ON THE COMPLETENESS OF GENETIC CODE: PART VII

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Abstract. In this seventh part of the work on the completeness of the genetic code, we present further relationships of different variants of Genetic Code Table and modified Rumer Table of nucleotide doublets within genetic code.

In previous six parts of this work[1] we have listed more examples of splittings and distinctions within genetic code, from which is obvious an analogy with the filling of orbitals in an atom: the classifications of AAs and codons within nucleotides triplet table (TT)[2] as well as nucleotides doublet table (DT)[3] are accompanied by increasing / decreasing (for one, two or more) of the specific quantities of number of atoms, or nucleons; all this in a strict relation to a specific and unique arithmetical system, consisting of the multiples of numbers 6-66-666 and their halves 3-33-333.[4]

In the first part of this paper we presented (Figure I/1) the multiples of the middle member of the lower sequence (number 33) in position of modular zero (in modulo 9) and its neighbors: (8 x 33 = 284), **(9 x 33 = 297)**, (10 x 33 = 330)[5] and showed that the number of atoms in the GC constituents in key distinctions (Py / Pu; 2 or 3 hydrogen bonds) corresponds with these numbering patterns. In this seventh part of the work on the completness of GC we will give some new examples. [For now we can not know why 6-66-666 sequence appears as a determinant of GC. A possible reason is the fact that the number 6 is the first perfect number, and we have already proved that perfect and friendly numbers are really determinants of GC (see: Figures 1.1 and 1.2 here, and: MMR, Genetic code as a unique system, p. 60, on my web site).]

In all presented cases, we follow the completeness of the genetic code, expressed through the unity and balance of physical and chemical properties of molecules (from one side) and arithmetical regularities, manifested in the number of atoms and nucleons (from the other side). By this we find, in the GCT, three sets of amino acids: 20 AAs (Table 1.1), 23 AAs (Table 2.1) and 61 AAs (Table 3.1).

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[1] The "Part I" as: "On the completeness of genetic code: some new examples" (viXra:1412.0274); "Part II" as: "On the completeness of genetic code: Part II" (viXra:1501.0117) etc., until the sixth part as: "On the completeness of genetic code: Part VI" (viXra:1502.0041).

[2] The nucleotides triplet table (TT) as Standard Genetic Code Table (GCT), valid for the so-called "Standard Genetic Code".

[3] The nucleotides doublet table (DT) as "Modified Rumer's Table", presented in Part II of this work as Table 2 (in other words: Table II/2).

[4] The ratio of the whole and its half boils down to the fact of "the symmetry in the simplest case" (Marcus, 1989).

[5] In modular formulation: ±0 and ±1.

1st lett.	2nd letter: U		C		A		G		3rd lett.
	U		C		A		G		
U	**00.** UUU		**08.** UCU		**32.** UAU		**40.** UGU	**C**	*U*
	01. UUC	**F**	**09.** UCC		**33.** UAC	**Y**	**41.** UGC		*C*
	02. UUA		**10.** UCA	**S**	**34.** UAA		**42.** UGA	CT	*A*
	03. UUG	**L**	**11.** UCG		**35.** UAG	CT	**43.** UGG	**W**	*G*
C	**04.** CUU		**12.** CCU		**36.** CAU		**44.** CGU		*U*
	05. CUC		**13.** CCC		**37.** CAC	**H**	**45.** CGC		*C*
	06. CUA	**L**	**14.** CCA	**P**	**38.** CAA		**46.** CGA	**R**	*A*
	07. CUG		**15.** CCG		**39.** CAG	**Q**	**47.** CGG		*G*
A	**16.** AUU	**I**	**24.** ACU		**48.** AAU		**56.** AGU		*U*
	17. AUC		**25.** ACC	**T**	**49.** AAC	**N**	**57.** AGC	**S**	*C*
	18. AUA		**26.** ACA		**50.** AAA		**58.** AGA		*A*
	19. AUG	**M**	**27.** ACG		**51.** AAG	**K**	**59.** AGG	**R**	*G*
G	**20.** GUU		**28.** GCU		**52.** GAU		**60.** GGU		*U*
	21. GUC		**29.** GCC		**53.** GAC	**D**	**61.** GGC		*C*
	22. GUA	**V**	**30.** GCA	**A**	**54.** GAA		**62.** GGA	**G**	*A*
	23. GUG		**31.** GCG		**55.** GAG	**E**	**63.** GGG		*G*

Figure 1.1. The GCT corresponds with 6-bit binary-code tree (Rakočević, 1998, Biosystems, 46, pp. 283-291). In such a case, the key distinctions (Py/Pu) are determined with the first four perfect numbers. So, the first distinction is with the natural numbers 0-3 whose sum is 6 (first perfect number); the second one 0-7 with the sum 28 (second perfect number); and the third distinction with the sequence 0-31 which numbers give the sum of 496 (third perfect number); finally, the cycling sequence 0-63-0 (from the beginning to the end and vice versa) gives a sum of 8128 (fourth perfect number).

