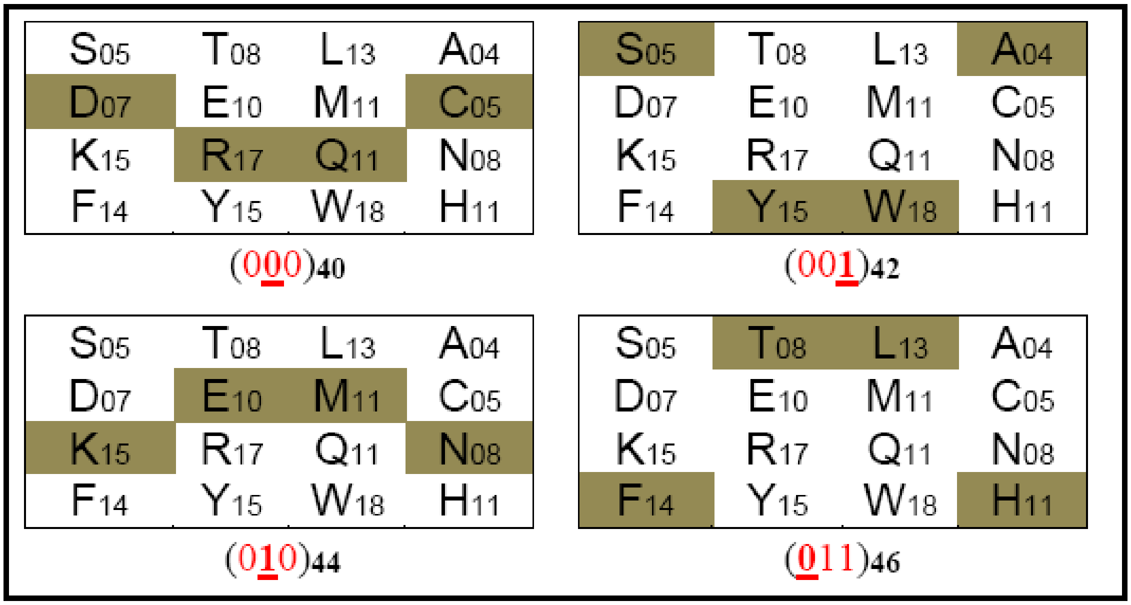
	Odd / Odd	
GVIKQ 25+**50**+139 = 214	NSCFW 75+**50**+191 = 316	→ **530**
	Last / First	
LKRQE 40+66+207 = 313	NDSTC 65+33+129 = 227	→ **540**
	First / Last	
GAVPI 15+36+91 = 142	MFYWH 90+69+259 = 418	→ **560**
	Even / Even	
APLRE 30+**52**+159 = 241	DTMYH 80+**52**+197 = 329	→ **570**

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



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



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

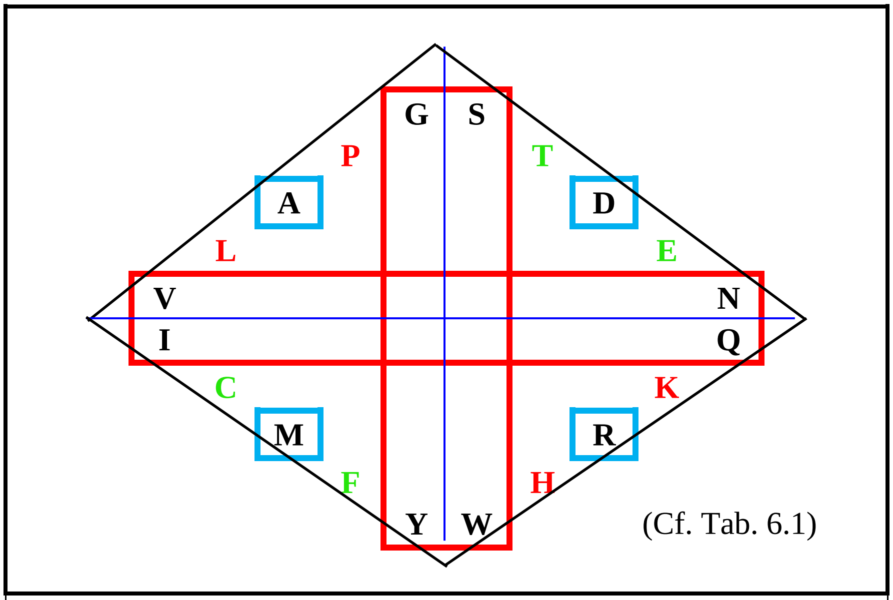
S05	T08	L13	A04
D07	E10	M11	C05
K15	R17	Q11	N08
F14	Y15	W18	H11

(010)44

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

(011)46

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



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

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

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

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

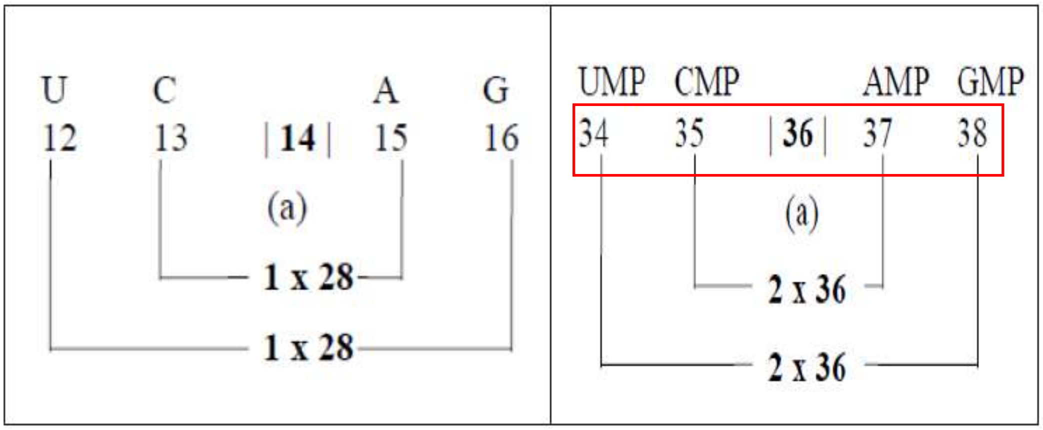


Figure 5. From (MMR, 1997b, pp. 62-63, Equ. 25-29). Distinctions as [(1 x 28) : (2 x 36)]. Quantities 12, 13, [14], 15, 16, as well as quantities 34, 35, [36], 37 38 are also found in one unique series of natural numbers (Survey 8).

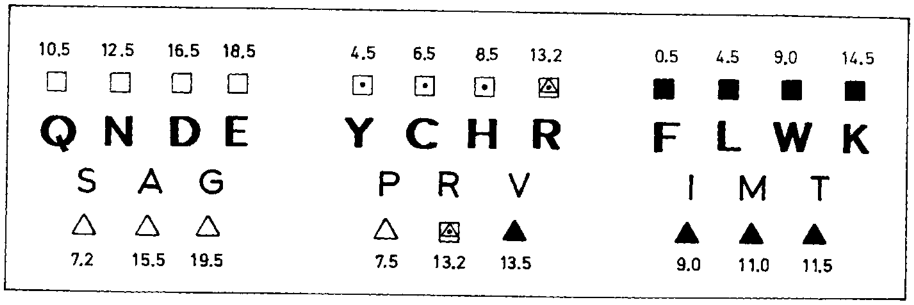


Figure 6. Taken from (MMR, 1997b, Figure 5, pp. 26-27 and from MMR, 2021b, Fig. A1): "Here are given the amino acids from Space-3 (triangles) and Space-4 (squares) [of Boolean space] depending on the binary value (strict order per rising values in each group) …The mean binary values are given in Figure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

SURVEYS

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

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

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

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

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

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

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

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

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

12 + 210 = 222 = 6 x 37

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

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

Survey 6. Relations of quantities 51 and 66

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

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

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

1	$\boxed{1}$, 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, $\boxed{\mathbf{25}}$, 30**)**, **35**, 40, **45**	**35**
6	6, 12, **(**18, 24, 30, $\boxed{\mathbf{36}}$**)**, **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, …

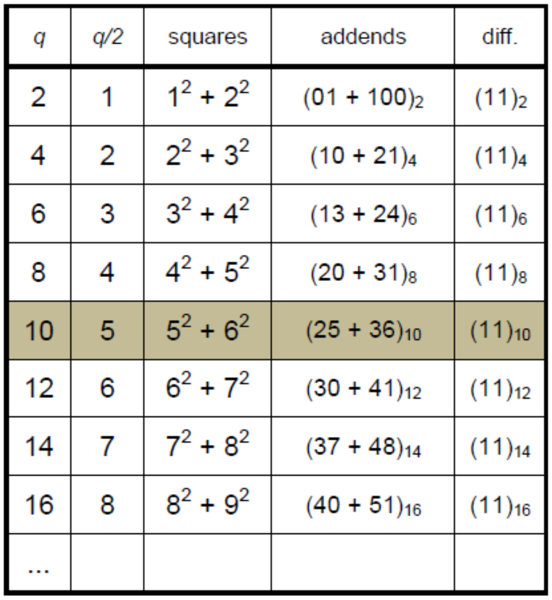
Quantities 28 and 35 are found as realities of the genetic code (Table 8.1); quantities 21 and 42 as the harmonic mean on the 6-binary tree, in reading from one side and the other (MMR, 1998, Fig. 1). [Cf. Table 8.1.)

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

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

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

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



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

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

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

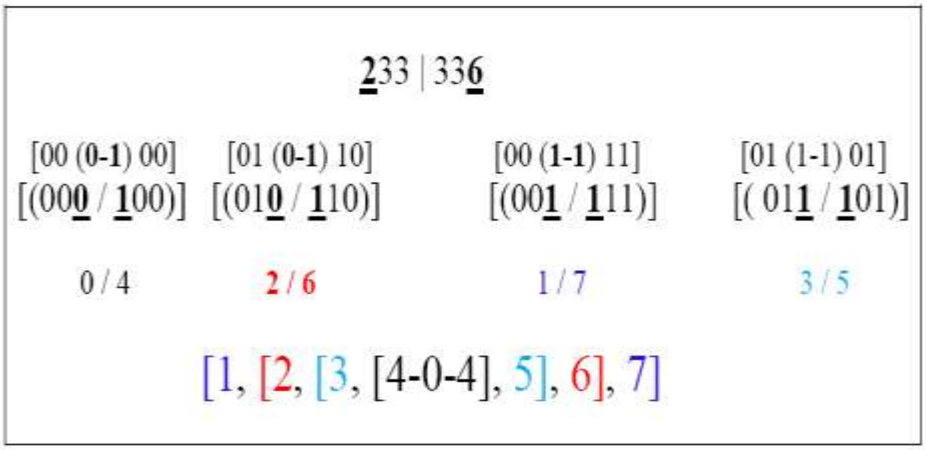
1, (2), 3, 4 → 1, 7, 8
6
3, (4), 5, 6 → 3, 11, 14
6
5, (**6**), 7, 8 → 5, 15, **20**
6
7, (8), 9, 10 → 7, 19, 26
. . .

1 x 5
3 x 5
4 x 5

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

Correspondences: Table 3,2 and Figure 5.

Survey 9. Mirroring of neutron number in PPAASS



233 | 33**6**

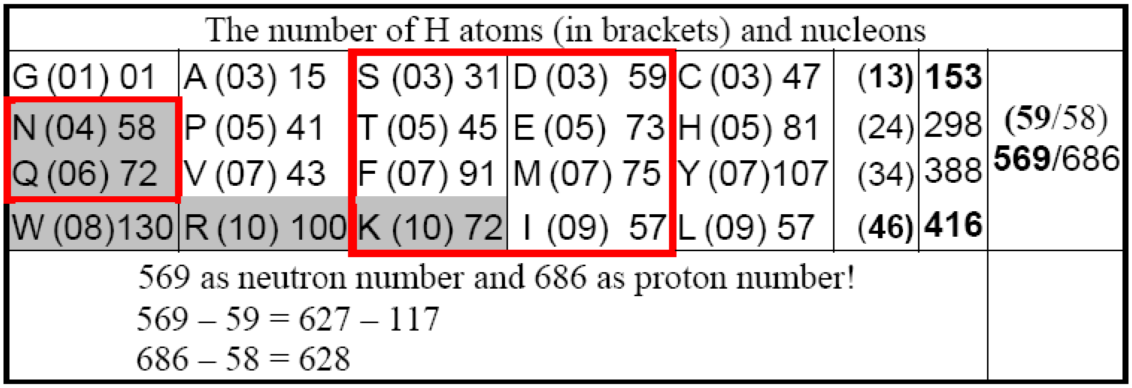
[00 (**0**-**1**) 00]	[01 (**0**-**1**) 10]	[00 (**1**-**1**) 11]	[01 (1-1) 01]
[(00**0** / **1**00)]	[(01**0** / **1**10)]	[(00**1** / **1**11)]	[(01**1** / **1**01)]
0 / 4	**2 / 6**	1 / 7	3 / 5

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

Correspondences: Table 5.2 and 5.3

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

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

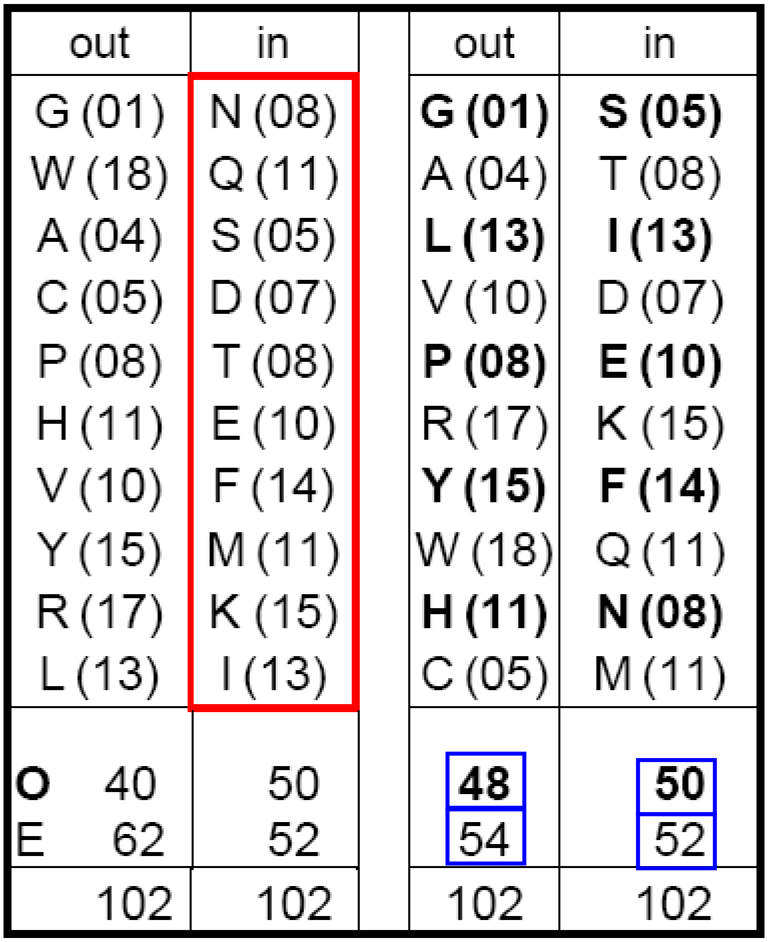


The number of H atoms (in brackets) and nucleons							
G (01) 01	A (03) 15	S (03) 31	D (03) 59	C (03) 47	**(13)**	**153**	
N (04) 58	P (05) 41	T (05) 45	E (05) 73	H (05) 81	(24)	298	(59/58)
Q (06) 72	V (07) 43	F (07) 91	M (07) 75	Y (07)107	(34)	388	**569**/686
W (08)130	R (10) 100	K (10) 72	I (09) 57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

569 as neutron number and 686 as proton number!
569 – 59 = 627 – 117
686 – 58 = 628

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

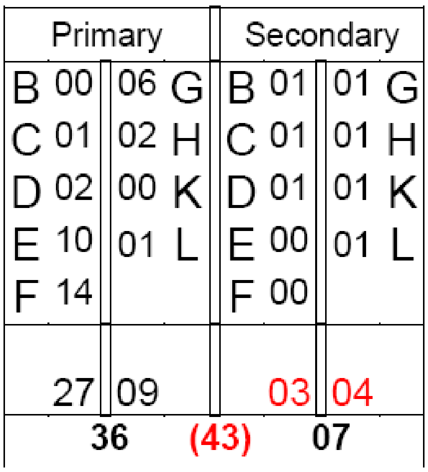
Table A2. Distribution of AAs according to the number of hydrogen atoms (II)



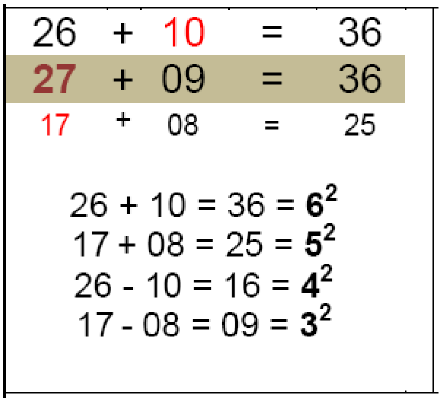
out	in		out	in
G (01)	N (08)		**G (01)**	**S (05)**
W (18)	Q (11)		A (04)	T (08)
A (04)	S (05)		**L (13)**	**I (13)**
C (05)	D (07)		V (10)	D (07)
P (08)	T (08)		**P (08)**	**E (10)**
H (11)	E (10)		R (17)	K (15)
V (10)	F (14)		**Y (15)**	**F (14)**
Y (15)	M (11)		W (18)	Q (11)
R (17)	K (15)		**H (11)**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

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

Table A3. The key of Darwin's Diagram



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



26	+	10	=	36
27	+	09	=	36
17	+	08	=	25

$26 + 10 = 36 = \mathbf{6^2}$

$17 + 08 = 25 = \mathbf{5^2}$

$26 - 10 = 16 = \mathbf{4^2}$

$17 - 08 = 09 = \mathbf{3^2}$

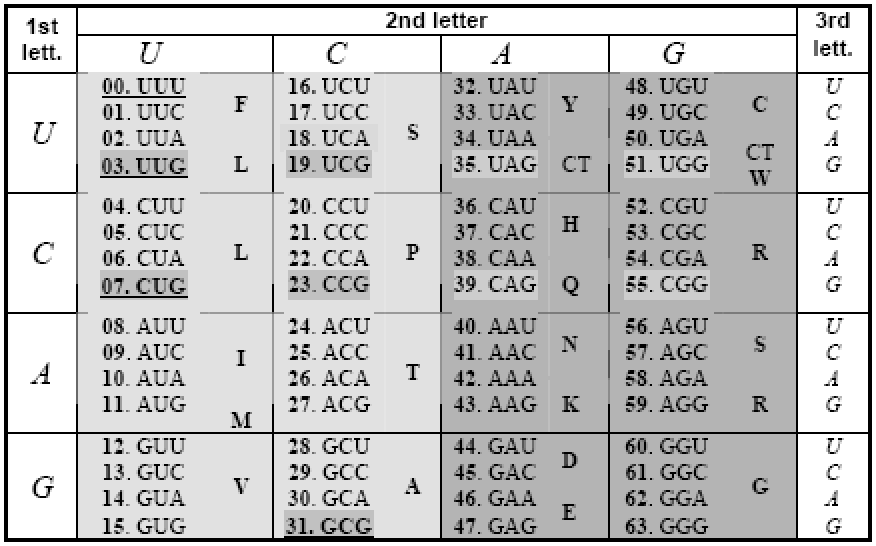
Mendel's result:
$1^n - 2^n - 3^n - 4^n$

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

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

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



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

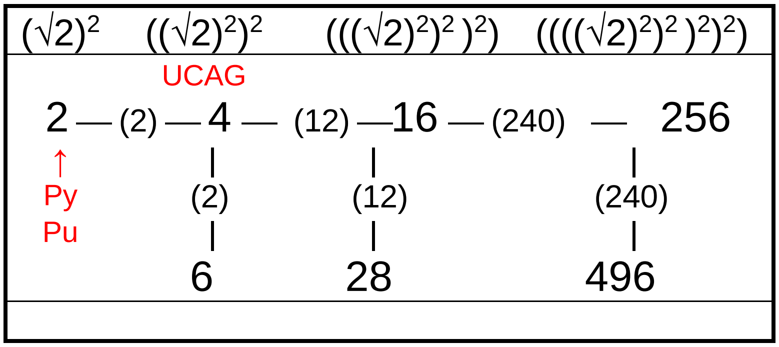
Quantitative-qualitative distinctions:
[(0 – 3) (UUU – UUG) → 6], [(0 – 7) (UUU – CUG) → 28], [(0 – 31) (UUU – GCG) → 496],
{[(0 – 63) (UUU – GGG)] + [(64 – 127) (GGG – UUU) → 8128]}
6 + 28 + 496 + 8128 = 8658 = 7770 + 088 = 6 x 1443

