Amino acid numbering, ultimate numbers and the 3/2 ratio

Connections between genetic code and number theory

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Abstract. An unprecedented numbering of the twenty proteinogenic amino acids, itself deduced from a logical numbering of the sixty-four DNA triplets, reveals connections between the mechanism of the genetic code, of the field of Biology, and the number theory field, of which more precisely the notion of ultimate number, one of the four classes of Mathematics entities proposed to constitute the set of whole numbers. These connections are revealed in an physico-arithmetic organization of the genetic code in various ratios of 3/2 value as global configurations.

1 Introduction

After having introduced the concept of ultimate number which allows the constitution of a class of number merging the sequence of the prime numbers with the exotic numbers o (zero) and 1 (one), is presented, from the field of Biology, a numbering of the twenty proteinogenic amino acids and of sixty four codons, primordial entities of the genetic code. A cross-investigation of these different concepts reveals arithmetic connections manifesting themselves in various ratios of value 3/2 simultaneously from the field of Mathematics and that of molecular Biology.

2 The ultimate numbers

The concept of numbers ultimity has been introduced in the article *"The ultimate numbers and the 3/2 ratio"* [1] where singular arithmetic phenomena are presented in relation to the different classifications of numbers deduced from this new concept. In a second paper *"New Whole Numbers Classification"* [2], a new classification of whole numbers was therefore proposed and introduced. These two papers describes how the set $\mathbb{N}$ (of whole numbers) can be organized into subsets with arithmetic properties proper and unique but also, simultaneously interactive.

2.1 Concept of ultimate number

The definition of thus called *prime numbers* did not allow the numbers zero (0) and one (1) to be included in this set of primes. Thus, the set of whole numbers was scattered in four entities: prime numbers, non-prime numbers, but also ambiguous numbers *zero* and *one* at exotic arithmetic characteristics. The double definition of ultimate and non-ultimate numbers proposed here makes it possible to properly divide the set of whole numbers into two groups of numbers with well-defined and absolute characteristics: a number is either ultimate or non-ultimate. In addition to its non-triviality, the fact of specifying the numerically lower nature of a divisor to any envisaged number effectively allows that there is no difference in status between the ultimate numbers zero (0) and one (1) and any other number* described as ultimate.

* In statements, when this is not specified, the term "number" always means "whole number". It is therefore agreed that the number zero (0) is well integrated into the set of whole numbers.

2.1.1 Definition of an ultimate number

Considering the set of whole numbers, these are organized into two sets: ultimate numbers and non-ultimate numbers.

Ultimate numbers definition:

> ***An ultimate number not admits any non-trivial divisor (whole number) being less than it.***

Non-ultimate numbers definition:

> ***A non-ultimate number admits at least one non-trivial divisor (whole number) being less than it.***

Note: a non-trivial divisor of a whole number *n* is a whole number which is a divisor of *n* but distinct from *n* and from 1 (which are its trivial divisors).

2.1.2 Other definitions

Let *n* be a whole number (belonging to $\mathbb{N}$), this one is ultimate if no divisor (whole number) lower than its value and other than 1 divides it.

Let *n* be a whole number (belonging to $\mathbb{N}$), this one is non-ultimate if at least one divisor (whole number) lower than its value and other than 1 divides it.

2.2. The four classes of whole numbers: the NWNC

The segregation of whole numbers into two sets of entities qualified as ultimate and non-ultimate is only a first step in the investigation of this type of numbers. Here is a further exploration of this set of numbers revealing its organization into four subsets of entities with their own but interactive properties.

2.2.1 Four different types of numbers

From the definition of ultimate numbers introduced above, it is possible to differentiate the set of whole numbers into four final classes, inferred from the three source classes and progressively defined according to these criteria:

Whole numbers are subdivided into these two categories:

- **ultimates**: an ultimate number not admits any non-trivial divisor (whole number) being less than it.

- **non-ultimates**: a non-ultimate number admits at least one non-trivial divisor (whole number) being less than it.

Non-ultimate numbers are subdivided into these two categories:

- **raiseds**: a raised number is a non-ultimate number, power of an ultimate number.

- **composites**: a composite number is a non-ultimate and not raised number admitting at least two different divisors.

Composite numbers are subdivided into these two categories:

- **pure composites**: a pure composite number is a non-ultimate and not raised number admitting no raised number as divisor.

- **mixed composites**: a mixed composite number is a non-ultimate and not raised number admitting at least a raised number as divisor.

2.2.2 Degree of complexity of number classes

The table in Figure 1 summarizes these different definitions. It is more fully developed in Figure 5 Chapter 5.1 where the interactions of the four classes of whole numbers are highlighted.

<table>
<tr><th colspan="4">The whole numbers:</th></tr>
<tr><th>The ultimates:</th><th colspan="3">The non-ultimates:</th></tr>
<tr><td rowspan="5">an ultimate number not admits any non-trivial divisor (whole number) being less than it</td><td colspan="3">A non-ultimate number admits at least one non-trivial divisor (whole number) being less than it</td></tr>
<tr><th>The raiseds:</th><th colspan="2">The composites:</th></tr>
<tr><td rowspan="3">a raised number is a non-ultimate number, power of an ultimate number</td><td colspan="2">a composite number is a non-ultimate and not raised number admitting at least two different divisors</td></tr>
<tr><th>The pure composites:</th><th>The mixed composites:</th></tr>
<tr><td>a pure composite number is a non-ultimate and not raised number admitting no raised number as divisor</td><td>a mixed composite number is a non-ultimate and not raised number admitting at least a raised number as divisor</td></tr>
<tr><th>level 1</th><th>level 2</th><th>level 3</th><th>level 4</th></tr>
<tr><td colspan="4">degree of complexity of the final four classes of numbers</td></tr>
</table>

Fig. 1 Classification of whole numbers from the definition of ultimate numbers (see Fig. 5 and 7 also).

