

Vsevolod Y Makeev

List of Publications by Year in descending order

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96
papers

6,897
citations

172457

29
h-index

69250

77
g-index

103
all docs

103
docs citations

103
times ranked

13020
citing authors

#	ARTICLE	IF	CITATIONS
1	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
2	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	17.5	1,121
3	HOCOMOCO: towards a complete collection of transcription factor binding models for human and mouse via large-scale ChIP-Seq analysis. <i>Nucleic Acids Research</i> , 2018, 46, D252-D259.	14.5	660
4	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456
5	HOCOMOCO: expansion and enhancement of the collection of transcription factor binding sites models. <i>Nucleic Acids Research</i> , 2016, 44, D116-D125.	14.5	215
6	HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. <i>Nucleic Acids Research</i> , 2013, 41, D195-D202.	14.5	206
7	Exploring Massive, Genome Scale Datasets with the GenometriCorr Package. <i>PLoS Computational Biology</i> , 2012, 8, e1002529.	3.2	167
8	Homotypic Regulatory Clusters in <i>Drosophila</i> . <i>Genome Research</i> , 2003, 13, 579-588.	5.5	140
9	Deep and wide digging for binding motifs in ChIP-Seq data. <i>Bioinformatics</i> , 2010, 26, 2622-2623.	4.1	139
10	Identification of Proteins Associated with Murine Cytomegalovirus Virions. <i>Journal of Virology</i> , 2004, 78, 11187-11197.	3.4	138
11	GTRD: an integrated view of transcription regulation. <i>Nucleic Acids Research</i> , 2021, 49, D104-D111.	14.5	137
12	De novo sequencing and characterization of floral transcriptome in two species of buckwheat (<i>Fagopyrum</i>). <i>BMC Genomics</i> , 2011, 12, 30.	2.8	132
13	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
14	A Gibbs sampler for identification of symmetrically structured, spaced DNA motifs with improved estimation of the signal length. <i>Bioinformatics</i> , 2005, 21, 2240-2245.	4.1	95
15	Short fuzzy tandem repeats in genomic sequences, identification, and possible role in regulation of gene expression. <i>Bioinformatics</i> , 2006, 22, 676-684.	4.1	88
16	A Novel Model System for Design of Biomaterials Based on Recombinant Analogs of Spider Silk Proteins. <i>Journal of NeuroImmune Pharmacology</i> , 2009, 4, 17-27.	4.1	77
17	Extraction of Functional Binding Sites from Unique Regulatory Regions: The <i>Drosophila</i> Early Developmental Enhancers. <i>Genome Research</i> , 2002, 12, 470-481.	5.5	75
18	Distance preferences in the arrangement of binding motifs and hierarchical levels in organization of transcription regulatory information. <i>Nucleic Acids Research</i> , 2003, 31, 6016-6026.	14.5	74

