

# 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<sup>1</sup> 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)<sup>2</sup> as well as nucleotides doublet table (DT)<sup>3</sup> 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.<sup>4</sup>

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)<sup>5</sup> 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 completeness 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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<sup>1</sup> 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).

<sup>2</sup> The nucleotides triplet table (TT) as Standard Genetic Code Table (GCT), valid for the so-called "Standard Genetic Code".

<sup>3</sup> 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).

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

<sup>5</sup> In modular formulation:  $\pm 0$  and  $\pm 1$ .

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

<pre> /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   64 </pre>
<pre> /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 </pre>

**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](https://arxiv.org/abs/q-bio/0703011v2) [q-bio.OT])

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:  $(3 \times H) + (1 \times C) + (1 \times O) = (3 \times 1) + (3 \times 2) + (1 \times 12) + (1 \times 13) + (1 \times 16) + (1 \times 17) + (1 \times 18) = 85$ ]; NN-1—the nucleon number within first nuclide [example for serine:  $(3 \times 1) + (1 \times 12) + (1 \times 16) = 31$ ]; PN—the number of protons [example for serine:  $(3 \times 1) + (1 \times 6) + (1 \times 8) = 17$ ]; Isot. N—the number of isotopes (nuclides) [example for serine:  $(3 \times 2)H + (1 \times 2)C + (1 \times 3)O = 11$ ]; 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).<sup>6</sup> 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:  $(3 \times H) + (1 \times C) + (1 \times O) = (3 \times 1) + (3 \times 2) + (1 \times 12) + (1 \times 13) + (1 \times 16) + (1 \times 17) + (1 \times 18) = 85$ ]; NN-1—the nucleon number within first nuclide [example for serine:  $(3 \times 1) + (1 \times 12) + (1 \times 16) = 31$ ]; PN—the number of protons [example for serine:  $(3 \times 1) + (1 \times 6) + (1 \times 8) = 17$ ]; Isot. N—the number of isotopes (nuclides) [example for serine:  $(3 \times 2)H + (1 \times 2)C + (1 \times 3)O = 11$ ]; 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

<sup>6</sup> For this reason, D and E have to go 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.)

	AN	M. Mass	NN-T	NN-1	PN	Isot. N	Conf. N
Odd	102-1	1369-1	<b>15</b> 3	627-1	343-1	210-1	203+1
Even	102+1	1369+1	15 <b>3</b>	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				3rd	
	U	C	A	G		
U	UUU	UCU	UAU	UGU	U	70
	UUC <b>F</b>	UCC <b>S</b>	UAC <b>Y</b>	UGC <b>C</b>	C	
	UUA	UCA	UAA <b>CT</b>	UGA <b>W</b>	A	
	UUG <b>L</b>	UCG	UAG	UGG	G	
C	CUU	CCU	CAU	CGU	U	60
	CUC <b>L</b>	CCC <b>P</b>	CAC <b>H</b>	CGC <b>R</b>	C	
	CUA	CCA	CAA <b>Q</b>	CGA	A	
	CUG	CCG	CAG	CGG	G	
A	AUU	ACU	AAU	AGU	U	77
	AUC <b>I</b>	ACC <b>T</b>	AAC <b>N</b>	AGC <b>S</b>	C	
	AUA	ACA	AAA <b>K</b>	AGA	A	
	AUG <b>M</b>	ACG	AAG	AGG <b>R</b>	G	
G	GUU	GCU	GAU	GGU	U	32
	GUC <b>V</b>	GCC <b>A</b>	GAC <b>D</b>	GGC <b>G</b>	C	
	GUA	GCA	GAA <b>E</b>	GGA	A	
	GUG	GCG	GAG	GGG	G	
	74	25	77	63		
(74 + 63 = <b>137</b> ) (25 + 77 = <b>102</b> ) / (70 + 32 = <b>1102</b> ) (60 + 77 = <b>137</b> )						

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

**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	<b>147</b>	<b>137</b>	127	<b>117</b>	107	97	87
82	<b>92</b>	<b>102</b>	112	<b>122</b>	132	142	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								3rd			
	U		C		A		G					
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			
		<b>54</b>		<b>20</b>		<b>30</b>		<b>28</b>				
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			
		<b>52</b>		<b>32</b>		<b>44</b>		<b>68</b>				
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			
		<b>50</b>		<b>32</b>		<b>46</b>		<b>44</b>				
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			
		<b>40</b>		<b>16</b>		<b>34</b>		<b>04</b>				
	<b>196</b>		<b>100</b>		<b>154</b>		<b>144</b>					
	<b>296 (306-10)</b>			<b>298 (288+10)</b>								
	<b>297±1</b>											

**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).

<b>266</b>	276	286	<b>296</b>	<b>306</b>	316	326	...
<b>328</b>	318	308	<b>298</b>	<b>288</b>	278	268	...
(Tab. VII/3.1) <sup>7</sup>			(Tab. I/1.2) <sup>8</sup>	(Tab. VII/3.2) <sup>9</sup>			

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

<sup>7</sup> Tables VII / 3.1; 3.3; 3.4.

