

Yuriy L. Orlov

List of Publications by Year in descending order

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Version: 2024-02-01

129
papers

9,071
citations

218677

26
h-index

43889

91
g-index

143
all docs

143
docs citations

143
times ranked

14352
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. <i>Cell</i> , 2008, 133, 1106-1117. | 28.9 | 2,279 |
| 2 | An oestrogen-receptor- β -bound human chromatin interactome. <i>Nature</i> , 2009, 462, 58-64. | 27.8 | 1,537 |
| 3 | Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98. | 28.9 | 1,096 |
| 4 | Whole-Genome Mapping of Histone H3 Lys4 and 27 Trimethylations Reveals Distinct Genomic Compartments in Human Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2007, 1, 286-298. | 11.1 | 536 |
| 5 | Global mapping of c-Myc binding sites and target gene networks in human B cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17834-17839. | 7.1 | 462 |
| 6 | The Nuclear Receptor Nr5a2 Can Replace Oct4 in the Reprogramming of Murine Somatic Cells to Pluripotent Cells. <i>Cell Stem Cell</i> , 2010, 6, 167-174. | 11.1 | 424 |
| 7 | A genome-wide RNAi screen reveals determinants of human embryonic stem cell identity. <i>Nature</i> , 2010, 468, 316-320. | 27.8 | 407 |
| 8 | Tbx3 improves the germ-line competency of induced pluripotent stem cells. <i>Nature</i> , 2010, 463, 1096-1100. | 27.8 | 261 |
| 9 | Eset partners with Oct4 to restrict extraembryonic trophoblast lineage potential in embryonic stem cells. <i>Genes and Development</i> , 2009, 23, 2507-2520. | 5.9 | 218 |
| 10 | Non-coding RNAs and Their Roles in Stress Response in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 301-312. | 6.9 | 150 |
| 11 | Integrative model of genomic factors for determining binding site selection by estrogen receptor α . <i>Molecular Systems Biology</i> , 2010, 6, 456. | 7.2 | 139 |
| 12 | <i>FRIZZY PANICLE</i> Drives Supernumerary Spikelets in Bread Wheat. <i>Plant Physiology</i> , 2014, 167, 189-199. | 4.8 | 131 |
| 13 | Graded Nodal/Activin Signaling Titrates Conversion of Quantitative Phospho-Smad2 Levels into Qualitative Embryonic Stem Cell Fate Decisions. <i>PLoS Genetics</i> , 2011, 7, e1002130. | 3.5 | 80 |
| 14 | Complexity: an internet resource for analysis of DNA sequence complexity. <i>Nucleic Acids Research</i> , 2004, 32, W628-W633. | 14.5 | 73 |
| 15 | Integrative analysis of the human cis -antisense gene pairs, miRNAs and their transcription regulation patterns. <i>Nucleic Acids Research</i> , 2010, 38, 534-547. | 14.5 | 69 |
| 16 | Repeats, longevity and the sources of mtDNA deletions: evidence from Δ -deletional spectra TM . <i>Trends in Genetics</i> , 2010, 26, 340-343. | 6.7 | 48 |
| 17 | Metabolic model of central carbon and energy metabolisms of growing <i>Arabidopsis thaliana</i> in relation to sucrose translocation. <i>BMC Plant Biology</i> , 2016, 16, 262. | 3.6 | 43 |
| 18 | Dysfunction in Ribosomal Gene Expression in the Hypothalamus and Hippocampus following Chronic Social Defeat Stress in Male Mice as Revealed by RNA-Seq. <i>Neural Plasticity</i> , 2016, 2016, 1-6. | 2.2 | 42 |

