Genetic Patterns

Mathematical Patterns in the Genetic Code

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_VS.htm



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: Letter: Value:	1 % 1	2 ⊐ 2	3 1 3	4 7 4	5 ก 5	6 1 6	7 7 7	8 n 8
Place: Letter: Value:	9 ២ 9	10 10	11 ⊃ 7 20	12 5 30	13 ねロ 40	14 3 7 50	15 D 60	16 ນ 70
Place: Letter: Value:	17 ១ ៗ 80	18 Υγ 90	19 ア 100	20 7 200	21 W 300	22 ☐ 400		

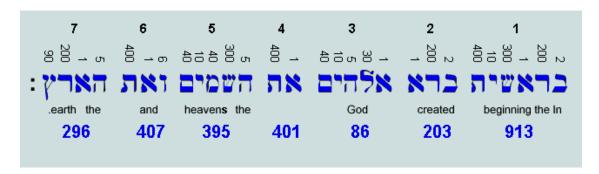
The practice that existed then was to record numbers on an *additive* basis, i.e. the value represented by a string of letters was simply the sum of the tabular values assigned to each. The *characteristic value* (CV) of a conventional Hebrew word, name, or phrase, is obtained in this manner. As an illustration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

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 –

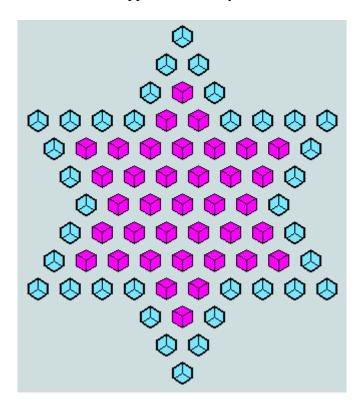


This verse consists of 7 Hebrew words. The sum of the number values for these **7** words add to **2701**. There are two factors of 2701; they are 37 and 73

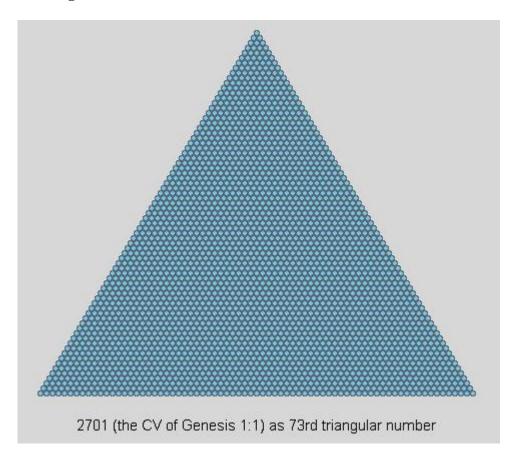
 $2701 = 37 \times 73$.

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



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.

$$913 \times 203 \times 86 \times 401 \times 395 \times 407 \times 296 = 304,153,525,784,175,760$$

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

$$304 + 153 + 525 + 784 + 175 + 760 = 37 \times 73$$

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

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

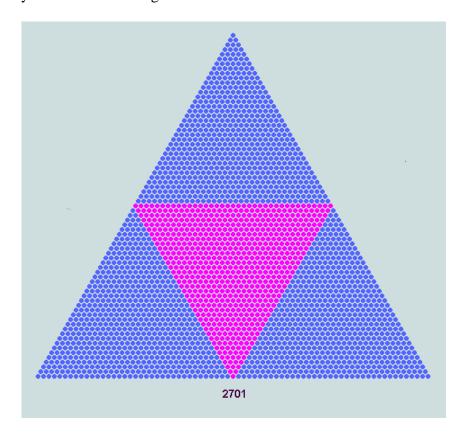
But are the individual words also multiples of 37?

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 –



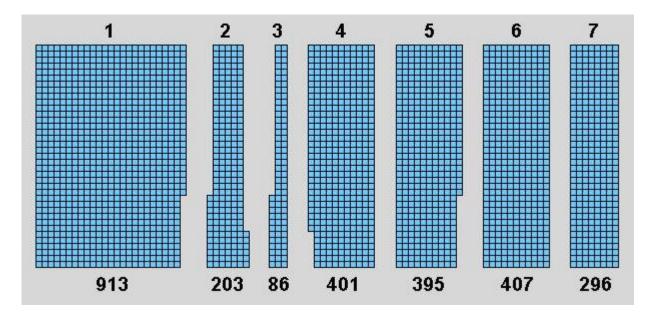
The 703 triangle is shown in pink. The three blue triangles surrounding it each have a value of 666, and the total triangle has a value of 2701.