2.2.3. New Whole Numbers Classification

By the previous definitions and demonstrations, we propose the classification of the set of whole numbers into four subset or classes of numbers:

- the ultimate numbers called ***ultimates*** (***u***),
- the raised numbers called ***raiseds*** (***r***),
- the pure composite numbers called ***composites*** (***c***),
- the mixed composite numbers called ***mixes*** (***m***).

2.2.3.1 Conventional number denominations

So it is agree that designation "ultimates" designates ultimate numbers (as "primes" designates prime numbers). Also it is agree that designation "raiseds" designates raised numbers, designation "composites" designates pure composite numbers and designation "mixes" designates mixed composite numbers. It is also agreed that is called u an ultimate number, r a raised number, c a pure composite and m a mixed composite number.

2.2.4 Hierarchical organization charts of whole numbers

Thus this set ℕ can be described by a hierarchical organization of its components. At the end of the hierarchy are the four new classes of numbers previously introduced. Figure 2 illustrates this organization.

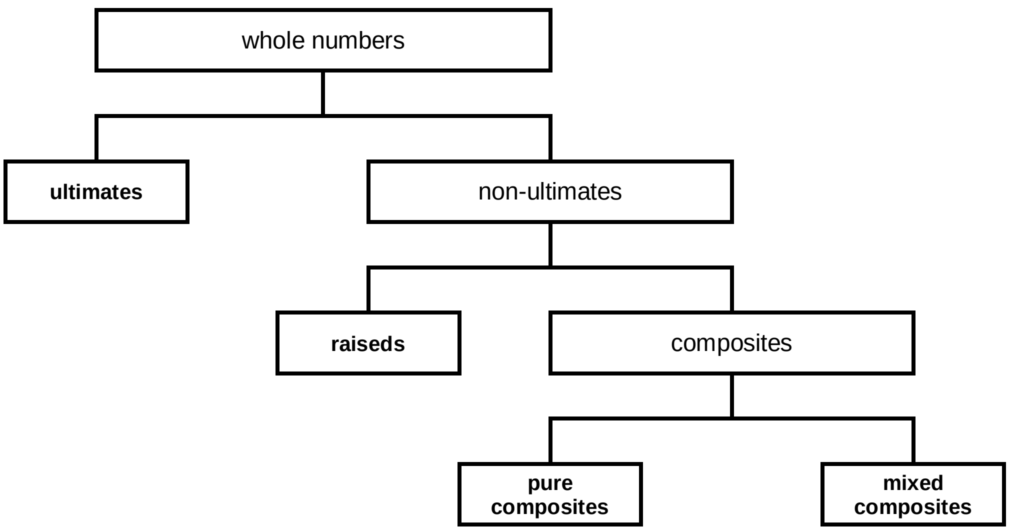


Fig. 2 Hierarchical classification of whole numbers since the definition of ultimate numbers.

This new classification of the whole numbers is called *"New Whole Numbers Classification"* and and *NWNC* for short.

2.3 NWNC and 3/2 ratio

The progressive differentiation of source classes and final classes of whole numbers is organized (Figure 3) into a powerful arithmetic arrangement generating transcendent ratios of value 3/2. Thus, the source set of whole numbers includes, among its first ten numbers, 6 ultimate numbers against 4 non-ultimate numbers. The next source set, that of the non-ultimates, includes, among its first ten numbers, 4 raised numbers against 6 composite numbers. Finally, the source set of composites includes, among its first ten numbers, 6 pure composites against 4 mixed composites.

The first 10 whole numbers: 0 1 2 3 4 5 6 7 8 9

6 ultimates: 0 1 2 3 5 7 **← 3/2 ratio →** 4 non-ultimates: 4 6 8 9

The first 10 non-ultimates: 4 6 8 9 10 12 14 15 16 18

4 raiseds: 4 8 9 16 **← 2/3 ratio →** 6 composites: 6 10 12 14 15 18

The first 10 composites: 6 10 12 14 15 18 20 21 22 24

6 pure: **← 3/2 ratio →** 4 mixed:

0 1 2 3 5 7	**← 3/2 ratio →**	**4 8 9 16**	**← 2/3 ratio →**	**6 10 14 15 21 22**	**← 3/2 ratio →**	**12 18 20 24**
11 13 17 19	**← 2/3 ratio →**	25 27 32 49 64 81	**← 3/2 ratio →**	26 30 33 34	**← 2/3 ratio →**	28 36 40 44 45 48
3/2 ratio		**2/3 ratio**		**3/2 ratio**		**2/3 ratio**
The first 10 ultimates		*The first 10 raiseds*		*The first 10 pure composites*		*The first 10 mixed composites*

10 mixed composites

20 composites (pure and mixed)

