# Nikolay A Kolchanov

List of Publications by Year
in descending order

| 138 | 3,948 | 201674 | 133252 |
|:---:|:---:|:---:|:---:|
| papers | citations | 27 | 59 |
| | | h-index | g-index |

| 140 | 140 | 140 | 4538 |
|:---:|:---:|:---:|:---:|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Databases on transcriptional regulation: TRANSFAC, TRRD and COMPEL. Nucleic Acids Research, 1998, 26, 362-367. | 14.5 | 1,345 |
| 2 | Can three-dimensional contacts in protein structures be predicted by analysis of correlated mutations?. Protein Engineering, Design and Selection, 1994, 7, 349-358. | 2.1 | 262 |
| 3 | TRANSFAC, TRRD and COMPEL: towards a federated database system on transcriptional regulation. Nucleic Acids Research, 1997, 25, 265-268. | 14.5 | 141 |
| 4 | Eukaryotic mRNAs encoding abundant and scarce proteins are statistically dissimilar in many structural features. FEBS Letters, 1998, 440, 351-355. | 2.8 | 97 |
| 5 | A compilation of composite regulatory elements affecting gene transcription in vertebrates. Nucleic Acids Research, 1995, 23, 4097-4103. | 14.5 | 96 |
| 6 | Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. BMC Genomics, 2014, 15, S11. | 2.8 | 75 |
| 7 | The role of alternative translation start sites in the generation of human protein diversity. Molecular Genetics and Genomics, 2005, 273, 491-496. | 2.1 | 61 |
| 8 | ANDSystem: an Associative Network Discovery System for automated literature mining in the field of biology. BMC Systems Biology, 2015, 9, S2. | 3.0 | 58 |
| 9 | uORFs, reinitiation and alternative translation start sites in human mRNAs. FEBS Letters, 2008, 582, 1293-1297. | 2.8 | 57 |
| 10 | Combined in silico/in vivo analysis of mechanisms providing for root apical meristem self-organization and maintenance. Annals of Botany, 2012, 110, 349-360. | 2.9 | 55 |
| 11 | An Experimental Verification of the Predicted Effects of Promoter TATA-Box Polymorphisms Associated with Human Diseases on Interactions between the TATA Boxes and TATA-Binding Protein. PLoS ONE, 2013, 8, e54626. | 2.5 | 55 |
| 12 | TATA box polymorphisms in human gene promoters and associated hereditary pathologies. Biochemistry (Moscow), 2009, 74, 117-129. | 1.5 | 54 |
| 13 | Isolation of prospective microalgal strains with high saturated fatty acid content for biofuel production. Algal Research, 2015, 12, 368-376. | 4.6 | 47 |
| 14 | AUG_hairpin: prediction of a downstream secondary structure influencing the recognition of a translation start site. BMC Bioinformatics, 2007, 8, 318. | 2.6 | 46 |
| 15 | A step-by-step model of TBP/TATA box binding allows predicting human hereditary diseases by single nucleotide polymorphism. Doklady Biochemistry and Biophysics, 2008, 419, 88-92. | 0.9 | 42 |
| 16 | The Mechanism by which TATA-Box Polymorphisms Associated with Human Hereditary Diseases Influence Interactions with the TATA-Binding Protein. Human Mutation, 2014, 35, 601-608. | 2.5 | 41 |
| 17 | Molecular analysis of the benthos microbial community in Zavarzin thermal spring (Uzon Caldera,) Tj ETQq1 1 0.784314 rgBT /Overloc | 2.8 | 39 |
| 18 | CRASP: a program for analysis of coordinated substitutions in multiple alignments of protein sequences. Nucleic Acids Research, 2004, 32, W64-W68. | 14.5 | 37 |

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|---|---------|-----|-----------|
| 19 | Effective transcription factor binding site prediction using a combination of optimization, a genetic algorithm and discriminant analysis to capture distant interactions. BMC Bioinformatics, 2007, 8, 481. | 2.6 | 35 |
| 20 | Time-course human urine proteomics in space-flight simulation experiments. BMC Genomics, 2014, 15, S2. | 2.8 | 35 |
