

**RESEARCH ARTICLE****C-skeleton in the genetic code from a basic series  $5 \rightarrow 0$ , guiding valences and other numeral features in the code****Authors**

Åsa Wohlin

Möregatan 10, 118 27 Stockholm, Sweden

E-mail address: [a.wohlin@u5d.net](mailto:a.wohlin@u5d.net)**Abstract**

The search for regularities in the background for the genetic code and its codon assignments is here further developed, earlier shown to have many correlations with numeral series of integers  $5 \rightarrow 0$  with different exponents. The atomic mass analysis here counts on  $20 + 4$  double-coded amino acids, here including Ile AUA as such.

A central finding here is that the C-skeleton seems to build on an hierarchical development of the mentioned basic series giving top numbers equal to those returning in side-chain divisions and on first three levels those of C-atoms in base-pair domains. It can very elementary explain the  $3/2$ -division in the weight series.

A few main results from earlier articles are shortly recapitulated, since it's shown here that an  $x^3$ -series times 15 ( $x = \text{integers } 5 \rightarrow 0$ ) joins those earlier aspects and add new ones.

It's found also that atoms with valences  $4 + 3$  relative those with  $2 + 1$  make up a 3 to 1-division in both base-pair groups of codon domains, strengthening the earlier observation of valences as one important guiding principle in the relation between codons and domains of amino acids; valences of the atoms which in themselves make up a basic series  $5 \rightarrow 0$  in the code when phosphorus P is included.

Finally, fundamental factors in the code are gathered, where step  $4 \rightarrow 3$  seems reign at bottom of the code and number 7, exactly mean value of all atoms.

**Keywords:** Numeral series, Weight series of amino acids,  $x^3$ -series, Codon distribution, Mass analysis

## 1. INTRODUCTION

### 1.1. General aspects:

This is a follow-up of earlier<sup>1, 2</sup> views, shortly recapitulated in the text, with new results from mass analysis of the genetic code. It departs from a table on 24 codons, thus including two sets of 4 amino acids (aa) with 2 codons. Hence, it deviates from other researchers counting on 20-23 codons in including not only Arg, Ser and Leu but also Ile2, only differing in 3rd base *type* (AUA, AU-U/C).

The different aspects regarded such as divisions related to different pairs of codon domains, side chains (R) versus backbone chains (B). 3-base-coded aa versus aa with “degenerated”, here called “2B-coded” aa, grouped aa after atom kinds in R ( molecular groups), origin from stations in glycolysis versus those from citrate cycle, aa lighter than mean value (Mv) and those heavier than Mv.

Mass as property seems obviously a deeper level than charge and is now accepted as a field, since the so called Higgs boson was detected. (A suggestion here is that Mass is related to the braking of acceleration or  $1/acc.$ , Charge as a braking of velocity or  $1/v.$ )

On the atomic level there are numeral formulas, e.g. the  $2x^2$ -series 50 - 32- 18 - 8 - 2 illustrating the additions for whole shells and orbital numbers s-p-d-f... in the steps. So also in Rydberg’s formulas for spectral lines of hydrogen<sup>1</sup>. Why not on the molecular level? Life as the fusion in suns outsourced to planets? The search of some guiding principle in the coding system is reasonable. A suggestion<sup>1</sup> was to see the relation codons — amino acids on an underlying level as the two different ways to read a hexagonal pattern in planar projection as points with three radii, (the 4th, R, to next level), equal to tetrahedrons of aa, or as hexagons, three of which define the points with radii. (The bases in codons are mainly synthesized by aa.)

### 1.2. The mathematical underground:

A mathematical underground might be assumed, numbers as such having their roots, their origin in divisions. Numeral series in accordance with

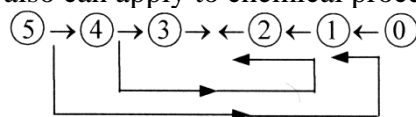
those on the atomic level mentioned above and hierarchical development of levels seem natural to search for. Types of operators are here elementary: +, −, ×, /,  $\sqrt{\quad}$ ,  $x^n$  and inversions (here signed  $\wedge$ .)

More or less of such famous geometrical relations as the Golden section, Fibonacci series and Pythagorean numbers have been found in the genetic code by many through different calculations, so too in this research<sup>1,2</sup>).

### 1.3. Actual background:

The actual background for this research<sup>1</sup> was an elementary 5-dimensional model proposed by the author for interpretations in physics and other sciences, (<https://www.u5d.net/index.html>).

The Entirety taken as 5-dimensional (one degree deeper than the standard 4-dimnsional “space-time”) stepwise polarized into complementary, conceptual structures defining next lower degree,  $4 \rightarrow 3 \rightarrow 2 \rightarrow 1 \rightarrow 0/00$  (the degree of pure kinetic energy), while lost degrees in the steps get transformed to motions or in a closed system meeting the other way around in synthesizing direction. D-degree 4 redefined as Direction, defined by poles center — anti-center, “0—00”. The model only shortly mentioned here because the structure, figure 1, reflects some arithmetical features referred to in the text and also can apply to chemical processes.



**Fig. 1** *The dimension model.*

*Figure from reference<sup>1</sup>, licence: cc.by-nc-nd.*

The thought was that if such a model should have any relevance, it should somehow appear in the genetic code.

Now, also apart from that model, a basic series of integers  $5 \rightarrow 0$  appears as involved in the code in different ways. Just to mention a few examples here:

- The valences of atoms in the code, including phosphorus P are 5-4-3-2-1.
- Flower plants have 5-4-3-merous plans, certainly genetically founded<sup>1</sup>.

- Number of coding bases is 5: T-U-G-C-A-U: 4 inwards DNA, 4 outwards in mRNA → 3 and 2 (not indifferent bases) in codons → 1 in co-enzymes<sup>1</sup>.

- Triplet numbers read in the basic series give approximately the atomic mass sum of nucleons in R<sup>1</sup>, 1504 +2.

- There was also the interesting formula  $1/55 \times 1/555$  which gave the total sum, R+B, of 24 aa = 3276 as decimal periodic number. a 2/3-division of fives multiplied, the inversion of fives giving mass numbers of H<sub>2</sub>O and a hexagon as fructose as periodic numbers<sup>1</sup>.

Here the genetic code is apprehended as a multidimensional system of deeply interdependant dimensions; in protein folding there are steps from d-degree 1→2→3 (to 4, proteins as co-enzymes or as n times globular forms?). As authors Taylor & Coates<sup>3</sup> underlined: “There are multiple levels at which selective forces operate, and an explanation at one level does not eliminate those operating at other levels”.

#### 1.4. A cell as an inversion

In certain aspects a cell: might be regarded as an inversion of an atom. There is the relative negative charge inside the cell, the positive outside it<sup>1</sup>. Further, the strong force in the nuclei of an atom might be seen as inverted to the hydrophobic bonds in lipids of its surrounding surface membrane. (Related turns inside out appear e.g. in lipids.).

A numerical aspect might be noted here. The superposed series to the basic 5 → 0 series = 9 - 7 - 5 - 3 - 1. These digits read as two triplets 975 and 531 might give the quotient  $975 \times 10^3 / 531 = 1836.158$ , close to ( ~ ) mass quotient p/e, the inversion of which is  $544.6 \times 10^{-6}$ , number 544 returning in these calculations.<sup>1</sup>. (About the repeated 5 in the quotient it might point to a two-way direction in series? The electron furthest in is also said to sometimes be located within the nucleon.)

#### 1.5. Calculations:

It started here with a table<sup>1</sup>, (in Appendix), on 24 codons, with two sets of the 4 aa with 2 codons (including both Ile AUA and AUU, differing only

in 3rd type, which deviates from other researchers, (a few among references here<sup>4-9</sup>). 24 codons =  $2(5+4+3)$ , gets divided  $2 \times 5$  on G1 and C1,  $2 \times 7$  on U1 and A1. Numbers  $10 - 8 - 6 = aa$  in G1+C1, A1 and U1 respectively.

Why 24 codons? It's possible to imagine an early 2-base code (2B) with 16 codons, half of which gets developed with a 3rd base (either a purine or a pyrimidine), thus giving 16 codons to the 8 “2B-coded” ones. It was observed that mass of 16 bases, 4 times G, C, A and U, transformed (TR) to number base system 8 (nb-8) gave the sum R+B of the 24 aa (+/-1 in R)<sup>1</sup>. Cf. +8 aa with the so called “degenerated” codons.

The table concerns the side-chains of aa (R), Most common isotopes were used.

Atomic mass as number of nucleons (mass) were noted, so was its division on neutrons (N) and protons (Z) and the sums for each base domain in 1<sup>st</sup> and 2<sup>nd</sup> base order:

G1 = the mass sum of all aa side-chains (R) with base G as 1<sup>st</sup> base in the triplet of bases in codons, G2 = all aa with G as 2<sup>nd</sup> base etc.

The 4 bases from which the triplet codons are taken, bind in pairs in DNA: G with C, A with T, hence natural to pair also these domains: A+U and G+C refer to sums of these domains of aa that astonishingly got equal in 1st and 2nd position of the codon bases. It led<sup>1</sup> to the construction of 12 aa with mixed codons (Mx) in 1st and 2nd position, one from each pair: GA-GU, CA-CU, UG-UC. AG-AC and 12 aa with non-mixed codons (Nmx): AA-AU, UU-UA and GG-GC-CG-CC.

Another feature in the table to observe: according to reference<sup>10</sup> the basic Arg1, Arg2 and Lys at start were taken as charged, which implies -1 H in their backbone parts (B-chains, B), the parts shared by all aa that bind them to proteins through peptide bonds. It implies a total sum of R = 1504, a total sum of B = 1772, the whole 3276.