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

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

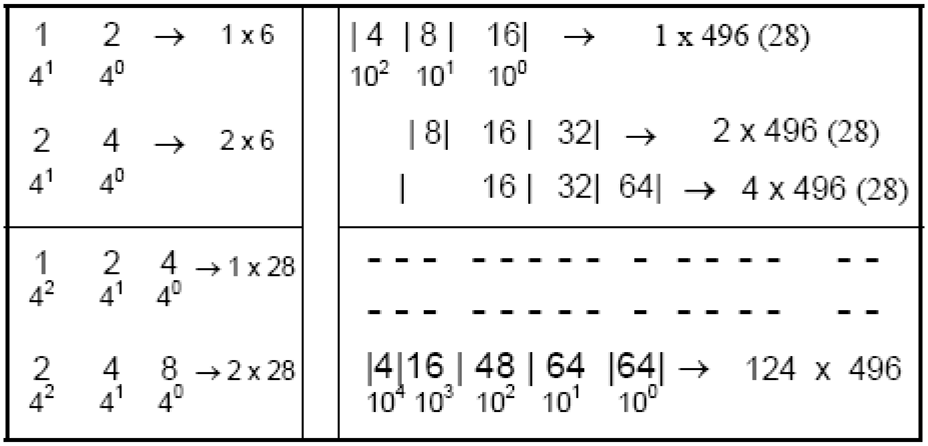
0 – 3 → 6		1^3	1	
0 – 7 → 28		**3^3**	**27**	**28**
0 – 31 → 496		5^3	125	
0 – 127 → 8128		**7^3**	**343**	**496**
		9^3	729	
2^1 x 3 = 6		11^3	1331	
2^2 x 7 = 28		13^3	2197	
2^4 x 31 = 496		**15^3**	**3375**	**8128**
2^6 x 127 = 8128				
(0 – 63) + (64 – 127) = 8128 (63 as 64) & (0 as 127)				

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



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

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



1 2 → 1 x 6 4^1 4^0 2 4 → 2 x 6 4^1 4^0		| 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)
1 2 4 → 1 x 28 4^2 4^1 4^0 2 4 8 → 2 x 28 4^2 4^1 4^0		- |4|16 | 48 | 64 |64| → 124 x 496 10^4 10^3 10^2 10^1 10^0

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

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

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

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

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

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

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

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

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

ADDENDUM 1

Chemia Naissensis

ISSN 2620-1895

July 2019 Volume 2, Issue 1

www.pmf.ni.ac.rs/chemianaissensis

Cover Designer
Jovana Janković

Chemia Naissensis (ISSN 2620-1895)

Published only in electronic form

Volume 2, Number 1, July 2019

Publisher:

Faculty of Sciences and Mathematics, University of Niš

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Chemia Naissensis, Vol 2, Issue 1, RESEARCH ARTICLE, 1-43

Protein amino acids as a complete (periodic) system

Miloje M. Rakočević[*]

Faculty of Science and Mathematics, Department of Chemistry, Višegradska 33, 18000 Niš, Serbia (retired from 2003)

ABSTRACT

Referring to the results of previous research on the Cipher of genetic code and analogies of genetic and chemical code – two overall complete natural systems – this paper presents the results of the study on the most complete Protein Amino Acids System (PAAS). It is shown that 20 protein amino acids appear to be a complete system – ordered, coherent, and harmonic. In such a system, all chemical distinctions within the system are accompanied by specific arithmetical and algebraic regularities, including the existence of amino acid ordinal numbers from 1 to 20. The classification of amino acids into two decades (1-10 and 11-20) appears to be in a strict correspondence with the balances of the number of atoms. From the existence of harmonic structures and arrangements of AAs, regardless of whether they are or not the constituents of the genetic code follow the conclusions that the genetic code, through its main constituents – 20 AAs and 4 Py-Pu bases – was complete even in prebiotic conditions.

Keywords: *Protein amino acids, Amino acid code, Genetic code, Binary tree, Gray code, Golden mean, Fibonacci series.*

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[*] University of Niš, Faculty of Science and Mathematics, Department of Chemistry, Višegradska 33, 18000 Niš, Serbia, e-mail: mirkovmiloje@gmail.com

Introduction

This paper is a step further in argumentation of the completeness of the system of protein amino acids (AAs),[1] in the sense that it is a Mendeleevian type of system, whose organization is based on the principles of continuity and minimum change, that is, on the principles of balancing the properties[2] of its elements (within the system). In other words, it is a coherent and harmonious system, both in biotic and prebiotic conditions. In this case, the harmonicity is understood as the correspondence with the golden mean and the Fibonacci series.[3] As such, the system is inevitably in relation to one specific periodic system of numbers (PSN) [Figure A1 in relation to Table B5 and Figures C2 & C3], correspondent (analog) with the periodic system of chemical elements (PSE).
„Regarding the application of theoretical-numerical representations, even Mendeleev considered as appropriate to look for an analytical expression for the law of periodicity, based on theory of numbers." (Trifonov, Dmitriev, 1981, p. 237).]

Previously we have shown that the completeness of PAAS is recognized when protein AAs are observed as constituents of the genetic code (GC) (Rakočević, 1998b; 2004a; 2011a, b; 2018a, b). In this paper, however, we are starting with a *working hypothesis* (Box 1) that the same holds true when the set of 20 protein AAs is observed regardless of their positions in the genetic code displays [in the standard Genetic code Table (Crick,

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[1] When we say that the genetic code (GC) was complete even in prebiotic conditions, then we mean on constituents of standard GC, the 20 protein amino acids (AAs) and 4 nucleotide bases. If within this paper we give convincing arguments for the completeness of the system of 20 protein AAs (PAAS), whether they are GC constituents or are just a set of free molecules independent of the positions of the AAs in the Standard GC Table, then we provide evidence also for the completeness of the set of 4 Py-Pu bases, according to the scenario we gave in previous work (Rakočević, 2018a, Section 2, p. 32).

[2] The notions of *balancing* related to the state of the amino acid (genetic) code, as well as the conditions of the system of protein amino acids (PAAS), will be used in the sense of Definitions 1 and 2, given in our previous paper (Rakočević, 2018a, p. 33). Under these assumptions, in this paper we consider that these states are analogous to the same states found in the Periodic system of chemical elements (PSE), when Mendeleev discovered the elements and interpreted their properties by the method of interpolation (Kedrov, 1997, p. 231). [Encyclopedia Britannica: "Interpolation, in mathematics, the determination or estimation of the value of f(x), or a function of x, from certain known values of the function".]

[3] On determination of PSE by the golden mean and the Fibonacci series see in (Trifonov, Dmitriev, 1981) and (Rakočević, 1998a). On the determination of the protein amino acid system (as constituents of the genetic code), also with the golden mean and the Fibonacci series, see in: (Rakočević, 1998b; 2011b).

1966; Rumer, 1966)[4]; in Gray code model of GC (Swanson, 1984) and GC binary tree (Rakočević, 1998b)]. In the argumentation of the working hypothesis, we consider that the coexistence of GC with Boolean spaces (Swanson, 1984; Rakočević, 1994, 1997b, 1998b)[5], analogy with quantum physics (Shcherbak, 1994, 2008),[6] analogy of genetic and chemical code (Rakočević, 2018b) and the existence of "arithmetic inside the universal genetic code" (Shcherbak, 2003) are established facts.

Box 1. *The statements of the working hypothesis*

1. The protein amino acid system (PAAS) is an ordered, coherent, and harmonic system. [Ordered as in Figure 1 in this paper; coherent as in (Rakočević, 2011a, b); harmonic as in (Rakočević, 2004a); with the expectation that all three attributes are applying, while when the protein amino acids are not positioned in the genetic code then they are freely present in the world of molecules.].

2. The order of PAAS is also expressed through the existence of the order of AAs from the first to the 20th [The order according to the logic that each subsequent molecule is similar to the previous one.].

3. "The Little Gauss' algorithm" (Rakočević, 2011b, p. 833) is contained in the Periodic system of numbers (PSN) (Fig. A1)- it is a modified algorithm of "Little Gauss", in the sense that not the numbers are going from 1 to 100 but from 1 to 101. This phenomenon

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[4] The sense of deviation, that is of the degree of freedom in deviation from the standard GC as in: (Rakočević, 2018a, Box 2, p. 41). Under the same "degree of freedom" we can now include the "21th" AA Selenocysteine (encoded by the UGA codon found in every domain of life on Earth), as well as the "22nd" AA Pyrrolysine (coded by UAG in Archaea), and we will not consider them within these considerations. Because they are encoding by stop codons, they do not disturb the order within the system of standard protein AAs. It is quite certain that it makes sense to investigate the possible completeness, coherence and harmony and for the system of "22" protein AAs, as well as the trend towards completeness; also makes sense to investigate the completeness of other potential biomolecular systems (Kostić et al., 1998 a,b, pp. 189-194; 195-200).

[5] Rakočević, 1998b, p. 46: “Swanson (1984) has shown that ‘the genetic code is almost an example of a Gray code… an example of minimum change binary code’ ... If so, then the genetic code can be represented in the form of a binary-code tree, according to the natural numbers sequence 0–63”; Rakočević, 1994, p. 36: „The basic concept from that we start is the Boolean logical square. This square exists within Gray code model of genetic code, [which] code can be *per se* developed in two types of the binary tree: (1) the binary tree which keeps the logic of the Gray code. ... (2) the binary tree with the logic of natural numbers series”; Rakočević, 1997b, p. 5: „Boolean spaces are the main determinants and invariants of the genetic code“.

[6] For details about analogies of genetic code and quantum physics see in preprint form of paper (Rakočević, 2018b), OSF Preprints, DOI: 10.31219/osf.io/mxecj (created on October 07, 2017).

was the only analogy that could be found in relations to results in previous three works (Rakočević, 2006; 2011a,b); however, it can now be shown that this arrangement is "taken off" from the PSN (the right picture in Figure 1 in relation to Figure A1).

4. PAAS correspond with PSN [It refers to the correspondences mentioned in the preceding paragraph, but also to others that is first shown.].

5. The pattern 35-36-61 in the chemical code refers to the number of unstable and stable elements respectively in a set of 61 multi-isotopic elements; and in the genetic code refers to the number of codons encoding less and more complex AAs respectively in a set of 61 amino acid codons; and is also valid for the number of atoms in the PAAS [As stated, and what we found in Darwin's diagram (Rakočević, 2015), *i.e.* in his "computer program" (first two columns in Table C1 in relation to the third quadrant of Table C2].

6. PAAS corresponds to the uniqueness of the six-bit binary tree and correspondent Farey tree (both trees in: Rakočević, 1998b, Figures 1 & 2, pp. 284-285) [The uniqueness of the six-bit tree is in its horizontal and vertical mirror symmetry; it is the first and only possible binary tree with one mirror (010/101), as shown in Figure 2 and Figure A2, on the left. Notice that the mirror symmetry for the binary records on the genetic code of the binary tree (Rakočević, 1998b, Figure 1, p. 284) is a face to back, while for the *amino* or *oxo* functional groups is a face to face: *amino vs. amino* and *oxo vs. oxo* group, in reading the binary tree on the left half: from left to right, and on the right half: from the right to the left; the same logic – *amino vs. amino* and *oxo vs. oxo* is valid in reading two Rumer's octets of nucleotide doublets (Rakočević, 2018a, Table 2A, p. 34). Notice also that the comparable position („terminal position“) of the functional group must be the amino group in adenine because it does not have an oxo group.][7].

7. PAAS is (evolutionarily) generated through the unity of the mirror symmetry of the AAs and the mirror symmetry of the correspondent numbers [It is shown that the mirror symmetry 2 *vs.* 5 (010/101) mapped from the six-bit binary tree to the standard Genetic

---

[7] “The four [bases] are mutually distinguishable by three main characteristics: the type of base (purine, Pu, or pyrimidine, Py); the type of functional group in terminal position (position 6 in purine, position 4 in pyrimidine) – either oxo or amino; and the number of hydrogen bonds linking them in the system codon-anticodon” (Rakočević, 1988, p. 112).

code Table (GCT) has a quantitative meaning of the number of atoms (Table 3 in relation to Table 7 and Figure 2).].

8. PAAS corresponds with the uniqueness of the decimal number system [The uniqueness of the decimal number system: the 9 non-zero digits correspond to the Cantor triadic set: 123 / 456 / 789, which quantities we found as natural entities (Rakočevič, 2018a, Fig. 4 and Rakočević, 2018b, Equations 1 & 2 and Table 4). Notice that the generation of a binary tree represents *ipso facto* a permanent correspondence with the Cantor triad set.) On the other hand, the decimal number system is the only one that has a direct connection with the golden mean (Table B6, the second row where we find the original golden triangle, whose one cathetus is the square root of number 5. Thus, the first cathetus a = q/2, the second cathetus b = 2 and hypotenuse c = 3 = $\Phi^2 + \phi^2$ (Table B6 in relation to Table A1, second column).

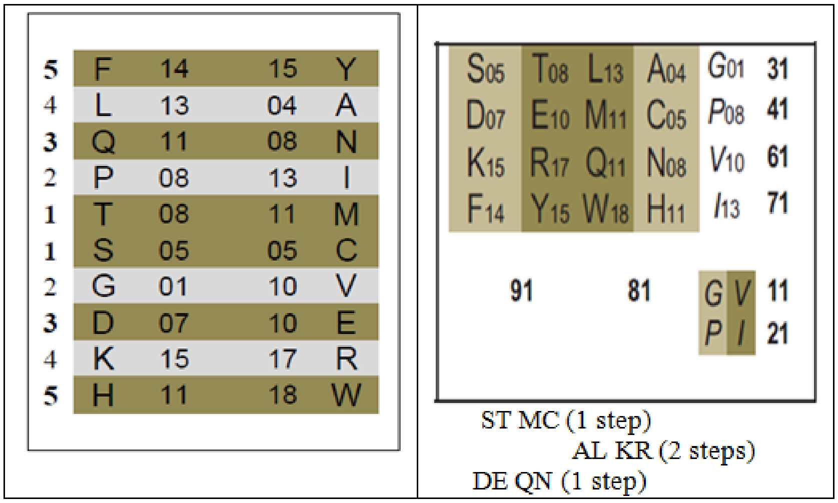
9. PAAS corresponds with the uniqueness of the golden mean and the Fibonacci series of numbers. [This statement applies to PAAS when it is a component of the genetic code we have shown in several papers; we mention now only two (Rakočević, 1998b, 2004b). Here, however, we show that this fact applies to PAAS, regardless of the genetic code.]

The procedure for proving *the working hypothesis* will be realized by presenting the relevant facts in the two main segments of this paper: in the Preliminaries, we give new aspects and new knowledge about the previously presented arrangements of the AAs within the GC and/or outside of it, while in the Section "New insights" we provide new insights into the universal completeness of PAAS.

Preliminaries

Already the act of mapping the Gray code model from "A unifying concept for the amino acid code" (Swanson, 1984) into a binary code tree (Rakočević, 1998b, Figure 1, p. 284) was a hint of the existence of a complete – ordered, coherent and harmonious – system of protein AAs. [The Gray code model as in Figure C2, down on the left.] And when, with this act, the sequence of "golden" AAs, existing on positions ϕ^0 to ϕ^9, on the binary code tree, the sequence (G-Q-T-P-S-L-F), was transmitted in a sequence of Mendeleevian order, according to the growing masses of amino acid molecules: (G-S-T-

P-Q-L-F) (Rakočević, 2011b, Fig. 6, p. 832), then PAAS was obvious (Figure 1 in this paper) (Box 2).



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

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)

Figure 1. The left picture: Cyclic Invariant Periodic System (CIPS) of AAs (Rakočević, 2011b, Fig. 6, p. 832). The right picture from Rakočević (2011b, Fig. 9, p. 834) (Box 2).

Box 2. *The explanation of Figure 1*

In Figure 1, the left picture from Rakočević (2011b, Fig. 6, p. 832): "The Cyclic Invariant Periodic System (CIPS) of canonical AAs: 1) at the inner side – the atom number within amino acid side chains; 2) in the middle position there are chalcogen AAs (S, T & C, M); 3) follow - in next ‘cycle’ – the AAs of nonalanine stereochemical types (G, P & V, I); 4) then two double acidic AAs with two their amide derivatives (D, E & N, Q), 5) the two original aliphatic AAs with two amine derivatives (A, L & K, R); and, finally, 6) four aromatic AAs (F,Y & H, W) – two up and two down. The mentioned five classes belong to two superclasses: primary superclass in light areas and secondary superclass in dark areas. Notice that each amino acid position in this CIPS is strictly determined, and none can be changed".[8] New comment, for the left picture: 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.

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[8] Rakočević, 1998b, p. 289: "Within seven ‘golden’ amino acids (within side chains) [GSTPQLF] there are 60 atoms; within their seven complements [VCMINAY] there are [60+(1×6)] and within six non-complements [DE, KR, HW] there are {[60+(1×6)]+(2×6)} of atoms. [Notice that the differences are 1×6, 2×6 and 3×6 which means realization of minimum change principle and continuity principle at the same time."]

The right picture from Rakočević (2011b, Fig. 9, p. 834): "Dark tones: Class I of amino acids handled by class I of enzymes aminoacyl-tRNA synthetases [except T]; light tones: Class II [except C]." New comment for the right picture (about exceptions C & M) is given in footnote 9.

New comment for both pictures: going from left to the right picture it is evident that chemically related groups of AAs come down for 0, 1 and 2 steps, respectively; for zero "steps" in aromatics FY-WH; for one step in chalcogen AAs ST-MC and in carboxylic DE-QN (carboxylic AAs D & E in relation with their amides N & Q); for two steps in AL-KR.

In support of the completeness of the system on the left picture goes also the splitting according to the ratio 8:12 (2:3) in molecule number: (FYLA + KRHW = 107 atoms); (QNPI + TMSC + GVDE = 97 atoms). In support of the completeness of the system on the right picture go also the relations within the set of 16 AAs of alanine stereochemical type, the balanced relations between rows and columns:

I. (STLA + KRQN = 81) (LA+MC+QN+WH = 81); LAQN = 4 x 9 = 36; STKR = MCWH = 5 x 9 = 45

II. (DEMC + FYWH = 91) (ST+DE+KR+FY = 91); DEFY = 36+10 = 46; MCWH = STKR = 5 x 9 = 45

(The cited previous papers available in www.rakocevcode.rs)

The determination of the amino acid (genetic) code with the golden mean leads to the CIPS (Cyclic Invariant Periodic System) (Figure 1, the picture on the left), in which the positions of five classes of AAs are strictly determined, two in the less complex and three in the more complex superclass: 1. (**SC-TM**), 2. (GV-PI), 3. (**DE-NQ**), 4. (AL-KR), 5. (**FY-HW**); less complex in the 2nd and 4th class and more complex in the remaining three classes (1st, 3rd and 5th), with the following distinction within the side chains of two super classes: H, C, N / N-O, O, S plus aromatic AAs.

As we can see, the CIPS is indeed a complete amino acid system, but AAs positions within the genetic code determine it, and according to our working hypothesis it must be a Mendeleevian type of system, in which AAs are ordered from the first to the last, the 20th amino acid. This condition is fulfilled in certain percentages by the arrangement of the AAs that we find on the right picture of Figure 1 as if it was mapped from one of the PSN diagonals. (In PSN, Figure A1, this diagonal is in black tones.) At the same time, this arrangement is identical to the arrangement presented on the right picture of Table B1, if the quartets of the AAs are read in a circular direction (as in the Gray code model within Boolean spaces): STLA, DEMC, KRQN, FYWH. Both these mappings, to some extent, confirms the statements of the working hypothesis: 1, 3, and 4. We say "to some extent" because we still do not have the order of AAs from the first to the last, but we have arrangements of AAs in which their positions are independent of positions in GC (the right picture of Figure 1 in relation to the right illustration in Table B1). [The left illustration of Table B1 also shows the correspondence with the pattern 25-36-61, as it is presented in the legend of Table B1.]

It is noteworthy to mention the fact that in all presented AAs pairs, in right picture of Figure 1, the first member, as a smaller molecule, belongs to the class II of AAs, handled by class II of enzymes aminoacyl-tRNA synthetases, and the second to class I. The exceptions are only T and C.[9] [About two classes of AAs, handled by class I & II of enzymes aminoacyl-tRNA synthetases see in: (Wetzel, 1995) and (Rakočević, 1997a); also, in Box 3 in this paper.]

Box 3. *Aminoacyl-tRNA synthetases*

There are two classes of aminoacyl-tRNA synthetases. Class I consists of synthetases with two highly conserved sequence motifs, which aminoacylate at the 2'-OH of an adenosine nucleotide, and they are usually monomeric or dimeric (one or two subunits, respectively). Class II of synthetases contains three highly conserved sequence motifs, and they aminoacylate at the 3'-OH of the same adenosine, and they are usually dimeric or tetrameric (two or four subunits, respectively). Although phenylalanine-tRNA synthetase belongs to a class II, it aminoacylates at the 2'-OH. Within the standard genetic code’s Table it does not follow a full distinction of AAs in relation to two classes of the aminoacyl-tRNA synthetases (Wetzel, 1995, Fig. l, p. 546), but within the ″Codon path cube″ it follows with only one exception (Rakočević, 1997a, Fig. 1, p. 646).