| 21 | How to Use SNP_TATA_Comparator to Find a Significant Change in Gene Expression Caused by the Regulatory SNP of This Gene's Promoter via a Change in Affinity of the TATA-Binding Protein for This Promoter. BioMed Research International, 2015, 2015, 1-17. | 1.9 | 34 |
| 22 | Computational genomics at BGRSSB-2016: introductory note. BMC Genomics, 2016, 17, 996. | 2.8 | 33 |
| 23 | Point mutations within 663-666 bp of intron 6 of the human TDO2 gene, associated with a number of psychiatric disorders, damage the YY-1 transcription factor binding site. FEBS Letters, 1999, 462, 85-88. | 2.8 | 32 |
| 24 | Modification of cellulose as a promising direction in the design of new materials. Polymer Science - Series B, 2013, 55, 409-429. | 0.8 | 31 |
| 25 | Molecular evolution of cyclin proteins in animals and fungi. BMC Evolutionary Biology, 2011, 11, 224. | 3.2 | 30 |
| 26 | Combined experimental and computational approaches to study the regulatory elements in eukaryotic genes. Briefings in Bioinformatics, 2007, 8, 266-274. | 6.5 | 28 |
| 27 | Molecular evolution of the hyperthermophilic archaea of the Pyrococcus genus: analysis of adaptation to different environmental conditions. BMC Genomics, 2009, 10, 639. | 2.8 | 28 |
| 28 | Genetic basis of olfactory cognition: extremely high level of DNA sequence polymorphism in promoter regions of the human olfactory receptor genes revealed using the 1000 Genomes Project dataset. Frontiers in Psychology, 2014, 5, 247. | 2.1 | 28 |
| 29 | Impact of Terahertz Radiation on Stress-Sensitive Genes of E.Coli Cell. IEEE Transactions on Terahertz Science and Technology, 2016, 6, 435-441. | 3.1 | 28 |
| 30 | Transcription Regulatory Regions Database (TRRD): its status in 1999. Nucleic Acids Research, 1999, 27, 303-306. | 14.5 | 27 |
| 31 | Studying the non‐thermal effects of terahertz radiation on <i>E. coli</i>/pKatG‐GFP biosensor cells. Bioelectromagnetics, 2013, 34, 15-21. | 1.6 | 26 |
| 32 | Molecular association of pathogenetic contributors to pre-eclampsia (pre-eclampsia associome). BMC Systems Biology, 2015, 9, S4. | 3.0 | 25 |
| 33 | Obesity-related known and candidate SNP markers can significantly change affinity of TATA-binding protein for human gene promoters. BMC Genomics, 2015, 16, S5. | 2.8 | 24 |
| 34 | Somatic hypermutagenesis in immunoglobulin genes. III. Somatic mutations in the chicken light chain locus. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1996, 1306, 171-178. | 2.4 | 23 |
| 35 | Candidate SNP Markers of Familial and Sporadic Alzheimer's Diseases Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. Frontiers in Aging Neuroscience, 2017, 9, 231. | 3.4 | 23 |
| 36 | A strategy to eradicate well-developed Krebs-2 ascites in mice. Oncotarget, 2016, 7, 11580-11594. | 1.8 | 23 |

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|---|---------|-----|-----------|
| 37 | Candidate SNP markers of reproductive potential are predicted by a significant change in the affinity of TATA-binding protein for human gene promoters. BMC Genomics, 2018, 19, 0. | 2.8 | 22 |
| 38 | A fast genetic algorithm for RNA secondary structure analysis. Russian Chemical Bulletin, 2002, 51, 1135-1144. | 1.5 | 21 |
| 39 | Insights into pathophysiology of dystropy through the analysis of gene networks: an example of bronchial asthma and tuberculosis. Immunogenetics, 2014, 66, 457-465. | 2.4 | 21 |
| 40 | Candidate SNP Markers of Chronopathologies Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. BioMed Research International, 2016, 2016, 1-21. | 1.9 | 21 |
| 41 | NotI flanking sequences: a tool for gene discovery and verification of the human genome. Nucleic Acids Research, 2002, 30, 3163-3170. | 14.5 | 20 |