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 $703 + 666 = 37 \times 37$

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:

$$1998 = 666 + 666 + 666$$

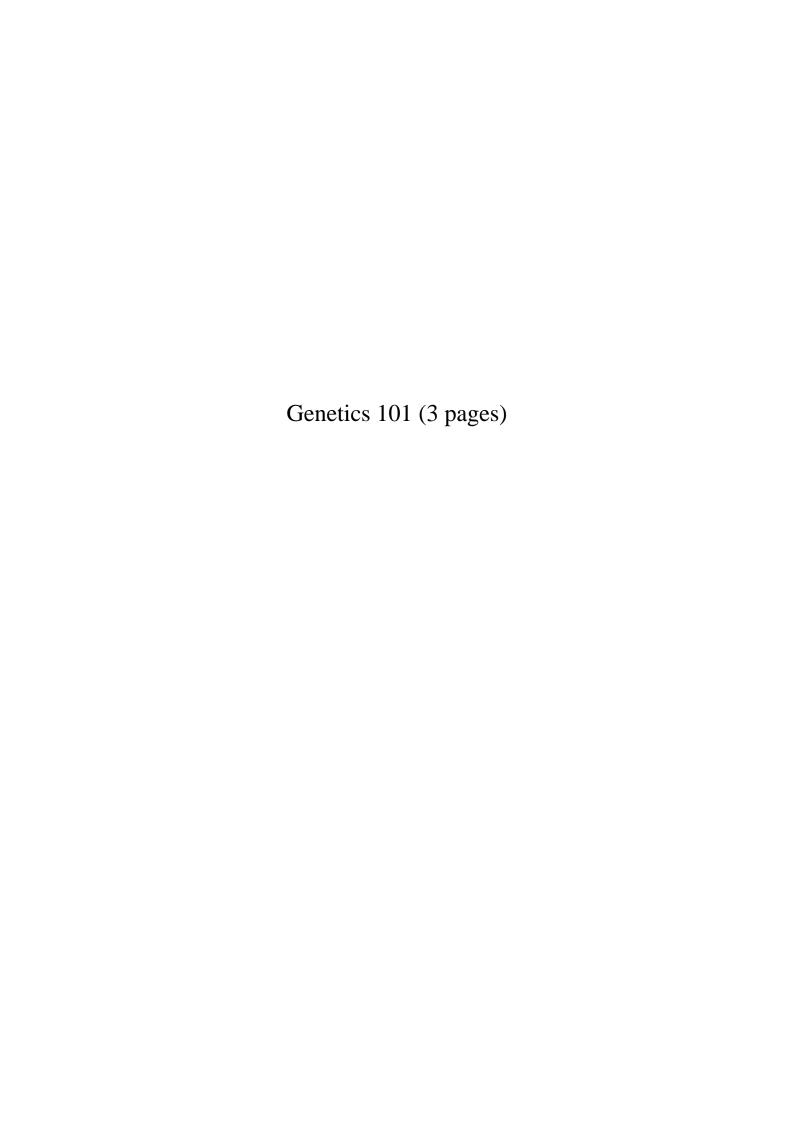
This numerical phenomena is called a cyclic permutation. The numbers always add to 666 + 666 + 666, no matter how they are read!

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?