All mass numbers refer to side-chains (R) if nothing else is mentioned.

**RESULTS, Sections 2→7**

**2. The C-skeleton of 24 amino acids**

Why 80 Cs in the 24 aa? A background scheme for the C-skeleton might be found in the hierarchical development of the basic series of integers 5 → 0 where 6 levels of the pyramid leads to the top number 80. The two-peak numbers are equal to those returning in side-chain divisions of aa in the genetic code and first three levels those of Cs in base-pair domains. It can very elementary explain the 3/2-division in the weight series. As found earlier<sup>1</sup>:

Cs in 24 R = mass 960, equal to whole mass in A+U-domains R

Re in 24 R = mass 544, equal to whole mass in G+C-domains R

Why this equivalence appears is of cause a very central issue.

The A+U-domains 960 were in two ways divided ≈ 2/3, 384 and 576 (-/+1); for a third way see section 3. These polarities in the code are shortly recapitulated and explained with figures below, the ES-series<sup>1</sup> and the weight-series<sup>2</sup>. L-chain is aa lighter than mean value (MV) of R, H-chain aa heavier than Mv:

In the weight-series<sup>2</sup>, L-chain 384 -1, H-chain 576 +1.

In Mx-coded<sup>1</sup> aa 384 +1, in Nmx-coded<sup>1</sup> aa 576 -1.

A number pyramid built on the basic series of integers 5 → 0, and this times 12, gives the top number 960 and the two-peak top numbers 576 and 384:

<b>80</b>					Levels	0	Rows	960							
<b>48</b>		<b>32</b>				<b>1</b>		<b>576</b>		<b>384</b>		= 960			
28	20	12				<b>2</b>		336	240	144		= 720			
16	12	8	4			<b>3</b>		<b>192</b>	144	96	48		= 480		
9	7	5	3	1		<b>4</b>		<b>108</b>		<b>84</b>		60	36	12	= 300
5 — 4 — 3 — 2 — 1 — 0						<b>5</b>		60 — 48 — 36 — 24 — 12 — 0				= 180			

**Fig. 2.1:** Number pyramid on the basic series 5→0 and times mass of C-atom à 12

*Some first notations:*

- First three rows give the total of Cs, top sum 960.
- Inner shared part of these three rows = 540, the sum of Re if basic aa are taken as uncharged and -1, see below.
- Row 4, 108 and 84 are the sums of Cs in Trp, the heaviest aa, and Phe (and Tyr), the 3 aromatic aa from 3-P-enolpyruvate.
- The two-peak numbers return in B-chains also.
- 48 × 32 happens to be 1536, the total sum of Cs in 24 aa R+B.

*B-chains:*

In the common B-chains of aa the equal sums reappear, most clearly in the bound B-chains:

$$\begin{aligned}
 48 \text{ Cs} &= 576 \\
 24 \text{ }^{16}\text{O} &= 384 \\
 24 \text{ }^{14}\text{N} &= 336, + 48 \text{ H} = 384.
 \end{aligned}$$

**The 3-2-division:**

The two-peak pyramid explains in a very elementary way the 3/2-division in the weight series:

$$\begin{aligned}
 \text{Pyramid } 384 &- \text{ on basic numbers } 4 \rightarrow 0 = 10 \\
 \text{Pyramid } 576 &- \text{ on basic numbers } 5 \rightarrow 1 = 15
 \end{aligned}$$

*L—H<sup>2</sup>: total sums 900 — 600:*

Also the sum of all atoms in the H—L-chains, when counting on a total of 1500, is given in rows 5, 4, 3 as if substituents represented a number of Cs; this when counting the shared part two times.

Excluding the numbers furthest to the right gives 180 + 300 + 480 - 60 = 900. Excluding numbers furthest to the left gives 960 - 360 = 600.

$$\begin{aligned}
 576: \text{ Rows } 5+4+3 &= 180 + 288 + 432 = 900 \\
 384: \text{ Rows } 5+4+3 &= 120 + 192 + 288 = 600
 \end{aligned}$$

Base-pair domains A+U and G+C in R:  
Cs in A1+U1 = 53, Cs in G1+C1 = 27; such a division is shown in figure 2.2, three bottom levels of the pyramid:

16	12	8	4	3
9	7	5	3	1
5	4	3	2	1
53				27

**Fig. 2.2.** Number of Cs in base-pair domains. A1+U1 = 53, G1+C1 = 27

Masses for instance:

A1+U1 summed up horizontally, sum 53 Cs:  
9 Cs = 108, 16 Cs = 192, 28 Cs = 336, Sum 636.

G1+C1 summed up vertically, sum 27:  
16 Cs = 192, 9 Cs = 108, 2 Cs = 24, Sum 324.

Amino-/keto pairing:

It could be remembered<sup>1</sup> that the amino-/keto pairing of codon domains in 2<sup>nd</sup> base order gave the Cs-division of the two-peak numbers on level 1:

$$A2 + C2 = 25 + 7 \text{ Cs} = 32, \rightarrow \text{mass } 384$$

$$G2 + U2 = 19 + 29 \text{ Cs} = 48, \rightarrow \text{mass } 576$$

## 2.2. Recapitulations of earlier results:

### 2.2.1. The weight series and L-H-chains<sup>2</sup>:

Gly	Asp	Gln	Trp
1	59	72	130
L-chain	Mv	H-chain	
600		900 + 4	
Division of total mass of aa R			

**Fig.2.3.** Serial order of aa divided around the mean value Mv.

Figure from reference 2, licence:cc- by.

L-chain - domains			H-chain - domains		
Re	216	+1 = G1+C1	Re	328	-1 = G1+C1
Cs	384	-1 = A1+U1	Cs	576	+1 = A1+U1
600			900 + 4		

**Fig.2.4.** Mass of R divided on Cs and Re: 14 aa lighter than Mv, the L-chain, and 10 aa heavier than Mv, the H-chain. The similarity (-/+1) with paired codon domains are included to the right in the columns .New figure built on reference 2,licence cc- by..

If Lys and the two Arg were taken as uncharged, the total mass becomes 1500 +1; eventually, if assuming only e.g. Glu charged, it gives a total of 1500, 100 times the basic series. Then also the Re-numbers here would be exactly divided in quotient 2/3. It got nearly exactly divided in the quotient 3/2, as the division of Cs 576 and 384.

The closely equal division on codon domains is striking. The aa in this division:

L-chain: 14 aa:

G1: Gly, Ala, Val, Asp	= 118
C1: Pro, Leu1	= 99...Sum 217
A1: Ser2, Thr, Ile1, Ile2, Asn	= 248
U1: Ser1, Cys, Leu2	= 135...Sum 383

H-chain, 10 aa:

G1: Glu	= 73
C1: Arg1, Gln, His	= 254...Sum 327
A1: Arg2, Lys, Meth	= 249
U1: Trp, Tyr, Phe	= 328...Sum 577

Added here: The implication that Re in A1+U1-domains 324 equals Cs in G1+C1 is an essential feature. The same equivalence appears, -/+1, in L- and H-chains *separately*, which indicates that this relation has a deeper root in the code:

L-chain: Re in A1+U1 = 155, +1 = Cs in G1+C1 = 156

H-chain: Re in A1+U1 = 169, -1 = Cs in G1+C1 = 168

It was suggested<sup>2</sup> that the many similarities in numbers +/-1 of this kind represent a change to another coordinate axis.

(A move of Ile AUA to combine with Meth in the H-chain gives in R: L-chain 543, in H-chain 961, close to the G+C — A+U-division; in R+B it

gives L-chain  $1636 - 133 = 1502$ , in H-chain  $1641 + 133 = 1774$ , close to the division on R- and B-chains.)

### 2.2.2. The ES-series<sup>1</sup>

The series of integers  $5 \rightarrow 0$  with exponent  $2/3$  times  $10^2$ , baptized ES, with abbreviated numbers = 292 — 252 — 208 — 159 — 100; the numbers in such series referred to as 5', 4', 3', 2', 1'. Additions and intervals in this series showed up to correlate more or less exactly with the atomic mass of aa summed in codon domains of different kinds. The operations  $-/+$  lower numbers on the series gave ( $-/+1$ ) individual domains. .

Two times first three numbers in the chain gave the total of R for the 24 aa and were divided on codon domains as shown in figure 5:

$$5' + 4' + 3' = 752, - 3' = 544 = G+C\text{-domains},$$

$$5' + 4' + 2 \times 3' = 960 = A+U\text{-domains}$$

The very number 24 of aa correlates with two times  $5 + 4 + 3$  in the basic series.

$5^{2/3}$	$4^{2/3}$	$3^{2/3}$	$2^{2/3}$	$1^{2/3}$	$0$	$\times 10^2$
= 292,4	252,0	208,0	158,7	100		
<hr/>		<hr/>		<hr/>		
292	252	208	159	100		
<hr/>		<hr/>		<hr/>		
752		259				
<hr/>		<hr/>		<hr/>		
544		$\times 2 = 416$				
<hr/>						
$2 \times 752 = 1504$ , total sum of 24 aa R.						
<hr/>						
$544 = G+C\text{-coded aa} \dots \dots$				$= 752 - 208$		
$544 + 416 = 960 = U+A\text{-coded aa}$				$= 752 + 208$		

**Fig. 2.5.** The ES-series, where  $5'+4' = G+C$  544,  $5'+4'+2 \times 3' = A+U$  960. Figure from reference <sup>1</sup>, license cc-by-nc-nd.

