Yasubumi Sakakibara

List of Publications by Year
in descending order

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	Development and preliminary validation of a machine learning system for thyroid dysfunction diagnosis based on routine laboratory tests. Communications Medicine, 2022, 2, .	4.2	9
2	Informative RNA base embedding for RNA structural alignment and clustering by deep representation learning. NAR Genomics and Bioinformatics, 2022, 4, lqac012.	3.2	15
3	Performance of a deep learning-based identification system for esophageal cancer from CT images. Esophagus, 2021, 18, 612-620.	1.9	21
4	RNA secondary structure prediction using deep learning with thermodynamic integration. Nature Communications, 2021, 12, 941.	12.8	181
5	Deep learning integration of molecular and interactome data for protein–compound interaction prediction. Journal of Cheminformatics, 2021, 13, 36.	6.1	8
6	Chromosomal-scale de novo genome assemblies of Cynomolgus Macaque and Common Marmoset. Scientific Data, 2021, 8, 159.	5.3	9
7	MetaVelvet-DL: a MetaVelvet deep learning extension for de novo metagenome assembly. BMC Bioinformatics, 2021, 22, 427.	2.6	8
8	Genomic style: yet another deep-learning approach to characterize bacterial genome sequences. Bioinformatics Advances, 2021, 1, .	2.4	0
9	An improved de novo genome assembly of the common marmoset genome yields improved contiguity and increased mapping rates of sequence data. BMC Genomics, 2020, 21, 243.	2.8	9
10	Poly-γ-glutamic acid production of Bacillus subtilis (natto) in the absence of DegQ: A gain-of-function mutation in yabJ gene. Journal of Bioscience and Bioengineering, 2019, 128, 690-696.	2.2	8
11	Comprehensive evaluation of non-hybrid genome assembly tools for third-generation PacBio long-read sequence data. Briefings in Bioinformatics, 2019, 20, 866-876.	6.5	86
12	Convolutional neural network based on SMILES representation of compounds for detecting chemical motif. BMC Bioinformatics, 2018, 19, 526.	2.6	114
13	A max-margin training of RNA secondary structure prediction integrated with the thermodynamic model. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840025.	0.8	32
14	Time-Series Analysis of Tumorigenesis in a Murine Skin Carcinogenesis Model. Scientific Reports, 2018, 8, 12994.	3.3	6
15	Convolutional neural networks for classification of alignments of non-coding RNA sequences. Bioinformatics, 2018, 34, i237-i244.	4.1	59
16	DEclust: A statistical approach for obtaining differential expression profiles of multiple conditions. PLoS ONE, 2017, 12, e0188285.	2.5	20
17	Probabilistic Context-Free Grammars. , 2017, , 1013-1017.		1
18	SHARAKU: an algorithm for aligning and clustering read mapping profiles of deep sequencing in non-coding RNA processing. Bioinformatics, 2016, 32, i369-i377.	4.1	3

