

Revelations of a Biological Abacus

1. Preamble

Over the past few years, a number of world-class scientists have reported the discovery of numerical patterns in the universal genetic code. Thus, from France (Boulay), Russia (Gusev and Petroukhov), Kazakhstan (shCherbak), Serbia (Rakocevic) and Algeria (Negadi) - none of whom can be assumed to espouse the Judeo-Christian cause - we hear of the reality of what must be widely regarded as *interesting news*. However, such news, when interpreted in the light of what has already been established in the pages of this site as hard fact, threatens to lead to some uninvited and serious consequences - not least, in man's understanding of who and what he is.

This page focuses attention exclusively on the work of **Vladimir shCherbak**, as documented in his paper *Arithmetic inside the universal genetic code**. However, before these significant findings can be offered to the eye of the general reader, it is necessary that certain relevant and generally accepted technicalities be briefly introduced and explained. Following this, all that remains is to allow the numbers to speak for themselves.

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2. Introduction

2.1 - The Amino Acids

Central to the chemical processes that occur to maintain the life of living organisms are the 20 *amino acids* (Table 1). They are the basic raw materials from which *proteins* are synthesised - these being substances that perform the essential structural and functional roles required in all living things. The amino acids, in turn, derive from the coded instructions contained in the organism's DNA (deoxyribonucleic acid) and RNA (ribonucleic acid). Each of these instructions (known as a *codon*) takes the form of an ordered string of 3 letters drawn from a *genetic alphabet* of just 4 characters, viz T, C, A and G (for DNA) and U, C, A and G (for RNA). Clearly, there exists only 64 unique arrangements of each of these (Table 2).

Amino Acid	
Name	Abb'n
Alanine	Ala
Arginine	Arg
Asparagine	Asn
Aspartic acid	Asp
Cysteine	Cys
Glutamic acid	Glu
Glutamine	Gln
Glycine	Gly
Histidine	His
Isoleucine	Ile
Leucine	Leu
Lysine	Lys
Methionine	Met
Phenylalanine	Phe
Proline	Pro
Serine	Ser
Threonine	Thr
Tryptophan	Trp
Tyrosine	Tyr
Valine	Val

Table 1

The 20 amino acids involved
in the metabolic processes of
all things living

DNA		SECOND BASE				THIRD BASE
		T	C	A	G	
FIRST BASE	T	TTT TTC TTA TTG	TCT TCC TCA TCG	TAT TAC TAA TAG	TGT TGC TGA TGG	T C A G
	C	CTT CTC CTA CTG	CCT CCC CCA CCG	CAT CAC CAA CAG	CGT CGC CGA CGG	T C A G
	A	ATT ATC ATA ATG	ACT ACC ACA ACG	AAT AAC AAA AAG	AGT AGC AGA AGG	T C A G
	G	GTT GTC GTA GTG	GCT GCC GCA GCG	GAT GAC GAA GAG	GGT GGC GGA GGG	T C A G

RNA		SECOND BASE				THIRD BASE
		U	C	A	G	
FIRST BASE	U	UUU UUC UUA UUG	UCU UCC UCA UCG	UAU UAC UAA UAG	UGU UGC UGA UGG	U C A G
	C	CUU CUC CUA CUG	CCU CCC CCA CCG	CAU CAC CAA CAG	CGU CGC CGA CGG	U C A G
	A	AUU AUC AUA AUG	ACU ACC ACA ACG	A AU AAC AAA AAG	AGU AGC AGA AGG	U C A G
	G	GUU GUC GUA GUG	GCU GCC GCA GCG	GAU GAC GAA GAG	GGU GGC GGA GGG	U C A G

Table 2

Organised presentations of
the 64 triple-base codons
of DNA and RNA

2.2 - Their Composition

The chemical elements involved in the structure of amino acids are tabulated below together with the numbers of protons and neutrons in their nuclei - the latter relating specifically to the most common isotope of each (Table 3). Of course, these elements, as they occur naturally, will be *mixtures* of isotopes, and it is important that we realise what the term 'common isotope' implies in this context (Table 4).

