Creation of the Genetic Code

By Craig Paardekooper BSc

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Title: Creation of the Genetic Code

Sub Title : Review of the paper by Rakocevic "A Harmonic Structure of the Genetic Code"

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Abstract

This paper is a review of the research of Rakocevic as presented in his paper "A Harmonic Structure of the Genetic Code". Rakocevic's findings are confirmed. A strong symmetry is revealed in Rakocevic's table – both horizontally and vertically. New data reveals that Rakocevic's patterns are framed around 5 key numbers - the prime numbers 37 and 73, and their midpoint 55, and the triangular numbers 666 and 703. A simple geometric pattern is proposed that integrates all 5 numbers. It is shown that 666 and 703 are the constituent triangles of the 73^{rd} triangular number 2701 (37 x 73), and 703 itself is the 37^{th} triangular number. These findings have implications for the origin of the amino acids, suggesting the operation of a primordial arithmetic process, and concur in this respect with the findings of Shcherbak.

Keywords: Symmetry, mathematics, prime number, arithmetic, triangular.

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1. Introduction

The objective of this research was to review the findings of Rakocevic [1] who proposed the existence of a mathematical symmetry inherent in the molecular masses of the 20 amino acids. Rakocevic arranged the 20 amino acids into a 4 x 5 table as shown in table 1. He found that the molecular masses of the amino acids formed a pattern with horizontal and vertical symmetry, structured around multiples of the prime number 37. In particular, Rakocevic identified 666 and 703 as key numbers in the pattern.

However, based on Rakocevic's own data, his patterns were only approximate. So the initial aim was to check Rakocevic's calculations against accurate values of the amino acid masses obtained from Wikipedia [2]. A second objective was to see if any additional patterns would be found.

1.1 Rakocevic's pattern

In Table 1 you can see each amino acid together with the molecular masses used by Rakocevic.

Table 1 : Showing the amino acid molecular masses used by Rakocevic

Aspartic Acid Mass 133.10	Asparagine Mass 132.12	Alanine Mass 89.09	Leucine Mass 131.18	Total Mass 485.49
Arginine Mass 174.2	Phenyl Alanine Mass 165.19	Proline Mass 115.13	Isoleucine Mass 131.18	Total Mass 585.7
Lysine Mass 146.19	Tyrosine Mass 181.19	Threonine Mass 119.12	Methionine Mass 149.21	Total Mass 595.71
Histidine Mass 155.16	Tryptophan Mass 204.10	Serine Mass 105.09	Cysteine Mass 121.16	Total Mass 585.64
Glutamic Acid Mass 147.13	Glutamine Mass 146.15	Glycine Mass 75.07	Valine Mass 117.15	Total Mass 485.5
Total Mass 755.78	Total Mass 828.88	Total Mass 503.5	Total Mass 649.88	Grand Total Mass 2738

2 x 666

2 x 703

2738 =
2 x 37 x 37

Rakocevic’s table of amino acid masses shows symmetry about the central row, and the total mass for all 20 amino acids is given as 2 x the square of a prime number 37.

What is more, the sum of the inner two columns is given as 2 x 666, also a multiple of 37, and the sum of the outer two columns is given as 2 x 703, also a multiple of 37

It so happens that 703 – 666 = 37, and 703 + 666 = 37 x 37. Consequently

outer columns - inner columns = 2 x 37
outer columns + inner columns = 2 x 37 x 37

If you draw a horizontal line through the central row, the masses are arranged symmetrically about the central row, so the horizontal line creates two sections each of mass = 703 + 666 or 37 x 37.

So we have horizontal and vertical symmetry – a true harmony.

It seems remarkable that such a simple and integrated pattern of symmetry should exist in the amino acid masses, and more so since it is centred on a large prime number – 37.

One might add that, since there are 20 amino acids, the average mass for each amino acid is 37 x 3.7 or 70.3 + 66.6.

1.2. Is Rakocevic’s pattern precise?

As remarkable as this harmony of masses seems, Rakocevic’s harmonies are only approximate.

The sum of the inner two columns only approximates to 2 x 666. It’s actual value, according to the amino acid masses shown in Rakocevic’s table, is 2 x 666 + 0.38.

Similarly, the sum of the two outer columns only approximates to 2 x 703. It’s actual value, according to the amino acid masses shown in Rakocevic’s table, is 2 x 703 – 0.34.

Also, the total mass for all 20 amino acids is 2738.04 rather than 2738.

1.3 A revised table containing precise data

Data of the exact molecular masses of all 20 of the amino acids is readily available on Wikipedia. [2] The masses are accurate to the second decimal place. These amino acid masses were collected by Stephen Coneglan and are shown in Table 2 below -

> *“Dear Craig,*
> *I individually checked the molecular weights for each of the 20 standard amino acids on Wikipedia. There were a few extremely slight errors in the weights of 5 amino acids that Rakocevic created. Amazingly, when these are adjusted to the Wikipedia values, exact divisions of the number 037 eventuate. Let me give you the details of the amendments that need to be made to the molecular weights for 5 of the amino acids. After you have considered the adjustments, perhaps you might want to comment on the exactness of the number 037 at your webpage.*
>
> *These are the 5 amino acids whose values should be adjusted in Rakocevic’s table to reflect the values found for*

each at Wikipedia:

1.Tryptophan (W): 204.23
2.Isoleucine (I): 131.17
3.Histidine (H): 155.15
4.Leucine (L): 131.17
5.Glutamine (Q): 146.14

By adjusting the values for these 5 amino acids in Rakocevic's table, the following data apply in respect of the columns:

***Column 1**:*

1.Aspartic acid: 133.1
2.Arginine: 174.2
3.Lysine: 146.19
4.Histidine: 155.15
5.Glutamic acid: 147.13

The total for Column 1 is:

•133.1 + 174.2 + 146.19 + 155.15 + 147.13 = 755.77

***Column 2**:*

1.Asparagine: 132.12
2.Phenylalanine: 165.19
3.Tyrosine: 181.19
4.Tryptophan: 204.23
5.Glutamine: 146.14

The total for column 2 is:

•132.12 + 165.19 + 181.19 + 204.23 + 146.14 = 828.87

Column 3:

1.Alanine: 89.09
2.Proline: 115.13
3.Threonine: 119.12
4.Serine: 105.09
5.Glycine: 75.07

The total for Column 3 is:

•89.09 + 115.13 + 119.12 + 105.09 + 75.07 = 503.5

***Column 4**:*

1.Leucine: 131.17
2.Isoleucine: 131.17
3.Methionine: 149.21
4.Cysteine: 121.16
5.Valine: 117.15

The total for Column 4 is:

•131.17 + 131.17 + 149.21 + 121.16 + 117.15 = 649.86

From the Wikipedia data, the totals for all four columns are:

1.755.77
2.828.87
3.503.5
4.649.86

The following sums apply:

•Column 1 + Column 4 = 755.77 + 649.86 = 1405.63 = (2 x 703) - 0.37
•Column 2 + Column 3 = 828.87 + 503.5 = 1332.37 = (2 x 666) + 0.37
•Column 1 + Column 2 + Column 3 + Column 4 = 755.77 + 828.87 + 503.5 + 649.86 = 2738 = 2 x 37 x 37

The adjusted totals for the 5 rows are:

1.485.48
2.585.69
3.595.71
4.585.63
5.485.49

Incredibly, the combined molecular weight for all 20 amino acids comes out to an exact integer. That integer is 2738. There is no decimal remainder. The difference between the sums for Columns 1 + 4, and Columns 2 + 3, is mediated by a remainder of 0.37."

Stephen Coneglan (personal communication February 2010)

Table 2: Showing the amino acid molecular masses collected by Stephen Coneglan from Wikipedia

Aspartic Acid Mass 133.10	**Asparagine** Mass 132.12	**Alanine** Mass 89.09	**Leucine** Mass 131.17	**Total** Mass 485.48
Arginine Mass 174.2	**Phenyl Alanine** Mass 165.19	**Proline** Mass 115.13	**Isoleucine** Mass 131.17	**Total** Mass 585.69
Lysine Mass 146.19	**Tyrosine** Mass 181.19	**Threonine** Mass 119.12	**Methionine** Mass 149.21	**Total** Mass 595.71
Histidine Mass 155.15	**Tryptophan** Mass 204.23	**Serine** Mass 105.09	**Cysteine** Mass 121.16	**Total** Mass 585.63
Glutamic Acid Mass 147.13	**Glutamine** Mass 146.14	**Glycine** Mass 75.07	**Valine** Mass 117.15	**Total** Mass 485.49
Total Mass 755.77	**Total** Mass 828.87	**Total** Mass 503.5	**Total** Mass 649.86	**Grand Total** Mass 2738

485.48 +
585.69 +
half of 595.71

= 703 + 666 + 0.025

485.49 +
585.63 +
half of 595.71

= 703 + 666 - 0.025

2 x 666 + 0.37

2 x 703 - 0.37

2. Results

The results are intriguing, to say the least.

2.1 Pattern built around 37 and 0.37

The sum of the two inner columns now comes to 2 x 666 + 0.37.
And the sum of the two outer columns comes to 2 x 703 – 0.37.
See Table 2 above.

What is remarkable is the inter-relationship between 666, 703 and 37. As mentioned above, 666 + 37 = 703 and 703 – 37 = 666, so it is quite coincidental that the “fine-tuning” 0.37 should be added to 666 and subtracted from 703.

Also, with the more accurate data, the sum of all 20 amino acid masses becomes 2 x 37 x 37 precisely!!

2 x 666 + 0.37 can be rewritten as 2 x 703 – 2 x 37 + 0.37
2 x 703 – 0.37 can be rewritten as 2 x 666 + 2 x 37 – 0.37

The reason for rewriting these expressions will soon become obvious.

2.2 Pattern built around 73 and 0.73

On closer inspection, I noticed a new pattern.
The sum of the odd columns = 755.77 + 503.5 = 2 x 703 – 2 x 73 – 0.73
The sum of the even columns = 828.87 + 649.86 = 2 x 666 + 2 x 73 + 0.73

Comparing these equations with the ones we found previously you can see the extraordinary similarity of form –

Sum of inner columns = **2 x 703 – 2 x 37 + 0.37**

Sum of outer columns = **2 x 666 + 2 x 37 – 0.37**

Sum of odd columns = **2 x 703 – 2 x 73 – 0.73**

Sum of even columns = **2 x 666 + 2 x 73 + 0.73**

See Table 3

Table 3: Table of amino acid masses showing how column sums are related

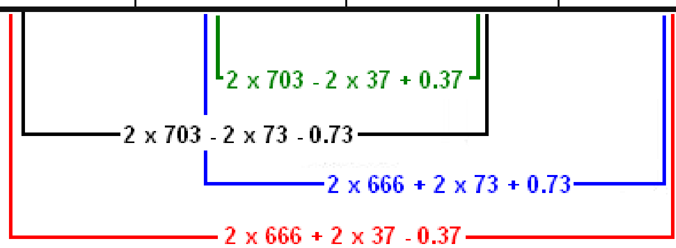
Aspartic Acid Mass 133.10	**Asparagine** Mass 132.12	**Alanine** Mass 89.09	**Leucine** Mass 131.17	**Total** Mass 485.48
Arginine Mass 174.2	**Phenyl Alanine** Mass 165.19	**Proline** Mass 115.13	**Isoleucine** Mass 131.17	**Total** Mass 585.69
Lysine Mass 146.19	**Tyrosine** Mass 181.19	**Threonine** Mass 119.12	**Methionine** Mass 149.21	**Total** Mass 595.71
Histidine Mass 155.15	**Tryptophan** Mass 204.23	**Serine** Mass 105.09	**Cysteine** Mass 121.16	**Total** Mass 585.63
Glutamic Acid Mass 147.13	**Glutamine** Mass 146.14	**Glycine** Mass 75.07	**Valine** Mass 117.15	**Total** Mass 485.49
Total Mass 755.77	**Total** Mass 828.87	**Total** Mass 503.5	**Total** Mass 649.86	**Grand Total** Mass 2738

485.48 +
585.69 +
half of 595.71

= 703 + 666 + 0.025

485.49 +
585.63 +
half of 595.71

= 703 + 666 - 0.025



The sums of the inner columns and the sums of the outer columns are built around the prime number 37 and 0.37.