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19	Resequencing of the common marmoset genome improves genome assemblies and gene-coding sequence analysis. Scientific Reports, 2015, 5, 16894.	3.3	32
20	Whole-Genome Sequencing and Comparative Genome Analysis of Bacillus subtilis Strains Isolated from Non-Salted Fermented Soybean Foods. PLoS ONE, 2015, 10, e0141369.	2.5	32
21	Nordihydroguaiaretic Acid Disrupts the Antioxidant Ability ofHelicobacter pylorithrough the Repression of SodB ActivityIn Vitro. BioMed Research International, 2015, 2015, 1-8.	1.9	8
22	MetaVelvet-SL: an extension of the Velvet assembler to a de novo metagenomic assembler utilizing supervised learning. DNA Research, 2015, 22, 69-77.	3.4	89
23	Whole Genome Complete Resequencing of Bacillus subtilis Natto by Combining Long Reads with High-Quality Short Reads. PLoS ONE, 2014, 9, e109999.	2.5	41
24	An extended genovo metagenomic assembler by incorporating paired-end information. PeerJ, 2013, 1, e196.	2.0	14
25	DAFS: simultaneous aligning and folding of RNA sequences via dual decomposition. Bioinformatics, 2012, 28, 3218-3224.	4.1	40
26	COPICAT: a software system for predicting interactions between proteins and chemical compounds. Bioinformatics, 2012, 28, 745-746.	4.1	18
27	MetaVelvet: an extension of Velvet assembler to de novo metagenome assembly from short sequence reads. Nucleic Acids Research, 2012, 40, e155-e155.	14.5	562
28	An efficient algorithm for de novo predictions of biochemical pathways between chemical compounds. BMC Bioinformatics, 2012, 13, S8.	2.6	32
29	Fast and accurate clustering of noncoding RNAs using ensembles of sequence alignments and secondary structures. BMC Bioinformatics, 2011, 12, S48.	2.6	16
30	Operon structure optimization by random self-assembly. Natural Computing, 2010, 9, 173-181.	3.0	2
31	Robust and accurate prediction of noncoding RNAs from aligned sequences. BMC Bioinformatics, 2010, 11, S3.	2.6	1
32	Whole genome assembly of a natto production strain Bacillus subtilis natto from very short read data. BMC Genomics, 2010, 11, 243.	2.8	87
33	Murasaki: A Fast, Parallelizable Algorithm to Find Anchors from Multiple Genomes. PLoS ONE, 2010, 5, e12651.	2.5	30
34	A NON-PARAMETRIC BAYESIAN APPROACH FOR PREDICTING RNA SECONDARY STRUCTURES. Journal of Bioinformatics and Computational Biology, 2010, 08, 727-742.	0.8	11
35	Integrating Statistical Predictions and Experimental Verifications for Enhancing Protein-Chemical Interaction Predictions in Virtual Screening. PLoS Computational Biology, 2009, 5, e1000397.	3.2	53
36	Genome-wide searching with base-pairing kernel functions for noncoding RNAs: computational and expression analysis of snoRNA families in Caenorhabditis elegans. Nucleic Acids Research, 2009, 37, 999-1009.	14.5	11

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37	A Non-parametric Bayesian Approach for Predicting RNA Secondary Structures. Lecture Notes in Computer Science, 2009, , 286-297.	1.3	1
38	Sequence and Structural Analyses forÂFunctional Non-coding RNAs. Natural Computing Series, 2009, , 63-79.	2.2	0
39	Directed acyclic graph kernels for structural RNA analysis. BMC Bioinformatics, 2008, 9, 318.	2.6	14
40	Software.ncrna.org: web servers for analyses of RNA sequences. Nucleic Acids Research, 2008, 36, W75-W78.	14.5	5
41	STEM KERNELS FOR RNA SEQUENCE ANALYSES. Journal of Bioinformatics and Computational Biology, 2007, 05, 1103-1122.	0.8	18
42	Statistical prediction of proteinâ€"chemical interactions based on chemical structure and mass spectrometry data. Bioinformatics, 2007, 23, 2004-2012.	4.1	91
43	PSSMTS: position specific scoring matrices on tree structures. Journal of Mathematical Biology, 2007, 56, 201-214.	1.9	3
44	Guest editorial to the special issue on grammatical inference. Machine Learning, 2007, 66, 3-5.	5.4	1
45	Learning context-free grammars using tabular representations. Pattern Recognition, 2005, 38, 1372-1383.	8.1	43
46	Pair stochastic tree adjoining grammars for aligning and predicting pseudoknot RNA structures. Bioinformatics, 2005, 21, 2611-2617.	4.1	62
47	RNA secondary structural alignment with conditional random fields. Bioinformatics, 2005, 21, ii237-ii242.	4.1	42
48	Grammatical inference in bioinformatics. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2005, 27, 1051-1062.	13.9	52
49	DNA-based algorithms for learning Boolean formulae. Natural Computing, 2003, 2, 153-171.	3.0	5
50	Pair hidden Markov models on tree structures. Bioinformatics, 2003, 19, i232-i240.	4.1	44
51	Learning Context-Free Grammars from Partially Structured Examples. Lecture Notes in Computer Science, 2000, , 229-240.	1.3	23
52	Recent advances of grammatical inference. Theoretical Computer Science, 1997, 185, 15-45.	0.9	127
53	Stochastic context-free grammers for tRNA modeling. Nucleic Acids Research, 1994, 22, 5112-5120.	14.5	317
54	Efficient learning of context-free grammars from positive structural examples. Information and Computation, 1992, 97, 23-60.	0.7	127

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55	Learning context-free grammars from structural data in polynomial time. Theoretical Computer Science, 1990, 76, 223-242.	0.9	101