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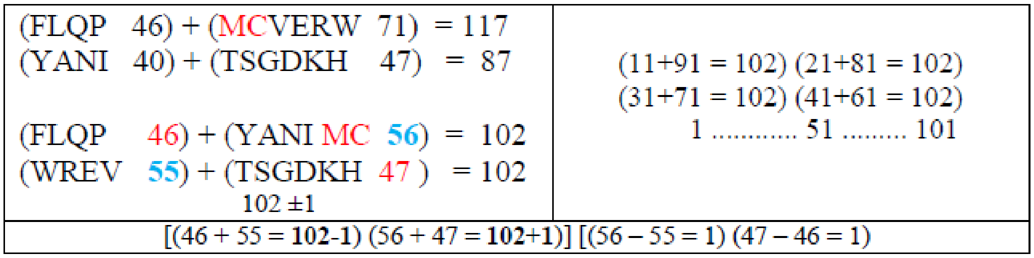
[9] The 18 AAs are built with four elements, one from the first (H), and three from the second period of PSE (C, N, O). The remaining two AAs have one element more (sulfur). These two sulfur AAs (C-M) have exactly two chemical analogues among the previous 18 AAs (S-T). It would be expected that in both cases, the smaller molecule belongs to Class II, and the larger to Class I; however, this is not the case: a stronger hierarchy (among periods) has the advantage: S-T, which do not reach the third period belong to Class II and C-M, which can be achieved belong to class I.

Presented classification of AAs within CIPS into classes and superclasses (left picture of Figure 1), in correspondence with two classes of aminoacyl-tRNA synthetases, can be continued further to obtain subclasses and families. Such a sophisticated classification can be useful in analyzing the structure and classification of proteins (Rakočević, 2011b, Figure 7, p. 833).

However, apart from the all above, we are now able to present new balances in CIPS. In Survey 1 it was shown that they have the meaning of the distinctions not only of the half the number of molecules *vs.* the second half, in systems and subsystems (in the ratio 1:1), but also of the distinctions with the ratio 4:6 or 6:4 which means 2:3 or 3:2 (Tables B1, B2 and B3 in relation to Table B6). The ratio 2:3/3:2 we find in the second row of Table B6, containing the system of the generalized golden mean; also 2/3 is the harmonic mean of a whole and its half, and 3/2 also represents the limit of "golden numbers" (Moore, 2004, p. 211.)[10]

Survey 1. The relationships within two systems presented in Figure 1



(FLQP 46) + (MCVERW 71) = 117 (YANI 40) + (TSGDKH 47) = 87 (FLQP 46) + (YANI MC 56) = 102 (WREV 55) + (TSGDKH 47) = 102 102 ±1	(11+91 = 102) (21+81 = 102) (31+71 = 102) (41+61 = 102) 1 .... 51 101
[(46 + 55 = **102-1**) (56 + 47 = **102+1**)] [(56 – 55 = 1) (47 – 46 = 1)	

The left area in this Survey (Survey 1) is related to the left picture in Figure 1, and the right area to the right one. The members of AAs pairs are symmetrically distributed (F-Y, L-A, *etc.*). See details in the text.

As it is self-evident (from Table B6), in the special case of generalization, the order values of generalized golden mean are related to the series of natural numbers (0, 1), (1,

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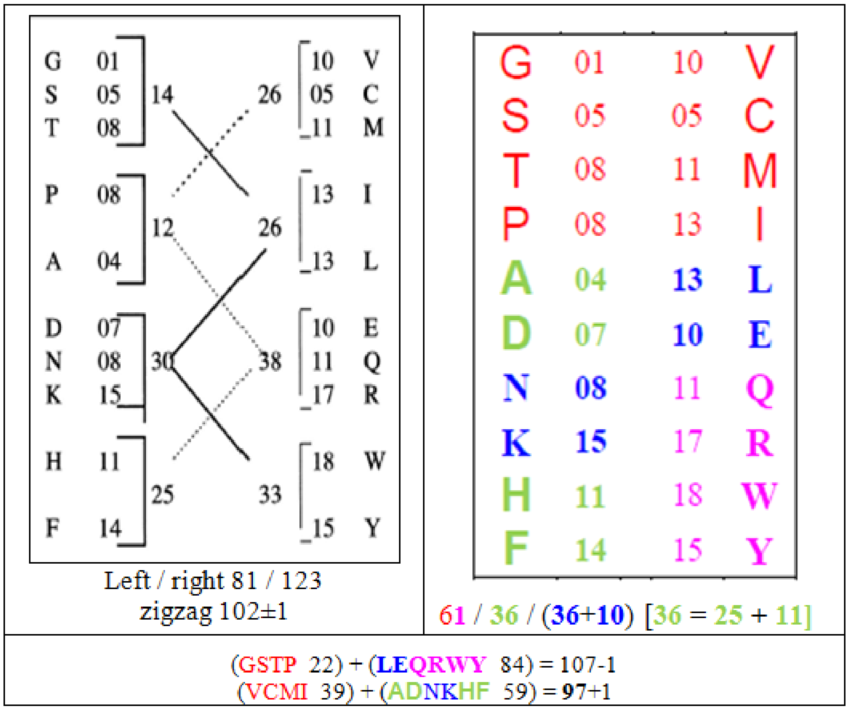
[10] Except of direct relationship of 2/3 (Tables B1 & B2) with the golden mean (Table B6, 2nd row), there is an indirect relationship in the following sense. In the cases presented here: 4 AAs *vs.* 6 AAs. But this is at the same time the 3/2 ratio as: 6 AAs *vs.* 4 AAs, and it is known that 3/2 represents "the limit of the golden numbers" (Moore, 2004, p. 211: "Our concern here is the study of the sequence $\{g_n\}$ of "golden numbers". A computer analysis of this sequence of roots indicated that the odd-indexed subsequence of $\{g_n\}$ was monotonically increasing and convergent to 3/2 from below, while the even-indexed subsequence was monotonically decreasing and convergent to 3/2 from above").

2), (2, 3) *etc*., and to Hückel rule at the same time (the right illustration in Table B5: the first column in relation to the far right column); also to the squares of natural numbers sequence: (1, 2), (2, 3), (3, 4), ..., when they correspond to the balance "11" (Table A1).

Table 1. The order of protein amino acids based on two classes aminoacyl-tRNA synthetases



G	01	14	26	10	V
S	05			05	C
T	08			11	M
P	08	12	26	13	I
A	04			13	L
D	07	30	38	10	E
N	08			11	Q
K	15			17	R
H	11	25	33	18	W
F	14			15	Y

Left / right 81 / 123
zigzag 102±1

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

61 / 36 / (36+10) [36 = 25 + 11]

(GSTP 22) + (LEQRWY 84) = 107-1
(VCMI 39) + (ADNKHF 59) = 97+1

The left illustration of this Table (Table 1) follows from Rakočević (1998b, Survey 4, p. 290): „On the first (full) zigzag line, there are 102+1 atoms whereas on the second (dotted) line there are 102−1 atoms. The arithmetic means for both: 102±1. Class II handles the smaller amino acids within the pairs (on the left), whereas class I aminoacyl-tRNA synthetases handled the larger amino acids (on the right).“ The right illustration is a new arrangement for this paper. See details in the text.

Now we go back to CIPS (left picture of Figure 1 in relation to Survey 1). When the first four of the AAs from the first column are added to six of the AAs from the second one, and *vice versa* (Figure 1 in relation to Survey 1), in these groups of AAs the number of atoms corresponds to the quantities indicated between the fifth and sixth row of Table

A2: 87 as (97 – 10) and 117 as (107 + 10)[11] [Notice that 87 = 86 + 01]. Here, it is particularly interesting the fact that only two sulfur AAs (C & M) appear as a tongue on balance: by moving them from one subgroup to another, the balance 87: 117 turns into a balance of 102: 102. [In the side chains of 20 standard AAs there are 117 hydrogen and 87 non-hydrogen atoms (Sukhodolets, 1985; Rakočević, 2011b, Table 7, p. 830).]. But the balancing also exists when the distinctions from the state 4 *vs.* 6 AAs, or 5 *vs.* 5 (in the shaded and non-shaded space) go on and in a different way as shown in Tables B2 & B3 and the accompanying Survey B1. In doing so, the quantization from the ratio 87: 117 goes to 97: 107.

In the left part of Figure 1, we see also that at the center of the CIPS system, there is a subsystem with high molecular diversity. Two and two AAs of non-alanine types (G-P and V-I) have "captured" the only two sulfur AAs (with sulfur existing in the third period and the sixth group of PSE: cysteine and methionine) and their two oxygen analogues (existing in the second period and a sixth group of PSE: serine and threonine). Realizing that here we have a Mendeleevian order (continuity and minimum change in atom number) with glycine in front: G-S-T-P, it makes sense to bring it in connection also with Mendeleev's based subsystem of the remaining 12 AAs of alanine type, led by alanine and presented in left picture of Table B1. [The only change in this process of connecting the two subsystems is that C and T exchange their positions.] The two subsystems thus connected give a new system, presented in Table 1.

The left illustration in Table 1 was firstly published in 1998, and then in 2004 (Rakočević, 1998b, Survey 4, p. 290; 2004a, Fig. 1, p. 222). With all provided information there, we now show distinctions from the aspect of division into 4: 6 amino acids. The illustration on the right side of Table 1 shows that the pattern 25–36–61 is really "played" here, which we already had with the genetic code and chemical code (Rakočević, 2018a and 2018b). On the right side is the first-class of amino acids, and on

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[11] Relationships with quantities 97/107 we can find in all essential arrangements of AAs: Table 1 & 2, Tables B2 & B3, and Survey B1.

the left side is the second class of amino acids.[12] Each molecule from the second class is smaller than the paring member in the first class.

At the bottom of the first class, there are four amino acids in which there are exactly 61 atoms, and at the top, there is the amino acid quartet which, together, with their in the second-class partners (total of eight amino acids) together also have 61 atoms. The two quartets in the right column are separated by a doublet L-E, while in the left column the quartet A-D-H-F is splitting into doublet A-D and doublet H-F; the H-F exactly with 25 atoms, and A-D with 11 atoms; a total within the quartet of 36 atoms. In two "breakable" doublets (diagonally connected) there is 23+23 = 36+10 atoms. Altogether exactly as it is predicted by working hypothesis (statements 4 & 5), and showed in Table A2 (the fifth and sixth row).

New insights

From a chemical point of view the first step of classification of protein amino acids (AAs), must be the classification into aliphatic and aromatic AAs, where on a hierarchical scale of changes by similarity and complexity, aliphatic AAs must precede the aromatic. For the same reason of the chemical hierarchy, within the class of aliphatic AAs at the beginning must be the hydrocarbon AAs (possessing in the side chain carbon and hydrogen, or hydrogen only, in the case of glycine), and at the end two sulfur AAs, quite different from preceeded non-sulphuric AAs. It means that two sulfur AAs (as the last in the class of aliphatic amino acids) must be found in direct contact to the aromatic.

Full certainty

In the further course of the sequencing of AAs, in terms of changes by similarity, from the aspect of the AAs singlets and/or doublets, *i.e.*, pairs, the appropriate distinctions in three areas should be considered: hydrocarbon, aromatic, and those between them. In the set of aromatic AAs, Phe came the first, as the simplest, followed

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[12] The class I is realized by AAs handled by class I, while class II is realized by AAs handled by class II of enzymes aminoacyl-tRNA synthetases, respectively.

by Tyr, and Trp, all three with possession of a benzene ring.[13] At the very end ultimately must be His, the only one which does not possess the aromatic benzene ring (Table 2 in relation to Survey 2).

In the set of hydrocarbon AAs, at the very beginning must be Gly as the simplest AA, followed by Ala as the first possible case of hydrocarbon series with an open carbon chain. At the same time, for chemical reasons, it seems that Gly-Ala can be considered as a pair of AAs. Then comes the par Val-Pro, both with three carbon atoms in the side chain, rather than Leu and Ile with four carbon atoms. Val with half-cyclic chain precedes Pro. [On the relations between valine and proline, such that the valine is bound by the vertices, and the proline by the side of the isopropyl "triangle" for the amino acid functional group, see in (Rakočević and Jokić, 1996).]

Order uncertainty

After the pair Val-Pro, it follows the pair Leu-Ile or Ile-Leu? One possible solution is that Ile precedes leucine (Table 2) because it has already been demonstrated that Ile chemically best suits to the proline (Rakočević and Jokić, 1996, Survey 1.2), and in addition it is a derivative and pairing-member of valine within a set of only two AAs of the valine stereochemical type (Rakočević and Jokić, 1996; Rakočević, 1998b, Survey 4, p. 290). In this solution, Ile has the status of "the first and only" possible derivative, the valine derivative, from the aspect of the change at the end of the valine side chain ("non-standard" hydrocarbon amino acid in the set of 20 AAs due to the above-mentioned "triangle" in the amino acid side chain); and the leucine has the status of "the first possible case" from the aspect of hydrocarbon chain branching.

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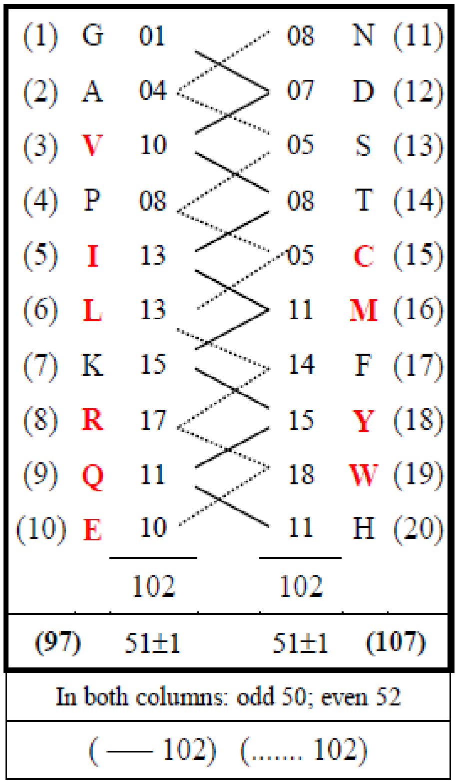
[13] In fact, it is a toluene ring, as a condition of belonging to the alanine stereochemical type, with one CH_2 group between the "head" and "the body" of amino acid molecule (Rakočević and Jokić, 1996. [The 16 AAs of alanine stereochemical type; the 04 AAs of non-alanin stereochemical types: glycine type with only glycine, proline type with only proline and valin type with valine and isoleucine (Popov, 1989; Rakočević and Jokić, 1996).]

Table 2. The order of protein amino acids based on chemical similarity



(1)	G	01	08	N	(11)
(2)	A	04	07	D	(12)
(3)	V	10	05	S	(13)
(4)	P	08	08	T	(14)
(5)	I	13	05	C	(15)
(6)	L	13	11	M	(16)
(7)	K	15	14	F	(17)
(8)	R	17	15	Y	(18)
(9)	Q	11	18	W	(19)
(10)	E	10	11	H	(20)
		102	102		
(97)		51±1	51±1		(107)

In both columns: odd 50; even 52

(—— 102) (....... 102)

The 20 protein AAs are arranged into two decades in accordance to ordinal amino acid number, 1-10 and 11-20; the numbers presented outer: the ordinal numbers 1-20; the numbers presented inner: the number of atoms within side chain of the responding amino acid. In red color AAs handled by class I aminoacyl-tRNA synthetases. In both columns: odd 50 and even positions 52 atoms. Within two decades there are 120 atoms in each; in both zigzag lines also 102 and 102 atoms. First four plus six last equals 97/107 respectively [(GAVP) + (CMFYWH) = 97] [(NDST) + (ILKRQE) = 107][VILRQE = CMFYWH = 74] [GAPK = NDST = CMYW = 28][(1 x 74 = 74) (3 x 28 = 84)]. See details in the text.

Another possibility is that Leu precedes the isoleucine to the following logic and chemical similarity: In the relation of Val-Pro *vs.* Leu-Ile, the Leu chemically corresponds more to valine and Ile to proline (Table B4). "Paradoxically," there is a change of status: now Leu has the status of "the first and only" possible derivative, in a set of only two AAs, in the pair of Val-Leu, where happens the splitting into the valine and alanine stereochemical types. In doing so, the derivation occurs at the beginning of the valine side chain, in contact with the amino acid "head", *i.e.*, amino acid functional group. [This uniqueness of the two-member set also follows from the above said uniqueness of the isopropyl group "triangle".] On the other hand, Ile gets now the status of the "first possible case" from the aspect of the branching.

However, this "paradox" should not be surprising. If the analogy with quantum physics is already on the scene, then this kind of analogy with Heisenberg's uncertainty principle can be expected.

The "between" area

Finally, it remains to determine the chemical distinctions of AAs in "between" area. We have already said that sulfur amino acid pair, Cys-Met, precede aromatic amino acids. As chalcogen AAs, they must be in contact with other two chalcogen amino acids, Ser-Thr. By this, the contact has to be made *via* Cys because it possesses SH group, correspondent to OH group in Ser as well as in Thr.

It is to be understood that a pair of oxygen AAs with the hydroxyl (OH) functional group in side chain must be in contact with a pair of two also oxygen AAs, but which possesses the carboxyl (COOH) functional group: Asp-Glu. However, the problem is that both of these two AAs have their amide derivatives (Asn-Gln) and it is not easy when determining the distinctions, which here proceeds and which follows.

It turns out, however, that the problem is easier to solve when returning to the beginning, in the area of hydrocarbon AAs, to the "point" of the pair Ile-Leu. Further must follow the pair of nitrogen derivatives, Lys-Arg, and Lysine must come first with four carbon atoms in the side chain, which number is also valid for Leucine; and then, with the validity of both principles – the continuity and minimum of change – comes Arginine with three atoms (not counting carbon atom in the guanidino group). Then, chemically speaking, it is very natural that after Arginine comes Gln with its precursor, the glutamic amino acid, both (Gln-Glu) with two carbon atoms in the side chain; it is natural indeed that, in terms of chemical similarity, after 3C atoms occurs changes into 2C atoms, better than into 1C atom, like in the pair Asn-Asp. [As in the case of the guanidino-functional group in arginine, no carbon atom is counting in the carboxylic or amide functional group.] With this, chemical sequencing of series of 20 AAs closes, starting from the first, glycine, and ending with very different histidine (Table 2).

Survey 2. The relationships in the system presented in Table 2

GAVP 23 CMFYWH 74 (**97**) ILKRQE = 79 NDST = 28 (**107**)	VILRQE 74 / CMYW 49 → 123 GAPK 28 / NDSTFH 53 → 81 74 + 53 = **127** 49 + 28 = **77**
(GAVP 23) + (NDST 28) = **51 x 1** (ILKRQE 79) + (CMFYWH 74) = **51 x 3** (23 + 79 = **51 x 2**) / (28 + 74 = **51 x 2**)	

The Survey (Survey 2) presents the relationships in Table 2. The key results appear to be in relation to the quantity 97 which follow from the pattern 25-36-61 [(25+36 = 61) (61+36 = 97)]; the adding as in Fibonacci series; cf. Table A2 rows 5 & 6); other balance quantities: 102 and 51 as the ½ and ¼ of quantity 204 as the total number of atoms within 20 amino acid side chains. [Rakočević, 2004a, a legend to Fig. 1, p. 222: "within AAs (side chains) in class II there are 81, whereas in the class I the 0123 of atoms. Notice that 81 (as 9 x 9) is the first possible (zeroth) arithmetic square in module 9, and 0-1-2-3 is the first possible (zeroth) logical square (as 00-01-10-11)."]

The main result

The main result of this pure chemical sequencing of AAs, presented in Table 2, shows that these chemical distinctions are accompanied by specific arithmetic regularities, including the existence of amino acid ordinal numbers from 1 to 20, with two decades (1-10 and 11-20); and also shows the full balance of the number of atoms in the 20 amino acid molecules: 102±0 atoms in two decades, as well as on two zigzag lines, where such a system with two zigzag lines represents the first possible *periodic system* with two periods.