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|----|--|-----|-----------|
| 19 | Transcription Factors for the Modulation of Pluripotency and Reprogramming. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 237-244. | 1.1 | 40 |
| 20 | Genome Wide Analysis Reveals Zic3 Interaction with Distal Regulatory Elements of Stage Specific Developmental Genes in Zebrafish. PLoS Genetics, 2013, 9, e1003852. | 3.5 | 35 |
| 21 | Association of AMD-like retinopathy development with an Alzheimer's disease metabolic pathway in OXYS rats. Biogerontology, 2013, 14, 753-762. | 3.9 | 34 |
| 22 | Computational genomics at BGRSSB-2016: introductory note. BMC Genomics, 2016, 17, 996. | 2.8 | 33 |
| 23 | Genomic landscape of CpG rich elements in human. BMC Evolutionary Biology, 2017, 17, 19. | 3.2 | 33 |
| 24 | Computational models in genetics at BGRSSB-2016: introductory note. BMC Genetics, 2016, 17, 155. | 2.7 | 30 |
| 25 | Serotonergic genes in the development of anxiety/depression-like state and pathology of aggressive behavior in male mice: RNA-seq data. Molecular Biology, 2017, 51, 251-262. | 1.3 | 29 |
| 26 | Blurring of High-Resolution Data Shows that the Effect of Intrinsic Nucleosome Occupancy on Transcription Factor Binding is Mostly Regional, Not Local. PLoS Computational Biology, 2010, 6, e1000649. | 3.2 | 27 |
| 27 | Association Analysis of Genetic Variants with Type 2 Diabetes in a Mongolian Population in China. Journal of Diabetes Research, 2015, 2015, 1-7. | 2.3 | 27 |
| 28 | Editorial: Bioinformatics of Genome Regulation and Systems Biology. Frontiers in Genetics, 2020, 11, 625. | 2.3 | 27 |
| 29 | Computational Errors and Biases in Short Read Next Generation Sequencing. Journal of Proteomics and Bioinformatics, 2017, 10, . | 0.4 | 26 |
| 30 | Comparative Expression Analysis of Stress-Inducible Candidate Genes in Response to Cold and Drought in Tea Plant [Camellia sinensis (L.) Kuntze]. Frontiers in Genetics, 2020, 11, 611283. | 2.3 | 25 |
| 31 | Clinical aspects of TP53 gene inactivation in diffuse large B-cell lymphoma. BMC Medical Genomics, 2019, 12, 35. | 1.5 | 24 |
| 32 | STATISTICAL MEASURES OF THE STRUCTURE OF GENOMIC SEQUENCES: ENTROPY, COMPLEXITY, AND POSITION INFORMATION. Journal of Bioinformatics and Computational Biology, 2006, 04, 523-536. | 0.8 | 21 |
| 33 | Heterogeneity of Brain Ribosomal Genes Expression Following Positive Fighting Experience in Male Mice as Revealed by RNA-Seq. Molecular Neurobiology, 2018, 55, 390-401. | 4.0 | 21 |
| 34 | Medical Genetics, Genomics and Bioinformatics Aid in Understanding Molecular Mechanisms of Human Diseases. International Journal of Molecular Sciences, 2021, 22, 9962. | 4.1 | 21 |
| 35 | Introductory note for BGRSSB-2014 special issue. Journal of Bioinformatics and Computational Biology, 2015, 13, 1502001. | 0.8 | 20 |
| 36 | Changes in the expression of dopaminergic genes in brain structures of male mice exposed to chronic social defeat Stress: An RNA-seq study. Molecular Biology, 2016, 50, 161-163. | 1.3 | 18 |