/00 - 07/	08 - 15/	16 - 23/	24 - 31//	32 - 39/	40 - 47/	48 - 55/	56 - 63/
28	92	156	220	284	348	412	476
64	64	64	64	64	64	64	

/00 - 07/	00 - 15/	00 - 23/	00 - 31//	00 - 39/	00 - 47/	00 - 55/	00 - 63/
28	120	276	496	780	1128	1540	2016
92	156	220	284	348	412	476	

Table 3. The eight octets within 6-bit binary-code tree (Rakočević, 1998) as well as within GCT are determined with the first pair of friendly numbers (220 & 284) and third perfect number (496). For details see the text, especially Remarks 1 & 2.

Figure 1.2. The eight octets within 6-bit binary-code tree (Rakočević, 1998) as well as within GCT have determined with the first pair of friendly numbers (220 & 284) and third perfect number (496). (After **arXiv:q-bio/0703011v2 [q-bio.OT]**)

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Table 7
The AAs sequence taken from GCT as well as from binary-code tree of Genetic Code (Rakočević, 1998a)

Conf. N	12	22	20	20	08	12	24	38	16	66
Isot. N	28	26	26	24	20	31	22	23	17	30
PN	49	33	33	41	25	57	43	39	31	41
NN-1	91	57	57	75	43	107	81	72	58	72
NN-T	196	127	127	231	96	247	173	173	142	159
M. Mass	165.19	131.18	131.18	149.21	117.15	181.19	155.16	146.15	132.12	146.19
AN	14	13	13	11	10	15	11	11	08	15
	+	+	+	+	+	−	−	−	−	−
	F	L	I	M	V	Y	H	Q	N	K
	S	P	T	A	C	W	R	G	E	D
	−	−	−	+	+	−	−	−	−	−
AN	05	08	08	04	05	18	17	01	10	07
M. Mass	105.09	115.13	119.12	089.09	121.16	204.23	174.20	075.07	147.13	133.10
NN-T	85	90	116	34	169	278	217	03	192	161
NN-1	31	41	45	15	47	130	100	01	73	59
PN	17	23	25	09	25	69	55	01	39	31
Isot. N	11	16	17	08	12	36	34	02	22	16
Conf. N	09	02	08	03	21	24	66	04	20	10

After AAs encoded by middle "U" codons come AAs encoded by middle "A" codons; then follow AAs encoded by middle "G" and "C" in a cyclic organized system. The system can be seeing also as a sequence of the pairs (F-S, L-P, etc.). The data are as follows: The sign "+" and "–" for non-polar and polar AAs, respectively (after hydropathy index); AN-the number of atoms within AA side chain; M Mass—the molecule mass of AA molecule; NN-T—the total nucleon number within AA side chain [example of calculation for serine: (3 × H) + (1 × C) + (1 × O) = (3 × 1) + (3 × 2) + (1 × 12) + (1 × 13) + (1 × 16) + (1 × 17) + (1 × 18) = 85]; NN-1— the nucleon number within first nuclide [example for serine: (3 × 1) + (1 × 12) + (1 × 16) = 31]; PN—the number of protons [example for serine: (3 × 1) + (1 × 6) + (1 × 8) = 17]; Isot. N—the number of isotopes (nuclides) [example for serine: (3 × 2)H + (1 × 2)C + (1 × 3)O = 11]; Conf. N—the number of conformations, as in Popov (1989, Table 8, p. 88). (Note: nucleon number and proton number for proline is calculated as in Shcherbak, 1994, and as in Dlyasin, 1998: one H atom from side chain, must be, in calculation, associated with the AA "head", because the same AA "head" must be referent system for all 20 canonical AAs).

Table 1.1. The amino acids sequences taken from GCT for two and two columns, after hydrogen bonds between nucleotides (UA versus CG). [All references for Part VII in this article.]

