Genetic code as a semiotic system (Vers. 1)

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

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.
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Pergamon Press Ltd.

A UNIFYING CONCEPT FOR THE AMINO ACID CODE

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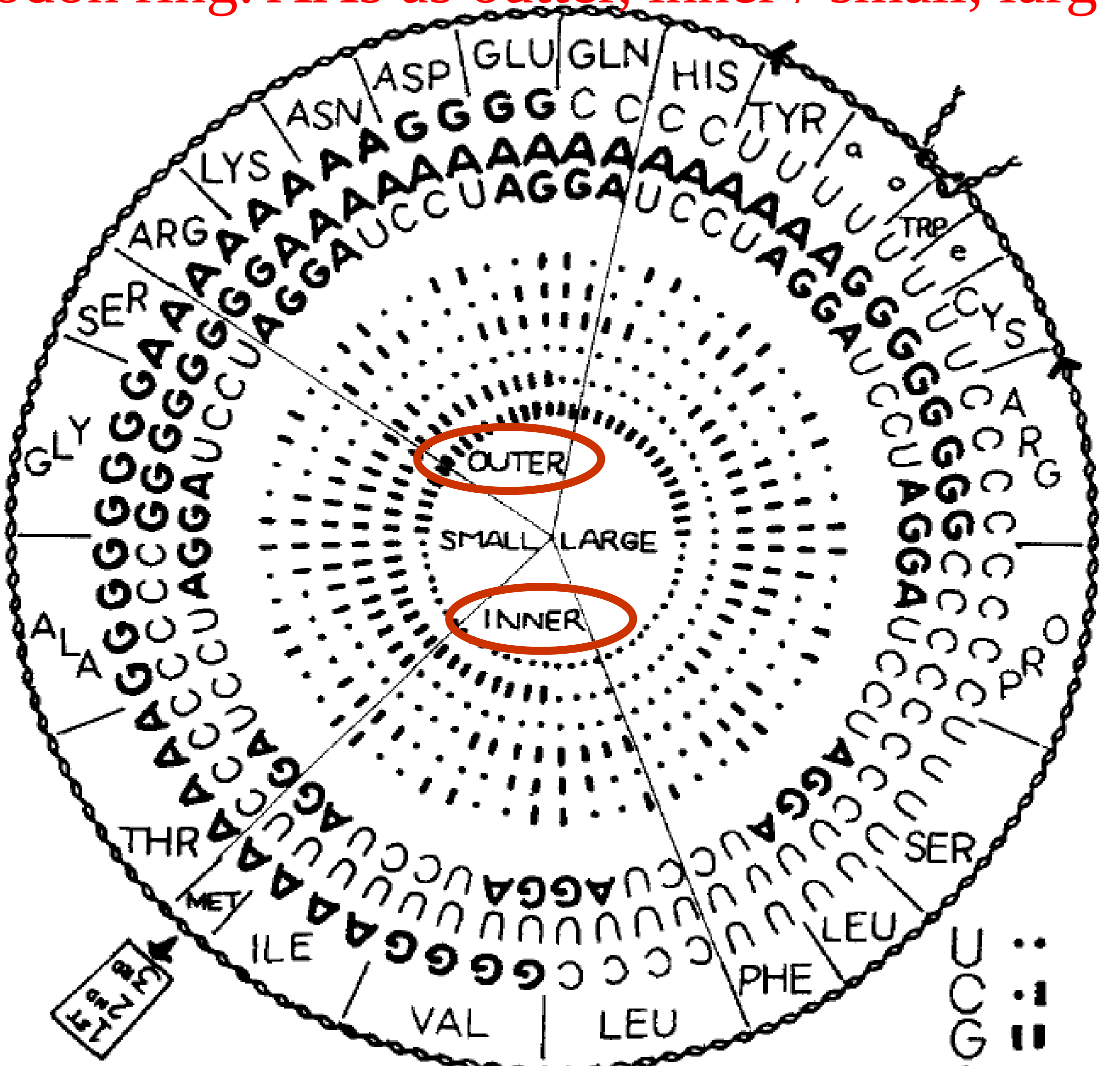
The structure of the genetic code is related to a Gray code, which is a plausible theoretical model for an amino acid code. The proposed model implies that the most important

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

Determination by the Golden Mean

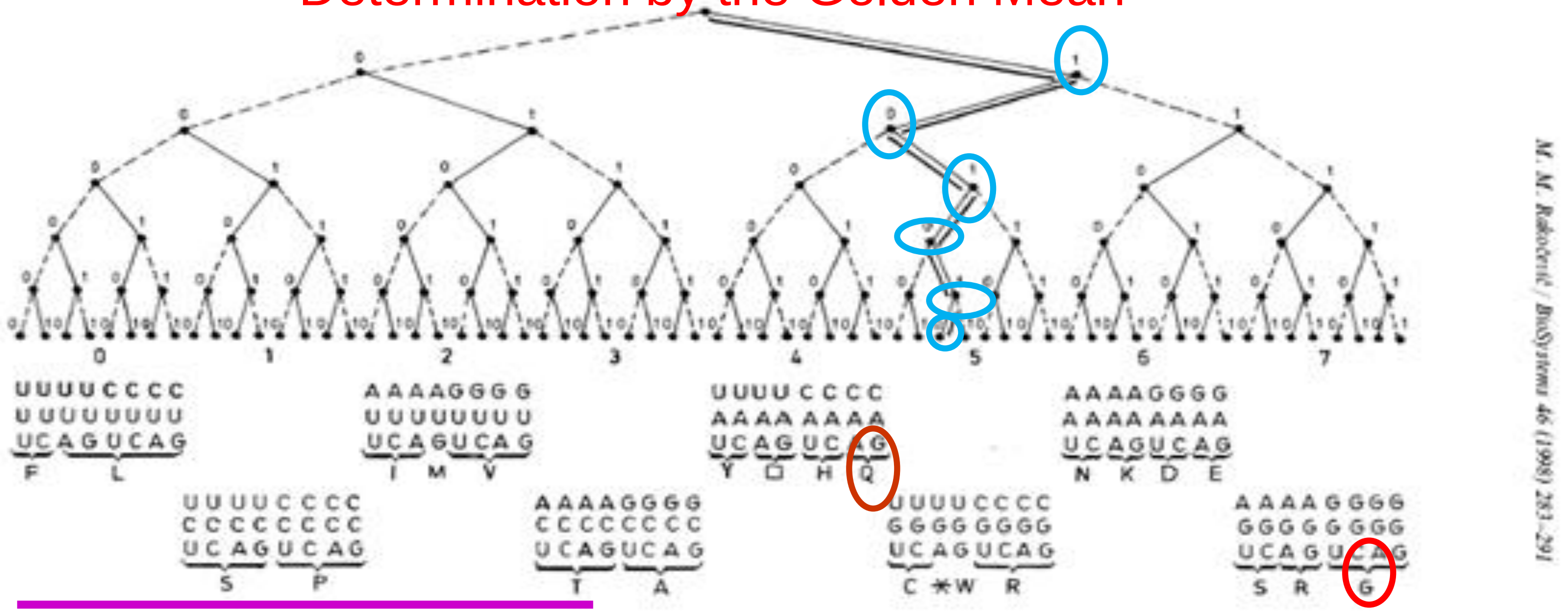


Fig. 1. Genetic code as a binary-code tree. The full lines: the routes of the greater (faster) changes from pyrimidine to purine or from two to three hydrogen bonds and vice versa. The dotted lines: the routes of the less (slower) changes. The double full line: the route of the maximum possible (fastest) 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

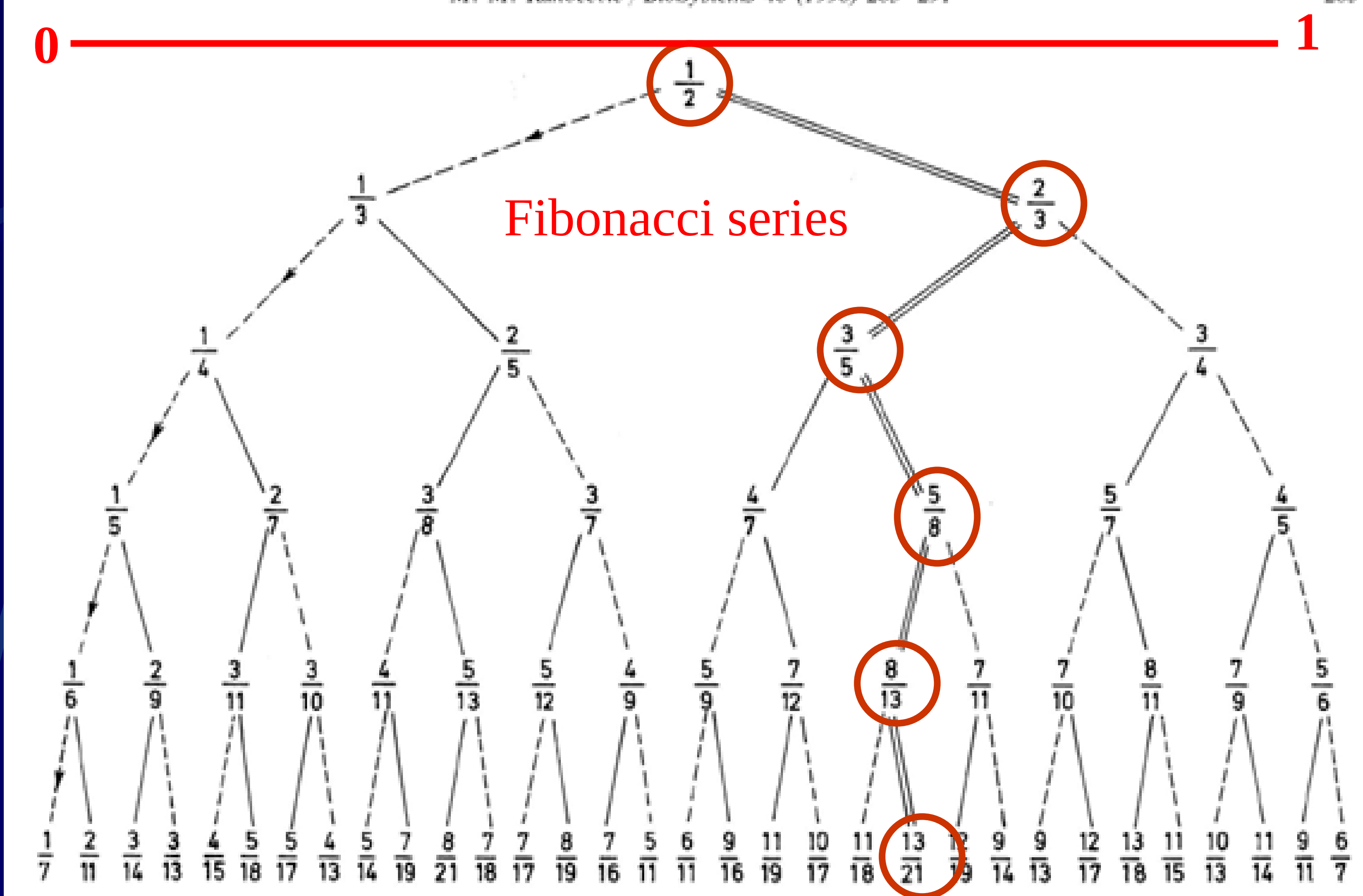


Fig. 2. The Farey binary-code tree as a representation of rational numbers relationships within the interval (0, 1). The full lines: the

