

Yasubumi Sakakibara

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,749
citations

257450

24
h-index

189892

50
g-index

64
all docs

64
docs citations

64
times ranked

3150
citing authors

#	ARTICLE	IF	CITATIONS
1	MetaVelvet: an extension of Velvet assembler to de novo metagenome assembly from short sequence reads. <i>Nucleic Acids Research</i> , 2012, 40, e155-e155.	14.5	562
2	Stochastic context-free grammars for tRNA modeling. <i>Nucleic Acids Research</i> , 1994, 22, 5112-5120.	14.5	317
3	RNA secondary structure prediction using deep learning with thermodynamic integration. <i>Nature Communications</i> , 2021, 12, 941.	12.8	181
4	Efficient learning of context-free grammars from positive structural examples. <i>Information and Computation</i> , 1992, 97, 23-60.	0.7	127
5	Recent advances of grammatical inference. <i>Theoretical Computer Science</i> , 1997, 185, 15-45.	0.9	127
6	Convolutional neural network based on SMILES representation of compounds for detecting chemical motif. <i>BMC Bioinformatics</i> , 2018, 19, 526.	2.6	114
7	Learning context-free grammars from structural data in polynomial time. <i>Theoretical Computer Science</i> , 1990, 76, 223-242.	0.9	101
8	Statistical prediction of protein-chemical interactions based on chemical structure and mass spectrometry data. <i>Bioinformatics</i> , 2007, 23, 2004-2012.	4.1	91
9	MetaVelvet-SL: an extension of the Velvet assembler to a de novo metagenomic assembler utilizing supervised learning. <i>DNA Research</i> , 2015, 22, 69-77.	3.4	89
10	Whole genome assembly of a natto production strain <i>Bacillus subtilis</i> natto from very short read data. <i>BMC Genomics</i> , 2010, 11, 243.	2.8	87
11	Comprehensive evaluation of non-hybrid genome assembly tools for third-generation PacBio long-read sequence data. <i>Briefings in Bioinformatics</i> , 2019, 20, 866-876.	6.5	86
12	Pair stochastic tree adjoining grammars for aligning and predicting pseudoknot RNA structures. <i>Bioinformatics</i> , 2005, 21, 2611-2617.	4.1	62
13	Convolutional neural networks for classification of alignments of non-coding RNA sequences. <i>Bioinformatics</i> , 2018, 34, i237-i244.	4.1	59
14	Integrating Statistical Predictions and Experimental Verifications for Enhancing Protein-Chemical Interaction Predictions in Virtual Screening. <i>PLoS Computational Biology</i> , 2009, 5, e1000397.	3.2	53
15	Grammatical inference in bioinformatics. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2005, 27, 1051-1062.	13.9	52
16	Pair hidden Markov models on tree structures. <i>Bioinformatics</i> , 2003, 19, i232-i240.	4.1	44
17	Learning context-free grammars using tabular representations. <i>Pattern Recognition</i> , 2005, 38, 1372-1383.	8.1	43
18	RNA secondary structural alignment with conditional random fields. <i>Bioinformatics</i> , 2005, 21, ii237-ii242.	4.1	42

#	ARTICLE	IF	CITATIONS
19	Whole Genome Complete Resequencing of <i>Bacillus subtilis</i> Natto by Combining Long Reads with High-Quality Short Reads. <i>PLoS ONE</i> , 2014, 9, e109999.	2.5	41
20	DAFS: simultaneous aligning and folding of RNA sequences via dual decomposition. <i>Bioinformatics</i> , 2012, 28, 3218-3224.	4.1	40
21	An efficient algorithm for de novo predictions of biochemical pathways between chemical compounds. <i>BMC Bioinformatics</i> , 2012, 13, S8.	2.6	32
22	Resequencing of the common marmoset genome improves genome assemblies and gene-coding sequence analysis. <i>Scientific Reports</i> , 2015, 5, 16894.	3.3	32
23	Whole-Genome Sequencing and Comparative Genome Analysis of <i>Bacillus subtilis</i> Strains Isolated from Non-Salted Fermented Soybean Foods. <i>PLoS ONE</i> , 2015, 10, e0141369.	2.5	32
24	A max-margin training of RNA secondary structure prediction integrated with the thermodynamic model. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840025.	0.8	32
25	Murasaki: A Fast, Parallelizable Algorithm to Find Anchors from Multiple Genomes. <i>PLoS ONE</i> , 2010, 5, e12651.	2.5	30
26	Learning Context-Free Grammars from Partially Structured Examples. <i>Lecture Notes in Computer Science</i> , 2000, , 229-240.	1.3	23
27	Performance of a deep learning-based identification system for esophageal cancer from CT images. <i>Esophagus</i> , 2021, 18, 612-620.	1.9	21
28	DEclust: A statistical approach for obtaining differential expression profiles of multiple conditions. <i>PLoS ONE</i> , 2017, 12, e0188285.	2.5	20
29	STEM KERNELS FOR RNA SEQUENCE ANALYSES. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 1103-1122.	0.8	18
30	COPICAT: a software system for predicting interactions between proteins and chemical compounds. <i>Bioinformatics</i> , 2012, 28, 745-746.	4.1	18
31	Fast and accurate clustering of noncoding RNAs using ensembles of sequence alignments and secondary structures. <i>BMC Bioinformatics</i> , 2011, 12, S48.	2.6	16
32	Informative RNA base embedding for RNA structural alignment and clustering by deep representation learning. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac012.	3.2	15
33	Directed acyclic graph kernels for structural RNA analysis. <i>BMC Bioinformatics</i> , 2008, 9, 318.	2.6	14
34	An extended genovo metagenomic assembler by incorporating paired-end information. <i>PeerJ</i> , 2013, 1, e196.	2.0	14
35	Genome-wide searching with base-pairing kernel functions for noncoding RNAs: computational and expression analysis of snoRNA families in <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2009, 37, 999-1009.	14.5	11
36	A NON-PARAMETRIC BAYESIAN APPROACH FOR PREDICTING RNA SECONDARY STRUCTURES. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 727-742.	0.8	11