A central finding was the division of aa on aa with “mixed” (Mx) and “non-mixed” (Nmx) codons, 12 aa in each. “Mixed” codons (Mx) here meaning one of the first two bases in the triplets from the G+C-group, one from the U+A-group:

$$\text{Mass of Mx} = 2(5' + 4' - 2'),$$

$$\text{Mass of Nmx} = 2(3' + 2')$$

The table, figure 2.6, on mixed coded aa gave an astonishingly regular 2D-table (or 3D if the N-Z-division should be included): the 3 rows adding up to  $385 - 209 - 176$  and the 4 columns adding up to

$209 -/+1$  and  $176 -/+1$ . ( $N = 2 \times 176 - 1$ ,  $Z = 2 \times 209 + 1$ .)

GA	Glu	CA	His	UG	Trp	AG	Arg2	$\rightarrow 385$
GA	Asp	CA	Gln	UG	Cys	AG	Ser2	$\rightarrow 209$
Gu	Val	CU	Leu	UC	Ser	AC	Thr	$\rightarrow 176$
<hr/>		<hr/>		<hr/>		<hr/>		
175		210		208		177		
<hr/>				<hr/>				
385				385				$\Sigma 770$

**Fig. 2.6.** The 12 mixed coded aa, first two bases and sums of mass.

$A+U\text{-coded aa} = 384 + 1$ .

Figure from reference <sup>1</sup>, license: cc-by-nc-nd.

Non-mixed aa:

$$A+U\text{-coded aa} = 575 = 2 \times 3' + 2' = 576 - 1.$$

$$G+C\text{-coded aa} = 159 = 2'$$

Some of the other found patterns in this ES-series<sup>1</sup>:

$$G1 = 191 = 5' - 1', -1. \quad C2 = 133 = 5' - 2'$$

$$C1 = 353 = 4' + 1', +1*. \quad G2 = 411 = 4' + 2'$$

\* as a displacement of  $\text{Arg}^+$  101 from  $\text{GG} \rightarrow \text{CG}$

A similar displacement of Tyr,  $107 = 3' - 1' - 1$  from U2 to A2 gave:

$$5' + 4' = 544, - 107 = 437 = U2$$

$$2 \times 3' = 416, + 107 = 523 = A2$$

The purine-pyrimidine polarity:

$$G2 + A2 = 934 = 2 \times 467 = 2(3' + 2' + 1')$$

$$U2 + C2 = 570 = 2 \times 285 = 2(5' + 4' - 2' - 1')$$

The interval  $2' - 1' = 59$  ( $-/+1$ ) seemed to function as an exchange file:

$$G1 - 58 = C2, C1 + 58 = G2.$$

$$A1 - 60 = U2, U1 + 60 = A2.$$

With an addition here: The aa-domains  $G1+A1$  (688) versus  $U1+C1$  (816) divide in Cs: 396 and 564, equal to numbers  $384 + 12$  and  $584 - 12$  in the two-peak pyramid, figure 2.1, or as  $576 -/+ 180 =$  row 1 in the pyramid. Re was divided 292 and 252 in this pairing, i.e. as 5' and 4' in the ES-series. This division gives  $+/- 101$  ( $101 \sim \text{Arg}^+$  R) the four single base domains:

$$396 + 101 = 497 = A1; 564 - 101 = 463 = U1$$

$$292 - 101 = 191 = G1; 252 + 101 = 353 = C1$$

### 2.3. Some fundamental numbers

In the number pyramid, figure 2.1, there was the superposed series on the basic one on level 4: 9-7-5-3-1 This series added times 12 gives the fundamental factors 192 and 108, 16 and 9 times 12, at bottom 4 and 3 squared.

$$\frac{108 - 84 - 60 - 36 - 12}{192 \quad 108}$$

They were also intervals in the ES-series<sup>1</sup>, 5' → 1' and 3' → 1' with difference 84 = 5' → 3'.

$$5^2 \times 12 = 300, \times 5 \sim \text{total mass as } 1500.$$

$$4^2 \times 12 = 192, \times 5 \sim \text{Cs } 960, = \text{A+U-domains,}$$

$$3^2 \times 12 = 108, \times 5 \sim \text{Re } 540, = \text{G+C-domains}^*$$

\*When calculation on a total 1500.

It shows on the close correlations with the Pythagorean numbers. (The factors 192 - 108 and interval 84 gave also associations to the synthesis of hexoses<sup>2</sup> as it usually is summarized.)

### 2.4. Number 60

The central number 5 in the superposed chain 9-7-5-3-1, row 4 on the number pyramid, figure 2.1, with mass number 60, is shared by both pyramids. (Could they eventually represent the C-atoms of Gln and Asn in some contexts, e.g. as in oxytocine?) This central position might elucidate the many operations -/+ 60 that lead to new polarities in the code:

Domains:

$$576 + 60 = 636 = \text{Cs in A1+U1}$$

$$384 - 60 = 324 = \text{Cs in G1+C1}$$

Mx — Nmx:

$$576 - 60 = 516 = \text{Cs in Nmx-coded aa}$$

$$384 + 60 = 444 = \text{Cs in Mx-coded aa}$$

L—H-chains in the weight-series:

Domains                      L—H-chains

G1: Cs 108, + 60 = 168 = Cs in G1+C1 in H-chain

C1: Cs 216, -60 = 156 = Cs in G1+C1 in L-chain

U1: Cs 348, +60 = 408 = Cs in A1+U1 in H-chain

A1: Cs 288, -60 = 228 = Cs in A1+U1 in L-chain

Apart from Cs-numbers it reminds of the addition of 60 A in the synthesis of the coding bases: Gly 75+ 60 = A-base 135, Asp + carbamoyl~(P) ~ + 60 in the first step of the U-base synthesis. To this

come the addition of acetyl~(Coa) + H in the citrate cycle. Isocitrate with mass 192 read “horizontally” has the parts 59 - 58 - 75: here 75 (= Gly) becomes the part that develops to B-chains and. 59-58 are equivalent with R of Asp and Asn.

It might be added that the sum of *valences* in 12 N and 12 O+S in R = 36 and 24, sum 60:

$$\text{Row 5: } 60 - 48 - \frac{36 - 24}{12} - 0 \text{ (Sum 180.)}$$

N O+S

Sum of valences in R

In the ES-series<sup>1</sup>,  $x^{2/3}$  ( $x=5 \rightarrow 0$ ),  $\times 10^2$ , the interval 108 was divided 49 — 59, here 48 — 60, (an opposite order in ES). The number 59 was shown to be a kind of ‘exchange file’ with similar operations as with number 60 here. Some examples:

$$\text{Half G2} + \text{A2} = 467, - 59 = 408, = \frac{1}{2} (\text{U1} + \text{C1})$$

$$\text{Half C2} + \text{U2} = 285, + 59 = 344, = \frac{1}{2} (\text{G1} + \text{A1})$$

And with additions here:

The 12-group Mx-coded aa,  $2 \times 385$ :

$$385 - 59 = 326 = \text{Re}$$

$$\frac{385 + 59}{2} = 444 = \text{Cs}$$

$$\text{Cs in G1+C1} = 228, - 59 = 169 = \text{Re U+A,}$$

$$\text{Re in G1+C1} = 157, + 59 = 216 = \text{Cs U+A}$$

The 12-group Nmx-coded aa,  $2 \times 367$ :

$$\text{G1} + \text{C1} = 159, + 59 = 218 = \text{Re}$$

$$\text{A1} + \text{U1} = 575, - 59 = 516 = \text{Cs}$$

### 2.5. Molecular groups

When the aa were<sup>2</sup> divided according to significant atom kinds in R, it gave three groups: those with only CHx, those including nitrogen, NHx, and those with oxygen or sulfur: O/SHx. The sums got close to the same division on CHx- and NHx-groups versus the O/SHx group: 904 (+1) — 600 -1, than between the L-H-chains, figure 2.7., along another axis.

<b>CHx-series:</b>	<b>L</b>	<b>H</b>
Ala-Pro-Val-2 Ile-2 Leu — Phe = 328		91
<b>NHx-series:</b>		
— Lys,-2 Arg-His-Trp	= 0	486
	<u>Σ 328</u>	<u>577</u>
		= 904 +1
<b>O/SHx-series:</b>		
Gly-2 Ser-Thr-Cys-Asn-Asp		
— Gln-Glu-Met-Tyr	Σ = 272	327
		<u>        </u>
		= 600 -1

**Fig. 2.7.** Molecular groups of 24 aa divided in accordance with significant atoms on those lighter and heavier than the mean value. Gln and Asn here referred to the O/SHx-series. Figure from reference<sup>2</sup>, license: cc-by.

C-atoms in the groups: 30 Cs in CHx, 25 in NHx, 25 in O/SHx. In the pyramid, figure 2.1:

CHx: 30 Cs = 2 × 180 (row 5)

NHx + O/SHx = 25 + 25 Cs = 2 × 300 (row 4)

Total sums<sup>2</sup>, Cs + Re, in this pairing gives close to the division of triplets in the basic series:

O/SHx + NHx = 1085 = 2 × 543, -1

CHx = 419 = 2 × 210, -1

It can here be added that a move of Asn, one of the two aa with questionable position, to the NHx-group, it gives the following nice division:

CHx + O/SHx = 419 + 599, -58 = 960

NHx = 486 + 58 = 544

Thus it gives sums equal to the division on codon domains A+U and G+C and on Cs versus ‘substituents’ totally. 544 equal to sum of all Re.