There is also another result, also directly "taken up" from the Periodic system of numbers (PSN), which simultaneously corresponds to the unique situation in the PSN (Figure A1) and the number of atoms in 20 AAs: 26-42-59-77, within side chains of 4 x 5 of AAs which grouping follows from four amino acid diversity types[14] (Rakočević, 2011b, Figure 3, p. 828). Since these four results are obtained from the "center" of the PSN, it makes sense to compare them with four results obtained from the diagonal of the same system, presented in the right picture of Figure 1 (Equation 1). By this, it makes sense to assume that the quantities "2" and "5" should be understood in the same manner as in Figure 2 (as well as the quantities "1" and "6"), „taken up” from the six-bit binary tree, as shown in Equation 2 (in relation to Figure C3).

$$\begin{array}{cccc} 31 & 41 & 61 & 71 \\ 5 & 1 & 2 & 6 \\ 26 & 42 & 59 & 77 \end{array} \rightarrow (5+2=1+6=7) \ldots\ldots\ldots\ldots (1)$$

$$\begin{array}{cc} 5 & 6 \\ 101 & 110 \\ 010 & 001 \\ 2 & 1 \end{array} \quad \begin{array}{c} (101+010=111) \\ (110+001=111) \end{array} \quad \ldots\ldots\ldots\ldots (2)$$

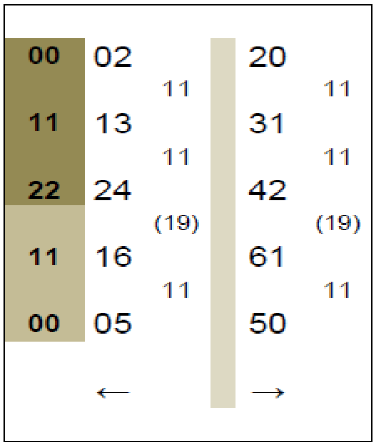


Figure 2. The arrangement is "taken off" from the Periodic Number System (PNS, Figure A1), from where the significant diagonal connects with the initial triangle in Boolean space: 0,1,2 (000, 001, 010). On the left side (shaded) there is a doubled sequence 0-1-2, connected and superposed with its mirror image. Following the logic given in statement 6 of the working hypothesis (Box 1), it makes sense to add the "2" and "5" quantities in the best balance relations. The numbers 02, 13, 24, 16, 05 are obtained, and their mirror image in the tenth step, as shown in Table A3.

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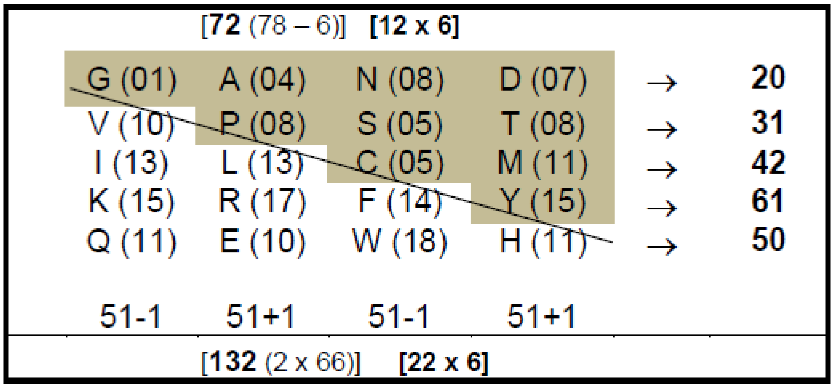
[14] $(G_1+A_4+C_5+N_8+P_8 = \mathbf{26})$; $(S_5+D_7+T_8+Q_{11}+H_{11} = \mathbf{42})$; $(Y_{15}+M_{11}+E_{10}+V_{10}+L_{13} = \mathbf{59})$; $(W_{18}+R_{17}+F_{14}+I_{13}+K_{15} = \mathbf{77})$. These four sets of AAs follow from four amino acid diversity types (see explanation of Table 6 in Box 4).

Table 3. The order of five quartets of protein amino acids following from Table 2 (I)



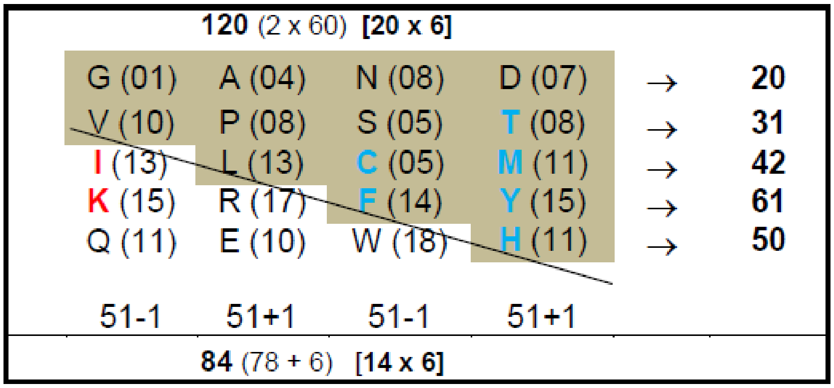
[**72** (78 – 6)] **[12 x 6]**

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**
51-1	51+1	51-1	51+1		

[**132** (2 x 66)] **[22 x 6]**

This Table (Table 3) follows from Table 2 and PSN (Figure A1), from a doubled starting triangle from the top of the last column; triangle switched with its mirror image and superimposed: (00-11-22 / 22-11-00 → 00-11-**22**-11-00 (Table 2 and Table A3). Now we can see that with this arrangement the distinctions and classifications of protein AAs follow another multiplication of number 6 more than was found in the golden mean determination of CIPS (see the legend of Figure 1). Together with the results: (10 x 6 = 60), (11 x 6 = 66), (13 x 6 = 78), we now have the result (12 x 6 = 72). There is still no result (14 x 6 = 84), so if it will occur, then – bingo, the only mirror logical square in the series of natural numbers is reached, also included in Darwin's "computer program". [On the only Darwin's diagram in his famous book *Origin of species*, we see that at the top of the branch "m", between the written numbers 10 and 14, the positions of unwritten numbers 11, 12 and 13 are also indicated (Figure C1).]

Table 4. The order of five quartets of protein amino acids following from Table 2 (II)



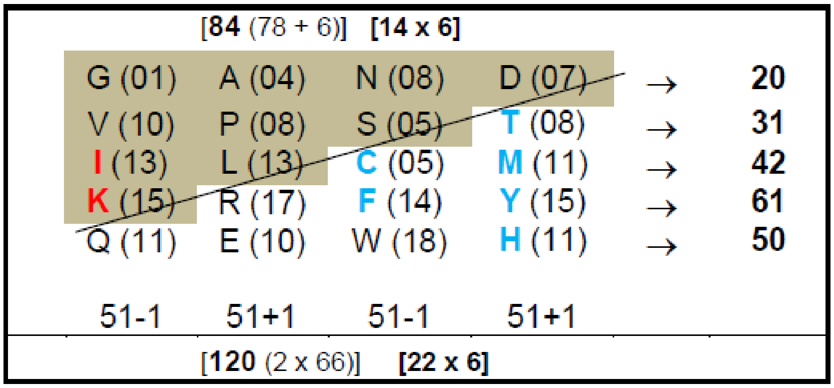
120 (2 x 60) **[20 x 6]**

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**
51-1	51+1	51-1	51+1		

84 (78 + 6) **[14 x 6]**

In this Table (Table 4), all is the same as in Table 3, but with the diagonal one step lower. The colors are used to indicate the AAs that are repeated in the "84 atoms" and "120 atoms" quantities in Table 5. From that crossing a specific amino acid distinction follows: at the beginning of dark area the **8** AAs (G, A, V, P, L, N, D, S) as the first possible cases, and at the beginning of light area the **2** AAs (I, K) as "non-standard" AAs: Ile, as the only one derivative within the valine stereochemical type, and Lys as the fourth case, instead of the first as in the Ser and Cys case. In the light area follow the **4** AAs (Q, E, R, W) as the second (Gln, Glu) or different (Arg, Trp); in the dark area follow the **6** AAs (C, M, F, Y, H, T), two sulfur, three aromatic and one with hydroxide functional group. (Cf. legends of Tables 5 & 6.) [It is possible to see the "rotation" in the Ile-Leu pair, depending on which precedes, and which follows in PAAS, presented in Table 2, what is explained in the Section "Order uncertainty".]

Table 5. The order of five quartets of protein amino acids following from Table 2 (III)



[**84** (78 + 6)] **[14 x 6]**

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**
51-1	51+1	51-1	51+1		

[**120** (2 x 66)] **[22 x 6]**

In this Table (Table 5) all is the same as in Table 3, but with the opposite diagonal in relation to diagonal in Table 3, and colors as in Table 4.

Survey 3. The balance relationships between the arrangements in Tables 4 and 5

IK QREW GV IK APLNSD	IK 28 + QREW 56 = 84 IK 28 + GVAPLNSD 56 = 84
GVAPLNS CF D TMYH QRE CFWTMYH	GVAPLNSD 56 + CFTMYH 64 = 120 QREW 56 + CFTMYH 64 = 120
[(7 x 4 = 28) (7 x 8 = 56) (8 x 8 = 64)] [(6 x 14 = 84) (6 x 20 = 120)] (120 – 84 = 36 = 6 x 6)	

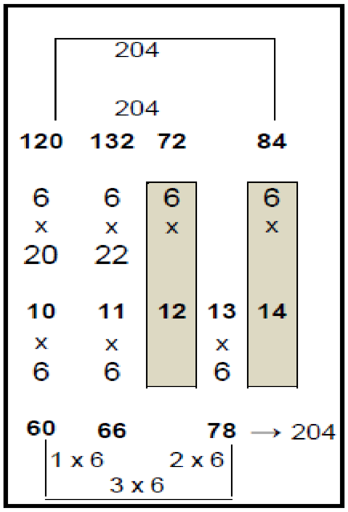
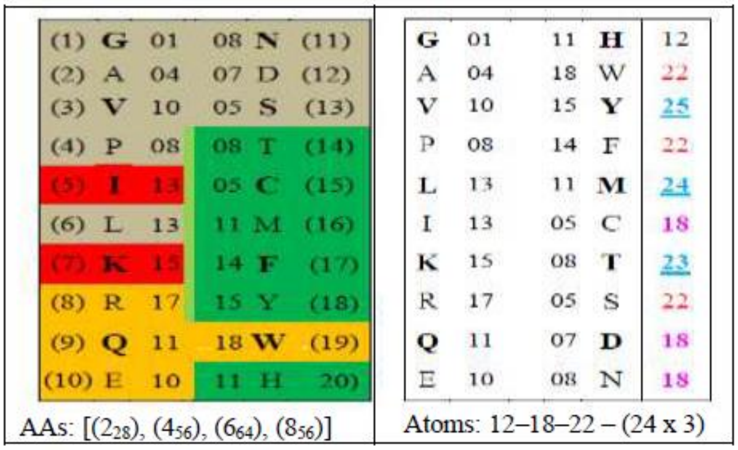


Figure 3. The multiplication of number 6 found in arrangements of AAs in Figure 1 and Tables 3, 4 and 5: the multiples of 10, 11, 12, 13, 14. (The unique sequence as in Table A4 and in top of Darwin's Diagram (Figure C1: $m^{10} – m^{14}$).

Table 6. New splitting within the arrangement presented in Table 2



(1)	G	01	08	N	(11)
(2)	A	04	07	D	(12)
(3)	V	10	05	S	(13)
(4)	P	08	08	T	(14)
(5)	I	13	05	C	(15)
(6)	L	13	11	M	(16)
(7)	K	15	14	F	(17)
(8)	R	17	15	Y	(18)
(9)	Q	11	18	W	(19)
(10)	E	10	11	H	20)

AAs: [(2_{28}), (4_{56}), (6_{64}), (8_{56})]

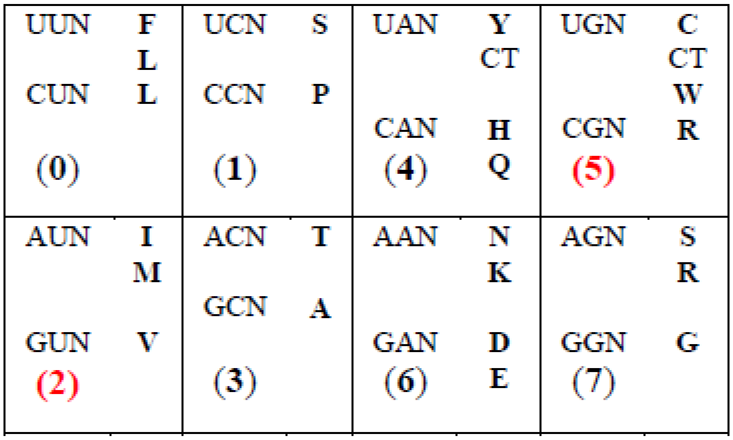
G	01	11	H	12
A	04	18	W	22
V	10	15	Y	25
P	08	14	F	22
L	13	11	M	24
I	13	05	C	18
K	15	08	T	23
R	17	05	S	22
Q	11	07	D	18
E	10	08	N	18

Atoms: 12–18–22 – (24 x 3)

Box 4. *The explanation of Table 6*

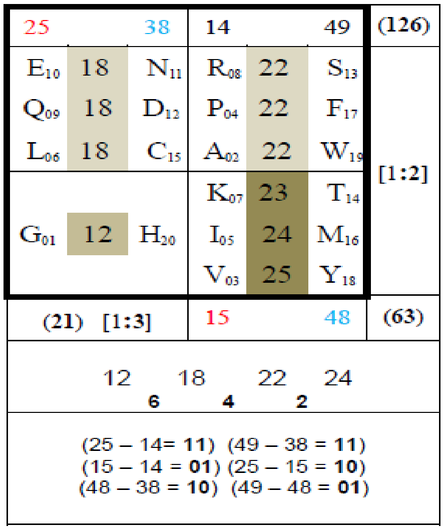
The left illustration in Table 6 follows from Survey 3 and Table 4, while the right illustration follows from Table 2 by rotating the second decade by 180 degrees. [This rotation process is a kind of cyclization; thus, the amino acid arrangement in Table 2 we can call CIPS II versus CIPS I in left picture of Figure 1.] The left illustration contains the result of the crossing of Table 4 with Table 5. Four "new types" of amino acid diversity, comparable to those previously found (Rakočević, 2011b), were obtained. The new types: [(G, A, V, P, L, N, D, S); (C, M, F, Y, H, T); (Q, E, R, W); (I, K)]: the 8 AAs as the first possible cases; the 2 AAs as "non-standard" (as it is explained in the legend of Table 4); the 4 AAs as the second (Gln, Glu) or different (Arg, Trp); the 6 AAs, all the same as the 6 AAs in the "old types" of diversity (Rakočević, 2011b), all but one, Thr instead of Trp. [Thr is the only "black sheep" in the set of 16 AAs of the alanine stereochemical type, given that one of its hydrogen atoms in the CH_2 group, between the head and the body, is replaced by one CH_3 group; on the other hand, Trp is the only "black sheep" in the set of aromatic AAs, having two rings.] "Old type": [(G, P); (A, L, V, I); (C, M, F, Y, W, H); (R, K, Q, N, E, D, T, S)]: the 4 hydrocarbon AAs; the 2 as different, "non-standard" hydrocarbon; the 8 AAs that within the side chain ("body") have a functional group mapped from the "head"; the 6 AAs in which there is no mapping of functional groups from head to body.

Table 7. The generalized Table of standard Genetic code



UUN F L CUN L (0)	UCN S CCN P (1)	UAN Y CT CAN H (4) Q	UGN C CT W CGN R (5)
AUN I M GUN V (2)	ACN T GCN A (3)	AAN N K GAN D (6) E	AGN S R GGN G (7)

Table 7 presents the codon families and their positions on the six-bit binary tree (Rakočević, 1998b, Figure 1). By comparing the positions of codons and AAs on this binary tree, we find that the arrangement is determined by cross-mirror symmetry, in contrast to 000 FLL/111 SRG on the left diagonal and 010 IMV/101 CWR on the right one. In doing so, the key contrasts are: on the least change path Phe UUU 000 000 *vs.* 111 111 GGG Gly crossed with Val GUC 010 101 *vs.* 101 010 UGA "stop" on the path of the maximal changes, when each zero number follows the number one and vice versa. [Notice that "The path of the maximal changes" (101 010 etc., on the correspondent Farey tree is "The golden ruth" as it is presented in Figure 2 in (Rakočević, 1998b).]



25		38	14		49	(126)
E_{10}	18	N_{11}	R_{08}	22	S_{13}	[1:2]
Q_{09}	18	D_{12}	P_{04}	22	F_{17}	
L_{06}	18	C_{15}	A_{02}	22	W_{19}	
			K_{07}	23	T_{14}	
G_{01}	12	H_{20}	I_{05}	24	M_{16}	
			V_{03}	25	Y_{18}	
(21) [1:3]			15		48	(63)

12 18 22 24

6 4 2

(25 – 14= **11**) (49 – 38 = **11**)
(15 – 14 = **01**) (25 – 15 = **10**)
(48 – 38 = **10**) (49 – 48 = **01**)

Figure 4. This arrangement of PAAS follows from the right illustration in Table 6 (from CIPS II). The expression of the principle of balancing, through the interconnection of the chemical properties of AAs, the number of atoms and the ordinal number of AAs in CIPS II, is self-evident. Confirmation of V. Shcherbak's hypothesis (1994) on the analogy of the amino acid (genetic) code with quantum physics also.

However, the result of the most surprising is the result shown in Table 3 (in relations with Tables 4 & 5). It is indeed a mirror image of our hypothetical result, which we gave with a working hypothesis (the statement 6 in relations to the statements 2, 4, 7 and 8): 20 -31-42-61-50 *vs.* 02-13-24-16-05 (Figure 2 in relation to Table A3). In the system presented in Table A3, the result is found in the 10th step, with sum 204, as well as the number of atoms in 20 AAs, in their side chains. As a curiosity or something more than that, the right neighbor is the number 220 (the first friendly number), the lower vertical neighbor is the number 284 (the second friendly number) and the top 124 the fourth of the third perfect number (124 x 4 = 496).][15]

Altogether these are systematic natural arrangements, whose organization and determination correspond with the principle of self-similarity.[16] The already well-known facts that genetic code represents an analogy with natural (verbal) language[17] are joined now to the facts about analogies between genetic code arrangements and specific arrangements within the set of natural numbers.[18]

Conclusion

The facts and arguments presented in this paper fully confirm all nine statements of the working hypothesis (Box 1) about the existence of a complete system of protein amino acids (PAAS), both in biotic as well as in prebiotic conditions, *i.e.* within the amino acid (genetic) code, and independently from it. The existence of such facts also supports our hypothesis that the genetic code, viewed through its chemical constituents, was still prebiotic complete (Rakočević, 2004a). Also, everything that is discussed in this paper is in favor of our attitude that both genetic and chemical code corresponds to one specific spontaneous, intelligent design (SPID) (Rakočević, 2018a, Box 4).[19]

---

[15] A hypothesis on the determination of the genetic code with the perfect and friendly numbers we have presented in the book (Rakočević, 1997b). (www.rakocevcode.rs) [Perfect numbers: 6, 28, 496, 8128, *etc.*; the pairs of the friendly numbers: (220-284), (1184-1210), (17296-18416) *etc.*]

[16] "In correspondence with this, Complete Genetic Code must be based on several key principles. We are going to list only those considered to be the most important: 1. The principle of systemic self-related and self-similar organization. …" (Rakočević, 2004a, p. 231).

[17] "Rumer (1966) suggests that encoding by dinucleotide aggregations is mediated by 'grammatical' formalism (the relation between words and the root of the word), semantics (one-meaning and multy-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 'significant' and 'signifié'" [(Rakočević, 2018a, pp. 31-32 in relation to (De Saussure, 1985, p. 99) (Cf. De Saussure's logical square of natural language in relation with the genetic code language in Figure C2)].

[18] "In determination of the genetic code, except two inherent alphabets – twenty amino acids and four amino bases (two pyrimidines & two purines – is involved still one 'hidden alphabet', the series of natural numbers, with all its regularities and laws" (Rakočević, 2011a, p. 4). An "unfaithless Tomas" may consider this to be numerology, but the facts are the facts. For any theory of probability, it is not possible to prove that all these "downloads" of chemical facts from the Periodic system of numbers (PSN) are mere coincidence.

[19] In further research, it may be possible to get a better term (and notion) by analogy with Carl Jung's term "Synchronizität" ("Synchronicity": Jung, 1993), but with the opposite meaning. This new term could be

Acknowledgment

I am very grateful to the Editorial Board of the Journal *Chemia Naissensis* for the kind invitation to write this paper. This invitation refreshed my beautiful memories on the 15 final years of my professional work at the Department of Chemistry, Faculty of Science and Mathematics, University of Niš. Especially I thank to Vesna Stankov Jovanović, Editor-in-Chief and to Biljana Arsić, Deputy Editor-in-Chief, for the great help in the editing of the paper. Also, I am very grateful to Dejan Raković for helpful and stimulating discussions in the preparation of the paper for publishing.

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"Harmonizität" ("Harmonicity"), but while Synchronicity refers to acausal "meaningful coincidences", the Harmonycity refers to indirect-causal meaningful correspondences. These correspondences follow from interpolation relationships within PSE, with the validity of two Mendeleevian principles (continuity and minimum change), both for chemical elements and for compounds that build complete and consistent molecular systems.