Element		Nucleons		
Name	Symbol	Protons	Neutrons	Total
Hydrogen	H	1	0	1
Carbon	C	6	6	12
Nitrogen	N	7	7	14
Oxygen	O	8	8	16
Sulphur	S	16	16	32

Table 3

The elements of amino acids with their idealised atomic masses

Element	Approx Atomic Mass of most common isotope	Atomic Mass natural isotope mixture
H	1	1.008
C	12	12.011
N	14	14.007
O	16	15.999
S	32	32.066

Table 4

The elements as they are found to occur naturally

Clearly, the whole-number totals of nucleons recorded in Table 3 appear well-justified and, based upon these figures, the masses of the amino acid molecules may now be computed. However, before proceeding to do that, it is necessary that we consider an important structural feature of amino acids.

2.3 - Standard Block and Side Chain

It transpires that **19** of the amino acids comply with the generic formula:



Here, the lower component represents the so-called *standard block* - designated **B**. The variety in amino acid characteristics derives entirely from **R** - the unique *side chain*. The one exception to this general rule is *Proline* which has one less hydrogen bonded to the nitrogen of its standard block. Thus, applying the data of Table 3 to the elements of the standard block, we deduce the molecular masses to be

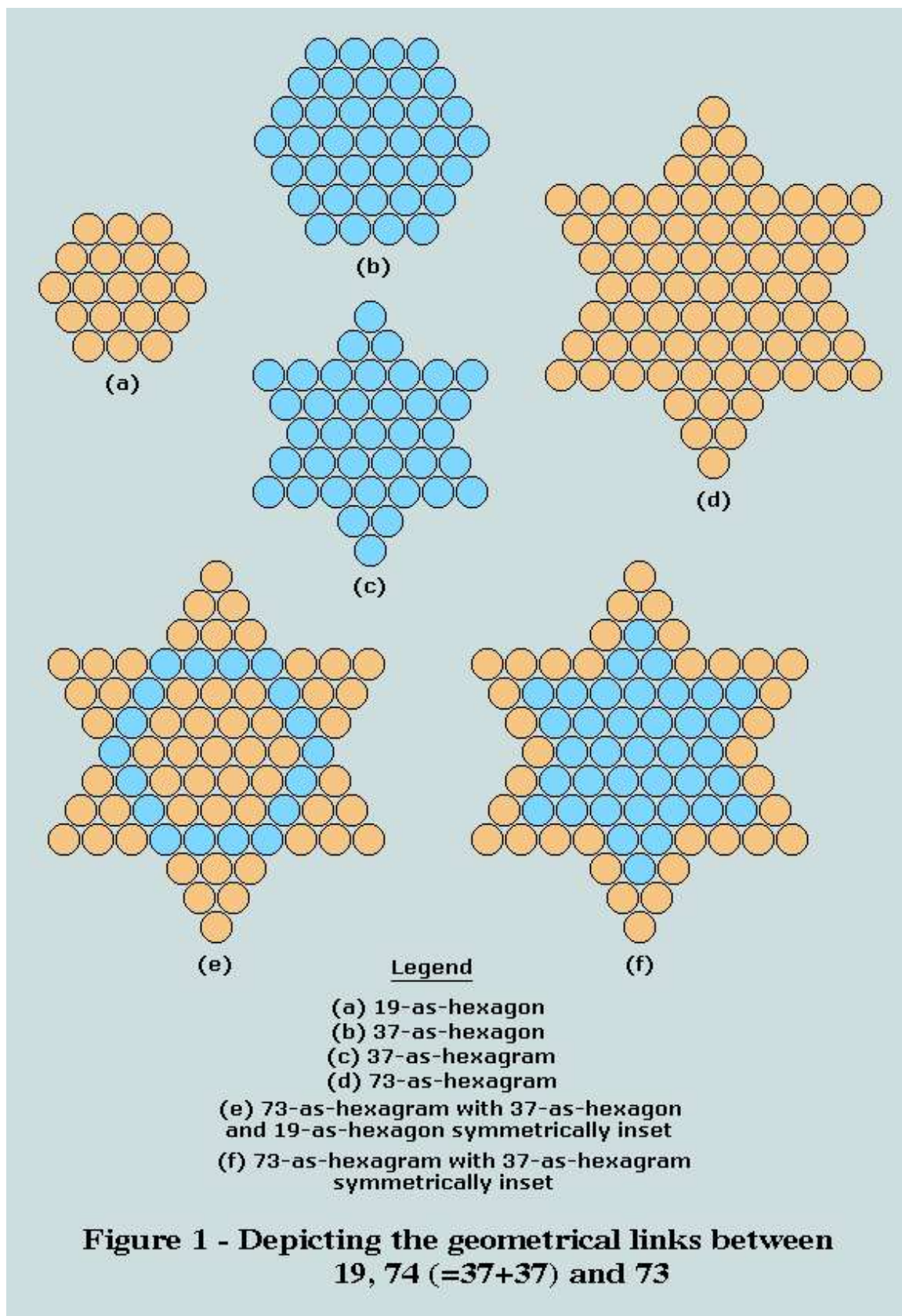
$2 + 14 + 12 + 1 + 12 + 32 + 1 = 74$ (for all amino acids excluding Proline), and **73** for Proline.

