

# Maria Anisimova

## List of Publications by Year in descending order

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55  
papers

21,814  
citations

230014

27  
h-index

182931

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62  
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62  
docs citations

62  
times ranked

36287  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Use of the Rare TTA Codon in Streptomyces Genes: Significance of the Codon Context?. Indian Journal of Microbiology, 2021, 61, 24-30.	1.5	2
2	TRAL 2.0: Tandem Repeat Detection With Circular Profile Hidden Markov Models and Evolutionary Aligner. Frontiers in Bioinformatics, 2021, 1, .	1.0	9
3	Beyond Microsatellite Instability: Intrinsic Disorder as a Potential Link Between Protein Short Tandem Repeats and Cancer. Frontiers in Bioinformatics, 2021, 1, .	1.0	1
4	ProPIP: a tool for progressive multiple sequence alignment with Poisson Indel Process. BMC Bioinformatics, 2021, 22, 518.	1.2	5
5	Impact of Diabetes Mellitus on Voice : A Methodological Commentary. Journal of Voice, 2020, , .	0.6	1
6	A New Census of Protein Tandem Repeats and Their Relationship with Intrinsic Disorder. Genes, 2020, 11, 407.	1.0	45
7	Accelerating phylogeny-aware alignment with indel evolution using short time Fourier transform. NAR Genomics and Bioinformatics, 2020, 2, lqaa092.	1.5	3
8	Selection Acting on Genomes. Methods in Molecular Biology, 2019, 1910, 373-397.	0.4	9
9	Evolutionary Genomics. Methods in Molecular Biology, 2019, , .	0.4	18
10	Tandem repeats lead to sequence assembly errors and impose multi-level challenges for genome and protein databases. Nucleic Acids Research, 2019, 47, 10994-11006.	6.5	236
11	Enabling semantic queries across federated bioinformatics databases. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	23
12	Genomic Insights into Evolution of AdpA Family Master Regulators of Morphological Differentiation and Secondary Metabolism in Streptomyces. Journal of Molecular Evolution, 2018, 86, 204-215.	0.8	20
13	Genomes reveal marked differences in the adaptive evolution between orangutan species. Genome Biology, 2018, 19, 193.	3.8	18
14	Accounting for Programmed Ribosomal Frameshifting in the Computation of Codon Usage Bias Indices. G3: Genes, Genomes, Genetics, 2018, 8, 3173-3183.	0.8	3
15	Progressive multiple sequence alignment with indel evolution. BMC Bioinformatics, 2018, 19, 331.	1.2	19
16	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. Current Biology, 2017, 27, 3487-3498.e10.	1.8	192
17	Functional assignment to positively selected sites in the core type <scp>Ill</scp> effector <scp>RipG</scp> 7 from <scp><i>R</i></scp><i>alstonia solanacearum</i>. Molecular Plant Pathology, 2016, 17, 553-564.	2.0	39
18	DNA polymorphism and selection at the bindin locus in three Strongylocentrotus sp. (Echinoidea). BMC Genetics, 2016, 17, 66.	2.7	4

#	ARTICLE	IF	CITATIONS
19	Statistical Approaches to Detecting and Analyzing Tandem Repeats in Genomic Sequences. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 31.	2.0	19
20	TRAL: tandem repeat annotation library. <i>Bioinformatics</i> , 2015, 31, 3051-3053.	1.8	17
21	Antibody-Specific Model of Amino Acid Substitution for Immunological Inferences from Alignments of Antibody Sequences. <i>Molecular Biology and Evolution</i> , 2015, 32, 806-819.	3.5	25
22	Maximum-Likelihood Tree Estimation Using Codon Substitution Models with Multiple Partitions. <i>Molecular Biology and Evolution</i> , 2015, 32, 2208-2216.	3.5	14
23	Darwin and Fisher meet at biotech: on the potential of computational molecular evolution in industry. <i>BMC Evolutionary Biology</i> , 2015, 15, 76.	3.2	10
24	The evolution and function of protein tandem repeats in plants. <i>New Phytologist</i> , 2015, 206, 397-410.	3.5	54
25	Unraveling Patterns of Site-to-Site Synonymous Rates Variation and Associated Gene Properties of Protein Domains and Families. <i>PLoS ONE</i> , 2014, 9, e95034.	1.1	17
26	Deep Conservation of Human Protein Tandem Repeats within the Eukaryotes. <i>Molecular Biology and Evolution</i> , 2014, 31, 1132-1148.	3.5	62
27	Natural Selection on Coding and Noncoding DNA Sequences Is Associated with Virulence Genes in a Plant Pathogenic Fungus. <i>Genome Biology and Evolution</i> , 2014, 6, 2368-2379.	1.1	31
28	State-of the art methodologies dictate new standards for phylogenetic analysis. <i>BMC Evolutionary Biology</i> , 2013, 13, 161.	3.2	51
29	Repertoire, unified nomenclature and evolution of the Type III effector gene set in the <i>Ralstonia solanacearum</i> species complex. <i>BMC Genomics</i> , 2013, 14, 859.	1.2	206
30	CodonPhyML: Fast Maximum Likelihood Phylogeny Estimation under Codon Substitution Models. <i>Molecular Biology and Evolution</i> , 2013, 30, 1270-1280.	3.5	99
31	Graph-based modeling of tandem repeats improves global multiple sequence alignment. <i>Nucleic Acids Research</i> , 2013, 41, e162-e162.	6.5	25
32	Repeat or not repeat? Statistical validation of tandem repeat prediction in genomic sequences. <i>Nucleic Acids Research</i> , 2012, 40, 10005-10017.	6.5	47
33	ALF: A Simulation Framework for Genome Evolution. <i>Molecular Biology and Evolution</i> , 2012, 29, 1115-1123.	3.5	130
34	Gene copy number variation and its significance in cyanobacterial phylogeny. <i>BMC Microbiology</i> , 2012, 12, 177.	1.3	36
35	Selection on the Protein-Coding Genome. <i>Methods in Molecular Biology</i> , 2012, 856, 113-140.	0.4	26
36	Parametric models of codon evolution. , 2012, , 12-33.		23