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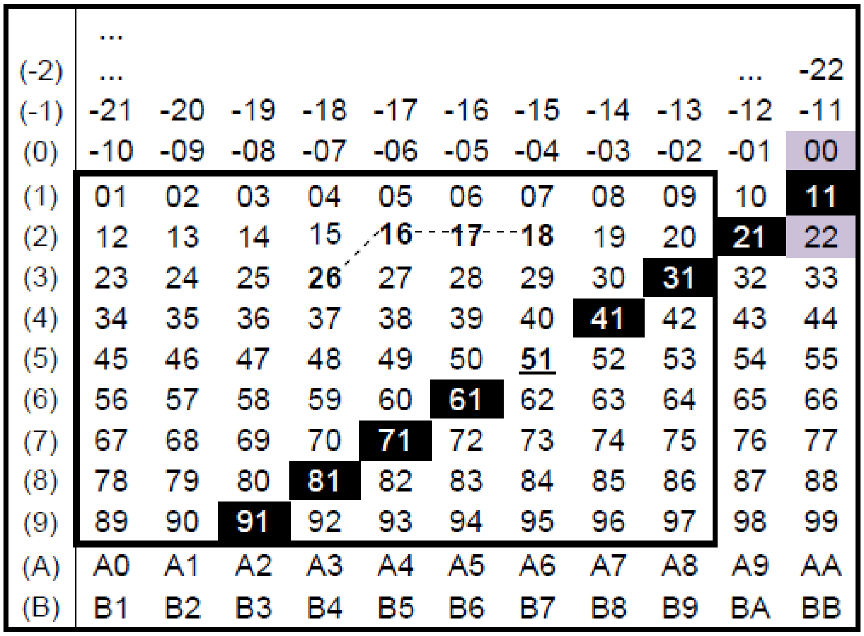
APPENDIX A

Periodic system of the numbers

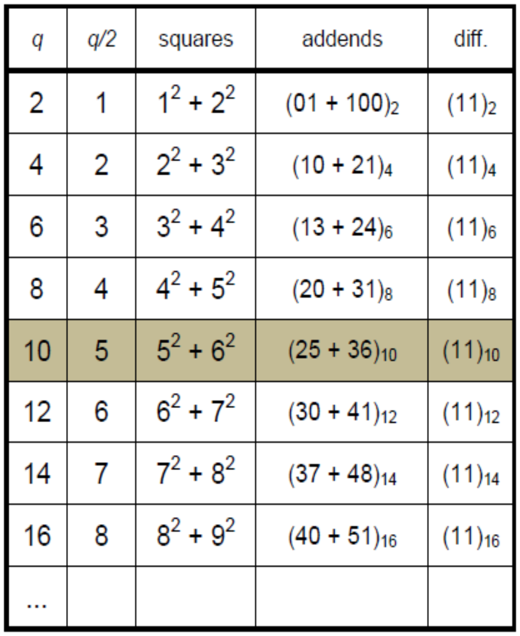
The periodic number system (PSN) was originally given in: (Rakočević, 2011a, Table 4, p. 12 and 2011b, Table 4, p. 826), and here is only a different shading and one relevant diagonal with its own source in the double starting "triangle": (00-11-22). [We say "triangle" thinking that this number series corresponds with the first possible "triangle" in Boolean space (0-1-2, i.e. 000-001-010). However, this is a special topic that remains outside of the scope of this paper, for some other occasion.] In both previous presentations, in order to avoid misunderstanding in the scientific public as "pure numerology," I only labeled it "Table of minimal adding". Now I can no longer run back, and here I am presenting it as a PSN, as a reality.



	...										
(-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
(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 A1. The first three non-negative numbers in the far right column correspond with the zeroth triangle (0,1,2) in Boolean spaces, and the first four (0,1,2,3) with the logical square (as in Figures C2 & C3). The end right column can also be read as (0,1), (1,2), (2,3), (3,4) and so on, as in the last column of Table B5.

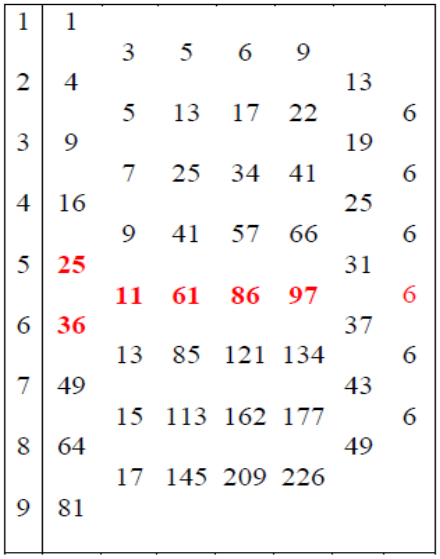
Table A1. Possible periodic systems of numbers



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

The row "10" in this Table follows from PSN presented in Table A1; all other rows follow from analog number systems. From the fact that pattern 25-36-61, valid both in genetic and chemical codes, follows the conclusion that in the case of the existence of biomolecules, only decimal number system has "passed" through Darwin's selective sieve. What is surprising, however, is the fact that Darwin's sieve is matched with the "pulse" of Bing Bang.

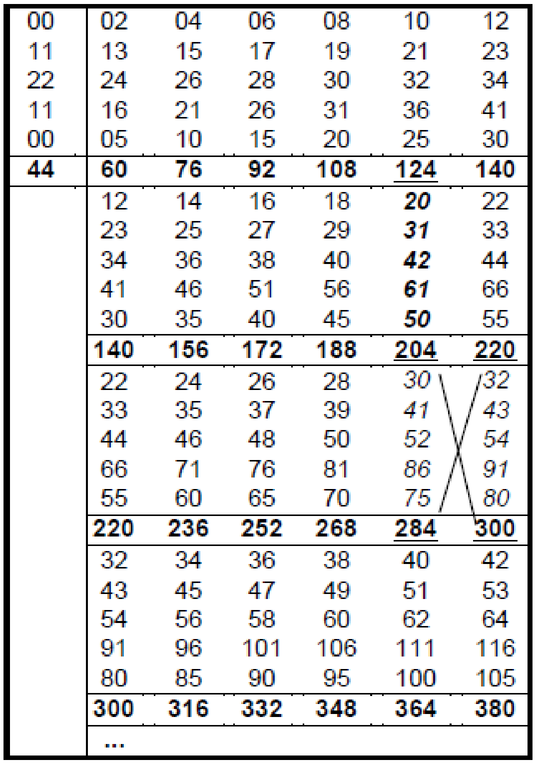
Table A2. A double Fibonaccian step



1	1						
		3	5	6	9		
2	4					13	
		5	13	17	22		6
3	9					19	
		7	25	34	41		6
4	16					25	
		9	41	57	66		6
5	**25**					31	
		11	**61**	**86**	**97**		6
6	**36**					37	
		13	85	121	134		6
7	49					43	
		15	113	162	177		6
8	64					49	
		17	145	209	226		
9	81						

The Table presents – in the red area – a double Fibonaccian step. From the fact that pattern 25-36-61 is valid both in genetic and chemical codes, and patterns 25-36-61-86 & 25-36-61-86-97 are valid in genetic code, follows the conclusion that in Nature realy exists such a double Fibonaccian step. [These are not Fibonacci numbers, but it is the Fibonacci rule.]

Table A3. The source of PAAS mirror symmetry

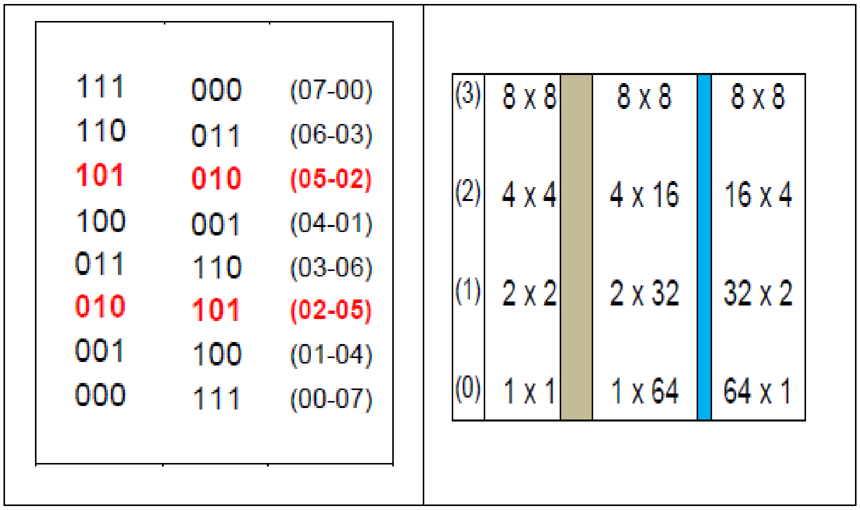


00	02	04	06	08	10	12
11	13	15	17	19	21	23
22	24	26	28	30	32	34
11	16	21	26	31	36	41
00	05	10	15	20	25	30
44	**60**	**76**	**92**	**108**	**<u>124</u>**	**140**
	12	14	16	18	***20***	22
	23	25	27	29	***31***	33
	34	36	38	40	***42***	44
	41	46	51	56	***61***	66
	30	35	40	45	***50***	55
	140	**156**	**172**	**188**	**<u>204</u>**	**<u>220</u>**
	22	24	26	28	*30*	*32*
	33	35	37	39	*41*	*43*
	44	46	48	50	*52*	*54*
	66	71	76	81	*86*	*91*
	55	60	65	70	*75*	*80*
	220	**236**	**252**	**268**	**<u>284</u>**	**<u>300</u>**
	32	34	36	38	40	42
	43	45	47	49	51	53
	54	56	58	60	62	64
	91	96	101	106	111	116
	80	85	90	95	100	105
	300	**316**	**332**	**348**	**364**	**380**
	...					

The arrangement represents the Table of distinct 2-5 adding (TDA) with starting column 00-11-22-11-00 which follows from PSN (Periodic system of numbers: Figure A1) in decimal number system by overlapping the real sequence of doubled the first possible triangle in Boolean space (0-1-2) with its mirror image through compression and superposition at the point "22"). In the 10th step we have a realization of the sequence (20-31-42-61-50), the same with the number of atoms in five AAs classes (20, 31, 42, 61, 50) as it is here presented: all five results in the 10th step are mirror image of the first step. (Cf. Figure 2 and see details in the text.)

Table A4. Mirror symmetry within the sequence 11-12-13-14 in the decimal number system (Rakočević, 1994, p. 235)

0	$11 \times 1 = 11$ $11 \times 2 = 22$ $11 \times 3 = 33$	$11 \times 1 = 11$ $11 \times 2 = 22$ $11 \times 3 = 33$	$11^2 = 121$
1	$12 \times 1 = 12$ $12 \times 2 = 24$ $12 \times 3 = 36$	$21 \times 1 = 21$ $21 \times 2 = 42$ $21 \times 3 = 63$	$12^2 = 144$ $21^2 = 441$
2	$13 \times 1 = 13$ $13 \times 2 = 26$ $13 \times 3 = 39$	$31 \times 1 = 31$ $31 \times 2 = 62$ $31 \times 3 = 93$	$13^2 = 169$ $31^2 = 961$
3	$14 \times 1 = 14$ $14 \times 2 = 28$ $14 \times 3 = ?$	$41 \times 1 = 41$ $41 \times 2 = 82$ $41 \times 3 = ?$	$14^2 = 196$



111	000	(07-00)
110	011	(06-03)
101	010	(05-02)
100	001	(04-01)
011	110	(03-06)
010	101	(02-05)
001	100	(01-04)
000	111	(00-07)

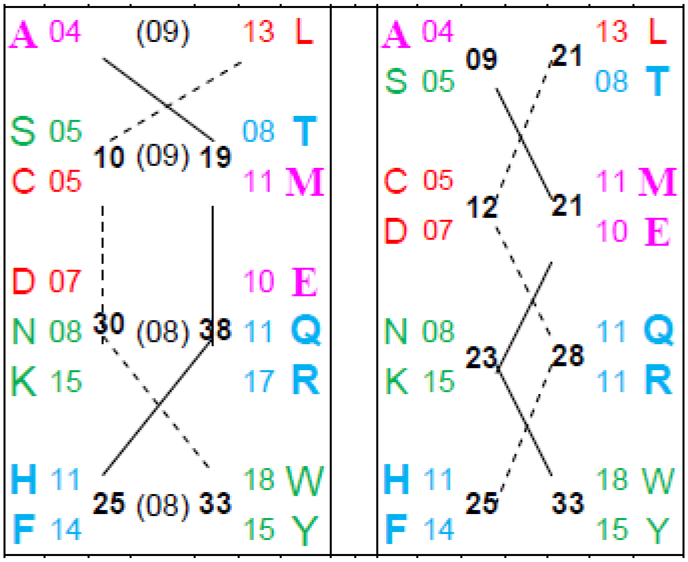
(3)	8 x 8	8 x 8	8 x 8
(2)	4 x 4	4 x 16	16 x 4
(1)	2 x 2	2 x 32	32 x 2
(0)	1 x 1	1 x 64	64 x 1

Figure A2. Mirror symmetry within the binary number record on the Boolean cube (on the left). Mirror symmetry within the codon distribution to a six-bit binary tree; an example: two branches, each with 32 codons *vs.* 32 codon pairs (on the right).

APPENDIX B

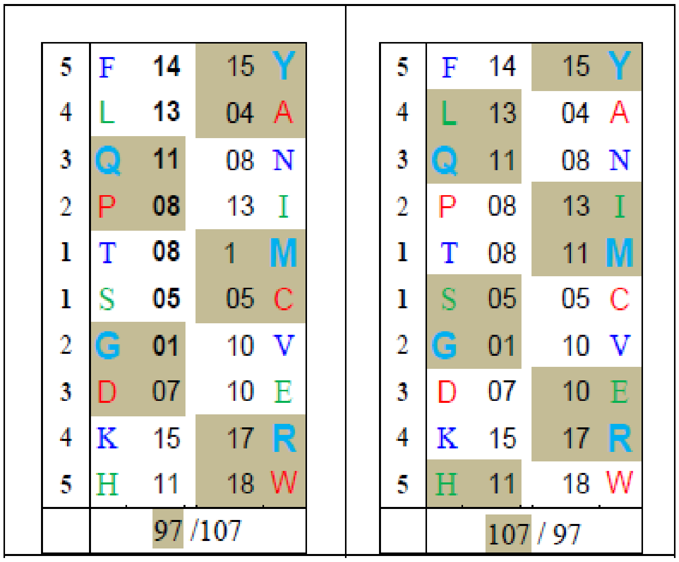
Harmonic amino acid structures

Table B1. The distinctions of 16 AAs of alanine stereochemical type



In the Table it is given a classification of 16 AAs of alanine stereochemical type into 8 chemically adequate pairs. In both crossing lines there are 86±0 atoms. [86 + GV 11 = 97 and 86 + PI 21 = 107 (cf. Table A2, 5th and 6th row)]. The differences 8 and 9 (9 - 8 = 1) express the minimum change relation among the amino acids [as in Gray code model of GC (Swanson, 1984, p. 191)]. The order (ordinal number) follows from the atom number hierarchy. Notice that within outer class (2:4 = 1:2 AAs or amino acid pairs) there is a balance of the number of atoms: [(4 + 33 = **37**) + (13 + 25 = **38**) = 75 (86 – 11)]; and within inner class (4:6 = 2:3) [(10 + 38 = **37** + 11) + (19 + 30 = **38** + 11) = 97 (86 + 11)] (All examples as Shcherbak’s analogies with quantum physics.) Notice also the realization of 25-36-61 pattern: AME = LCD = 25. [This 25 + (GV 11) from non-alanine types equals 36.]; on the other hand, AAs in green as well as AAs in blue equals 61 atoms. The right illustration contains the algorithm for the generation of a variant ("wobble" variant!) of CIPS as it is the right picture in Figure 1, by reading as from a logical square in the Gray code model: STLA, DEMC, KRQN, FYWH. (Left illustration from: Rakočević and Jokić, 1996, Survey 1, p. 346; right illustration from: Rakočević, 2011b, Table 2.1, p. 823.)

Table B2. The significant distinctions in CIPS (I)

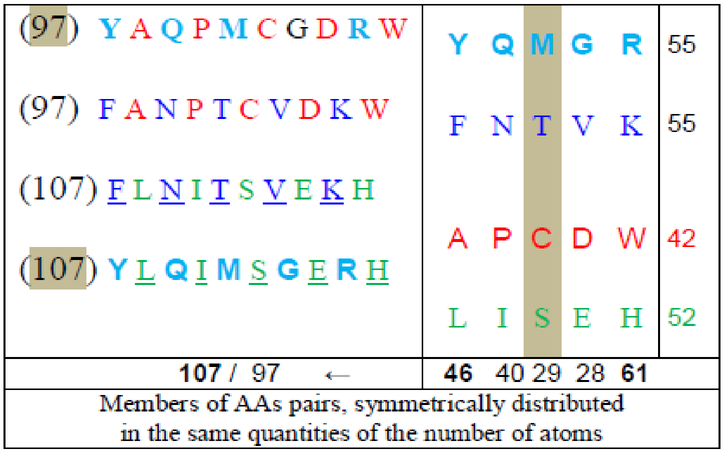


5	F	14	15	Y
4	L	13	04	A
3	Q	11	08	N
2	P	08	13	I
1	T	08	1	M
1	S	05	05	C
2	G	01	10	V
3	D	07	10	E
4	K	15	17	R
5	H	11	18	W
		97 /107		

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
		107 / 97		

The distinctions of AAs after the ratio 4: 6 = 2:3 on the left and 5:5 = 1:1 on the right. The resulting relationships are analyzed in Table B3 and Survey B1.

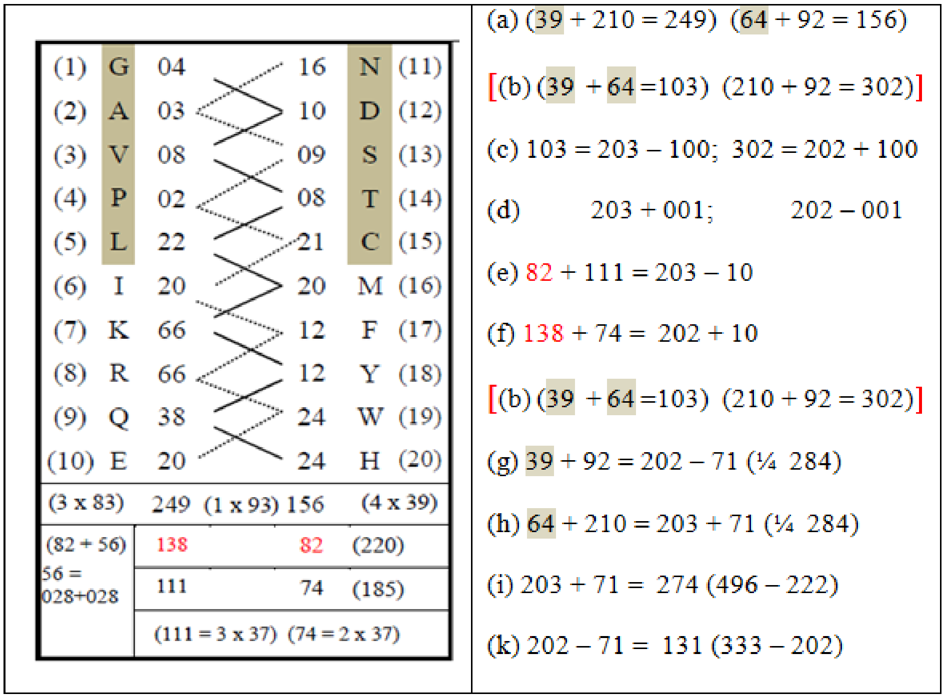
Table B3. The significant distinctions in CIPS (II)



(97) Y A Q P M C G D R W	Y	Q	M	G	R	55
(97) F A N P T C V D K W	F	N	T	V	K	55
(107) F L N I T S V E K H	A	P	C	D	W	42
(107) Y L Q I M S G E R H	L	I	S	E	H	52
107 / 97 ←	46	40	29	28	61	
Members of AAs pairs, symmetrically distributed in the same quantities of the number of atoms						

The analysis of relationships in Table B2 after crossing of quantities 97 and 107. New order in relation to left picture in Figure 1: [(YF AL) → aliphatic and carboaromatic]; [(QN PI) → the first three nitrogens, the fourth one links P with valine, *i.e. via* isopropyl group "triangle"] [GV DE → *vs.* PI QN]; [RK WH → all are nitrogens]; [On the left (AL FY) → initial aliphatic and initial aromatic; On the right (RK WH) → right end: all are nitrogenous]. In the middle of the system are chalcogenes. All four columns correspond to CIPS on the left picture in Figure 1: two and two rows from top to bottom.