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	cctccgagaggggagaccaggggccatgacaagctccaggctttggttttcgctgctggc
000065	ggcagcgttcgcaggacggcgacggccctctggccctggcctcagaacttccaaacctccgac
000129	cagogota cgt cottta coogaa caa ctt to a attocag tacgat g to a gotogoog cg cago
000193	coggetgete agteetega cgaggeette cagegetategtgacetgettt teggtteegggte
000257	ttggccccgtccttacctcacagggaaacggcatacactggagaagaatgtgttggttg
000321	gtagt cacacctgg atgta accag ctt cot a ctttgg ag t cag tgg ag a attatac cct g acca
000385	taaatgatgaccagtgtttactcctctctgagactgtctggggagctctccgaggtctggagac
000449	ttttagccagcttgtttggaaatctgctgagggcacattctttatcaacaagactgagattgag
000513	gactttccccgctttcctcaccggggcttgctgttggatacatctcgccattacctgccactct
000577	ctag cate ctgg a cactetg g at gte at gg e g tae a at a a at tg a a e g t g t te e a e t g g e at e t g e g e g e g e g e g e g e g e g
000641	ggtagatgatcottcottcocatatgagagottcacttttcoagagotcatgagaaaggggtco
000705	taca accet g teace cacate taca cag cacagg at g tga agg agg teat tga at acge acgg cacagg cacagg and the second cacagg at g tacagg and the second cacagg at g tacagg at g tacagg at g tacagg acg and the second cacagg at g tacagg at g ta
000769	tooggggtatccgtgtgcttgcagagtttgacactcctggccacactttgtcctggggaccagg
000833	tatecotggattactgactcottgctactctgggtctgagccctctggcacctttggaccagtg
000897	${\tt aat} cocagte tea {\tt aat} a {\tt aat} a cotat {\tt gag} tteat {\tt gag} cae {\tt at} tet tet ta {\tt gaa} {\tt gag} teaget et {\tt gt} tet {\tt gag} teaget {\tt gag} teag$
000961	to coagatt tt tatct to a tottg g agg ag at g agg tt g at tt cacct g ct g
001025	agagate coagga ctttat gagga agaa aggette ggtgagga ette aageagetggagte ette
001089	tacate cagac getgetgga categ tetet tettat ggea agggetat gtggtgtggeaggagg
001153	tgtttgataataaagtaaagattcagccagacacaatcatacaggtgtggcgagaggatattcc
001217	${\bf agtgaactatatgaaggagctggaactggtcaccaaggccggcttccgggcccttctctctgcc}$
001281	ccctgg tacctgaaccg tatatcct at ggccctgactggaaggatt tctacgtagtggaacccc
001345	tgg catttg aaggtacccctg ag cag aaggctctgg tgattgg tgg ag aggcttg tatgtgggg
001409	aga atat gtggaca acaca acctggtcccc aggctctggccc agagcaggggctgttgccga a
001473	${\bf aggetgtggagcaacaagttgacatctgacctgacatttgcctatgaacgtttgtcacacttcc}$
001537	gotgtgagttgotgaggcgaggtgtccaggcccaacccctcaatgtaggcttctgtgagcagga
001601	$\tt gtttgaacagacctgagccccaggcaccgaggagggtgctggctg$
001665	coagget to cact geat cot gg coaggg gaggac gag coeft t geot to gt geo cot t geot get
001729	gcccctgtgcttggagagaaaggggccggtgctggcgctcgcattcaataaagagtaatgtggc
001793	atttttctataataaacatggattacctgtgtttaaaaaaaa
001857	agggcacagccaggctggagtcagtgtctgcccctgaggtcttttaagttgagggctgggaatg
001921	${\tt aaacctatagcotttgtgctgttctgccttgcctgtgagctatgtcactcccctcccactcctg}$
001985	${\tt accatattccagacacctgccctaatcctcagcctgctcacttcacttctgcattatatctcca}$
002049	${\tt aggcgttggtatatggaaaaagatgtaggggcttggaggtgttctggacagtggggagggctcc}$
002113	agaccea acctgg teacaa agag cete teccee at geatacteat ceace teccete cectaga
002177	$gotattotoottt {\tt gggtttottgotgotgoa} {\tt attttatacaa} {\tt ccattatttaa} {\tt attattaa}$
002241	cacatattgttctct

These letters are the "software code".

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.

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

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.

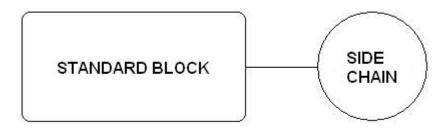
So atoms can be represented by numbers.

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	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	73
Block																				
Side	58	72	31	100	57	75	45	59	73	1	43	15	107	47	130	91	57	81	72	42
Chain																				

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 $74 = 2 \times 37$. 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.