Leibnitz's interpretation of binary system

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

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

x Clarke 1899

1900 *March* — 1900 март

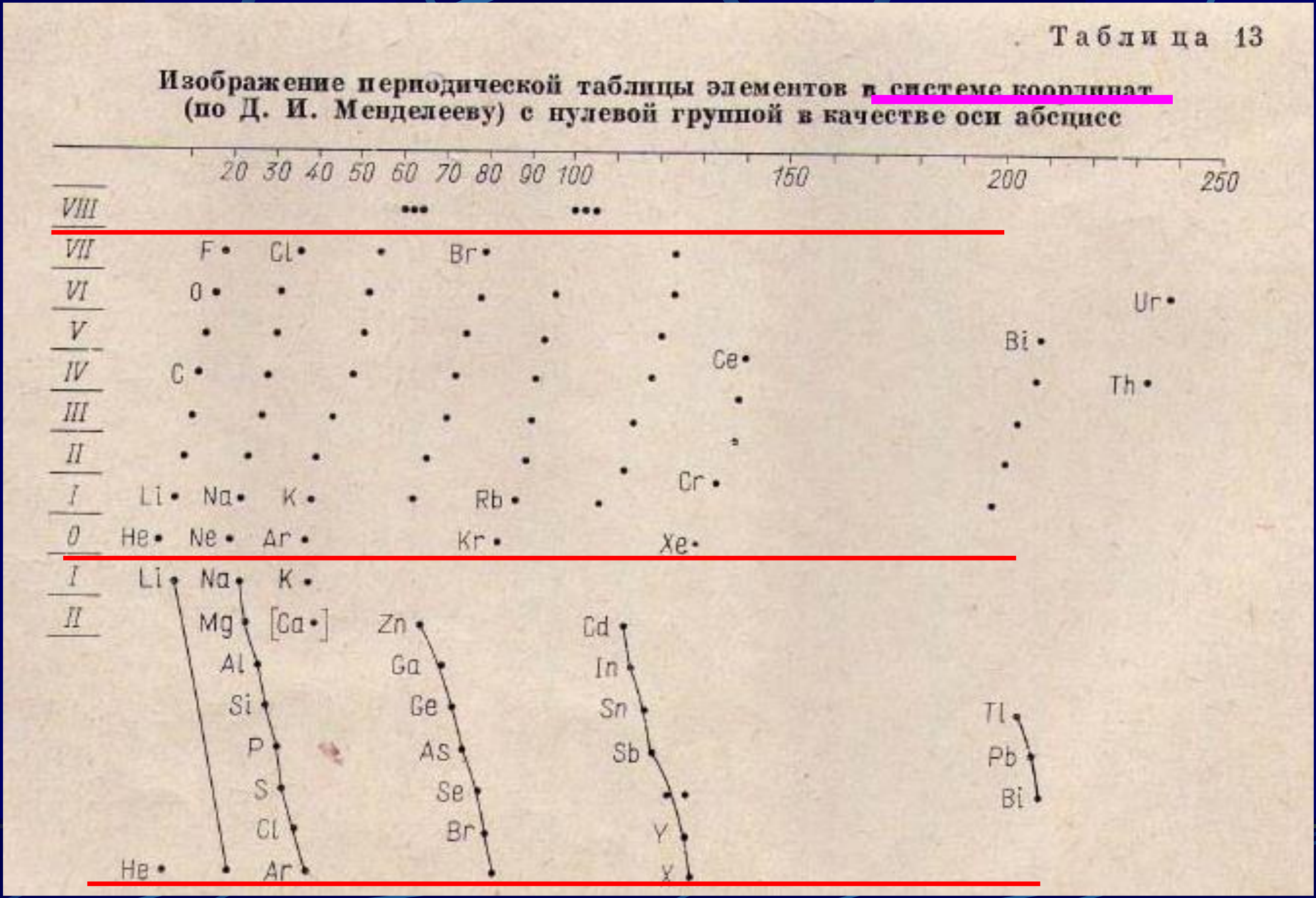
	H=1,008 x																
He=4	Li=7,03 x	Be=9,1 x	B=11,0 x	C=12,00 x											N=14,04 x	O=16	F=19,05 x
Ne=20	Na=23,05 x	Mg=24,36 x24,3	Al=27,0 x27,1	Si=28,4 x											P=31,0 x	S=32,06 x32,07	Cl=35,45 x
A=38	K=39,14 39,11 x	Ca=40,1 x	Sc=44,0 x44,1	Ti=48,2 x48,15	V=51,4 x	Cr=52,1 , x	Mn=55,0 x	Fe÷56,0 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=112,2 112,4 x	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=1[illegible],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

Noble gases in the zeroth and VIII group



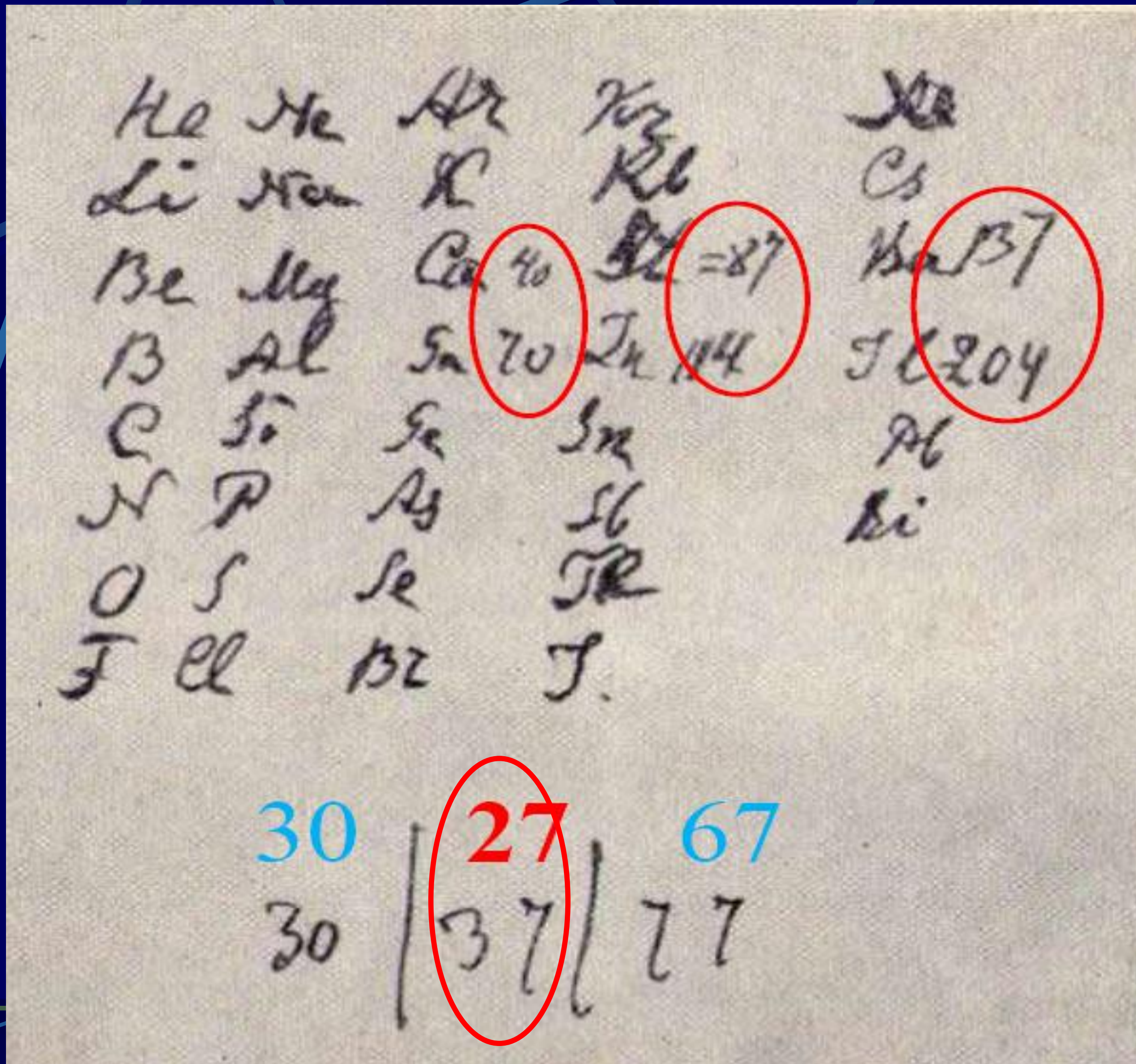
"Periodic system of elements by groups and rows"

Періодическая система элементовъ по группамъ и рядамъ.

Ряды.	ГРУППЫ ЭЛЕМЕНТОВЪ: 0	I	II	III	IV	V	VI	VII	VIII
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 окисы:	R	R^2O	RO	R^2O^3	RO^2	R^2O^5	RO^3	R^2O^7	RO^4
Высшія газообразныя водородныя соединенія:					RH^4	RH^3	RH^2	RH	

Д. Менделѣевъ.
1869 — 1905.

Mendeleev's „error", which it is not



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**

51

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

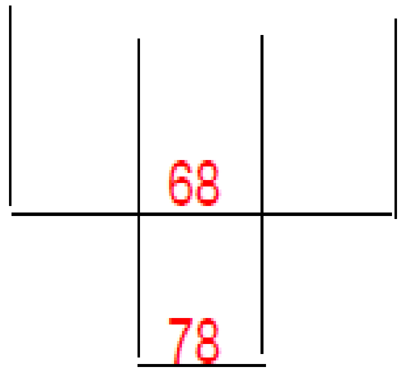
GPVI + **DENQ** = 68±0

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

(Cf. Tab. A2)

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	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 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}		G_{01} A_{04} N_{08} D_{07} → 20
A_{04}	D_{07}		+11
V_{10}	S_{05}		V_{10} P_{08} S_{05} T_{08} → 31
P_{08}	T_{08}		+11
I_{13}	C_{05}		I_{13} L_{13} C_{05} M_{11} → 42
L_{13}	M_{11}		
K_{15}	F_{14}		K_{15} R_{17} F_{14} Y_{15} → 61
R_{17}	Y_{15}		-11
Q_{11}	W_{18}		Q_{11} E_{10} W_{18} H_{11} → 50
E_{10}	H_{11}		
102 51 ± 0**1**	102 51 ± 0**1**		(102 + **1**0) / (102 – **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

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

496 as third PN

(~~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		000		000
11	+ 2	=	13		31	11		011		110
22	+ 2	=	24	→	42	22	→	022	→	220
11	+ 5	=	16		61	11		011		110
00	+ 5	=	05		50	00		000		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					**645** | 546			
554 – 10 = 544)[1]					546 + 10 = 556)[2]			

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

Odd / Odd

(50 = **51** – 1)