Table B4. The number of conformations (total: 202 + 203 = 405)



(1)	G	04	16	N	(11)
(2)	A	03	10	D	(12)
(3)	V	08	09	S	(13)
(4)	P	02	08	T	(14)
(5)	L	22	21	C	(15)
(6)	I	20	20	M	(16)
(7)	K	66	12	F	(17)
(8)	R	66	12	Y	(18)
(9)	Q	38	24	W	(19)
(10)	E	20	24	H	(20)
(3 x 83)		249	(1 x 93) 156		(4 x 39)
(82 + 56) 56 = 028+028		138	82	(220)	
		111	74	(185)	
		(111 = 3 x 37)	(74 = 2 x 37)		

(a) (39 + 210 = 249) (64 + 92 = 156)

[(b) (39 + 64 =103) (210 + 92 = 302)]

(c) 103 = 203 – 100; 302 = 202 + 100

(d) 203 + 001; 202 – 001

(e) 82 + 111 = 203 – 10

(f) 138 + 74 = 202 + 10

[(b) (39 + 64 =103) (210 + 92 = 302)]

(g) 39 + 92 = 202 – 71 (¼ 284)

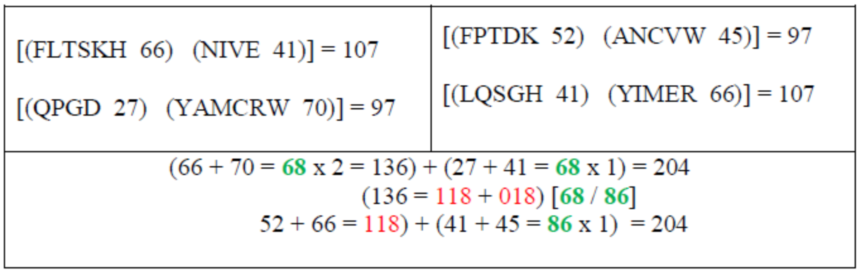
(h) 64 + 210 = 203 + 71 (¼ 284)

(i) 203 + 71 = 274 (496 – 222)

(k) 202 – 71 = 131 (333 – 202)

This Table is the same as Table 2, except that Leu proceeds Isoleucine, and instead of the number of atoms in AAs, is given the number of conformations, as in Popov (1989, Table 8, p. 88). The balancing of conformation as follows: From (a) to (c) the difference in the number of conformations in two columns (decades) in relation to the middle pair 202-203, with a change for ± 100; (d) from: (Rakočević, 2004a, Table 8, p. 228) and (Rakočević, 2018a, Table 8, p. 44) where is shown the change in the number of conformations for ± 001 in the GC Table, if the order of AAs follows the order of their coding codons, in the hierarchy of the number of hydrogen bonds; from (e) to (f) the number of conformations in odd positions in relation to multiples of Shcherbak's "Prime quantum 37" with a change for ± 10; from (g) to (h) the number of conformations in relation to the second friendly number; (i) the number of conformations in relation to the second friendly and the third perfect number; (k) the number of conformations in relation to the second friendly number and to the significant determinant of GC, as is the number 333 (Rakočević, 2018a, p. 37: the sixth column in Survey 2).

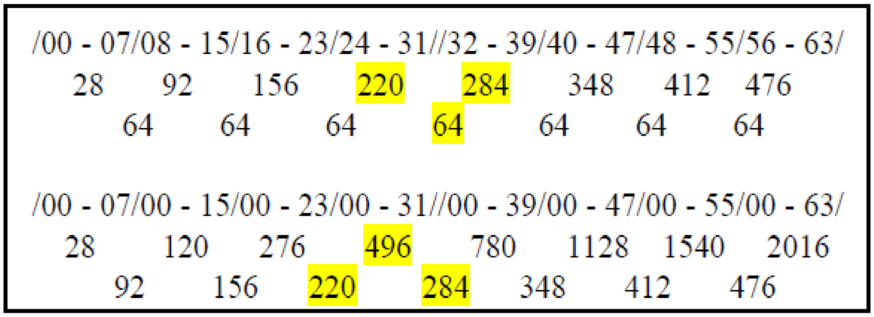
Survey B1. The relationships within two arrangements presented in Table B2



[(FLTSKH 66) (NIVE 41)] = 107 [(QPGD 27) (YAMCRW 70)] = 97	[(FPTDK 52) (ANCVW 45)] = 97 [(LQSGH 41) (YIMER 66)] = 107

(66 + 70 = 68 x 2 = 136) + (27 + 41 = 68 x 1) = 204
(136 = 118 + 018) [68 / 86]
52 + 66 = 118) + (41 + 45 = 86 x 1) = 204

Survey B2. The determinations on the six-bit binary tree

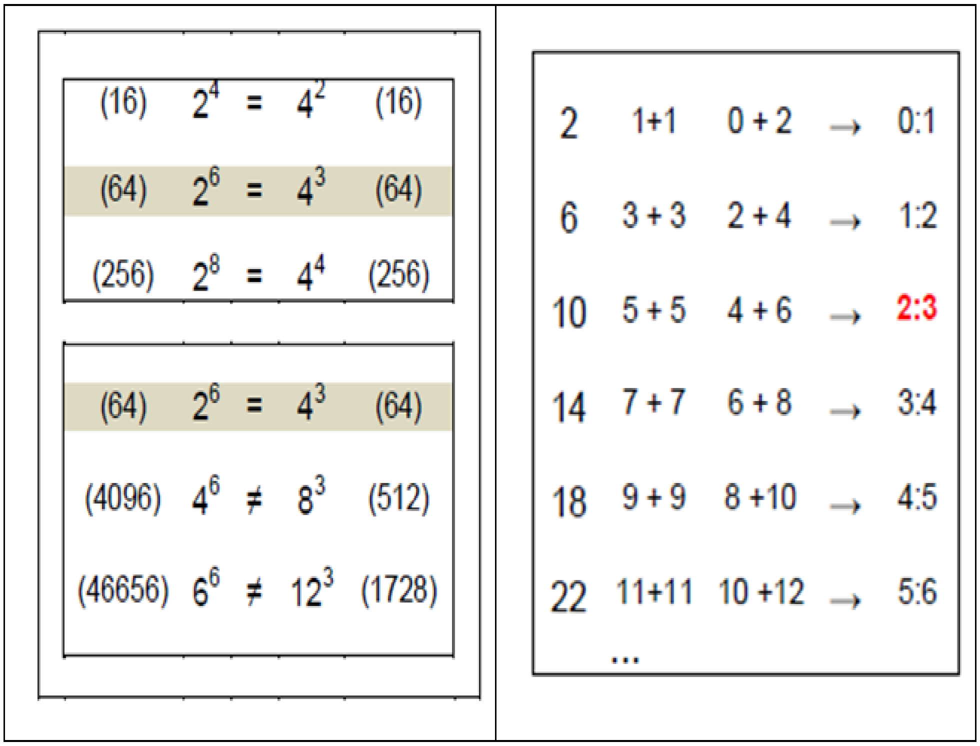


/00 - 07/08 - 15/16 - 23/24 - 31//32 - 39/40 - 47/48 - 55/56 - 63/
28 92 156 220 284 348 412 476
64 64 64 64 64 64 64

/00 - 07/00 - 15/00 - 23/00 - 31//00 - 39/00 - 47/00 - 55/00 - 63/
28 120 276 496 780 1128 1540 2016
92 156 220 284 348 412 476

The Survey follows from (Rakočević, 1997b, Figure 7, p. 60): "The determination of the series of the numbers 0-63. When we look closely into the structure of the sequence 0-63 of the series of the natural numbers we come to the obvious and self-evident explanation of the reason why the genetic code must be six-bit code, no matter if it is the manifestation in the form of the Gray Code model (Swanson, 1984, p 188), or it is in the form of the Binary tree (Rakočević, 1994, p 38). There must be 8 codons, *i.e.* amino acid classes. The structure of the sequence 0-63 is strictly determined by third perfect number (496) and the sum consisted of the first pair of the friendly numbers (220+284). Along with this, the specific Boolean square is being made and it is the restrictive factor, in a sense that it is not possible to ‘go on’ any further - not ahead, not back: (0) 220+284=504; (1) 156+348=504; (2) 92+412=504; (3) 28+476=504. The key distinctions within the genetic code are obviously self-evident: entity 64 as a series of continuity (correspondent with 64 codons); entity 20 from 496 (III PN)-476=20 (correspondent with 20 amino acids) *etc.*"

Table B5. Some number systms: the unique arrangements and situations



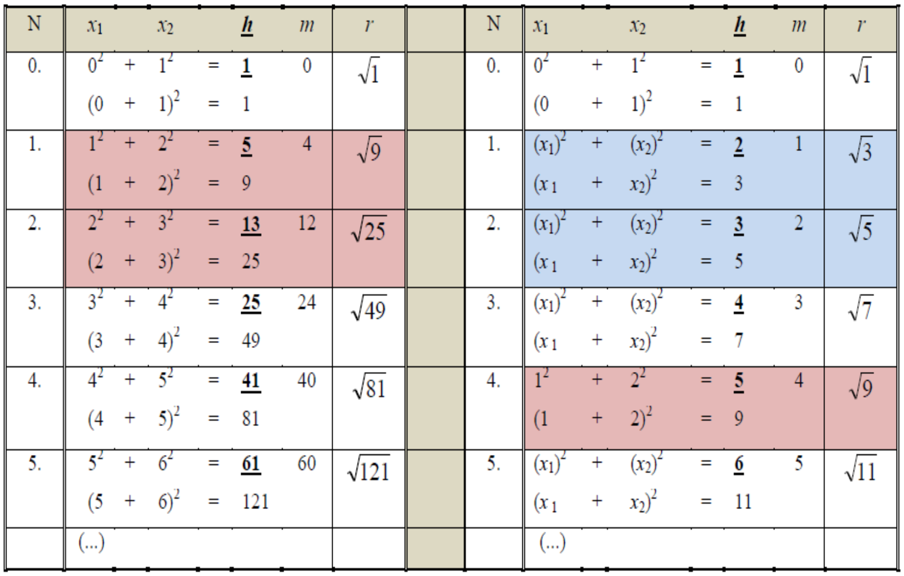
(16)	2^4	=	4^2	(16)
(64)	2^6	=	4^3	(64)
(256)	2^8	=	4^4	(256)

(64)	2^6	=	4^3	(64)
(4096)	4^6	≠	8^3	(512)
(46656)	6^6	≠	12^3	(1728)

2	1+1	0 + 2	→	0:1
6	3 + 3	2 + 4	→	1:2
10	5 + 5	4 + 6	→	2:3
14	7 + 7	6 + 8	→	3:4
18	9 + 9	8 +10	→	4:5
22	11+11	10 +12	→	5:6
...				

The Table corresponds with PSN (Figure A1) through the ratio 1:2 on the left above and 2:3 on the right, the third row. The left illustration shows unique arrangements and situations corresponding to 16 doublets and 64 triplets of nucleotides in the genetic code. The right illustration shows the changes by ± 1 in relation to $q/2$ of number systems whose numerical basis (q) corresponds to the values that follow from Hükel's rule (the first column). It can be seen that only in the case of the decimal number system we have a direct correspondance with the golden mean (footnote 10).

Table B6. The relationships within Generalized Golden mean (Rakočević, 2004b)



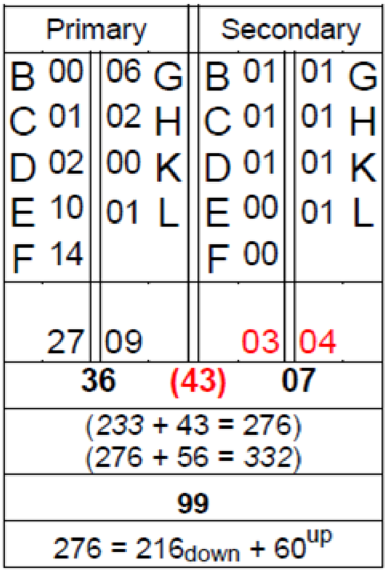
N	x_1		x_2		**h**	m	r		N	x_1		x_2		**h**	m	r
0.	0^2	+	1^2	=	**1**	0	$\sqrt{1}$		0.	0^2	+	1^2	=	**1**	0	$\sqrt{1}$
	$(0$	+	$1)^2$	=	1					$(0$	+	$1)^2$	=	1		
1.	1^2	+	2^2	=	**5**	4	$\sqrt{9}$		1.	$(x_1)^2$	+	$(x_2)^2$	=	**2**	1	$\sqrt{3}$
	$(1$	+	$2)^2$	=	9					$(x_1$	+	$x_2)^2$	=	3		
2.	2^2	+	3^2	=	**13**	12	$\sqrt{25}$		2.	$(x_1)^2$	+	$(x_2)^2$	=	**3**	2	$\sqrt{5}$
	$(2$	+	$3)^2$	=	25					$(x_1$	+	$x_2)^2$	=	5		
3.	3^2	+	4^2	=	**25**	24	$\sqrt{49}$		3.	$(x_1)^2$	+	$(x_2)^2$	=	**4**	3	$\sqrt{7}$
	$(3$	+	$4)^2$	=	49					$(x_1$	+	$x_2)^2$	=	7		
4.	4^2	+	5^2	=	**41**	40	$\sqrt{81}$		4.	1^2	+	2^2	=	**5**	4	$\sqrt{9}$
	$(4$	+	$5)^2$	=	81					$(1$	+	$2)^2$	=	9		
5.	5^2	+	6^2	=	**61**	60	$\sqrt{121}$		5.	$(x_1)^2$	+	$(x_2)^2$	=	**6**	5	$\sqrt{11}$
	$(5$	+	$6)^2$	=	121					$(x_1$	+	$x_2)^2$	=	11		
	(...)									(...)						

APPENDIX C

Some additional harmonic structures

The Darwin's equation

Table C1. The key of Darwin's Diagram (I)

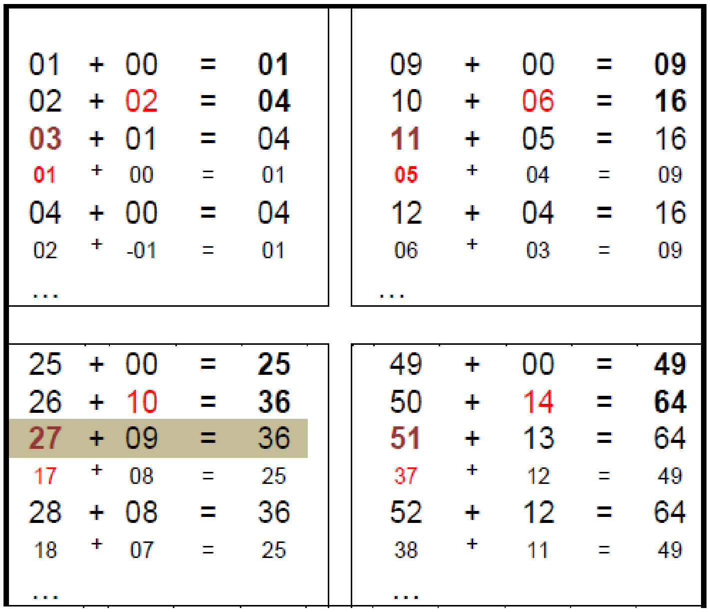


Primary		Secondary	
B 00	06 G	B 01	01 G
C 01	02 H	C 01	01 H
D 02	00 K	D 01	01 K
E 10	01 L	E 00	01 L
F 14		F 00	
27	09	03	04
36	(43)		07
(233 + 43 = 276) (276 + 56 = 332)			
99			
$276 = 216_{down} + 60^{up}$			

"All branches (primary + secondary) for "other nine species" for the left and the right part of the Diagram, at all 15 levels. The equation 27 + 09 = 36 appears to be a special Darwin's equation, valid to determination of the genetic code (Figure 6, 7 & 8 and Table 6.1); and the equation 03 + 04 = 07 corresponds to the first three members of Lucas number series (Figure D.1). The number 233 comes from Table 4.5 and together with this result (43) makes 276 which is the total number of branches within the Diagram. In addition: 56 = 46 nodes plus 10 branchings, and from that all "branch" entities/quantities equal 332 as a mirror pattern of the 233" (Rakočević, 2015, Table 5, p. 47).
(http://dx.doi.org/10.17605/OSF.IO/QZG69)
(www.rakocevcode.rs)

The Darwin's equation (27 + 9 = 36) is the "missing link" that allows understanding of the pattern 25-36-61, contained in two linear equations, determinants of genetic and chemical code (Rakočević, 2018b, Survey 2a, 2b, 3a and 3b, p. 296). At the same time, it is also the key of Darwin's Diagram (Rakočević, 2015, Figure 1.1, p. 19; here Figure C1).

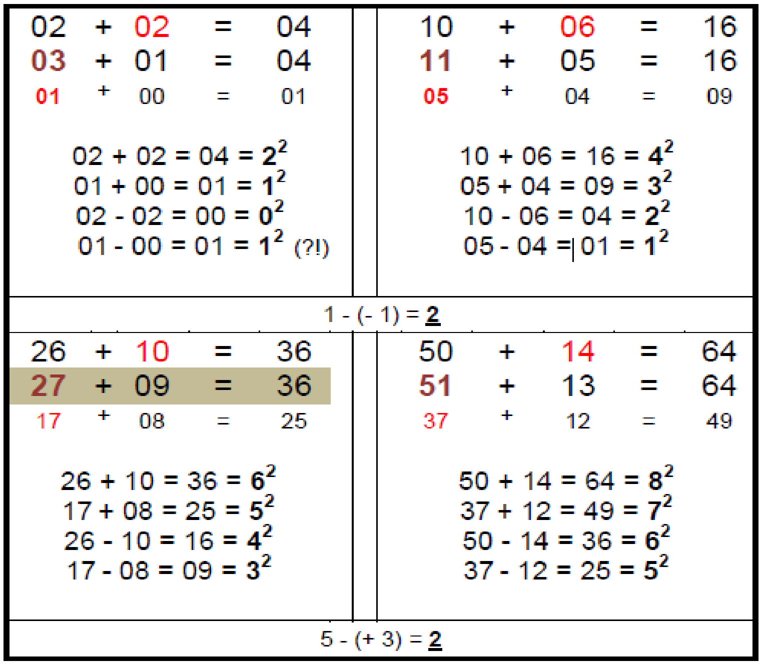
Table C2. The key of Darwin's Diagram (II)



01	+	00	=	**01**	09	+	00	=	**09**
02	+	02	=	**04**	10	+	06	=	**16**
03	+	01	=	04	**11**	+	05	=	16
01	+	00	=	01	**05**	+	04	=	09
04	+	00	=	04	12	+	04	=	16
02	+	-01	=	01	06	+	03	=	09
…					…				
25	+	00	=	**25**	49	+	00	=	**49**
26	+	10	=	**36**	50	+	14	=	**64**
27	+	09	=	36	**51**	+	13	=	64
17	+	08	=	25	37	+	12	=	49
28	+	08	=	36	52	+	12	=	64
18	+	07	=	25	38	+	11	=	49
…					…				

This illustration is from Figure 6 in "Darwin Enigma" (Rakočević, 2015): „The generation of the squares of natural numbers through two linear equations. Darwin's equation is in the third quadrant, in the area of dark tones surrounded by two linear equations valid in the genetic code." Notice that the second member of the equation (the second row in all four quadrants) follows from Hückel's rule (2, 6, 10, 14); the differences between the third and fourth row also from Hückel rule: (3-1 = 2), (11-5 = 6), (**27-17** = **10**), (51-37 = 14). On the other hand, the first member of the equation (2, 10, 26, 50) increases by 8n (n = 1, 2 and 3). Notice also that with the first quadrant we have the generation of the squares of the first two natural numbers 1 and 2, in second 3 and 4, in third 5 and 6 (in relation to the pattern 25-36-61) and in the forth 7 and 8. [The next step in generating would already be in the area of double-digit numbers.]

Table C3. The key of Darwin's Diagram (III)



02 + 02 = 04 03 + 01 = 04 01 + 00 = 01 $02 + 02 = 04 = \mathbf{2}^2$ $01 + 00 = 01 = \mathbf{1}^2$ $02 - 02 = 00 = \mathbf{0}^2$ $01 - 00 = 01 = \mathbf{1}^2$ (?!)	10 + 06 = 16 11 + 05 = 16 05 + 04 = 09 $10 + 06 = 16 = \mathbf{4}^2$ $05 + 04 = 09 = \mathbf{3}^2$ $10 - 06 = 04 = \mathbf{2}^2$ $05 - 04 = 01 = \mathbf{1}^2$
$1 - (- 1) = \underline{\mathbf{2}}$	
26 + 10 = 36 27 + 09 = 36 17 + 08 = 25 $26 + 10 = 36 = \mathbf{6}^2$ $17 + 08 = 25 = \mathbf{5}^2$ $26 - 10 = 16 = \mathbf{4}^2$ $17 - 08 = 09 = \mathbf{3}^2$	50 + 14 = 64 51 + 13 = 64 37 + 12 = 49 $50 + 14 = 64 = \mathbf{8}^2$ $37 + 12 = 49 = \mathbf{7}^2$ $50 - 14 = 36 = \mathbf{6}^2$ $37 - 12 = 25 = \mathbf{5}^2$
$5 - (+ 3) = \underline{\mathbf{2}}$	

The Table as in (Rakočević, 2015, Table 5, p. 47): "This Figure follows from the previous. Three linear equations within each of the four quadrants in relation to the quadruplets of natural numbers' squares. In the third quadrant: two equations are valid in the genetic code and one (in the middle position, dark tone) is given as Darwin's equation [Notice a paradox (Darwin's paradox), valid for number 1 in the first quadrant: the negative value of number 1 cannot be – negative?!]."