| 42 | Extraction of quantitative characteristics describing wheat leaf pubescence with a novel image-processing technique. Planta, 2012, 236, 1943-1954. | 3.2 | 20 |
| 43 | Introductory note for BGRSSB-2014 special issue. Journal of Bioinformatics and Computational Biology, 2015, 13, 1502001. | 0.8 | 20 |
| 44 | Candidate SNP markers of aggressiveness-related complications and comorbidities of genetic diseases are predicted by a significant change in the affinity of TATA-binding protein for human gene promoters. BMC Genomics, 2016, 17, 995. | 2.8 | 20 |
| 45 | SNPS IN THE HIV-1 TATA BOX AND THE AIDS PANDEMIC. Journal of Bioinformatics and Computational Biology, 2010, 08, 607-625. | 0.8 | 19 |
| 46 | SNP TATA Comparator genomewide landmarks for preventive personalized medicine. Frontiers in Bioscience - Scholar, 2017, 9, 276-306. | 2.1 | 19 |
| 47 | Genome analysis identifies the mutant genes for common industrial Silverblue and Hedlund white coat colours in American mink. Scientific Reports, 2019, 9, 4581. | 3.3 | 19 |
| 48 | NPRD: Nucleosome Positioning Region Database. Nucleic Acids Research, 2004, 33, D67-D70. | 14.5 | 17 |
| 49 | INTRODUCTORY NOTE FOR BGRS-2012 SPECIAL ISSUE. Journal of Bioinformatics and Computational Biology, 2013, 11, 1302001. | 0.8 | 17 |
| 50 | Permanent proteins in the urine of healthy humans during the Mars-500 experiment. Journal of Bioinformatics and Computational Biology, 2015, 13, 1540001. | 0.8 | 17 |
| 51 | Candidate SNP Markers of Gender-Biased Autoimmune Complications of Monogenic Diseases Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. Frontiers in Immunology, 2016, 7, 130. | 4.8 | 17 |
| 52 | Gene expression profiling of tumor-initiating stem cells from mouse Krebs-2 carcinoma using a novel marker of poorly differentiated cells. Oncotarget, 2017, 8, 9425-9441. | 1.8 | 17 |
| 53 | Properties of internalization factors contributing to the uptake of extracellular DNA into tumor-initiating stem cells of mouse Krebs-2 cell line. Stem Cell Research and Therapy, 2016, 7, 76. | 5.5 | 16 |
| 54 | Potential of microalgae as a source of bioenergy. Catalysis in Industry, 2012, 4, 202-208. | 0.7 | 15 |

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| 55 | A compendium of human genes regulating feeding behavior and body weight, its functional characterization and identification of GWAS genes involved in brain-specific PPI network. BMC Genetics, 2016, 17, 158. | 2.7 | 15 |
| 56 | ARGO: a web system for the detection of degenerate motifs and large-scale recognition of eukaryotic promoters. Nucleic Acids Research, 2005, 33, W417-W422. | 14.5 | 14 |
| 57 | Natural Selection Equally Supports the Human Tendencies in Subordination and Domination: A Genome-Wide Study With in silico Confirmation and in vivo Validation in Mice. Frontiers in Genetics, 2019, 10, 73. | 2.3 | 14 |
| 58 | Pluripotency gene network dynamics: System views from parametric analysis. PLoS ONE, 2018, 13, e0194464. | 2.5 | 14 |
| 59 | A new form of Miscanthus (Chinese silver grass, Miscanthus sinensisâ€"Andersson) as a promising source of cellulosic biomass. Advances in Bioscience and Biotechnology (Print), 2010, 01, 167-170. | 0.7 | 14 |
| 60 | Recognition of interferon-inducible sites, promoters, and enhancers. BMC Bioinformatics, 2007, 8, 56. | 2.6 | 13 |
| 61 | SUBCELLULAR LOCALIZATION CHARTS: A NEW VISUAL METHODOLOGY FOR THE SEMI-AUTOMATIC LOCALIZATION OF PROTEIN-RELATED DATA SETS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340005. | 0.8 | 13 |
| 62 | Human Genes Encoding Transcription Factors and Chromatin-Modifying Proteins Have Low Levels of Promoter Polymorphism: A Study of 1000 Genomes Project Data. International Journal of Genomics, 2015, 2015, 1-15. | 1.6 | 13 |