The sums of the odd columns and the sums of the even columns are built around the prime number 73 and 0.73, the digital reflection of 37 and 0.37 !!

These new patterns have been reviewed by Stephen Coneglan, and found to be PRECISELY correct –

> *"Craig,*
> *I just checked out your latest findings and saw the stuff involving the number 73. You have already demonstrated how the number 37 plays the leading role in the organisation of Rakocevic's table of the amino acids. To see the number 73 also playing a fine-tuning role to the '37-dependent' phenomena is really quite astounding. I had to double check your results for veracity.*
>
> *Indeed, I have found your contentions concerning the columns to be exactly correct! The following sums attain:*
>
> 1. *C1 + C3 = 755.77 + 503.50 = 1259.27 = (2 x 703) - (2 x 73) - 0.73*
> 2. *C2 + C4 = 828.87 + 649.86 = 1478.73 = (2 x 666) + (2 x 73) + 0.73*
>
> *Thus, you are perfectly correct when you assert that the number 73 plays the leading role in fine-tuning the data*

for these columns. We saw previously that the number 37 played the fine-tuning role for the respective outer and inner column sums of 1405.63 and 1332.37."

Stephen Coneglan (private communication February 2011)

2.3 Pattern of alternating cells built around 0.55

Vernon Jenkins compared the sums of alternating cells within the amino acid table. [3] See Table 4.

He found that –

Sum of odd cells (coloured white) = 1331.45 = 2 x 666 – 0.55
Sum of even cells (coloured blue) = 1406.55 = 2 x 703 + 0.55

Stephen Coneglan observed that 55 is the exact midpoint between 0.37 and 0.73

0.55 = 0.73 – 0.18
0.55 = 0.37 + 0.18

Table 4: Table showing amino acid masses - summing alternate cells

Aspartic Acid Mass 133.10	Asparagine Mass 132.12	Alanine Mass 89.09	Leucine Mass 131.17
Arginine Mass 174.2	Phenyl Alanine Mass 165.19	Proline Mass 115.13	Isoleucine Mass 131.17
Lysine Mass 146.19	Tyrosine Mass 181.19	Threonine Mass 119.12	Methionine Mass 149.21
Histidine Mass 155.15	Tryptophan Mass 204.23	Serine Mass 105.09	Cysteine Mass 121.16
Glutamic Acid Mass 147.13	Glutamine Mass 146.14	Glycine Mass 75.07	Valine Mass 117.15

3. Discussion

3.1 The genetic code is organized around arithmetic structures

To quote Rakocevic –

> *"There is synchronic coherency with simple arithmetic structures, in the sense that a unity of form and essence is realised."*
>
> *"One should notice that even amino acids and their biosynthetic precursors are determined by basic arithmetic structures."*
>
> *"Still, there is more. The same pattern of coherency is demonstrated for the number of nucleons within the first nucleon, and for the molecule mass where other nuclides are participating."*

3.2 The pattern possesses irreducible complexity, and so constrains variation

Here are quotations from Rakocevic –

> *"The results show that if only one amino acid should be replaced within the 5 x 4 table of amino acids, then all symmetry will be lost – there will no longer be any balance or coherency."*

Given the arithmetic integration of the genetic code, Rakocevic comments –

> *"It is hard to see how any other kind of 'original form of life', could have been built with fewer than 4 purine-pyrimidine bases, and fewer than 20 amino acids, or with anything other than the twenty standard amino acid molecules."*
>
> *"That is the reason we can only consider an abiotic origin, and not by any means a biotic evolution of the genetic code."*

Rakocevic argues that the genetic code has remained unchanged since it was first created at the very beginning of life, and that physical and chemical determinants are inadequate to explain the patterns.

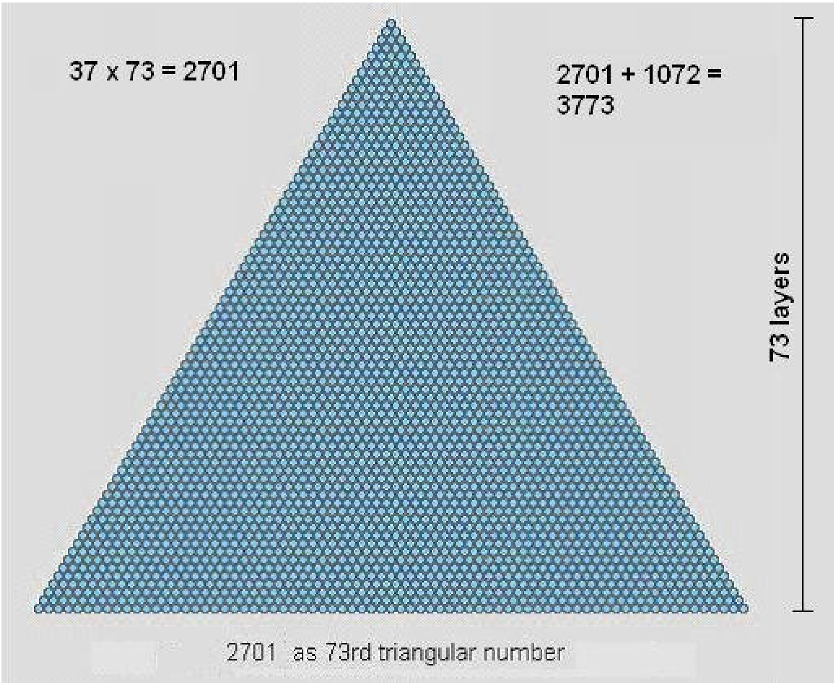
> *"However, with the knowledge of the synergy influence of previously discussed principles, particularly the principle of compromise, and the principle of coherence with simple arithmetic structures and regularities, it becomes clear that physical and chemical influences are limited. On the other hand, the genetic code is "frozen", but not during biotic evolution, but immediately at the very beginning from the very moment the code was created."*

3.3 The arithmetic structures integrate into a single geometrical pattern

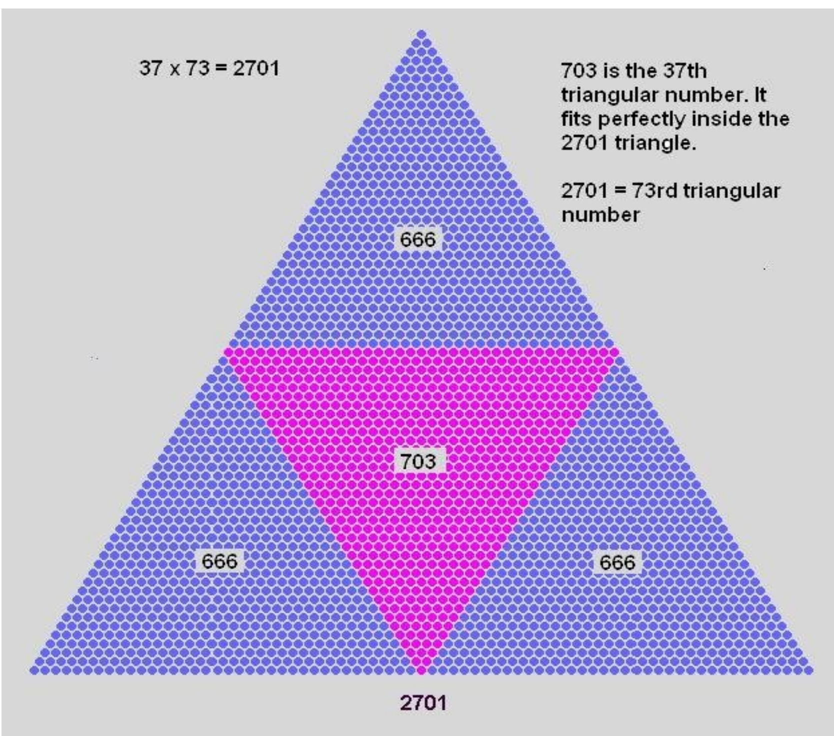
We might ask why the symmetrical patterns are constructed around a set of 5 numbers (37, 55, 73, 666 and 703). Is there any relationship between these numbers?

Curiously these 5 numbers integrate in a single geometrical pattern.

37 x 73 = 2701 = 73rd triangular number. It can be represented as a triangle with 73 layers thus –



703 is the **37th** triangular number and so it can be represented as a triangle with 37 layers. The 703 triangle fits perfectly within the 2701 triangle thus –

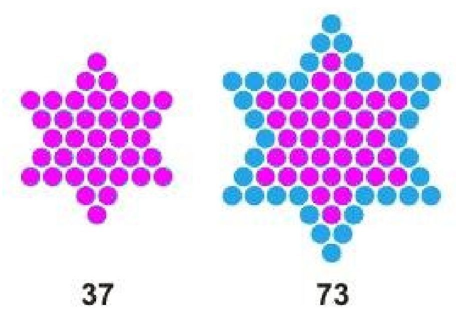


And the three triangles surrounding the 703 triangle each sum to 666 !!

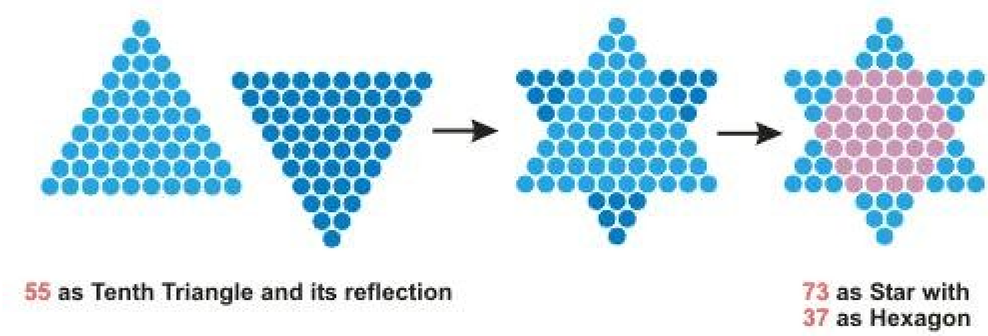
So this single geometric pattern integrates all 5 of the numbers found in the amino acid patterns. The 73rd triangle (37 x 73) incorporates the 37th triangle (703) and the number 666, and 55 is itself the mean of 37 and 73

3.4. The connection between 37, 73 and 55

Both 37 and 73 are prime numbers, and each is the digital reflection of the other. In addition, 73 can be represented as a hexagram, or star number, and 37 is the hexagram that fits perfectly inside the hexagram of 73.



55 is the midpoint between 73 and 37. In addition, the 73 hexagram is formed by the intersection of two triangles, each of 55.



So we can see how 37, 73 and 55 form an integrated geometry, and how 37 x 73 (the 73rd triangular number) integrates with 703 (the 37th triangular number) and 666.

Concluding Remarks

Accurate values of the amino acid masses confirm Rakocevic's findings – the pattern of amino acid masses possesses strong vertical and horizontal symmetry.

Furthermore, this symmetry is precisely structured around 5 numbers – 37, 55, 73, 666 and 703 , and these numbers are found to be integral to a single geometric pattern – the 73^{rd} triangular number 2701, itself a multiple of 37 (37 x 73)

These arithmetic regularities suggest that a primordial arithmetic process may have been involved in shaping the genetic code. If so then we should expect to discover much similar regularity in the future. So these arithmetic patterns may have predictive value.

What's more, these arithmetic regularities may lay additional constraints upon variation. The mathematical harmonies appear to be intact, and must have remained so since the genesis of the code.