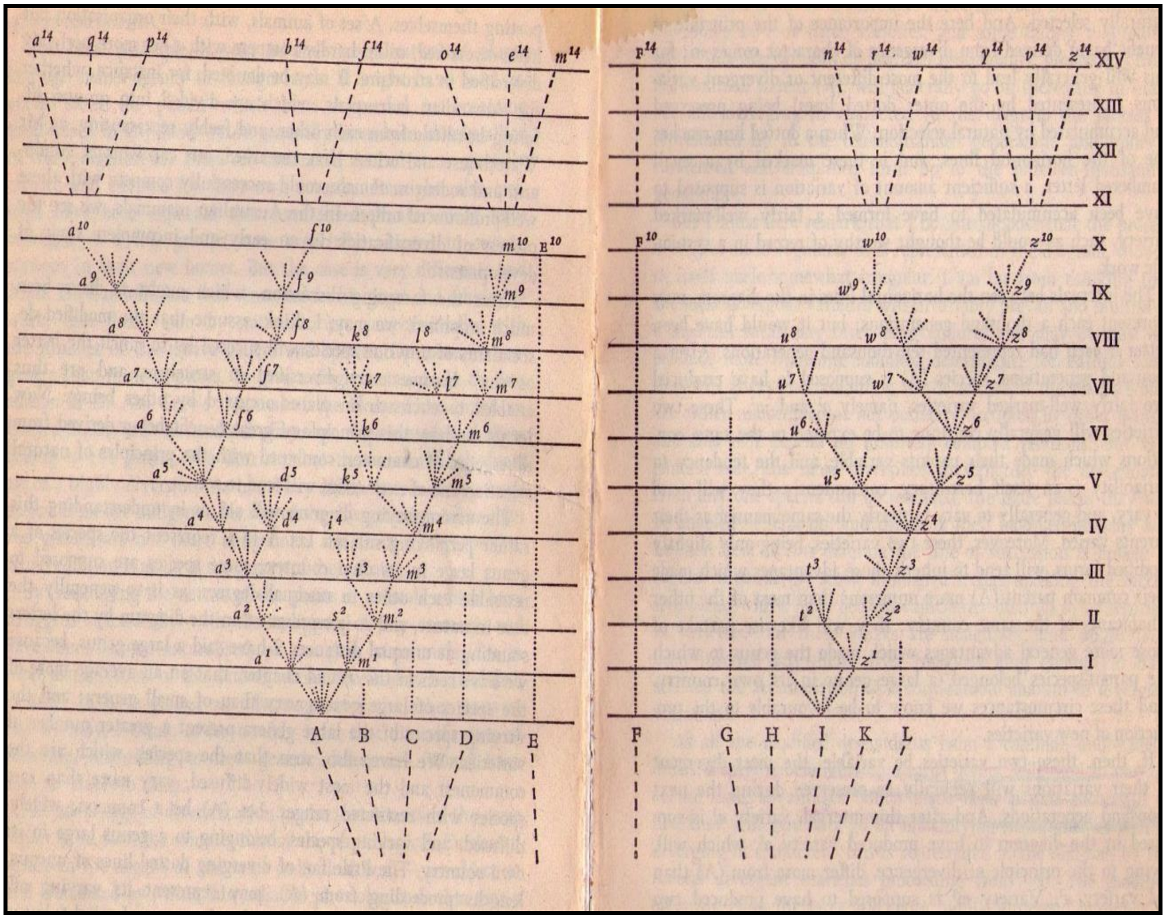


Figure C1. The "accompanying diagram" in Darwin's book "On the Origin of Species" (London, 1859)

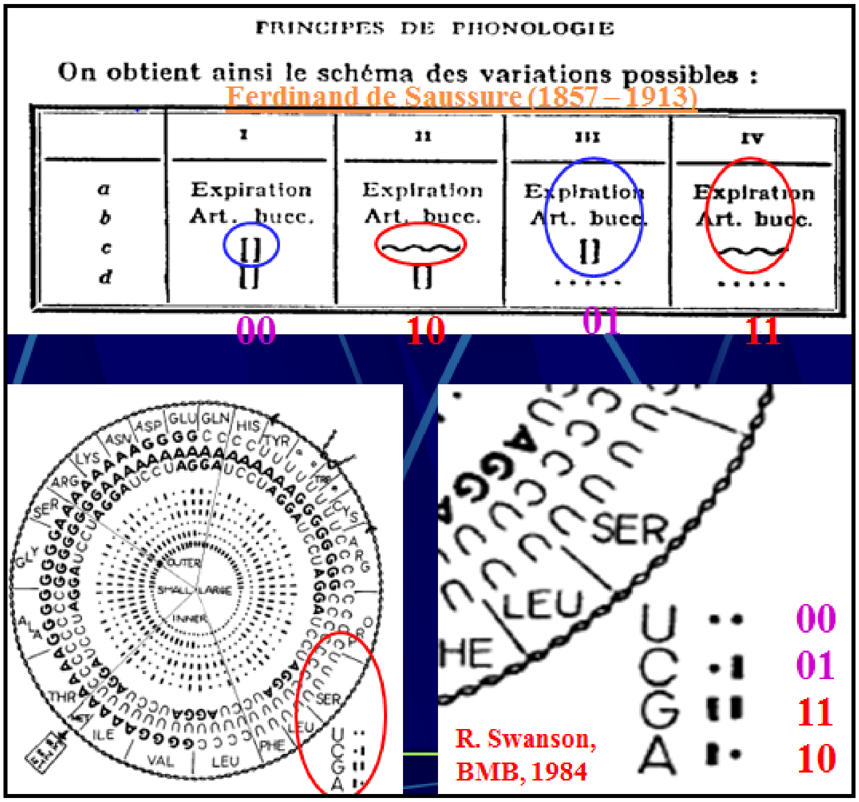


Figure C2. The correspondence with PSN (Fig. A1) through the relations between the logical square 00-01-10-11 and the first four levels in PSN: 00-11-22-33. The binary records of the logical square: up for the human language (De Saussure, 1985, p. 70); down: for the genetc language (Swanson, 1984, p. 188).

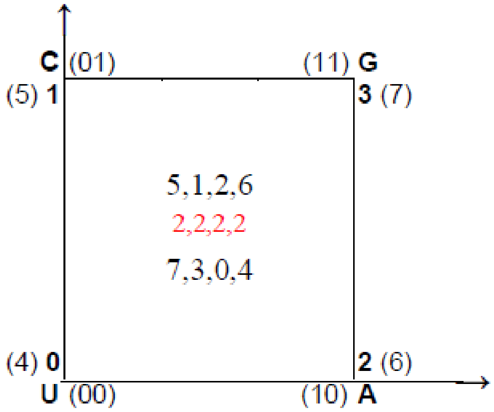


Figure C3. The correspondence with PSN (Figure A1) through the relations between the logical square 00-01-10-11 and the first four levels in PSN: 00-11-22-33. The unit Boolean logical square: **0** (00), **1** (01), **2** (01), **3** (11) in correspondence with the unit Boolean logical cube and/or with eight branches on the binary-code tree of Genetic code (Rakočević, 1998b, Figure 1, p. 284): **0** (000), **1** (001), **2** (010), **3** (011); **4** (100), **5** (101), **6** (110), **7** (111). The mirror symmetry on the binary-code tree of Genetic code: [010 / 101 → AUA / CGC etc.]; [001 / 110 → UCC / GAA etc.]. The Py-Pu logical square: U (00) → simpler ring, simpler H bond; C (01) → simpler ring, more complex H bond; A (10) → more complex ring, simpler H bond; G (11) → more complex ring, more complex H bond. From the 24 permutations of the UCAG sequence, only this, as the first, consistently follows the chemical hierarchy; the remaining 23 are in relation to it. (Cf. footnote 7; also, the sequence 5-1-2-6 with the same sequence in Equation 1.)

Chemia Naissensis, Vol 2, Issue 1,RESEARCH ARTICLE, 44

Preoteinske amino kiseline kao potpuni (periodni) sistem

Miloje M. Rakočević

Univerzitet u Nišu, Prirodno-matematički fakultet, Departman za hemiju, Višegradska 33, 18000 Niš, Srbija (u penziji od 2003)

SAŽETAK

Pozivajući se na rezultate prethodnog istraživanja o šifri genetskog koda i analogijama genetskog i hemijskog koda– dva u svemu kompletna prirodna sistema – ovaj rad predstavlja rezultate izučavanja najpotpunijeg Sistema proteinskih amino kiselina (engl. PAAS). Pokazano je da 20 proteinskih amino kiselina predstavljaju potpuni sistem-uređen, koherentan, i harmoničan. U takvom sistemu, sve hemijske razlike unutar Sistema su praćene specifičnim aritmetičkim i algebarskim pravilnostima, uključujući postojanje aminokiselinskih rednih brojeva od 1 do 20. Klasifikacija amino kiselina u dve dekade (1-10 i 11-20) u strogoj je korespondenciji sa balansima broja atoma. Postojanje harmonijskih struktura i rasporeda amino kiselina, bez obzira da li su ili nisu konstituenti genetskog koda, prati zaključke da je genetski kod, kroz svoje glavne konstituente-20 aminokiselina i 4 pirimidin-purinskih baza- bio kompletan čak i u prebiotskim uslovima.

Ključne reči: Proteinske amino kiseline, amino kiselinski kod, genetski kod, binarno stablo, Gray kod, Zlatna sredina, Fibonacci-jev niz.

Chemia Naissensis, Vol 2, Issue 1, RESEARCH ARTICLE, 45

Acides aminés protéiques en tant que système complet (périodique)

Miloje M. Rakočević

Université de Niš, Faculté des sciences naturelles et des mathématiques, Département de chimie, Višegradska 33, 18000 Niš, Serbie (à la retraite depuis 2003)

RÉSUMÉ

Se référant aux résultats des recherches antérieures sur le Chiffrage du code génétique et les analogies des codes génétique et chimique – deux systèmes presque naturels et complets – cet article présente les résultats de l'étude du Système le plus complet des acides aminés protéiques (PAAS, angl.). Il est démontré que 20 acides aminés protéiques semblent constituer un système complet, système étant ordonné, cohérent et harmonique. Dans une telle organisation, toutes les distinctions chimiques au sein du Système sont accompagnées de régularités spécifiques du type arithmétique et algébrique, y compris l'existence des nombres ordinaux d'acides aminés de 1 à 20. La classification des acides aminés en deux décades (celle de 1 à 10 et celle de 11 à 20) paraît être dans une stricte correspondance avec les équilibres du nombre d'atomes. L'existence des structures harmoniques et de la disposition des acides aminés, qu'ils soient ou non des constituants du code génétique, s'accorde avec les conclusions suivant lesquelles le code génétique, à travers ses constituants principaux – 20 acides aminés et 4 bases puriques et pyrimidiques – était complet même dans les conditions prébiotiques.

Mots-clés : acides aminés protéiques, code des acides aminés, code génétique, arbre binaire, code Gray, juste milieu, série de Fibonacci.

Белковые аминокислоты как целостная (периодическая) система

Милое М. Ракочевич

Университет в Нише, Факультет естественных наук и математики, Департамент химии, ул. Вышеградская 33, 18000 Ниш, Сербия (на пенсии с 2003 года)

АННОТАЦИЯ

Ссылаясь на результаты предыдущих исследований шифра генетического кода и аналогий генетического и химического кодов – двух общих целостных природных систем – в настоящем документе представлены результаты исследования наиболее полной белковой аминокислотной системы (PAAS). Показано, что 20 белковых аминокислот представляют собой целостную систему – упорядоченную, связную и гармоничную. В такой системе все химические различия внутри системы сопровождаются конкретными арифметическими и алгебраическими закономерностями, в том числе наличием порядковых номеров аминокислот от 1 до 20. Классификация аминокислот по двум числовым рядам (1-10 и 11-20), по-видимому, находится в строгом соответствии с балансами числа атомов. Существование гармонических структур и расположений белковых аминокислот, независимо от того, являются ли они составляющими генетического кода или нет, соответствуют выводам о том, что генетический код через его основные составляющие – 20 БА и 4 основания ПУ-ПИ, был завершен даже в пребиотических условиях.

Ключевые слова: белковые аминокислоты, аминокислотный код, генетический код, двоичное дерево, код Грея, золотое сечение, ряд Фибоначчи.

Chemia Naissensis, Vol 2, Issue 1, RESEARCH ARTICLE, 47

Protein-Aminosäuren als vollständiges (Perioden)System

Miloje M. Rakočević

Universität in Niš, Mathematisch-Naturwissenschaftliche Fakultät, Lehrstuhl für Chemie, Višegradska 33, 18000 Niš, Serbien (im Ruhestand seit 2003)

ABSTRAKT

In Bezug auf die bisherigen Ergebnisse früherer Forschungen über die Verschlüsselung des genetischen Codes und Analogien des genetischen und chemischen Codes – zwei fast vollständige natürliche Systeme – stellt diese Arbeit die Forschungsergebnisse des vollständigsten Systems der Protein-Aminosäuren dar (engl. PAAS). Es wird gezeigt, dass 20 Protein-Aminosäuren ein vollständiges System zu seien scheinen – geordnet, kohärent und harmonisch. In einem solchen System wird allen chemischen Unterschieden innerhalb des Systems von spezifischen, arithmetischen und algebraischen Regelmäßigkeiten gefolgt, einschließlich der Existenz von Aminosäure-Ordinalzahlen von 1 bis 20. Die Klassifikation von Aminosäuren in zwei Dekaden (1-10 und 11-20) scheint in enger Korrespondenz mit den Balancen der Anzahl der Atome zu stehen. Das Bestehen harmonischer Strukturen und Anordnungen von Aminosäuren, unabhängig davon, ob sie Bestandteile des genetischen Codes sind oder nicht, folgt den Schlussfolgerungen, dass der genetische Code durch seine Hauptbestandteile – 20 Aminosäuren und 4 Pyrimidin-Purinbasen, sogar in präbiotischen Zuständen vollständig war.

Schlüsselwörter: Protein-Aminosäuren, Aminosäure-Code, genetischer Code, Binärbaum, Goldener Schnitt, Fibonacci-Folge

ADDENDUM 2

Quantitative Biology > Biomolecules

[Submitted on 22 Jun 2021 (v1), last revised 14 Aug 2021 (this version, v4)]

A new type of mirror symmetry in the set of protein amino acids

Miloje M. Rakocevic

In several previous works, I presented the mirror symmetry in the set of protein amino acids, expressed through the number of atoms. Here, however, the same thing is shown but over the number of nucleons and molecules mass. Compared to the previous version of the paper, minimal changes have been made, and Display 2 as well as Figures 3 and 4 have been added.

Comments: 16 pages, 6 tables, 4 figures, 2 displays and 2 surveys

Subjects: **Biomolecules (q-bio.BM)**

Cite as: arXiv:2108.01563 **[q-bio.BM]**
(or arXiv:2108.01563v4 **[q-bio.BM]** for this version)
https://doi.org/10.48550/arXiv.2108.01563
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Submission history

From: Miloje M. Rakocevic [view email]

[v1] Tue, 22 Jun 2021 19:15:04 UTC (466 KB)

[v2] Fri, 6 Aug 2021 07:20:40 UTC (468 KB)

[v3] Wed, 11 Aug 2021 05:40:10 UTC (481 KB)

[v4] Sat, 14 Aug 2021 13:04:13 UTC (502 KB)

A new type of mirror symmetry in the set of protein amino acids

Miloje M. Rakočević
University of Niš, Faculty of Sciences and Mathematics, Department of Chemistry,
Višegradska 33, 18000 Niš, Serbia

Abstract. In several previous works, I presented the mirror symmetry in the set of protein amino acids, expressed through the number of atoms. Here, however, the same thing is shown but over the number of nucleons and molecules mass. Compared to the previous version of the paper, minimal changes have been made, and Display 2 as well as Figures 3 and 4 have been added.

Canonical AAs mirroring

Atom number		Nucleon numb.	
02	20	981	189
	11		100
13	31	982	289
	11		010
24	42	**992**	**299**
			010
16	61	982	289
	11		100
05	50	981	189

Synopsis of **Graphical abstract**: Records of the number of atoms and nucleons as *original* and the *image* in the mirror. Reducing the distances between the quantities of the number of atoms and/or of nucleons to the level "filled" exclusively with units, directly supports Shcherbak's hypothesis on the "analogies with quantum physics" (Shcherbak, 1994).

Key words. Genetic code; protein amino acids; periodic system of numbers; perfect numbers; friendly numbers.

The new type of the mirror symmetry, in the set of protein amino acids (AAs), which is the matter in this brief communication, was go in the form of a hint in a previous my work (MMR, 2004, Table 1, p. 223).[1] But then it was not allowed to say something like that [mirror symmetry of the numbers ?!], because it would be declared as numerology.[2] Now when that symmetry is the factual state, expressed though the number of atoms (Box 1), it makes sense to represent it also through the number of nucleons (Table 1 in relation to Figure 1), and through molecules mass (Tables 2, 3 and 4).[3]

We look now at Tables 1 and 2 together with Figure 1 and Survey 1. If we place a mirror at the middle row of Table 1, either from above or from below, we always see one and the same sequence-image; for the number of nucleons: 299, 289, 189 and for the molecule mass: 596, 586, 485, as indicated in Figure 1.[4] This is directly obvious mirror

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[1] The word is about a new type of mirror symmetry, in relation to enantiomer symmetry of amino acid molecules (MMR, 2018a, Solution 1, p. 42).

[2] It is the fact, however, that this new type of symmetry I have presented in some of the previous papers published only in preprint form; also once in the official journal, in a regular article (MMR, 2018a, at the end of page 38, in relation to Figure 4, p. 37.).

[3] We are talking here about the set of standard protein amino acids that have the status of "canonical amino acids" because their incorporation into proteins is mediated by the genetic code.

[4] In the middle row, in Table 1 and Figure 1, respectively, the number of nucleons 299 and the quantity of mass 596 irresistibly "invoke" the third perfect number: the quantity 596 because of the difference 596 -

symmetry, but it is existing a hidden one. The full meaning of balancing and nuancing, expressed through distinctions and differences between quantities, it appears only when the original and/or the mirror image of the double value of the third perfect number is included: the image as in Table 2, and original as in Table 3; both Tables taken together as a single system).[5]

Remark 1. One can note in Table 2, in the area of the quantities of molecules mass, the difference **100** (bold) in the middle row, and in area of nucleons number the difference **000** (bold). The difference of difference is 100. On the other hand, in Survey 1 we find that the difference between the sums and the sums in Table 2 is also 100. As we see the principle of self-similarity is at work also here as well.

Box 1. *Mirror symmetry through the number of atoms as a unity of numerical quantities and chemical qualities*

Start: a unique sequence of Periodic System of Numbers (PSN) in front of a mirror, with superposition; then "crossing" with a unique 6-bit binary tree sequence (Box 2): 010/101 as 2 / 5 (3 x 2 and 2 x 5):

00-11-22 / 22-11-00 → **00-11-22-11-00** → 02, 13, 24, 16, 05

Then mirroring with the result as in Display 1 and Fig. 2 (MMR, 2019, Fig. 2, p. 17 and Tab. A3, p. 30; 2021, Fig. 2, p. 55 and Fig. A2, p. 88). PSN as in (MMR, 2019, Fig. A1, p. 28).

Display 1. The unity of chemism and semiosis (I)

(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

According to our idea, Display 1 should be proof of our prediction (given at the end of the paper) that the Genetic code represents the unity of chemism and semiosis. The number of atoms in each of the five rows of AAs represents a mirror image of the number that arises in a specific crossing of PSN and the 6-bit binary tree. And the arrangement according to chemism is as follows. In the left (un-bolded) decade, AAs are sorted into pairs by chemical similarity: 1. "G" has the simplest possible side chain (it has only one hydrogen atom), and the side chain of "A" has one carbon atom in addition to three hydrogen; 2. "V" has the simplest semi-cyclic hydrocarbon chain and "P" has the simplest cyclic one; 3. "I" and "L" are the only two AAs (in this set) that are structural isomers; 4. "K" and "R" are the only two AAs with amino group in the side chain; 5. the fifth pair of the first decade forms a chemical unity (by similarity) with the 1st pair of the second decade: the only two AAs with the carboxyl group in the side chain ("E" and "D") with their amides, "Q" and "N", respectively; 2nd pair of second decade consists of only two AAs with the hydroxyl group in the side chain; 3rd pair are the only two sulfur AAs; 4th pair are the only two carbocyclic aromatic AAs; and 5th pair are the only two heterocyclic aromatic AAs.

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496 is equal to 100, and the number 299 because that record is actually a mirror image of the double value of the third perfect number.

[5] That perfect and friendly numbers are determinants of the genetic code I have repeatedly explained, especially in a monograph from 25 years ago (MMR, 1997b, pp. 60-64). www.rakocevcode.rs

Display 2. The unity of chemism and semiosis (II)

01G 01	**11**N 08	**06**L 13	**16**M 11		**01**G 01	**02**A 04	**11**N 08	**12**D 07
02A 04	**12**D 07	**07**K 15	**17**F 14		**03**V 10	**04**P 08	**13**S 05	**14**T 08
03V 10	**13**S 05	**08**R 17	**18**Y 15		**05**I 13	**06**L 13	**15**C 05	**16**M 11
04P 08	**14**T 08	**09**Q 11	**19**W 18		**07**K 15	**08**R 17	**17**F 14	**18**Y 15
05I 13	**15**C 05	**10**E 10	**20**H 11		**09**Q 11	**10**E 10	**19**W 18	**20**H 11

On the right side the arrangement of AAs is the same as in Display 1 (20 AAs as two decades), except that the order of amino acids (in the similarity), from the first to the last, is indicated here. (Cf. MMR, 2019, Table 2, p. 14.) The AAs decades placed on the left are divided into quintets: the first with the third, and the second with the fourth. Such an arrangement shows the unity of chemism and semiosis in a different way (different from this presented in Box 1), as it is represented in Figure 3. Furthermore, Figure 4 shows a more complete unity of chemism and semiosis through the chemical properties of molecules, the number of atoms in them, as well as through ordinal number of AAs in the system of chemical similarity of molecules as such.