| 63 | A New Stochastic Model for Subgenomic Hepatitis C Virus Replication Considers Drug Resistant Mutants. PLoS ONE, 2014, 9, e91502. | 2.5 | 12 |
| 64 | Efficacy of a new cancer treatment strategy based on eradication of tumor-initiating stem cells in a mouse model of Krebs-2 solid adenocarcinoma. Oncotarget, 2018, 9, 28486-28499. | 1.8 | 12 |
| 65 | HOW MULTIPLE AUXIN RESPONSIVE ELEMENTS MAY INTERACT IN PLANT PROMOTERS: A REVERSE PROBLEM SOLUTION. Journal of Bioinformatics and Computational Biology, 2013, 11, 1340011. | 0.8 | 11 |
| 66 | Editorial â€" Bioinformatics development at the BGRSSB conference series: 10th anniversary. Journal of Bioinformatics and Computational Biology, 2017, 15, 1702001. | 0.8 | 11 |
| 67 | Cancer Stem Cells: Emergent Nature of Tumor Emergency. Frontiers in Genetics, 2018, 9, 544. | 2.3 | 11 |
| 68 | Visualization and analysis of a cardio vascular disease- and MUPP1-related biological network combining text mining and data warehouse approaches. Journal of Integrative Bioinformatics, 2010, 7, 148. | 1.5 | 11 |
| 69 | Generating Programs for Predicting the Activity of Functional Sites. Journal of Computational Biology, 1997, 4, 83-90. | 1.6 | 10 |
| 70 | Visualization and Analysis of a Cardio Vascular Diseaseand MUPP1-related Biological Network combining Text Mining and Data Warehouse Approaches. Journal of Integrative Bioinformatics, 2010, 7, . | 1.5 | 10 |
| 71 | Specific/nonspecific binding of TBP to promoter DNA of the auxin response factor genes in plants correlated with ARFs function on gene transcription (activator/repressor). Doklady Biochemistry and Biophysics, 2010, 433, 191-196. | 0.9 | 10 |
| 72 | Modeling evolution of spatially distributed bacterial communities: a simulation with the haploid evolutionary constructor. BMC Evolutionary Biology, 2015, 15, S3. | 3.2 | 9 |

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| 73 | Dynamic properties of SOD1 mutants can predict survival time of patients carrying familial amyotrophic lateral sclerosis. Journal of Biomolecular Structure and Dynamics, 2017, 35, 645-656. | 3.5 | 9 |
| 74 | Domestication Explains Two-Thirds of Differential-Gene-Expression Variance between Domestic and Wild Animals; The Remaining One-Third Reflects Intraspecific and Interspecific Variation. Animals, 2021, 11, 2667. | 2.3 | 9 |
| 75 | INTERACTION OF RECOMBINANT TATA-BINDING PROTEIN WITH MAMMALS GENES PROMOTER TATA. Ecological Genetics, 2007, 5, 44-49. | 0.5 | 9 |
| 76 | Stress Reactivity, Susceptibility to Hypertension, and Differential Expression of Genes in Hypertensive Compared to Normotensive Patients. International Journal of Molecular Sciences, 2022, 23, 2835. | 4.1 | 9 |
| 77 | Bioinformatical and experimental approaches to investigation of transcription factor binding sites in vertebrate genes. Biochemistry (Moscow), 2007, 72, 1187-1193. | 1.5 | 8 |
| 78 | Mathematical model of auxin distribution in the plant root. Russian Journal of Developmental Biology, 2007, 38, 374-382. | 0.5 | 8 |
| 79 | Program complex SNP-MED for analysis of single-nucleotide polymorphism (SNP) effects on the function of genes associated with socially significant diseases. Russian Journal of Genetics: Applied Research, 2014, 4, 159-167. | 0.4 | 8 |
| 80 | Prediction of tissue-specific effects of gene knockout on apoptosis in different anatomical structures of human brain. BMC Genomics, 2015, 16, S3. | 2.8 | 8 |
| 81 | Apoptosis Gene Network: Description in the GeneNet and TRRD Databases. Annals of the New York Academy of Sciences, 2003, 1010, 16-18. | 3.8 | 7 |