30 non-ultimates

The 40 primordial numbers

Fig. 3 From the first ten numbers of the three source classes of whole numbers, generation inside 3/2 ratios of the first ten numbers of each of the four final number classes: the 40 primordials. See Fig. 1 and Fig. 2 also. See referenced papers [1] and [2], A very strong entanglement links all these sets of numbers which oppose in multiple ways in ratios of value 3/2 (or reversibly of ratios 2/3). For example, the first 6 ultimates (0-1-2-3-5-7) are simultaneously opposed to the 4 non-ultimates (4-6-8-9) among the first 10 natural numbers, to the 4 raiseds of the first 10 non-ultimates (4-8-9-16) and to the 4 ultimates beyond the first 10 whole numbers (11-13-17-19). This is just an overview of many arithmetic phenomena presented in referenced papers [1] and [2],

3. Numbering of the twenty proteinogenic amino acids

The concept of numbering of the twenty proteinogenic amino acids has been introduced in the article *"Numbering of the twenty proteinogenic amino acids: 3/2 ratios inside the genetic code"* [3] where singular arithmetic phenomena are presented in relation to the different attributes of the amino acids and the nature of their respective codons.

From a subtle numbering of the 64 codons of the universal genetic code, we propose a numbering (from 0 to 19) of the twenty amino acids. These two numbering systems, including the first proposed by Professor Sergey Petoukhov [4], are very directly dependent on the physico-chemical properties of the four nucleobases that make up DNA. They are therefore very legitimate to be used for the study of the genetic code mechanism. By "genetic code", we consider in this paper the totality of its components, namely simultaneously the 64 codons and the twenty encoded amino acids.

3.1 Codons numbering

In order to be able to number the twenty proteinogenic amino acids, we must first proceed to a numbering of the 64 codons of the universal genetic code. Also, this numbering of amino acids must depend on the physico-chemical character of the nucleobases constituting the codons. To this end, we use the very original numbering devised by Professor Sergey Petoukhov, which is based on the possible deamination and depurination of the four nucleobases.

3.1.1 Petoukhov's numbering of the 64 genetic code codons

In his investigations of the genetic code [4] Sergey Petoukhov assigns a number from 0 to 63 to each of the sixty-four codons. This Petoukhov numbering is directly dependent on the physico-chemical properties of the four DNA coding bases.

	111	*110*	*101*	*100*	*011*	*010*	*001*	*000*
111	CCC Pro 63 111111	CCA Pro 62 111110	CAC His 61 111101	CAA Gln 60 111100	ACC Thr 59 111011	ACA Thr 58 111010	AAC Asn 57 111001	AAA Lys 56 111000
110	CCT Pro 55 110111	**CCG** **Pro** **54** **110110**	**CAT** **His** **53** **110101**	**CAG** **Gln** **52** **110100**	ACT Thr 51 110011	**ACG** **Thr** **50** **110010**	**AAT** **Asn** **49** **110001**	**AAG** **Lys** **48** **110000**
101	CTC Leu 47 101111	CTA Leu 46 101110	CGC Arg 45 101101	CGA Arg 44 101100	ATC Ile 43 101011	ATA Ile 42 101010	AGC Ser 41 101001	AGA Arg 40 101000
100	CTT Leu 39 100111	CTG Leu 38 100110	CGT Arg 37 100101	CGG Arg 36 100100	**ATT** **Ile** **35** **100011**	**ATG** **Met** **34** **100010**	AGT Ser 33 100001	**AGG** **Arg** **32** **100000**
011	TCC Ser 31 011111	TCA Ser 30 011110	TAC Tyr 29 011101	TAA Stop 28 011100	GCC Ala 27 011011	GCA Ala 26 011010	GAC Asp 25 011001	GAA Glu 24 011000
010	TCT Ser 23 010111	**TCG** **Ser** **22** **010110**	**TAT** **Tyr** **21** **010101**	TAG Stop 20 010100	GCT Ala 19 010011	**GCG** **Ala** **18** **010010**	**GAT** **Asp** **17** **010001**	**GAG** **Glu** **16** **010000**
001	TTC Phe 15 001111	TTA Leu 14 001110	TGC Cys 13 001101	TGA Stop 12 001100	GTC Val 11 001011	GTA Val 10 001010	GGC Gly 9 001001	GGA Gly 8 001000
000	**TTT** **Phe** **7** **000111**	**TTG** **Leu** **6** **000110**	**TGT** **Cys** **5** **000101**	**TGG** **Trp** **4** **000100**	GTT Val 3 000011	**GTG** **Val** **2** **000010**	GGT Gly 1 000001	**GGG** **Gly** **0** **000000**

Fig. 4 Numbering of the 64 codons according to Sergey Petoukhov genetic code investigations [4] and distinction (grey areas) of the first appearance of each of the 20 coded amino acids. See Fig.5 and A2 (Appendix) also.

Using a very sophisticated method (see Appendix for more details about this), Sergey Petoukhov manages to classify the full sixty-four codons set using a binary language. Depending on whether each nucleobase can undergo deamination or not, Sergey Petoukhov assigns them either the value 1 or the value 0. Also, depending on whether each nucleobase can undergo depurination or not, Sergey Petoukhov assigns them either the value 0 or the value 1. This double criterion makes it possible, for each codon, to create a six-digit binary number by juxtaposition of two three-digit numbers.

Sergey Petoukhov then classifies very subtly in superimposed squares of 4, 16 and 64 boxes the 64 codons and numbers them in the order of the bases G→T→A→C for the first, second and third bases. In this numbering imagined by Sergey Petoukhov, the GGG codon thus bears the number 0 (binary 000000) and the CCC codon the number 63 (binary 111111). Figure 4 illustrates this complet numbering of the 64 genetic code codons set.