GVIKQ 25+**<u>50</u>**+139 = 214 / NSCFW 75+**<u>50</u>**+191 = 316 → **530**

Last / First

LKRQE 40+66+207 = 313 / NDSTC 65+33+129 = 227 → **540**

↑

First / Last 550

↓

GAVPI 15+36+91 = 142 / MFYWH 90+69+259 = 418 → **560**

Even / Even

(52 = **51** + 1)

APLRE 30+**<u>52</u>**+159 = 241 / DTMYH 80+**<u>52</u>**+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			
$A_{04}L_{13}$	$K_{15}R_{17}$	$F_{14}Y_{15}$	$D_{07}N_{08}$	$E_{10}Q_{11}$	$H_{11}W_{18}$	$S_{05}C_{05}$	$T_{08}M_{11}$	$G_{01}V_{10}$	$P_{08}I_{13}$	→	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	$S_{05}C_{05}$	$T_{08}M_{11}$	$G_{01}V_{10}$	10	→	122	82
											11	11
1	$K_{15}R_{17}$	$F_{14}Y_{15}$	4	$E_{10}Q_{11}$	6	7	$T_{08}M_{11}$	$G_{01}V_{10}$	$P_{08}I_{13}$	→	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	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	26 = 26	37 = 37
15 + 05 = 20	26 + 16 = 42	37 + 27 = 64
20 + 06 = 26	42 + 17 = 59	64 + 28 = 92
26 + 07 = 33	59 + 18 = 77	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 U	2nd letter C	2nd letter A	2nd letter G	3rd lett.
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 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*

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

(n) 4V+1M+3I+4A+**2L**+**4L**+**2F**+2C = 22 molecules

40+ 11+39+16+26 + 52 +28+10 = 2**2**2 atoms (42**0**)

(o) 4V+1M+3I+4A+**2Y**+**4R**+**1W**+2C = 21 molecules

40+ 11+39+16+ 30 + 68 +18+ 10 = 2**3**2 atoms (42**1**)

(p) 4G+2K+2N+4P+**2Y**+**4R**+**1W**+2E+2D+4T+2R+2S+2Q+2H+4S = 39

04+30+16+32+30 + 68+ 18+ 20 +14+ 32+ 34+10+22+22 + 20 = 3**7**2 (72**3**)

(i) 4G+2K+2N+4P+**2L**+**4L**+**2F**+2E+2D+4T+2R+2S+2Q+2H+4S = 40

04+30+16+32+26+52 + 28+20+ 14+32+ 34 +10+22+ 22+ 20 = 3**6**2 (72**2**)

"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	**S II**	*U*
	AUC	**Ile I**	**ACC**		AAC	**N II**	AGC		*C*
	AUA		**ACA**	**T II**	AAA		AGA	**R I**	*A*
	AUG	**M I**	**ACG**		AAG	**K II**	AGG		*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 (86) 32	$F_2S_4P_4T_4A_4H_2N_2K_2D_2S_2G_4$ 32 (224) 32
	08 16
(o) FLLSDESRG 09 (85) 24	$F_2L_2L_4S_4D_2E_2S_2R_2G_4$ 24 (208) 24
(I) LLIMVYQECWRR 12 (153) 29	$L_2L_4I_3M_1V_4Y_2Q_2E_2C_2W_1R_4R_2$ 29 (370) 29
	08 16
(i) IMVPTAYHQNKCWR 14 (154) 37	$I_3M_1V_4P_4T_4A_4Y_2H_2Q_2N_2K_2C_2W_1R_4$ 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 [(<u>1</u> x 68) + (<u>2</u> 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	**4**	5
(1 + 5 = 6) (2 + 3 = 5)				
2	3	4	**5**	6
(2 + 6 = 8) (3 + 4 = 7)				
3	4	5	**6**	7
(3 + 7 = 10) (4 + 5 = 9)				
4	**5**	**6**	**7**	**8**
(4 + 8 = 12) (5 + 6 = 11)				
5	6	7	**8**	9
(5 + 9 = 14) (6 + 7 = 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			$[12_8 = (2 \times 5)_{10}]$ $[14_8 = (24 : 2)_{10}]$						
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			$[12_{10} = (2 \times \underline{6})_{10}]$ $[14_{10} = (\underline{28} : 2)_{10}]$						
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			$[12_{12} = (2 \times 7)_{10}]$ $[14_{12} = (32 : 2)_{10}]$						
	...												

Plato's unique arithmetic existing in the genetic code

Harmonic mean (h)	Arithmetic mean (m)
$h = \frac{2ab}{a+b}$	$m = \frac{a+b}{2}$

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

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

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

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

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

384		432		486		512		576		648		729		768	
	48		54		26		64		72		81		39		(384)

The unity of chemistry type and the position

Py-Py
Py-Py

Py-Pu
Py-Pu

1st	2nd letter: U		C		A		G		3rd
U	UUU		UCU		UAU		UGU		U
	UUC	F II	UCC		UAC	Y I	UGC	C I	C
	UUA		UCA	S II	UAA		UGA		A
	UUG	L I	UCG		UAG	CT	UGG	CT 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	S II	U
	AUC	Ile I	ACC		AAC	N II	AGC		C
	AUA		ACA	T II	AAA		AGA	R I	A
	AUG	M I	ACG		AAG	K II	AGG		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

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)]

3. Slides explanations

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

[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

[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. ...

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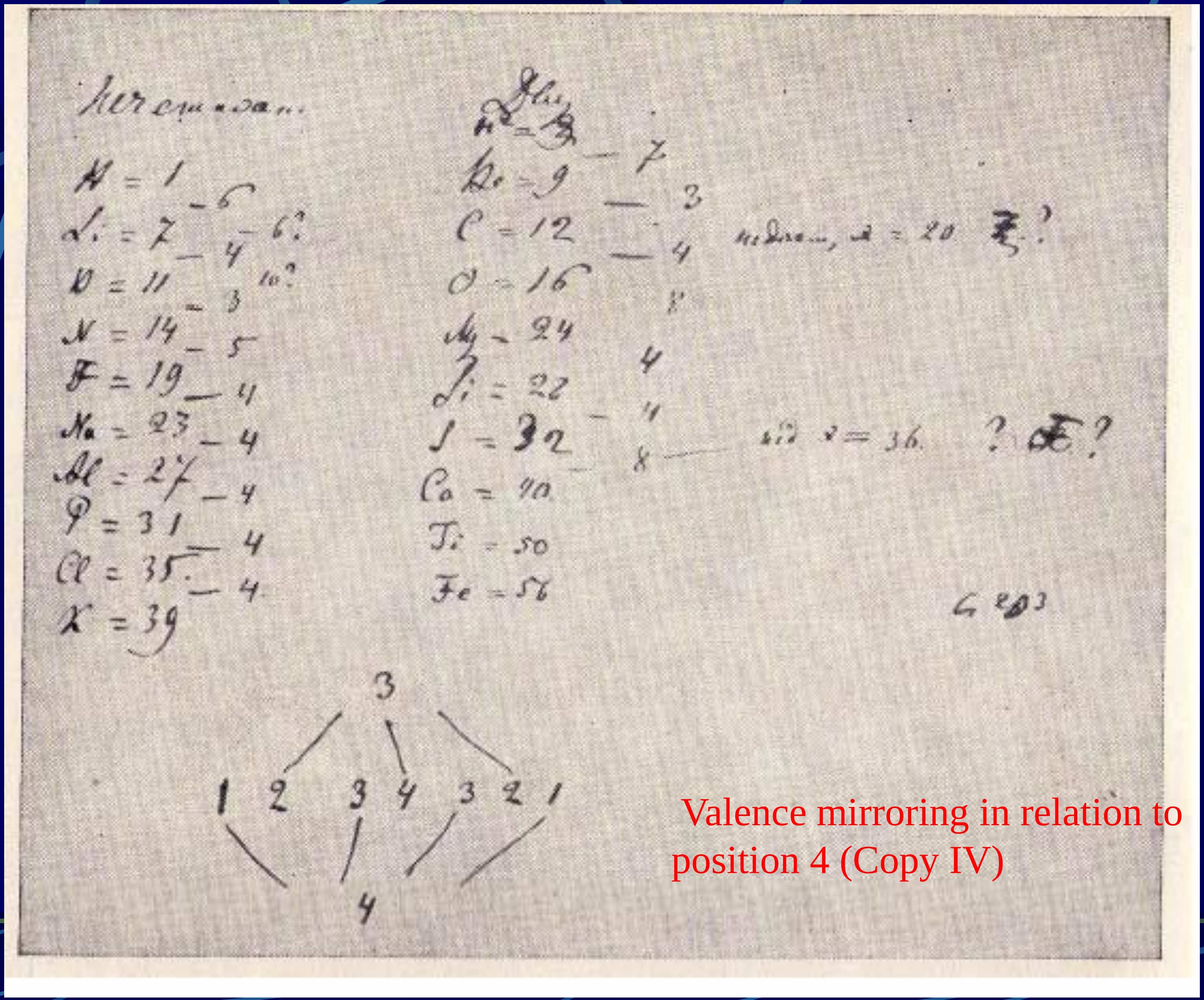
APPENDIX