PATTERN 1

					F	irst Base)				
		A		G		Т			С		
		AAT Asn AAC Asn AAA Lys AAG Lys		GAC	Glu S = 73 : B = 74			S = 107 : B = 74	CAT CAC CAA CAG	His His Gln Gln	S = 81 : B = 74 S = 72 : B = 74
Second Base	G	AGT Ser AGC Ser AGA Arg AGG Arg	S = 31 : B = 74 S = 100 : B = 74	GGT GGC GGA GGG	Gly	TGT TGC TGA TGG	Cys Stop	S = 47 : B = 74 S = 130 : B = 74	CGT CGC CGA CGG	Arg	S = 100 : B = 74
	т	ATT IIe ATC IIe ATA IIe ATG Met	S = 57 : B = 74 S = 75 : B = 74	GTC GTA	Val S = 43 : B = 74 Val Val Val	TTT TTC TTA TTG	Phe Phe Leu Leu	S = 91 : B = 74 S = 57 : B = 74	CTC	Leu	S = 57 : B = 74
		ACT Thr ACC Thr ACA Thr ACG Thr	S = 45 : B = 74	GCC GCA	Ala S = 15 : B = 74 Ala Ala Ala	TCT TCC TCA TCG	Ser Ser Ser Ser	S = 31 : B = 74	CCC	Pro Pro Pro	S = 42-1 : B = 73+1

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.

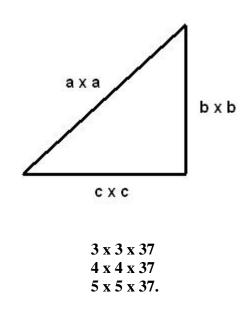
Taking the amino acids found in the yellow-shaded cells, **Shcherbak** counted the number of nucleons in the amino acids and found the following. Here are Shcherbak's calculations in full.

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

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

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



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

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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	=	30×37
•	number of nucleons in the side-chains comes to	1110	=	30×37
•	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 $30 \times 37 = 1110$ appears here; because 3×37 , like 7×37 , 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). $1110 = 30 \times 37$, 3×37 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 $259 = 7 \times 37$, 7×37 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.

					F	irst Bas	е				
		A		G		Т			С		
	Α	AAT Asn AAC Asn AAA Lys AAG Lys		GAC A	sp S = 59 : B = 74 sp lu S = 73 : B = 74 lu		Tyr Tyr Stop Stop	S = 107 : B = 74	CAC	His His Gln Gln	S = 81 : B = 74 S = 72 : B = 74
Second Base	G	AGT Ser AGC Ser AGA Arg AGG Arg		GGC G	ly S = 1 : B = 74 ly ly ly	TGC	Cys Cys Stop Trp	S = 47 : B = 74 S = 130 : B = 74	CGT CGC CGA CGG	Arg	S = 100 : B = 74
	т	ATT IIe ATC IIe ATA IIe ATG Met	S = 57 : B = 74 S = 75 : B = 74	GTT V GTC V GTA V GTG V	al al	TTT TTC TTA TTG	Phe Phe Leu Leu	S = 91 : B = 74 S = 57 : B = 74	CTC	Leu Leu Leu Leu	S = 57 : B = 74
	С	ACT Thr ACC Thr ACA Thr ACG Thr	S = 45 : B = 74	GCT A GCC A GCA AI GCG A	la a	TCT TCC TCA TCG	Ser Ser Ser Ser	S = 31 : B = 74		Pro Pro	S = 42-1 : B = 73+1

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 $= 814 = 22 \times 37$
- number of nucleons in the side-chain part of the amino acids $= 814 = 22 \times 37$
- 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

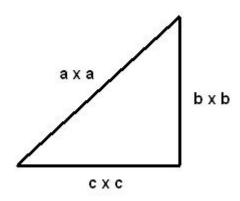
In the Pyrimidine group we have a perfect balance again between the standard block and the side-chain, both having a nucleon sum of 814, which is a multiple of 37. This is a similar pattern to the balance we found in Pattern 1, where the standard block and side chain both had a nucleon sum of 1110.