Explanation of Table 1.1: After AAs encoded by middle ''U'' codons come AAs encoded by middle ''A'' codons; then follow AAs encoded by middle ''G'' and ''C'' in a cyclic organized system. (The cyclization itself is also tested through symmetry: first 10 versus second 10 AAs (Table 1.2.)[6] The system can be seeing also as a sequence of the pairs (F-S, L-P, etc.). The data are as follows: The sign ''+'' and ''–'' for nonpolar and polar AAs, respectively (after hydropathy index); AN—the number of atoms within AA side chain; M. Mass—the molecule mass of AA molecule; NN-T—the total nucleon number within AA side chain [example of calculation for serine: (3 x H) + (1 x C) + (1 x O) = (3 x 1) + (3 x 2) + (1 x 12) + (1 x 13) + (1 x 16) + (1 x 17) + (1 x 18) = 85]; NN-1— the nucleon number within first nuclide [example for serine: (3 x 1) + (1 x 12) + (1 x 16) = 31]; PN—the number of protons [example for serine: (3 x 1) + (1 x 6) + (1 x 8) = 17]; Isot. N—the number of isotopes (nuclides) [example for serine: (3 x 2) H + (1 x 2) C + (1 x 3) O = 11]; Conf. N—the number of conformations, as in Popov (1989, Table 8, p. 88). (Note: nucleon number and proton number for proline is calculated as in Shcherbak, 1994, and as in

[6] For this reason, D and E have to go to into the second row. On the other hand, AAs that are located in two families of codons (L,S,R) appear only once in its first position each (in accordance with the principle of "all or nothing").

Dlyasin, 1998: one H atom from side chain, must be, in calculation, associated with the AA ‘‘head’’, because the same AA ‘‘head’’ must be referent system for all 20 canonical AAs.)

Table 8
The results of calculations from data given in Table 7

	AN	M. Mass	NN-T	NN-1	PN	Isot. N	Conf. N
Odd	102-1	1369-1	1513	627-1	343-1	210-1	203 + 1
Even	102 + 1	1369 + 1	1503	628 + 1	343 + 1	211 + 1	202-1

All designations as in Table 7. The sums are given for AAs pairs in odd (bold) as well as in even positions within the system in Table 7. For example, within five AAs pairs [(F–S), (I–T), (V–C), (H–Y), (N–E)], existing in odd positions, there are 10 AAs molecules with molecules mass of 1368 units and with atom number of 101 atoms, etc., as it is presented in this table. The balances are self-evident.

Table 1.2. The results of calculations for the parameters given in Table 1.1.

1st	2nd letter U		2nd letter C		2nd letter A		2nd letter G		3rd	
U	UUU	**F**	UCU	**S**	UAU	**Y**	UGU	**C**	*U*	70
	UUC		UCC		UAC		UGC	CT	*C*	
	UUA	**L**	UCA		UAA	CT	UGA	**W**	*A*	
	UUG		UCG		UAG		UGG		*G*	
C	CUU	**L**	CCU	**P**	CAU	**H**	CGU	**R**	*U*	60
	CUC		CCC		CAC		CGC		*C*	
	CUA		CCA		CAA	**Q**	CGA		*A*	
	CUG		CCG		CAG		CGG		*G*	
A	AUU	**I**	ACU	**T**	AAU	**N**	AGU	**S**	*U*	77
	AUC		ACC		AAC		AGC		*C*	
	AUA	**M**	ACA		AAA	**K**	AGA	**R**	*A*	
	AUG		ACG		AAG		AGG		*G*	
G	GUU	**V**	GCU	**A**	GAU	**D**	GGU	**G**	*U*	32
	GUC		GCC		GAC		GGC		*C*	
	GUA		GCA		GAA	**E**	GGA		*A*	
	GUG		GCG		GAG		GGG		*G*	
		74		25		77		63		

(74 + 63 = **137**) (25 + 77 = **102**) / (70 + 32 = **1102**) (60 + 77 = **137**)

Table 2.1. The standard Genetic Code Table (GCT): 64 codons and 23 amino acids; the arrangement by **second** letter (U, C, A, G: 16 times each in middle position within codons). Position hierarchy: II – I – III as II (16) – I (4) – III (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