2.4 - The Portent

Let us immediately observe that these are interesting figures - and for the following reasons:

2.4.1 - The juxtaposition of 19, 74 ($=2 \times 37$) and 73 will already be familiar to those acquainted with the pages of this site. Genesis 1:1 - as originally delivered in Hebrew - has the numerical value 2701, or 37×73 ; and the sum of its two final words, translated "and the earth", has the value 703, or 19×37 . Further, both 2701 and 703 are *coordinated* triangular numbers. [Further details [here](#)]

2.4.2 - But the factors themselves are also related figurate numbers (Figure 1).



2.4.3 - 74 and 73 are each the penultimate term of a *decimal* sequence specified by the rule: $S(r)$ - the r th term - is formed as the sum of the cubes of the digits of $S(r-1)$ - the term immediately preceding. The ultimate term in respect of 74 is 407 (value of the 6th word of the Bible's first verse); and of 73, 370 (a cyclic rotation of 703 - the sum of words 6 and 7).^{*} It should not pass unnoticed that 74, 407 and 370 are multiples of the unique *trifigurate* number 37; and that 73 is its decimal digit reflection. One further observation: the sum of 407 and 370 is 777, or $3 \times 7 \times 37$.

* There are just 4 natural numbers, base 10, that equal the sum of the cubes of their respective digits. Along with 407 and 370, we have 371 (duration, in days, of the Noahic Flood) and 153 (the miraculous catch of fishes described in John 21:11). Remarkably, the last is the terminal value of any sequence (as described) that begins with a multiple of 3.

Since shCherbak's findings take us further along this route in which the prime number 37 dominates - *but only when Proline is harmonised with the other 19 amino acids by transferring one hydrogen from R to B* - in the circumstances, we believe this adjustment to be fully justified.

2.5 - The Molecular Masses - We are now in a position to evaluate the molecular masses (or nucleon counts) of the 20 amino acids. Here are the details:

Amino Acid		Empirical Composition					Nucleons		
		C	H	N	O	S	Protons	Neutrons	Total
Alanine	[Ala]	3	7	1	2	0	48	41	89
Arginine	[Arg]	6	14	4	2	0	94	80	174
Asparagine	[Asn]	4	8	2	3	0	70	62	132
Aspartic acid	[Asp]	4	7	1	4	0	70	63	133
Cysteine	[Cys]	3	7	1	2	1	64	57	121
Glutamic acid	[Glu]	5	9	1	4	0	78	69	147
Glutamine	[Gln]	5	10	2	3	0	78	68	146
Glycine	[Gly]	2	5	1	2	0	40	35	75
Histidine	[His]	6	9	3	2	0	82	73	155
Isoleucine	[Ile]	6	13	1	2	0	72	59	131
Leucine	[Leu]	6	13	1	2	0	72	59	131
Lysine	[Lys]	6	14	2	2	0	80	66	146
Methionine	[Met]	5	11	1	2	1	80	69	149
Phenylalanine	[Phe]	9	11	1	2	0	88	77	165
Proline	[Pro]	5	9	1	2	0	62	53	115
Serine	[Ser]	3	7	1	3	0	56	49	105
Threonine	[Thr]	4	9	1	3	0	64	55	119
Tryptophan	[Trp]	11	12	2	2	0	108	96	204
Tyrosine	[Tyr]	9	11	1	3	0	96	85	181
Valine	[Val]	5	11	1	2	0	64	53	117

