

# ON THE COMPLETENESS OF GENETIC CODE: PART II

Miloje M. Rakočević

Department of Chemistry, Faculty of Science, University of Nish, Serbia  
(E-mail: milemirkov@open.telekom.rs; [www.rakocevcode.rs](http://www.rakocevcode.rs))

**Abstract.** As in first part of this work, in this second part we present the chemically meaningful splitting of codons after pyrimidine / purine distinctions; the splitting which is also in relation to Rumer nucleotide doublet Table.

Starting from our hypothesis of prebiotic completeness of the genetic code (Rakočević, 2004), we have presented several new examples of that completeness, in Part I of this work (Rakočević, 2014). Now, in this part (Part II) we present the relationships between the nucleotide triplets table (TT) and nucleotide doublets Table (DT) through the said completeness.

As first step we show the Rumer's Table of 16 nucleotide doublets and the Modified Rumer's Table (Tables 1 & 2 in relation to Tables 3 & 4) (Rakočević, 2014a). By this, the presented balances of the number of nucleons as well as atoms within amino acid side chains are valid for the set of 23 AAs. In a new Table (Table 5), however, we show the relationships only through the balances of the number of atoms, but in the set of 61 amino acid molecules.

The conclusion is the same as in Part I.

01. G	GG (6)	02. F	UU (4)	03. L
04. P	CC (6)	05. N	AA (4)	06. K
07. R	CG (6)	08. I	AU (4)	09. M
10. A	GC (6)	11. Y	UA (4)	12. St.
13. T	AC (5)	14. H	CA (5)	15. Q
16. V	GU (5)	17. C	UG (5)	18. W
19. S	UC (5)	20. D	GA (5)	21. E
22. L	CU (5)	23. S	AG (5)	24. R

**Table 1.** Rumer's Table of nucleotide doublets

01. G	GG (6)	02. F	UU (4)	03. L
04. P	CC (6)	05. N	AA (4)	06. K
07. A	GC (6)	08. Y	UA (4)	09. St.
10. R	CG (6)	11. I	AU (4)	12. M
13. V	GU (5)	14. C	UG (5)	15. W
16. T	AC (5)	17. H	CA (5)	18. Q
19. L	CU (5)	20. S	AG (5)	21. R
22. S	UC (5)	23. D	GA (5)	24. E

**Table 2.** The modified Rumer's Table: four quadruplets, each with 1<sup>st</sup>, 2<sup>nd</sup>, 3<sup>rd</sup>, 4<sup>th</sup> doublet.

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

**Table 3.** Distributions of AAs after nucleotide doublets presented in Table 2: Four squares with more dark tones (outer) contain four first doublets from Table 2 and four less dark tones (inner) contain four second doublets. In amino acids, within their side chains (in the set of 23 AAs) at outer/inner areas there are 369/369 nucleons and 61/61 atoms, respectively. All AAs in outer area are nonpolar whereas those in inner area are polar, measured by cloister energy. [Cloister energy as in Swanson, 1984.]

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

**Table 4.** Distributions of AAs after nucleotide doublets presented in Table 2: Four squares with more dark tones contain four third doublets from Table 2 and four with less dark tones contain four fourth doublets; two and two doublets on the right, and two and two on the left. In amino acids (within their side chains), in right/left areas there are 369/369-33 nucleons and 59/58 atoms, respectively. All AAs on the right together with D & E from the left are polar and other on the left are nonpolar. Because the balance is realized in relation to diagonal and not in relation to the type of nucleotide doublets (third or fourth) it follows that positions 3 & 4 in DT are not invariant, but only positions 1 & 2 as it is shown in Table 3.