Stephen Coneglan says –

> *"These findings provide overwhelming proof that the number pairs (37, 73) and (666, 703) - are present in the fine-tuning of the molar masses of the amino acids. These molar masses are not a matter of private interpretation. They were taken from an open source website, Wikipedia, and are available for all to peer review and critique.*
>
> *The fact that the sums, above, wherein the numbers 37 and 73 play the fine-tuning role, are EXACT is surely something to behold.*
>
> *The breath-taking simplicity with which the sets of equations obey almost the same form…..*
>
> *It is quite amazing that the number 73 should also appear as a fine-tuning mechanism for the columns.*
>
> *I had wondered if there was any significance to the alternating values having an orb of allowance of 0.55.*
>
> *I think Craig's latest finding helps to answer this question. The values [37 - 55 - 73] have a profound numero-geometrical presence.*
>
> *To find their decimal expressions as the fine-tuning mechanisms for three essential divisions of Rakocevic's table (RT) is simply astonishing."*
>
> *Stephen Coneglan (private communication February 2011)*

Acknowledgements

Stephen Coneglan BA

Vernon Jenkins MSc.

References

[1] “A Harmonic Structure of the Genetic Code”, Journal of Theoretical Biology 229 (2004) 221-234, Miloje M. Rakocevic

[2] Here are the Wikipedia links for amino acid masses

http://en.wikipedia.org/wiki/Alanine
http://en.wikipedia.org/wiki/Arginine
http://en.wikipedia.org/wiki/Asparagine
http://en.wikipedia.org/wiki/Aspartic_acid
http://en.wikipedia.org/wiki/Cysteine
http://en.wikipedia.org/wiki/Glutamic_acid
http://en.wikipedia.org/wiki/Glutamine
http://en.wikipedia.org/wiki/Glycine
http://en.wikipedia.org/wiki/Histidine
http://en.wikipedia.org/wiki/Isoleucine
http://en.wikipedia.org/wiki/Leucine
http://en.wikipedia.org/wiki/Lysine
http://en.wikipedia.org/wiki/Methionine
http://en.wikipedia.org/wiki/Phenylalanine
http://en.wikipedia.org/wiki/Proline
http://en.wikipedia.org/wiki/Serine
http://en.wikipedia.org/wiki/Threonine
http://en.wikipedia.org/wiki/Tryptophan
http://en.wikipedia.org/wiki/Tyrosine
http://en.wikipedia.org/wiki/Valine

[3] Vernon Jenkins – web reference: http://www.whatabeginning.com/Misc/Genetics/Rakbou.htm

About the Author

Craig Paardekooper has a long term interest in genetics, in the mathematical patterns found in nature, and a long term interest in philosophy. He graduated with a BSc in Psychology in 1990, and has studied and written on philosophical issues since then. He currently works freelance as a software developer and writer in London.

Genetic Patterns

Mathematical Patterns in the Genetic Code

by Craig Paardekooper

Abstract

Are there mathematical patterns in the Genetic Code??

Well, scientists are discovering new and intriguing patterns, though the reason why these patterns exist and what function they serve is as yet unknown.

Background

Previously, Vernon Jenkins, discovered a mathematical pattern encoded within the Hebrew text of the Old Testament creation narratives. His work is displayed here.

http://www.otherbiblecode.com

Then, over the last decade scientists around the world have begun exploring the mathematical patterns found within DNA.

Putting the Pieces Together

Vernon's pattern is intriguing, and it is tempting to take a look at the genetic code, to see if, perhaps, the same pattern is there too.

Results

In 2007, I came across the work of Shcherbak, a mathematician and geneticist. What was quite surprising was the resemblance between the Shcherbak's genetic patterns and those found by Vernon in the creation narratives. I have summarised Shcherbak's work in this booklet.

Vernon has independently investigated and confirmed these resemblances and has created his own web page where the findings are clearly depicted -

http://www.whatabeginning.com/Misc/Genetics/Genetics_VS.htm

A Pattern in Genesis

The Book of Genesis, which is the first book of the Bible, was originally written in Hebrew. The Hebrews did not have separate symbols for numbers, as we do today. Rather, they used the letters of their alphabet to represent numbers. Because of this, it is legitimate to convert each letter of the biblical text into a corresponding number. When this is done, striking mathematical patterns emerge.

The Hebrew Alphabetic Numbering Scheme

The Hebrew alphabet has 22 letters - five with 'end forms', i.e. variants used only when words end with one or other of these letters. From circa 200 BC, as the following table reveals, each letter was made to function as a numeral - thus copying the earlier Greek model (c 600 BC).

Place:	1	2	3	4	5	6	7	8
Letter:	א	ב	ג	ד	ה	ו	ז	ח
Value:	1	2	3	4	5	6	7	8
Place:	9	10	11	12	13	14	15	16
Letter:	ט	י	כ ך	ל	מ ם	נ ן	ס	ע
Value:	9	10	20	30	40	50	60	70
Place:	17	18	19	20	21	22		
Letter:	פ ף	צ ץ	ק	ר	ש	ת		
Value:	80	90	100	200	300	400		

The practice that existed then was to record numbers on an *additive* basis, i.e. the value represented by a string of letters was simply the sum of the tabular values assigned to each. The *characteristic value* (CV) of a conventional Hebrew word, name, or phrase, is obtained in this manner. As an illustration of the procedure, the characteristic value of the name *SIMEON* is derived below. We observe that all Hebrew reading proceeds from right to left.

(50)	(6)	(70)	(40)	(300)
ן	ו	ע	מ	ש

Thus, CV (SIMEON) = 50 + 6 + 70 + 40 + 300 = 466

.

Several years ago, a mathematician named Vernon Jenkins, (formerly Senior Lecturer of the Department of Mathematics and Computer Science, University of Glamorgan, Wales), discovered what seemed to be a mathematical pattern encoded within the Creation story of Genesis in the Bible.

Here is a summary of the pattern he found.

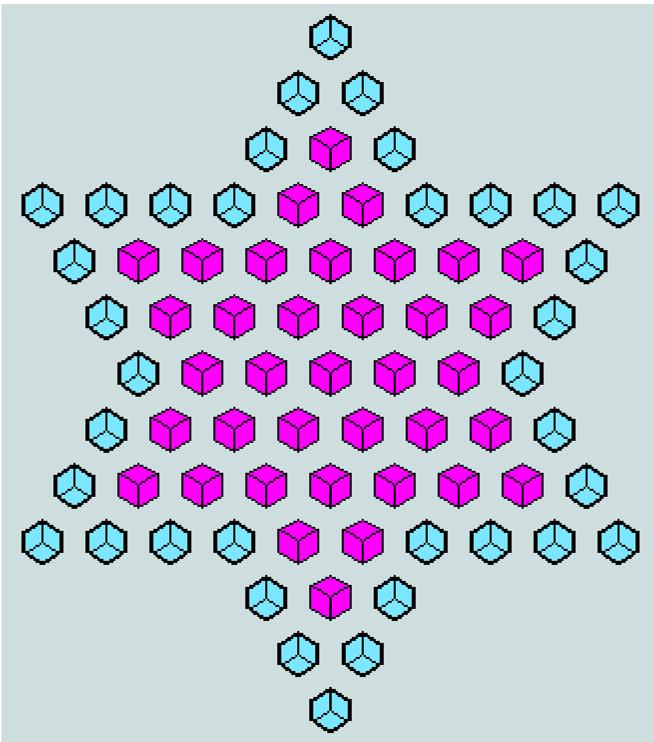
Taking the first verse of the Book of Genesis, Vernon calculated the numerical values of the words as follows –

This verse consists of 7 Hebrew words. The sum of the number values for these **7** words add to **2701**. There are two factors of 2701; they are 37 and 73

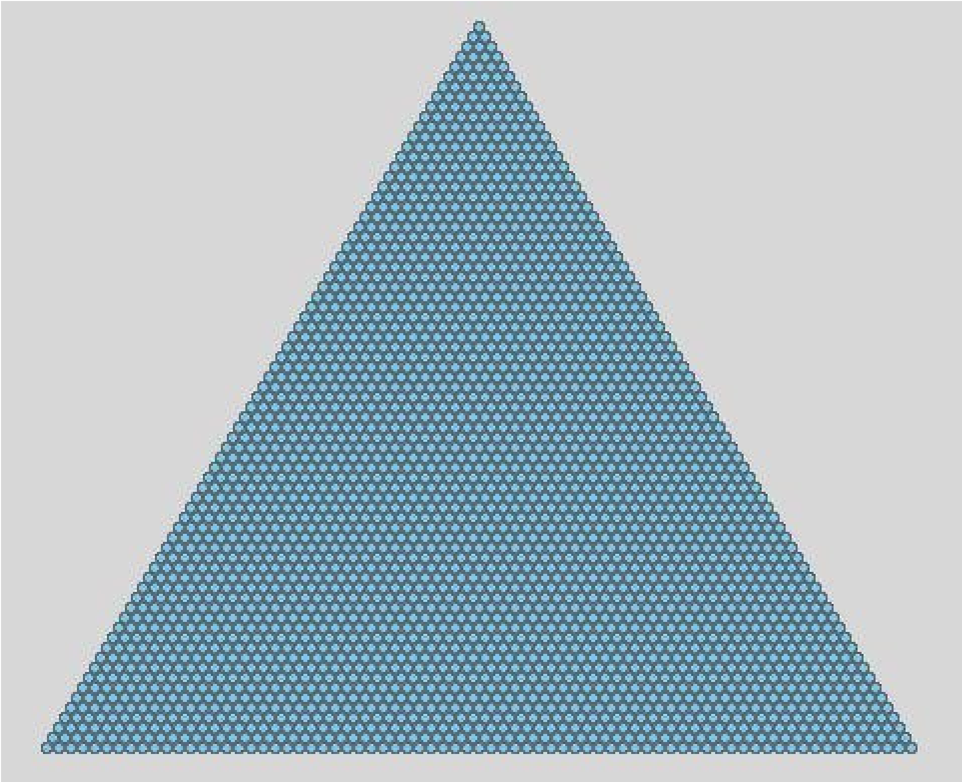
2701 = 37 x 73.

Here are some intriguing coincidences regarding 37 and 73

1. Both 37 and 73 are **PRIME** numbers, meaning that they are not divisible by any number except themselves and one.
2. Secondly, 37 and 73 are digital **REFLECTIONS** of each other.
3. Thirdly, both 37 and 73 can be arranged as **HEXAGRAMS** that fit neatly inside each other – it is a coincidence that the Star of David should appear in the very first verse



4. It is a coincidence that when 2701 counters are arranged into a triangle, the triangle produced has 73 layers; 2701 is the **73rd triangular number** – thus



2701 (the CV of Genesis 1:1) as 73rd triangular number

So the whole verse is a multiple of 37, and it's gross numerical value embodies no less than 4 numerical coincidences.

Vernon obtained the number 2701 by adding the numerical value of each word. But what happens when we multiply the value of each word instead.

913 x 203 x 86 x 401 x 395 x 407 x 296 = 304,153,525,784,175,760

The result can be divided up into 6 groups each of 3 digits. When these are then added we get an interesting result –

304 + 153 + 525 + 784 + 175 + 760 = **37 x 73**

What's more, if we add the individual digits we get –

3 + 0 + 4 + 1 + 5 + 3 + 5 + 2 + 5 + 7 + 8 + 4 + 1 + 7 + 5 + 7 + 6 + 0 = **73**

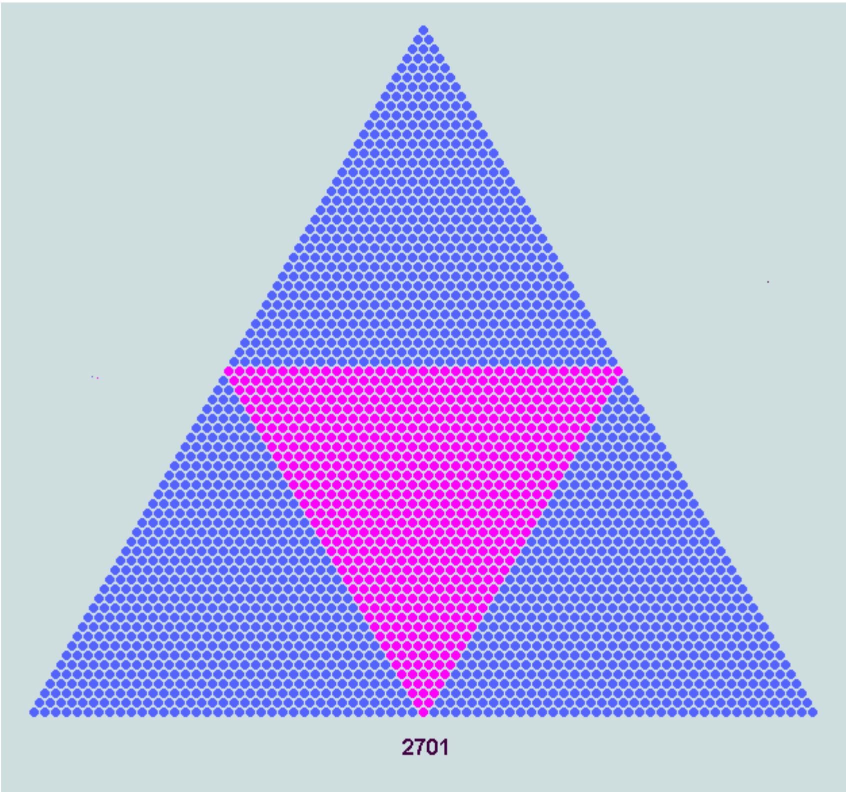
But are the individual words also multiples of 37?

