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Design primers for LAMP-amplification

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For successful loop-mediated isothermal amplification (LAMP) [1] it is necessary to correctly select sets of at least four primers, and find their occurrences in the complete genome or target site. The selection of primers for LAMP is a non-trivial task due to the large number of primers and the length of the genome, and therefore special computer programs are required. This paper presents an overview of the existing most popular computer programs for the design of primers for LAMP. The main parameters that must be taken into account when selecting primers are described. The analysis of mathematical algorithms for searching for a sample in a string is carried out. To implement the search and selection of primers in the genome, a new algorithm for selecting primers based on direct search was developed. A new computer program "LAMPrimers iQ" has been developed that takes into account a number of requirements for the selection of primers, searches for them, analyzes compliance with recommended conditions and groups them into sets, taking into account the absence of homo- and heterodimers, as well as the minimum difference in the melting temperature of primers in one set. One set contains four primers: FIP (forward inner primer), F3 (forward outer primer), BIP (backward inner primer) and B3 (backward outer primer). Primers location scheme used to initiate the LAMP process is shown in the Fig. 1 [2].

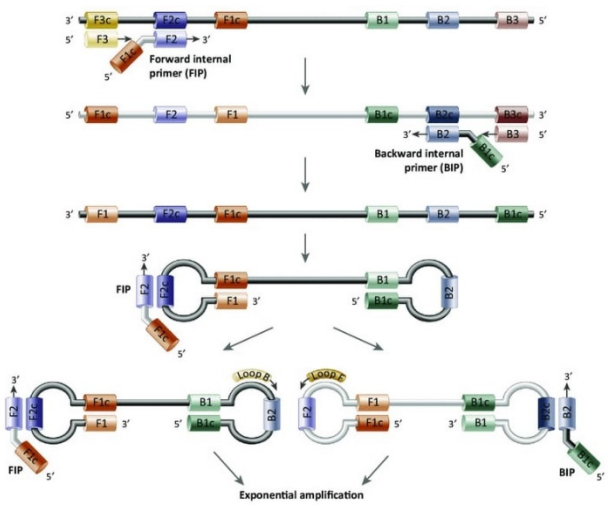

Fig. 1. Primer location scheme for loop-mediated isothermal amplification (LAMP)

This application implements work with files (plain text format, FASTA, GenBank) of sequences, it is also possible to insert a sequence through the clipboard. The results can be saved in Excel format or continue working with another file or sequence.

The program is implemented in the Python 3.10 programming language using the Biopython library, which contains a number of different submodules for general bioinformatics tasks and allows you to use different genetic databases and the Qt framework to create applications with a graphical interface.

Further, it is planned to expand the functionality of the program to increase the specificity of the reaction, namely, to add loop primers (LoopF, LoopB) [3] and a hybridization probe with an independent annealing site. Test the obtained sets of primers in the laboratory.

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