| 82 | Genomics at Belyaev conference â€" 2017. BMC Genomics, 2018, 19, 79. | 2.8 | 7 |
| 83 | Candidate SNP Markers of Atherogenesis Significantly Shifting the Affinity of TATA-Binding Protein for Human Gene Promoters Show Stabilizing Natural Selection as a Sum of Neutral Drift Accelerating Atherogenesis and Directional Natural Selection Slowing It. International Journal of Molecular Sciences, 2020, 21, 1045. | 4.1 | 7 |
| 84 | A Bioinformatics Model of Human Diseases on the Basis of Differentially Expressed Genes (of Domestic) Tj ETQq0 0 0 rgBT /Overlock 10 Changes. International Journal of Molecular Sciences, 2021, 22, 2346. | 4.1 | 7 |
| 85 | Novel genes identified by manual annotation and microarray expression analysis in the pancreas. Genomics, 2006, 88, 752-761. | 2.9 | 6 |
| 86 | Molecular dynamics simulations of the Nip7 proteins from the marine deep- and shallow-water Pyrococcus species. BMC Structural Biology, 2014, 14, 23. | 2.3 | 6 |
| 87 | Identification of the relationship between the variability of the expression of signaling pathway genes in the human brain and the affinity of TATA-binding protein to their promoters. Russian Journal of Genetics: Applied Research, 2015, 5, 626-634. | 0.4 | 6 |
| 88 | Mechanical Behavior of Cells within a Cell-Based Model of Wheat Leaf Growth. Frontiers in Plant Science, 2016, 7, 1878. | 3.6 | 6 |
| 89 | Introduction to the 9th Young Scientists School on Systems Biology and Bioinformatics (SBBâ€™2017). Journal of Bioinformatics and Computational Biology, 2018, 16, 1802001. | 0.8 | 6 |
| 90 | Simulation of coevolution in community by using the "Evolutionary Constructor" program. In Silico Biology, 2007, 7, 261-75. | 0.9 | 6 |

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| 91 | SitEx: a computer system for analysis of projections of protein functional sites on eukaryotic genes. Nucleic Acids Research, 2012, 40, D278-D283. | 14.5 | 5 |
| 92 | Computer modeling of genome complexity variation trends in prokaryotic communities under varying habitat conditions. Ecological Modelling, 2012, 224, 124-129. | 2.5 | 5 |
| 93 | Neurometabolic Effect of Altaian Fungus *Ganoderma lucidum* (Reishi Mushroom) in Rats Under Moderate Alcohol Consumption. Alcoholism: Clinical and Experimental Research, 2015, 39, 1128-1136. | 2.4 | 5 |
| 94 | Application of reproductive technologies to improve dairy cattle genomic selection. Russian Journal of Genetics: Applied Research, 2016, 6, 321-329. | 0.4 | 5 |
| 95 | Argo_CUDA: Exhaustive GPU based approach for motif discovery in large DNA datasets. Journal of Bioinformatics and Computational Biology, 2018, 16, 1740012. | 0.8 | 5 |
| 96 | Web-Based Computational Tools for the Prediction and Analysis of Posttranslational Modifications of Proteins. Methods in Molecular Biology, 2019, 1934, 1-20. | 0.9 | 5 |
| 97 | Genomics research at Bioinformatics of Genome Regulation and Structure Systems Biology (BGRSSB) conferences in Novosibirsk. BMC Genomics, 2019, 20, 322. | 2.8 | 5 |
| 98 | The Phylogeny of Class B Flavoprotein Monooxygenases and the Origin of the YUCCA Protein Family. Plants, 2020, 9, 1092. | 3.5 | 5 |
| 99 | Disruptive Selection of Human Immunostimulatory and Immunosuppressive Genes Both Provokes and Prevents Rheumatoid Arthritis, Respectively, as a Self-Domestication Syndrome. Frontiers in Genetics, 2021, 12, 610774. | 2.3 | 5 |
| 100 | GeneNet database: description and modeling of gene networks. In Silico Biology, 2002, 2, 97-110. | 0.9 | 5 |
| 101 | Study of a one-dimensional model, accounting for cell division, of regulation of the renewing zone size in a biological tissue. Journal of Applied and Industrial Mathematics, 2011, 5, 601-611. | 0.4 | 4 |
