Description
A computer system GeneExpress2 provides an access to the information resources developed at the Institute of Cytology and Genetics. It is designed for solving topical tasks of molecular biology and genetics, gene engineering, as well as for working out biomedical and biotechnological applications and for training specialists in modern biology and bioinformatics.

The system follows the latest trends in information and program resources concerned with gene expression regulation, spatial structures and functions of biological macromolecules (DNA, RNA, and proteins). GeneExpress 2 applies advanced Internet technologies for integration of and navigation over integrated resources. The architecture of GeneExpress 2 provides large information capacity and supplies users with necessary supportive tools such as a developed system of interactive assistance, comments and demonstration samples. More than 40 databases and over 20 program packages are integrated in GeneExpress 2. Each package contains up to several dozens of programs for identification and analysis of functional elements of biological macromolecules and fundamental molecular-genetic processes. The GeneExpress2 system is organized with regard to the natural hierarchical levels of molecular-genetic systems of organisms and has four large sections: (1) DNA Level, (2) RNA Level, (3) Protein Level, and (4) GeneNet Level. GeneExpress2 belongs to the class of super-scale information resources in bioinformatics and has no analogs worldwide. Not only analogs of the whole system, but also those of most of its constituents are unavailable abroad.

Technical appraisal and economic benefits
System GeneExpress 2 involves a huge variety of computer resources, in particular databases on gene and genomic sequences, structural-functional organization of genes and mechanisms of their regulation, structural organization of RNA, primary and spatial protein structures,
ways of transmitting signals and gene nets controlling biochemical, physiological processes, growth and development of organisms, as well programs for analyzing genomic DNA of various functional specificity, identification of genes and prediction of their functions, estimating the effect of mutations on the function of gene regulatory areas, analyzing and modeling the structural-functional organization of RNA and proteins, molecular interactions between them, studying the effect of mutations on the structure and function of DNA, RNA, and proteins, programs for analyzing and modeling gene nets and metabolic processes. These resources support reliable and precise solving of bioinformatics tasks, exceeding in this respect the existing systems.

**Application areas**
Molecular biology, genetics, gene engineering, biotechnology, pharmacology, medicine, bioinformatics, training students and specialists.

**Development stage**
The system is ready for application. It can be used by pharmacological companies, research institutes and universities for comprehensive analysis of experimental data in cytogenetics, molecular biology, molecular genetics, molecular medicine, etc.; for computer analysis aimed at revealing molecular-genetic defects; for studying and modeling the mechanisms of genetic pathologies; for molecular design of pharmacological preparations, etc.

**Patent situation**
RF patents.

**Commercial offers**
License agreement.

**Estimated cost**
To be negotiated.

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