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 $259 = 7 \times 37$)

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



3 squared + 4 squared = 5 squared

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 $259 = 7 \times 37$) 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 $111 = 3 \times 37$.

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

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	Т	С
	Α		GAC Asp GAA Glu S = 73 · B = 74	TAT Tyr S = 107 : B = 74 TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA GIn S = 72 : B = 74 CAG GIn
Second Base	G	AGC Ser AGA Arg S = 100 : B = 74	GGC Gly GGA 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
	Т	ATC IIe ATA IIe	GTC 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
	С	ACC Thr ACA Thr	GCC 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
 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
 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	Т	С
	Α	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 GIn S = 72 : B = 74 CAG GIn
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
	Т	ATT IIe S = 57: B = 74 ATC IIe ATA IIe 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
	С	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

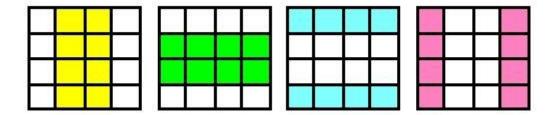
Here Shcherbak demonstrates more symmetry and balance within the genetic code - such that

the **GREEN** group + **YELLOW** group =
$$39 \times 37$$

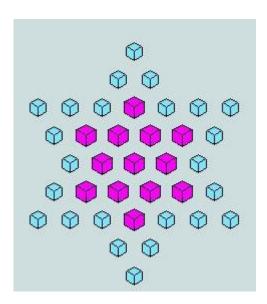
the **PINK** group + **BLUE** group =
$$39 \times 37$$

the **YELLOW** group + the **PINK** group =
$$39 \times 37$$

the **GREEN** group + the **BLUE** group =
$$39 \times 37$$



- 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 — 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

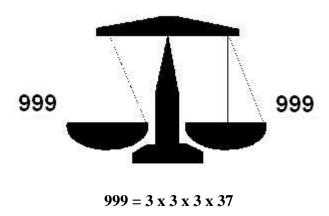
			Firs	t Base	
		A	G	Т	С
	Α	AAT Asn S = 58 : B = 74 AAC Asn AAA Lys S = 72 : B = 74 AAG Lys	GAT Asp S = 59: B = 74 GAC Asp GAA Glu S = 73: B = 74 GAG Glu	TAT Tyr TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA GIn S = 72 : B = 74 CAG GIn
Second Base	G	AGT Ser S = 31 : B = 74 AGC Ser AGA Arg 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
	Т	ATT IIe S = 57 : B = 74 ATC IIe ATA IIe 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
	С	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

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 $37 = 3 \times 3 \times 3 \times 37$



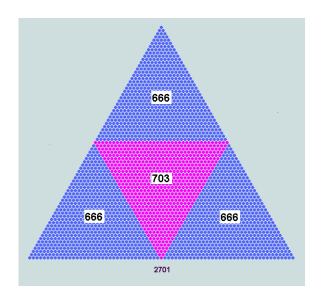
The total nucleon sum for the standard block part of amino acids =

$$1332 + 1258 = 70 \times 37$$

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

			Fir	st Base	
		A	G	Т	С
	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 TAC Tyr TAA Stop TAG Stop	CAT His S = 81 : B = 74 CAC His CAA GIn S = 72 : B = 74 CAG GIn
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
	Т	ATT IIe S = 57 : B = 74 ATC IIe ATA IIe 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
	С	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 - 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

	Amino Acids with three IDENTICAL BASES							
TTT	Phe S = 91 : B = 74		GGG	Gly S	= 1 : B = 74			
AAA	Lys $S = 72 : B = 74$		CCC	Pro S	= 42-1 : B = 73 + 1			
		Amino Acids	with three	UNIQUE	BASES			
TCA CAT ATC	Ser S = 31 : B = 74 His S = 81 : B = 74 Ile S = 57 : B = 74	Clockwise	C	TAC T	S = 45 : B = 74 Syr S = 107 : B = 74 eu S = 57 : B = 74	Anti-Clockwise		
GCT CTG TGC	Ala S = 15 : B = 74 Leu S = 57 : B = 74 Cys S = 47 : B = 74	Clockwise	C	GTC V	er S = 31 : B = 74 Val S = 43 : B = 74 arg S = 100 : B = 74	Anti-Clockwise		
TGA GAT ATG	Stop S = 0 : B = 0 Asp S = 59 : B = 0 Met S = 75 : B = 74	Clockwise	G	TAG S	er S = 31 : B = 74 top S = 0 : B = 0 Yal S = 43 : B = 74	Anti-Clockwise		
CAG AGC GCA	Gln S = 72 : B = 74 Ser S = 31 : B = 74 Ala S = 15 : B = 74	Clockwise	C G	CGA A	Asp S = 59 : B = 74 Arg S = 100 : B = 74 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				

