

Vsevolod Y Makeev

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2110347/publications.pdf>

Version: 2024-02-01

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	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
2	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
3	GTRD: an integrated view of transcription regulation. <i>Nucleic Acids Research</i> , 2021, 49, D104-D111.	14.5	137
4	Landscape of allele-specific transcription factor binding in the human genome. <i>Nature Communications</i> , 2021, 12, 2751.	12.8	55
5	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
6	Assessing Ribosome Distribution Along Transcripts with Polarity Scores and Regression Slope Estimates. <i>Methods in Molecular Biology</i> , 2021, 2252, 269-294.	0.9	1
7	Cyclical fate restriction: a new view of neural crest cell fate specification. <i>Development (Cambridge)</i> , 2021, 148, .	2.5	20
8	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
9	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	5.5	109
10	Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study. <i>Genome Biology</i> , 2020, 21, 114.	8.8	39
11	Signaling Pathways Potentially Responsible for Foam Cell Formation: Cholesterol Accumulation or Inflammatory Response—What is First?. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2716.	4.1	16
12	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
13	Heteroplasmic Variants of Mitochondrial DNA in Atherosclerotic Lesions of Human Aortic Intima. <i>Biomolecules</i> , 2019, 9, 455.	4.0	13
14	Defensin-like peptides in wheat analyzed by whole-transcriptome sequencing: a focus on structural diversity and role in induced resistance. <i>PeerJ</i> , 2019, 7, e6125.	2.0	17
15	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
16	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
17	Role of structural water for prediction of cation binding sites in apoproteins. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 221-232.	3.5	2
18	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

#	ARTICLE	IF	CITATIONS
19	Genome-wide map of human and mouse transcription factor binding sites aggregated from ChIP-Seq data. <i>BMC Research Notes</i> , 2018, 11, 756.	1.4	19
20	Modified LDL Particles Activate Inflammatory Pathways in Monocyte-derived Macrophages: Transcriptome Analysis. <i>Current Pharmaceutical Design</i> , 2018, 24, 3143-3151.	1.9	29
21	Transcriptome analysis of human macrophages reveals genes regulating cellular cholesterol efflux. <i>Atherosclerosis</i> , 2018, 275, e48.	0.8	0
22	Transcriptome analysis revealed inflammatory genes responsible for foam cell formation. <i>Atherosclerosis</i> , 2018, 275, e116.	0.8	4
23	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
24	HDL activates expression of genes stimulating cholesterol efflux in human monocyte-derived macrophages. <i>Experimental and Molecular Pathology</i> , 2018, 105, 202-207.	2.1	11
25	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456
26	Genes associated with cholesterol accumulation in macrophages (transcriptome analysis). <i>Atherosclerosis</i> , 2017, 263, e117.	0.8	2
27	Prevalent function of genome loci associated with development of multiple sclerosis as revealed by GWAS and eQTL analysis. <i>Russian Journal of Genetics</i> , 2017, 53, 982-987.	0.6	0
28	Use of Primary Macrophages for Searching Novel Immunocorrectors. <i>Current Pharmaceutical Design</i> , 2017, 23, 915-920.	1.9	3
29	The single nucleotide variant rs12722489 determines differential estrogen receptor binding and enhancer properties of an IL2RA intronic region. <i>PLoS ONE</i> , 2017, 12, e0172681.	2.5	10
30	Negative selection maintains transcription factor binding motifs in human cancer. <i>BMC Genomics</i> , 2016, 17, 395.	2.8	16
31	Preservation of methylated CpG dinucleotides in human CpG islands. <i>Biology Direct</i> , 2016, 11, 11.	4.6	15
32	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
33	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
34	Phenomenon of individual difference in human monocyte activation. <i>Experimental and Molecular Pathology</i> , 2015, 99, 151-154.	2.1	11
35	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
36	PERFECTOS-APE - Predicting Regulatory Functional Effect of SNPs by Approximate P-value Estimation. , 2015, , .		28

#	ARTICLE	IF	CITATIONS
37	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
38	Complete Genome Sequence of <i>Bifidobacterium longum</i> GT15: Unique Genes for Russian Strains. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
39	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
40	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
41	DNA Sequence Motif. <i>Advances in Protein Chemistry and Structural Biology</i> , 2013, 91, 135-171.	2.3	13
42	Predictive biology using systems and integrative analysis and methods. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 1-3.	3.5	0
43	Jaccard index based similarity measure to compare transcription factor binding site models. <i>Algorithms for Molecular Biology</i> , 2013, 8, 23.	1.2	53
44	Mutual disposition of nucleosomes and exons differs from common genome pattern at DNA segments containing periodic nucleotide sequences. <i>Biophysics (Russian Federation)</i> , 2013, 58, 851-853.	0.7	0
45	Identification of self-consistent modulons from bacterial microarray expression data with the help of structured regulon gene sets. <i>Journal of Biomolecular Structure and Dynamics</i> , 2013, 31, 115-124.	3.5	1
46	HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. <i>Nucleic Acids Research</i> , 2013, 41, D195-D202.	14.5	206
47	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
48	Exploring Massive, Genome Scale Datasets with the GenometriCorr Package. <i>PLoS Computational Biology</i> , 2012, 8, e1002529.	3.2	167
49	CORECLUST: identification of the conserved CRM grammar together with prediction of gene regulation. <i>Nucleic Acids Research</i> , 2012, 40, e93-e93.	14.5	9
50	Correlations between clusters of protein-DNA binding sites and the binding experimental data allow predicting a structure of regulatory modules. <i>Biophysics (Russian Federation)</i> , 2012, 57, 138-139.	0.7	0
51	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
52	A GENERALIZED HIDDEN MARKOV MODEL FOR PREDICTION OF CIS-REGULATORY MODULES IN EUKARYOTE GENOMES AND DESCRIPTION OF THEIR INTERNAL STRUCTURE. , 2012, , .		0
53	Preferred distances between transcription factor binding sites. <i>Biophysics (Russian Federation)</i> , 2011, 56, 114-116.	0.7	2
54	Using operonic gene pairs to set the threshold correlation coefficient for differently expressed genes. <i>Biophysics (Russian Federation)</i> , 2011, 56, 1041-1042.	0.7	1

