

Yuriy L. Orlov

List of Publications by Year in descending order

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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	Editorial: Association Between Individuals' Genomic Ancestry and Variation in Disease Susceptibility. <i>Frontiers in Genetics</i> , 2022, 13, 831320.	2.3	3
2	Population Analysis of <i>Diospyros lotus</i> in the Northwestern Caucasus Based on Leaf Morphology and Multilocus DNA Markers. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2192.	4.1	3
3	Statistical estimates of multiple transcription factors binding in the model plant genomes based on ChIP-seq data. <i>Journal of Integrative Bioinformatics</i> , 2022, 19, .	1.5	6
4	Plant Biology and Biotechnology: Focus on Genomics and Bioinformatics. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6759.	4.1	4
5	Novel ChIP-seq simulating program with superior versatility: isChIP. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	5
6	In situ dissecting the evolution of gene duplication with different histone modification patterns based on high-throughput data analysis in <i>Arabidopsis thaliana</i> . <i>PeerJ</i> , 2021, 9, e10426.	2.0	2
7	Molecular characteristic of treatment failure clinical isolates of <i>Leishmania major</i> . <i>PeerJ</i> , 2021, 9, e10969.	2.0	4
8	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
9	Estimation of the probability of daily fluctuations of incidence of COVID-19 according to official data. <i>PeerJ</i> , 2021, 9, e11049.	2.0	1
10	Medical Genetics, Genomics and Bioinformatics Aid in Understanding Molecular Mechanisms of Human Diseases. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9962.	4.1	21
11	Bioinformatics Applications to Reveal Molecular Mechanisms of Gene Expression Regulation in Model Organisms. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11973.	4.1	7
12	Editorial: Bioinformatics of Genome Regulation, Volume II. <i>Frontiers in Genetics</i> , 2021, 12, 795257.	2.3	5
13	Glioblastoma gene network reconstruction and ontology analysis by online bioinformatics tools. <i>Journal of Integrative Bioinformatics</i> , 2021, 18, .	1.5	4
14	Life: Computational Genomics Applications in Life Sciences. <i>Life</i> , 2021, 11, 1211.	2.4	3
15	Recent Trends in Cancer Genomics and Bioinformatics Tools Development. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12146.	4.1	15
16	Editorial: Bioinformatics of Genome Regulation, Volume I. <i>Frontiers in Genetics</i> , 2021, 12, 803273.	2.3	1
17	Entropy Analysis of Protein Sequences Reveals a Hierarchical Organization. <i>Entropy</i> , 2021, 23, 1647.	2.2	2
18	Bioinformatics research at SBB-2019. <i>BMC Bioinformatics</i> , 2020, 21, 366.	2.6	3

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19	Consideration of pathogenicity of nsSNVs in CDKN2A gene, as a new tumor marker for leukemia, using bioinformatics methods. , 2020, , .		0
20	Medical genomics at the Systems Biology and Bioinformatics (SBB-2019) school. BMC Medical Genomics, 2020, 13, 127.	1.5	4
21	Reconstruction of Dementia Gene Network Using Online Bioinformatics Tools. , 2020, , .		0
22	Editorial: Bioinformatics of Genome Regulation and Systems Biology. Frontiers in Genetics, 2020, 11, 625.	2.3	27
23	Statistical problems of clusters of transcription factor binding sites in plant genomes. , 2020, , .		0
24	Medical genetics studies at the SBB-2019 and MGNGS-2019 conferences. BMC Medical Genetics, 2020, 21, 186.	2.1	1
25	Bioinformatics Methods in Medical Genetics and Genomics. International Journal of Molecular Sciences, 2020, 21, 6224.	4.1	12
26	Genomics and Systems Biology at the "Centenary of Human Population Genetics" conference. BMC Genomics, 2020, 21, 592.	2.8	6
27	Microbiology research at the systems biology and bioinformatics - 2019 (SBB-2019) school. BMC Microbiology, 2020, 20, 348.	3.3	3
28	Comparative Expression Analysis of Stress-Inducible Candidate Genes in Response to Cold and Drought in Tea Plant [<i>Camellia sinensis</i> (L.) Kuntze]. Frontiers in Genetics, 2020, 11, 611283.	2.3	25
29	Genetics research at the "Centenary of human population genetics" conference and SBB-2019. BMC Genetics, 2020, 21, 109.	2.7	3
30	The rs78378222 prevalence and the copy loss of the protective allele A in the tumor tissue of diffuse large B-cell lymphoma. PeerJ, 2020, 8, e10335.	2.0	4
31	Physiological, biochemical and genetic responses of Caucasian tea (<i>Camellia sinensis</i> (L.) Kuntze) genotypes under cold and frost stress. PeerJ, 2020, 8, e9787.	2.0	18
32	The Geographic Information System of the Russian Ministry of Health. Smart Innovation, Systems and Technologies, 2020, , 403-411.	0.6	1
33	Bioinformatics of genome regulation and structure "2020 papers collection. Journal of Integrative Bioinformatics, 2020, 17, .	1.5	1
34	Integrated Computer Analysis of Genomic Sequencing Data Based on ICGenomics Tool. Advances in Intelligent Systems and Computing, 2020, , 154-164.	0.6	3
35	Computer genomics research at the bioinformatics conference series in Novosibirsk. BMC Genomics, 2019, 20, 537.	2.8	8
36	Medical genetics studies at BGRS conference series. BMC Medical Genetics, 2019, 20, 50.	2.1	2

