

Kiyoshi Asai

List of Publications by Year in descending order

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Version: 2024-02-01

123
papers

9,195
citations

66343

42
h-index

42399

92
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129
all docs

129
docs citations

129
times ranked

9664
citing authors

#	ARTICLE	IF	CITATIONS
1	ConsAlifold: considering RNA structural alignments improves prediction accuracy of RNA consensus secondary structures. <i>Bioinformatics</i> , 2022, 38, 710-719.	4.1	6
2	QRNAstruct: a method for extracting secondary structural features of RNA via regression with biological activity. <i>Nucleic Acids Research</i> , 2022, , .	14.5	0
3	A streamlined strain engineering workflow with genome-wide screening detects enhanced protein secretion in <i>Komagataella phaffii</i> . <i>Communications Biology</i> , 2022, 5, .	4.4	6
4	PBSIM2: a simulator for long-read sequencers with a novel generative model of quality scores. <i>Bioinformatics</i> , 2021, 37, 589-595.	4.1	81
5	m ⁶ A modification of HSATIII lncRNAs regulates temperature-dependent splicing. <i>EMBO Journal</i> , 2021, 40, e107976.	7.8	36
6	A robust model for quantitative prediction of the silencing efficacy of wild-type and A-to-I edited miRNAs. <i>RNA Biology</i> , 2020, 17, 264-280.	3.1	1
7	lncRNA-dependent nuclear stress bodies promote intron retention through SR protein phosphorylation. <i>EMBO Journal</i> , 2020, 39, e102729.	7.8	99
8	Free-Energy Calculation of Ribonucleic Inosines and Its Application to Nearest-Neighbor Parameters. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 5923-5935.	5.3	5
9	Finding the direct optimal RNA barrier energy and improving pathways with an arbitrary energy model. <i>Bioinformatics</i> , 2020, 36, i227-i235.	4.1	2
10	Exchange of endogenous and heterogeneous yeast terminators in <i>Pichia pastoris</i> to tune mRNA stability and gene expression. <i>Nucleic Acids Research</i> , 2020, 48, 13000-13012.	14.5	37
11	COSMO: A dynamic programming algorithm for multicriteria codon optimization. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1811-1818.	4.1	6
12	RintC: fast and accuracy-aware decomposition of distributions of RNA secondary structures with extended logsumexp. <i>BMC Bioinformatics</i> , 2020, 21, 210.	2.6	0
13	Improving the prediction accuracy of protein abundance in <i>Escherichia coli</i> using mRNA accessibility. <i>Nucleic Acids Research</i> , 2020, 48, e81-e81.	14.5	20
14	RNA Structure Prediction. , 2019, , 575-584.		1
15	Estimating Energy Parameters for RNA Secondary Structure Predictions Using Both Experimental and Computational Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1645-1655.	3.0	4
16	Secure Division Protocol and Applications to Privacy-preserving Chi-squared Tests. , 2018, , .		8
17	Jointly aligning a group of DNA reads improves accuracy of identifying large deletions. <i>Nucleic Acids Research</i> , 2018, 46, e18-e18.	14.5	3
18	Combining probabilistic alignments with read pair information improves accuracy of split-alignments. <i>Bioinformatics</i> , 2018, 34, 3631-3637.	4.1	0