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37	Complex Interplay of Evolutionary Forces in the ladybird Homeobox Genes of <i>Drosophila melanogaster</i> . PLoS ONE, 2011, 6, e22613.	1.1	7
38	Markov Models of Amino Acid Substitution to Study Proteins with Intrinsically Disordered Regions. PLoS ONE, 2011, 6, e20488.	1.1	36
39	Functional diversification of the <i>GAL4</i> type III effector family contributes to <i>Ralstonia solanacearum</i> adaptation on different plant hosts. New Phytologist, 2011, 192, 976-987.	3.5	97
40	Coevolution of amino acid residues in the key photosynthetic enzyme Rubisco. BMC Evolutionary Biology, 2011, 11, 266.	3.2	28
41	Evolution of cyanobacterial morphotypes. Communicative and Integrative Biology, 2011, 4, 424-427.	0.6	27
42	Survey of Branch Support Methods Demonstrates Accuracy, Power, and Robustness of Fast Likelihood-based Approximation Schemes. Systematic Biology, 2011, 60, 685-699.	2.7	912
43	Evolution of cyanobacterial morphotypes: Taxa required for improved phylogenomic approaches. Communicative and Integrative Biology, 2011, 4, 424-7.	0.6	14
44	Finding the balance between the mathematical and biological optima in multiple sequence alignment. Trends in Evolutionary Biology, 2010, 2, 7.	0.4	30
45	PANDITplus: toward better integration of evolutionary view on molecular sequences with supplementary bioinformatics resources. Trends in Evolutionary Biology, 2010, 2, 1.	0.4	6
46	New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. Systematic Biology, 2010, 59, 307-321.	2.7	15,166
47	Investigating Protein-Coding Sequence Evolution with Probabilistic Codon Substitution Models. Molecular Biology and Evolution, 2009, 26, 255-271.	3.5	141
48	Origin and Evolution of GAL4-LRR, a New Member of the CC-LRR Subfamily: From Plants to Bacteria?. PLoS ONE, 2008, 3, e1694.	1.1	46
49	Multiple Hypothesis Testing to Detect Lineages under Positive Selection that Affects Only a Few Sites. Molecular Biology and Evolution, 2007, 24, 1219-1228.	3.5	197
50	Phylogenomic analysis of natural selection pressure in <i>Streptococcus</i> genomes. BMC Evolutionary Biology, 2007, 7, 154.	3.2	47
51	Positive and Negative Selection in the $\beta$ -Esterase Gene Cluster of the <i>Drosophila melanogaster</i> Subgroup. Journal of Molecular Evolution, 2006, 62, 496-510.	0.8	9
52	Approximate Likelihood-Ratio Test for Branches: A Fast, Accurate, and Powerful Alternative. Systematic Biology, 2006, 55, 539-552.	2.7	2,426
53	Molecular Evolution of the Hepatitis Delta Virus Antigen Gene: Recombination or Positive Selection?. Journal of Molecular Evolution, 2004, 59, 815-826.	0.8	38
54	Accuracy and Power of Bayes Prediction of Amino Acid Sites Under Positive Selection. Molecular Biology and Evolution, 2002, 19, 950-958.	3.5	388

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55	Accuracy and Power of the Likelihood Ratio Test in Detecting Adaptive Molecular Evolution. Molecular Biology and Evolution, 2001, 18, 1585-1592.	3.5	658