UUU (F)	UCU(S)	UAU(Y)	UGU(C)	UUU (F)	UCU(S)	UAU(Y)	UGU(C)
UUC (F)	UCC(S)	UAC(Y)	UGC(C)	UUC (F)	UCC(S)	UAC(Y)	UGC(C)
UUA (L)	UCA(S)	UAA(ct)	UGA(ct)	UUA (L)	UCA(S)	UAA(ct)	UGA(ct)
UUG (L)	UCG(S)	UAG(ct)	UGG(W)	UUG (L)	UCG(S)	UAG(ct)	UGG(W)
CUU (L)	CCU(P)	CAU(H)	CGU(R)	CUU (L)	CCU(P)	CAU(H)	CGU(R)
CUC (L)	CCC(P)	CAC(H)	CGC(R)	CUC (L)	CCC(P)	CAC(H)	CGC(R)
CUA (L)	CCA(P)	CAA(Q)	CGA(R)	CUA (L)	CCA(P)	CAA(Q)	CGA(R)
CUG (L)	CCG(P)	CAG(Q)	CGG(R)	CUG (L)	CCG(P)	CAG(Q)	CGG(R)
AUU (I)	ACU(T)	AAU(N)	AGU(S)	AUU (I)	ACU(T)	AAU(N)	AGU(S)
AUC (I)	ACC(T)	AAC(N)	AGC(S)	AUC (I)	ACC(T)	AAC(N)	AGC(S)
AUA (I)	ACA(T)	AAA(K)	AGA(R)	AUA (I)	ACA(T)	AAA(K)	AGA(R)
AUG (M)	ACG(T)	AAG(K)	AGG(R)	AUG (M)	ACG(T)	AAG(K)	AGG(R)
GUU(V)	GCU(A)	GAU(D)	GGU(G)	GUU(V)	GCU(A)	GAU(D)	GGU(G)
GUC(V)	GCC(A)	GAC(D)	GGC(G)	GUC(V)	GCC(A)	GAC(D)	GGC(G)
GUA(V)	GCA(A)	GAA(E)	GGA(G)	GUA(V)	GCA(A)	GAA(E)	GGA(G)
GUG(V)	GCG(A)	GAG(E)	GGG(G)	GUG(V)	GCG(A)	GAG(E)	GGG(G)
(c) = 330/264 (blue+dark) vs (red+light)				(d) = 296/298 (red+dark) vs (blue+light)			
UUU (F)	UCU(S)	UAU(Y)	UGU(C)	UUU (F)	UCU(S)	UAU(Y)	UGU(C)
UUC (F)	UCC(S)	UAC(Y)	UGC(C)	UUC (F)	UCC(S)	UAC(Y)	UGC(C)
UUA (L)	UCA(S)	UAA(ct)	UGA(ct)	UUA (L)	UCA(S)	UAA(ct)	UGA(ct)
UUG (L)	UCG(S)	UAG(ct)	UGG(W)	UUG (L)	UCG(S)	UAG(ct)	UGG(W)
CUU (L)	CCU(P)	CAU(H)	CGU(R)	CUU (L)	CCU(P)	CAU(H)	CGU(R)
CUC (L)	CCC(P)	CAC(H)	CGC(R)	CUC (L)	CCC(P)	CAC(H)	CGC(R)
CUA (L)	CCA(P)	CAA(Q)	CGA(R)	CUA (L)	CCA(P)	CAA(Q)	CGA(R)
CUG (L)	CCG(P)	CAG(Q)	CGG(R)	CUG (L)	CCG(P)	CAG(Q)	CGG(R)
AUU (I)	ACU(T)	AAU(N)	AGU(S)	AUU (I)	ACU(T)	AAU(N)	AGU(S)
AUC (I)	ACC(T)	AAC(N)	AGC(S)	AUC (I)	ACC(T)	AAC(N)	AGC(S)
AUA (I)	ACA(T)	AAA(K)	AGA(R)	AUA (I)	ACA(T)	AAA(K)	AGA(R)
AUG (M)	ACG(T)	AAG(K)	AGG(R)	AUG (M)	ACG(T)	AAG(K)	AGG(R)
GUU(V)	GCU(A)	GAU(D)	GGU(G)	GUU(V)	GCU(A)	GAU(D)	GGU(G)
GUC(V)	GCC(A)	GAC(D)	GGC(G)	GUC(V)	GCC(A)	GAC(D)	GGC(G)
GUA(V)	GCA(A)	GAA(E)	GGA(G)	GUA(V)	GCA(A)	GAA(E)	GGA(G)
GUG(V)	GCG(A)	GAG(E)	GGG(G)	GUG(V)	GCG(A)	GAG(E)	GGG(G)
(a) = 280/314 (red+blue) vs (light)				(b) = 298/296 (red+dark) vs (blue+light)			

**Table 5.** Distributions of AAs after nucleotide doublets presented in Tables 2, 3 and 4: The (a) as Table 3 here, and as Table 3, under (b) in Part I (Rakočević, 2014b). In (b) at red squares (four first doublets in Table 2) there are 126 atoms; in four squares with dark tones (four forth doublets in Table 2) 172 atoms ( $126 + 172 = 298 = 297 + 1$ )  $[(9 \times 33) + 1]$ . In (b) at blue squares (four second doublets in Table 2) there are 154 atoms; in four light squares (four third doublets in Table 2) there are 142 atoms ( $154 + 142 = 296 = 297 - 1$ )  $[(9 \times 33) - 1]$ . In (c) there are 154 atoms at blue squares, plus 176 atoms in four squares on the right (with dark tones) equals 330 atoms  $[(9+1) \times 33]$ ; on the other hand, 126 atoms at the red squares, plus 138 atoms in four light squares on the left equals 264 atoms  $[(9-1) \times 33]$ . In (d) there are 126 atoms at red squares, plus 170 atoms in four squares above (with dark tones) equals  $296 = 297 - 1$  atoms  $[(9 \times 33) - 1]$ ; on the other hand, 154 atoms at the blue squares, plus 144 atoms in four light squares down equals  $298 = 297 + 1$  atoms  $[(9 \times 33) + 1]$ . (By all these balances one must notice that number patterns 296 / 298 and 264 / 330 correspond with the same patterns in Table 1.2, within Part I of this work (Rakočević, 2014b).)

## REFERENCES

Rakočević, M. M. (2004) A harmonic structure of the genetic code, *J. Theor. Biol.* 229, 463-465.

Rakočević, M. M. (2014a) Golden and harmonic mean in the genetic code, Proceedings of the 2nd International Conference “Theoretical Approaches to BioInformation Systems” (TABIS 2013), September 17 – 22, 2013 Belgrade.

Rakočević, M. M. (2014b) On the completeness of genetic code: some new examples, viXra:1412.0274.

Swanson, R. (1984) A unifying concept for the amino acid code, *Bull. Math. Biol.* 46, 187–207.