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37	Medical genomics research at BGRS-2018. BMC Medical Genomics, 2019, 12, 36.	1.5	11
38	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
39	Genomics research at Bioinformatics of Genome Regulation and Structure Systems Biology (BGRSSB) conferences in Novosibirsk. BMC Genomics, 2019, 20, 322.	2.8	5
40	The differences in brain stem transcriptional profiling in hypertensive ISIAH and normotensive WAG rats. BMC Genomics, 2019, 20, 297.	2.8	14
41	Clinical aspects of TP53 gene inactivation in diffuse large B-cell lymphoma. BMC Medical Genomics, 2019, 12, 35.	1.5	24
42	Evolutionary biology and biodiversity research at BGRS-2018. BMC Evolutionary Biology, 2019, 19, 43.	3.2	5
43	Plant biology research at BGRS-2018. BMC Plant Biology, 2019, 19, 56.	3.6	9
44	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
45	Challenges of in vitro conservation of <i>Diptera</i> germplasm resources. Vavilovskii Zhurnal Genetiki i Seleksii, 2019, 23, 24-28.	1.1	3
46	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
47	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
48	Novel read density distribution score shows possible aligner artefacts, when mapping a single chromosome. BMC Genomics, 2018, 19, 92.	2.8	6
49	Neuroscience researches at Belyaev conference-2017. BMC Neuroscience, 2018, 19, 14.	1.9	7
50	Medical genomics at Belyaev Conference “ 2017. BMC Medical Genomics, 2018, 11, 11.	1.5	9
51	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
52	Genomics at Belyaev conference “ 2017. BMC Genomics, 2018, 19, 79.	2.8	7
53	CpG islands™ clustering uncovers early development genes in the human genome. Computer Science and Information Systems, 2018, 15, 473-485.	1.0	1
54	Editorial “ Bioinformatics development at the BGRSSB conference series: 10th anniversary. Journal of Bioinformatics and Computational Biology, 2017, 15, 1702001.	0.8	11