Vernon found that only 2 of the 7 words in this verse were multiples of 37 on their own. These were the last two Hebrew words of the verse, which translate as - “and the earth”. The numerical value of these last two words comes to 407 + 296 = **703**.

So we have some more coincidences –

5. The two words add to 703, which **reflects** 73 and 37.
6. It is curious that 703 is also a **triangular** number.
7. 703 counters form a triangle with 37 layers – 703 happens to be the **37th triangular number**!

The 703 triangle fits neatly into the 2701 triangle like so –



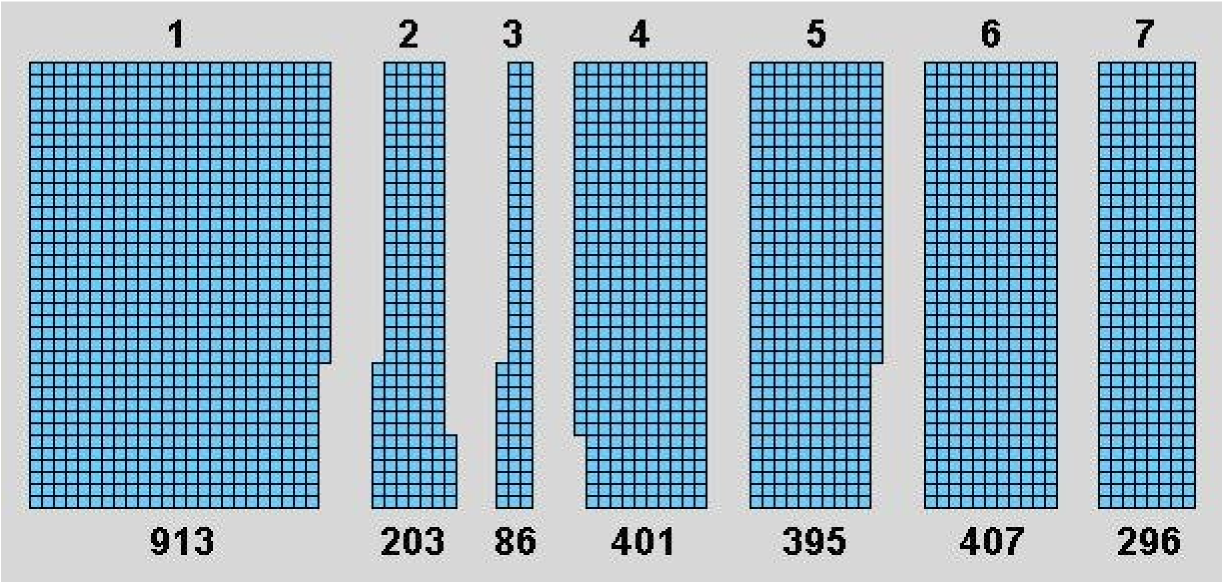
The 703 triangle is shown in pink. The three blue triangles surrounding it each have a value of 666, and the total triangle has a value of 2701.

We see that the number 703 is geometrically related to 2701 such that it forms a triangle that fits perfectly inside the triangle of 2701.

It is a further coincidence that 703 – 666 = 37, and 703 + 666 = 37 x 37

But what of the remaining 5 words whose numbers are 913, 203, 86, 401 and 395? Individually they are not multiples of 37, but as a group they add to 666 + 666 + 666, which is a multiple of 37.

Secondly, when we look at the numbers for each individual word in the verse, we notice a strange pattern –



Here is a diagram where each word is represented by a block of height 37. Notice that the words form a kind of jigsaw, where each number varies from a whole multiple of 37 by a multiple of 6. Strangely enough, all of the words vary from a multiple of 37 by either 0 x 6, 1 x 6 or 2 x 6. This is quite a big coincidence. I think you will agree that the jigsaw nature of this verse is very apparent.

Finally, these 5 words possess another strange property.

As shown above, the numbers for these 5 words are – 913, 203, 86, 401, and 395. Their sum is 1998. When written in reverse, the sum of these 5 numbers is still 1998 - as it is when the same cyclic permutation is applied to the digits of the individual values (rows 2 and 3), or to the block of five (rows 4 and 5), thus:

913 + 203 + 086 + 401 + 395	= 1998 =	593 + 104 + 680 + 302 + 319
391 + 320 + 608 + 140 + 539	= 1998 =	359 + 410 + 068 + 230 + 931
139 + 032 + 860 + 014 + 953	= 1998 =	935 + 041 + 806 + 023 + 193
591 + 320 + 308 + 640 + 139	= 1998 =	959 + 310 + 468 + 030 + 231
959 + 132 + 030 + 864 + 013	= 1998 =	195 + 931 + 046 + 803 + 023

1998 = 666 + 666 + 666

This numerical phenomena is called a cyclic permutation. The numbers always add to 666 + 666 + 666, no matter how they are read!

Criteria of Comparison

Vernon's patterns can be summarised as

1) PRIME numbers
2) multiples of the prime number 37, in particular 7 x 37, 3 x 37 and 73 x 37
3) symmetries (just as 37 was a "reflection" of 73)
4) specific multiples of the prime number 37, in particular 703, and 666 (703 – 37)
5) cyclic permutations, particularly based on 666.

Do we find the genetic code structured around these patterns?

Genetics 101 (3 pages)

The 4 Chemical Letters of the Code

The genetic code consists of a string of chemical letters. In DNA there are 4 different letters A, G, C and T.

