44. The Latest Achievements in the Field of Structural Genomics

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Introduction. The subject of structural genomics is the creation and comparison of different types of genome maps and large-scale DNA sequencing. The Human Genome Project and less known Plant Genome Research Program are the most large-scale studies of structural genomics. The tasks of structural genomics also include the identification, localization and preparation of genes' characteristics. As a result of implementation of private and public projects in structural genomics there were created maps of genomes and decoded the DNA sequence of a large number of organisms, including agricultural plants, pathogenic bacteria and viruses, yeasts, nitrogen-fixing bacteria, Plasmodium malaria and mosquitoes and micro-organisms used by man in a variety of industrial processes. Due to the fact that the genetic code is universal and all living organisms are able to decipher the genetic information of other organisms and to carry out its biological functions, any gene identified in the course of any given genome project can be used in a wide range of practical applications:

- for purposeful change the properties of plants and give them the desired characteristics;

- selection of specific recombinant molecules or micro-organisms;

- identification of genes involved in the implementation of complex processes that are controlled by many genes, and also independent of the influence the environment;

- detection of microbial infections of cell cultures and other Form that accepts a protein molecule depends on amino acid sequence, however, all the mechanisms of twisting and folding of amino acid chains is not fully understood. Scientists in the proteomics are now in a similar position: they need to develop a sufficient number of methods and techniques that could provide efficient operation over a huge number of questions:

- cataloguing of all proteins synthesized in different cell types;

- clarification of the nature of the influence of age, environmental conditions and disease on synthesized by the cell proteins;

- clarification of the functions of the identified proteins;

- study of the interaction of different proteins with other proteins inside the cell and in the extracellular space.

Conclusions. A huge amount of information that has become available as a result of successful completion of the project "human Genome", should play a special role in the development of methods of diagnostics of hereditary diseases, such as type I diabetes, cystic fibrosis, Alzheimer's and Parkinson's. Earlier diseases of this class are diagnosed only after the onset of clinical symptoms; the latest methods to allow the onset of clinical signs to identify groups at risk and susceptible to such diseases.

References:

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