Box 2. *The determination of the series of the numbers 0-63 on the 6-bit binary tree*

/00 - 07/08 - 15/16 - 23/24 - 31//32 - 39/40 - 47/48 - 55/56 - 63/
28 92 156 **220** **284** 348 412 476
64 64 64 64 64 64 64

/00 - 07/00 - 15/00 - 23/00 - 31//00 - 39/00 - 47/00 - 55/00 - 63/
28 120 276 **496** 780 1128 1540 2016
92 156 **220** **284** 348 412 476

"The determination of the series of the numbers 0-63 [on the 6-bit binary tree]. When we look closely into the structure of the sequence 0-63 of the series of the natural numbers we come to the obvious and self-evident explanation of the reason why the genetic code must be six-bit code, no matter if it is the manifestation in the form of the Gray Code model (Swanson, 1984, p 188), or it is in the form of the Binary tree (Rakočević, 1994, p. 38) [Rakočević, 1998, Fig. 1, p. 284]. There must be 8 codon i.e. amino acid classes. The structure of the sequence 0-63 is strictly determined by third perfect number (496) and the sum cbonsisted of the first pair of the friendly numbers (220 + 284 = 504) …" (Rakočević, 1997b, Fig. 7, p. 60) www.rakocevcode.rs

Remark 2. About "strange result" in Figure 1, where from differences of the quantities of molecules mass and the number of nucleons follows the number of atoms in the AAs molecules it is difficult to give any explanation. Instead that, we give only the facts. In the previous paper (MMR, Table 3a, p. 224) we showed that in the first two columns of GCT there are 196 + 100 = 296 atoms; the other two columns have 154 + 144 = 298 atoms. It is also indicated that in the first two columns there are 297–1 and in the other two columns there are 297 + 1 atoms.

Remark 3. The three equations we find reviewed in Survey 2 (very bottom, right) are also found in the standard GCT (MMR, 2004, Table 3a, p. 224).

*

Our expectations are that over time it will turn out that the presented results are strong support for two hypotheses and two predictions. The first hypothesis is the hypothesis of Vladimir Shcherbak, according that "The laws of additive-positions of numbers … have analogies with quantum physics" (Shcherbak, 1994, p. 476, last passage). The second hypothesis is our hypothesis given in a previous paper, whose this brief communication is a specific supplement: "Hypothesis on a complete [prebiotic] genetic code" (MMR, 2004, Section 7.1, p. 231).

The first prediction we give here for the first time boils down to the expectation that future researches will show that the view of mirror symmetry, presented here, has a direct or indirect connection with the choice of only the left amino acid enantiomers in the act of the generating of life.

According to the second prediction, it is expected that future researches will show that each of the mirror images of quantities (of number of atoms and / or nucleons, as well as of the sums of molecules mass of amino acids), presented here, can be considered as "signifier" of the "signified" in a semiotic sense, in the manner as we presented in the previous paper for Rumer's system of nucleotide doublets.[6] In such a case, "signifier" represents a mirror image, and "signified" is the corresponding chemical entity.

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[6] MMR, 2018a, pp. 31-31: "Rumer (1966) suggests that encoding by dinucleotide aggregations is mediated by 'grammatical' formalism (the relation between words and the root of the word), semantics (one-meaning and multy-meaning codon families) and by semiology, i.e. semiotics (the classification of nucleotide doublets after the number of their hydrogen bonds which appear here as 'signifiant' and 'signifié' (signifier and signified) at the same time, that is as their unity (De Saussure, 1985, p. 99)."

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Tables

Table 1. *"The harmonic structure with two 'acidic' and three 'basic' amino acid quartets"*

Amino acids				n	Molecule mass
D 59	N 58	A 15	L 57	189	485.49 ≈ 485 /486
R 100	F 91	P 41	I 57	289	585.70 ≈ 586 /586
K 72	Y 107	T 45	M 75	**299**	595.71 ≈ **596** /596
H 81	W 130	S 31	C 47	289	585.64 ≈ 586 /586
E 73	Q 72	G 01	V 43	189	485.50 ≈ 485 /486
				1255	2738.04 2738 = 2 x (037 x 037)

Minimally reduced and technically adjusted Table from previous work (MMR, 2004, Table 1, p. 223). Designation (n): The number of nucleons within 20 AAs side chains, calculated from the first, the lightest nuclide (H-1, C-12, N-14, O-16, S-32); One can notice that molecule mass within five rows is realized through the same logic-patterns of notations as the first nuclide, i.e. isotope. [*Note*: Integer upper values of molecules mass in all five rows end with the number 6, and the lower with the number 5 (485 + 585, etc.). The sum of the five lower values (485 + 585 +595 + 585 + 485) equals 2735, which number is the same as the number of nucleons in the whole molecules: in their "bodies", i.e. side chains (1255) and in "heads", i.e. amino acid functional groups (1480).]

Table 2. *The number of nucleons and the quantities of molecules mass in Table 1, in relation to the third perfect number and the mirror image of its double value*

992 - 011	981 / 189			(496 - 010)	486	485	
		100					*101*
992 - 010	982 / 289			(496 + 090)	586	586	
		010					*010*
992 ± **000**	992 / 299			496 + **100**	596	596	
		010					*010*
992 - 010	982 / 289			(496 + 090)	586	586	
		100					*101*
992 - 011	981 / 189			(496 - 010)	486	485	
042		*220*		300			*222*

The sums of differences (the sums of absolute values) correspond to two numbers (220 and 300) in the "logical square" in Figure 2 [(0). 204, **(1). 220**, (2). 284, **(3). 300**]. The other two vertices off the logic square, the numbers 284 and 204, exist through the relation with the golden mean, as shown in Survey 1, below right, in relation to Survey 2. If total molecules mass (M) follows according to column "485", then M = **2** x (037 x 037) (**2738**); if according to column "486", then M = 1 x (1370 + 1370) (**2740**) (Cf. shaded area in Table 4). If both results are taken into account, then the "hidden" mirror symmetry of Dirac's type **1**37 / **0**37 (0 vs 1 as electron vs positron) is also revealed. The degree of freedom between the integer in these two columns and the original non-integer, given in Table 1, was determined by the isotope contribution of the chemical elements.

Table 3. *The number of nucleons and the quantities of molecules mass in Table 1, in relation to the third perfect number (for nucleons) and its double value (for molecules mass)*

496 - 307	189			(992 - 507)	485	
		100				*101*
496 - 207	289			(992 - 406)	586	
		010				*010*
496 - 197	299			992 - 396	596	
		010				*010*
496 - 207	289			(992 - 406)	586	
		100				*101*
496 - 307	189			(992 - 507)	485	
1225		*220*		2222		*222*

(1225 + 220 = **1445**) / (2222 + 222 = **2444**) → 999

Last result in Shcherbak's Table: 27 x 37 = 999
(Shcherbak, 1994, Table 1, p. 476)

The relatively small changes in the status of the third perfect number in this Table in relation to Table 2, lead to the large changes in the result. Here it does not follow from the logical square in Figure 2 but follows from two specific arithmetical system-arrangements, presented in Tables 3.1 and 3.2.

Table 3.1. *Specific Arithmetical System-Arrangement*
(SASA I)

0	15	+	0	=	15
1	1**2**5	+	20	=	145
2	**1225**	**+**	**220**	**=**	**1445**
3	12225	+	2220	=	14445
	…				
0	15	+	9	=	24
1	1**4**5	+	99	=	244
2	**1445**	**+**	**999**	**=**	**2444**
3	14445	+	9999	=	24444
	…				

This arithmetical system-arrangement, taken together with the results in Table 3, is a proof more that the key determinant of the Multiplication Table in the decimal number system (3 x 5 = 15) also the determinant of the genetic code (MMR, 2021a, Survey 8 and Tables C2 and C3). The numbers 2 and 4 are emphasized in both subsystems, upper and lower, to indicate the fact that the ratio of number 4 and its half, the number 2, is manual in the genetic code as we have shown in previous works, as also follows from the system-arrangement shown in Table 3.2 (MMR, 2018b, Eq. II in Solution 3, on page 293).

Table 3.2. *Specific Arithmetical System-Arrangement*
(SASA II)

1	2	+	22	=	24
2	22	+	222	=	244
3	**222**	**+**	**2222**	**=**	**2444**
4	2222	+	22222	=	24444
	…				

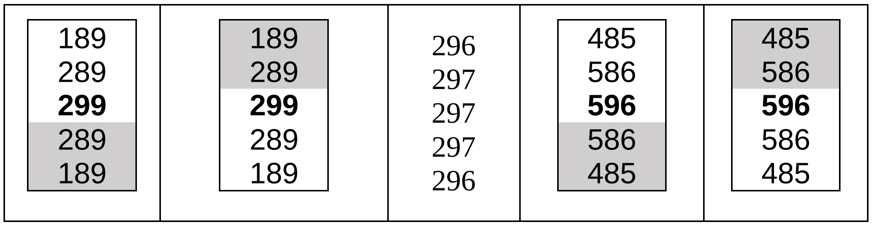
For the explanation see Legend of Table 3.1.

Table 4. *Arithmetic system corresponding (in the shaded part) with the mass of 20 amino acid molecules*

2 x (007 x 007) = 98	1 x (1070 + 1070) = 2140	+ 2042	280	
2 x (017 x 017) = 578	1 x (1170 + 1170) = 2340	+ 1762	680	400
2 x (027 x 027) = 1458	1 x (1270 + 1270) = 2540	+ 1082	1080	400
2 x (037 x 037) = **2738**	1 x (1370 + 1370) = 2740	+ 2	1480	400
2 x (047 x 047) = 4418	1 x (1470 + 1470) = 2940	- 1478	1880	400
2 x (057 x 057) = 6498	1 x (1570 + 1570) = 3140	- 3358	2280	400
2 x (067 x 067) = 8978	1 x (1670 + 1670) = 3340	- 5638		
. . .				

The optimal number "2738" corresponds to the mass of 20 amino acid molecules (according to Table 1). Hence the optimality of (prebiotic) selection of 20 protein AAs of standard GC. The difference in relation to the experimental value of only 0.04 is negligible, and is within the limit of experimental error. Nevertheless, the honor goes to the experimenters who determined the atomic masses of the chemical elements that make up amino acid molecules.

Figures



189	189	296	485	485
289	289	297	586	586
299	**299**	297	**596**	**596**
289	289	297	586	586
189	189	296	485	485

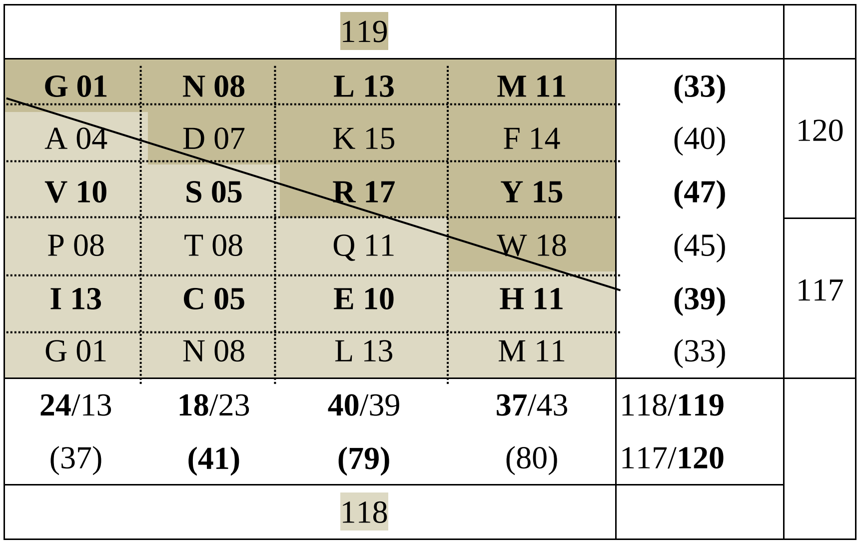
Figure 1. The mirror symmetry of the quantities contained in Table 1. In the middle area there are the differences of the quantities of molecules mass and the number of nucleons per row, respectively. These differences simultaneously correspond to the quantities of the number of atoms in 61 amino acid molecules within the standard Genetic Code Table (GCT), from the aspect of pyrimidine-purine distinctions: on the left pyrimidine half 32 amino acid molecules have 296 atoms and on the right purine half 29 amino acid molecules have 298 atoms; which means that the mean value of the left and right sides is 297.

(0)	(1)	(2)	(3)	(4)	(5)	(6)
00	*02*	04	06	08	10	12
11	*13*	15	17	19	21	23
22	*24*	26	28	30	32	34
11	*16*	21	26	31	36	41
00	*05*	10	15	20	25	30
44	**60**	**76**	**92**	**108**	**124**	**140**
	12	14	16	18	***20***	22
	23	25	27	29	***31***	33
	34	36	38	40	***42***	44
	41	46	51	56	***61***	66
	30	35	40	45	***50***	55
	140	**156**	**172**	**188**	**204**	**220**
	22	24	26	28	*30*	*32*
	33	35	37	39	*41*	*43*
	44	46	48	50	*52*	*54*
	66	71	76	81	*86*	*91*
	55	60	65	70	*75*	*80*
	220	**236**	**252**	**268**	**284**	**300**
	…					

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

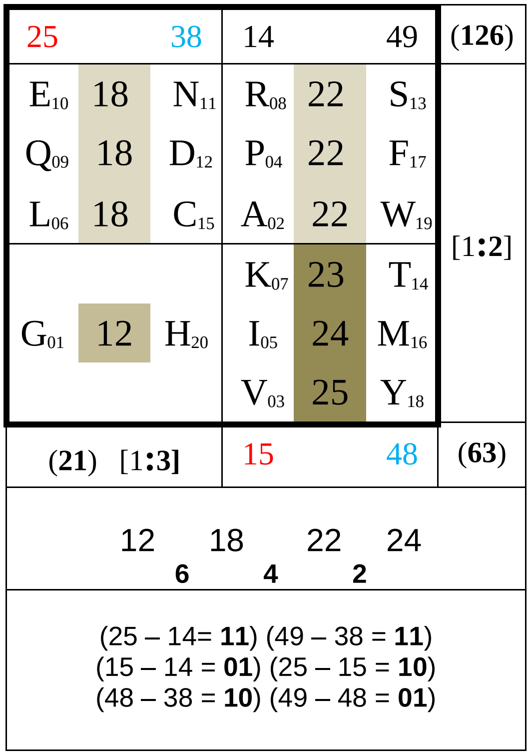
(220 + 284 = **504**) (204 + 300 = **504**)

Figure 2. "The arrangement represents the Table of distinct 2-5 adding (TDA) with starting column 00- 11-22-11-00 which follows from PSN (Periodic system of numbers: Figure A1) in decimal number system by overlapping the real sequence of doubled the first possible triangle in Boolean space (0-1-2) with its mirror image through compression and superposition at the point ‘22’. In the 10th step we have a realization of the sequence (20-31-42-61-50), the same with the number of atoms in five AAs classes … as it is here presented: all five results in the 10th step are mirror image of the first step." (MMR, 2019, Table A3, p. 30).



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**	
118					

Figure 3. <u>The unity of chemism and semiosis</u> (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. (Cf. footnote 6).]



25		38	14		49	**(126)**
E_{10}	18	N_{11}	R_{08}	22	S_{13}	[1**:2**]
Q_{09}	18	D_{12}	P_{04}	22	F_{17}	
L_{06}	18	C_{15}	A_{02}	22	W_{19}	
			K_{07}	23	T_{14}	
G_{01}	12	H_{20}	I_{05}	24	M_{16}	
			V_{03}	25	Y_{18}	
(21) [1**:3]**			15		48	**(63)**

12 **6** 18 **4** 22 **2** 24

(25 – 14= **11**) (49 – 38 = **11**)
(15 – 14 = **01**) (25 – 15 = **10**)
(48 – 38 = **10**) (49 – 48 = **01**)

Figure 4. The unity of chemism and semiosis (IV): "This arrangement of AAs follows from the [logic: first with last and so on]. … The expression of the principle of balancing and nuancing, through the interconnection of the chemical properties of AAs, the number of atoms and the ordinal number of AAs … is self-evident. Confirmation of V. Shcherbak's hypothesis (1994) on the analogy of the amino acid (genetic) code with quantum physics also" (MMR, 2019, Figure 4, p. 22). [*Note 1*: Distances 6–4–2 correspond to the distribution of the number of atoms in 20 AAs as follows. As the number of atoms in the side amino acid chain, the 6 numbers appear once (G-1, A-4, D-7, F-14, R-17, W-18); 4 numbers appear twice (S-5, C-5, V-10, E-10, I-13, L-13, K-15, Y-15); and 2 numbers appear three times (N-8, P-8, T-8, M-11, Q-11, H-11). Hence, follows this pattern: 6_1 – 4_2 – 2_3 which says the following: six numbers appear once; four numbers appear twice; and two numbers appear three times (MMR, 2018b, Table 4, p. 295). *Note 2*: If we multiply the basic number and the number in the index, we get a new pattern: 6-8-6. If we read this pattern as a three-digit number in the decimal number system (686), then in the case of GC that number can refer to the number of protons, because there are just as many of them in 20 AAs, in their side chains. All together, we can perhaps say (in the future, with a possible positive outcome of the prediction), that not only the principle of self-similarity is at work here, but also the principle of semiosis. For proton number and corresponding data, see in: MMR, 2011, Table 7, p. 830).]

Surveys

Survey 1. *The relationships of quantities contained in Table 2*

(042 + 300 = **342**) (*220* + *222* = ***442***) [*442* – 342 = **100**]

(*220* + *284* = *504*) (300 + $\boxed{204}$ = 504)[a]

(504 – 342 = $\underline{\mathbf{1}}$62) (504 – *442* = $\underline{\mathbf{0}}$62)[b]

[162 + 062 = 8 x 28][c] [162 = 666 – 504] [162 = 2 x 81][d]

100: 162 = 0.617 … ≈ 0.618 … (Golden mean)

342 + 442 = **784** **784** = 28 x 28 **384** = 204 + 180 (300 + (2 x 042) = **384)**[e] **384** = 496 – (4 x 28)	(222 = 284 – $\underline{\mathbf{0}}$62)[b] 042 = 204 – $\underline{\mathbf{1}}$62 0.62 ≈ 0.618 … 1.62 ≈ 1.618 …

[a] The four quantities contained in the logical square in Figure 2; two of them are also in Table 2, and other two are indirectly present through a relation with the golden mean. [b] Mediation by golden mean. [c] Mediation with the Golden mean and athe second perfect number, the number 28. [d] The quantities (81 versus 123) as the number of atoms in two classes of AAs, classified according to two classes of the enzymes aminoacyl-tRNA synthetases. [MMR, 2004, Fig. 1, p. 222: "Notice that '81' (as 9 x 9) is the first possible (zeroth) arithmetic square in module 9, and 0-1-2-3 is the first possible (zeroth) logical square (as 00-01-10-11)."] [About the said two classes of AAs one can see in (MMR, 1997a).] [e] The quantity 384 as the total number of atoms in 20 standard protein amino acids (204 in "bodies" and 180 in "heads") is also found in Plato's Timaeus as the main result of the "harmonization" of geometric progression (MMR, 2011, Table A.2., p. 839).

Survey 2. *Golden mean, expressed in different number systems,*
in relation to the quantities in Tables 2 and 3

<table>
<tr><td>Sum of (I)</td><td>Golden mean</td><td rowspan="4"></td><td rowspan="2">504 – 162 = 342
504 – 062 = 442</td></tr>
<tr><td>…
$(770)_8$
$(504)_{10}$</td><td>$(1.474\ \ldots)_8$
$(1.618\ \ldots)_{10}$</td></tr>
<tr><td>$(1F8)_{16}$
…</td><td>$(1.9E3\ \ldots)_{16}$</td><td rowspan="2">342 = 300 + 042
442 = 220 + 222</td></tr>
<tr><td colspan="2">"I" → The first friendly pair of numb.</td></tr>
<tr><td colspan="4"></td></tr>
<tr><td colspan="2">222 + 042 = 264
220 + 300 = 264 + **256**
384 = 256 + ½ 256</td><td colspan="2">256 = 16 x 16
256 = 8 x 32
264 = 8 x 33
297 = 9 x 33
330 = 10 x 33</td></tr>
</table>

For the three equations listed in Remark 3 (very bottom, right), the arithmetical template can be also found as in (MMR, 2018a, Survey 2, positions 8, 9 and 10) or in (MMR, 2021a, Table C10, with corrected cipher errors in line 3 and 27).