In many contexts it’s found<sup>1,2</sup> that the division Cs — Re (or N—Z) equals the division on the same aa as along another coordinate axes (+/-1). Here the NHx-group, without a move of Asn, seems represent the Re-part, O/SHx the Cs-part:

NHx:	Cs 300	Re 186	Sum 485 +1
O/SHx:	Cs 300	Re 299	Sum 600 -1
	<u>600</u>	<u>485</u>	

(Chemically the OHx-group appears closer to the CHx-group, C and O with valences 4 and 2 and closer to the origin of aa in relation to the NHx-group.)

### 3. The x<sup>3</sup>-series times 15 as a background scheme?

In this scheme from 4’ → 0 the two-peak numbers from the pyramid, figure 2.1, reappear, the 3/2-division of Cs in 576 and 384; factor 15 here divided 9 — 6.

#### 3.1. The x<sup>3</sup>-series, x = integers 5 → 0:

125 — 64 — 27 — 8 — 1 — 0

The series, times a factor 15, i.e. the sum of the basic series 5 → 0, gives from 4’ to 0 the total sum as 1500, 960 + 540.

In the ES-series<sup>1</sup> it was counted on a total R of 1504, with charged Lys and 2 Arg (according to reference<sup>10</sup> (Karlson 1976, an early source, since this research started in the beginning of the 1980th).

Below these aa are taken as uncharged with an added assumption of -1, eventually only Glu charged? It would give the beautiful total 1500 in R. The x<sup>3</sup>-series, vertically here, times 15 in columns gives figure 3.1:

x <sup>3</sup>	× 5	× 4	× 3	× 2	× 1	Sum
<b>125</b>	625	500	375	250	125	<b>1875</b>
<b>64</b>	320	256	192	128	64	<b>960</b>
<b>Sums</b>	<b>576</b>		<b>384</b>			
<b>27</b>	135	108	81	54	27	405
<b>8</b>	40	32	24	16	8	120
<b>1</b>	5	4	3	2	1	15
<b>Sums</b>	180	144	108	72	36	<b>540*</b>
	<b>324</b>		<b>216</b>			
Total	500	400	300	200	100	
Total	<b>900</b>		<b>600</b>			

**Fig. 3.1.** The x<sup>3</sup>-series, x = integers 5 → 0 times 5-4-3-2-1. Total sum of Re in 24 aa reduced with 4 H = 1500.

Factor 64 times 15 = sum of A+U-domains, 960,

Factor 36 (3’+2’+1’) times 15 = sum of G+C-domains 540

when reduced with 4 H.

Sum of the whole x<sup>3</sup>-series = 225 = 15<sup>2</sup>.

The marked sums in figure 3.1 give the sums of Cs and Re in the weight series, figure 2.4 above,



in the H- and L-chains (when 328 reduced with 4 H): 576 — 324 and 384 — 216.

These numbers are all appearing in the Pythagorean musical scale according to data from Negadi<sup>8</sup>.

Some notations:

- In the Nmx-series the mass of A+U-domains as 576 -1 was divided in A1 320 and U1 256 -1. It's noteworthy that this division appears in row 4', columns 5 and 4 here.

- As pointed to above the numbers 576 and 384 return in the B-chains also.

- It was earlier<sup>1</sup> noted about this x<sup>3</sup>-series that 6 × 5' = 750, +/- 6 times 3' + 2' = 210 gives the sums 960 and 540.

- Cs in G1 + C1 divided: 6 × 3' = 162, -/+ 6(2'+1') = 108 = Cs in G1 and 216 = Cs in C1.

- It can be recaptulated<sup>1</sup> that the figures in the middle of the x<sup>3</sup>-series 27 and 8 appeared in the G+C-domains in a curious way:

$$\sqrt{27/8} \rightarrow \wedge, \times 10^3 = 544.33$$

$$3^{3/2}, \wedge, \times 10^3 = 192.45. \sim G1 + 1.$$

$$2^{3/2}, \wedge, \times 10^3 = 353.55. \sim C1... \text{ Sum } 546.$$

It was noted with an association to 27 and 8 in particle physics and group theory by Gell-Man and Neéman<sup>11</sup> in "The Eightfold way" 1964.

- Sums in column ×3 vertically = 192 and 108, intervals 5' to 1' and 3' to 1' in ES-series.

- The total sums of columns from 4', 500 - 400 - 300 etc... in the figure 3.1 read as

a) numbers in nb-8 = row 4,

b) numbers in nb-6 = rows 3'+2'+1'.

- About the Mx-Nmx-division on codon domains, it was stressed before<sup>1</sup> that the middle numbers 27 and 8 in the x<sup>3</sup>-series with interval 19 appeared essential, times a factor 11 giving the strikingly regular mass structure for Mx-coded aa in figure 2.6 .

The Cs divide on Mx 384 + 60 = 444, on Nmx 576 - 60 = 516.

The Re divide as crosswise in figure 3.1 above: on Mx as 324, on Nmx 216, (+2 in both when calculating on a total R of 1504).

However, factor 11 is hardly explained in figure 3.1. Calculating with columns ×5, ×4, ×3, - column ×1 = 11 gives a figure as 3.2:

Row 3' 27: ×12 = 324, - 27 = 297 → ×2 = 594
-19 <span style="float: right;"> -209</span>
Row 2' 8: ×12 = 96, - 8 = 88 → ×2 = 176
385

**Fig. 3.2.** Mx-coded aa as first three columns in figure 3.1. - last column, times 2. Sum 770.

### 3.2. The sum 1500, 12 times 5'

The whole sum R as 1500 is given from first columns ×5, ×4, ×3 at row 5', 125, in figure 3.3:

x <sup>3</sup>	× 5	× 4	× 3	× 2	× 1	Sum
125	625	500	375	250	125	1875
	1500					

**Fig. 3.3.** Detail from figure 3.1.

Row 5' (= 125) × 5, ×4, ×3 = 1500, total R here.

In following steps 4' → 3' → 2' → 1' this sum 1500 might be seen as "developed" with columns × 1 and × 2. It reminds of the background model mentioned in the Introduction, figure 1.1, where lower dimensions (d-degrees) 1 and 2 are debranched at steps 5 → 4 and 4 → 3 and expressed as external motions or meeting the other way around in synthesizing direction.

The series 625 — 500 — 375 = 625 + 875 represent the Mv of 10 and 14 aa: numbers in aa G1+C1 = 5 + 5 aa, in A1+U1 14 aa, in 1st base order divided 8 in A1, 6 in U1, in 2nd base order = 7 + 7. 10 and 14 was also the division of aa in the weight series on H- and L-chains respectively.

Mv R + B = 3276/24 = 136.5, minus a B-chain à 74 = 62.5, Mv of aa R when calculating with -4 in R.

Compared with numbers in the ES-series, where 5' × 2 = 584 and 3' × 2 = 416, the division times 3/2 gives the equal division.

$$416 \times 3/2 = 624 = 5 \times 125 - 1$$

$$584 \times 3/2 = 876 = 7 \times 125 + 1$$

The exact quotients give naturally exactly 625 and 875. The order is in the x<sup>3</sup>-series reversed in relation to the ES-series! (Interval 876 - 624 = 252 = 4' in ES; 252 - 2, × 3/2 = 375.)

(A cross-adding of domains gives similar divisions, e.g. C1 + A2 = 876, G1 + U2 = 628.)

About this row 5 in figure 3.1 and the division of the total as 1500, see further about the division on atom kinds in section 5.

It was observed<sup>1</sup> that the ES-digits as decimals were approximately given as elementary quotients of 24, the total number of aa,  $\times 10^x$ :

$$14/24 = 0.583.33., \quad 12/24 = 0.500, \quad 10/24 = 0.416.66.$$

### 3.3. The number 1875, 15 times 5'?

1875 times  $10^{-4}$  is the same number as the factor in Rydberg's formula for second spectral line of hydrogen in the Balmer series. Cf. earlier notations<sup>1</sup> of quotients between these factors in the Balmer series times  $10^2$  giving mass sums of U-, A- and ~ G-bases.

### 3.4. Sums and intervals in the $x^3$ -series $\times 15$ :

Intervals:	61	37	19	7	1	
	125	64	27	8	1	0
Sums	189	91	35	9	1	

**Fig. 3.4.** Intervals and sums in the  $x^3$ -series  $\times 15$ .  $x = \text{integers } 5 \rightarrow 0$ .

Some notations:

- Sum 91 =  $4' + 3'$ ,  $64 + 27$ :

It's a factor in sums of aa R+B:  $91 \times 36 = 3276$ , the total of aa R+B unbound,

The whole series  $15 \times 91 = 1365$ , 10 times 136.5, the Mv of one aa R+B when calculating with - 4 H in R. A 3/2-division of the Mv-sum of 2 aa R + B in step  $4' - 3'$ :

$$91 \text{ times } 5 - 4 - 3 - 2 - 1 = \\ = \frac{455 - 364 - 273 - 182 - 91}{819 \quad 546^*}$$

$$819 = 1/4 = \text{the total } 24 \text{ aa R+B} = 3276$$

\* 546 was the approximate sum of  $1/\sqrt{27} + 1/\sqrt{8} \times 10^3$  divided on G1- and C1-domains.

- Interval 37 =  $4' - 3'$ ,  $64 - 27$ :

37 is half the normal B-chain 74 as unbound.

The division of 64 in 37 and 27, two numbers that are each other's periodic inversions, might be a factor in this step  $4' \rightarrow 3'$  to observe (?). (The quotient  $27/37$  is the square of 27 as decimal

period.) The relation between numbers 5 - 2 through inversions lies behind these inversions.