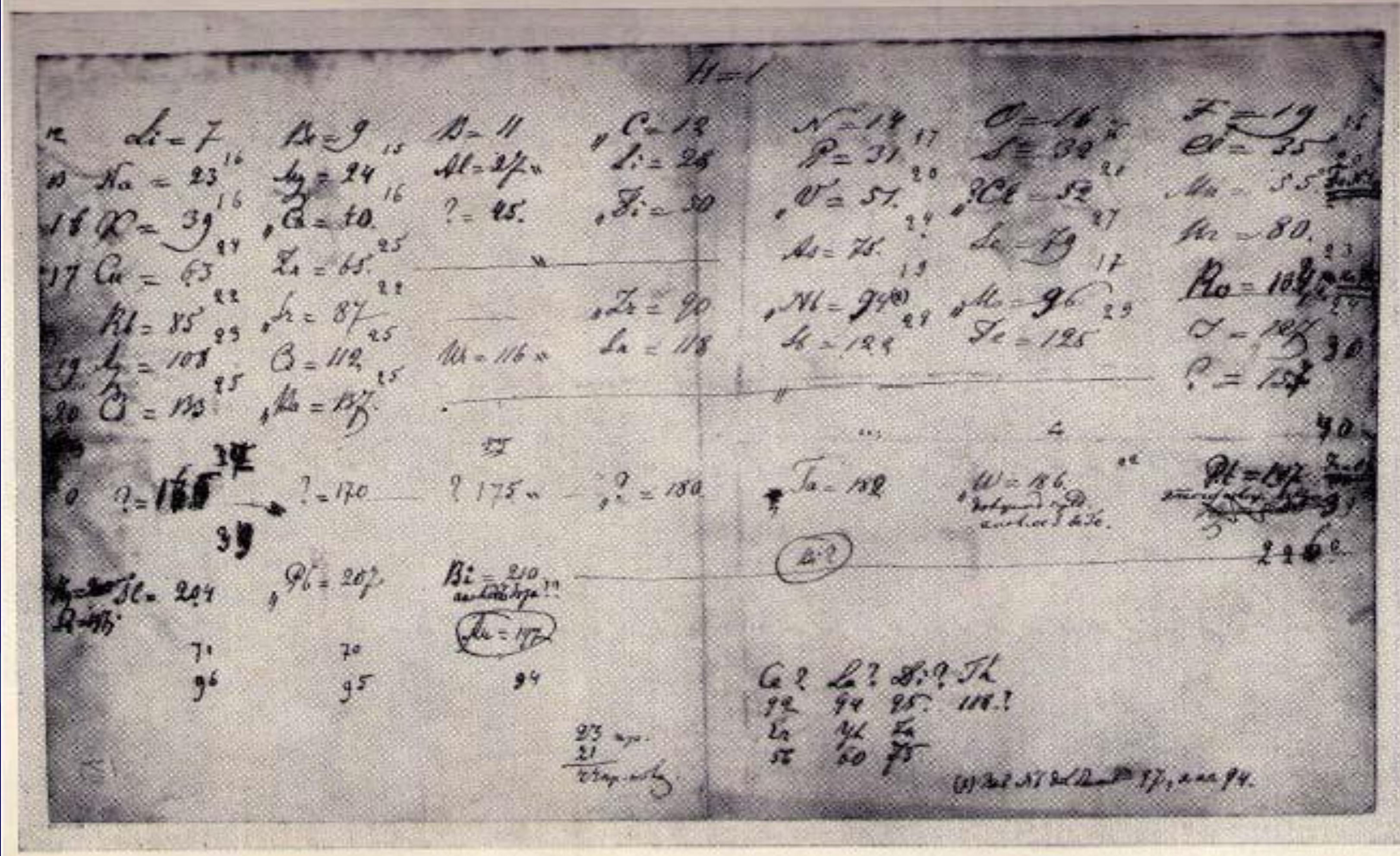
1. Appendix Slides presentation

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



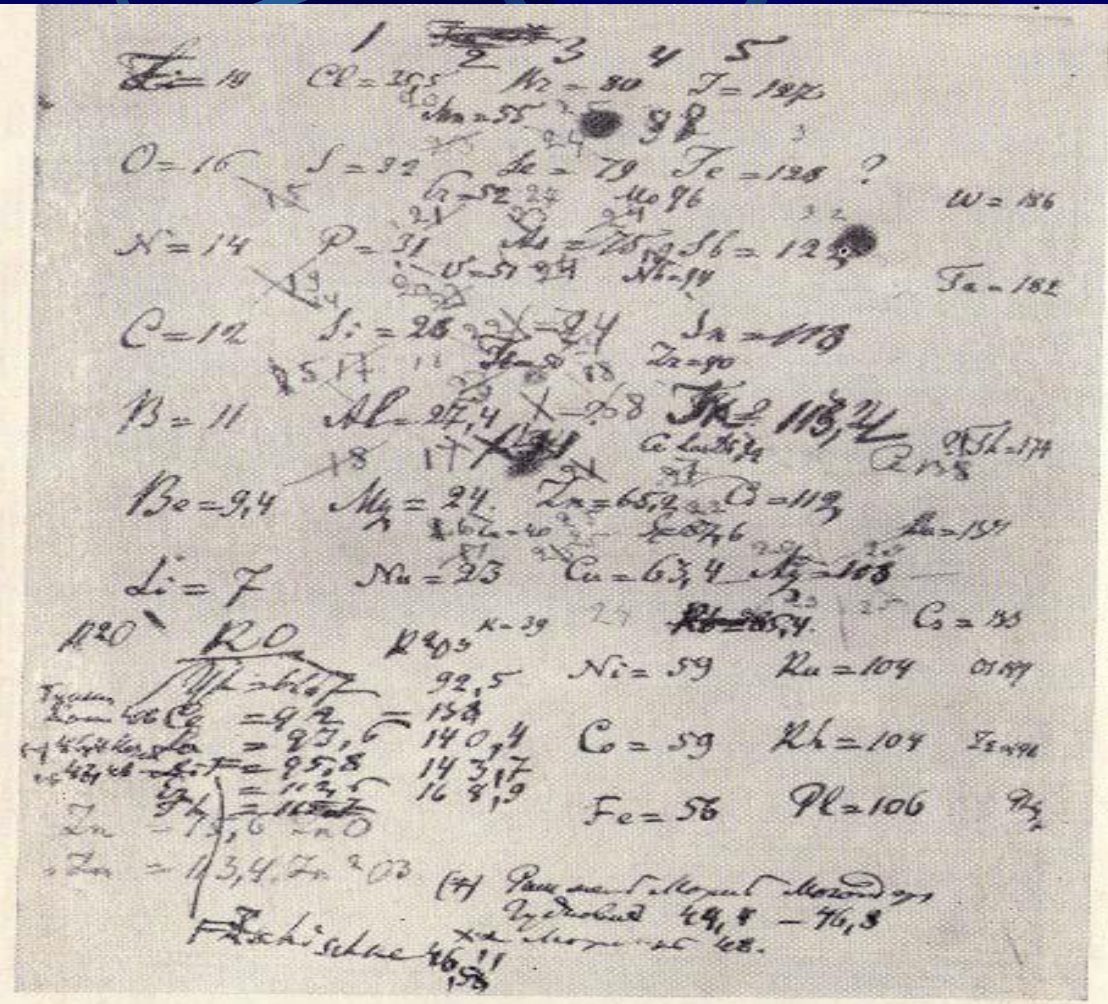
Valence mirroring in relation to position 4 (Copy IV)

Hydrogen on the right side of the Periodic System



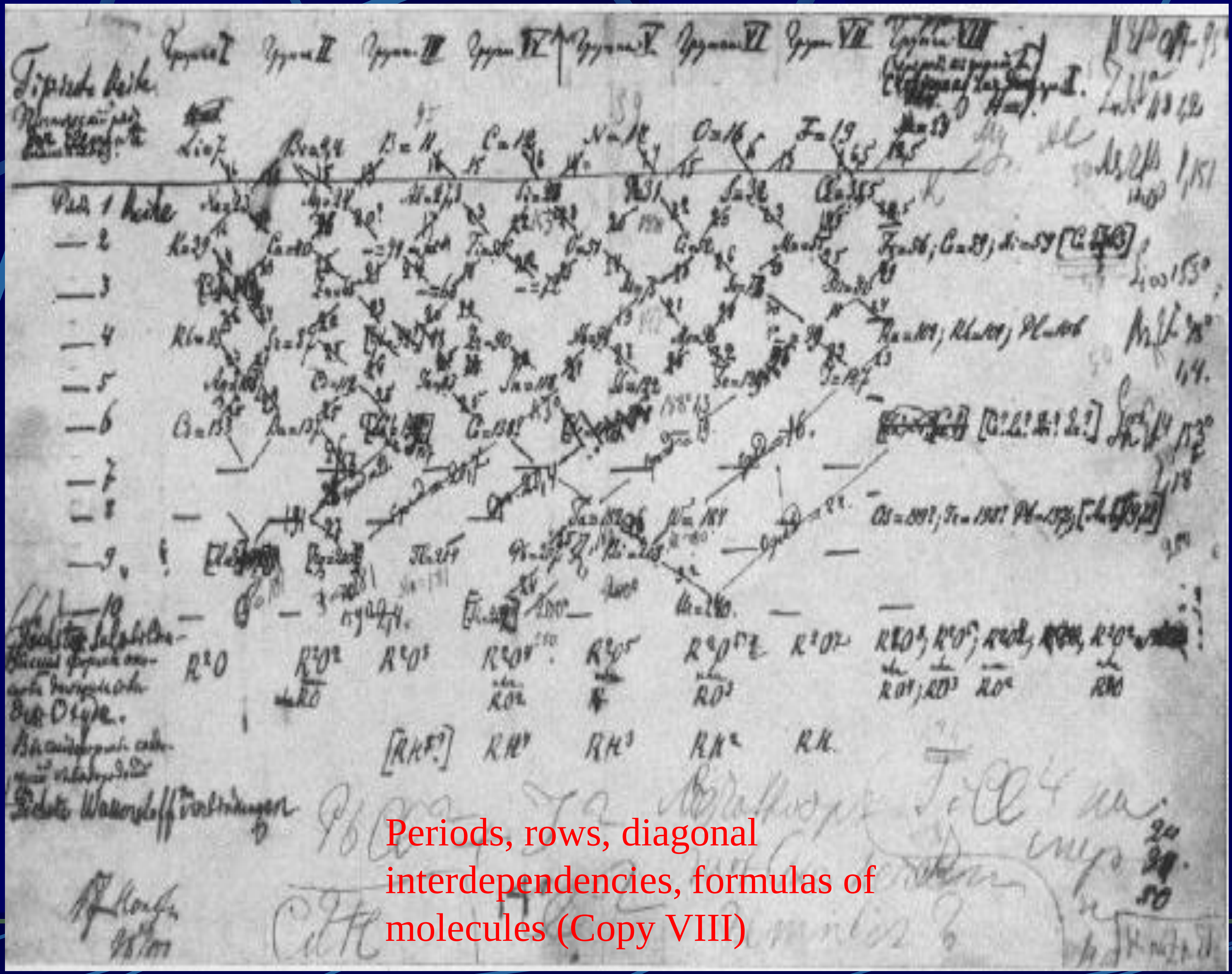
Фотокопия V. Первый вариант короткой таблицы элементов с подразделением рядов на чет-ные и нечетные. Февраль/март 1869 г.