3.2 Amino acid numbering

From this numbering system, in order to assign a number to each of the twenty proteinogenic amino acids, the most logical procedure is therefore proposed here, which is to follow the order of appearance of the amino acids according to this numbering of the codons (from 0 to 63) of the table by Sergey Petoukhov (Figure 4).

3.2.1 Numbering of the twenty proteinogenic amino acids

By this process, it is thus assigned (Figure 5) number 0 to Glycine, number 1 to Valine and to Proline, the last amino acid to appear according to this order of numbering of the sixty-four genetic code codons, 19 as number.

Pro	Pro	His	Gln	Thr	Thr	Asn	Lys
Pro	**19 Pro**	**18 His**	**17 Gln**	Thr	**16 Thr**	**15 Asn**	**14 Lys**
Leu	Leu	Arg	Arg	Ile	Ile	Ser	Arg
Leu	Leu	Arg	Arg	**13 Ile**	**12 Met**	Ser	**11 Arg**
Ser	Ser	Tyr	*Stop*	Ala	Ala	Asp	Glu
Ser	**10 Ser**	**9 Tyr**	*Stop*	Ala	**8 Ala**	**7 Asp**	**6 Glu**
Phe	Leu	Cys	*Stop*	Val	Val	Gly	Gly
5 Phe	**4 Leu**	**3 Cys**	**2 Trp**	Val	**1 Val**	Gly	**0 Gly**

Fig. 5 Assigning a single only one number to each of 20 proteinogenic amino acids in the table of the complete genetic code. See Figure 4 and Figure 6 also.

3.2.1 Symmetrical break-up of the 20 AAs in 3/2 ratio

Fig. 6 Conventional representation of 20 proteinogenic amino acids numbering in symmetry graphics. From paper [3].

Now that we have determined a numbering of amino acids by assigning them a unique and personal number, we propose to isolate these twenty entities in two sets of unequal size. We therefore distinguish a first set of 12 entities then a second set of 8 other entities.

As illustrated in Figure 6, these two sets then oppose each other in a ratio of value 3/2. Using symmetry graphics, thereby, each of the 20 amino acids is symmetrically positioned to the one of opposite numbering in relation to the numbering order of these 20 AAs*: 0Gly versus 19Pro, 1Val versus 18His, etc.

Also, we therefore isolate two numbering zones:

- an area called “external” with inside the six first and six last numbered AAs
- an area called “internal” with inside the two times four centrally numbered AAs.

** To simplify, in some parts of text and tables, AA (or AAs) is used to replace amino acid appellation.*

This is only by this way that appears many singular arithmetic arrangements about amino acids attributes. These singular phenomena are very amply presented in the paper *"Numbering of the twenty proteinogenic amino acids: 3/2 ratios inside the genetic code"* [3]. We will just present here the connections between these phenomena and the concept of ultimate numbers.

4 Amino acid numbering and NWNC

We are now going to present connections between two concepts which however seem very different:

- the ultimity (and other classes of number) of whole numbers,
- the numbering of proteinogenic amino acids and of them respective codons.

The universal genetic code is therefore organized with 64 coding entities, the 64 DNA triplets themselves a combination of four different nucleobases (adenine, thymine, guanine and cytosine), and 20 coded entities, the twenty proteinogenic amino acids.

In chapter 3 we presented a numbering, from 0 to 63, of the 64 coding entities. From this first numbering, we have presented a numbering, from 0 to 19, of the 20 coded entities. All these entities, coding and coded, are therefore here expressed by numbers, more precisely by whole numbers. In chapter 2 we presented a classification of whole numbers into four different sets. Thus, an number can be either an ultimate, or a raised, or a composite, or a mixed.

AA	***the 64 codons numbered as:***			
	ultimate	***raised***	***composite***	***mixed***
00Gly	**0 - 1**	**8 - 9**		
01Val	**2 - 3 - 11**		**10**	
02Trp		**4**		
03Cys	**5 - 13**			
04Leu	**47**		**6 - 14 - 38 - 39 - 46**	
05Phe	**7**		**15**	
06Glu		**16**		**24**
07Asp	**17**	**25**		
08Ala	**19**	**27**	**26**	**18**
09Tyr	**29**		**21**	
10Ser	**23 - 31 - 41**		**22 - 30 - 33**	
11Arg	**37**	**32**		**36 - 40 - 44 - 45**
12Met			**34**	
13Ile	**43**		**35 - 42**	
14Lys				**48 - 56**
15Asn		**49**	**57**	
16Thr	**59**		**51 - 58**	**50**
17Gln				**52 - 60**
18His	**53 - 61**			
19Pro			**55 - 62**	**54 - 63**
STOP signal				*12 - 20 - 28*
external area →	**12 ultimates**	**4 raiseds**	**12 composites**	**7 mixes**
internal area →	**8 ultimates**	**4 raiseds**	**8 composites**	**6 mixes**
total count	**20 ultimates**	**8 raiseds**	**20 composites**	**13** *(+3)* **mixes**

Fig. 7 Distribution of codon numbers according to the 4 classes of whole numbers for the twenty amino acids* including 12 of external numbering (grey area) and 8 of internal numbering (clear area). See Figures 4 and 6 also. * AAs are listed using alphanumeric nomenclature proposed in referenced paper [3].