2nd	1st letter U	1st letter C	1st letter A	1st letter G	3rd	
U	UUU UUC **F** UUA UUG **L**	CUU CUC CUA **L** CUG	AUU AUC **I** AUA AUG **M**	GUU GUC **V** GUA GUG	*U* *C* *A* *G*	74
C	UCU UCC UCA **S** UCG	CCU CCC CCA **P** CCG	ACU ACC ACA **T** ACG	GCU GCC GCA **A** GCG	*U* *C* *A* *G*	25
A	UAU UAC **Y** UAA CT UAG	CAU CAC **H** CAA CAG **Q**	AAU AAC **N** AAA AAG **K**	GAU GAC **D** GAA GAG **E**	*U* *C* *A* *G*	77
G	UGU **C** UGC CT UGA **W** UGG	CGU CGC CGA **R** CGG	AGU AGC **S** AGA AGG **R**	GGU GGC GGA **G** GGG	*U* *C* *A* *G*	63
	70	60	77	32		
(70 + 32 = **102**) (60 + 77 = **137**) / (74 + 63 = **137**) (25 + 77 = **102**)						

Table 2.2. The second variant of standard GCT with the set of 23 amino acids; the arrangement is given by **first** letter (U, C, A, G: 16 times each in first position within codons). Position hierarchy: I –II – III as I (16) – II (4) – III (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

157 82	**147** **92**	**137** **102**	127 112	**117** **122**	107 132	97 142	87 152
	Tab. IV/3	Tab. VII/2.2		Tab. IV/2	Tab. IV/2		

Survey 1. The atom number patterns within the set of 23 AAs (Cf. Survey IV/ 3.)

1st	2nd letter U		2nd letter C		2nd letter A		2nd letter G		3rd			
U	UUU	**F**	UCU	**S**	UAU	**Y**	UGU	**C**	*U*	**132**	328	
	UUC	**F**	UCC	**S**	UAC	**Y**	UGC	**C**	*C*			
	UUA	**L**	UCA	**S**	UAA	*	UGA	*	*A*			
	UUG	**L**	UCG	**S**	UAG	*	UGG	**W**	*G*			
		54		**20**		**30**		**28**				
C	CUU	**L**	CCU	**P**	CAU	**H**	CGU	**R**	*U*	196		290/ **304**
	CUC	**L**	CCC	**P**	CAC	**H**	CGC	**R**	*C*			
	CUA	**L**	CCA	**P**	CAA	**Q**	CGA	**R**	*A*			
	CUG	**L**	CCG	**P**	CAG	**Q**	CGG	**R**	*G*			
		52		**32**		**44**		**68**				
A	AUU	**I**	ACU	**T**	AAU	**N**	AGU	**S**	*U*	**172**	266	
	AUC	**I**	ACC	**T**	AAC	**N**	AGC	**S**	*C*			
	AUA	**I**	ACA	**T**	AAA	**K**	AGA	**R**	*A*			
	AUG	**M**	ACG	**T**	AAG	**K**	AGG	**R**	*G*			
		50		**32**		**46**		**44**				
G	GUU	**V**	GCU	**A**	GAU	**D**	GGU	**G**	*U*	94		
	GUC	**V**	GCC	**A**	GAC	**D**	GGC	**G**	*C*			
	GUA	**V**	GCA	**A**	GAA	**E**	GGA	**G**	*A*			
	GUG	**V**	GCG	**A**	GAG	**E**	GGG	**G**	*G*			
		40		**16**		**34**		**04**				
		196		**100**		**154**		**144**				
	296 (306-10)				**298** (288+10)							
	297±1											

Table 3.1. The first variant of standard GCT with 61 amino acids and 16 nucleotides in **second** position of codons; the arrangement by second letter (U, C, A, G: 16 times each in middle position within codons). Position hierarchy: II – I – III as II (16) – I (4) – III (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

266 **328**	276 318	286 308	**296** **298**	**306** **288**	316 278	326 268	... ...
(Tab. VII/3.1)[7]			(Tab. I/1.2)[8]	(Tab. VII/3.2)[9]			

Survey 2. The atom number patterns within the set of 61 AAs (I)

[7] Tables VII / 3.1; 3.3; 3.4.
[8] Fig. I/1; Tables: I / 1.2 (a); 5 (a, b); II/5 (b, d); III/ 2;
[9] Tables VII / 3.2, 3.4, 3.5, 3.6.