Table 5

The empirical compositions and nucleon counts of the amino acids

The separation of the B and R nucleons completes the picture, thus:

Amino Acid	Gly	Ala	Ser	Pro	Val	Thr	Cys	Leu	Ile	Asn
St'd Block (B)	74	74	74	73+1 =74	74	74	74	74	74	74
Side Chain (R)	1	15	31	42-1 =41	43	45	47	57	57	58
Total Nucleons	75	89	105	115	117	119	121	131	131	132

Amino Acid	Asp	Gln	Lys	Glu	Met	His	Phe	Arg	Tyr	Trp
St'd Block (B)	74	74	74	74	74	74	74	74	74	74
Side Chain (R)	59	72	72	73	75	81	91	100	107	130
Total Nucleons	133	146	146	147	149	155	165	174	181	204

Table 6

The nucleons allocated to standard block (B)
and side chain (R)

3. The Genetic Code

The genetic code can be expressed in terms of either DNA codons or RNA codons. Here are the details, as they may be found in any standard textbook on the subject:

DNA										RNA									
					SECOND BASE														

Table 7

The Universal Genetic Code

Observe that the only difference between these tables is that the thymidine (T) of DNA is replaced by the uridine (U) of RNA. Both incorporate 'Stop' instructions (which contribute nothing to the nucleon count); 'Start' is represented by the codons ATG and AUG, respectively, and is associated with the production of the amino acid

Methionine. Our chief interest in these matters concerns the amino acids and their related codons. Consequently, the order in which the (codon)-(amino acid) relationships are presented may vary, at the discretion of those who work in this area. For reasons which will become obvious, shCherbak has chosen to use an RNA arrangement of his own.

4. shCherbak's Patterns

4.1 - The First Pattern - Here we see the 16 x 4-codon cells divided into two identical interlocking areas based on the observation that 8 (coloured orange) contain codons, all of which code for same amino acid, and the remainder (coloured blue) that do not.

The respective counts of nucleons for orange and blue areas are summarised below.

		FIRST BASE			
		A	G	U	C
SECOND BASE	A	AAU Asn AAC Asn AAA Lys AAG Lys	GAU Asp GAC Asp GAA Glu GAG Glu	UAU Tyr UAC Tyr UAA Stop UAG Stop	CAU His CAC His CAA Gln CAG Gln
	G	AGU Ser AGC Ser AGA Arg AGG Arg	GGU Gly GGC Gly GGA Gly GGG Gly	UGU Cys UGC Cys UGA Stop UGG Trp	CGU Arg CGC Arg CGA Arg CGG Arg
	U	AUU Ile AUC Ile AUA Ile AUG Met	GUU Val GUC Val GUA Val GUG Val	UUU Phe UUC Phe UUA Leu UUG Leu	CUU Leu CUC Leu CUA Leu CUG Leu
	C	ACU Thr ACC Thr ACA Thr ACG Thr	GCU Ala GCC Ala GCA Ala GCG Ala	UCU Ser UCC Ser UCA Ser UCG Ser	CCU Pro CCC Pro CCA Pro CCG Pro

shCherbak's First Pattern

(a)

Codon	Amino Acid	R	B	Total Nucleons
GG(U,C,A,G)	Gly	1	74	75
CG(U,C,A,G)	Arg	100	74	174
GU(U,C,A,G)	Val	43	74	117
CU(U,C,A,G)	Leu	57	74	131
AC(U,C,A,G)	Thr	45	74	119
GC(U,C,A,G)	Ala	15	74	89
UC(U,C,A,G)	Ser	31	74	105
CC(U,C,A,G)	Pro	41	74	115
Nucleon Sums:		333	592	925