The table in Figure 7 lists the numbers of all the codons of the twenty amino acids (and of Stop signal codons) distinguishing between the four classes of whole numbers previously defined.

It turns out that from 0 to 63, there are very precisely 5*x* ultimate numbers and that this number is in fact equal to 20 entities. It also turns out that from 0 to 63, there are also very precisely 5*x* composite numbers and that this number is in fact still equal to 20 entities.

Thus, among the 64 coding entities that are the DNA triplets, 20 are numbered by an ultimate number. Also, 20 other codons are numbered by a composite number. Also none Stop signal codon is numbered by an ultimate or a composite number, so these two sets of 20 numbered codons always code for an amino acid.

We also note that very singularly, the three Stop signal codons are all numbered in a single number class, that of the mixed ones: TGA→12, TAG→20 and TAA→28. Also, these three codons appear on the same column of the Petoukhov table (Figure 4) and are therefore numbered from 8 to 8 values. These two numbering aspect are surely not by chance, but this will not discuss here.

The distribution of twenty codons with ultimate numbering in the two groups of amino acids qualified as external and internal according to their own numbering (from 0 to 19) is organized in various ratios of exact value 3/2 according to different criteria linked to this numbering. To a lesser extent, a similar phenomenon operates with respect to the distribution of the twenty composite numbered codons.

4.1 Ultimate numbered codons and AA numbering

ultimate numbering codons per amino acid

0Gly	1Val	2Trp	3Cys	4Leu	5Phe
0 - 1	2 - 3 11	-	5 - 13	47	7

6Glu	7Asp	8Ala	9Tyr
-	17	19	29

10Ser	11Arg	12Met	13Ile
23 - 31 41	37	-	43

14Lys	15Asn	16Thr	17Gln	18His	19Pro
-	-	59	-	53 - 61	-

20 ultimate codon numbers (5*x* ultimates → *x* = 4)

12 ultimates **(3*x* ultimates)**	**← 3/2 ratio →**	**8 ultimates** **(2*x* ultimates)**

Fig. 8 Ultimate numbering codons per amino acid. See Figure 6 and 7 also.

As it appears in Figure 8, the twenty ultimate numbered codons are distributed in a 3/2 ratio in the two sets of 12 and 8 amino acids respectively qualified as external and internal.

4.2 Ultimate codons and AA numbering parity

Also, among these twenty codons, ten code for an even numbered AA and another ten for an odd numbered AA. As it appears in Figure 9, these two sets of ten ultimate numbered codons are distributed in a 3/2 ratio in the four subsets of 6 and 4 amino acids respectively qualified as external and internal and of even or odd numbering.

ultimate numbering codons of 10 even numbered AAs

0Gly	1Val	**2Trp**	3Cys	**4Leu**	5Phe
0 - 1	2 - 3 11	**-**	5 - 13	**47**	7
	6Glu	7Asp	**8Ala**	9Tyr	
	-	17	**19**	29	
	10Ser	11Arg	**12Met**	13Ile	
	23 - 31 41	37	**-**	43	
14Lys	15Asn	**16Thr**	17Gln	**18His**	19Pro
-	-	**59**	-	**53 - 61**	-

10 ultimate numbers (5*x* ultimates → *x* = 2)

6 ultimates (3*x* ultimates) ← **3/2 ratio** → **4 ultimates (2*x* ultimates)**

ultimate numbering codons of 10 odd numbered AAs

0Gly	**1Val**	2Trp	**3Cys**	4Leu	**5Phe**
0 - 1	**2 - 3 11**	-	**5 - 13**	47	**7**
	6Glu	**7Asp**	8Ala	**9Tyr**	
	-	**17**	19	**29**	
	10Ser	**11Arg**	12Met	**13Ile**	
	23 - 31 41	**37**	-	**43**	
14Lys	**15Asn**	16Thr	**17Gln**	18His	**19Pro**
-	**-**	59	**-**	53 - 61	**-**

10 ultimate numbers (5*x* ultimates → *x* = 2)

6 ultimates (3*x* ultimates) ← **3/2 ratio** → **4 ultimates (2*x* ultimates)**

Fig. 9 Ultimate numbered codons per amino acid and according to numbering parity of AAs. See Figure 7 and 8 also.

4.3 Ultimate codons and opposed numbering amino acids

The difference (in absolute value) in the ultimate numbered codons between two amino acids of opposite numbering (0 versus 19, 1 versus 18, etc.) also overall generates an opposition of values in an exact 3/2 ratio in the two predefined areas of 12 external AAs and 8 internal AAs. Figure 10 illustrate that.

gaps of ultimate codons between opposed numbering amino acids

0Gly	**1Val**	**2Trp**	**3Cys**	**4Leu**	**5Phe**
↑**2**↓	↑**1**↓	↑**0**↓	↑**1**↓	↑**1**↓	↑**1**↓
19Pro	**18His**	**17Gln**	**16Thr**	**15Asn**	**14Lys**
	6Glu	**7Asp**	**8Ala**	**9Tyr**	
	↑**1**↓	↑**1**↓	↑**0**↓	↑**2**↓	
	13Ile	**12Met**	**11Arg**	**10Ser**	

10 ultimate codon gaps (5*x* gaps → *x* = 2)

6 ultimate codon gaps (3*x* gaps→ *x* = 2) ← **3/2 ratio** → **4 ultimate codon gaps (2*x* gaps→ *x* = 2)**

Fig. 10 Ultimate codon gaps between opposed numbering amino acids. See Fig 8 also.