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|----|--|-----|-----------|
| 37 | Physiological, biochemical and genetic responses of Caucasian tea (<i>Camellia sinensis</i> (L.) Kuntze) genotypes under cold and frost stress. <i>PeerJ</i> , 2020, 8, e9787. | 2.0 | 18 |
| 38 | Quality assessment of the Affymetrix U133A&B probesets by target sequence mapping and expression data analysis. <i>In Silico Biology</i> , 2007, 7, 241-60. | 0.9 | 18 |
| 39 | INTRODUCTORY NOTE FOR BGRS-2012 SPECIAL ISSUE. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1302001. | 0.8 | 17 |
| 40 | Computer Analysis of Glioma Transcriptome Profiling: Alternative Splicing Events. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, . | 1.5 | 17 |
| 41 | Evolutionary biology at BGRSSB-2016. <i>BMC Evolutionary Biology</i> , 2017, 17, 21. | 3.2 | 15 |
| 42 | Recent Trends in Cancer Genomics and Bioinformatics Tools Development. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12146. | 4.1 | 15 |
| 43 | Computational plant bioscience at BGRSSB-2016: introductory note. <i>BMC Plant Biology</i> , 2016, 16, 243. | 3.6 | 14 |
| 44 | The differences in brain stem transcriptional profiling in hypertensive ISIAH and normotensive WAG rats. <i>BMC Genomics</i> , 2019, 20, 297. | 2.8 | 14 |
| 45 | Evolutionary Biology at Belyaev Conference “ 2017. <i>BMC Evolutionary Biology</i> , 2017, 17, 260. | 3.2 | 12 |
| 46 | Bioinformatics Methods in Medical Genetics and Genomics. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6224. | 4.1 | 12 |
| 47 | Editorial “ Bioinformatics development at the BGRSSB conference series: 10th anniversary. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1702001. | 0.8 | 11 |
| 48 | Computer analysis of colocalization of the TFs™ binding sites in the genome according to the ChIP-seq data. <i>Russian Journal of Genetics: Applied Research</i> , 2017, 7, 513-522. | 0.4 | 11 |
| 49 | Medical genomics research at BGRS-2018. <i>BMC Medical Genomics</i> , 2019, 12, 36. | 1.5 | 11 |
| 50 | SITEVIDEO: a computer system for functional site analysis and recognition. Investigation of the human splice sites. <i>Bioinformatics</i> , 1993, 9, 617-627. | 4.1 | 10 |
| 51 | Regulatory single nucleotide polymorphisms at the beginning of intron 2 of the human KRAS gene. <i>Journal of Biosciences</i> , 2015, 40, 873-883. | 1.1 | 10 |
| 52 | Biological Big Bytes: Integrative Analysis of Large Biological Datasets. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, . | 1.5 | 10 |
| 53 | Plant Biology at Belyaev Conference “ 2017. <i>BMC Plant Biology</i> , 2017, 17, 257. | 3.6 | 9 |
| 54 | Medical genomics at Belyaev Conference “ 2017. <i>BMC Medical Genomics</i> , 2018, 11, 11. | 1.5 | 9 |

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|----|--|-----|-----------|
| 55 | Plant biology research at BGRS-2018. BMC Plant Biology, 2019, 19, 56. | 3.6 | 9 |
| 56 | Regulatory genomics: Combined experimental and computational approaches. Russian Journal of Genetics, 2015, 51, 334-352. | 0.6 | 8 |
| 57 | Computer genomics research at the bioinformatics conference series in Novosibirsk. BMC Genomics, 2019, 20, 537. | 2.8 | 8 |
| 58 | Analysis of differential gene expression by RNA-seq data in brain areas of laboratory animals. Journal of Integrative Bioinformatics, 2016, 13, 1-15. | 1.5 | 7 |
| 59 | Neuroscience researches at Belyaev conference-2017. BMC Neuroscience, 2018, 19, 14. | 1.9 | 7 |
| 60 | Genomics at Belyaev conference " 2017. BMC Genomics, 2018, 19, 79. | 2.8 | 7 |
| 61 | Bioinformatics Applications to Reveal Molecular Mechanisms of Gene Expression Regulation in Model Organisms. International Journal of Molecular Sciences, 2021, 22, 11973. | 4.1 | 7 |
| 62 | Aggressive behavior: Genetic and physiological mechanisms. Russian Journal of Genetics: Applied Research, 2015, 5, 413-429. | 0.4 | 6 |
| 63 | Introduction to the 9th Young Scientists School on Systems Biology and Bioinformatics (SBB™2017). Journal of Bioinformatics and Computational Biology, 2018, 16, 1802001. | 0.8 | 6 |
| 64 | Novel read density distribution score shows possible aligner artefacts, when mapping a single chromosome. BMC Genomics, 2018, 19, 92. | 2.8 | 6 |
| 65 | Genomics and Systems Biology at the "Century of Human Population Genetics" conference. BMC Genomics, 2020, 21, 592. | 2.8 | 6 |
| 66 | Statistical estimates of multiple transcription factors binding in the model plant genomes based on CHIP-seq data. Journal of Integrative Bioinformatics, 2022, 19, . | 1.5 | 6 |
| 67 | Computer and Statistical Analysis of Transcription Factor Binding and Chromatin Modifications by CHIP-seq data in Embryonic Stem Cell. Journal of Integrative Bioinformatics, 2012, 9, 88-100. | 1.5 | 5 |
| 68 | Cognitive Architecture of Collective Intelligence Based on Social Evidence. Procedia Computer Science, 2016, 88, 475-481. | 2.0 | 5 |
| 69 | Genomics research at Bioinformatics of Genome Regulation and Structure Systems Biology (BGRSSB) conferences in Novosibirsk. BMC Genomics, 2019, 20, 322. | 2.8 | 5 |
| 70 | Evolutionary biology and biodiversity research at BGRS-2018. BMC Evolutionary Biology, 2019, 19, 43. | 3.2 | 5 |
| 71 | Novel ChIP-seq simulating program with superior versatility: isChIP. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 5 |
| 72 | Role of apoptosis genes in aggression revealed using combined analysis of ANDSystem gene networks, expression and genomic data in grey rats with aggressive behavior. Vavilovskii Zhurnal Genetiki i Selektzii, 2017, 21, 911-919. | 1.1 | 5 |