Tables S1

(b)

Codon	Amino Acid	R	B	Total Nucleons
AA(U,C)	Asn	58	74	132
AA(A,G)	Lys	72	74	146
GA(U,C)	Asp	59	74	133
GA(A,G)	Glu	73	74	147
UA(U,C)	Tyr	107	74	181
UA(A,G)	Stop	0	0	0
CA(U,C)	His	81	74	155
CA(A,G)	Gln	72	74	146
AG(U,C)	Ser	31	74	105
AG(A,G)	Arg	100	74	174
UG(U,C)	Cys	47	74	121
UG(A)	Stop	0	0	0
UG(G)	Trp	130	74	204
AU(U,C,A)	Ile	57	74	131
AU(G)	Met	75	74	149
UU(U,C)	Phe	91	74	165
UU(A,G)	Leu	57	74	131
Nucleon sums:		1110	1110	2220

Observe that (a) yields the {R,B,(R+B)} sequence {333,592,925}, or {9x37,16x37,25x37} in which the multipliers of 37 are the squares associated with the classical pythagorean example. Of course, if all 4 codons producing the same amino acid are taken into account, these figures are quadrupled to produce {1332,2368,3700}. Remarkably, these same figures are found together on the breastplate of the high priest (the details may be found [here](#)).

With respect to (b): we observe an even division of the total of nucleons between R and B. It is remarkable that there should be this exact balance between the contributions from standard blocks and side-chains, and that the balance should again be a multiple of 37.

4.2 - The Second Pattern - It has been established that the 64 RNA codons (the 3-letter codes) divide into 2 groups - those that begin with A or G, and those that begin with C or U. These groups are referred to as *the Purines* (coloured blue in the following table) and *the Pyrimidines* (coloured orange), respectively.

		FIRST BASE			
		A	G	U	C
SECOND BASE	A	AAU Asn AAC Asn AAA Lys AAG Lys	GAU Asp GAC Asp GAA Glu GAG Glu	UAU Tyr UAC Tyr UAA Stop UAG Stop	CAU His CAC His CAA Gln CAG Gln
		AGU Ser AGC Ser AGA Arg AGG Arg	GGU Gly GGC Gly GGA Gly GGG Gly	UGU Cys UGC Cys UGA Stop UGG Trp	CGU Arg CGC Arg CGA Arg CGG Arg
	U	AUU Ile AUC Ile AUA Ile AUG Met	GUU Val GUC Val GUA Val GUG Val	UUU Phe UUC Phe UUA Leu UUG Leu	CUU Leu CUC Leu CUA Leu CUG Leu
		ACU Thr ACC Thr ACA Thr ACG Thr	GCU Ala GCC Ala GCA Ala GCG Ala	UCU Ser UCC Ser UCA Ser UCG Ser	CCU Pro CCC Pro CCA Pro CCG Pro

shCherbak's Second Pattern

The Purines

Codon	Amino Acid	R	B	Total Nucleons
AA(U,C)	Asn	58	74	132
AA(A,G)	Lys	72	74	146
GA(U,C)	Asp	59	74	133
GA(A,G)	Glu	73	74	147
AG(U,C)	Ser	31	74	105
AG(A,G)	Arg	100	74	174
GG(U,C,A,G)	Gly	1	74	75
AU(U,C,A)	Ile	57	74	131
AU(G)	Met	75	74	149
GU(U,C,A,G)	Val	43	74	117
AC(U,C,A,G)	Thr	45	74	119
GC(U,C,A,G)	Ala	15	74	89
Nucleon Sums :		629	888	1517

The Pyrimidines

Codon	Amino Acid	R	B	Total Nucleons
UA(U,C)	Tyr	107	74	181
UA(A,G)	Stop	0	0	0
CA(U,C)	His	81	74	155
CA(A,G)	Gln	72	74	146
UG(U,C)	Cys	47	74	121
UG(A)	Stop	0	0	0
UG(G)	Trp	130	74	204
CG(U,C,A,G)	Arg	100	74	174
UU(U,C)	Phe	91	74	165
UU(A,G)	Leu	57	74	131
CU(U,C,A,G)	Leu	57	74	131
UC(U,C,A,G)	Ser	31	74	105
CC(U,C,A,G)	Pro	41	74	115
Nucleon Sums:		814	814	1628

Tables S2

Observe that for the pyrimidines we again have a perfect balance between R and B. Both groups yield further multiples of 37.