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	Intergenic, gene terminal, and intragenic CpG islands in the human genome. <i>BMC Genomics</i> , 2010, 11, 48.	2.8	67
58	The GC skew near Pol II start sites and its association with SP1-binding site variants. <i>Biophysics (Russian Federation)</i> , 2010, 55, 901-907.	0.7	0
59	Deep and wide digging for binding motifs in ChIP-Seq data. <i>Bioinformatics</i> , 2010, 26, 2622-2623.	4.1	139
60	EMPIRICAL POTENTIALS FOR ION BINDING IN PROTEINS. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 427-435.	0.8	5
61	Motif discovery and motif finding from genome-mapped DNase footprint data. <i>Bioinformatics</i> , 2009, 25, 2318-2325.	4.1	35
62	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
63	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
64	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
65	Stochastic modeling of noninteracting probes in the protein structure space for construction of knowledge-based potentials for atom-atom interactions. <i>Biophysics (Russian Federation)</i> , 2008, 53, 189-194.	0.7	0
66	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
67	In vitro selection of optimal RelB/p52 DNA-binding motifs. <i>Biochemical and Biophysical Research Communications</i> , 2008, 365, 583-588.	2.1	29
68	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
69	Atomic hydration potentials using a Monte Carlo Reference State (MCRS) for protein solvation modeling. <i>BMC Structural Biology</i> , 2007, 7, 19.	2.3	9
70	A model of evolution with constant selective pressure for regulatory DNA sites. <i>BMC Evolutionary Biology</i> , 2007, 7, 125.	3.2	0
71	Relationship of micro-and minisatellites in the human genome. <i>Biophysics (Russian Federation)</i> , 2006, 51, 581-586.	0.7	1
72	ClusterTree-RS: A binary tree algorithm identifying coregulated genes by clustering regulatory signals. <i>Molecular Biology</i> , 2006, 40, 465-473.	1.3	0

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	Comparative Genomics and Evolution of Bacterial Regulatory Systems. , 2006, , 111-119.		0
76	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	17.5	1,121
77	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
78	Evolution of transcription factor DNA binding sites. <i>Gene</i> , 2005, 347, 255-263.	2.2	18
79	Identification of Proteins Associated with Murine Cytomegalovirus Virions. <i>Journal of Virology</i> , 2004, 78, 11187-11197.	3.4	138
80	Segmentation of Heteropolymer Sequences Specifying Subsequences with Different Composition and Statistical Properties. <i>Macromolecular Theory and Simulations</i> , 2003, 12, 604-613.	1.4	7
81	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
82	Homotypic Regulatory Clusters in <i>Drosophila</i> . <i>Genome Research</i> , 2003, 13, 579-588.	5.5	140
83	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
84	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
85	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
86	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	12
87	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
88	Segmentation of long genomic sequences into domains with homogeneous composition with BASIO software. <i>Bioinformatics</i> , 2001, 17, 1065-1066.	4.1	7
89	DNA Segmentation Through the Bayesian Approach. <i>Journal of Computational Biology</i> , 2000, 7, 215-231.	1.6	36
90	G and T Nucleotide Contents Show Specie-Invariant Negative Correlation for All Three Codon Positions. <i>Journal of Biomolecular Structure and Dynamics</i> , 1997, 14, 629-639.	3.5	11

#	ARTICLE	IF	CITATIONS
91	Search of periodicities in primary structure of biopolymers: a general Fourier approach. Bioinformatics, 1996, 12, 49-54.	4.1	16
92	The third nucleotide of the Gly coding triplet remembers the periodicity of the collagen chain. FEBS Letters, 1995, 366, 33-36.	2.8	1
93	Dynamics of nonlinear excitations in soft quasi-one-dimensional molecular chains. , 1991, , .		0
94	Positional weight matrices have sufficient prediction power for analysis of noncoding variants. F1000Research, 0, 11, 33.	1.6	1
95	Positional weight matrices have sufficient prediction power for analysis of noncoding variants. F1000Research, 0, 11, 33.	1.6	0
96	Positional weight matrices have sufficient prediction power for analysis of noncoding variants. F1000Research, 0, 11, 33.	1.6	3