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

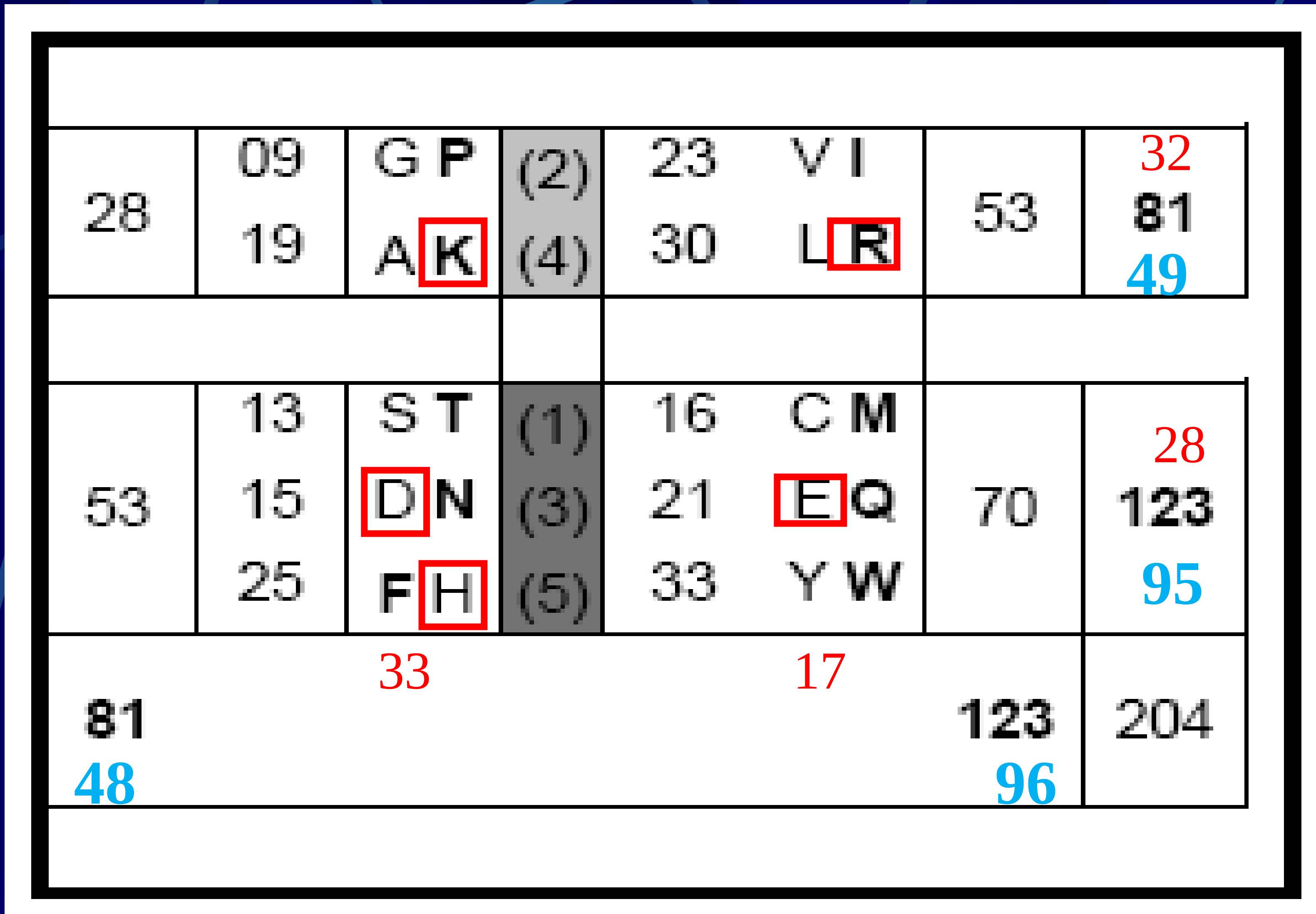


Фотокопия VI. Набросок короткой таблицы элементов с выявленным диагональным направлением. Лето или осень 1870 г.

The law of diagonal interdependence

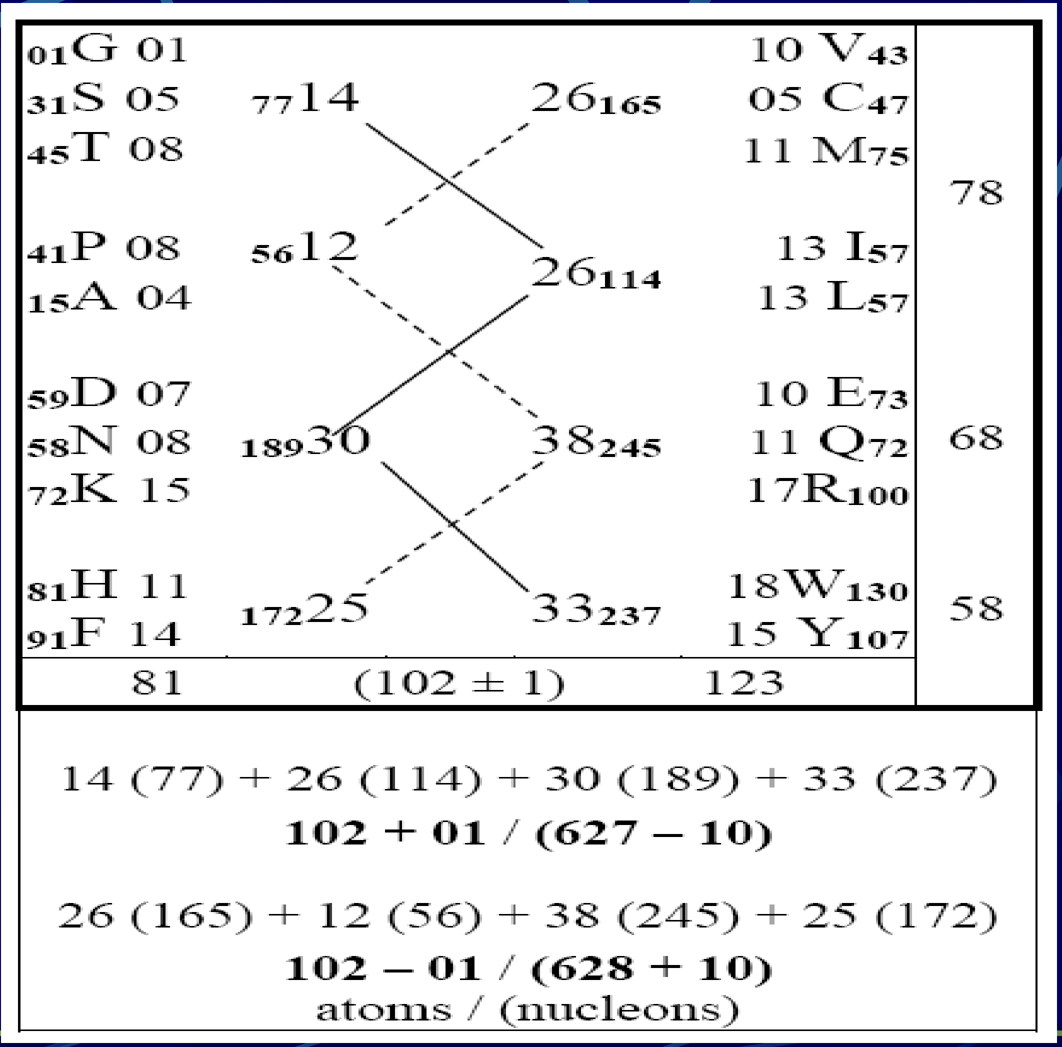


Periods, rows, diagonal interdependencies, formulas of molecules (Copy VIII)



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

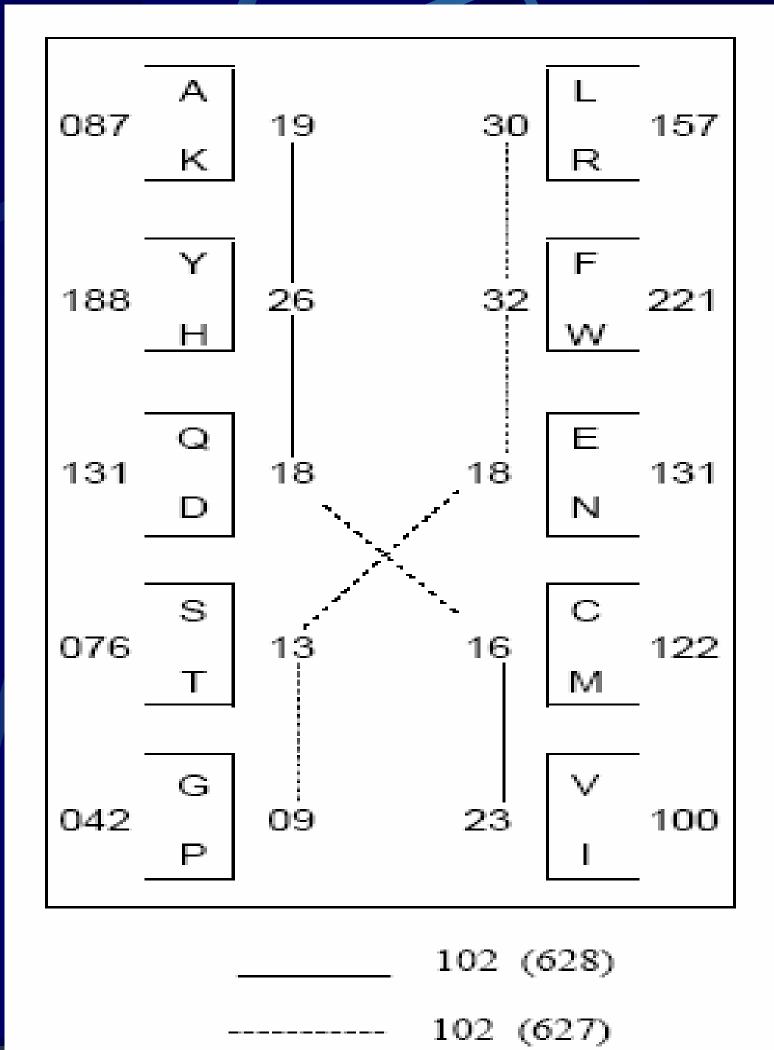
Two classes of amino acids related to two classes of synthetases

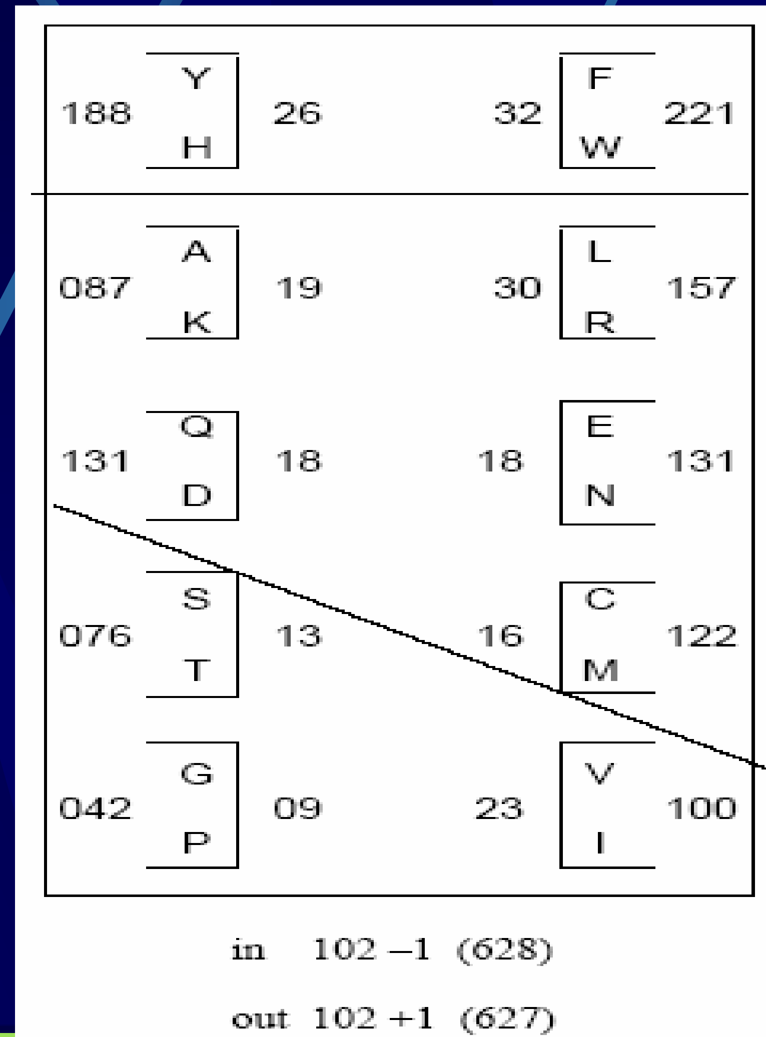


Rakočević, 1998a, Surv. 4, p. 290

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**	(119)	**89**	125
	116		108	
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**	(120)	**84**	114
	106		118	
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		39		48	
38	(10)	39	(00)	47	(01)
66		78		60+35	