4.3 - The Third Pattern - Here we examine two symmetrical divisions of the genetic code. The first, involving the amalgamation of the two central columns; the second, the amalgamation of the two

central rows.

Division 1

		FIRST BASE			
		A	G	U	C
SECOND BASE	A	AAU Asn AAC Asn AAA Lys AAG Lys	GAU Asp GAC Asp GAA Glu GAG Glu	UAU Tyr UAC Tyr UAA Stop UAG Stop	CAU His CAC His CAA Gln CAG Gln
	G	AGU Ser AGC Ser AGA Arg AGG Arg	GGU Gly GGC Gly GGA Gly GGG Gly	UGU Cys UGC Cys UGA Stop UGG Trp	CGU Arg CGC Arg CGA Arg CGG Arg
	U	AUU Ile AUC Ile AUA Ile AUG Met	GUU Val GUC Val GUA Val GUG Val	UUU Phe UUC Phe UUA Leu UUG Leu	CUU Leu CUC Leu CUA Leu CUG Leu
	C	ACU Thr ACC Thr ACA Thr ACG Thr	GCU Ala GCC Ala GCA Ala GCG Ala	UCU Ser UCC Ser UCA Ser UCG Ser	CCU Pro CCC Pro CCA Pro CCG Pro

shCherbak's Third Pattern (1)

Codon	Amino Acid	R	B	Total Nucleons
AA(U,C)	Asn	58	74	132
AA(A,G)	Lys	72	74	146
CA(U,C)	His	81	74	155
CA(A,G)	Gln	72	74	146
AG(U,C)	Ser	31	74	105
AG(A,G)	Arg	100	74	174
CG(U,C,A,G)	Arg	100	74	174
AU(U,C,A)	Ile	57	74	131
AU(G)	Met	75	74	149
CU(U,C,A,G)	Leu	57	74	131
AC(U,C,A,G)	Thr	45	74	119
CC(U,C,A,G)	Pro	41	74	115
Nucleon Sums: 789 888 1677				

Codon	Amino Acid	R	B	Total Nucleons
GA(U,C)	Asp	59	74	133
GA(A,G)	Glu	73	74	147
UA(U,C)	Tyr	107	74	181
UA(A,G)	Stop	0	0	0
GG(U,C,A,G)	Gly	1	74	75
UG(U,C)	Cys	47	74	121
UG(A)	Stop	0	0	0
UG(G)	Trp	130	74	204
GU(U,C,A,G)	Val	43	74	117
UU(U,C)	Phe	91	74	165
UU(A,G)	Leu	57	74	131
GC(U,C,A,G)	Ala	15	74	89
UC(U,C,A,G)	Ser	31	74	105
Nucleon Sums: 654 814 1468				

Tables S3(1)

Observe that for the blue group, the total number of nucleons in the radical (R) component of the amino acids is 789; and for the orange group, 654. The total represented in this category is therefore 1443, or 39×37 .

Division 2

		FIRST BASE			
		A	G	U	C
SECOND BASE	A	AAU Asn AAC Asn AAA Lys AAG Lys	GAU Asp GAC Asp GAA Glu GAG Glu	UAU Tyr UAC Tyr UAA Stop UAG Stop	CAU His CAC His CAA Gln CAG Gln
	G	AGU Ser AGC Ser AGA Arg AGG Arg	GGU Gly GGC Gly GGA Gly GGG Gly	UGU Cys UGC Cys UGA Stop UGG Trp	CGU Arg CGC Arg CGA Arg CGG Arg
	U	AUU Ile AUC Ile AUA Ile AUG Met	GUU Val GUC Val GUA Val GUG Val	UUU Phe UUC Phe UUA Leu UUG Leu	CUU Leu CUC Leu CUA Leu CUG Leu
	C	ACU Thr ACC Thr ACA Thr ACG Thr	GCU Ala GCC Ala GCA Ala GCG Ala	UCU Ser UCC Ser UCA Ser UCG Ser	CCU Pro CCC Pro CCA Pro CCG Pro

shCherbak's Third Pattern (2)