266 **328**	276 318	286 308	**290** **304**	**306** **288**	316 278	326 268	… …
	(Tab. VII/4.3)		(Tab. VII/3.5)[10]	(Tab. VII/3.2)[11]			

Survey 3. The atom number patterns within the set of 61 AAs (II)

3rd	2nd letter								1st	a	b
	U		C		A		G				
U	UUU	**F**	UCU	**S**	UAU	**Y**	UGU	**C**	*U*	144	288
	CUU	**L**	CCU	**P**	CAU	**H**	CGU	**R**	*C*		
	AUU	**I**	ACU	**T**	AAU	**N**	AGU	**S**	*A*		
	GUU	**V**	GCU	**A**	GAU	D	GGU	**G**	*G*		
		50		**25**		**41**		**28**			
C	UUC	**F**	UCC	**S**	UAC	**Y**	UGC	**C**	*U*	144	
	CUC	**L**	CCC	**P**	CAC	**H**	CGC	**R**	*C*		
	AUC	**I**	ACC	**T**	AAC	**N**	AGC	**S**	*A*		
	GUC	**V**	GCC	**A**	GAC	**D**	GGC	**G**	*G*		
		50		**25**		**41**		**28**			
A	UUA	**L**	UCA	**S**	UAA	*	UGA	*	*U*	145	306
	CUA	**L**	CCA	**P**	CAA	**Q**	CGA	**R**	*C*		
	AUA	**I**	ACA	**T**	AAA	**K**	AGA	**R**	*A*		
	GUA	**V**	GCA	**A**	GAA	**E**	GGA	**G**	*G*		
		49		**25**		**36**		**35**			
G	UUG	**L**	UCG	**S**	UAG	*	UGG	**W**	*U*	161	
	CUG	**L**	CCG	**P**	CAG	**Q**	CGG	**R**	*C*		
	AUG	**M**	ACG	**T**	AAG	**K**	AGG	**R**	*A*		
	GUG	**V**	GCG	**A**	GAG	**E**	GGG	**G**	*G*		
		47		**25**		**36**		**53**			
		196		**100**		**154**	**144**				
	296 (306-10)				**298** (288+10)						
	297±1										

Table 3.2. The second variant of standard GCT with 61 amino acids and 16 nucleotides in **second** position of codons; the arrangement by second letter (U, C, A, G: 16 times each in middle position within codons). Position hierarchy: II – III – I as II (16) – III (4) – I (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

[10] Tables I / 3 (a).

[11] Tables: I/4(a); III/ 1(b); VII / 3.4; 3.5; 3.6.

2nd	1st letter U	1st letter C	1st letter A	1st letter G	3rd			
U	UUU **F**	CUU **L**	AUU **I**	GUU **V**	*U*	**196**	296	
	UUC **F**	CUC **L**	AUC **I**	GUC **V**	*C*			
	UUA **L**	CUA **L**	AUA **I**	GUA **V**	*A*			
	UUG **L**	CUG **L**	AUG **M**	GUG **V**	*G*			
	54	**52**	**50**	**40**				
C	UCU **S**	CCU **P**	ACU **T**	GCU **A**	*U*	100		264-10 / **330+10**
	UCC **S**	CCC **P**	ACC **T**	GCC **A**	*C*			
	UCA **S**	CCA **P**	ACA **T**	GCA **A**	*A*			
	UCG **S**	CCG **P**	ACG **T**	GCG **A**	*G*			
	20	**32**	**32**	**16**				
A	UAU **Y**	CAU **H**	AAU **N**	GAU **D**	*U*	154	298	
	UAC **Y**	CAC **H**	AAC **N**	GAC **D**	*C*			
	UAA *****	CAA **Q**	AAA **K**	GAA **E**	*A*			
	UAG *	CAG **Q**	AAG **K**	GAG **E**	*G*			
	30	**44**	**46**	**34**				
G	UGU **C**	CGU **R**	AGU **S**	GGU **G**	*U*	**144**		
	UGC **C**	CGC **R**	AGC **S**	GGC **G**	*C*			
	UGA *****	CGA **R**	AGA **R**	GGA **G**	*A*			
	UGG **W**	CGG **R**	AGG **R**	GGG **G**	*G*			
	28	**68**	**44**	**04**				
	132	**196**	**172**	**94**				
	328		**266**					

Table 3.3. The first variant of standard GCT with 61 amino acids and 16 nucleotides in **first** position of codons; the arrangement by first letter (U, C, A, G: 16 times each in first position within codons). Position hierarchy: I – II – III as I (16) – II (4) – III (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