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55	Serotonergic genes in the development of anxiety/depression-like state and pathology of aggressive behavior in male mice: RNA-seq data. <i>Molecular Biology</i> , 2017, 51, 251-262.	1.3	29
56	Genomic landscape of CpG rich elements in human. <i>BMC Evolutionary Biology</i> , 2017, 17, 19.	3.2	33
57	The evolution of CpG islands by tandem duplications. <i>Russian Journal of Genetics: Applied Research</i> , 2017, 7, 538-549.	0.4	0
58	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
59	Non-coding RNAs and Their Roles in Stress Response in Plants. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 301-312.	6.9	150
60	Differential alternative splicing in brain regions of rats selected for aggressive behavior. <i>Molecular Biology</i> , 2017, 51, 759-768.	1.3	0
61	Computer Analysis of Glioma Transcriptome Profiling: Alternative Splicing Events. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	17
62	Evolutionary biology at BGRSSB-2016. <i>BMC Evolutionary Biology</i> , 2017, 17, 21.	3.2	15
63	Biological Big Bytes: Integrative Analysis of Large Biological Datasets. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.5	10
64	Evolutionary Biology at Belyaev Conference “ 2017. <i>BMC Evolutionary Biology</i> , 2017, 17, 260.	3.2	12
65	Plant Biology at Belyaev Conference “ 2017. <i>BMC Plant Biology</i> , 2017, 17, 257.	3.6	9
66	Computational Errors and Biases in Short Read Next Generation Sequencing. <i>Journal of Proteomics and Bioinformatics</i> , 2017, 10, .	0.4	26
67	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
68	Role of apoptosis genes in aggression revealed using combined analysis of ANDSystem gene networks, expression and genomic data in grey rats with aggressive behavior. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2017, 21, 911-919.	1.1	5
69	Computer tools for analysis of transcriptomics data: program complex ExpGene. <i>Program Systems Theory and Applications</i> , 2017, 8, 45-68.	0.1	1
70	Program for analysis of genome distribution of chromosome contacts in cell nucleus by the data obtained using ChIA-PET and Hi-C technologies. <i>Program Systems Theory and Applications</i> , 2017, 8, 219-242.	0.1	2
71	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
72	Flanking monomer repeats determine decreased context complexity of single nucleotide polymorphism sites in the human genome. <i>Russian Journal of Genetics: Applied Research</i> , 2016, 6, 809-815.	0.4	1

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73	Changes in the expression of dopaminergic genes in brain structures of male mice exposed to chronic social defeat Stress: An RNA-seq study. <i>Molecular Biology</i> , 2016, 50, 161-163.	1.3	18
74	Cognitive Architecture of Collective Intelligence Based on Social Evidence. <i>Procedia Computer Science</i> , 2016, 88, 475-481.	2.0	5
75	Transcriptome profiles of gene expression in brain of male mice with repeated experience of aggression as revealed by RNA-Seq. <i>European Neuropsychopharmacology</i> , 2016, 26, S179.	0.7	0
76	Analysis of differential gene expression by RNA-seq data in brain areas of laboratory animals. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 1-15.	1.5	7
77	Computational models in genetics at BGRSSB-2016: introductory note. <i>BMC Genetics</i> , 2016, 17, 155.	2.7	30
78	Computational genomics at BGRSSB-2016: introductory note. <i>BMC Genomics</i> , 2016, 17, 996.	2.8	33
79	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
80	Computational plant bioscience at BGRSSB-2016: introductory note. <i>BMC Plant Biology</i> , 2016, 16, 243.	3.6	14
81	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
82	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
83	Association Analysis of Genetic Variants with Type 2 Diabetes in a Mongolian Population in China. <i>Journal of Diabetes Research</i> , 2015, 2015, 1-7.	2.3	27
84	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
85	Introductory note for BGRSSB-2014 special issue. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1502001.	0.8	20
86	Regulatory genomics: Combined experimental and computational approaches. <i>Russian Journal of Genetics</i> , 2015, 51, 334-352.	0.6	8
87	Aggressive behavior: Genetic and physiological mechanisms. <i>Russian Journal of Genetics: Applied Research</i> , 2015, 5, 413-429.	0.4	6
88	Computer analysis of the data on gene expression in brain cells obtained by microarray tests and high-throughput sequencing. <i>Russian Journal of Genetics: Applied Research</i> , 2014, 4, 259-266.	0.4	0
89	<i>FRIZZY PANICLE</i> Drives Supernumerary Spikelets in Bread Wheat. <i>Plant Physiology</i> , 2014, 167, 189-199.	4.8	131
90	Translation efficiency in yeasts correlates with nucleosome formation in promoters. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 96-102.	3.5	2