One way to describe the relation between unbound B-chains and number 37 is dividing it according to valences of the atoms (+/-1): C-C-N, valences 4 and 3, mass  $37 + 1$ , O-O-4H, valences 2 and 1 = mass  $37 - 1$ .

Cf.  $5 \times 27$  in row 3' = 135, the mass of the A-base, gives inverted 74 as a periodic number:  $135 \wedge 740740740... \times 10^x$ .

The whole series  $15 \times 37$  has the sum 555. (Here we have numbers 37 and 111 that Shcherbak<sup>4,5,6</sup> has found as mass factors when counting on 23 aa, dividing them in 8 with "degenerated" codons and the other 15.)

The number 555 reminds of the operations of inversions that gave half and whole mass of 24 aa R+B as periodic numbers, mentioned in introduction<sup>1</sup>. A note about those numbers 555 and 55 may be added: In the decimal period  $1/3276 = 305 \ 250 \ 305 \ 250$  the sum  $305 + 250 = 555$  and the difference = 55. (55 is the sum of an  $x^2$ -series  $25 - 16 - 9 - 4 - 1$ ,  $1/55 = 18$ , H<sub>2</sub>O as periodic.)

$111 = 3 \times 37$ , is the mass of the C-base (often the methylated in epigenetic context).

- Sum 35 =  $3' + 2'$ ,  $27 + 8$ :

The numbers were commented on in section 3.2 and figure 3.2 above on Mx-coded aa =  $2 \times 385$ ,  $2 \times 11 \times 35$ .

- Interval 19 =  $3' - 2'$  =  $27 - 8$ :

A first note: intervals  $37 + 19 = 4' - 2'$  = 56, the sum of a bound B-chain.

The series  $19 \times 15 = 95 - 76 - 57 - 38 - 19$ , sum 285.

The sum 285 is half the mass R of domains C2 + U2. The aa in these groups contain the main hydrophobic aa. (perhaps Ile and Leu doubled in codons to give strength to globular proteins?) Here the middle number 57 is the mass R of the 2 Ile and 2 Leu,  $4 \times 57 = 228$ .

$$C2 = 133 = 7 \times 19.$$

$$U2 = 437 = 23 \times 19.$$

$$C2: \text{ Ala GC} + \text{ Pro CC} = 57 = 3/7$$

$$\text{ Ser UC} + \text{ Thr AC} = 76 = 4/7$$

U2:  $437 = 2 \text{ Ile} + 2 \text{ Leu}$ , sum 228 ( $12 \times 19$ ) + rest 209 =  $11 \times 19$ :

$$\begin{aligned} \text{Val GU} + \text{Phe UU} &= 134, 7 \times 19 + 1, \\ \text{Met AUG} &= 75, 4 \times 19 - 1. \end{aligned}$$

H-atoms<sup>1</sup>, 152 in the total 1504, were  $8 \times 19$ , divided on domains G1 19, C1 38 -1, U1 38 -1, and A1 57 + 2,  $\sim 1/8, 2/8, 2/8, 3/8$ .

285, -/+ 152 gives the domains C2 — U2,  $133 - 437 = 570$  (as ten Leu or Ile).  
(Quotient  $285/152 = 15/8 = 1.875$ , this Rydberg-factor again  $\times 10^x$ .)

*A note about intervals and carbohydrates:*

Intervals of first order in the  $x^3$ -series = 61-37-19-7-1, times first column 5 in the  $x^3$ -series = 305 - 185 - 95 - 35 - 5. Secondary intervals = 120 - 90 - 60 - 30 might point to underlying sugar pieces, as 90 + 60 at middle steps 27 - 8 representing a ribose, with + 30 an hexose.

Same secondary intervals of the  $x^3$ -series times 1 = 24 - 18 - 12 - 6. Intervals 18 -12 at the middle numbers 27 - 8 might represent H2O and the C-atom,  $\rightarrow \text{HCOH}$ .

**4. Valences — and a view on the doubly encoded aa**

Valences of atoms in the genetic code represents a series 5  $\rightarrow$  1:

P	C	N	O/S	H
5	4	3	2	1

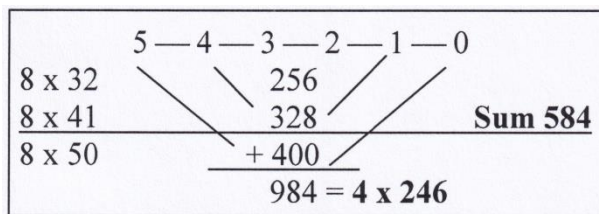
An atom as P with valence 5 seems necessary for development of life! (Bonds notably divided 3+2 to oxygen around phosphorus,)

In the background model an angled view on the 5-dimensional basic chain implies 3 polarizations of 5 into 5 — 0, 4 — 1 and 3 — 2.

In synthesis of the bases and in other contexts the molecules that add C-atoms, valence 4, to the rings replace H-atoms, valence 1, and N-atoms, valence 3, replace oxygen O, valence 2. It gives in terms of valences synthesizing steps 3 $\leftarrow$  2 and 4 $\leftarrow$  1, to compare with the basic chain (5 $\rightarrow$  0) regarded as three polarizations of 5.

Reading the steps as 2-digit numbers outwards gives the sum  $50 + 41 + 32 = 123$ . The angled

”loop” view, figure 4.1, on the total sum of valences in 24 aa = 984, R+B:



**Fig.4.1.** The total sum of valences in 24 aa R+B= 984. An angled view on the basic series. (584 = 2 x 5’ in the ES-series).

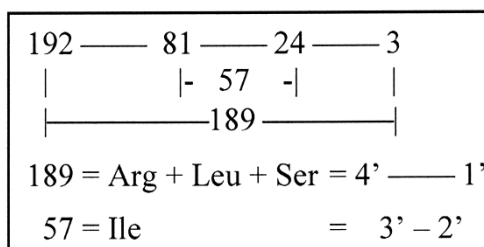
Sum of valences when B-chains bound:  $984 - 24 \text{ H}_2\text{O} (= - 96) = 888$ .

If counting on a total mass of R 1500 and all B-chains bound à mass 56, valences get divided on B-chains  $24 \times 15 = 360$  and on R = 528.

Sum of valences R + B in all 24 aa unbound are divided:

$$\begin{aligned} 4 \times 128 \text{ C} + 1 \times 244 \text{ H} + 3 \times 36 \text{ N} + 2 \times 58 \text{ O} + 2 \text{ S}: \\ \text{Valences } 4 + 1 = 756 = 4 \times 189 \\ \text{Valences } 3 + 2 = 228 = 4 \times 57 \dots \text{ Sum } 984 = 4 \times 246. \end{aligned}$$

Now, the numbers 189 and 57 appear as intervals in the  $x^3$ -series, column  $\times 3$ , and coincide with the atomic masses of the 4 doubly encoded aa, figure 4.2:



**Fig. 4.2.** Interval numbers in column  $\times 3$  of the  $x^3$ -series  $\times 15$ . One suggested view on the 4’extra’ aa.

Cf. Column  $\times 3$  equivalent with sum of columns  $\times 1$  and  $\times 2$ , which in a dimensional aspect might be regarded as debranched “d-degrees” from steps 5  $\rightarrow$  4  $\rightarrow$  3, as “extras” ( $5-4-3-2-1 = 5-4-3-3 = 5-4-6^*$ , a note below.)

The 4 aa seem to line up elementary polarities in the basic chain. A possible function? How the relation between the properties Valences versus

Mass should be interpreted, if some relevance in this figure, is here left as an open question. (Valences as potential bonds might be seen as expression of forces on an underlying level of higher d-degree, which as such and generally gets realized as mass on next lower degree (this also implying development of the side chains R.) What's clear is that the 4 aa represent at least two basic polarities, the one between hydrophobic and more polar aa and that within the AG-pair Arg — Ser, the N — O polarity.

Mass sum of the 4 aa R = 246, 6 times 41, ¼ of total valences.

R+B: Arg<sup>2</sup> + Leu<sup>2</sup> + Ser<sup>2</sup> = 410, + Ile<sup>2</sup> = 541. The sum of valences, number 984, appears in the x<sup>3</sup>-series as a difference in step 3-2:

$$12(4^3 + 3^3, 91) = 1092.$$

12(2<sup>3</sup> + 1<sup>3</sup> = 9) = 108. Difference 1092 – 108 = 984.

\*Bonds in nucleotide pairs get in the Mx-Nmx-division ordered: 5 in Mx-coded aa, 4 in A-U-group of Nmx-coded aa, 6 in G+C-coded aa. The same order 5-4-6 concerns the Cs-numbers of keto acids in the citrate cycle from α-keto-glutarate. 5-4-6 as an instruction sign?

### 5. The 3/1-division of atom kinds, also ~ valences

The valences of the atoms appear as one important guiding factor of the whole code.

It was earlier observed<sup>2</sup> that in the division of atom kinds in side chains (R) the sums of Cs and N became three times the sum of O+S+H, a division of mass on atoms with valences 4+3 versus 2+1, counting on the total 1504 in R.

$$Cs + N = 1128$$

$$O+S+H = 376... \text{Quotient } 3/1$$

It can here be observed that these numbers equal the first three columns in the x<sup>3</sup>-series × 15, figure 3.1 above when reduced with 4 H, row 5', n × 125:

$$\text{Columns } (5 + 4) \times 5' = 1125 = 1128-3$$

$$\text{Column } 3 \times 5' = 375 = 376-1$$

Obviously it's the atom group O+H+S with valences 2+1 that is separated here, the mass division between Cs and N not concerned.