3rd	1st letter				2nd			
	U	C	A	G				
U	UUU **F** UCU **S** UAU **Y** UGU **C** **39**	CUU **L** CCU **P** CAU **H** CGU **R** **49**	AUU **I** ACU **T** AAU **N** AGU **S** **34**	GUU **V** GCU **A** GAU **D** GGU **G** **22**	*U* *C* *A* *G*	**144**		288
C	UUC **F** UCC **S** UAC **Y** UGC **C** **39**	CUC **L** CCC **P** CAC **H** CGC **R** **49**	AUC **I** ACC **T** AAC **N** AGC **S** **34**	GUC **V** GCC **A** GAC **D** GGC **G** **22**	*U* *C* *A* *G*	144	290-1 / 304 + 1	
A	UUA **L** UCA **S** UAA * UGA * **18**	CUA **L** CCA **P** CAA **Q** CGA **R** **49**	AUA **I** ACA **T** AAA **K** AGA **R** **53**	GUA **V** GCA **A** GAA **E** GGA **G** **25**	*U* *C* *A* *G*	**145**		306
G	UUG **L** UCG **S** UAG * UGG **W** **36**	CUG **L** CCG **P** CAG **Q** CGG **R** **49**	AUG **M** ACG **T** AAG **K** AGG **R** **51**	GUG **V** GCG **A** GAG **E** GGG **G** **25**	*U* *C* *A* *G*	161		
	132	**196**	**172**	**94**				
	328		**266**					

Table 3.4. The second variant of standard GCT with 61 amino acids and 16 nucleotides in **first** position of codons; the arrangement by first letter (U, C, A, G: 16 times each in first position within codons). Position hierarchy: I – III – II as I (16) – III (4) – II (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

1st	3rd letter				2nd			
	U	C	A	G				
U	UUU **F** UCU **S** UAU **Y** UGU **C** **39**	UUC **F** UCC **S** UAC **Y** UGC **C** **39**	UUA **L** UCA **S** UAA * UGA * **18**	UUG **L** UCG **S** UAG * UGG **W** **36**	*U* *C* *A* *G*	**132**	328	
C	CUU **L** CCU **P** CAU **H** CGU **R** **49**	CUC **L** CCC **P** CAC **H** CGC **R** **49**	CUA **L** CCA **P** CAA **Q** CGA **R** **49**	CUG **L** CCG **P** CAG **Q** CGG **R** **49**	*U* *C* *A* *G*	196		290 / **304**
A	AUU **I** ACU **T** AAU **N** AGU **S** **34**	AUC **I** ACC **T** AAC **N** AGC **S** **34**	AUA **I** ACA **T** AAA **K** AGA **R** **53**	AUG **M** ACG **T** AAG **K** AGG **R** **51**	*U* *C* *A* *G*	**172**	266	
G	GUU **V** GCU **A** GAU **D** GGU **G** **22**	GUC **V** GCC **A** GAC **D** GGC **G** **22**	GUA **V** GCA **A** GAA **E** GGA **G** **25**	GUG **V** GCG **A** GAG **E** GGG **G** **25**	*U* *C* *A* *G*	94		
	144	**144**	**145**	**161**				
		288		**306**				

Table 3.5. The first variant of standard GCT with 61 amino acids and 16 nucleotides in **third** position of codons; the arrangement by third letter (U, C, A, G: 16 times each in third position within codons). Position hierarchy: III – I – II as III (16) – I (4) – II (1), in the sense: 16 and 4 the same nucleotides in a continual sequence, then four times of 1 different nucleotides (UCAG).

