

# Victor V Solovyev

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

14,137

citations

38

h-index

66

g-index

66

ext. papers

16,201

ext. citations

14.2

avg, IF

6.53

L-index

#	Paper	IF	Citations
62	New insights from <i>Opisthorchis felinus</i> genome: update on genomics of the epidemiologically important liver flukes. <i>BMC Genomics</i> , <b>2019</b> , 20, 399	4.5	17
61	Epigenetic-genetic chromatin footprinting identifies novel and subject-specific genes active in prefrontal cortex neurons. <i>FASEB Journal</i> , <b>2019</b> , 33, 8161-8173	0.9	7
60	Promoter analysis and prediction in the human genome using sequence-based deep learning models. <i>Bioinformatics</i> , <b>2019</b> , 35, 2730-2737	7.2	46
59	TSSPlant: a new tool for prediction of plant Pol II promoters. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e65	20.1	35
58	Recognition of prokaryotic and eukaryotic promoters using convolutional deep learning neural networks. <i>PLoS ONE</i> , <b>2017</b> , 12, e0171410	3.7	114
57	Nucleotide patterns aiding in prediction of eukaryotic promoters. <i>PLoS ONE</i> , <b>2017</b> , 12, e0187243	3.7	14
56	Rule Mining Techniques to Predict Prokaryotic Metabolic Pathways. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1613, 311-331	1.4	1
55	Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D1075-D1081	10.1	137
54	Evidence-based gene models for structural and functional annotations of the oil palm genome. <i>Biology Direct</i> , <b>2017</b> , 12, 21	7.2	14
53	Prediction of Metabolic Pathway Involvement in Prokaryotic UniProtKB Data by Association Rule Mining. <i>PLoS ONE</i> , <b>2016</b> , 11, e0158896	3.7	11
52	SNP-Seek II: A resource for allele mining and analysis of big genomic data in <i>Oryza sativa</i> . <i>Current Plant Biology</i> , <b>2016</b> , 7-8, 16-25	3.3	29
51	Karect: accurate correction of substitution, insertion and deletion errors for next-generation sequencing data. <i>Bioinformatics</i> , <b>2015</b> , 31, 3421-8	7.2	50
50	Nsite, NsiteH and NsiteM computer tools for studying transcription regulatory elements. <i>Bioinformatics</i> , <b>2015</b> , 31, 3544-5	7.2	22
49	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> , <b>2015</b> , 3,		1
48	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , <b>2014</b> , 15, 86	4.5	284
47	The ctenophore genome and the evolutionary origins of neural systems. <i>Nature</i> , <b>2014</b> , 510, 109-14	50.4	459
46	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , <b>2014</b> , 24, 2077-89	9.7	74

45	The PlantProm DB: Recent Updates <b>2012</b> ,		2
44	Towards the integration of genomics, epidemiological and clinical data. <i>Genome Medicine</i> , <b>2011</b> , 3, 48	14.4	7
43	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , <b>2011</b> , 21, 2224-41	9.7	364
42	Genome sequence of the pea aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , <b>2010</b> , 8, e1000313	9.7	732
41	Identification of promoter regions and regulatory sites. <i>Methods in Molecular Biology</i> , <b>2010</b> , 674, 57-83	1.4	92
40	Functional and evolutionary insights from the genomes of three parasitoid <i>Nasonia</i> species. <i>Science</i> , <b>2010</b> , 327, 343-8	33.3	682
39	Community-wide assessment of GPCR structure modelling and ligand docking: GPCR Dock 2008. <i>Nature Reviews Drug Discovery</i> , <b>2009</b> , 8, 455-63	64.1	236
38	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , <b>2009</b> , 324, 522-8	33.3	863
37	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , <b>2008</b> , 452, 949-55	50.4	1043
36	nGASP--the nematode genome annotation assessment project. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 549	3.6	51
35	INTENSIFICATION OF NANOPOROUS GLASS PRODUCING BY POWERFUL ULTRASONIC FIELDS. <i>Integrated Ferroelectrics</i> , <b>2008</b> , 103, 60-65	0.8	
34	A high quality draft consensus sequence of the genome of a heterozygous grapevine variety. <i>PLoS ONE</i> , <b>2007</b> , 2, e1326	3.7	779
33	Automatic annotation of eukaryotic genes, pseudogenes and promoters. <i>Genome Biology</i> , <b>2006</b> , 7 Suppl 1, S10.1-12	18.3	461
32	Performance assessment of promoter predictions on ENCODE regions in the EGASP experiment. <i>Genome Biology</i> , <b>2006</b> , 7 Suppl 1, S3.1-13	18.3	54
31	The genome of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , <b>2006</b> , 314, 941-52	33.3	886
30	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , <b>2006</b> , 443, 931-49	50.4	1414
29	Plant promoter prediction with confidence estimation. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 1069-76	20.1	92
28	Automated whole-genome multiple alignment of rat, mouse, and human. <i>Genome Research</i> , <b>2004</b> , 14, 685-92	9.7	69