<table>
<tr><th>a</th><th colspan="3">b</th><th>c</th><th></th><th>d</th><th>e</th><th>f</th></tr>
<tr><td>01</td><td>10</td><td>11</td><td>13</td><td>34</td><td></td><td>11 + [((1 x 1) + 5)] = 034:2</td><td>13 | 31</td><td>(2 x 9)</td></tr>
<tr><td>02</td><td>20</td><td>22</td><td>26</td><td>68</td><td></td><td>22 + [((2 x 2) + 8)] = 068:2</td><td></td><td></td></tr>
<tr><td>03</td><td>30</td><td>33</td><td>39</td><td>102</td><td></td><td>33 + [((3 x 3) + 9)] = 102:2</td><td>51</td><td></td></tr>
<tr><td>04</td><td>40</td><td>44</td><td>52</td><td>136</td><td></td><td>44 + [((4 x 4) + 8)] = 136:2</td><td></td><td></td></tr>
<tr><td>05</td><td>50</td><td>55</td><td>65</td><td>170</td><td></td><td>55 + [((5 x 5) + 5)] = 170:2</td><td></td><td></td></tr>
<tr><td>06</td><td>60</td><td>66</td><td>78</td><td>204</td><td></td><td>66 + [((6 x 6) ± 0)] = 204:2</td><td>78 | 87</td><td>(1 x 9)</td></tr>
<tr><td>07</td><td>70</td><td>77</td><td>91</td><td>238</td><td></td><td>77 + [((7 x 7) – 7)] = 238:2</td><td></td><td></td></tr>
<tr><td>08</td><td>80</td><td>88</td><td>104</td><td>272</td><td></td><td>88 + [((8 x 8) – 16)] = 272:2</td><td></td><td></td></tr>
<tr><td>09</td><td>90</td><td>99</td><td>117</td><td>306</td><td></td><td>99 + [((9 x 9) – 27)] = 306:2</td><td>117 | 711</td><td>594 (66 x 9)</td></tr>
<tr><td>0A</td><td>A0</td><td>AA</td><td>130</td><td>340</td><td></td><td>AA + [((10 x 10) – 40)] = 340:2</td><td colspan="2" rowspan="2">34 = 2 x 17
51 = 3 x 17</td></tr>
<tr><td>0B</td><td>B0</td><td>BB</td><td>143</td><td>374</td><td></td><td>BB + [((11 x 11) – 55)] = 374:2</td></tr>
<tr><td colspan="6">34 + 374 = 2 x 204
68 + 340 = 2 x 204</td><td>102 + 306 = 2 x 204
136 + 272 = 2 x 204
170 + 238 = 2 x 204</td><td colspan="2">374 = 2 x 187
187 + 197 = 384</td></tr>
</table>

5 8 9 8 5 0 7 16 27 40 55	→	180	264
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	022
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 = 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	Tc	(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>|4 |8| 16| → 1 x 496 (28)
10^2 10^1 10^0

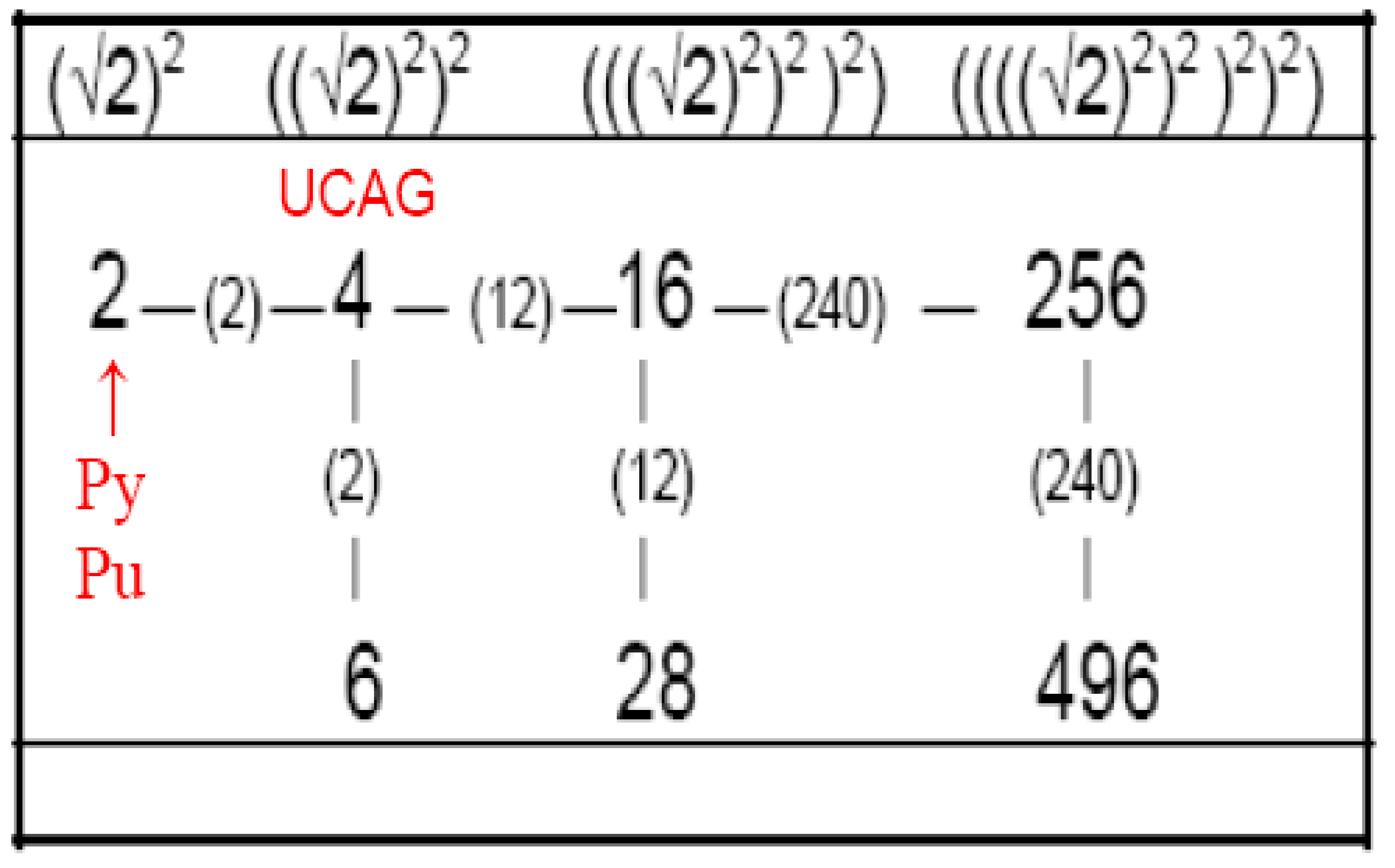
|8| 16 | 32| → 2 x 496 (28)
| 16 | 32| 64| → 4 x 496 (28)</td>
</tr>
<tr>
<td>1 2 4 → 1 x 28
4^2 4^1 4^0

2 4 8 → 2 x 28
4^2 4^1 4^0</td>
<td>- - - - - - - - - - - - - - - -
- - - - - - - - - - - - - - - -

|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



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
(3)	5^3	125	
(4)	$\underline{7}^3$	343	496
(5)	9^3	729	
(6)	11^3	1331	
(7)	13^3	2197	
(8)	$\underline{15}^3$	3375	8128