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|----|---|-----|-----------|
| 73 | Editorial: Bioinformatics of Genome Regulation, Volume II. <i>Frontiers in Genetics</i> , 2021, 12, 795257. | 2.3 | 5 |
| 74 | Computational analysis and modeling of genome-scale avidity distribution of transcription factor binding sites in chip-pet experiments. <i>Genome Informatics</i> , 2007, 19, 83-94. | 0.4 | 5 |
| 75 | Analysis of differential gene expression by RNA-seq data in brain areas of laboratory animals. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 292. | 1.5 | 5 |
| 76 | Title is missing!. <i>Molecular Biology</i> , 2001, 35, 810-817. | 1.3 | 4 |
| 77 | Genome-wide statistical analysis of multiple transcription factor binding sites obtained by chip-seq technologies. , 2009, , . | | 4 |
| 78 | Medical genomics at the Systems Biology and Bioinformatics (SBB-2019) school. <i>BMC Medical Genomics</i> , 2020, 13, 127. | 1.5 | 4 |
| 79 | Molecular characteristic of treatment failure clinical isolates of <i>Leishmania major</i> . <i>PeerJ</i> , 2021, 9, e10969. | 2.0 | 4 |
| 80 | Biodistribution of 10B in Glioma Orthotopic Xenograft Mouse Model after Injection of L-para-Boronophenylalanine and Sodium Borocaptate. <i>Biomedicines</i> , 2021, 9, 722. | 3.2 | 4 |
| 81 | Genetic polymorphisms and related risk factors of ischemic stroke in a Mongolian population in China. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2017, 21, 581-587. | 1.1 | 4 |
| 82 | The rs78378222 prevalence and the copy loss of the protective allele A in the tumor tissue of diffuse large B-cell lymphoma. <i>PeerJ</i> , 2020, 8, e10335. | 2.0 | 4 |
| 83 | Clioblastoma gene network reconstruction and ontology analysis by online bioinformatics tools. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, . | 1.5 | 4 |
| 84 | Computer and statistical analysis of transcription factor binding and chromatin modifications by CHIP-seq data in embryonic stem cell. <i>Journal of Integrative Bioinformatics</i> , 2012, 9, 211. | 1.5 | 4 |
| 85 | Editorial: High-Throughput Sequencing-Based Investigation of Chronic Disease Markers and Mechanisms. <i>Frontiers in Genetics</i> , 0, 13, . | 2.3 | 4 |
| 86 | Plant Biology and Biotechnology: Focus on Genomics and Bioinformatics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6759. | 4.1 | 4 |
| 87 | Development of new SSR markers for homoeologous WFZP gene loci based on the study of the structure and location of microsatellites in gene-rich regions of chromosomes 2AS, 2BS, and 2DS in bread wheat. <i>Russian Journal of Genetics: Applied Research</i> , 2016, 6, 330-337. | 0.4 | 3 |
| 88 | Bioinformatics research at SBB-2019. <i>BMC Bioinformatics</i> , 2020, 21, 366. | 2.6 | 3 |
| 89 | Microbiology research at the systems biology and bioinformatics - 2019 (SBB-2019) school. <i>BMC Microbiology</i> , 2020, 20, 348. | 3.3 | 3 |
| 90 | Genetics research at the "Centenary of human population genetics" conference and SBB-2019. <i>BMC Genetics</i> , 2020, 21, 109. | 2.7 | 3 |