(With the ES-series the 3 atom groups could be derived in a simple way<sup>2</sup>:

$$584 - 208 = 376 = O+H+S$$

$$+ \frac{376 - 208}{2} = 168 = N$$

$$= 960 \quad 416 \quad 544$$

Cs = 960 = A+U-domains, Re 544 = G+C-domains of aa.).

Now, this same relation to atoms O+H+S shows up also in the separate base-pair groups A1+U1 and G1+C1, figures 5.1 and 5.2. (There are equal numbers of N and O in R-chains of these groups, 6 N and 5 O:

$$G + C, \text{ mass R} = 544 = 4 \times 136:$$

$$G1+C1: 27 C + 6 N + 5 O + 56 H.$$

Valences, signed v

$4^v + 3^v$		$1^v + 2^v$	
Cs 324	— (-268) —	56 H	
N 84	— (-4) —	80 O	
408	↓	136	<i>Quotient 3 / 1.</i>
	-272		
	$\frac{1}{2} \times 544$		

**Fig. 5.1.** *Quotient 3/1 in mass of (Cs+N)/(O+S+H) in G1+C1-domains*

$$A+U, \text{ mass R } 960 = 4 \times 240:$$

$$A1+U1: 53 C + 6 N + 5 O + 96 H, +2 S$$

$4^v + 3^v$		$1^v + 2^v$	
Cs 636	— (-540) —	96 H	96
N 84	— (-4) —	80 O	+ 64 S = 144
720	↓	176	240
	-544		
720	↓	240	<i>Quotient 3 / 1</i>
	480		
	$\frac{1}{2} \times 960$		

**Fig. 5.2.** *Quotient 3/1 in mass of (Cs + N)/(O+S+H) in A1+U-domains*

The difference between codon groups, (A1+U1) – (G1+C1) in Cs+N = 720 – 408 = 312, in O+S+H = 240 – 136 = 104. Sum 416 (2× 3' in ES), divided 3/1.

About the marked intervals without sulfur S above it might also be remembered<sup>1</sup> that mass of domains G + C = 544, + 272 = 816 = U1 + C1, and A+U = 960, – 272 = 688 = G1 + A1.

*Why this strict 3/1-division in valences of atoms?*

One association goes to the more general exclusion of water in glycolysis and synthesizing processes. Another to the background model, figure 1.1 where lower d-degrees are seen debranched from higher steps, meeting the other way around.

The “octet rule” demonstrates on the atomic level the 1/3-quotient: the power or forces that drive atoms to seek 6 electrons in their outer shell above 2 in an inner, deeper shell, the octet rule (not fully understood) implies this 3 - 1-relation, p- versus s-orbitals. (So it also seems to be with the division of gluons as 6 + 2 in the nuclei of atoms.)

If the basic series is taken as a dimensional evolution towards lower degrees there is the step  $4 \rightarrow 3, + 1$ , thus into a quotient  $3/1$ .

Cf. also the missing electrons in the p-shell of the C-atom, 1 “outwards”, 3 “inwards”, as in the tetrahedron of an amino acid.

The equal division within these *base-pair* domains supports a view that it's these base-pairing, in DNA or at the meeting of mRNA-tRNA at ribosomes that is relevant for the distribution of codons.

## 6. Theme 81 — 47

Another example of a relation equally showing up in the separate *base-pair* groups, as in section 5 above, is the number of Cs in R+B in relation to all atoms in R, shortly mentioned earlier<sup>2</sup>, with more comments here:

### 6.1. Cs and number of atoms:

All C-atoms in 24 aa,  $R+B = 128$ .

All atoms in R are twice that number = 256.

Number of C-atoms divided on main domains, R + B:

Cs:  $G1+C1 = 47$  (B+R), all atoms in R =  $2 \times 47$

Cs:  $A1+U1 = 81$  (B+R), all atoms in R =  $2 \times 81$

This is only valid for the base-pairs, not for single domains.

The question Why? remains unanswered.

## 6.2 Cys and His

Cys 47 (UGY) + His 81 (CAY), mass numbers in R, are the active aa in the enzyme dividing fructose at start of the glycolysis<sup>10</sup>. (Their codons, first two bases, are each other's anti-codons if read in opposite directions.)

### 6.3. B-R-chains:

The division  $-/+1$  happens to correspond with the one between number of Cs in B- and R-chains, cf. section 2. However, it's hard to find a relation to this division on B and R, sooner the opposite.

$$47 + 1 = \text{C-atoms in B-chains } 48$$

$$81 - 1 = \text{C-atoms in R-chains } 80$$

### 6.4. Domains from $-/+ 81$ and 47:

#### 6.4.1. Single base domains:

Partly noted earlier<sup>1</sup> was that these numbers,  $-/+1$ , in the ES-series gave single base domains of aa in R:

$$\underline{544 = 5' + 4'}, \underline{416 = 2 \times 3'}:$$

$$544/2, - 81 = 191 = G1 \text{ and } + 81 = 353 = C1.$$

$$544 - 81 = 463 = U1 \text{ and } 416 + 81 = 497 = A1$$

$$544 - 47 = 497 = A1, 416 + 47 = 463 = U1.*$$

(\*Cys 47 from Meth AUG to an U1-code?)

#### 6.4.2. Nmx, division within the A1+U1-group:

$$A1 = 320, + 47 = 367 = 3' + 2' \text{ in ES-series}$$

$$U1 = 255, - 47* = 208 = 3' \text{ in ES-series}$$

(\*Cys here still as belonging to AUG?)

#### 6.4.3. Nmx and Mx:

Division of aa R on  $688 = G1+A1$  and  $816 = U1+C1$  in a total of R 1504 has the difference 128, ~ Cys + His. Mass difference 34. Relation to mass of Mx- and Nmx-coded aa with masses 770 and 734 with the difference 36 (~ 2 H<sub>2</sub>O):

$$+/- 47: U1+C1 = 816, - 47 = 769 = Mx 770, -1$$

$$G1+A1 = 688, + 47 = 735 = Nmx 734, +1$$

$$-/+ 81: U1+C1 = 816, - 81 = 735 = Nmx 734, +1$$

$$G1+A1 = 688, + 81 = 769 = Mx 770, -1$$

The role of His and Cys-Cys-bonds (-2H) in structuring the proteins?

## 7. Fundamental numbers

*A gathering of annotations*

**7.1. Numbers 4 → 3 squared = 16 - 9. Interval 7**

Much indicates that the step 4→3 is fundamental in the code, with 4 – 3 as factors. One aspect is that these numbers are the valences of C and N, characterizing proteins.

4 and 3 squared times 12 (= 4 × 3) gives 192 — (84) — 108, figure 7.1.

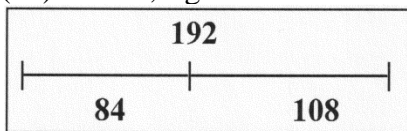


Fig. 7.1. 12 times 16, 7 and 9

192 is a factor in Cs, 84 in total N-atoms.

$5 \times 192 = 960 = \text{A+U-domains} = \text{all } 80 \text{ Cs in R.}$

$5 \times | -84 = 420, \text{ interval}^*$

$5 \times 108 = 540 = \text{G+C-domains } (-4^{**})$

\*420 also the sum of the molecular group of 8 aa with only C-atoms and/or H in R.

Displacement of 4 units from 420 to 540 gives the numbers 416 and 544 in the ES-series.

\*\*540 = Re – 4H (Lys + 2 Arg uncharged, + Glu assumed charged, for a total of 1500).

Total sum of Cs R+B =  $8 \times 192$ , in R =  $5 \times 192$ , divided 3 — 2 in the two-peak pyramid, on the basic series 5 → 0, figure 2.1. = 576 and 384.

Total sum of B-chains in 24 bound aa is  $7 \times 192 = 960 + 384$  in figure 2.1. (For another view on number 192, see Négadi<sup>8</sup>.)

The factors 192 - 84 - 108 were intervals in the ES-series<sup>1</sup>.

$5' \rightarrow 1' = 192, 5' \rightarrow 3' = 84, 3' \rightarrow 1' = 108$

Number  $84 \times 2 =$  the sum of the 12 N-atoms in 24 aa R.

In the *weight series*<sup>2</sup> the same factors appeared in its parts, the L—H-chains (when counting on a total R as 1500, (– 4 H in Re):

Cs:  $192 \times 2 = 384, \times 3 = 576$  Sum 960

Re:  $108 \times 2 = 216, \times 3 = 324$  Sum 540

L 600      H 900

It might be added that the sum of *valences* of atoms in R of G1 + C1-domains sum up to 192:

Cs = 108 (4 × 27) and Re = 84. (Valences)

The  $x^2$ -series times 60 gives the simplest derivation of the main codon domains:

$4^2 = 16, \text{ times } 60 = 960 = \text{A+U} = \text{Cs}$

$3^2 = 9, \text{ times } 60 = 540 = \text{G+C } (-4) = \text{Re}$

Factor 60 from  $5 \times 4 \times 3$ .

(Why squares of what can be identified with valences? Cf. Rydberg’s formula for spectral lines of orbitals in hydrogen, factors from intervals between inverted squares.)

It could be added that the  $2x^2$ -series behind shells and orbitals in the Periodic system times  $\log 2$  (or 0.3) ×  $10^2$  gives the approximate division of aa on codon pairs and Cs — Re from 5’-4’-3’:

$50 - 32 - 18, \times \log 2 \times 10^2 = 1505. - 963. - 542.$

*A note on B-chains:*

Triplets in the basic series of integers 5 → 0 read in opposite directions, inwards and outwards (giving mass number 135 for the A-base):

$543 \rightarrow + \leftarrow 012 = 555, \wedge = 18181818... \times 10^x$

$345 \leftarrow - \rightarrow 210 = 135, \wedge = 74074074... \times 10^x$

Difference:  $560560560... \times 10^x$ , bound B-chains.