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• **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°3, pp. 187-209 [23 page(s) (article)]

Appendix A

Structure of the Amino Acids

AMINO ACID	Abr	Chemical Formula	Number of Nucleons in Base	Number of Nucleons in Side-chain
Glycine	Gly	Ħ 0	СООН—СНNН2	Н
		н—с—с—о—н N—н	74	1
		H H		
Alanine	Ala	H H O	COOH—CH—NH2	CH3
		н—с—с—с—о—н	74	15
		H N—H		
Serine	Ser	н н ү	СООН—СН—NH2	СН2-ОН
		H-0-C-C-C-C-H	74	31
		H H		
Proline	Pro	H H O	COOH—CH—NH2	CH2—CH2—CH2
		н с с с он	73	42
		H C H H	A single hydrogen transfer to base from side-chain gives	A single hydrogen transfer to base from side-chain gives
		STATES ASSOCI	74	41
Valine	Val	H	СООН—СН—NH2	СН—СН3—СН3
		н—С—н н Н О	74	43
		Н—С—С—С—С—О—Н 		
		H		

Threonine	Thr	н н н о	COOH—CH—NH2	СН3СН—ОН
		Н—С—С—С—С—О—Н Н О И—Н	74	45
		н н		
Leucine	Leu	Ț	COOH—CH—NH2	СН2—СН—СН3—СН3
		H-C-H H H H O H-C-C-C-C-C-C-O-H H H H N-H	74	57
Arginine	Arg	н н н ю	COOH—CH—NH2	CH2—CH2—CH2—NH— CNH—NH2
		H—N—C—N—C—C—C—C—C—O—H	7.4	
			74	100
Cysteine	Cys	н н о	COOH—CH—NH2	CH2—SH
		H—S—C—C—C—O—H 	74	47
Isoleucine	Ile	并	COOH—CH—NH2	СН—СН3—СН2—СН3
		H H H C H C O H H C C O H H H H H H H H	74	57
Asparagine	Asn	н н о	СООН—СН—NH2	CH2—CO—NH2
		H—N—C—C—C—C—O—H	74	58

Aspartic	Asp	governor survivos pagamentos	COOH—CH—NH2	СН2—СО—ОН
Acid	Asp	H H O H H O H H O H H O H N H	74	59
		Ĥ		
Glutamine	Gln	H—N—C—C—H H—C—H H—C—H	COOH—CH—NH2 74	CH2—CH2—CO—NH2 72
Histidine	His	·n	COOH—CH—NH2	CH2—C3N2H4
Tilstidile		$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	74	81
Phenyl-	Phe	н н	COOH—CH—NH2	CH2 – C6H5
alanine			74	91
Tyrosine	Tyr	н н	COOH—CH—NH2	СН2—С6Н4—ОН
		H-0-C C C C C C C C C C H H H H H H H H H H	74	107
Methionine	Met	Н Н Н Н О Н—С—S—С—С—С—С—О—Н Н Н Н Н	COOH—CH—NH2 74	CH2—CH2S—CH3 75

Tryptophan	Trp	H	СООН—СН—NH2	CH2—C8H5—NH2
		H C H	74	130
		H H O H H O H H O H H O H H O H O H O H		
		拍		
Lysine	Lys	H H H H O	СООН—СН—NH2	CH2—CH2—CH2— CH2—NH2
		Н—N—С—С—С—С—С—С—О—Н 	74	72
		Ħ		
Glutamic Acid	Glu	н н н о	СООН—СН—NH2	СН2—СН2—СО—ОН
Acid		н—о—с—с—с—с—с—о—н	74	73
		Ö Й Й <mark>√—Н</mark> Н		

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