Codon	Amino Acid	R	B	Total Nucleons
AA(U,C)	Asn	58	74	132
AA(A,G)	Lys	72	74	146
GA(U,C)	Asp	59	74	133
GA(A,G)	Glu	73	74	147
UA(U,C)	Tyr	107	74	181
UA(A,G)	Stop	0	0	0
CA(U,C)	His	81	74	155
CA(A,G)	Gln	72	74	146
AC(U,C,A,G)	Thr	45	74	119
GC(U,C,A,G)	Ala	15	74	89
UC(U,C,A,G)	Ser	31	74	105
CC(U,C,A,G)	Pro	41	74	115
Nucleon Sums: 654 814 1468				

Codon	Amino Acid	R	B	Total Nucleons
AG(U,C)	Ser	31	74	105
AG(A,G)	Arg	100	74	174
GG(U,C,A,G)	Gly	1	74	75
UG(U,C)	Cys	47	74	121
UG(A)	Stop	0	0	0
UG(G)	Trp	130	74	204
CG(U,C,A,G)	Arg	100	74	174
AU(U,C,A)	Ile	57	74	131
AU(G)	Met	75	74	149
GU(U,C,A,G)	Val	43	74	117
UU(U,C)	Phe	91	74	165
UU(A,G)	Leu	57	74	131
CU(U,C,A,G)	Leu	57	74	131
Nucleon Sums: 789 888 1677				

Tables S3(2)

Here, we see the results of the earlier analysis duplicated. Once more a perfect symmetry is displayed - again involving multiples of 37.

4.4 - The Fourth Pattern - Here we identify and colour code those codons whose triplets include two identical letters. Thus, those codons highlighted in blue each incorporate a pair of Us; those in yellow, a pair of Gs... and so on.

		FIRST BASE			
		A	G	U	C
SECOND BASE	A	AAU Asn AAC Asn AAA Lys AAG Lys	GAU Asp GAC Asp GAA Glu GAG Glu	UAU Tyr UAC Tyr UAA Stop UAG Stop	CAU His CAC His CAA Gln CAG Gln
	G	AGU Ser AGC Ser AGA Arg AGG Arg	GGU Gly GGC Gly GGA Gly GGG Gly	UGU Cys UGC Cys UGA Stop UGG Trp	CGU Arg CGC Arg CGA Arg CGG Arg
	U	AUU Ile AUC Ile AUA Ile AUG Met	GUU Val GUC Val GUA Val GUG Val	UUU Phe UUC Phe UUA Leu UUG Leu	CUU Leu CUC Leu CUA Leu CUG Leu
	C	ACU Thr ACC Thr ACA Thr ACG Thr	GCU Ala GCC Ala GCA Ala GCG Ala	UCU Ser UCC Ser UCA Ser UCG Ser	CCU Pro CCC Pro CCA Pro CCG Pro

shCherbak's Fourth Pattern

Codon	Amino Acid	R	B	Total Nucleons
AAU	Asn	58	74	132
AAC	Asn	58	74	132
AAG	Lys	72	74	146
GAA	Glu	73	74	147
UAA	Stop	0	0	0
CAA	Gln	72	74	146
AGA	Arg	100	74	174
AUA	Ile	57	74	131
ACA	Thr	45	74	119
Nucleon Sums: 535 592				

Codon	Amino Acid	R	B	Total Nucleons
GAG	Glu	73	74	147
AGG	Arg	100	74	174
GGU	Gly	1	74	75
GGC	Gly	1	74	75
GGA	Glv	1	74	75
UGG	Trp	130	74	204
CGG	Arg	100	74	174
GUG	Val	43	74	117
GCG	Ala	15	74	89
Nucleon Sums: 464 666				