(Sum 690 equal to 3 P-ribose-groups à 230, 98 + 150 – 18.)

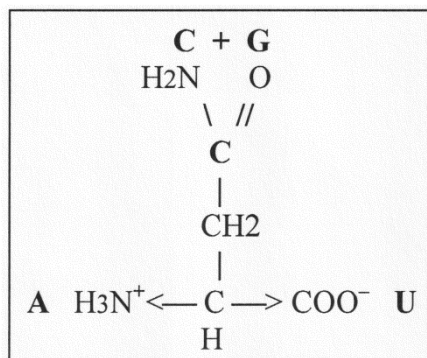
**7.2. The coding bases and numbers 192 — 108 — 84**

A base-pair A+U or G+C has 9 C — 6 N in the rings:

Masses: Cs: 108 — N: 84 = sum 192.

This fact might be one reason why these types of bases are chosen, or inversely, which groups of aa are chosen — and the fact that the bases mainly are constructed by aa. The sum of external additions or “tags” to the 4 bases of H, O and N = 125 =  $15^2$ , equal to 5’ in the  $x^3$ -series, A = 19, U = 36, G = C = 35 in mass. 35 is the sum of 3’ + 2’ in the  $x^3$ -series, 19 the interval. The low number of A might be connected with its special role.

The aa Asn, figure 7.2, or Gln can illustrate the distribution of external tags to the bases: backbone part the opposition N — O as additions to A- and U-base, the R-chain with both N and O the G and C-bases.



**Fig. 7.2.** *The amino acid Asn. Coding bases marked at their addends. Not to mix with the relation aa - codons*

In this sense the backbone chains as dipoles might be regarded as longitudinal waves in d-degree 4, developing side-chains as T-waves<sup>1</sup>, representing d-degree 3 in this context; corresponding to A+U-domains = total Cs, valence 4, and G+C-domains to Re-sums, valences 3 and 2+1.

It was noted<sup>1</sup> that the mass of main aa building the coding bases was Gly 75 = 3/4 × 10<sup>2</sup> (purines) and Asp 133 ≈ 4/3 × 10<sup>2</sup> (pyrimidines). Numbers 4, 3 to observe.

**7.3. Transformations between number base systems:**

Transformations (TR) between number base systems (nb-x) was introduced<sup>1</sup> as a hypothetical internal reference system, (assuming a background in dimensions), since mass of the 4 coding bases in 4 sets transformed to nb-8 gave masses of the coded aa R+B (+/-1 in G+C) and many more astonishing things. First to note about 192 and 108:

192 in nb-10 → 300 in nb-8, growth 108.

108 in nb-10 → 300 in nb-6, growth 192.

And 300 in nb-16 = 3276 in nb-6, the total sum of 24 aa R+B in nb-10.

A similar "reference pattern" was found in the L-H-series.<sup>2</sup>

Here codon bases times 4 is shown to give the aa sums R+B in another way; nb-x given as only index digits below and A- and U-bases with operator ×4 after transformation.

Numbers in nb-8 and nb-6 are here as before freely rewritten using digits from higher nb-

systems, as 638 and 640 in nb-8 give the same amount when transformed to nb-10:

$$4 \times G \ 151 = 604-10 = 1134-8$$

$$\underline{U \ 112-10 = 160-8, \times 4 = 640-8 = 638-8}$$

$$\text{Sum } 1772-8, \sim 24 \text{ B-chains in nb-10}$$

$$4 \times C \ 111 = 444-10 = 674-8$$

$$\underline{A \ 135-10 = 207-8, \times 4 = 828-8 = 830-8}$$

$$\text{Sum } 1504-8, \sim 24 \text{ R-chains in nb-10}$$

$$4 \text{ G+C-bases in nb-8} = 1808 = A1 + C1 \text{ in nb-10}$$

$$4 \text{ A+U-bases in nb-8} = 1468 = G1 + U1 \text{ in nb-10}$$

The 4 base-pairs give the same numbers as for aa domains in nb-10 with an exchange between G1 and A1-domains. (It's said that editing RNA often implies an exchange A to G. Why?)

(More on such transformations and other material on the author's home page: <https://u5d.net/Genetic-code/index.html>)

**7.4. The basic series of integers 5 → 0**

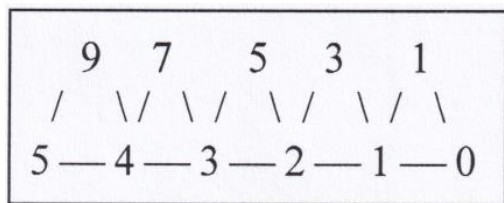
$$\text{The basic series: } 5 \frac{\text{---}}{9} 4 \text{---} \frac{\text{---}}{6} 3 \text{---} 2 \text{---} 1 \text{---} 0.$$

It might be noted again that the 3/2-division (as in L—H-chains when counting on a total 1500 appears in step 4→3 in this basic series.

The main codon groups A1+U1 = 9-6-0 and G1+C1 as = 5-4-0 might simply be read directly from this basic series, as this might be summed up 5-4-3-3 or 546, which times 6 = gives total mass R+B of aa, 3276, and equals Mv of 4 aa R+B, 2 × 273.

A speculative association: 1/9 + 1/6 ~ 0.2777 = 2 × 0.13888, = 2 times the factor (1/4 – 1/9) in Rydberg's formula on the 3rd level for spectral lines of hydrogen in the Balmer series. (1/6 – 1/9 = 0.0555... = the inversion of 18, ~ H2O.)

The superposed series, figure 7.3, gives the 16 — 9 division at 3 in the basic series, (9 + 7) and (5+3+1):



**Fig. 7.3.** The basic series with the next superposed one, equal to row 5 and 4 in the number pyramid, figure 2.1..

If read as two triplets, 975 and 531 with sum 1506, a single displacement of 15 gives the two base-pair domains R with + 2 in G+C-domains:

$$975 - 15 = 960 = \text{A+U-domains, R}$$

$$531 + 15 = 546 = \text{G+C-domains} + 2, \text{R} *$$

Ala, GC-coded, mass 15, equals the sum of the underlying series.

In number of aa there is the division 7 – 5: A+U-coded aa, 2 × 7 with mass sum 60 × 16, (9 + 7), and G+C -coded aa 2 × 5 with mass sum 60 × 9 (5+3+1).

The superposed series approximates the division of aa in classes I and II: 977 and 527 in the total 1504.

Sum of all R-chains = 2 times 7-5-3 = 1506 – 2 when calculating with R = 1504.

\* It might be remembered<sup>1</sup> that summing 4 two-digit numbers up and down in these combined series gave the sums 273 and in next step 207, also close to the masses of charged π-mesons and μ-leptons in electron mass:

$$\text{a) } 5 \rightarrow 3: 59 + 94 + 47 + 73 = 273, \times 2 = 546$$

$$\text{b) } 4 \rightarrow 2: 47 + 73 + 35 + 52 = 207, \times 2 = 414$$

$$\text{Sum } 960$$

## 7.5. Number 7 —the interval 16 —9

### 7.5.1. Number of atoms 468 and total mass:

Total number of atoms in 24 aa R+B = 468. (In 20 aa 2 × 192, + in 4 double-coded aa 84.)

Total mass sum of 24 aa R+B = 3276 = 7 × 468. Thus, Mv of mass of an atom in the 24 aa becomes exactly 7 (as Z of the characterizing nitrogen N or sum of valences C+N, 4 + 3). Mv mass of an atom is close to 7 also in separate domains A1+U1 and G1+C:

$$\text{A1+U1} = 286 \text{ atoms. R+B} = 1994, /7 = 284.86.$$

$$\text{G1+C1} = 182 \text{ atoms. R+B} = 1282, /7 = 183.14.$$

### 7.5.2. Number of atoms without H in R+B in 24 aa:

$$468 - 244 \text{ H} = 224 = 7 \times 32.$$

$$4/7 = \text{C-atoms} = 128,$$

$$3/7 = \text{N+O+S-atoms} = 96 (36 + 58+2).$$

The 4-3-relation expressed in another form, R+B: Cs = 16 × 8, substituents N-O+S = 16 × 6, gives an association to intervals for orbitals in the 2x<sup>2</sup>-series: the octet rule and number 6 for the p-orbital. Or f-orbital 14 divided 8 - 6 as in 8 sphere quadrants and 6 poles of 3 coordinate axes.

### 7.5.3. Atoms with valences 3 —2 in R:

Mass sum 392 = 544 minus H-atoms 152 in a total R 1504: 392 = 292 + 100, 152 = 252 – 100 (in ES-numbers). Mass sums:

$$\text{O+S: } 224 = 4 \times 56. \text{ Sum of valences } 24$$

$$\text{N: } 168 = 3 \times 56. \text{ Sum of valences } 36$$

In sums of mass a 4/3-relation, in valences a 2/3-relation.

### 7.5.4. The number 468 as a sum of squares?

$$= 324 \rightarrow 18^2$$

$$+ 144 \rightarrow 12^2 \quad 18 = \text{H}_2\text{O}, 12 = \text{C-atom.}$$

The view gives a connection to sugar pieces. 324 – 144 = 180 (an hexose).

Quotient 324/144 = [3/2]<sup>2</sup> = 9/4 = 2.25, the sum of the x<sup>3</sup>-series × 10<sup>-2</sup>.

