

Victor V Solovyev

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

17,536
citations

81900

39
h-index

123424

61
g-index

66
all docs

66
docs citations

66
times ranked

23293
citing authors

#	ARTICLE	IF	CITATIONS
1	Community structure and metabolism through reconstruction of microbial genomes from the environment. <i>Nature</i> , 2004, 428, 37-43.	27.8	2,045
2	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006, 443, 931-949.	27.8	1,648
3	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	27.8	1,255
4	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
5	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006, 314, 941-952.	12.6	1,018
6	Ab initio Gene Finding in <i>Drosophila</i> Genomic DNA. <i>Genome Research</i> , 2000, 10, 516-522.	5.5	987
7	A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety. <i>PLoS ONE</i> , 2007, 2, e1326.	2.5	945
8	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	5.6	913
9	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	12.6	808
10	Automatic annotation of eukaryotic genes, pseudogenes and promoters. <i>Genome Biology</i> , 2006, 7, S10.	9.6	749
11	The ctenophore genome and the evolutionary origins of neural systems. <i>Nature</i> , 2014, 510, 109-114.	27.8	606
12	Analysis of canonical and non-canonical splice sites in mammalian genomes. <i>Nucleic Acids Research</i> , 2000, 28, 4364-4375.	14.5	520
13	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	5.5	443
14	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , 2014, 15, 86.	2.8	375
15	Predicting internal exons by oligonucleotide composition and discriminant analysis of spliceable open reading frames. <i>Nucleic Acids Research</i> , 1994, 22, 5156-5163.	14.5	333
16	Expression of Msl-2 causes assembly of dosage compensation regulators on the X chromosomes and female lethality in <i>Drosophila</i> . <i>Cell</i> , 1995, 81, 867-877.	28.9	310
17	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535.	27.8	298
18	Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , 2017, 45, D1075-D1081.	14.5	290

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19	Prediction of Protein Secondary Structure by Combining Nearest-neighbor Algorithms and Multiple Sequence Alignments. <i>Journal of Molecular Biology</i> , 1995, 247, 11-15.	4.2	280
20	Community-wide assessment of GPCR structure modelling and ligand docking: GPCR Dock 2008. <i>Nature Reviews Drug Discovery</i> , 2009, 8, 455-463.	46.4	260
21	PlantProm: a database of plant promoter sequences. <i>Nucleic Acids Research</i> , 2003, 31, 114-117.	14.5	240
22	SpliceDB: database of canonical and non-canonical mammalian splice sites. <i>Nucleic Acids Research</i> , 2001, 29, 255-259.	14.5	210
23	Recognition of prokaryotic and eukaryotic promoters using convolutional deep learning neural networks. <i>PLoS ONE</i> , 2017, 12, e0171410.	2.5	183
24	Identification of Promoter Regions and Regulatory Sites. <i>Methods in Molecular Biology</i> , 2010, 674, 57-83.	0.9	137
25	A novel type of RNase III family proteins in eukaryotes. <i>Gene</i> , 2000, 245, 213-221.	2.2	120
26	Sequence alignment kernel for recognition of promoter regions. <i>Bioinformatics</i> , 2003, 19, 1964-1971.	4.1	116
27	Protein secondary structure prediction using local alignments. <i>Journal of Molecular Biology</i> , 1997, 268, 31-36.	4.2	115
28	PromH: promoters identification using orthologous genomic sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3540-3545.	14.5	113
29	Plant promoter prediction with confidence estimation. <i>Nucleic Acids Research</i> , 2005, 33, 1069-1076.	14.5	106
30	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	5.5	102
31	Promoter analysis and prediction in the human genome using sequence-based deep learning models. <i>Bioinformatics</i> , 2019, 35, 2730-2737.	4.1	89
32	Automated Whole-Genome Multiple Alignment of Rat, Mouse, and Human. <i>Genome Research</i> , 2004, 14, 685-692.	5.5	79
33	Karect: accurate correction of substitution, insertion and deletion errors for next-generation sequencing data. <i>Bioinformatics</i> , 2015, 31, 3421-3428.	4.1	75
34	Performance assessment of promoter predictions on ENCODE regions in the EGASP experiment. <i>Genome Biology</i> , 2006, 7, S3.	9.6	61
35	nGASP – the nematode genome annotation assessment project. <i>BMC Bioinformatics</i> , 2008, 9, 549.	2.6	61
36	TSSPlant: a new tool for prediction of plant Pol II promoters. <i>Nucleic Acids Research</i> , 2017, 45, gkw1353.	14.5	59