Here is a picture of a typical DNA letter sequence.

```
Frame 3

000001     cctccgagaggggagaccagcgggccatgacaagctccaggctttggttttcgctgctgctggc
000065     ggcagcgttcgcaggacgggcgacggccctctggccctggcctcagaacttccaaacctccgac
000129     cagcgctacgtcctttacccgaacaactttcaattccagtacgatgtcagctcggccgcgcagc
000193     ccggctgctcagtcctcgacgaggccttccagcgctatcgtgacctgcttttcggttccgggtc
000257     ttggccccgtccttacctcacagggaaacggcatacactggagaagaatgtgttggttgtctct
000321     gtagtcacacctggatgtaaccagcttcctactttggagtcagtggagaattataccctgacca
000385     taaatgatgaccagtgtttactcctctctgagactgtctggggagctctccgaggtctggagac
000449     ttttagccagcttgtttggaaatctgctgagggcacattctttatcaacaagactgagattgag
000513     gactttccccgctttcctcaccggggcttgctgttggatacatctcgccattacctgccactct
000577     ctagcatcctggacactctggatgtcatggcgtacaataaattgaacgtgttccactggcatct
000641     ggtagatgatccttccttcccatatgagagcttcacttttccagagctcatgagaaaggggtcc
000705     tacaaccctgtcacccacatctacacagcacaggatgtgaaggaggtcattgaatacgcacggc
000769     tccggggtatccgtgtgcttgcagagtttgacactcctggccacactttgtcctggggaccagg
000833     tatccctggattactgactccttgctactctgggtctgagccctctggcacctttggaccagtg
000897     aatcccagtctcaataatacctatgagttcatgagcacattcttcttagaagtcagctctgtct
000961     tcccagatttttatcttcatcttggaggagatgaggttgatttcacctgctggaagtccaaccc
001025     agagatccaggactttatgaggaagaaaggcttcggtgaggacttcaagcagctggagtccttc
001089     tacatccagacgctgctggacatcgtctcttcttatggcaagggctatgtggtgtggcaggagg
001153     tgtttgataataaagtaaagattcagccagacacaatcatacaggtgtggcgagaggatattcc
001217     agtgaactatatgaaggagctggaactggtcaccaaggccggcttccgggcccttctctctgcc
001281     ccctggtacctgaaccgtatatcctatggccctgactggaaggatttctacgtagtggaacccc
001345     tggcatttgaaggtacccctgagcagaaggctctggtgattggtggagaggcttgtatgtgggg
001409     agaatatgtggacaacacaaacctggtccccaggctctggcccagagcaggggctgttgccgaa
001473     aggctgtggagcaacaagttgacatctgacctgacatttgcctatgaacgtttgtcacacttcc
001537     gctgtgagttgctgaggcgaggtgtccaggcccaacccctcaatgtaggcttctgtgagcagga
001601     gtttgaacagacctgagccccaggcaccgaggagggtgctggctgtaggtgaatggtagtggag
001665     ccaggcttccactgcatcctggccaggggacggagccccttgccttcgtgccccttgcctgcgt
001729     gcccctgtgcttggagagaaagggggccggtgctggcgctcgcattcaataaagagtaatgtggc
001793     atttttctataataaacatggattacctgtgtttaaaaaaaaaagtgtgaatggcgttagggta
001857     agggcacagccaggctggagtcagtgtctgcccctgaggtcttttaagttgagggctgggaatg
001921     aaacctatagcctttgtgctgttctgccttgcctgtgagctatgtcactcccctcccactcctg
001985     accatattccagacacctgccctaatcctcagcctgctcacttcacttctgcattatatctcca
002049     aggcgttggtatatggaaaaagatgtaggggcttggaggtgttctggacagtggggagggctcc
002113     agacccaacctggtcacaaaagagcctctcccccatgcatactcatccacctccctcccctaga
002177     gctattctcctttgggtttcttgctgctgcaattttatacaaccattatttaaatattattaaa
002241     cacatattgttctct
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These letters are the “software code”.

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The Code for Each Amino Acid

Every three letters (called a Codon) comprise an instruction to produce one of the 20 amino acids. There are also three-letter codes that instruct the amino acid production to start and stop.

Here are the three-letter codes that produce each of the 20 amino acids. The code is in **black**, and the amino acid is in **blue.**

		First Base			
		A	**G**	**T**	**C**
Second Base	**A**	AAT Asn S = 58 : B = 74 AAC Asn AAA Lys S = 72 : B = 74 AAG Lys	GAT Asp S = 59 : B = 74 GAC Asp GAA Glu S = 73 : B = 74 GAG Glu	TAT Tyr S = 107 : B = 74 TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA Gln S = 72 : B = 74 CAG Gln
	G	AGT Ser S = 31 : B = 74 AGC Ser AGA Arg S = 100 : B = 74 AGG Arg	GGT Gly S = 1 : B = 74 GGC Gly GGA Gly GGG Gly	TGT Cys S = 47 : B = 74 TGC Cys TGA Stop TGG Trp S = 130 : B = 74	CGT Arg S = 100 : B = 74 CGC Arg CGA Arg CGG Arg
	T	ATT Ile S = 57 : B = 74 ATC Ile ATA Ile ATG Met S = 75 : B = 74	GTT Val S = 43 : B = 74 GTC Val GTA Val GTG Val	TTT Phe S = 91 : B = 74 TTC Phe TTA Leu S = 57 : B = 74 TTG Leu	CTT Leu S = 57 : B = 74 CTC Leu CTA Leu CTG Leu
	C	ACT Thr S = 45 : B = 74 ACC Thr ACA Thr ACG Thr	GCT Ala S = 15 : B = 74 GCC Ala GCA Ala GCG Ala	TCT Ser S = 31 : B = 74 TCC Ser TCA Ser TCG Ser	CCT Pro S = 42-1 : B = 73+1 CCC Pro CCA Pro CCG Pro

This table is the standard depiction of the genetic code found in most text books on genetics.

So now you know which codes produce which amino acid. The table above shows all of the 64 possible combinations of three letters and the amino acids they produce.

Every amino acid can be represented by a number.

We are familiar with the Periodic Table, where an atom of any element may be represented by a number – it's ATOMIC NUMBER, which equals the number of protons in it's nucleus. An atom may also be represented by another number – it's MASS NUMBER, which equals the number of protons + neutrons in it's nucleus.

- ATOMIC NUMBER = Number of protons in the nucleus of an atom
- MASS NUMBER = Number of protons + neutrons in the nucleus of an atom
- A NUCLEON is either a proton or a neutron, so MASS NUMBER = number of nucleons.

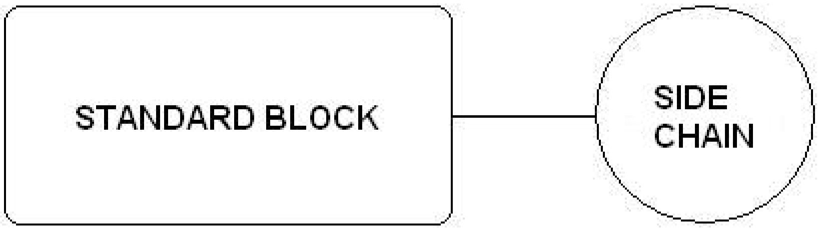
So atoms can be represented by numbers.

Amino acids are MOLECULES, meaning that they are made up of many atoms. This means that an amino acid can be represented by a number too. The MASS NUMBER of an amino acid is equal to the sum of the mass numbers of the atoms that it contains. Here are the mass numbers for each amino acid.

Asn	Lys	Ser	Arg	Ile	Met	Thr	Asp	Glu	Gly	Val	Ala	Tyr	Cys	Trp	Phe	Leu	His	Gln	Pro
132	146	105	174	131	149	119	133	147	75	117	89	181	121	204	165	131	155	146	115

Each Amino Acid has 2 Parts

Every amino acid consists of two parts – a STANDARD BLOCK part, which is the same in all amino acids, and a SIDE-CHAIN part, which varies in it's chemical structure quite widely from one amino acid to the next.



Here are the MASS NUMBERS for the two parts in each amino acid. Remember, the mass number is simply the number of protons and neutronside-chain the number of nucleons.

	Asn	Lys	Ser	Arg	Ile	Met	Thr	Asp	Glu	Gly	Val	Ala	Tyr	Cys	Trp	Phe	Leu	His	Gln	Pro
Standard Block	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	73
Side Chain	58	72	31	100	57	75	45	59	73	1	43	15	107	47	130	91	57	81	72	42

You can see that the mass number for the side-chain part varies greatly, but the mass number for the standard block part is nearly always 74 = 2 x 37. The one exception is PROLINE (Pro) where the mass number is 73.

The Hidden Patterns

The mathematical patterns found in the genetic code are based on the mass numbers of the amino acids. All of these patterns were discovered by the mathematician Vladimir I. Shcherbak, who published his findings in a paper called "Arithmetic Inside the Universal Genetic Code".

Shcherbak noticed that Proline was the odd one out because it's standard block was 73 instead of 74. He wondered what would be the effect of transferring 1 unit from the side chain of Proline to the standard block to give the standard block a value of 74, and the side chain a value of 41.

When he did this, he found that the genetic code suddenly displayed an extraordinary symmetry throughout, based on multiples of the number 37.

Shcherbak’s Patterns

PATTERN 1

		First Base			
		A	**G**	**T**	**C**
Second Base	**A**	AAT Asn S = 58 : B = 74 AAC Asn AAA Lys S = 72 : B = 74 AAG Lys	GAT Asp S = 59 : B = 74 GAC Asp GAA Glu S = 73 : B = 74 GAG Glu	TAT Tyr S = 107 : B = 74 TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA Gln S = 72 : B = 74 CAG Gln
	G	AGT Ser S = 31 : B = 74 AGC Ser AGA Arg S = 100 : B = 74 AGG Arg	GGT Gly S = 1 : B = 74 GGC Gly GGA Gly GGG Gly	TGT Cys S = 47 : B = 74 TGC Cys TGA Stop TGG Trp S = 130 : B = 74	CGT Arg S = 100 : B = 74 CGC Arg CGA Arg CGG Arg