The numbers are also squares of first whole shells in the Periodic system: 2 + 10 and 18.

### 7.5.5. The String theory:

It has been said that 7 dimensions are “undeveloped” in that theory. A curious statement since it seems extraordinary developed in the “property” of life. — and in our brains as a multitude of universes.

## 8. Discussion

Codes as such are often seen as of unlimited choice, as words for something in the thousands of human languages. Yet, in human construction of codes some principles are mostly used, as for instance in the early Morse alphabet with directions of signaling arms in different combinations. In the embryological development from morula to blastula etc. (from center to anti-center) of first cells the regional differentiation of



cells and definition of different coordinate axis and polarities of different kinds are some of the principles. That's a stepwise specification through polarized directions of first few cells that represents the "Whole", the stem cells. It wouldn't be astonishing if the genetic code showed up to have followed similar principles.

The thought that a "whole" have preceded the parts in the genetic code<sup>12</sup> is involved in this analysis as in many others. It is here an analysis in terms of *Mass*, and since mass as fields were physically accepted with the 'Higg's boson', such whole entities should be more easily imaginable. (Masses of aa, here defined as numbers of nuclei, become equivalent with abbreviations of aa masses with decimals.) To the mass fields come of cause the electromagnet ones. According to the background model in figure 1 it's also ambiguous what comes first and what last in the evolution.

Dimensional views are surely accurate as opposite directions, with numbers as such rooted in polarizations. A numerical approach to mass division in the genetic code would not be strange. Dimensions get apparent in protein folding as where on level 2 the helices of aa illustrate substantiated 3-dimensional motions (a linear path and a 2-dimensional circle) and  $\beta$ -sheets 2-dimensionally structured surfaces.

When a photon is split into two complementary and are sent in different directions, however far from each other, they still show a timeless, immediate connection, a mutual dependence. They seem to identify the concept of a dimension, not to mix with quantifiable distances, dimension as a deeper level of abstraction, yet physically identifiable in quantum mechanics. (Valences and bonds around atoms pointing out dimensions, defined as directions, as a "Morse alphabet"). When a hexose of 6 Cs as fructose (within two phosphorus with valence 5) is split into two halves, 3-3 Cs, at the start of glycolysis, they show up to be complementary: one being the backbone part of lipids, forming the *circular* peripheral structure of a cell, the other leading to the at first hand *radial* proteins; geometrical polarities one essential principle.

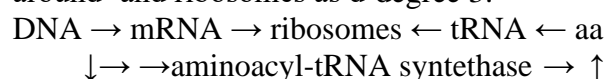
How to regard the equivalences, often  $-/+1$ , of mass numbers for differing groups of molecules

as for instance here in section 2, such similarities usually dismissed as incidental during reigning paradigm? It's proposed here that such correlations that seem to prove the relevance of an arithmetical approach, originate in principles on more elementary, deeper levels, showing up on higher, more differentiated ones;  $-/+1$  perhaps indicating a change to another coordinate axis when dimensions are seen as developed out of one another, deeply interdependant. And  $H^+$  and  $e^-$  represent elementary chemical forces.

The very fact that deviations exist in the code in some phyla (and in mitochondrial DNA) implies of cause that strict congruence with arithmetic patterns isn't a necessary condition for life, at least not in the further evolution. Underlying geometries and arithmetical patterns found in the code may have served as a stabilizing grid, a lattice to which it stepwise adapted, (as the scheme for the Periodic system on the atomic level), favoring its universality. Even if there are no known physical-chemical laws today that can explain such "wholes" or patterns, there is certainly more to discover in physics and quantum mechanics.

Why a  $5 \rightarrow 0$  of integers as the basic series here? (5 dimensions in the background model of this research, shortly mentioned in the introduction. As earlier pointed to there are for instance the 5-4-3-numerous plans in the realm of plants (and the number 5 in extremities more or less developed in vertebrates also). It is one degree more assumed for the whole, before creation of the standard 4-dimensional Space-Time (redefined in the background model). As noted in the text above the atoms of the genetic code, including phosphorus P, have valences forming this integer series 5-4-3-2-1. The sum of valences in 24 aa was 8(50, 41, 32), i.e. 8 times main polarizations of 5, which seems also to support this view.

It was suggested<sup>1</sup> also to see the whole process from codons to aa and peptides as 5 to 6 dimensional steps with aaRS as 'the other way around' and ribosomes as d-degree 3:



Life as fusion, developed and outsourced to planets, is essentially built by atoms with deficiencies, i.e. with respect to the “octet rule”, with social competence, not self-sufficient ones.

It was argued<sup>1</sup> that the enormous complexity of a cell only seems comprehensible as result of *internal* differentiations, inside a unit, demanding some unit already defined<sup>13</sup>.

### **Results:**

A number pyramid as the one in section 2, built on the basic series  $5 \rightarrow 0$ , that times  $4 \times 3$  gives the Cs-skeleton of 24 aa, implies a perpendicular evolution versus a serial one. Such a development along different coordinate axes seems to demand some form of enclosing of the series, including Stops, and the two-way-direction of the series as in figure 1.

Why “pyramids”? There are similar hierarchies in biological systems, e.g. in the protein folding. And what humans “invent” might be taken from their inner biological construction.

(Other number pyramids, there on the  $2x^2$ -series, are found in reference 2, Appendix.)

Perhaps essential to note: the sum of the basic series = 15 is related to the top number of the pyramid 80 as  $15/80 = 0.1875$ , the factor in 2nd spectral line of hydrogen in the Balmer series in Rydberg’s formula.

The  $x^3$ -series times 15 in section 3 implies serial development along two axes. There the division on Cs and Re (544 –4) in codon domains of aa showed up from  $4'$  and  $3'+2'+1'$

respectively, in accordance with valences of the atoms.

Sums and intervals in the  $x^3$ -series were shown to be factors in aa, e.g. 91 in the total R+B, 35 in the 12-group of aa with mixed codons, interval 19 the main factor in C2+U2-domains.

Valences as such of atom kinds, treated in section 4, are an own  $5 \rightarrow 0$ -series if phosphorus included. A remarkable fact, section 5, was that atoms with valences 2 plus 1 together make up exactly 1/3 of those with valences 4 and 3 in *both* base-pair domains A1+U1 and G1+C1.

An earlier noted similar equivalence between these base-pair domains in 1st position order (section 6) concerned number of nucleons and was further commented on Cs R+B times 2 = all atoms in side chains R. These facts might indicate that it is the *base-pairs* in codons (as in DNA or the tRNA-RNA meeting at ribosomes) that are decisive.

It’s also in the *base-pairs*, in their summed rings, the fundamental number 192 is found, divided  $9C = 108$ ,  $6N = 84$ , sum 15 atoms. The fundamental numbers in aa (gathered views in section 7) seem to have their origin in the squares of 4 and 3, the valences of C- and N-atoms. Mean value of all atoms in the code  $(468) = 7$ . Total sum  $R+B = 7 \times 468 = 3276$ .

### **Conflict of interest**

The author declares no conflict of interest

## References

1. Wohlin Å. Numeral series hidden in the distribution of atomic mass of amino acids to codon domains in the genetic code. *J Theor Biol.* 2015; 369: 95-109. [Crossref] <http://dx.doi.org/10.1016/j.jtbi.2015.01.013>
2. Wohlin Å. Numerical analysis of 3/2-relations in the genetic code and correlations with basic series of integers 5–0. *Biomed Genet Genomics.* 2016, Volume 1(4):1-15. DOI: 10.15761/BGG.1000118
3. Taylor F.J.R, Coates D. The code within the codons. *BioSystems.* 1989; 22:177-187. DOI: 10.1016/0303-2647(89)90059-2
4. Shcherbak VI. Twenty canonical amino acids of the genetic code: the arithmetical regularities. Part I. *Theor Biol.* 1993; 162(3): 399-401. dDOI: 10.1006.jtbi.1993.1096
5. Shcherbak VI. Sixty-four triplets and 20 canonical amino acids of the genetic code: the arithmetical regularities. Part II. *J Theor Biol.* 1994; 166(4): 475-477 DOI: 10.1006/jtbi.1994.1042.
6. Shcherbak VI. Arithmetic inside the universal genetic code. *Biosystems.* 2003; 70(3): 187- 209 doi.org/10.1016/S0303-2647(03)00066-2
7. Rakočević MM A harmonic structure of the genetic code. *J Theor. Biol.* 2004 Jul 21;229(2): 221-234. DOI: 10.1016/j.jtbi.2004.03.017
8. Négadi T. The multiplet structure of the genetic code, from one and small number. [[arxiv.org/pdf](https://arxiv.org/pdf/2011.1101.2983). 2011;1101.2983]
9. Dragovich B. Genetic code and number theory. *arXiv preprint arXiv:0911.4014*, 2009.arxiv.org
10. Karlson P. *Biokemi (Biochemistry). LiberLäromedel Lund.* 1976
11. Gell-Mann M, Néeman Y. *The Eightfold Way. W. A. Benjamin, Inc. New York, Amsterdam.* 1964; (e.g. pp 15, 29, 85)
12. Sukhodolets VV. The genetic code as a clue to understanding of molecular evolution. *J Theor.Biol.* 1989;141(3):379-89. [https://doi.org/10.1016/S0022-5193\(89\)80120-1](https://doi.org/10.1016/S0022-5193(89)80120-1)
13. Paleos C.M. A decisive step toward the origin of life. *Trends Biochem Sci.* 2015 Sep;40(9):487-8. doi: 10.1016/j.tibs.2015.06.001.