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19	Intergenic, gene terminal, and intragenic CpG islands in the human genome. <i>BMC Genomics</i> , 2010, 11, 48.	2.8	67
20	FROM BINDING MOTIFS IN CHIP-SEQ DATA TO IMPROVED MODELS OF TRANSCRIPTION FACTOR BINDING SITES. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1340004.	0.8	58
21	The complete genome sequence of <i>Pantoea ananatis</i> AJ13355, an organism with great biotechnological potential. <i>Applied Microbiology and Biotechnology</i> , 2012, 93, 331-341.	3.6	55
22	Landscape of allele-specific transcription factor binding in the human genome. <i>Nature Communications</i> , 2021, 12, 2751.	12.8	55
23	Jaccard index based similarity measure to compare transcription factor binding site models. <i>Algorithms for Molecular Biology</i> , 2013, 8, 23.	1.2	53
24	Evolution of exon-intron structure and alternative splicing in fruit flies and malarial mosquito genomes. <i>Genome Research</i> , 2006, 16, 505-509.	5.5	43
25	Single-Cell Analyses of ESCs Reveal Alternative Pluripotent Cell States and Molecular Mechanisms that Control Self-Renewal. <i>Stem Cell Reports</i> , 2015, 5, 207-220.	4.8	40
26	Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study. <i>Genome Biology</i> , 2020, 21, 114.	8.8	39
27	Discovery of DNA motifs recognized by transcription factors through integration of different experimental sources. <i>Biophysics (Russian Federation)</i> , 2009, 54, 667-674.	0.7	38
28	DNA Segmentation Through the Bayesian Approach. <i>Journal of Computational Biology</i> , 2000, 7, 215-231.	1.6	36
29	Motif discovery and motif finding from genome-mapped DNase footprint data. <i>Bioinformatics</i> , 2009, 25, 2318-2325.	4.1	35
30	Application of experimentally verified transcription factor binding sites models for computational analysis of ChIP-Seq data. <i>BMC Genomics</i> , 2014, 15, 80.	2.8	31
31	Exact p-value calculation for heterotypic clusters of regulatory motifs and its application in computational annotation of cis-regulatory modules. <i>Algorithms for Molecular Biology</i> , 2007, 2, 13.	1.2	29
32	In vitro selection of optimal RelB/p52 DNA-binding motifs. <i>Biochemical and Biophysical Research Communications</i> , 2008, 365, 583-588.	2.1	29
33	Modified LDL Particles Activate Inflammatory Pathways in Monocyte-derived Macrophages: Transcriptome Analysis. <i>Current Pharmaceutical Design</i> , 2018, 24, 3143-3151.	1.9	29
34	PERFECTOS-APE - Predicting Regulatory Functional Effect of SNPs by Approximate P-value Estimation. , 2015, , .		28
35	Cyclical fate restriction: a new view of neural crest cell fate specification. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	20
36	Complete Genome Sequence of <i>Bifidobacterium longum</i> GT15: Identification and Characterization of Unique and Global Regulatory Genes. <i>Microbial Ecology</i> , 2015, 70, 819-834.	2.8	19

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37	Genome-wide map of human and mouse transcription factor binding sites aggregated from ChIP-Seq data. BMC Research Notes, 2018, 11, 756.	1.4	19
38	Evolution of transcription factor DNA binding sites. Gene, 2005, 347, 255-263.	2.2	18
39	Defensin-like peptides in wheat analyzed by whole-transcriptome sequencing: a focus on structural diversity and role in induced resistance. PeerJ, 2019, 7, e6125.	2.0	17
40	Search of periodicities in primary structure of biopolymers: a general Fourier approach. Bioinformatics, 1996, 12, 49-54.	4.1	16
41	Negative selection maintains transcription factor binding motifs in human cancer. BMC Genomics, 2016, 17, 395.	2.8	16
42	Signaling Pathways Potentially Responsible for Foam Cell Formation: Cholesterol Accumulation or Inflammatory Response? What is First?. International Journal of Molecular Sciences, 2020, 21, 2716.	4.1	16
43	Preservation of methylated CpG dinucleotides in human CpG islands. Biology Direct, 2016, 11, 11.	4.6	15
44	DNA Sequence Motif. Advances in Protein Chemistry and Structural Biology, 2013, 91, 135-171.	2.3	13
45	Heteroplasmic Variants of Mitochondrial DNA in Atherosclerotic Lesions of Human Aortic Intima. Biomolecules, 2019, 9, 455.	4.0	13
46	Extraction of Functional Binding Sites from Unique Regulatory Regions: The Drosophila Early Developmental Enhancers. Genome Research, 2002, 12, 470-481.	5.5	12
47	G and T Nucleotide Contents Show Specie-Invariant Negative Correlation for All Three Codon Positions. Journal of Biomolecular Structure and Dynamics, 1997, 14, 629-639.	3.5	11
48	Phenomenon of individual difference in human monocyte activation. Experimental and Molecular Pathology, 2015, 99, 151-154.	2.1	11
49	HDL activates expression of genes stimulating cholesterol efflux in human monocyte-derived macrophages. Experimental and Molecular Pathology, 2018, 105, 202-207.	2.1	11
50	The single nucleotide variant rs12722489 determines differential estrogen receptor binding and enhancer properties of an IL2RA intronic region. PLoS ONE, 2017, 12, e0172681.	2.5	10
51	Atomic hydration potentials using a Monte Carlo Reference State (MCRS) for protein solvation modeling. BMC Structural Biology, 2007, 7, 19.	2.3	9
52	CORECLUST: identification of the conserved CRM grammar together with prediction of gene regulation. Nucleic Acids Research, 2012, 40, e93-e93.	14.5	9
53	Segmentation of long genomic sequences into domains with homogeneous composition with BASIO software. Bioinformatics, 2001, 17, 1065-1066.	4.1	7
54	Segmentation of Heteropolymer Sequences Specifying Subsequences with Different Composition and Statistical Properties. Macromolecular Theory and Simulations, 2003, 12, 604-613.	1.4	7