	T	ATT Ile S = 57 : B = 74 ATC Ile ATA Ile ATG Met S = 75 : B = 74	GTT Val S = 43 : B = 74 GTC Val GTA Val GTG Val	TTT Phe S = 91 : B = 74 TTC Phe TTA Leu S = 57 : B = 74 TTG Leu	CTT Leu S = 57 : B = 74 CTC Leu CTA Leu CTG Leu
	C	ACT Thr S = 45 : B = 74 ACC Thr ACA Thr ACG Thr	GCT Ala S = 15 : B = 74 GCC Ala GCA Ala GCG Ala	TCT Ser S = 31 : B = 74 TCC Ser TCA Ser TCG Ser	CCT Pro S = 42-1 : B = 73+1 CCC Pro CCA Pro CCG Pro

Each amino acid consists of a standard block and a side-chain. The standard block is the same in all amino acids, and consists of 74 nucleons, whilst the number of nucleons in the side-chain varies. The table shows the number of nucleons in the side-chain as **S = ..** and the number of nucleons in the standard block as **B =** ..

In each of the cells shaded yellow, all of the three-letter codes produce the same amino acid. For example, ACT, ACC, ACA and ACG, found in the bottom left cell, are all instructions for producing the amino acid Threonine**.** In the cells shaded white this is not the case.

This phenomenon divides the genetic code in half precisely – 8 cells belonging to each group.

Taking the amino acids found in the yellow-shaded cells, **Shcherbak** counted the number of nucleons in the amino acids and found the following. Here are Shcherbak's calculations in full.

Amino Acids in the yellow cells	**Symbol**	**Mass Number (nucleons) in standard block**	**Mass Number (nucleons) in side chain**
Threonine	Thr	74	45
Alanine	Ala	74	15
Valine	Val	74	43
Glycine	Gly	74	1
Serine	Ser	74	31
Arginine	Arg	74	100
Leucine	Leu	74	57
Proline	Pro	73 + 1	42 - 1
		592	**333**

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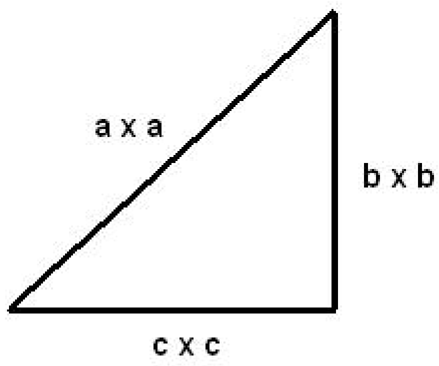
- Number of nucleons in the side-chain = **333** = **3 x 3 x 37.**
- Number of nucleons in the standard block = **592** = **4 x 4 x 37.**
- total number of nucleons in the amino acids coded = **925** = **5 x 5 x 37.**

Shcherbak points out that it is remarkable that each of these numbers (925, 592 and 333) is a multiple of 37. To his amazement, Shcherbak then realised that the three numbers formed a perfect Pythagorean Triangle

5 squared = 4 squared + 3 squared



3 x 3 x 37
4 x 4 x 37
5 x 5 x 37.

It is also interesting that 333 = 592 – 259. So the numbers 925, 592 and 592 – 259 are all **CYCLIC PERMUTATIONS** of 259 = **7 x 37.** Remember that 7 x 37 is central to the Creation story pattern. It is one of the multiples that we predicted we would find.

925
592
259

This is a truly remarkable the genetic code should contain such mathematical patterns.

The second part of Shcherbak's pattern concerns the remaining 8 cells that are shaded in white. Given the remarkable results from the first group, we might expect this group to display a mathematical pattern too. Shcherbak repeated the same procedure - counting the number of nucleons in each amino acid found in these cells.

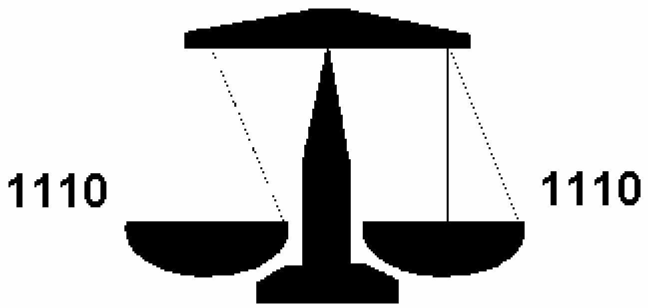
- number of nucleons in the standard blocks comes to **1110** = **30 x 37**
- number of nucleons in the side-chains comes to **1110** = **30 x 37**
- total number of nucleons comes to **2220** = **60 x 37**

There is a perfect balance between the number of nucleons in the standard blocks and the number of nucleons in the side-chains!! Just how strange and unexpected this is becomes apparent when we look at the amino acids that make up this group.

Amino Acids in the white cells	**Symbol**	**Mass Number (nucleons) in standard block**	**Mass Number (nucleons) in side chain**
Asparagine	Asn	74	58
Lysine	Lys	74	72
Serine	Ser	74	31
Arginine	Arg	74	100
Isoleucine	Ile	74	57
Methionine	Met	74	75
Aspartic Acid	Asp	74	59
Glutamic Acid	Glu	74	73
Tyrosine	Tyr	74	107
Cysteine	Cys	74	47
Tryptophan	Trp	74	130
Phenyl-alanine	Phe	74	91
Leucine	Leu	74	57
Histidine	His	74	81
Glutamine	Gln	74	72
		Total = 1110	**Total = 1110**

Notice that even though the side chain mass numbers vary considerably from one amino acid to the next, their total just happens to be the same as for the standard block.

Shcherbak states that it is remarkable that there should be this exact balance between the total nucleon numbers for the standard blocks and side-chains, and also that the balance should again be a multiple of 37. We might add that it is extraordinary that the number **30 x 37** = 1110 appears here; because 3 x 37, like 7 x 37, is one of the key multiples we predicted.



In summary, so far, the DNA codon table of amino acids divides naturally into 2 parts. The number of nucleons in each case displaying an interesting mathematical pattern viz -

PART 1 built on 3 x 37

a). 1110 (standard block) + 1110 (Side-chain) = 2220 - a perfect balance – a perfect symmetry.

b). 1110 = 30 x 37, 3 x 37 being one of the key multiples of 37 predicted from the Genesis patterns.

PART 2 built on 7 x 37

a). 333 (standard block) + 592 (Side-chain) = 925 (Total) - forms a Pythagorean triangle pattern.

b). 925 and 592 and (592 – 259) are cyclic permutations of 259 = 7 x 37, 7 x 37 being one of the key multiples of 37 predicted by the Genesis patterns.

In the first pattern alone we find startling patterns of symmetry –

- 1110 balanced with 1110
- 925 reflecting 592 reflecting 259, and forming a Pythagorean Triangle while doing so.
- 3 x 37 reflecting 7 x 37

And these patterns directly relate to the Creation story patterns.

PATTERN 2

		First Base			
		A	G	T	C
Second Base	A	AAT Asn S = 58 : B = 74 AAC Asn AAA Lys S = 72 : B = 74 AAG Lys	GAT Asp S = 59 : B = 74 GAC Asp GAA Glu S = 73 : B = 74 GAG Glu	TAT Tyr S = 107 : B = 74 TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA Gln S = 72 : B = 74 CAG Gln
	G	AGT Ser S = 31 : B = 74 AGC Ser AGA Arg S = 100 : B = 74 AGG Arg	GGT Gly S = 1 : B = 74 GGC Gly GGA Gly GGG Gly	TGT Cys S = 47 : B = 74 TGC Cys TGA Stop TGG Trp S = 130 : B = 74	CGT Arg S = 100 : B = 74 CGC Arg CGA Arg CGG Arg
	T	ATT Ile S = 57 : B = 74 ATC Ile ATA Ile ATG Met S = 75 : B = 74	GTT Val S = 43 : B = 74 GTC Val GTA Val GTG Val	TTT Phe S = 91 : B = 74 TTC Phe TTA Leu S = 57 : B = 74 TTG Leu	CTT Leu S = 57 : B = 74 CTC Leu CTA Leu CTG Leu
	C	ACT Thr S = 45 : B = 74 ACC Thr ACA Thr ACG Thr	GCT Ala S = 15 : B = 74 GCC Ala GCA Ala GCG Ala	TCT Ser S = 31 : B = 74 TCC Ser TCA Ser TCG Ser	CCT Pro S = 42-1 : B = 73+1 CCC Pro CCA Pro CCG Pro

The 64 DNA codons (the three-letter codes) divide into 2 groups - those that begin with A or G, and those that begin with C or T. This natural division is shown above.

The codons whose first base is A or G are called **PYRIMIDINES**, and the 8 cells shaded WHITE contain the amino acids coded by these codons.

The codons whose first base is C or T are called **PURINES**, and the 8 cells shaded YELLOW contain the amino acids coded by these codons.

As was mentioned before, each amino acid divides into two parts - a "standard block" part and a side-chain part. The standard block part always contains 74 nucleons, that is 37 x 2.

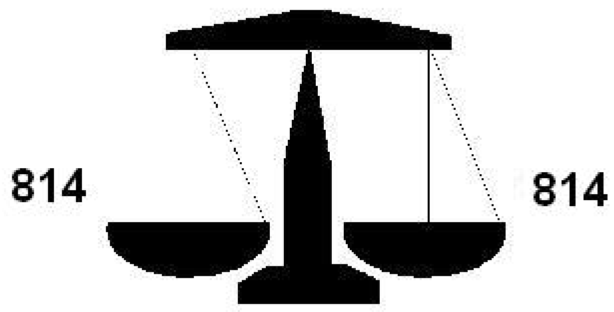
Here are the figures for the PYRIMIDINES (white group) -

- number of nucleons in the "standard blocks" of the amino acids = 814 = 22 x 37
- number of nucleons in the side-chain part of the amino acids = 814 = 22 x 37
- total number of nucleons is 1628

Here are the figures for the PURINES (yellow group) -

- number of nucleons in the "standard blocks" of the amino acids = 592 + 592/2
- number of nucleons in the "side-chain part of the amino acids = 333 + 592/2
- total number of nucleons = 925 + 592

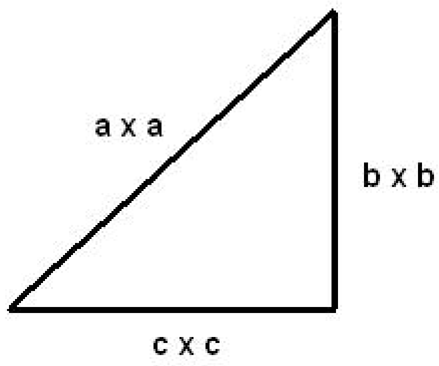
In the Pyrimidine group we have a perfect balance again between the standard block and the side-chain, both having a nucleon sum of 814, which is a multiple of 37. This is a similar pattern to the balance we found in Pattern 1, where the standard block and side chain both had a nucleon sum of 1110.