$0 - 3 \longrightarrow 2^2$

$(1 + 2 + 3 = 06$

$0 - 7 \longrightarrow 2^3$

$(1 + 2 \ldots + 6 + 7 = 28$

$1 \rightarrow 3 = 6$

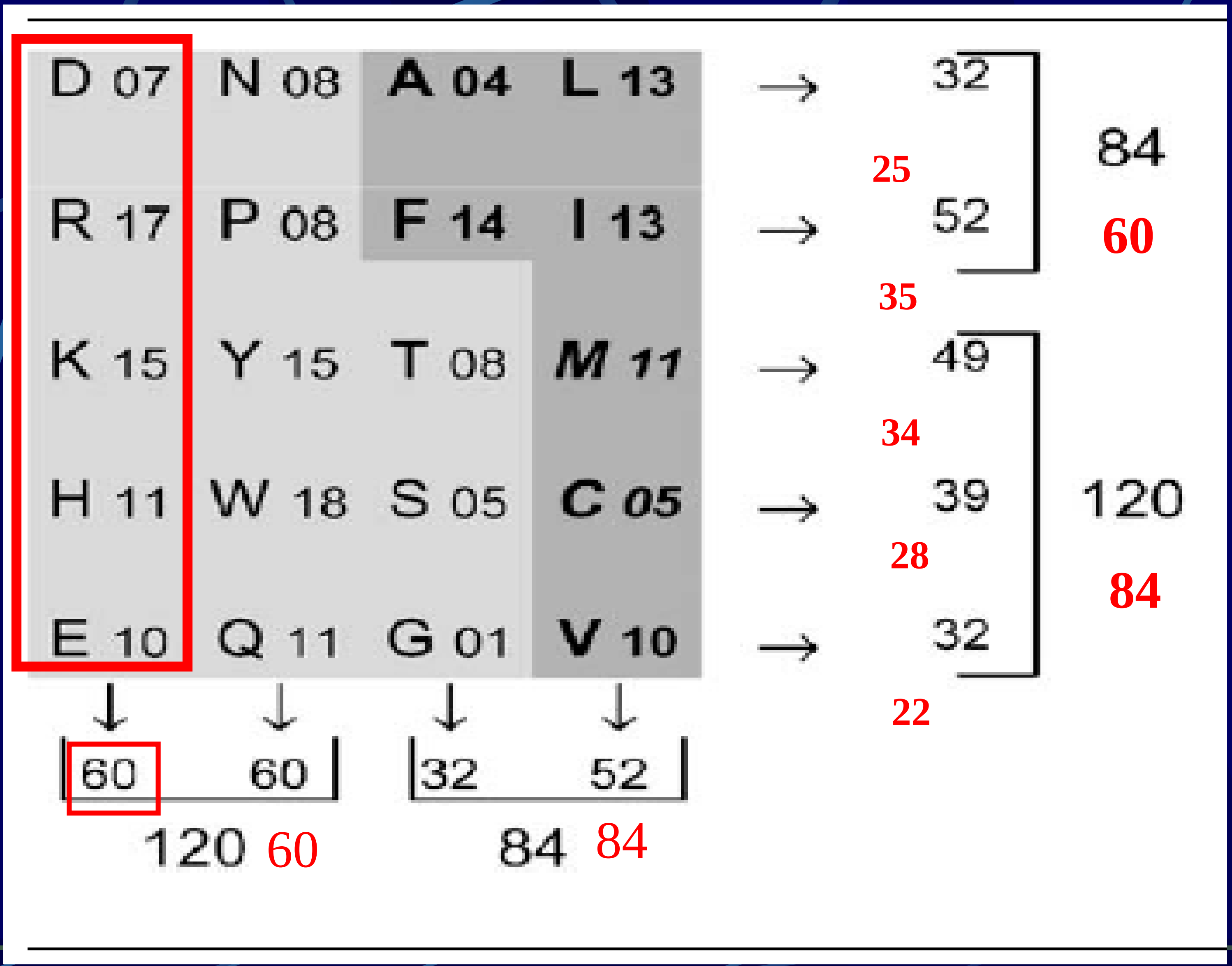
$1 \rightarrow 7 = 28$

$1 \rightarrow 31 = 496$

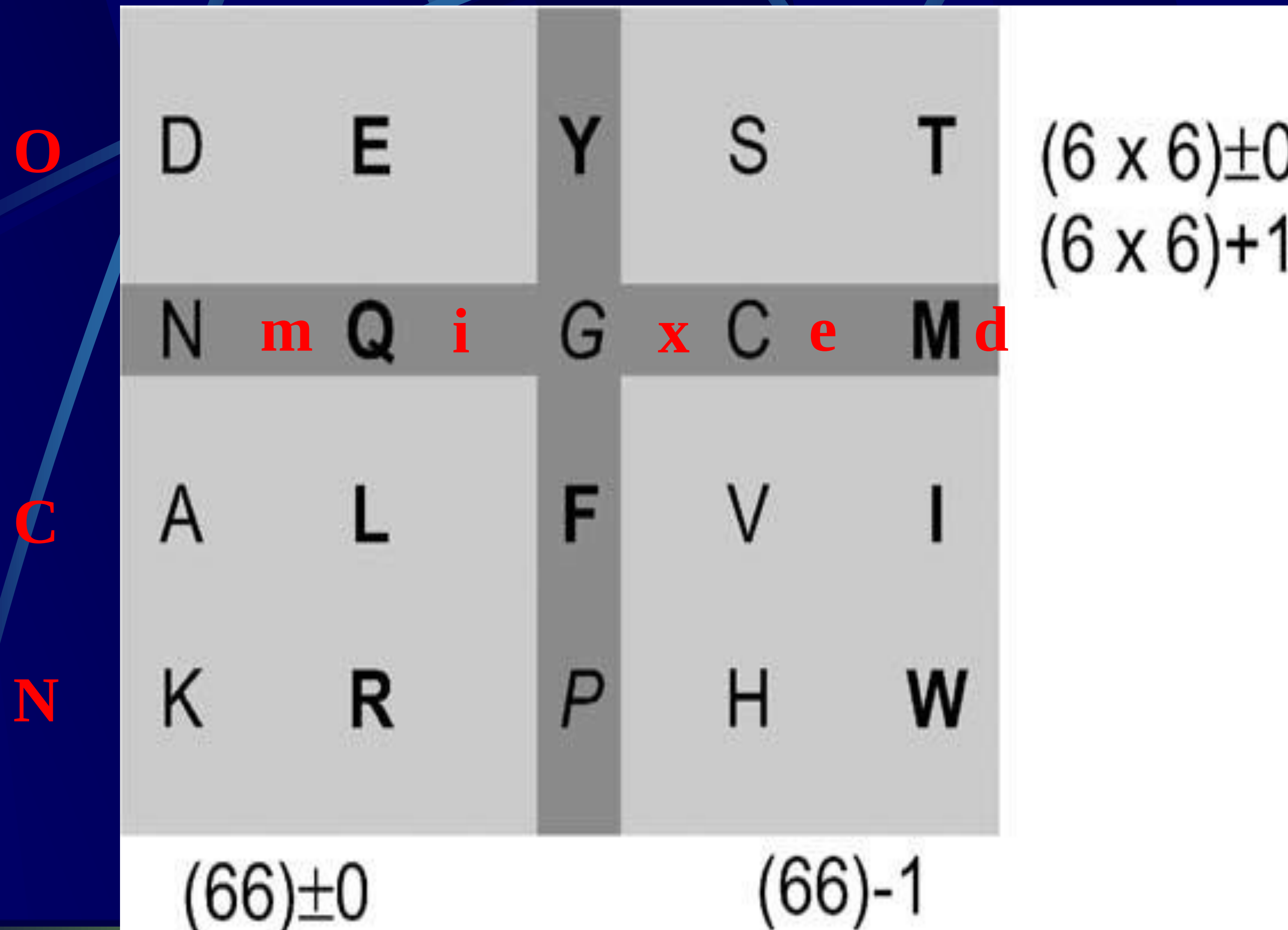
$1 \rightarrow 127 = 8128$

$0 - 15 \longrightarrow 2^4$

Rakočević, 2007a, Tab. 4, p. 82.


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

mixed



					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: U		C		A		G		3rd lett.
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	M	26. ACA		50. AAA	K	58. AGA	R	A
	19. AUG		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)

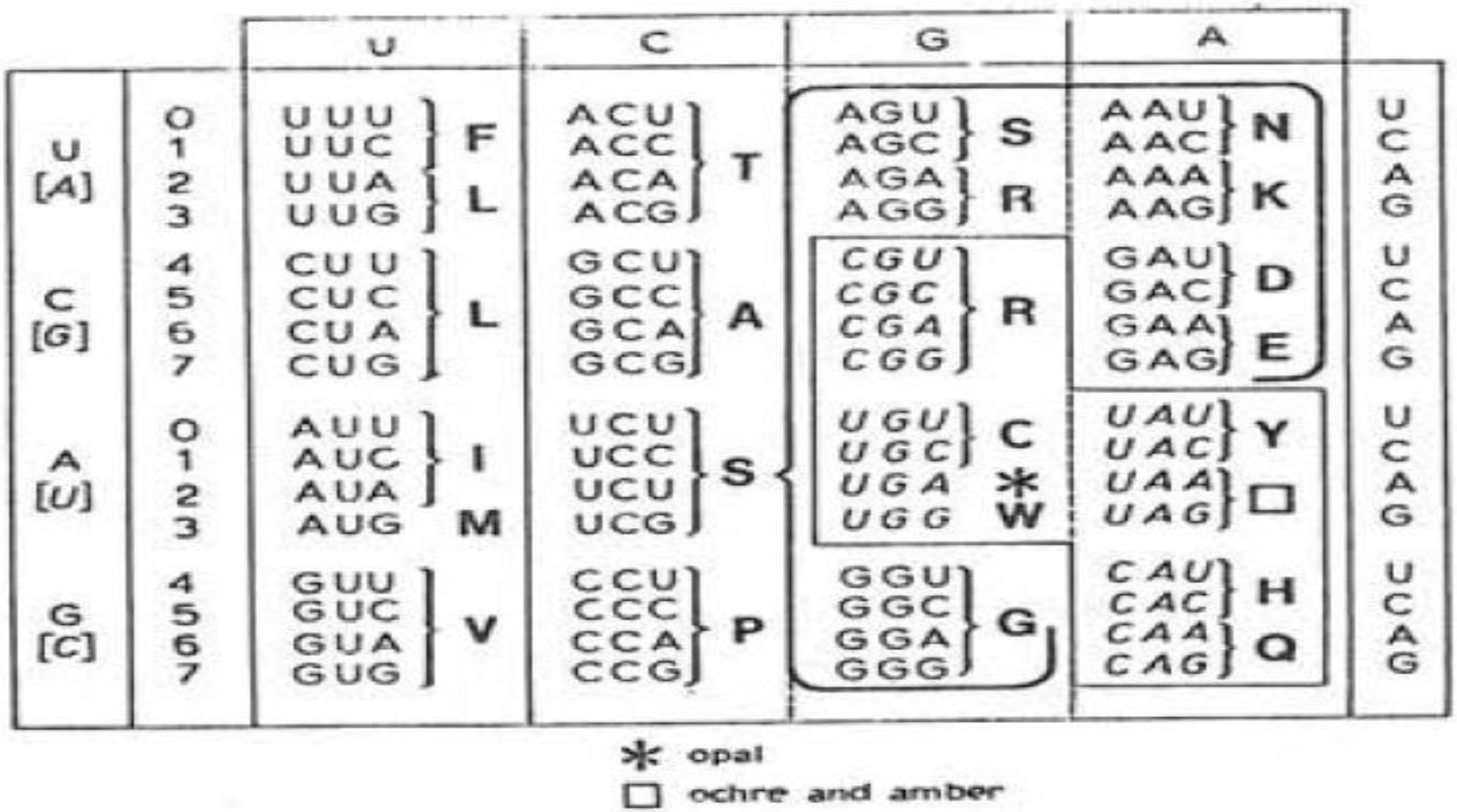
119 – 10
(12)

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				



[(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	957	759
726	726	↓	↓
693	693	**627**	**204**
		330	**555**
		225	
660	660		
627	627		
594	594		
561	561		
528	528		
495	495		
462	462		
429	429	924	429
396	396	↓	↓
363	363	**627**	**204**
		297	225
330	330	522	
297	297		
264	**264**		
231	231		
198	**198**		
165	165		
132	132		
99	99		
66	66		
33	33		

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

2. Appendix Slides explanations

3. *Explanation ...* :

4. *Explanation ...* :

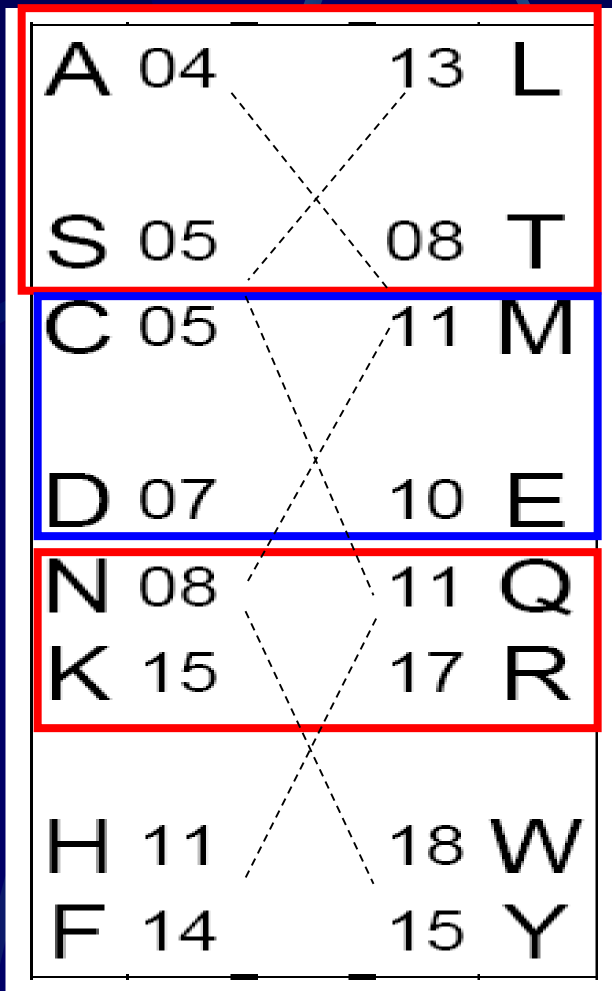
5. *Explanation ...* :