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|-----|--|-----|-----------|
| 91 | 5th International Scientific Conference of "Plant Genetics, Genomics, Bioinformatics, and Biotechnology" (24-29 June 2019, Novosibirsk, Russia). Journal of Food Quality and Hazards Control, 0, , . | 0.1 | 3 |
| 92 | Challenges of in vitro conservation of <i>Đ</i> itrus germplasm resources. Vavilovskii Zhurnal Genetiki i Seleksii, 2019, 23, 24-28. | 1.1 | 3 |
| 93 | Integrated Computer Analysis of Genomic Sequencing Data Based on ICGenomics Tool. Advances in Intelligent Systems and Computing, 2020, , 154-164. | 0.6 | 3 |
| 94 | Life: Computational Genomics Applications in Life Sciences. Life, 2021, 11, 1211. | 2.4 | 3 |
| 95 | Editorial: Association Between Individuals'™ Genomic Ancestry and Variation in Disease Susceptibility. Frontiers in Genetics, 2022, 13, 831320. | 2.3 | 3 |
| 96 | Population Analysis of <i>Diospyros lotus</i> in the Northwestern Caucasus Based on Leaf Morphology and Multilocus DNA Markers. International Journal of Molecular Sciences, 2022, 23, 2192. | 4.1 | 3 |
| 97 | Translation efficiency in yeasts correlates with nucleosome formation in promoters. Journal of Biomolecular Structure and Dynamics, 2013, 31, 96-102. | 3.5 | 2 |
| 98 | Medical genetics studies at BGRS conference series. BMC Medical Genetics, 2019, 20, 50. | 2.1 | 2 |
| 99 | Testing Safety of Genetically Modified Products of Rice: Case Study on Sprague Dawley Rats. Russian Journal of Genetics, 2019, 55, 962-968. | 0.6 | 2 |
| 100 | In situ dissecting the evolution of gene duplication with different histone modification patterns based on high-throughput data analysis in <i>Arabidopsis thaliana</i> . PeerJ, 2021, 9, e10426. | 2.0 | 2 |
| 101 | COMPUTATIONAL ANALYSIS AND MODELING OF GENOME-SCALE AVIDITY DISTRIBUTION OF TRANSCRIPTION FACTOR BINDING SITES IN CHIP-PET EXPERIMENTS. , 2007, , . | | 2 |
| 102 | Program for analysis of genome distribution of chromosome contacts in cell nucleus by the data obtained using ChIA-PET and Hi-C technologies. Program Systems Theory and Applications, 2017, 8, 219-242. | 0.1 | 2 |
| 103 | Entropy Analysis of Protein Sequences Reveals a Hierarchical Organization. Entropy, 2021, 23, 1647. | 2.2 | 2 |
| 104 | Statistical analysis of DNA sequences containing nucleosome positioning sites. Biophysics (Russian) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 | 0.7 | 1 |
| 105 | APMA Database for Affymetrix Target Sequences Mapping, Quality Assessment and Expression Data Mining. Lecture Notes in Computer Science, 2007, , 166-177. | 1.3 | 1 |
| 106 | Relatively conserved common short sequences in transcription factor binding sites and miRNA. Russian Journal of Genetics: Applied Research, 2012, 2, 238-242. | 0.4 | 1 |
| 107 | RatDNA: A database on microarray studies of rats bearing genes associated with age-related diseases. Russian Journal of Genetics: Applied Research, 2013, 3, 163-170. | 0.4 | 1 |
| 108 | Genome features and GC content in prokaryotic genomes in connection with environmental evolution. Paleontological Journal, 2013, 47, 1056-1060. | 0.5 | 1 |

