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ABSTRACTS

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45	WHAT EVOLUTION OF RYE SUBTELOMERIC REPEATS CAN TELL US ABOUT CEREALS SPECIATIONS? <i>Gunbin K.V., Levitsky V.G., Vershinin A.V.</i>	61
46	IMAGEJ ADDON FOR 2D ELECTROPHORESIS GEL ANALYSIS <i>Gurkov A.N., Kondratyeva E.M., Bedulina D.S.</i>	62
47	CONTROLLED VOCABULARIES AND INFORMATION TABLES FOR THE KNOWLEDGE BASE ON EPIGENETIC CONTROL OF HUMAN EMBRYONIC STEM CELLS <i>Ignatieva E.V.</i>	63
48	FUNCTIONAL CHARACTERISTICS OF HUMAN GENES CONTAINING LOW LEVEL OF PROMOTER POLYMORPHISM REVEALED FROM THE 1000 GENOMES PROJECT DATASET <i>Ignatieva E.V., Levitsky V.G., Kolchanov N.A.</i>	64
49	THE KNOWLEDGE BASE ON MOLECULAR GENETICS MECHANISMS CONTROLLING HUMAN LIPID METABOLISM <i>Ignatieva E.V.</i>	65
50	METHOD TO PREDICT THE PERCENTAGE OF CELL TYPES IN HUMAN BLOOD <i>Igolkina A.A., Samsonova M.G.</i>	66
51	ANALYSIS OF A TOMATO INTROGRESSION LINE, IL8-3, WITH INCREASED BRUX CONTENT USING THE WHOLE-GENOME SEQUENCE <i>Ikeda H., Kanayama Y.</i>	67
52	MATHEMATICAL MODELING OF LUNG INFECTION AND ANTIBIOTIC RESISTANCE <i>Ilin A., Islamov R., Kasenov S., Nurseitov D., Serovajsky S.</i>	68
53	FEATURES OF INTERACTIONS BETWEEN miR-1273 FAMILY AND mRNA OF TARGET GENES <i>Ivashchenko A.T., Berillo O.A., Pyrkova A.Y., Niyazova R.E.</i>	69
54	THE FEATURES OF BINDING SITES OF miR-619-5P, miR-5095, miR-5096 AND miR-5585-3P IN THE mRNAs OF HUMAN GENES <i>Ivashchenko A.T., Berillo O.A., Pyrkova A.Y., Niyazova R.E., Atambayeva S.A.</i>	70
55	MATHEMATICAL MODEL FOR SUBGENOMIC HEPATITIS C VIRUS REPLICATION: IMPACT OF DRUG RESISTANCE EMERGENCE ON LONG-TERM KINETICS OF NS3 PROTEASE INHIBITORS ACTION <i>Ivanisenko N., Mishchenko E., Akberdin I., Demenkov P., Kozlov K., Todorov D., Gursky V.V., Samsonova M.G., Samsonov A.M., Clausnitzer D., Kaderali L., Kolchanov N.A., Ivanisenko V.A.</i>	71
56	MOLECULAR MECHANISMS OF INTERACTION OF TUMOR NECROSIS FACTOR WITH TNF-BINDING ORTOPOXVIRAL PROTEINS C _{rmB} <i>Ivanisenko N.V., Tregubchak T.V., Saik O.V., Ivanisenko V.A., Shchelkunov S.N.</i>	72
57	NEW VERSIONS OF THE PDBSITE DATABASE AND PDBSITE SCAN TOOL: PREDICTION OF FUNCTIONAL SITES IN THE PROTEIN 3D STRUCTURE <i>Ivanisenko T.V., Demenkov P.S., Ivanisenko N.V., Ivanisenko V.A.</i>	73
58	METABOLOME AND TRANSCRIPTOME ANALYSES OF A TOMATO INTROGRESSION LINE CONTAINING A <i>SOLANUM PENNELLII</i> CHROMOSOME SEGMENT <i>Kanayama Y., Ikeda H.</i>	74
59	EVOLUTION OF RUBISCO ENCODING GENES IN PLANTS AND ITS IMPLICATIONS FOR RUBISCO ENGINEERING IN CROPS <i>Kapralov M.V., Whitney S.M.</i>	75