Codon	Amino Acid	R	B	Total Nucleons
UAU	Tyr	107	74	181
UGU	Cys	47	74	121
AUU	Ile	57	74	131
GUU	Val	43	74	117
UUC	Phe	91	74	165
UUA	Leu	57	74	131
UUG	Leu	57	74	131
CUU	Leu	57	74	131
UCU	Ser	31	74	105
Nucleon Sums: 547 666				

Codon	Amino Acid	R	B	Total Nucleons
CAC	His	81	74	155
CGC	Arg	100	74	174
CUC	Leu	57	74	131
ACC	Thr	45	74	119
GCC	Ala	15	74	89
UCC	Ser	31	74	105
CCU	Pro	41	74	115
CCA	Pro	41	74	115
CCG	Pro	41	74	115
Nucleon Sums: 452 666				

Tables S4

Observe the following:

- total nucleons in the R-component of paired A codons = 535
- G codons = 464
- these amino acids = 999

- total nucleons in the B-component of paired A codons = 592
- G codons = 666
- these amino acids = 1258

- total nucleons in the R-component of paired A codons = 547
- G codons = 452
- these amino acids = 999

- total nucleons in the B-component of paired A codons = 666
- G codons = 666
- these amino acids = 1332

The repunits 666 and 999 are a significant feature; again, each a multiple of 37 and directly involved in the Genesis 1:1 geometries.

4.5 - The Fifth Pattern - Switching here from an RNA to a DNA context, shCherbak focuses attention, (i) on the amino acids that arise from codons with 3 identical bases, viz TTT, AAA, GGG and CCC - appropriately, pairing T with A and G with C; and again, (ii) on all those that arise from codons with 3 unique bases. Here are the details:

Triplets of Identical Bases			
TTT Phe	R = 91 ; B = 74	GGG Gly	R = 1 ; B = 74
AAA Lys	R = 72 ; B = 74	CCC Pro	R = 41 ; B = 74

Clockwise Codons	Triplets of Unique Bases	AntiClockwise Codons
TCA Ser R = 31; B = 74 CAT His R = 81; B = 74 ATC Ile R = 57; B = 74	T A C	CTA Leu R = 57; B = 74 TAC Tyr R = 107; B = 74 ACT Thr R = 45; B = 74
GCT Ala R = 15; B = 74 CTG Leu R = 57; B = 74 TGC Cys R = 47; B = 74	G T C	CGT Arg R = 100; B = 74 GTC Val R = 43; B = 74 TCG Ser R = 31; B = 74
TGA Stop R = 0 ; B = 0 GAT Asp R = 59; B = 74 ATG Met R = 75; B = 74	T A G	GTA Val R = 43; B = 74 TAG Stop R = 0 ; B = 0 AGT Ser R = 31; B = 74
CAG Gln R = 72; B = 74 AGC Ser R = 31; B = 74 GCA Ala R = 15; B = 74	C G A	ACG Thr R = 45; B = 74 CGA Arg R = 100; B = 74 GAC Asp R = 59; B = 74

shCherbak's Fifth Pattern

Nucleon Totals			
R	B	R	B
703	962	703	962

Tables S5

Again, a perfect balance is observed, together with significant multiples of 37.

5. Conclusions

A reading of the Abstract to Vladimir shCherbak's paper *Arithmetic inside the universal genetic code* (it may be found [here](#)) reveals that he believes these numerical patterns - based on what he refers to as '**the criterion of divisibility by 037**' - created themselves - along with '**a primordial version of the genetic code and genetic texts**'. Further, he detects a 'base 10' number system underpinning all this; and even suggests that '**possibly a zero was invented and used by this mechanism**'.

Such highly imaginative thinking is quickly brought to earth when it is realised that there are more points of contact between the genetic code, the Hebrew of the Bible's first verse, the breastplate of the High Priest (Ex.28:15-21) and the Name and Title of our Creator - the Lord Jesus Christ - than can fairly be accounted for by chance.

The facts presented on this site, when combined with those now revealed to us by shCherbak, constitute invincible evidence of the truth of the Judeo-Christian Scriptures, and of the Being and Sovereignty of their Divine Author.

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<http://www.freewebs.com/genetics37>

www.otherbiblecode.com