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55	Complete Genome Sequence of <i>Bifidobacterium longum</i> GT15: Unique Genes for Russian Strains. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
56	ANANASTRA: annotation and enrichment analysis of allele-specific transcription factor binding at SNPs. <i>Nucleic Acids Research</i> , 2022, 50, W51-W56.	14.5	7
57	Upstream open reading frames regulate translation of the long isoform of SLAMF1 mRNA that encodes costimulatory receptor CD150. <i>Biochemistry (Moscow)</i> , 2014, 79, 1405-1411.	1.5	6
58	Chromosomal Translocations in NK-Cell Lymphomas Originate from Inter-Chromosomal Contacts of Active rDNA Clusters Possessing Hot Spots of DSBs. <i>Cancers</i> , 2021, 13, 3889.	3.7	6
59	EMPIRICAL POTENTIALS FOR ION BINDING IN PROTEINS. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 427-435.	0.8	5
60	A deeper look into transcription regulatory code by preferred pair distance templates for transcription factor binding sites. <i>Bioinformatics</i> , 2011, 27, 2621-2624.	4.1	5
61	The complete genome of the oil emulsifying strain <i>Thalassolituus oleivorans</i> K-188 from the Barents Sea. <i>Marine Genomics</i> , 2018, 37, 18-20.	1.1	4
62	Transcriptome analysis revealed inflammatory genes responsible for foam cell formation. <i>Atherosclerosis</i> , 2018, 275, e116.	0.8	4
63	Employing toxin-antitoxin genome markers for identification of <i>Bifidobacterium</i> and <i>Lactobacillus</i> strains in human metagenomes. <i>PeerJ</i> , 2019, 7, e6554.	2.0	4
64	Bayesian Approach to DNA Segmentation into Regions with Different Average Nucleotide Composition. <i>Lecture Notes in Computer Science</i> , 2001, , 57-73.	1.3	3
65	Left helix of polyproline II type and genesis of β -structures in spidroins 1 and 2 and their recombinant analogs. <i>Biophysics (Russian Federation)</i> , 2009, 54, 271-274.	0.7	3
66	Use of Primary Macrophages for Searching Novel Immunocorrectors. <i>Current Pharmaceutical Design</i> , 2017, 23, 915-920.	1.9	3
67	What Do Neighbors Tell About You: The Local Context of Cis-Regulatory Modules Complicates Prediction of Regulatory Variants. <i>Frontiers in Genetics</i> , 2019, 10, 1078.	2.3	3
68	A holistic view of mouse enhancer architectures reveals analogous pleiotropic effects and correlation with human disease. <i>BMC Genomics</i> , 2020, 21, 754.	2.8	3
69	The gene regulation knowledge commons: the action area of GREEKC. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194768.	1.9	3
70	Analysis of bacterial RM-systems through genome-scale analysis and related taxonomy issues. <i>In Silico Biology</i> , 2003, 3, 127-43.	0.9	3
71	Positional weight matrices have sufficient prediction power for analysis of noncoding variants. <i>F1000Research</i> , 0, 11, 33.	1.6	3
72	Regular location of exon starts in collagen I and VII genes with periods comparable to nucleosome repeat lengths. <i>Biophysics (Russian Federation)</i> , 2008, 53, 245-249.	0.7	2

