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Encoding of amino acids in DNA from position of physics of proteins

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The problem of encoding of sequence of amino acids in proteins is connected with two circumstances: analysis of functioning of molecules of RNA and consideration of all amino acids as if they were identical from the point of view of their physical properties. These two circumstances underlie of idea about three-position code words without skips, at least, for RNA. The question of redundancy of the third nucleotide in the genetic code of protein molecules periodically pops up in the literature [1-3], precisely because remains unclear how information about the structure of the proteins encoded in DNA molecules. Also it is unknown, how in the genetic code of RNA and DNA are reflected physical and structural properties of amino acids.

From the viewpoint of physics the protein it was shown that there exist not less than 11 "significant" acids. For them any error in its location in protein leads to a losing or deterioration of functionality. Consequently, DNA must have at least one code for each of these acids. It was also established the presence of not more than 9 "not significant" amino acids. Their mutual replacement will take place almost unnoticed to the functionality of the protein molecule therefore for them the possibility of several amino acids on one code is permitted. It is this last circumstance admits possibility for a two-position codeword with skip between words.

According to the results of our researches was proposed table of codes for the DNA (not RNA). This table takes into account all known on today properties of amino acids and proline.

1. Lagerkvist U. "Two out of three": An alternative method for codon reading // Proc. Natl. Acad. Sci. USA.-1978.-75, N 4.-P. 1759-1762.

2. *Crick F. H. C.* What mad pursuit: a personal view of scientific discovery // New York: Basic Books. 1988. 182 p.

3. *Ratner V. A.* Genetic code as a system // Soros Educational Journal.-2000.-6, N 3.-P. 17–22.