THE FEATURES OF BINDING SITES OF miR-619-5P, miR-5095, miR-5096 AND miR-5585-3P IN THE mRNAs OF HUMAN GENES

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Key words: miRNA, mRNA, miR-619, binding site, human

Motivation and Aim: The actions of miRNAs on the cell cycle, apoptosis, differentiation, growth and development in animals have been shown. Connections between miRNA expression and the development of various diseases has been established. miRNA concentrations change in cancer and cardiovascular diseases. Metabolic disturbances necessarily change miRNA concentrations in cells. It is possible to normalize some processes using miRNAs. The aforementioned roles do not encompass the full list of the biological processes in which miRNAs participate, which proves the importance of their biological functions. The connections between the majority of miRNAs and their target genes will remain unknown.

Methods and Algorithms: MirTarget program defines the localization of miRNA binding sites in the 5'UTRs, CDSs and 3'UTRs of the mRNAs; it calculates the free energy of hybridization (ΔG , kJ/mole) and the ratio $\Delta G/\Delta G_m$ (%), where ΔG_m equal to the free energy of miRNA binding with completely complementary nucleotide sequence. The binding sites of miRNAs with mRNAs were selected with $\Delta G/\Delta G_m$ ratio of 90% or more.

Results: The binding of 2,563 human miRNAs with the mRNAs of 12,175 human genes was calculated. It was established that miR-619-5p, miR-5095, miR-5096 and miR-5585-3p bind with high affinity to the mRNAs of the 1215, 832, 725 and 655 genes, respectively.

miR-619-5p has 1811 binding sites on 1215 target mRNAs. Of these, 1772 miR-619-5p binding sites are located in 3'UTRs, 26 sites are located in 5'UTRs and 13 sites are located in CDSs. The mRNAs of 197 genes have completely complementary binding sites for miR-619-5p ($\Delta G/\Delta G_m = 100\%$). The mRNAs of 27 genes have four binding sites. Seven genes have five binding sites, and the mRNAs of the *CATAD1*, *ICAIL*, *GK5*, *POLH* and *PRR11* genes have six binding sites, respectively. The mRNAs of the *OPA3* and *CYP20A1* genes have eight and ten binding sites, respectively. All of these sites are located in 3'UTRs. miR-5096 has 997 binding sites on 832 target mRNAs. Of these, 984 miR-5096 binding sites are located in 3'UTRs, nine sites are located in 5'UTRs and four sites are located in CDSs. The mRNAs of 42 genes have completely complementary binding sites for miR-5096 ($\Delta G/\Delta G_m = 100\%$). The mRNAs of the *IP09* gene have four binding sites. The *PRR11* gene have five binding sites. The mRNAs of the *OPA3* and *CYP20A1* genes have six and eleven miR-5096 binding sites, respectively. All of these sites are located in 3'UTRs. We found that 655 target gene mRNAs have 734 binding sites. Fourteen of these binding sites are located in 5'UTRs, eight sites are located in CDSs and 712 sites are located in 3'UTRs. The mRNAs of two genes have completely complementary binding sites for miR-5095. The mRNAs of the *OPA3*, and *SPN* genes each have four binding sites.

The mRNAs of 725 target gene have 844 binding sites for miR-5585-3p. Nine of these binding sites are located in 5'UTRs, two sites are located in CDSs and 833 sites are located in 3'UTRs. The mRNAs of the *CYP20A1* and *GPR155* genes each have four binding sites.

Conclusion: Studied miRNAs have binding sites in the 3'UTRs, CDSs and 5'UTRs. The mRNAs of many genes have multiple miR-619-5p, miR-5095, miR-5096 and miR-5585-3p binding sites. Groups of mRNAs with the ordering of the miR-619-5p, miR-5095, miR-5096 and miR-5585-3p binding sites were established.