

# Victor G Levitsky

## List of Publications by Year in descending order

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48  
papers

992  
citations

361413

20  
h-index

477307

29  
g-index

53  
all docs

53  
docs citations

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times ranked

1216  
citing authors

#	ARTICLE	IF	CITATIONS
1	Application of alternative &lt;i>de novo</i> motif recognition models for analysis of structural heterogeneity of transcription factor binding sites: a case study of FOXA2 binding sites. Vavilovskii Zhurnal Genetiki I Seleksii, 2021, 25, 7-17.	1.1	3
2	Transcriptional regulation in plants: Using omics data to crack the cis-regulatory code. Current Opinion in Plant Biology, 2021, 63, 102058.	7.1	9
3	Tissue-specific transcriptome profiling of the Arabidopsis inflorescence stem reveals local cellular signatures. Plant Cell, 2021, 33, 200-223.	6.6	48
4	Faint gray bands in Drosophila melanogaster polytene chromosomes are formed by coding sequences of housekeeping genes. Chromosoma, 2020, 129, 25-44.	2.2	5
5	Architecture of DNA elements mediating ARF transcription factor binding and auxin-responsive gene expression in <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24557-24566.	7.1	53
6	Asymmetric Conservation within Pairs of Co-Occurred Motifs Mediates Weak Direct Binding of Transcription Factors in ChIP-Seq Data. International Journal of Molecular Sciences, 2020, 21, 6023.	4.1	4
7	Nucleosome Positioning around Transcription Start Site Correlates with Gene Expression Only for Active Chromatin State in Drosophila Interphase Chromosomes. International Journal of Molecular Sciences, 2020, 21, 9282.	4.1	2
8	Specification and regulation of vascular tissue identity in the <i>Arabidopsis</i> embryo. Development (Cambridge), 2020, 147, .	2.5	24
9	Genes Containing Long Introns Occupy Series of Bands and Interbands in Drosophila melanogaster Polytene Chromosomes. Genes, 2020, 11, 417.	2.4	3
10	Architecture of Promoters of House-Keeping Genes in Polytene Chromosome Interbands of Drosophila melanogaster. Doklady Biochemistry and Biophysics, 2019, 485, 95-100.	0.9	2
11	A single ChIP-seq dataset is sufficient for comprehensive analysis of motifs co-occurrence with MCOT package. Nucleic Acids Research, 2019, 47, e139-e139.	14.5	28
12	Developing of WebMCOT Web-Service for Finding Cooperative Site-Binding TF DNA-Motifs. Vestnik NSU Series Information Technologies, 2019, 17, 74-86.	0.2	0
13	Spatial specificity of auxin responses coordinates wood formation. Nature Communications, 2018, 9, 875.	12.8	110
14	Diversity of cis-regulatory elements associated with auxin response in Arabidopsis thaliana. Journal of Experimental Botany, 2018, 69, 329-339.	4.8	45
15	Genetic Organization of Open Chromatin Domains Situated in Polytene Chromosome Interbands in Drosophila. Doklady Biochemistry and Biophysics, 2018, 483, 297-301.	0.9	3
16	Polytene Chromosomes – A Portrait of Functional Organization of the Drosophila Genome. Current Genomics, 2018, 19, 179-191.	1.6	30
17	Auxin regulates functional gene groups in a fold-change-specific manner in Arabidopsis thaliana roots. Scientific Reports, 2017, 7, 2489.	3.3	42
18	Protein and Genetic Composition of Four Chromatin Types in Drosophila melanogaster Cell Lines. Current Genomics, 2017, 18, 214-226.	1.6	15