The total number of nucleons in the Pyrimidine group comes to 814 + 814 = 1628. The total in Pattern 1 was 1110 + 1110 = 2220. Oddly enough -

2220 – 1628 = 592 (permutation of 259 = 7 x 37)

In the Purine group Shcherbak once again found a Pythagorean Triangle pattern –



3 squared + 4 squared = 5 squared

4 x 4 x 37 + 592/2
3 x 3 x 37 + 592/2
5 x 5 x 37 + 592

So in this way Pattern 2 is also similar to Pattern 1

Notice that the total number of nucleons in the Purine group is 925 + 592 (permutations of 259 = **7 x 37**) and that the additional 592 is distributed equally between the standard blocks and side chains. Also note that this total differs from the total for the Pyrimidine group by 111 = **3 x 37**.

1628 - (925 + 592) = **111**

So there is a strong similarity between Pattern 1 and Pattern 2; both patterns consist of multiples of 37; both exhibit a perfect balance in one half of the pattern, and a Pythagorean Triangle in the other. And in both, the total for the Pythagorean Triangle is either **925** or **925 + 592**!!

PATTERN 3

		First Base			
		A	**G**	**T**	**C**
	A	AAT Asn S = 58 : B = 74 AAC Asn AAA Lys S = 72 : B = 74 AAG Lys	GAT Asp S = 59 : B = 74 GAC Asp GAA Glu S = 73 : B = 74 GAG Glu	TAT Tyr S = 107 : B = 74 TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA Gln S = 72 : B = 74 CAG Gln
Second Base	**G**	AGT Ser S = 31 : B = 74 AGC Ser AGA Arg S = 100 : B = 74 AGG Arg	GGT Gly S = 1 : B = 74 GGC Gly GGA Gly GGG Gly	TGT Cys S = 47 : B = 74 TGC Cys TGA Stop TGG Trp S = 130 : B = 74	CGT Arg S = 100 : B = 74 CGC Arg CGA Arg CGG Arg
	T	ATT Ile S = 57 : B = 74 ATC Ile ATA Ile ATG Met S = 75 : B = 74	GTT Val S = 43 : B = 74 GTC Val GTA Val GTG Val	TTT Phe S = 91 : B = 74 TTC Phe TTA Leu S = 57 : B = 74 TTG Leu	CTT Leu S = 57 : B = 74 CTC Leu CTA Leu CTG Leu
	C	ACT Thr S = 45 : B = 74 ACC Thr ACA Thr ACG Thr	GCT Ala S = 15 : B = 74 GCC Ala GCA Ala GCG Ala	TCT Ser S = 31 : B = 74 TCC Ser TCA Ser TCG Ser	CCT Pro S = 42-1 : B = 73+1 CCC Pro CCA Pro CCG Pro

The 64 DNA codons can also be divided into 2 groups as shown above

Here are the figures for the YELLOW GROUP -

- number of nucleons in the side-chain part of the amino acids = 654
- number of nucleons in the standard block part of the amino acids = 814

Here are the figures for the PINK GROUP

- number of nucleons in the side-chain part of the amino acids = 789
- number of nucleons in the standard block part of the amino acids = 888

Total number of nucleons in the side-chains = 654 + 789
= 2368 – 925

Total number of nucleons in the standard block = 888 + 814

		First Base			
		A	**G**	**T**	**C**
Second Base	**A**	AAT Asn S = 58 : B = 74 AAC Asn AAA Lys S = 72 : B = 74 AAG Lys	GAT Asp S = 59 : B = 74 GAC Asp GAA Glu S = 73 : B = 74 GAG Glu	TAT Tyr S = 107 : B = 74 TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA Gln S = 72 : B = 74 CAG Gln
	G	AGT Ser S = 31 : B = 74 AGC Ser AGA Arg S = 100 : B = 74 AGG Arg	GGT Gly S = 1 : B = 74 GGC Gly GGA Gly GGG Gly	TGT Cys S = 47 : B = 74 TGC Cys TGA Stop TGG Trp S = 130 : B = 74	CGT Arg S = 100 : B = 74 CGC Arg CGA Arg CGG Arg
	T	ATT Ile S = 57 : B = 74 ATC Ile ATA Ile ATG Met S = 75 : B = 74	GTT Val S = 43 : B = 74 GTC Val GTA Val GTG Val	TTT Phe S = 91 : B = 74 TTC Phe TTA Leu S = 57 : B = 74 TTG Leu	CTT Leu S = 57 : B = 74 CTC Leu CTA Leu CTG Leu
	C	ACT Thr S = 45 : B = 74 ACC Thr ACA Thr ACG Thr	GCT Ala S = 15 : B = 74 GCC Ala GCA Ala GCG Ala	TCT Ser S = 31 : B = 74 TCC Ser TCA Ser TCG Ser	CCT Pro S = 42-1 : B = 73+1 CCC Pro CCA Pro CCG Pro

Here are the figures for the PINK GROUP -

- number of nucleons in the side-chain part of the amino acids = 789
- number of nucleons in the standard block part of the amino acids = 888

Here are the figures for the BLUE GROUP

- number of nucleons in the side-chain part of the amino acids = 654
- number of nucleons in the standard block part of the amino acids = 814

Total number of nucleons in the side-chains = 654 + 789
= 2368 – 925

Total number of nucleons in the standard blocks = 888 + 814

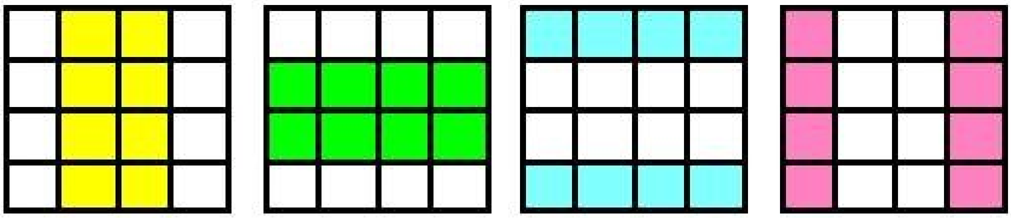
Here Shcherbak demonstrates more symmetry and balance within the genetic code - such that

the **GREEN** group + **YELLOW** group = 39 x 37

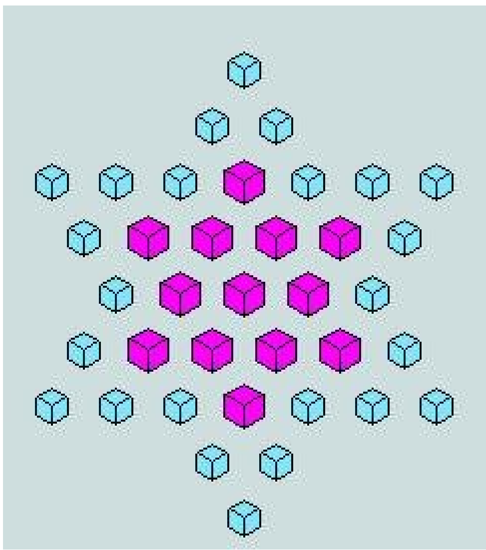
the **PINK** group + **BLUE** group = 39 x 37

the **YELLOW** group + the **PINK** group = 39 x 37

the **GREEN** group + the **BLUE** group = 39 x 37



1. **Once more a perfect symmetry is displayed**
2. **The symmetry involves multiples of 37**
3. **The totals come to 39 x 37 = 3 x 13 x 37**
   (13 and 37 being geometrically related as one hexagram inside of another)



All three of these observations were predicted in the Creation story pattern.

Six forms of REFLECTION –

Balance	– where one side is equal to another
Symmetry	– where one side is symmetrically arranged relative to the other
Division	– where both sides divide in such a way that one reflects the other
Permutation	– where one part is a cyclic permutation of another part
Geometric unity	– where one part has a geometric form that is in unity with the geometric form of another part
Progression	– where the parts form sequential steps in a mathematical progression.

Listed above are some of the forms of mathematical symmetry found in the code.

PATTERN 4

		First Base			
		A	G	T	C
Second Base	A	AAT Asn S = 58 : B = 74 AAC Asn AAA Lys S = 72 : B = 74 AAG Lys	GAT Asp S = 59 : B = 74 GAC Asp GAA Glu S = 73 : B = 74 GAG Glu	TAT Tyr S = 107 : B = 74 TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA Gln S = 72 : B = 74 CAG Gln
	G	AGT Ser S = 31 : B = 74 AGC Ser AGA Arg S = 100 : B = 74 AGG Arg	GGT Gly S = 1 : B = 74 GGC Gly GGA Gly GGG Gly	TGT Cys S = 47 : B = 74 TGC Cys TGA Stop TGG Trp S = 130 : B = 74	CGT Arg S = 100 : B = 74 CGC Arg CGA Arg CGG Arg
	T	ATT Ile S = 57 : B = 74 ATC Ile ATA Ile ATG Met S = 75 : B = 74	GTT Val S = 43 : B = 74 GTC Val GTA Val GTG Val	TTT Phe S = 91 : B = 74 TTC Phe TTA Leu S = 57 : B = 74 TTG Leu	CTT Leu S = 57 : B = 74 CTC Leu CTA Leu CTG Leu
	C	ACT Thr S = 45 : B = 74 ACC Thr ACA Thr ACG Thr	GCT Ala S = 15 : B = 74 GCC Ala GCA Ala GCG Ala	TCT Ser S = 31 : B = 74 TCC Ser TCA Ser TCG Ser	CCT Pro S = 42-1 : B = 73+1 CCC Pro CCA Pro CCG Pro

The amino acids highlighted in **yellow** are coded by codons with **two A's**

The amino acids highlighted in **green** are coded by codons with **two G's**

The amino acids highlighted in **blue** are coded by codons with **two T's**

The amino acids highlighted in **grey** are coded by codons with **two C's**

- total number of nucleons in the **side-chain** part of AA amino acids = 535
- total number of nucleons in the **side-chain** part of GG amino acids = 464

total = **999**

- total number of nucleons in the **side-chain** part of TT amino acids = 547
- total number of nucleons in the **side-chain** part of CC amino acids = 452

total = **999**

- total number of nucleons in the **standard block** part of AA amino acids = 592
- total number of nucleons in the **standard block** part of GG amino acids = 666

total = 1258

- total number of nucleons in the **standard block** part of TT amino acids = 666
- total number of nucleons in the **standard block** part of CC amino acids = 666

total = 1332

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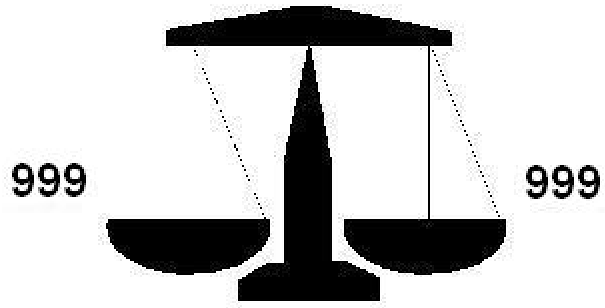
The AA + GG amino acid side-chain are in perfect balance with the TT + CC amino acid side-chains. In both cases the nucleon sum for the side-chains is 999. This is a multiple of 37 = **3 x 3 x 3 x 37**



999 = 3 x 3 x 3 x 37

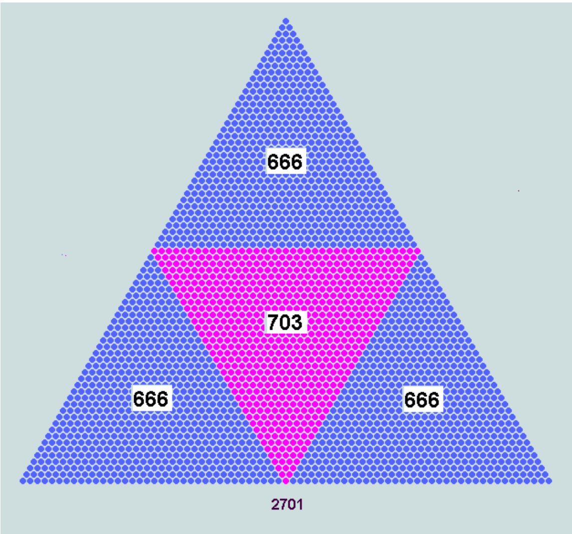
The total nucleon sum for the standard block part of amino acids **=**

1332 + 1258 = 70 x 37