2nd	3rd letter U		C		A		G		1st		
U	UUU	**F**	UUC	**F**	UUA	**L**	UUG	**L**	*U*		
	CUU	**L**	CUC	**L**	CUA	**L**	CUG	**L**	*C*		
	AUU	**I**	AUC	**I**	AUA	**I**	AUG	**M**	*A*	**196**	
	GUU	**V**	GUC	**V**	GUA	**V**	GUG	**V**	*G*		
		50		**50**		**49**		**47**			296
C	UCU	**S**	UCC	**S**	UCA	**S**	UCG	**L**	*U*		
	CCU	**P**	CCC	**P**	CCA	**P**	CCG	**P**	*C*		
	ACU	**T**	ACC	**T**	ACA	**T**	ACG	**T**	*A*	100	
	GCU	**A**	GCC	**A**	GCA	**A**	GCG	**A**	*G*		
		25		**25**		**25**		**25**			
A	UAU	**Y**	UAC	**Y**	UAA	**CT**	UAG	**CT**	*U*		
	CAU	**H**	CAC	**H**	CAA	**Q**	CAG	**Q**	*C*		
	AAU	**N**	AAC	**N**	AAA	**K**	AAG	**K**	*A*	**154**	
	GAU	**D**	GAC	**D**	GAA	**E**	GAG	**E**	*G*		
		41		**41**		**36**		**36**			
G	UGU	**C**	UGC	**C**	UGA	**CT**	UGG	**W**	*U*		298
	CGU	**R**	CGC	**R**	CGA	**R**	CGG	**R**	*C*		
	AGU	**S**	AGC	**S**	AGA	**R**	AGG	**R**	*A*	144	
	GGU	**G**	GGC	**G**	GGA	**G**	GGG	**G**	*G*		
		28		**28**		**35**		**53**			
		144		**144**		**145**		**161**			
		288					**306**				

Table 3.6. The second variant of standard GCT with 61 amino acids and 16 nucleotides in **third** position of codons; the arrangement by third letter (U, C, A, G: 16 times each in third position within codons). Position hierarchy: III – II – II as III (16) – II (4) – I (1).

I-II			I-II					
GG **GU**	GGGG VVVV	**44**	**UU** **UG**	FFLL CC*W	**82**	**126**	296 / **298**	280
CC **AC**	PPPP TTTT	**64**	**AA** **CA**	NNKK HHQQ	**90**	154		
GC **CU**	AAAA LLLL	**68**	**UA** **AG**	YY** SSRR	**74**	142		314
CG **UC**	RRRR SSSS	**88**	**AU** **GA**	IIIM DDEE	**84**	**172**		
	264			**330**				

Table 4.1. The nucleotide doublets as in Table II/2: positions I & II in the codon. (Cf. Fig. I/1.)

I-III			I-III				
GG	VAEG	**47**	**UU**	FSYC	**75**	**122**	306+ 1 = **307**
GU	VADG		**UG**	LS*W			
CC	LPHR	**83**	**AA**	ITKR	**102**	**185**	
AC	ITNS		**CA**	LPQR			
GC	VADG	**71**	**UA**	LS**	**69**	**140**	288 – 1 = **287**
CU	LPHR		**AG**	MTKR			
CG	LPQR	**88**	**AU**	LS**	**59**	**147**	
UC	FSYC		**GA**	MTKR			
288 + 1 =		**289**	306 – 1 =		**305**		

Table 4.2. The nucleotide doublets taken from positions I & III in the codon. The atom number pattern 289/305 corresponds (making a balance) to the atom number 290/304 in Table 3.1; also to the atom number 290-10 / 304 + 10 in Table 4.1. On the other hand, the atom number pattern 287/307 corresponds to the atom number 288/306 in Table 3.2.

II-III			II-III				
GG	WRRG	**81**	**UU**	FLIV	**97**	**178**	**306 – 1= 305**
GU	CRSG		**UG**	LLMV			
CC	SPTA	**66**	**AA**	QKE	**61**	**127**	
AC	YHND		**CA**	SPTA			
GC	CRSG	**53**	**UA**	LLIV	**85**	**138**	**288+1= 289**
CU	SPTA		**AG**	QKE			
CG	SPTA	**75**	**AU**	YHND	**76**	**151**	
UC	FLIV		**GA**	RRG			
276 – 1			**318 + 1**				

Table 4.3. The nucleotide doublets taken from positions II & III in the codon. The atom number pattern 289/305 corresponds (making a balance) to the same atom number pattern 289/305 in Table 4.2. On the other hand, the atom number pattern 276/318 corresponds to the same pattern in Survey 2.

* * *

Presented facts support the hypothesis that the genetic code was a complete code from very begining, from prebiotic times and conditions. On the other hand, such a complet code must be expressed into genotype and phenotype,[12] and that is the reason why all the presented relationships in the genetic code one needs to know.

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[12] „Britsh zoologist Richard Dawkins is best known for his popular science books. ... His most significant contribution to his field is his concept of the 'extended phenotype'. An organism's genotype is the sum of the instructions contained in its genetic code. Its phenotype is that which results from the expression of that code" (Hart-Davis et al, 2014).