27	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , <b>2004</b> , 428, 529-35	50.4	216
26	Community structure and metabolism through reconstruction of microbial genomes from the environment. <i>Nature</i> , <b>2004</b> , 428, 37-43	50.4	1710
25	PlantProm: a database of plant promoter sequences. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 114-7	20.1	196
24	Sequence alignment kernel for recognition of promoter regions. <i>Bioinformatics</i> , <b>2003</b> , 19, 1964-71	7.2	97
23	Abundance of plastid DNA insertions in nuclear genomes of rice and Arabidopsis. <i>Plant Molecular Biology</i> , <b>2003</b> , 52, 923-34	4.6	47
22	PromH: Promoters identification using orthologous genomic sequences. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3540-5	20.1	84
21	Genome-Wide Prokaryotic Promoter Recognition Based on Sequence Alignment Kernel. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 386-396	0.9	
20	SpliceDB: database of canonical and non-canonical mammalian splice sites. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 255-9	20.1	169
19	Ab initio gene finding in Drosophila genomic DNA. <i>Genome Research</i> , <b>2000</b> , 10, 516-22	9.7	836
18	Analysis of canonical and non-canonical splice sites in mammalian genomes. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 4364-75	20.1	411
17	A novel type of RNase III family proteins in eukaryotes. <i>Gene</i> , <b>2000</b> , 245, 213-21	3.8	108
16	INFOGENE: a database of known gene structures and predicted genes and proteins in sequences of genome sequencing projects. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 248-50	20.1	43
15	Protein secondary structure prediction using local alignments. <i>Journal of Molecular Biology</i> , <b>1997</b> , 268, 31-6	6.5	95
14	Analysis of mutation rates in the SMCY/SMCX genes shows that mammalian evolution is male driven. <i>Mammalian Genome</i> , <b>1997</b> , 8, 134-8	3.2	45
13	Expression of msl-2 causes assembly of dosage compensation regulators on the X chromosomes and female lethality in Drosophila. <i>Cell</i> , <b>1995</b> , 81, 867-77	56.2	261
12	Prediction of protein secondary structure by combining nearest-neighbor algorithms and multiple sequence alignments. <i>Journal of Molecular Biology</i> , <b>1995</b> , 247, 11-5	6.5	227
11	Predicting internal exons by oligonucleotide composition and discriminant analysis of spliceable open reading frames. <i>Nucleic Acids Research</i> , <b>1994</b> , 22, 5156-63	20.1	296
10	Predicting alpha-helix and beta-strand segments of globular proteins. <i>Bioinformatics</i> , <b>1994</b> , 10, 661-9	7.2	21

9	Assignment of position-specific error probability to primary DNA sequence data. <i>Nucleic Acids Research</i> , <b>1994</b> , 22, 1272-80	20.1	30
8	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> , <b>1993</b> , 9, 17-24	7.2	12
7	Fractal graphical representation and analysis of DNA and protein sequences. <i>BioSystems</i> , <b>1993</b> , 30, 137-60	9	15
6	New elements of glucocorticoid-receptor binding sites of hormone-regulated genes. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , <b>1991</b> , 1089, 367-76		7
5	Intercalary heterochromatin in <i>Drosophila</i> . III. Homology between DNA sequences from the Y chromosome, bases of polytene chromosome limbs, and chromosome 4 of <i>D. melanogaster</i> . <i>Chromosoma</i> , <b>1988</b> , 97, 247-53	2.8	23
4	Peculiarities of immunoglobulin gene structures as a basis for somatic mutation emergence. <i>FEBS Letters</i> , <b>1987</b> , 214, 87-91	3.8	30
3	Conformational changes in the globin family during evolution. 1. Analysis of the evolutionary role of insertions and deletions. <i>Journal of Molecular Evolution</i> , <b>1984</b> , 21, 42-53	3.1	9
2	A simple method for the calculation of low energy packings of alpha-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> , <b>1984</b> , 110, 67-91	2.3	2
1	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> , <b>1984</b> , 165, 72-8	3.8	3