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|-----|---|-----|-----------|
| 109 | Flanking monomer repeats determine decreased context complexity of single nucleotide polymorphism sites in the human genome. Russian Journal of Genetics: Applied Research, 2016, 6, 809-815. | 0.4 | 1 |
| 110 | Medical genetics studies at the SBB-2019 and MGNGS-2019 conferences. BMC Medical Genetics, 2020, 21, 186. | 2.1 | 1 |
| 111 | Estimation of the probability of daily fluctuations of incidence of COVID-19 according to official data. PeerJ, 2021, 9, e11049. | 2.0 | 1 |
| 112 | Computer tools for analysis of transcriptomics data: program complex ExpGene. Program Systems Theory and Applications, 2017, 8, 45-68. | 0.1 | 1 |
| 113 | CpG islandsâ€™ clustering uncovers early development genes in the human genome. Computer Science and Information Systems, 2018, 15, 473-485. | 1.0 | 1 |
| 114 | The Geographic Information System of the Russian Ministry of Health. Smart Innovation, Systems and Technologies, 2020, , 403-411. | 0.6 | 1 |
| 115 | Bioinformatics of genome regulation and structure â€™ 2020 papers collection. Journal of Integrative Bioinformatics, 2020, 17, . | 1.5 | 1 |
| 116 | Editorial: Bioinformatics of Genome Regulation, Volume I. Frontiers in Genetics, 2021, 12, 803273. | 2.3 | 1 |
| 117 | Software for Analysis of Gene Regulatory Sequences by Knowledge Discovery Methods. , 2006, , 491-498. | | 1 |
| 118 | Interstitial telomeric repeats as markers of evolutionary changes in the mammalian karyotype: Human chromosome 2. Biophysics (Russian Federation), 2006, 51, 535-540. | 0.7 | 0 |
| 119 | INTRODUCTION TO THE SELECTED PAPERS OF BGRS'06. Journal of Bioinformatics and Computational Biology, 2007, 05, vii-viii. | 0.8 | 0 |
| 120 | Computer analysis of the data on gene expression in brain cells obtained by microarray tests and high-throughput sequencing. Russian Journal of Genetics: Applied Research, 2014, 4, 259-266. | 0.4 | 0 |
| 121 | Transcriptome profiles of gene expression in brain of male mice with repeated experience of aggression as revealed by RNA-Seq. European Neuropsychopharmacology, 2016, 26, S179. | 0.7 | 0 |
| 122 | The evolution of CpG islands by tandem duplications. Russian Journal of Genetics: Applied Research, 2017, 7, 538-549. | 0.4 | 0 |
| 123 | Differential alternative splicing in brain regions of rats selected for aggressive behavior. Molecular Biology, 2017, 51, 759-768. | 1.3 | 0 |
| 124 | Triple Haplotypes of the TP53 Gene in Patients with Diffuse Small B-Cell Lymphoma. Russian Journal of Genetics, 2019, 55, 1564-1568. | 0.6 | 0 |
| 125 | Consideration of pathogenicity of nsSNVs in CDKN2A gene, as a new tumor marker for leukemia, using bioinformatics methods. , 2020, , . | | 0 |
| 126 | Reconstruction of Dementia Gene Network Using Online Bioinformatics Tools. , 2020, , . | | 0 |

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|-----|--|-----|-----------|
| 127 | Statistical problems of clusters of transcription factor binding sites in plant genomes. , 2020, , . | | 0 |
| 128 | RNA Polymrase II gene expression in clinical Leishmania major isolates with no-response-to-drug pattern. Biointerface Research in Applied Chemistry, 2019, 9, 4126-4130. | 1.0 | 0 |
| 129 | VMM: A Variable Memory Markov Model Prediction of Nucleosome Formation Sites. , 2006, , 85-95. | | 0 |