| 102 | A new variety of Chinese silver grass (Miscanthus sinensis Anderss.): A promising source of cellulose-containing raw material. Russian Journal of Genetics: Applied Research, 2011, 1, 29-32. | 0.4 | 4 |
| 103 | Computer analysis of metagenomic data—Pediction of quantitative value of specific activity of proteins. Doklady Biochemistry and Biophysics, 2012, 443, 76-80. | 0.9 | 4 |
| 104 | Association of anxiety level with polymorphic variants of serotonin transporter gene in Russians and Tuvinians. Russian Journal of Genetics: Applied Research, 2015, 5, 656-665. | 0.4 | 4 |
| 105 | Characterization of biological peculiarities of the radioprotective activity of double-stranded RNA isolated from Saccharomyces Ņerevisiae. International Journal of Radiation Biology, 2020, 96, 1173-1191. | 1.8 | 4 |
| 106 | Unannotated single nucleotide polymorphisms in the TATA box of erythropoiesis genes show in vitro positive involvements in cognitive and mental disorders. BMC Medical Genetics, 2020, 21, 165. | 2.1 | 4 |
| 107 | Meta-Analysis of Transcriptome Data Detected New Potential Players in Response to Dioxin Exposure in Humans. International Journal of Molecular Sciences, 2020, 21, 7858. | 4.1 | 4 |
| 108 | Computer analysis of the relation between hydrogen bond stability in SOD1 mutants and the survival time of amyotrophic lateral sclerosis patients. Journal of Molecular Graphics and Modelling, 2022, 110, 108026. | 2.4 | 4 |

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|---|---------|-----|-----------|
| 109 | The Importance of Changes to Microrna in the Evolution of Homo Neanderthalensis and Homo Denisova. Archaeology, Ethnology and Anthropology of Eurasia, 2012, 40, 22-30. | 0.2 | 3 |
| 110 | Research on the biodiversity of Western Siberia microalgae for third-generation biofuel production processes. Russian Journal of Genetics: Applied Research, 2013, 3, 487-492. | 0.4 | 3 |
| 111 | Abundances of microRNAs in human cells can be estimated as a function of the abundances of YRHB and RHHK tetranucleotides in these microRNAs as an ill-posed inverse problem solution. Frontiers in Genetics, 2013, 4, 122. | 2.3 | 3 |
| 112 | The evolution of Homo sapiens denisova and Homo sapiens neanderthalensis miRNA targeting genes in the prenatal and postnatal brain. BMC Genomics, 2015, 16, S4. | 2.8 | 3 |
| 113 | Identification of residues of the archaeal RNA-binding Nip7 proteins specific to environmental conditions. Journal of Bioinformatics and Computational Biology, 2017, 15, 1650036. | 0.8 | 3 |
| 114 | Search for new binding sites for the transcriptional factor SF-1 by the SITECON method: Experimental verification and analysis of regulatory regions of orthologous genes. Doklady Biochemistry and Biophysics, 2007, 415, 165-169. | 0.9 | 2 |
| 115 | The abundance of microRNA in Arabidopsis thaliana correlates with the presence of tetranucleotides WRHW and DRYD in their sequences. Doklady Biochemistry and Biophysics, 2008, 420, 150-154. | 0.9 | 2 |
| 116 | Genetic algorithm and optimized weight matrix application for peroxisome proliferator response elements recognition: Prerequisites of accuracy growth for wide genome research. Intelligent Data Analysis, 2008, 12, 513-526. | 0.9 | 2 |
| 117 | Development of computational methods to search for FoxA transcription factor binding sites, their experimental verification and application to the analysis of ChIP-seq data. Doklady Biochemistry and Biophysics, 2011, 436, 12-15. | 0.9 | 2 |
| 118 | Important role of hydrophobic interactions in high-pressure adaptation of proteins. Doklady Biochemistry and Biophysics, 2011, 438, 113-116. | 0.9 | 2 |