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19	Capturing alternative secondary structures of RNA by decomposition of base-pairing probabilities. <i>BMC Bioinformatics</i> , 2018, 19, 38.	2.6	8
20	Training alignment parameters for arbitrary sequencers with LAST-TRAIN. <i>Bioinformatics</i> , 2017, 33, 926-928.	4.1	70
21	Evolutionary design of multiple genes encoding the same protein. <i>Bioinformatics</i> , 2017, 33, 1613-1620.	4.1	10
22	Genome Sequence of <i>Ustilaginoidea virens</i> IPU010, a Rice Pathogenic Fungus Causing False Smut. <i>Genome Announcements</i> , 2016, 4, .	0.8	22
23	Class of cyclic ribosomal peptide synthetic genes in filamentous fungi. <i>Fungal Genetics and Biology</i> , 2016, 86, 58-70.	2.1	84
24	Genome sequence of <i>Aspergillus luchuensis</i> NBRC 4314. <i>DNA Research</i> , 2016, 23, 507-515.	3.4	48
25	Improved Accuracy in RNA-Protein Rigid Body Docking by Incorporating Force Field for Molecular Dynamics Simulation into the Scoring Function. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 4688-4697.	5.3	23
26	Comprehensive prediction of lncRNA-RNA interactions in human transcriptome. <i>BMC Genomics</i> , 2016, 17, 12.	2.8	54
27	<i>Rtools</i> : a web server for various secondary structural analyses on single RNA sequences. <i>Nucleic Acids Research</i> , 2016, 44, W302-W307.	14.5	21
28	CDSfold: an algorithm for designing a protein-coding sequence with the most stable secondary structure. <i>Bioinformatics</i> , 2016, 32, 828-834.	4.1	10
29	Bioinformatics tools for lncRNA research. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 23-30.	1.9	45
30	Privacy-preserving search for chemical compound databases. <i>BMC Bioinformatics</i> , 2015, 16, S6.	2.6	10
31	Learning chromatin states with factorized information criteria. <i>Bioinformatics</i> , 2015, 31, 2426-2433.	4.1	14
32	Guest Editorial for the 25th International Conference on Genome Informatics (GIW/ISCB-Asia 2014). <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 761-762.	3.0	1
33	A semi-supervised learning approach for RNA secondary structure prediction. <i>Computational Biology and Chemistry</i> , 2015, 57, 72-79.	2.3	12
34	Ustiloxins, fungal cyclic peptides, are ribosomally synthesized in <i>Ustilaginoidea virens</i> . <i>Bioinformatics</i> , 2015, 31, 981-985.	4.1	62
35	Predicting RNA Duplex Dimerization Free-Energy Changes upon Mutations Using Molecular Dynamics Simulations. <i>Journal of Physical Chemistry Letters</i> , 2015, 6, 4348-4351.	4.6	19
36	Hybrid De Novo Genome Assembly Using MiSeq and SOLiD Short Read Data. <i>PLoS ONE</i> , 2015, 10, e0126289.	2.5	6

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37	CapR: revealing structural specificities of RNA-binding protein target recognition using CLIP-seq data. <i>Genome Biology</i> , 2014, 15, R16.	9.6	80
38	Motif-Independent Prediction of a Secondary Metabolism Gene Cluster Using Comparative Genomics: Application to Sequenced Genomes of <i>Aspergillus</i> and Ten Other Filamentous Fungal Species. <i>DNA Research</i> , 2014, 21, 447-457.	3.4	44
39	Tertiary Structure Prediction of RNA-RNA Complexes Using a Secondary Structure and Fragment-Based Method. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 672-682.	5.4	6
40	Reference-free prediction of rearrangement breakpoint reads. <i>Bioinformatics</i> , 2014, 30, 2559-2567.	4.1	5
41	Efficient calculation of exact probability distributions of integer features on RNA secondary structures. <i>BMC Genomics</i> , 2014, 15, S6.	2.8	11
42	RNA Structural Alignments, Part II: Non-Sankoff Approaches for Structural Alignments. <i>Methods in Molecular Biology</i> , 2014, 1097, 291-301.	0.9	14
43	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. <i>Journal of Biomedical Semantics</i> , 2013, 4, 6.	1.6	26
44	Analysis of base-pairing probabilities of RNA molecules involved in protein-RNA interactions. <i>Bioinformatics</i> , 2013, 29, 2524-2528.	4.1	10
45	CentroidAlign-Web: A Fast and Accurate Multiple Aligner for Long Non-Coding RNAs. <i>International Journal of Molecular Sciences</i> , 2013, 14, 6144-6156.	4.1	4
46	PBSIM: PacBio reads simulator toward accurate genome assembly. <i>Bioinformatics</i> , 2013, 29, 119-121.	4.1	279
47	Finding Protein-Coding Genes through Human Polymorphisms. <i>PLoS ONE</i> , 2013, 8, e54210.	2.5	3
48	MIDDAS-M: Motif-Independent De Novo Detection of Secondary Metabolite Gene Clusters through the Integration of Genome Sequencing and Transcriptome Data. <i>PLoS ONE</i> , 2013, 8, e84028.	2.5	106
49	Shape-based alignment of genomic landscapes in multi-scale resolution. <i>Nucleic Acids Research</i> , 2012, 40, 6435-6448.	14.5	7
50	DAFS: simultaneous aligning and folding of RNA sequences via dual decomposition. <i>Bioinformatics</i> , 2012, 28, 3218-3224.	4.1	40
51	Transformations for the compression of FASTQ quality scores of next-generation sequencing data. <i>Bioinformatics</i> , 2012, 28, 628-635.	4.1	45
52	Rtips: fast and accurate tools for RNA 2D structure prediction using integer programming. <i>Nucleic Acids Research</i> , 2012, 40, W29-W34.	14.5	17
53	A mostly traditional approach improves alignment of bisulfite-converted DNA. <i>Nucleic Acids Research</i> , 2012, 40, e100-e100.	14.5	55
54	RecountDB: a database of mapped and count corrected transcribed sequences. <i>Nucleic Acids Research</i> , 2012, 40, D1089-D1092.	14.5	0