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19	Meta-analysis of transcriptome data identified TGTCNN motif variants associated with the response to plant hormone auxin in <i>Arabidopsis thaliana</i> L. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1641009.	0.8	31
20	Estimation of the role of single nucleotide polymorphism in lymphotoxin beta gene during pig domestication based on the bioinformatic and experimental approaches. <i>Russian Journal of Genetics: Applied Research</i> , 2016, 6, 816-824.	0.4	1
21	Hidden heterogeneity of transcription factor binding sites: A case study of SF-1. <i>Computational Biology and Chemistry</i> , 2016, 64, 19-32.	2.3	6
22	The expansion of heterochromatin blocks in rye reflects the co-amplification of tandem repeats and adjacent transposable elements. <i>BMC Genomics</i> , 2016, 17, 337.	2.8	32
23	The Interplay of Chromatin Landscape and DNA-Binding Context Suggests Distinct Modes of EIN3 Regulation in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 2044.	3.6	6
24	Effect of flanking sequences on the accuracy of the recognition of transcription factor binding sites. <i>Russian Journal of Genetics: Applied Research</i> , 2015, 5, 322-329.	0.4	1
25	Human Genes Encoding Transcription Factors and Chromatin-Modifying Proteins Have Low Levels of Promoter Polymorphism: A Study of 1000 Genomes Project Data. <i>International Journal of Genomics</i> , 2015, 2015, 1-15.	1.6	13
26	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. <i>Frontiers in Psychology</i> , 2014, 5, 247.	2.1	28
27	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
28	The roles of the monomer length and nucleotide context of plant tandem repeats in nucleosome positioning. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 115-126.	3.5	12
29	Computational analysis of auxin responsive elements in the <i>Arabidopsis thaliana</i> L. genome. <i>BMC Genomics</i> , 2014, 15, S4.	2.8	54
30	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
31	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
32	In Silico Prediction of Transcriptional Factor-Binding Sites. <i>Methods in Molecular Biology</i> , 2011, 760, 251-267.	0.9	6
33	Development of computational methods to search for FoxA transcription factor binding sites, their experimental verification and application to the analysis of ChIP-seq data. <i>Doklady Biochemistry and Biophysics</i> , 2011, 436, 12-15.	0.9	2
34	Genetic algorithm and optimized weight matrix application for peroxisome proliferator response elements recognition: Prerequisites of accuracy growth for wide genome research. <i>Intelligent Data Analysis</i> , 2008, 12, 513-526.	0.9	2
35	Combined experimental and computational approaches to study the regulatory elements in eukaryotic genes. <i>Briefings in Bioinformatics</i> , 2007, 8, 266-274.	6.5	28
36	Bioinformatical and experimental approaches to investigation of transcription factor binding sites in vertebrate genes. <i>Biochemistry (Moscow)</i> , 2007, 72, 1187-1193.	1.5	8

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37	Effective transcription factor binding site prediction using a combination of optimization, a genetic algorithm and discriminant analysis to capture distant interactions. <i>BMC Bioinformatics</i> , 2007, 8, 481.	2.6	35
38	Pattern of locally positioned dinucleotides correlates with MicroRNA abundance in plants. <i>Biophysics (Russian Federation)</i> , 2006, 51, 7-10.	0.7	1
39	Potential binding sites for SF-1: Recognition by the SiteGA method, experimental verification, and search for new target genes. <i>Molecular Biology</i> , 2006, 40, 454-464.	1.3	6
40	RECON: a program for prediction of nucleosome formation potential. <i>Nucleic Acids Research</i> , 2004, 32, W346-W349.	14.5	42
41	NPRD: Nucleosome Positioning Region Database. <i>Nucleic Acids Research</i> , 2004, 33, D67-D70.	14.5	17
42	Recognition of eukaryotic promoters using a genetic algorithm based on iterative discriminant analysis. <i>In Silico Biology</i> , 2003, 3, 81-7.	0.9	9
43	Locus Control Regions: Description in the LCR-TRRDatabase. <i>Molecular Biology</i> , 2001, 35, 802-809.	1.3	0
44	Computer Analysis and Recognition of <i>Drosophila melanogaster</i> Gene Promoters. <i>Molecular Biology</i> , 2001, 35, 826-832.	1.3	4
45	Nucleosome formation potential of exons, introns, and Alu repeats. <i>Bioinformatics</i> , 2001, 17, 1062-1064.	4.1	21
46	Nucleosome formation potential of eukaryotic DNA: calculation and promoters analysis. <i>Bioinformatics</i> , 2001, 17, 998-1010.	4.1	52
47	Nucleosomal DNA property database. <i>Bioinformatics</i> , 1999, 15, 582-592.	4.1	24
48	Investigating extended regulatory regions of genomic DNA sequences. <i>Bioinformatics</i> , 1999, 15, 644-653.	4.1	27