

This work is aimed at developing methods for the isolation and identification of proteins interacting with telomeric sequences of RNA and DNA.

A model yeast system for the isolation and identification of proteins interacting with telomere repeats of human RNA molecules has been developed.

A method for isolating and identifying proteins interacting with telomeric human sequences of RNA molecules was developed and optimized.

The identification of the identified proteins by mass spectrometry has been tested, the Ten1 protein involved in the regulation of telomere length has been identified.

Based on the lactose operon of *E. coli*, a model yeast system for the isolation and identification of proteins interacting with telomere repeats of human DNA molecules has been developed.

A specific interaction of the recombinant SUMO-LacI protein with PCR products of lactose operon sequences modified by human telomeric repeats is shown.

The final qualifying work includes the chapters "Introduction", "Literature review", "The purpose of the work", "The tasks of work", "Materials and methods", "Results", "Discussion of results", "Conclusions", "Acknowledgments", "References". The work takes 62 pages, illustrated by 19 figures and contains 3 tables. "References" includes 140 sources.

The "Introduction" justifies the relevance of these studies, there is no purpose and research objectives.

"The review of literature" is written in detail and it is quite enough to understand the essence of the work. The information on the structure and functions of telomeric sequences, mechanisms of replication and transcription is given. The chromatin structure of telomeric regions is described. The existing methods for studying telomeric sequences and proteins associated with them are described. The choice of the yeast model for the solution of the set tasks is substantiated.

Of the negative aspects, it should be noted a large number of stylistic errors and typos. Using slang vocabulary spoils the impression of this section. There are such phrases as "DNA-RNA hybrid", "human proteins", "DNA matrices". In describing the structure of telomeres of yeast *Saccharomyces cerevisiae* on page 7 there is no reference to figure 2. The logical structure of the section is broken, it is advisable to swap paragraphs 1.2 and 1.3. Existing methods for studying telomeric sequences are not fully described.

The purpose and objectives of the work are presented in the form of separate sections. It is striking inadequate formulation and stylistic errors. More reasonably, the tasks can be represented as follows:

1. Development of a model yeast system for the isolation and identification of proteins interacting with telomere repeats of human RNA molecules.

2. Development and optimization of methods for isolating and identifying proteins interacting with telomeric human sequences of RNA molecules.

3. Identification of identified proteins by mass spectrometry.

4. Development of a model yeast system based on the lactose operon of *E. coli* for the isolation and identification of proteins interacting with telomere repeats of human DNA molecules.

5. Verification of the specific interaction of the recombinant SUMO-LacI protein with PCR products of lactose operon sequences modified by human telomeric repeats.

In the section "Materials and Methods" the strains and plasmids used in the work are given. The methods of conducting research are described in sufficient detail. It should be noted that the author uses modern methods of molecular biology, bioinformatics and biochemistry, including the method of mass spectrometry. Unfortunately, there are still many stylistic errors and slang vocabulary. There are phrases like "Intron inserted human telomeric repeats in different orientations" and "The cassette is designed for the third chromosome near the origin of replication ARS306." When describing the oligonucleotides used in the work, annealing

temperatures are not presented. There is no justification for the use of the recombinant SUMO-LacI protein.

The chapter "Results" makes it possible to note that during the research interesting data were obtained that are of fundamental and practical importance. A list of proteins determined by mass spectrometry, interacting with telomeric sequences of RNA molecules, is given. A bioinformatic analysis of the sequence of Ten1 *S. cerevisiae* protein was performed. Still there are stylistic errors and typos. In Figure 14 there is a discrepancy between the signatures of track 41 and sample 43. There is no reference to figure 15. In the discussion of figure 17, the numbering of the gel tracks is confused. There are no indents to some paragraphs. I would like to see an appendix to the work containing the primary mass spectra of the proteins being analyzed. Also, it is necessary to think about additional control experiments on the binding of the SUMO-LacI protein to the lactose operon sequences modified by human telomeric repeats, since the interaction of the SUMO-LacI protein with PCR products was investigated in this work, and in the future it is planned to work with fragmented chromatin.

For the first time, the section "Discussion" is devoted to the important role of studying telomeric sequences and associated proteins, although it is more reasonable to imagine this in the Introduction. Next is a description of modern methods for identifying new proteins that interact with telomeric sequences, which is more in line with the Literature Review. Moreover, modern approaches to molecular spectroscopy (single molecule spectroscopy, selective laser spectroscopy, etc.) are not available, which can be used to independently confirm the results obtained. Only the last 1.5 pages of the section are devoted to the detected proteins - Ten1, Yra1, Mec1, Brn2. The structure, functions and features of the bioinformatic analysis of the Ten1 protein are described in detail. It remains a mystery why the discussion of such results as the development of a model yeast system based on the lactose operon of *E. coli* and the verification of the specific interaction of the recombinant SUMO-LacI protein with the PCR products of lactose operon sequences remains a mystery.

In general, the research was carried out at a high scientific and methodological level, interesting results were obtained, but the above remarks spoil the general impression and make the perception of the material difficult.