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37	Analysis of mutation rates in the SMCY/SMCX genes shows that mammalian evolution is male driven. <i>Mammalian Genome</i> , 1997, 8, 134-138.	2.2	52
38	Abundance of plastid DNA insertions in nuclear genomes of rice and Arabidopsis. <i>Plant Molecular Biology</i> , 2003, 52, 923-934.	3.9	51
39	SNP-Seek II: A resource for allele mining and analysis of big genomic data in <i>Oryza sativa</i> . <i>Current Plant Biology</i> , 2016, 7-8, 16-25.	4.7	48
40	INFOGENE: a database of known gene structures and predicted genes and proteins in sequences of genome sequencing projects. <i>Nucleic Acids Research</i> , 1999, 27, 248-250.	14.5	45
41	Nsite, NsiteH and NsiteM computer tools for studying transcription regulatory elements. <i>Bioinformatics</i> , 2015, 31, 3544-3545.	4.1	41
42	Predicting α -helix and β -strand segments of globular proteins. <i>Bioinformatics</i> , 1994, 10, 661-669.	4.1	37
43	Peculiarities of immunoglobulin gene structures as a basis for somatic mutation emergence. <i>FEBS Letters</i> , 1987, 214, 87-91.	2.8	34
44	Assignment of position-specific error probability to primary DNA sequence data. <i>Nucleic Acids Research</i> , 1994, 22, 1272-1280.	14.5	34
45	New insights from <i>Opisthorchis felinus</i> genome: update on genomics of the epidemiologically important liver flukes. <i>BMC Genomics</i> , 2019, 20, 399.	2.8	29
46	Evidence-based gene models for structural and functional annotations of the oil palm genome. <i>Biology Direct</i> , 2017, 12, 21.	4.6	24
47	Intercalary heterochromatin in <i>Drosophila</i> . <i>Chromosoma</i> , 1988, 97, 247-253.	2.2	23
48	A novel method of protein sequence classification based on oligopeptide frequency analysis and its application to search for functional sites and to domain localization. <i>Bioinformatics</i> , 1993, 9, 17-24.	4.1	19
49	Nucleotide patterns aiding in prediction of eukaryotic promoters. <i>PLoS ONE</i> , 2017, 12, e0187243.	2.5	19
50	Fractal graphical representation and analysis of DNA and protein sequences. <i>BioSystems</i> , 1993, 30, 137-160.	2.0	17
51	Towards the integration of genomics, epidemiological and clinical data. <i>Genome Medicine</i> , 2011, 3, 48.	8.2	15
52	Prediction of Metabolic Pathway Involvement in Prokaryotic UniProtKB Data by Association Rule Mining. <i>PLoS ONE</i> , 2016, 11, e0158896.	2.5	13
53	Epigenetic chromatin footprinting identifies novel and subject-specific genes active in prefrontal cortex neurons. <i>FASEB Journal</i> , 2019, 33, 8161-8173.	0.5	12
54	Conformational changes in the globin family during evolution. <i>Journal of Molecular Evolution</i> , 1984, 21, 42-53.	1.8	10

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55	New elements of glucocorticoid-receptor binding sites of hormone-regulated genes. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1991, 1089, 367-376.	2.4	9
56	A simple method for the calculation of low energy packings of α -helices – A threshold approximation. I. The use of the method to estimate the effects of amino acid substitutions, deletions and insertions in globins. <i>Journal of Theoretical Biology</i> , 1984, 110, 67-91.	1.7	4
57	The template RNAs of RNA polymerases can have compact secondary structure, formed by long double helices with partial violations of the complementarity. <i>FEBS Letters</i> , 1984, 165, 72-78.	2.8	4
58	The PlantProm DB: Recent Updates. , 2012, , .		2
59	Genome Sequence of a Multidrug-Resistant Strain of <i>Stenotrophomonas maltophilia</i> with Carbapenem Resistance, Isolated from King Abdullah Medical City, Makkah, Saudi Arabia. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
60	Rule Mining Techniques to Predict Prokaryotic Metabolic Pathways. <i>Methods in Molecular Biology</i> , 2017, 1613, 311-331.	0.9	2
61	Evolution and performance of electron and photon triggers in ATLAS in the year 2011. , 2012, , .		1
62	INTENSIFICATION OF NANOPOROUS GLASS PRODUCING BY POWERFUL ULTRASONIC FIELDS. <i>Integrated Ferroelectrics</i> , 2008, 103, 60-65.	0.7	0
63	Genome-Wide Prokaryotic Promoter Recognition Based on Sequence Alignment Kernel. <i>Lecture Notes in Computer Science</i> , 2003, , 386-396.	1.3	0