4.4 Ultimate codons and consecutive numbering amino acids

In similar phenomenon, the difference in the number of ultimate codons between two amino acids of consecutive numbering (0 versus 1, 2 versus 3, etc.) also overall generates an opposition of values in an exact 3/2 ratio. This, once more between the two sets of external and internal entities as shown in Figure 11.

gaps of ultimate codons between consecutive numbering amino acids

0Gly	2Trp	4Leu	14Lys	16Thr	18His
↑1↓	↑2↓	↑0↓	↑0↓	↑1↓	↑2↓
1Val	3Cys	5Phe	15Asn	17Gln	19Pro

6Glu	8Ala	10Ser	12Met
↑1↓	↑0↓	↑2↓	↑1↓
7Asp	9Tyr	11Arg	13Ile

10 ultimate codon gaps (5*x* gaps → *x* = 2)

↙ ↘

6 ultimate codon gaps (3*x* gaps→ *x* = 2)	← 3/2 ratio →	4 ultimate codon gaps (2*x* gaps→ *x* = 2)

Fig. 11 Ultimate gaps between consecutive numbering amino acids. See Fig 8 also.

This close investigation about connections between ultimate numbering of codons and numbering of the twenty proteinogenic amino acid.

4.5 Composite numbered codons and AA numbering

We have previously determined, from the tables of Figures 4 and 7, that twenty composite numbers, ie 5*x* entities, also encode the proteinogenic amino acids (none encoding a Stop signal).

As it appears in Figure 12, these twenty ultimate numbered codons are distributed in a 3/2 ratio in the two sets of 12 and 8 amino acids respectively qualified as external and internal. This, in the same way as the ultimate numbered codons are distributed like in Figure 8.

composite numbering codons per amino acid

0Gly	1Val	2Trp	3Cys	4Leu	5Phe
-	10	-	-	6 - 14 - 38 39 - 46	15

6Glu	7Asp	8Ala	9Tyr
-	-	26	21

10Ser	11Arg	12Met	13Ile
22 - 30 33	-	34	35 - 42

14Lys	15Asn	16Thr	17Gln	18His	19Pro
-	57	51 - 58	-	-	55 - 62

20 composite codon numbers (5*x* composites → *x* = 4)

↙ ↘

12 composites (3*x* composites)	← 3/2 ratio →	8 composites (2*x* composites)

Fig. 12 Composite numbering codons per amino acid. See Figure 7 and 8 also.

4.6 Composite codons and AA atom count

In preview article *"Numbering of the twenty proteinogenic amino acids: 3/2 ratios inside the genetic code"* [3 see Appendix also] connections have been demonstrated between the decimal system and the number of atoms contained in each of the twenty proteinogenic amino acids. Thus, see Figure A3 of the Appendix, it turns out that 10 AAs have a number of atoms of one ten and 10 other AAs are in two atom tens.

Also, among the twenty composite numbering codons, ten code for an AA at 1 ten of atom and another ten for an AA at 2 tens of atom. As it appears in Figure 13, these two sets of ten composite numbered codons are distributed in a 3/2 ratio in the four subsets of 6 and 4 amino acids respectively qualified as external and internal and of 1 ten or 2 tens of atoms.

composite numbering codons of 10 AAs at 1 ten of atom

0Gly	**1Val**	2Trp	**3Cys**	4Leu	5Phe
-	**10**	-	**-**	6 - 14 - 38 39 - 46	15

6Glu	**7Asp**	**8Ala**	9Tyr
-	**-**	**26**	21

10Ser	11Arg	12Met	13Ile
22 - 30 33	-	34	35 - 42

14Lys	**15Asn**	**16Thr**	17Gln	18His	**19Pro**
-	**57**	**51 - 58**	-	-	**55 - 62**

10 composite numbers (5x composites → x = 2)

6 composites (3x composites) ← **3/2 ratio** → **4 composites (2x composites)**

composite numbering codons of 10 AAs at 2 tens of atom

0Gly	1Val	**2Trp**	3Cys	**4Leu**	**5Phe**
-	10	**-**	-	**6 - 14 - 38 39 - 46**	**15**

6Glu	7Asp	8Ala	**9Tyr**
-	-	26	**21**

10Ser	**11Arg**	**12Met**	**13Ile**
22 - 30 33	**-**	**34**	**35 - 42**

14Lys	15Asn	16Thr	**17Gln**	**18His**	19Pro
-	57	51 - 58	**-**	**-**	55 - 62

10 composite numbers (5x ultimates → x = 2)

6 composites (3x composites) ← **3/2 ratio** → **4 composites (2x composites)**

Fig. 13 Composite numbered codons per amino acid and according to tens of atom number of AAs. See Figures 4 and 7 also.

5. Discussions and conclusions

The periodic table of elements is organized entirely by the numbers universe. The genetic code is the ultimate organization of matter from its simplest components (nucleons, atoms, molecules) to what is called living matter. It is therefore not insignificant that this genetic code, which we consider as an non-dissociable whole comprising 64 coding entities and 20 coded entities, is also entirely dominated by the field of numbers in its proteinogenic amino acids coding mechanism.

Thus we demonstrate that very exactly twenty codons, out of sixty-four, can be numbered by what we call "ultimate numbers". By a definition common to them, the ultimate numbers consist of the set of primes and the two exotic mathematical entities that are 0 and 1. The numbering of these codons depends on the physical properties of the DNA nucleobases of which they are combinations.