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73	Preferred distances between transcription factor binding sites. Biophysics (Russian Federation), 2011, 56, 114-116.	0.7	2
74	Genes associated with cholesterol accumulation in macrophages (transcriptome analysis). Atherosclerosis, 2017, 263, e117.	0.8	2
75	Role of structural water for prediction of cation binding sites in apoproteins. Journal of Biomolecular Structure and Dynamics, 2018, 36, 221-232.	3.5	2
76	The third nucleotide of the Gly coding triplet remembers the periodicity of the collagen chain. FEBS Letters, 1995, 366, 33-36.	2.8	1
77	Relationship of micro-and minisatellites in the human genome. Biophysics (Russian Federation), 2006, 51, 581-586.	0.7	1
78	Using operonic gene pairs to set the threshold correlation coefficient for differently expressed genes. Biophysics (Russian Federation), 2011, 56, 1041-1042.	0.7	1
79	Identification of self-consistent modulons from bacterial microarray expression data with the help of structured regulon gene sets. Journal of Biomolecular Structure and Dynamics, 2013, 31, 115-124.	3.5	1
80	Assessing Ribosome Distribution Along Transcripts with Polarity Scores and Regression Slope Estimates. Methods in Molecular Biology, 2021, 2252, 269-294.	0.9	1
81	Positional weight matrices have sufficient prediction power for analysis of noncoding variants. F1000Research, 0, 11, 33.	1.6	1
82	Dynamics of nonlinear excitations in soft quasi-one-dimensional molecular chains. , 1991, , .		0
83	ClusterTree-RS: A binary tree algorithm identifying coregulated genes by clustering regulatory signals. Molecular Biology, 2006, 40, 465-473.	1.3	0
84	A model of evolution with constant selective pressure for regulatory DNA sites. BMC Evolutionary Biology, 2007, 7, 125.	3.2	0
85	Stochastic modeling of noninteracting probes in the protein structure space for construction of knowledge-based potentials for atom-atom interactions. Biophysics (Russian Federation), 2008, 53, 189-194.	0.7	0
86	The GC skew near Pol II start sites and its association with SP1-binding site variants. Biophysics (Russian Federation), 2010, 55, 901-907.	0.7	0
87	Correlations between clusters of protein-DNA binding sites and the binding experimental data allow predicting a structure of regulatory modules. Biophysics (Russian Federation), 2012, 57, 138-139.	0.7	0
88	Predictive biology using systems and integrative analysis and methods. Journal of Biomolecular Structure and Dynamics, 2013, 31, 1-3.	3.5	0
89	Mutual disposition of nucleosomes and exons differs from common genome pattern at DNA segments containing periodic nucleotide sequences. Biophysics (Russian Federation), 2013, 58, 851-853.	0.7	0
90	Prevalent function of genome loci associated with development of multiple sclerosis as revealed by GWAS and eQTL analysis. Russian Journal of Genetics, 2017, 53, 982-987.	0.6	0

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91	Transcriptome analysis of human macrophages reveals genes regulating cellular cholesterol efflux. <i>Atherosclerosis</i> , 2018, 275, e48.	0.8	0
92	Heteroplasmic Variants and Copy Number of Mitochondrial DNA in Different Types of Atherosclerotic Lesions of Human Aorta. <i>Atherosclerosis Supplements</i> , 2018, 32, 102.	1.2	0
93	A GENERALIZED HIDDEN MARKOV MODEL FOR PREDICTION OF CIS-REGULATORY MODULES IN EUKARYOTE GENOMES AND DESCRIPTION OF THEIR INTERNAL STRUCTURE. , 2012, , .		0
94	The channel in transporters is formed by residues that are rare in transmembrane helices. <i>In Silico Biology</i> , 2003, 3, 197-204.	0.9	0
95	Comparative Genomics and Evolution of Bacterial Regulatory Systems. , 2006, , 111-119.		0
96	Positional weight matrices have sufficient prediction power for analysis of noncoding variants. <i>F1000Research</i> , 0, 11, 33.	1.6	0