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55	A Classification of Bioinformatics Algorithms from the Viewpoint of Maximizing Expected Accuracy (MEA). <i>Journal of Computational Biology</i> , 2012, 19, 532-549.	1.6	13
56	Prediction of Conserved Precursors of miRNAs and Their Mature Forms by Integrating Position-Specific Structural Features. <i>PLoS ONE</i> , 2012, 7, e44314.	2.5	12
57	Rchange: algorithms for computing energy changes of RNA secondary structures in response to base mutations. <i>Bioinformatics</i> , 2012, 28, 1093-1101.	4.1	17
58	Antagonistic RNA aptamer specific to a heterodimeric form of human interleukin-17A/F. <i>Biochimie</i> , 2011, 93, 1081-1088.	2.6	18
59	Generalized Centroid Estimators in Bioinformatics. <i>PLoS ONE</i> , 2011, 6, e16450.	2.5	15
60	Probabilistic alignments with quality scores: an application to short-read mapping toward accurate SNP/indel detection. <i>Bioinformatics</i> , 2011, 27, 3085-3092.	4.1	16
61	IPknot: fast and accurate prediction of RNA secondary structures with pseudoknots using integer programming. <i>Bioinformatics</i> , 2011, 27, i85-i93.	4.1	253
62	Improving the accuracy of predicting secondary structure for aligned RNA sequences. <i>Nucleic Acids Research</i> , 2011, 39, 393-402.	14.5	59
63	A detailed investigation of accessibilities around target sites of siRNAs and miRNAs. <i>Bioinformatics</i> , 2011, 27, 1788-1797.	4.1	62
64	CentroidHomfold-LAST: accurate prediction of RNA secondary structure using automatically collected homologous sequences. <i>Nucleic Acids Research</i> , 2011, 39, W100-W106.	14.5	22
65	Prediction of RNA secondary structure by maximizing pseudo-expected accuracy. <i>BMC Bioinformatics</i> , 2010, 11, 586.	2.6	24
66	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. <i>Journal of Biomedical Semantics</i> , 2010, 1, 8.	1.6	31
67	Discovery of short pseudogenes derived from messenger RNAs. <i>Nucleic Acids Research</i> , 2010, 38, 1163-1171.	14.5	15
68	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
69	RactIP: fast and accurate prediction of RNA-RNA interaction using integer programming. <i>Bioinformatics</i> , 2010, 26, i460-i466.	4.1	99
70	Conic Programming for Multitask Learning. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2010, 22, 957-968.	5.7	49
71	Sorting next generation sequencing data improves compression effectiveness. , 2010, , .		4
72	In search of true reads: A classification approach to next generation sequencing data selection. , 2010, , .		0