From this codon prime numbering, a resulting numbering of the twenty proteinogenic amino acids becomes naturally legitimate. These different notions can be mixed in various physico-arithmetic entanglements and these singular entanglements manifest themselves in the ratio 3/2. This ratio is just possible with an overall source value of 5x entities considered. And this is precisely what operates with the genetic code of 5x amino acids, 5x codons numbered as ultimate numbers, 5x as composite numbers, etc.

Since the singular arrangements involving different fields of study, which are unveiled, it therefore seems undeniable that we must not dissociate the physical aspects from the numeric aspects (in the etymological sense of this term) of matter organization in general, living matter in particular and whose genetic code represents the most sophisticated structure.

We therefore suggest always taking into account the numerical aspect of the different components of the genetic code in the study of its mechanism and also, but without restricting the fields, in the investigations of proteins and genetics in general. we believe that by these procedures surprising research results will appear.

Appendix

These developments are some excerpts from the author referenced articles [1 - 2 - 3].

A.1 Development of Chapter 2.1

Below are listed, to illustration of definition, some of the first ultimate or non-ultimate numbers defined above, especially particular numbers zero (0) and one (1).

- 0 is ultimate: although it admits an infinite number of divisors superior to it, **since it is the first whole number**, the number 0 does not admit any divisor **being inferior to it**.

- 1 is ultimate: since the division by 0 has no defined result, the number 1 does not admit any divisor (whole number) being less than it.

- 2 is ultimate: since the division by 0 has no defined result, the number 2 does not admit any divisor* being less than it.

- 4 is non-ultimate: the number 4 admits the number 2 (number being less than it) as divisor*.

- 6 is non-ultimate: the number 6 admits numbers 2 and 3 (numbers being less than it) as divisors*.

- 7 is ultimate: since the division by 0 has no defined result, the number 7 does not admit any divisor* being less than it. The non-trivial divisors 2, 3, 4, 5 and 6 cannot divide it into whole numbers.

- 12 is non-ultimate: the number 6 admits numbers 2, 3, 4 and 6 (numbers being less than it) as divisors*.

Thus, by these previous definitions, the set of whole numbers is organized into these two entities:

- the set of ultimate numbers, which is the fusion of the prime numbers sequence with the numbers 0 and 1.

- the set of non-ultimate numbers identifying to the non-prime numbers sequence, deduced from the numbers 0 and 1.

* non-trivial divisor.

A.1.1 The first ten ultimate numbers and the first ten non-ultimate numbers

Considering the previous double definition, the sequence of ultimate numbers is initialized by these ten numbers:

0 1 2 3 5 7 11 13 17 19

Considering the previous double definition, the sequence of non-ultimate numbers is initialized by these ten numbers:

4 6 8 9 10 12 14 15 16 18

A.2 Development of Chapter 3.1

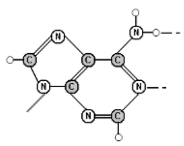
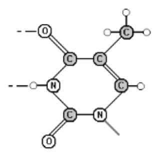
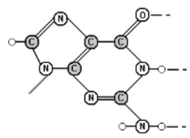
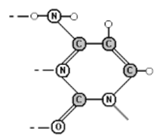
	Adenine	**Thymine**	**Guanine**	**Cytosine**
nucleobases				
Possible deamination: yes = 1 no = 0	1	0	0	1
Possible depurination: yes = 0 no = 1	0	1	0	1

Fig. A1 Method of assigning a double binary value to the four DNA nucleobases according to Sergey Petoukhov [4].

This double criterion makes it possible, for each codon, to create a six-digit binary number by juxtaposition of two three-digit numbers as described in Figure A2.

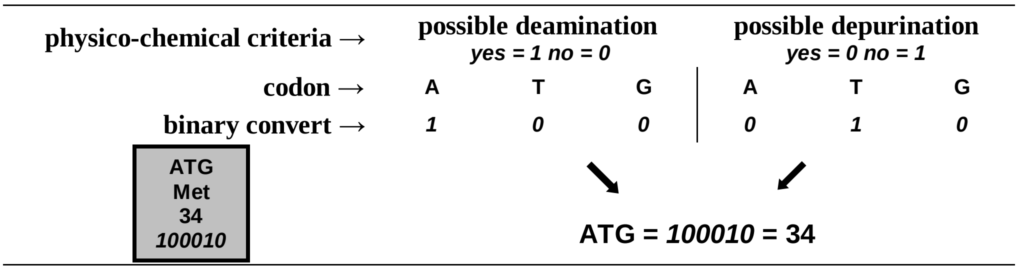


Fig. A2 Method of assigning a number to codons according to Sergey Petoukhov [4]. See Fig. A1 and Fig. 4 Chapter 3.1 also.

A.3 Development of Chapter 4.6

The number of atoms contained in each of the twenty amino acids, in their complete version (base + radical as presented in Figure A3) is related to the decimal system.

Indeed, it turns out that the smallest amino acid, Glycine has exactly 10 atoms. Also, the ten amino acids with the smallest number of atoms have 19 as maximum 19. The other ten have a number of atoms from 20 to 29 (27 more precisely for Tryptophan). Thus, we can say that 10 AAs have a number of atoms of ten and 10 others of two tens.