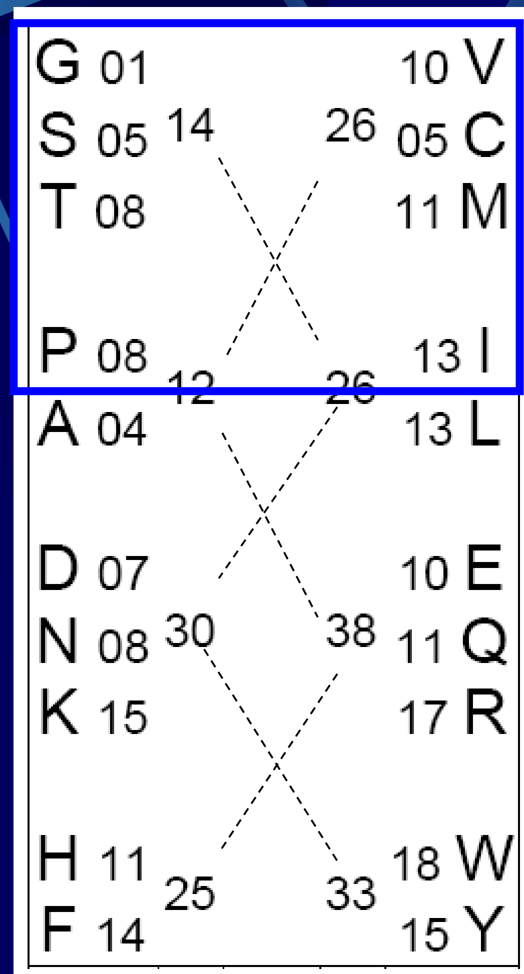
6. *Explanation ...* :

7. *Explanation ...* :

Materials (Slides) for future Supplements

Amino acid system-arrangements (Sis-ars)





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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"A harmonic structure of the genetic code"

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Journal of Theoretical Biology 229 (2004) 221–234

Journal of Theoretical Biology

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

124	124 +11	54	54 x 2		a	b	c	d	M
						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							
					1255	1255	1465	1465 + 9	2738.04

70 = 124 – 54; 30 =108 – 078 [60 + 66 = (2 x 063)]

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)

...

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

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

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

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

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

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

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

...

$780 - 078 = 6 \times 117$ (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

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	50		48	50
E	62	52		54	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 (407)

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

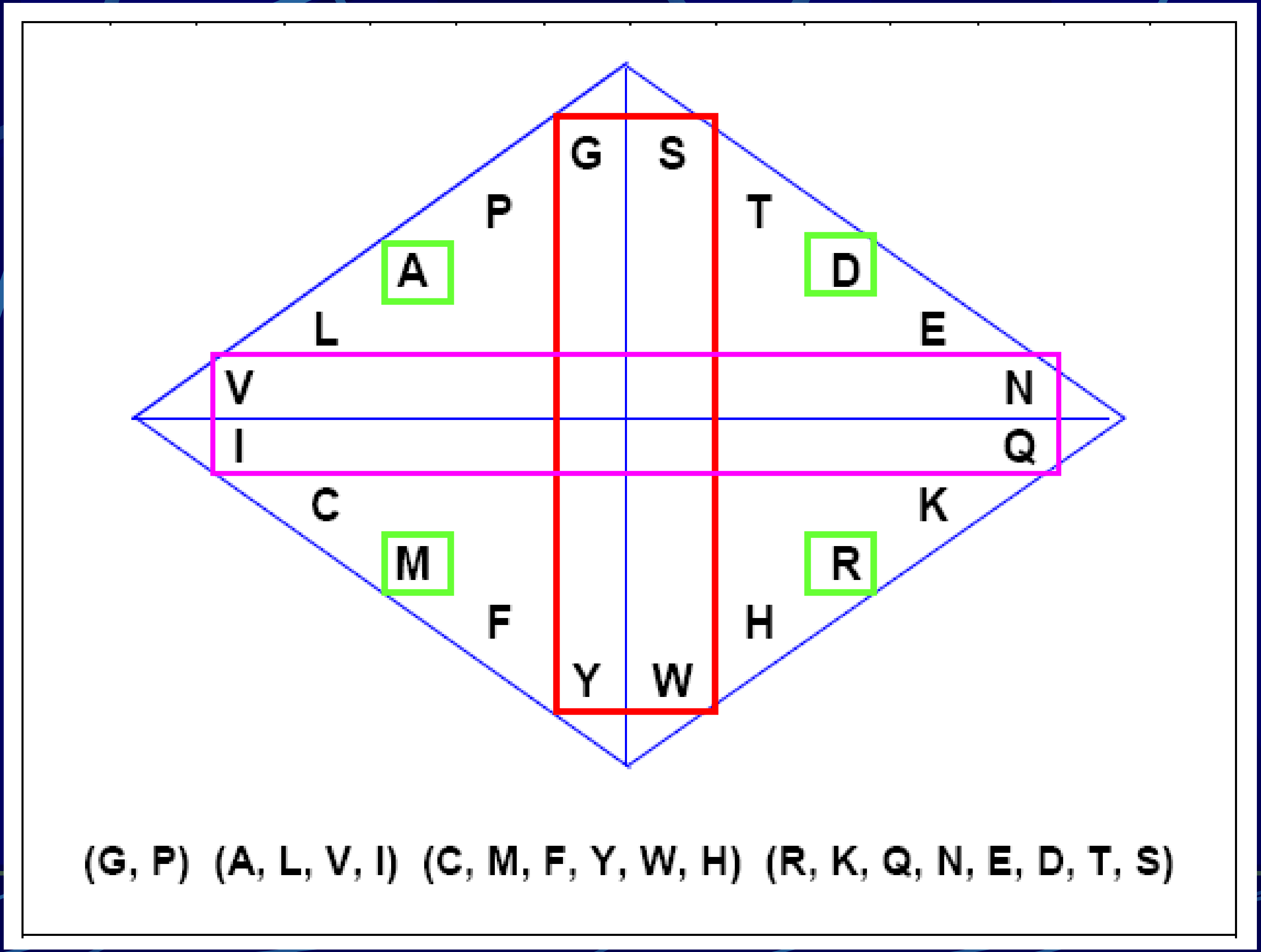
Perfect Protein Amino Acid Similarity System (PPAASS) [VI]

		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)

<table>
<tr><td>G 01</td><td>S 05</td><td>Y 15</td><td>W 18</td><td>39</td><td rowspan="2">54</td><td rowspan="3">67</td></tr>
<tr><td>A 04</td><td>D 07</td><td>M 11</td><td>R 17</td><td>15</td></tr>
<tr><td>C 05</td><td>T 08</td><td>E 10</td><td>F 14</td><td>27</td><td>13
14</td></tr>
<tr><td>N 08</td><td>Q 11</td><td>V 10</td><td>I 13</td><td>**42**</td><td>**63**</td><td>**77**</td></tr>
<tr><td>P 08</td><td>H 11</td><td>L 13</td><td>K 15</td><td>**21**</td><td></td><td></td></tr>
<tr><td>26</td><td>24</td><td>49</td><td>45</td><td></td><td></td><td></td></tr>
<tr><td colspan="2">(50)</td><td colspan="3">(50 + 044)</td><td colspan="2">144</td></tr>
<tr><td colspan="7">**60**, (66+1), (**78-1**) → 204</td></tr>
</table>

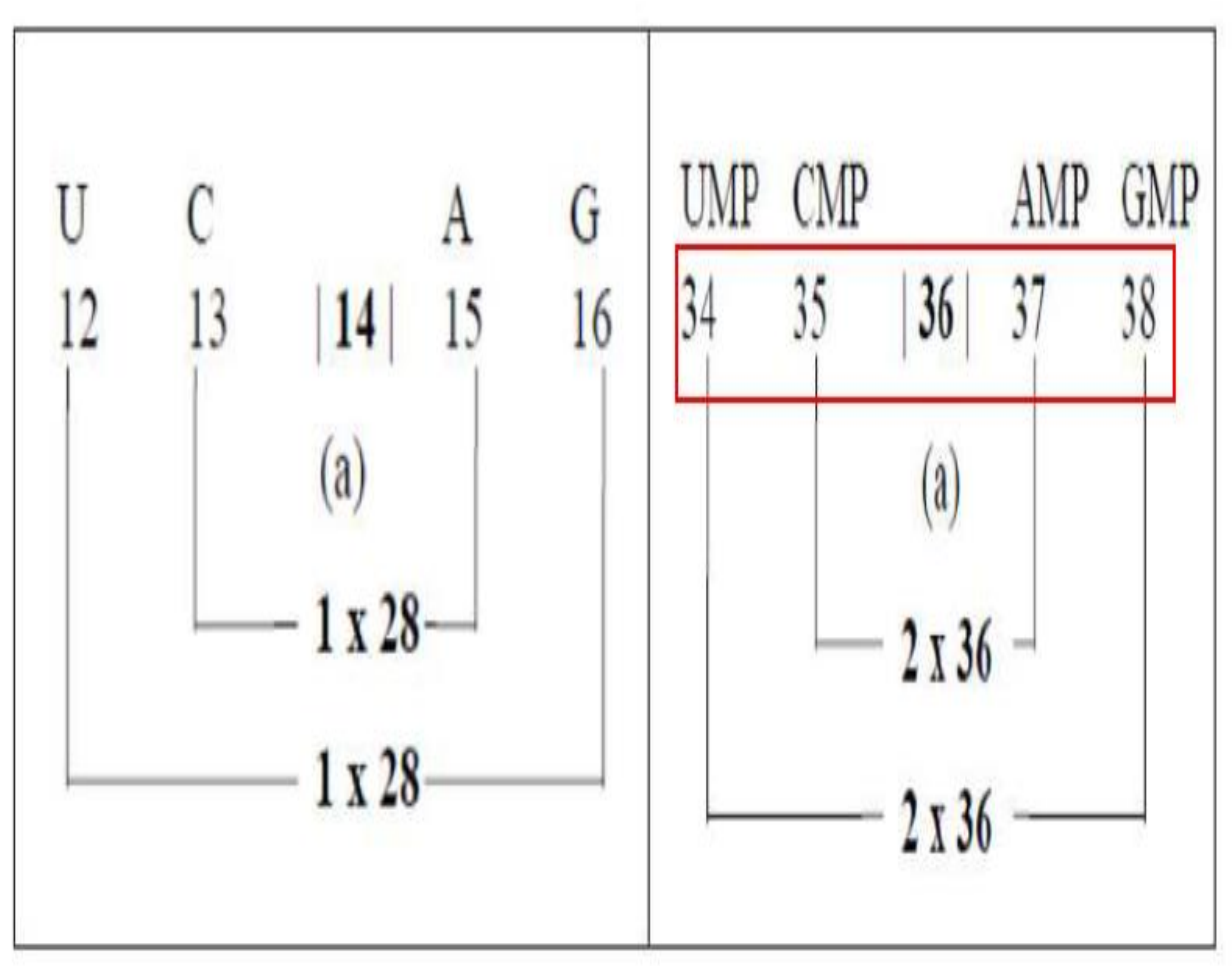
(26 + 45 = 72 – 1) (24 + 49 = 72 + 1)

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: A		G		C		U		3rd
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]
	08	+	04	+	08	+	05	+	14	=	39					
2	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]
	08	+	07	+	11	+	15	+	05	+	01	+	17	=	64	
2'	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 U	2nd letter C	2nd letter A	2nd letter G	3rd lett.	
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	.70
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	.32 / 28
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	.45 / 32
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	.15 / 17
	.74	.25	.34 / 43	.29 / 34		