| 119 | Effect of TATA Box polymorphisms in human β-globin gene promoter associated with β-thalassemia on interaction with TATA-binding protein. Russian Journal of Genetics: Applied Research, 2011, 1, 183-188. | 0.4 | 2 |
| 120 | Contextual DNA features significant for the DNA damage by the 193-nm ultraviolet laser beam. Doklady Biochemistry and Biophysics, 2012, 447, 267-272. | 0.9 | 2 |
| 121 | High temperature and pressure influence the interdomain orientation of Nip7 proteins from P. abyssi and P. furiosus: MD simulations. Journal of Biomolecular Structure and Dynamics, 2018, 36, 68-82. | 3.5 | 2 |
| 122 | Leave or Stay: Simulating Motility and Fitness of Microorganisms in Dynamic Aquatic Ecosystems. Biology, 2021, 10, 1019. | 2.8 | 2 |
| 123 | Single amino acid substitutions producing instability of globular proteins. Calculation of their frequencies in the entire mutational spectra of the α- and β-subunits of human hemoglobin. Journal of Molecular Evolution, 1988, 27, 154-162. | 1.8 | 1 |
| 124 | Adaptive evolution of genes of archaea belonging to the genus Pyrococcus associated with adaptation to life under high-pressure conditions. Doklady Biochemistry and Biophysics, 2009, 425, 91-93. | 0.9 | 1 |
| 125 | Acute immune response to the intranasal application of nanoparticles of SiO2 (Tarkosil 25) in mice of two strains. Nanotechnologies in Russia, 2011, 6, 763-772. | 0.7 | 1 |
| 126 | Change of TATA-binding protein affinity to oligonucleotides corresponding to TATA boxes in human gene promoters bearing polymorphisms associated with hereditary diseases. Russian Journal of Genetics: Applied Research, 2012, 2, 1-6. | 0.4 | 1 |

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|---|---------|-----|-----------|
| 127 | Computerized analysis of the relationship between allergenicity of microorganisms and their habitats. Russian Journal of Genetics: Applied Research, 2013, 3, 171-175. | 0.4 | 1 |
| 128 | Effect of flanking sequences on the accuracy of the recognition of transcription factor binding sites. Russian Journal of Genetics: Applied Research, 2015, 5, 322-329. | 0.4 | 1 |
| 129 | A quantitative method for determination of <scp>PPDK</scp> concentration in miscanthus leaves. GCB Bioenergy, 2017, 9, 262-269. | 5.6 | 1 |
| 130 | Spatial heterogeneity promotes antagonistic evolutionary scenarios in microbial community explained by ecological stratification: a simulation study. Ecological Modelling, 2019, 399, 66-76. | 2.5 | 1 |
| 131 | The evolution of key cell cycle proteins correlates with an increase in the complexity of eukaryotic organisms. Doklady Biochemistry and Biophysics, 2009, 426, 147-151. | 0.9 | 0 |
| 132 | Possibility spaces and evolution. Paleontological Journal, 2010, 44, 1491-1499. | 0.5 | 0 |
| 133 | From Published Expression and Phenotype Data to Structured Knowledge: The Arabidopsis Gene Net Supplementary Database and Its Applications. Lecture Notes in Computer Science, 2011, , 101-120. | 1.3 | 0 |
| 134 | Modeling of plant embryo morphodynamics at early developmental stages. Russian Journal of Genetics: Applied Research, 2013, 3, 176-183. | 0.4 | 0 |
| 135 | Mechanisms of the formation and propagation of sociobiological interactions: a computer simulation study. Russian Journal of Genetics: Applied Research, 2015, 5, 672-678. | 0.4 | 0 |
| 136 | Influence of serotonin transporter allele polymorphism on individual characteristics of cerebral hemodynamics in humans under the â€œStopâ€"Signalâ€•experimental paradigm. Russian Journal of Genetics: Applied Research, 2015, 5, 666-671. | 0.4 | 0 |
| 137 | Initiation Factors â˜†. , 2018, , . | | 0 |
| 138 | GPU Based Composite Elements Discovery In Large DNADatasets. , 2020, , . | | 0 |