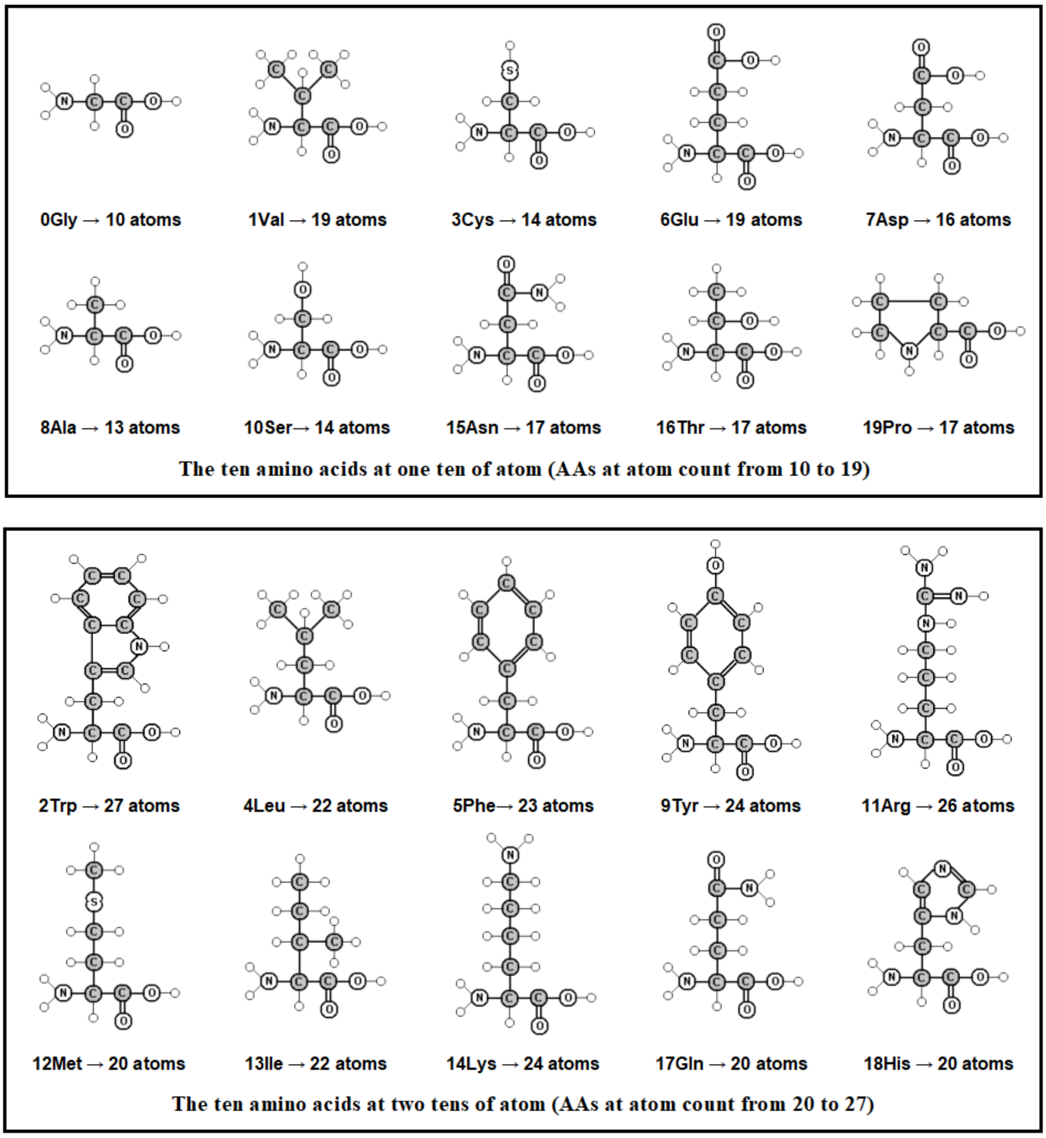


Fig. A3 Two set of AAs: 10 with an atom count at one ten and 10 with an atom count at two tens. Inspired graphics from S. Petoukhov paper [4].

These two sets of 10 AAs are distributed in perfect 3/2 ratios in accordance with the two predefined numbering zones as illustrated Figure A4.

10 amino acids with an atom count of 1 ten
→ from 10 to 19 atoms
(also the 10 AAs at lowest Van der Walls volume)

0Gly 10	**1Val 19**	2Trp 27	**3Cys 14**	4Leu 22	5Phe 23
	6Glu 19	**7Asp 16**	**8Ala 13**	9Tyr 24	
	10Ser 14	11Arg 26	12Met 20	13Ile 22	
14Lys 24	**15Asn 17**	**16Thr 17**	17Gln 20	18His 20	**19Pro 17**

6 AA ← **3/2 ratio** → **4 AA**

10 amino acids with an atom count of 2 tens
→ from 19 to 27 atoms
(also the 10 AAs at highest Van der Walls volume)

0Gly 10	1Val 19	**2Trp 27**	3Cys 14	**4Leu 22**	**5Phe 23**
	6Glu 19	7Asp 16	8Ala 13	**9Tyr 24**	
	10Ser 14	**11Arg 26**	**12Met 20**	**13Ile 22**	
14Lys 24	15Asn 17	16Thr 17	**17Gln 20**	**18His 20**	19Pro 17

6 AA ← **3/2 ratio** → **4 AA**

Fig. A4 Distribution of the two sets of the ten AAs at one ten number of atoms and at two tens numbers in 3/2 ratios according to internal and external numbering. See Figure A3.

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