

# 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

53  
times ranked

1216  
citing authors

#	ARTICLE	IF	CITATIONS
1	Spatial specificity of auxin responses coordinates wood formation. <i>Nature Communications</i> , 2018, 9, 875.	12.8	110
2	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
3	Computational analysis of auxin responsive elements in the <i>Arabidopsis thaliana</i> L. genome. <i>BMC Genomics</i> , 2014, 15, S4.	2.8	54
4	Architecture of DNA elements mediating ARF transcription factor binding and auxin-responsive gene expression in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24557-24566.	7.1	53
5	Nucleosome formation potential of eukaryotic DNA: calculation and promoters analysis. <i>Bioinformatics</i> , 2001, 17, 998-1010.	4.1	52
6	Tissue-specific transcriptome profiling of the <i>Arabidopsis</i> inflorescence stem reveals local cellular signatures. <i>Plant Cell</i> , 2021, 33, 200-223.	6.6	48
7	Diversity of cis-regulatory elements associated with auxin response in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 329-339.	4.8	45
8	RECON: a program for prediction of nucleosome formation potential. <i>Nucleic Acids Research</i> , 2004, 32, W346-W349.	14.5	42
9	Auxin regulates functional gene groups in a fold-change-specific manner in <i>Arabidopsis thaliana</i> roots. <i>Scientific Reports</i> , 2017, 7, 2489.	3.3	42
10	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
11	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
12	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
13	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
14	Polytene Chromosomes – A Portrait of Functional Organization of the <i>Drosophila</i> Genome. <i>Current Genomics</i> , 2018, 19, 179-191.	1.6	30
15	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
16	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
17	A single ChIP-seq dataset is sufficient for comprehensive analysis of motifs co-occurrence with MCOT package. <i>Nucleic Acids Research</i> , 2019, 47, e139-e139.	14.5	28
18	Investigating extended regulatory regions of genomic DNA sequences. <i>Bioinformatics</i> , 1999, 15, 644-653.	4.1	27

#	ARTICLE	IF	CITATIONS
19	Nucleosomal DNA property database. <i>Bioinformatics</i> , 1999, 15, 582-592.	4.1	24
20	Specification and regulation of vascular tissue identity in the <i>Arabidopsis</i> embryo. <i>Development</i> (Cambridge), 2020, 147, .	2.5	24
21	Nucleosome formation potential of exons, introns, and Alu repeats. <i>Bioinformatics</i> , 2001, 17, 1062-1064.	4.1	21
22	NPRD: Nucleosome Positioning Region Database. <i>Nucleic Acids Research</i> , 2004, 33, D67-D70.	14.5	17
23	Protein and Genetic Composition of Four Chromatin Types in <i>Drosophila melanogaster</i> Cell Lines. <i>Current Genomics</i> , 2017, 18, 214-226.	1.6	15
24	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
25	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
26	Transcriptional regulation in plants: Using omics data to crack the cis-regulatory code. <i>Current Opinion in Plant Biology</i> , 2021, 63, 102058.	7.1	9
27	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
28	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
29	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
30	In Silico Prediction of Transcriptional Factor-Binding Sites. <i>Methods in Molecular Biology</i> , 2011, 760, 251-267.	0.9	6
31	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
32	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
33	Faint gray bands in <i>Drosophila melanogaster</i> polytene chromosomes are formed by coding sequences of housekeeping genes. <i>Chromosoma</i> , 2020, 129, 25-44.	2.2	5
34	Computer Analysis and Recognition of <i>Drosophila melanogaster</i> Gene Promoters. <i>Molecular Biology</i> , 2001, 35, 826-832.	1.3	4
35	Asymmetric Conservation within Pairs of Co-Occurred Motifs Mediates Weak Direct Binding of Transcription Factors in ChIP-Seq Data. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6023.	4.1	4
36	Genetic Organization of Open Chromatin Domains Situated in Polytene Chromosome Interbands in <i>Drosophila</i> . <i>Doklady Biochemistry and Biophysics</i> , 2018, 483, 297-301.	0.9	3

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37	Genes Containing Long Introns Occupy Series of Bands and Interbands in <i>Drosophila melanogaster</i> Polytene Chromosomes. <i>Genes</i> , 2020, 11, 417.	2.4	3
38	Application of alternative & de novo motif recognition models for analysis of structural heterogeneity of transcription factor binding sites: a case study of FOXA2 binding sites. <i>Vavilovskii Zhurnal Genetiki I Seleksii</i> , 2021, 25, 7-17.	1.1	3
39	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
40	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
41	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
42	Architecture of Promoters of House-Keeping Genes in Polytene Chromosome Interbands of <i>Drosophila melanogaster</i> . <i>Doklady Biochemistry and Biophysics</i> , 2019, 485, 95-100.	0.9	2
43	Nucleosome Positioning around Transcription Start Site Correlates with Gene Expression Only for Active Chromatin State in <i>Drosophila</i> Interphase Chromosomes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9282.	4.1	2
44	Pattern of locally positioned dinucleotides correlates with MicroRNA abundance in plants. <i>Biophysics (Russian Federation)</i> , 2006, 51, 7-10.	0.7	1
45	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
46	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
47	Locus Control Regions: Description in the LCR-TRRDatabase. <i>Molecular Biology</i> , 2001, 35, 802-809.	1.3	0
48	Developing of WebMCOT Web-Service for Finding Cooperative Site-Binding TF DNA-Motifs. <i>Vestnik NSU Series Information Technologies</i> , 2019, 17, 74-86.	0.2	0