The nucleon sum for the side-chain part of amino acids =

666 + 666 + 666

Where have we seen a similar pattern before - multiple of 37 enclosed by 666 + 666 + 666?



In the Creation story pattern, 703, the 37th triangular number, was surrounded by three triangles each of 666.

And just as in the Creation pattern, the numbers that sum to 666 + 666 + 666 can be arranged in any order, forwards or backwards, and they will always sum to 666 + 666 + 666.

The numbers 535, 464, 547 and 452 form a cyclic permutation such that

535 + 464 + 547 + 452	=	**666 + 666 + 666**	=	254 + 745 + 464 + 535
354 + 645 + 474 + 525	=	**666 + 666 + 666**	=	525 + 474 + 546 + 453
546 + 454 + 745 + 253	=	**666 + 666 + 666**	=	352 + 547 + 454 + 645

No matter where you start, the total is always the same. You can repeat this procedure forwards or backwards.

PATTERN 5

		First Base			
		A	**G**	**T**	**C**
Second Base	**A**	AAT Asn S = 58 : B = 74 AAC Asn AAA Lys S = 72 : B = 74 AAG Lys	GAT Asp S = 59 : B = 74 GAC Asp GAA Glu S = 73 : B = 74 GAG Glu	TAT Tyr S = 107 : B = 74 TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA Gln S = 72 : B = 74 CAG Gln
	G	AGT Ser S = 31 : B = 74 AGC Ser AGA Arg S = 100 : B = 74 AGG Arg	GGT Gly S = 1 : B = 74 GGC Gly GGA Gly GGG Gly	TGT Cys S = 47 : B = 74 TGC Cys TGA Stop TGG Trp S = 130 : B = 74	CGT Arg S = 100 : B = 74 CGC Arg CGA Arg CGG Arg
	T	ATT Ile S = 57 : B = 74 ATC Ile ATA Ile ATG Met S = 75 : B = 74	GTT Val S = 43 : B = 74 GTC Val GTA Val GTG Val	TTT Phe S = 91 : B = 74 TTC Phe TTA Leu S = 57 : B = 74 TTG Leu	CTT Leu S = 57 : B = 74 CTC Leu CTA Leu CTG Leu
	C	ACT Thr S = 45 : B = 74 ACC Thr ACA Thr ACG Thr	GCT Ala S = 15 : B = 74 GCC Ala GCA Ala GCG Ala	TCT Ser S = 31 : B = 74 TCC Ser TCA Ser TCG Ser	CCT Pro S = 42-1 : B = 73+1 CCC Pro CCA Pro CCG Pro

Those amino acids with A or G as a UNIQUE BASE, ie where A or G are the only bases that occur once, are shown below, highlighted in blue.

Those amino acids with T or C as a UNIQUE BASE, ie where T or C are the only bases that occur once, are shown below shaded in yellow.

For A and G UNIQUE BASES

- The side-chains in these amino acids sum to 1110 = 30 x 37
- The standard blocks in these amino acids sum to 1258 = (666 - 37) + (666 - 37)

Total = 888 + 1480 = 2368

For T and C UNIQUE BASES

- The side-chains in these amino acids sum to 888
- The standard blocks in amino acids sum to 666 + 666 = 1480 - 148

Total = 888 + 1480 - 148 = 2220

All 4 numbers – 1110, 1258, 888 and (666 + 666) are multiples of 37

Please note that there seems to be a common pattern shared by the totals for the two groups shown above.

888 + 1480

888 + 1480 - 148

Remember that in Pattern 1 we had a total of 2220 for one half of the pattern, and 925 for the other half. Well now we have a total of 2220 for the T and C unique bases, and 2368 for the A and G unique bases.

Pattern 1 : 2220 + 925

Pattern 5 : 2220 + 2368

PATTERN 6

Amino Acids with three IDENTICAL BASES				
TTT Phe S = 91 : B = 74 **AAA Lys S = 72 : B = 74**			**GGG Gly S = 1 : B = 74** **CCC Pro S = 42-1 : B = 73 + 1**	
Amino Acids with three UNIQUE BASES				
TCA Ser S = 31 : B = 74 **CAT His S = 81 : B = 74** **ATC Ile S = 57 : B = 74**	**Clockwise**	**C** **T A**	**CTA Thr S = 45 : B = 74** **TAC Tyr S = 107 : B = 74** **ACT Leu S = 57 : B = 74**	**Anti-Clockwise**
GCT Ala S = 15 : B = 74 **CTG Leu S = 57 : B = 74** **TGC Cys S = 47 : B = 74**	**Clockwise**	**C** **G T**	**CGT Ser S = 31 : B = 74** **GTC Val S = 43 : B = 74** **TCG Arg S = 100 : B = 74**	**Anti-Clockwise**
TGA Stop S = 0 : B = 0 **GAT Asp S = 59 : B = 0** **ATG Met S = 75 : B = 74**	**Clockwise**	**G** **T A**	**GTA Ser S = 31 : B = 74** **TAG Stop S = 0 : B = 0** **AGT Val S = 43 : B = 74**	**Anti-Clockwise**
CAG Gln S = 72 : B = 74 **AGC Ser S = 31 : B = 74** **GCA Ala S = 15 : B = 74**	**Clockwise**	**A** **C G**	**ACG Asp S = 59 : B = 74** **CGA Arg S = 100 : B = 74** **GAC Thr S = 45 : B = 74**	**Anti-Clockwise**

The Yellow Group codons change in a CLOCKWISE fashion. Look at the three-letter triangle in the centre of the table. TCA is one clockwise cycle, then the next clockwise cycle is CAT, then ATC and so on. This is repeated for each of the 4 groups of unique bases.

The Blue Group codons change in an ANTI-CLOCKWISE fashion. Here CTA is followed by TAC, then ACT and so on. This is repeated for each of the 4 groups of unique bases

The Yellow Group :

- Number of nucleons in the side-chain part of the amino acids 703
- Number of nucleons in the standard block part of the amino acids 703 + 259
- Number of nucleons in total = 666 + 666 + 333

The Blue Group :

- Number of nucleons in the side-chain part of the amino acids 703
- Number of nucleons in the standard block part of the amino acids 703 + 259
- Number of nucleons in total = 666 + 666 + 333

Here we have a final example of perfect balance again - not just with the totals, but also with the side-chain total and standard block total

1. The side-chain and standard block nucleon numbers are 703 and 7 x 37 + 703 respectively

2. The standard block + side-chain total is centred on the number 666

Bibliography

On Patterns in the Creation story:

- **Vernon Jenkins** (formerly Senior Lecturer of the Department of Mathematics and Computer Science, University of Glamorgan, Wales):
  Website – www.otherbiblecode.com

On Patterns in the Genetic code :

- **Vladimir I. Shcherbak** (Department of Applied Mathematics, al-Faraby Kazakh National University, Kazakhstan):
  Paper - "Arithmetic Inside the Universal Genetic Code" Biosystems 2003, vol. 70, n^{o}3, pp. 187-209 [23 page(s) (article)]

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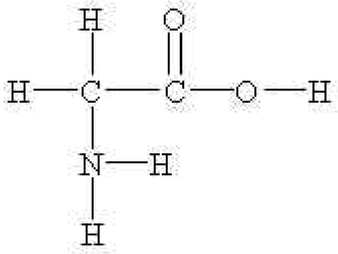
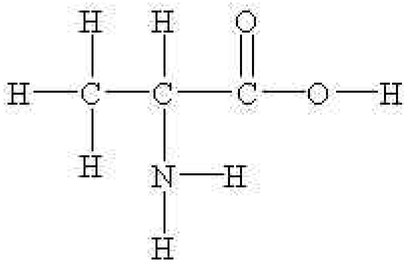
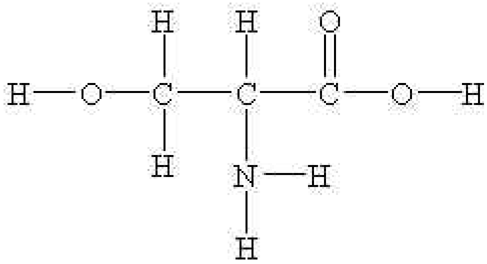
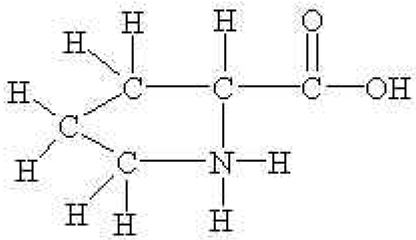
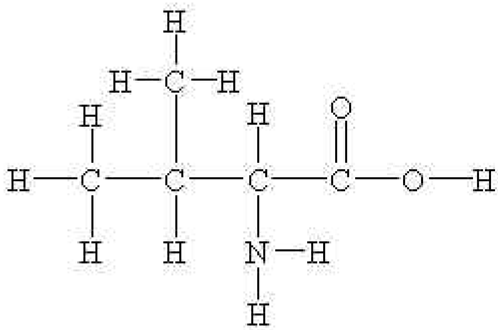
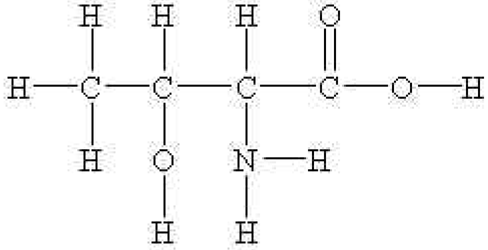
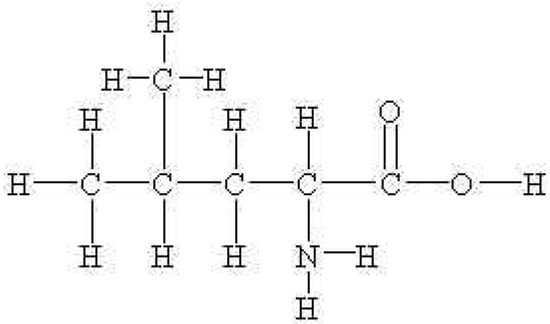
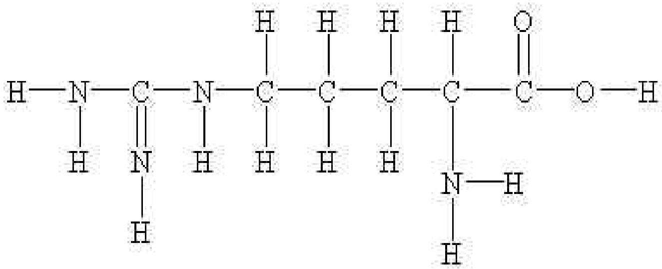
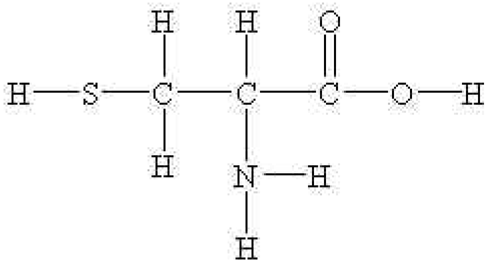
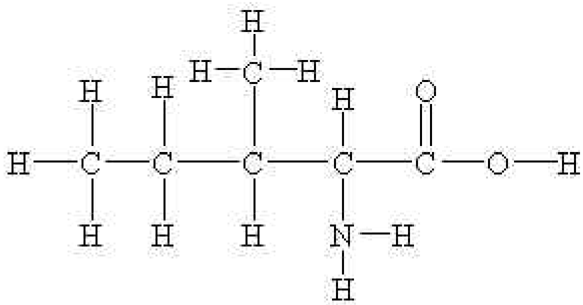
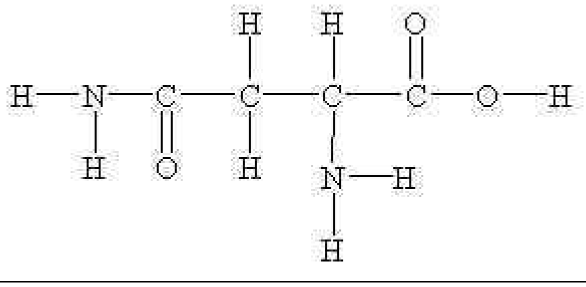
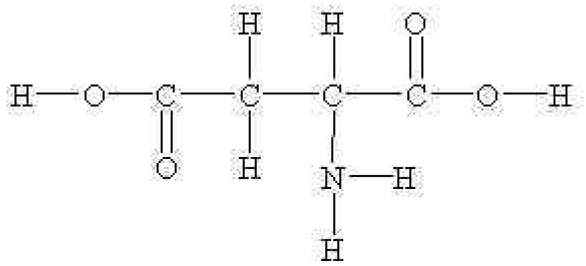
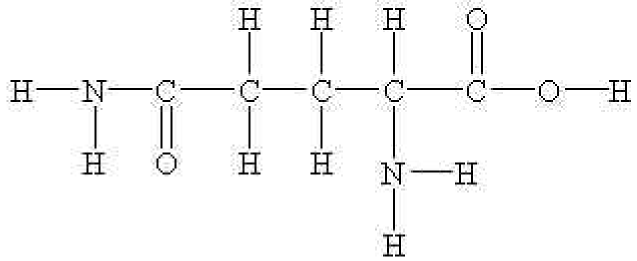
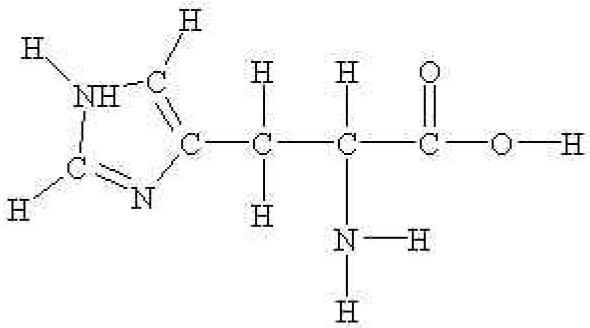
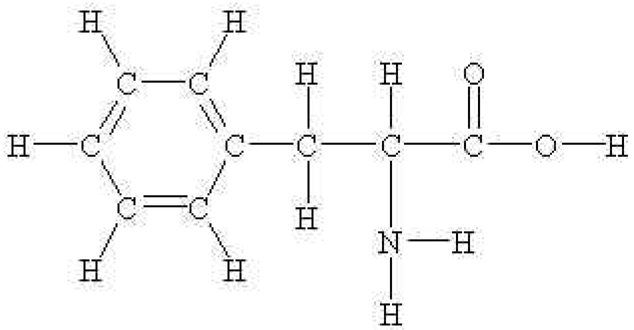
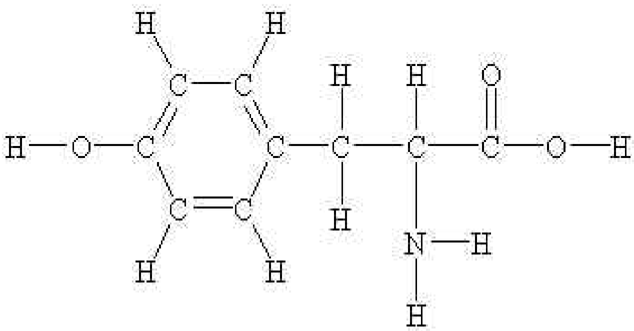
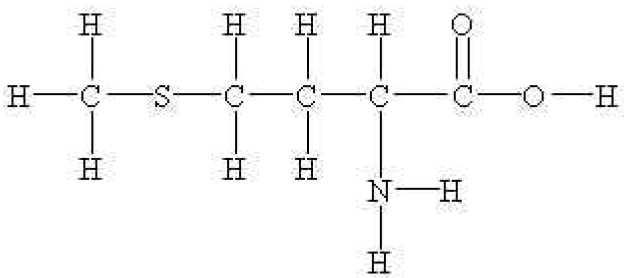
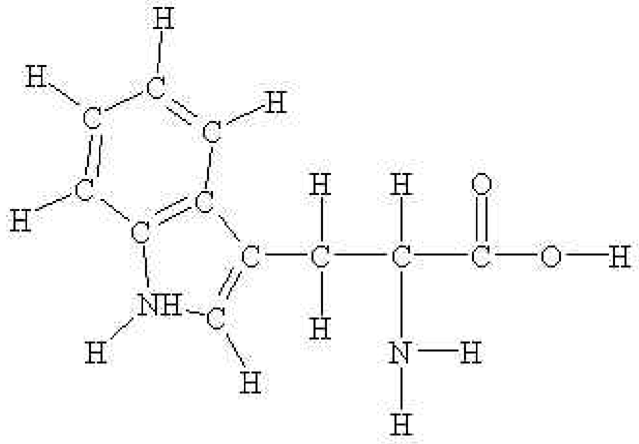
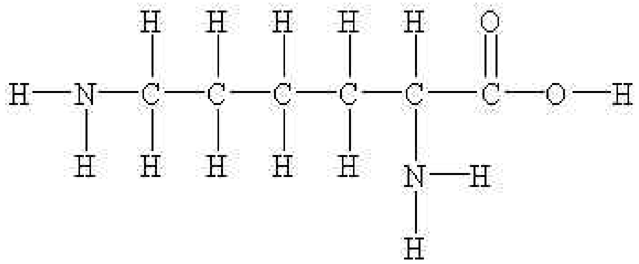
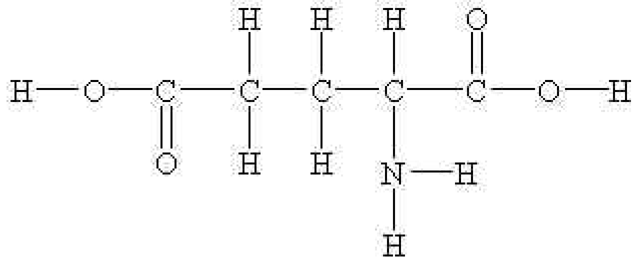
Appendix A

Structure of the Amino Acids

AMINO ACID	Abrev	Chemical Formula	Number of Nucleons in Base	Number of Nucleons in Side-chain
Glycine	Gly		COOH—CH--NH2 74	H 1
Alanine	Ala		COOH—CH—NH2 74	CH3 15
Serine	Ser		COOH—CH—NH2 74	CH2-OH 31
Proline	Pro		COOH—CH—NH2 73 A single hydrogen transfer to base from side-chain gives 74	CH2—CH2—CH2 42 A single hydrogen transfer to base from side-chain gives 41
Valine	Val		COOH—CH—NH2 74	CH—CH3—CH3 43

Threonine	Thr		COOH—CH—NH2 74	CH3--CH—OH 45
Leucine	Leu		COOH—CH—NH2 74	CH2—CH—CH3—CH3 57
Arginine	Arg		COOH—CH—NH2 74	CH2—CH2—CH2—NH—CNH—NH2 100
Cysteine	Cys		COOH—CH—NH2 74	CH2—SH 47
Isoleucine	Ile		COOH—CH—NH2 74	CH—CH3—CH2—CH3 57
Asparagine	Asn		COOH—CH—NH2 74	CH2—CO—NH2 58

Aspartic Acid	Asp		COOH—CH—NH2 74	CH2—CO—OH 59
Glutamine	Gln		COOH—CH—NH2 74	CH2—CH2—CO—NH2 72
Histidine	His		COOH—CH—NH2 74	CH2—C3N2H4 81
Phenyl-alanine	Phe		COOH—CH—NH2 74	CH2 – C6H5 91
Tyrosine	Tyr		COOH—CH—NH2 74	CH2—C6H4—OH 107
Methionine	Met		COOH—CH—NH2 74	CH2—CH2S—CH3 75

Tryptophan	Trp		COOH—CH—NH2 74	CH2—C8H5—NH2 130
Lysine	Lys		COOH—CH—NH2 74	CH2—CH2—CH2—CH2—NH2 72
Glutamic Acid	Glu		COOH—CH—NH2 74	CH2—CH2—CO—OH 73

For an online table of the amino acids see - http://dl.clackamas.cc.or.us/ch106-05/common.htm