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73	CENTROIDFOLD: a web server for RNA secondary structure prediction. <i>Nucleic Acids Research</i> , 2009, 37, W277-W280.	14.5	279
74	Prediction of RNA secondary structure using generalized centroid estimators. <i>Bioinformatics</i> , 2009, 25, 465-473.	4.1	203
75	CentroidAlign: fast and accurate aligner for structured RNAs by maximizing expected sum-of-pairs score. <i>Bioinformatics</i> , 2009, 25, 3236-3243.	4.1	45
76	Predictions of RNA secondary structure by combining homologous sequence information. <i>Bioinformatics</i> , 2009, 25, i330-i338.	4.1	51
77	Transcripts of unknown function in multiple-signaling pathways involved in human stem cell differentiation. <i>Nucleic Acids Research</i> , 2009, 37, 4987-5000.	14.5	51
78	A local multiple alignment method for detection of non-coding RNA sequences. <i>Bioinformatics</i> , 2009, 25, 1498-1505.	4.1	16
79	The Functional RNA Database 3.0: databases to support mining and annotation of functional RNAs. <i>Nucleic Acids Research</i> , 2009, 37, D89-D92.	14.5	119
80	A regulatory circuit for piwi by the large Maf gene traffic jam in <i>Drosophila</i> . <i>Nature</i> , 2009, 461, 1296-1299.	27.8	387
81	Large Scale Similarity Search for Locally Stable Secondary Structures among RNA Sequences. <i>IPSJ Transactions on Bioinformatics</i> , 2009, 2, 36-46.	0.2	1
82	A Non-parametric Bayesian Approach for Predicting RNA Secondary Structures. <i>Lecture Notes in Computer Science</i> , 2009, , 286-297.	1.3	1
83	<i>Drosophila</i> endogenous small RNAs bind to Argonaute2 in somatic cells. <i>Nature</i> , 2008, 453, 793-797.	27.8	417
84	Directed acyclic graph kernels for structural RNA analysis. <i>BMC Bioinformatics</i> , 2008, 9, 318.	2.6	14
85	A fast structural multiple alignment method for long RNA sequences. <i>BMC Bioinformatics</i> , 2008, 9, 33.	2.6	95
86	Expansion of signaling genes for adaptive immune system evolution in early vertebrates. <i>BMC Genomics</i> , 2008, 9, 218.	2.8	9
87	Retention of genes involved in the adenohipophysis-mediated endocrine system in early vertebrates. <i>Gene</i> , 2008, 412, 71-83.	2.2	1
88	Software.ncrna.org: web servers for analyses of RNA sequences. <i>Nucleic Acids Research</i> , 2008, 36, W75-W78.	14.5	5
89	Characterization of endogenous human Argonautes and their miRNA partners in RNA silencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7964-7969.	7.1	221
90	Rfold: an exact algorithm for computing local base pairing probabilities. <i>Bioinformatics</i> , 2008, 24, 367-373.	4.1	53