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91	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
92	Association of AMD-like retinopathy development with an Alzheimer's disease metabolic pathway in OXYS rats. Biogerontology, 2013, 14, 753-762.	3.9	34
93	Genome features and GC content in prokaryotic genomes in connection with environmental evolution. Paleontological Journal, 2013, 47, 1056-1060.	0.5	1
94	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
95	INTRODUCTORY NOTE FOR BGRS-2012 SPECIAL ISSUE. Journal of Bioinformatics and Computational Biology, 2013, 11, 1302001.	0.8	17
96	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
97	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	28.9	1,096
98	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
99	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, 211.	1.5	4
100	Graded Nodal/Activin Signaling Titrates Conversion of Quantitative Phospho-Smad2 Levels into Qualitative Embryonic Stem Cell Fate Decisions. PLoS Genetics, 2011, 7, e1002130.	3.5	80
101	Repeats, longevity and the sources of mtDNA deletions: evidence from Δ -deletional spectra. Trends in Genetics, 2010, 26, 340-343.	6.7	48
102	Tbx3 improves the germ-line competency of induced pluripotent stem cells. Nature, 2010, 463, 1096-1100.	27.8	261
103	A genome-wide RNAi screen reveals determinants of human embryonic stem cell identity. Nature, 2010, 468, 316-320.	27.8	407
104	Integrative analysis of the human cis-antisense gene pairs, miRNAs and their transcription regulation patterns. Nucleic Acids Research, 2010, 38, 534-547.	14.5	69
105	Integrative model of genomic factors for determining binding site selection by estrogen receptor. Molecular Systems Biology, 2010, 6, 456.	7.2	139
106	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
107	Transcription Factors for the Modulation of Pluripotency and Reprogramming. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 237-244.	1.1	40
108	The Nuclear Receptor Nr5a2 Can Replace Oct4 in the Reprogramming of Murine Somatic Cells to Pluripotent Cells. Cell Stem Cell, 2010, 6, 167-174.	11.1	424

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109	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
110	An oestrogen-receptor- β -bound human chromatin interactome. <i>Nature</i> , 2009, 462, 58-64.	27.8	1,537
111	Genome-wide statistical analysis of multiple transcription factor binding sites obtained by chip-seq technologies. , 2009, , .		4
112	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
113	INTRODUCTION TO THE SELECTED PAPERS OF BGRS'06. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, vii-viii.	0.8	0
114	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
115	APMA Database for Affymetrix Target Sequences Mapping, Quality Assessment and Expression Data Mining. <i>Lecture Notes in Computer Science</i> , 2007, , 166-177.	1.3	1
116	COMPUTATIONAL ANALYSIS AND MODELING OF GENOME-SCALE AVIDITY DISTRIBUTION OF TRANSCRIPTION FACTOR BINDING SITES IN CHIP-PET EXPERIMENTS. , 2007, , .		2
117	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
118	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
119	Interstitial telomeric repeats as markers of evolutionary changes in the mammalian karyotype: Human chromosome 2. <i>Biophysics (Russian Federation)</i> , 2006, 51, 535-540.	0.7	0
120	Statistical analysis of DNA sequences containing nucleosome positioning sites. <i>Biophysics (Russian)</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.7	1
121	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
122	STATISTICAL MEASURES OF THE STRUCTURE OF GENOMIC SEQUENCES: ENTROPY, COMPLEXITY, AND POSITION INFORMATION. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 523-536.	0.8	21
123	Software for Analysis of Gene Regulatory Sequences by Knowledge Discovery Methods. , 2006, , 491-498.		1
124	VMM: A Variable Memory Markov Model Prediction of Nucleosome Formation Sites. , 2006, , 85-95.		0
125	Complexity: an internet resource for analysis of DNA sequence complexity. <i>Nucleic Acids Research</i> , 2004, 32, W628-W633.	14.5	73
126	Title is missing!. <i>Molecular Biology</i> , 2001, 35, 810-817.	1.3	4

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127	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
128	5th International Scientific Conference of "Plant Genetics, Genomics, Bioinformatics, and Biotechnology" (24-29 June 2019, Novosibirsk, Russia). <i>Journal of Food Quality and Hazards Control</i> , 0, , .	0.1	3
129	Editorial: High-Throughput Sequencing-Based Investigation of Chronic Disease Markers and Mechanisms. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	4