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37	An improved de novo genome assembly of the common marmoset genome yields improved contiguity and increased mapping rates of sequence data. <i>BMC Genomics</i> , 2020, 21, 243.	2.8	9
38	Chromosomal-scale de novo genome assemblies of <i>Cynomolgus</i> Macaque and Common Marmoset. <i>Scientific Data</i> , 2021, 8, 159.	5.3	9
39	Development and preliminary validation of a machine learning system for thyroid dysfunction diagnosis based on routine laboratory tests. <i>Communications Medicine</i> , 2022, 2, .	4.2	9
40	Nordihydroguaiaretic Acid Disrupts the Antioxidant Ability of <i>Helicobacter pylori</i> through the Repression of SodB Activity In Vitro. <i>BioMed Research International</i> , 2015, 2015, 1-8.	1.9	8
41	Poly- γ -glutamic acid production of <i>Bacillus subtilis</i> (natto) in the absence of DegQ: A gain-of-function mutation in <i>yajL</i> gene. <i>Journal of Bioscience and Bioengineering</i> , 2019, 128, 690-696.	2.2	8
42	Deep learning integration of molecular and interactome data for protein-compound interaction prediction. <i>Journal of Cheminformatics</i> , 2021, 13, 36.	6.1	8
43	MetaVelvet-DL: a MetaVelvet deep learning extension for de novo metagenome assembly. <i>BMC Bioinformatics</i> , 2021, 22, 427.	2.6	8
44	Time-Series Analysis of Tumorigenesis in a Murine Skin Carcinogenesis Model. <i>Scientific Reports</i> , 2018, 8, 12994.	3.3	6
45	DNA-based algorithms for learning Boolean formulae. <i>Natural Computing</i> , 2003, 2, 153-171.	3.0	5
46	Software.ncrna.org: web servers for analyses of RNA sequences. <i>Nucleic Acids Research</i> , 2008, 36, W75-W78.	14.5	5
47	PSSMTS: position specific scoring matrices on tree structures. <i>Journal of Mathematical Biology</i> , 2007, 56, 201-214.	1.9	3
48	SHARAKU: an algorithm for aligning and clustering read mapping profiles of deep sequencing in non-coding RNA processing. <i>Bioinformatics</i> , 2016, 32, i369-i377.	4.1	3
49	Operon structure optimization by random self-assembly. <i>Natural Computing</i> , 2010, 9, 173-181.	3.0	2
50	Guest editorial to the special issue on grammatical inference. <i>Machine Learning</i> , 2007, 66, 3-5.	5.4	1
51	Robust and accurate prediction of noncoding RNAs from aligned sequences. <i>BMC Bioinformatics</i> , 2010, 11, S3.	2.6	1
52	A Non-parametric Bayesian Approach for Predicting RNA Secondary Structures. <i>Lecture Notes in Computer Science</i> , 2009, , 286-297.	1.3	1
53	Probabilistic Context-Free Grammars. , 2017, , 1013-1017.		1
54	Sequence and Structural Analyses for Functional Non-coding RNAs. <i>Natural Computing Series</i> , 2009, , 63-79.	2.2	0

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55	Genomic style: yet another deep-learning approach to characterize bacterial genome sequences. Bioinformatics Advances, 2021, 1, .	2.4	0