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91	STEM KERNELS FOR RNA SEQUENCE ANALYSES. Journal of Bioinformatics and Computational Biology, 2007, 05, 1103-1122.	0.8	18
92	miRRim: A novel system to find conserved miRNAs with high sensitivity and specificity. Rna, 2007, 13, 2081-2090.	3.5	51
93	Murlet: a practical multiple alignment tool for structural RNA sequences. Bioinformatics, 2007, 23, 1588-1598.	4.1	69
94	Genomics of <i>Aspergillus oryzae</i> . Bioscience, Biotechnology and Biochemistry, 2007, 71, 646-670.	1.3	163
95	Robust prediction of consensus secondary structures using averaged base pairing probability matrices. Bioinformatics, 2007, 23, 434-441.	4.1	51
96	A New Direction for the Computational Biology Research Center. Asia Pacific Biotech News, 2007, 11, 1027-1029.	0.0	0
97	fRNAdb: a platform for mining/annotating functional RNA candidates from non-coding RNA sequences. Nucleic Acids Research, 2007, 35, D145-D148.	14.5	134
98	Coordinated expression of ncRNAs and HOX mRNAs in the human HOXA locus. Biochemical and Biophysical Research Communications, 2007, 357, 724-730.	2.1	32
99	Identification and characterization of human non-coding RNAs with tissue-specific expression. Biochemical and Biophysical Research Communications, 2007, 357, 991-996.	2.1	33
100	Identification of Glycosyltransferases Focusing on Golgi Transmembrane Region. Trends in Glycoscience and Glycotechnology, 2007, 19, 41-47.	0.1	3
101	FLOW MODEL OF THE PROTEIN-PROTEIN INTERACTION NETWORK FOR FINDING CREDIBLE INTERACTIONS. , 2007, , .		1
102	Learning Kernels from Distance Constraints. IPSJ Digital Courier, 2006, 2, 441-451.	0.3	0
103	Network-based de-noising improves prediction from microarray data. BMC Bioinformatics, 2006, 7, S4.	2.6	13
104	Mining frequent stem patterns from unaligned RNA sequences. Bioinformatics, 2006, 22, 2480-2487.	4.1	40
105	SCARNA: fast and accurate structural alignment of RNA sequences by matching fixed-length stem fragments. Bioinformatics, 2006, 22, 1723-1729.	4.1	45
106	Genome sequencing and analysis of <i>Aspergillus oryzae</i> . Nature, 2005, 438, 1157-1161.	27.8	1,128
107	Genomic sequence of the pathogenic and allergenic filamentous fungus <i>Aspergillus fumigatus</i> . Nature, 2005, 438, 1151-1156.	27.8	1,272
108	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . Nature, 2005, 438, 1105-1115.	27.8	1,250

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109	Extracting relations between promoter sequences and their strengths from microarray data. <i>Bioinformatics</i> , 2005, 21, 1062-1068.	4.1	27
110	Accurate extraction of functional associations between proteins based on common interaction partners and common domains. <i>Bioinformatics</i> , 2005, 21, 2043-2048.	4.1	17
111	Selective integration of multiple biological data for supervised network inference. <i>Bioinformatics</i> , 2005, 21, 2488-2495.	4.1	58
112	Statistical evaluation of a bottom-up clustering for single particle molecular images. <i>Genome Informatics</i> , 2005, 16, 125-35.	0.4	2
113	Minimizing the Cross Validation Error to Mix Kernel Matrices of Heterogeneous Biological Data. <i>Neural Processing Letters</i> , 2004, 19, 63-72.	3.2	6
114	A New Variational Framework for Rigid-Body Alignment. <i>Lecture Notes in Computer Science</i> , 2004, , 171-179.	1.3	3
115	Inference of Euler angles for single-particle analysis by means of evolutionary algorithms. <i>BioSystems</i> , 2003, 72, 43-55.	2.0	1
116	Processing sequence annotation data using the Lua programming language. <i>Genome Informatics</i> , 2003, 14, 154-63.	0.4	7
117	Marginalized kernels for biological sequences. <i>Bioinformatics</i> , 2002, 18, S268-S275.	4.1	112
118	Modeling splicing sites with pairwise correlations. <i>Bioinformatics</i> , 2002, 18, S27-S34.	4.1	23
119	MOSBY: a molecular structure viewer program with portability and extensibility. <i>Journal of Molecular Graphics and Modelling</i> , 2002, 20, 411-413.	2.4	4
120	Marginalized kernels for RNA sequence data analysis. <i>Genome Informatics</i> , 2002, 13, 112-22.	0.4	10
121	Inference of Euler angles for single particle analysis by using Genetic Algorithms. <i>Genome Informatics</i> , 2002, 13, 133-42.	0.4	0
122	The voltage-sensitive sodium channel is a bell-shaped molecule with several cavities. <i>Nature</i> , 2001, 409, 1047-1051.	27.8	255
123	Prediction of protein secondary structure by the hidden Markov model. <i>Bioinformatics</i> , 1993, 9, 141-146.	4.1	86