<sup>8</sup> Fig. I/1; Tables: I / 1.2 (a); 5 (a, b); II/5 (b, d); III/ 2;

<sup>9</sup> Tables VII / 3.2, 3.4, 3.5, 3.6.

266	276	286	<b>290</b>	<b>306</b>	316	326	...
328	318	308	<b>304</b>	<b>288</b>	278	268	...
	(Tab. VII/4.3)		(Tab. VII/3.5) <sup>10</sup>	(Tab. VII/3.2) <sup>11</sup>			

**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		
		<b>50</b>		<b>25</b>		<b>41</b>		<b>28</b>			
C	UUC	F	UCC	S	UAC	Y	UGC	C	U	144	306
	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		
		<b>50</b>		<b>25</b>		<b>41</b>		<b>28</b>			
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		
		<b>49</b>		<b>25</b>		<b>36</b>		<b>35</b>			
G	UUG	L	UCG	S	UAG	*	UGG	W	U	161	306
	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		
		<b>47</b>		<b>25</b>		<b>36</b>		<b>53</b>			
		<b>196</b>		<b>100</b>		<b>154</b>		<b>144</b>			
		<b>296 (306-10)</b>			<b>298 (288+10)</b>						
		<b>297±1</b>									

**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).

<sup>10</sup> Tables I / 3 (a).

<sup>11</sup> Tables: I/4(a); III/ 1(b); VII / 3.4; 3.5; 3.6.

2nd	1st letter						3rd				
	U	C	A	G							
U	UUU	F	CUU	L	AUU	I	GUU	V	196	296	264-10 / 330+10
	UUC	F	CUC	L	AUC	I	GUC	V			
	UUA	L	CUA	L	AUA	I	GUA	V			
	UUG	L	CUG	L	AUG	M	GUG	V			
		54		52		50		40			
C	UCU	S	CCU	P	ACU	T	GCU	A	100	298	264-10 / 330+10
	UCC	S	CCC	P	ACC	T	GCC	A			
	UCA	S	CCA	P	ACA	T	GCA	A			
	UCG	S	CCG	P	ACG	T	GCG	A			
		20		32		32		16			
A	UAU	Y	CAU	H	AAU	N	GAU	D	154	298	264-10 / 330+10
	UAC	Y	CAC	H	AAC	N	GAC	D			
	UAA	*	CAA	Q	AAA	K	GAA	E			
	UAG	*	CAG	Q	AAG	K	GAG	E			
		30		44		46		34			
G	UGU	C	CGU	R	AGU	S	GGU	G	144	298	264-10 / 330+10
	UGC	C	CGC	R	AGC	S	GGC	G			
	UGA	*	CGA	R	AGA	R	GGA	G			
	UGG	W	CGG	R	AGG	R	GGG	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	CUU	L	AUU	I	GUU	V	U	144	288	
	UCU	S	CCU	P	ACU	T	GCU	A	C			
	UAU	Y	CAU	H	AAU	N	GAU	D	A			
	UGU	C	CGU	R	AGU	S	GGU	G	G			
		<b>39</b>		<b>49</b>		<b>34</b>		<b>22</b>				
C	UUC	F	CUC	L	AUC	I	GUC	V	U	144	288	
	UCC	S	CCC	P	ACC	T	GCC	A	C			
	UAC	Y	CAC	H	AAC	N	GAC	D	A			
	UGC	C	CGC	R	AGC	S	GGC	G	G			
		<b>39</b>		<b>49</b>		<b>34</b>		<b>22</b>				
A	UUA	L	CUA	L	AUA	I	GUA	V	U	145	306	290-1 / 304 + 1
	UCA	S	CCA	P	ACA	T	GCA	A	C			
	UAA	*	CAA	Q	AAA	K	GAA	E	A			
	UGA	*	CGA	R	AGA	R	GGA	G	G			
		<b>18</b>		<b>49</b>		<b>53</b>		<b>25</b>				
G	UUG	L	CUG	L	AUG	M	GUG	V	U	161	306	
	UCG	S	CCG	P	ACG	T	GCG	A	C			
	UAG	*	CAG	Q	AAG	K	GAG	E	A			
	UGG	W	CGG	R	AGG	R	GGG	G	G			
		<b>36</b>		<b>49</b>		<b>51</b>		<b>25</b>				
		<b>132</b>		<b>196</b>		<b>172</b>		<b>94</b>				
		<b>328</b>				<b>266</b>						

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

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

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

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

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

**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 beginning, from prebiotic times and conditions. On the other hand, such a complete code must be expressed into genotype and phenotype,<sup>12</sup> and that is the reason why all the presented relationships in the genetic code one needs to know.

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<sup>12</sup> „British 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.“