Kiyoshi Asai

List of Publications by Year
in descending order

123 papers	9,195 citations	66343 42 h-index	42399 92 g-index
129 all docs	129 docs citations	129 times ranked	9664 citing authors

#	Article	IF	Citations
1	Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature, 2005, 438, 1151-1156.	27.8	1,272
2	Sequencing of Aspergillus nidulans and comparative analysis with A. fumigatus and A. oryzae. Nature, 2005, 438, 1105-1115.	27.8	1,250
3	Genome sequencing and analysis of Aspergillus oryzae. Nature, 2005, 438, 1157-1161.	27.8	1,128
4	Drosophila endogenous small RNAs bind to Argonaute‰2 in somatic cells. Nature, 2008, 453, 793-797.	27.8	417
5	A regulatory circuit for piwi by the large Maf gene traffic jam in Drosophila. Nature, 2009, 461, 1296-1299.	27.8	387
6	CENTROIDFOLD: a web server for RNA secondary structure prediction. Nucleic Acids Research, 2009, 37, W277-W280.	14.5	279
7	PBSIM: PacBio reads simulator—toward accurate genome assembly. Bioinformatics, 2013, 29, 119-121.	4.1	279
8	The voltage-sensitive sodium channel is a bell-shaped molecule with several cavities. Nature, 2001, 409, 1047-1051.	27.8	255
9	IPknot: fast and accurate prediction of RNA secondary structures with pseudoknots using integer programming. Bioinformatics, 2011, 27, i85-i93.	4.1	253
10	Characterization of endogenous human Argonautes and their miRNA partners in RNA silencing. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7964-7969.	7.1	221
11	Prediction of RNA secondary structure using generalized centroid estimators. Bioinformatics, 2009, 25, 465-473.	4.1	203
12	Genomics of <i>Aspergillus oryzae</i>. Bioscience, Biotechnology and Biochemistry, 2007, 71, 646-670.	1.3	163
13	fRNAdb: a platform for mining/annotating functional RNA candidates from non-coding RNA sequences. Nucleic Acids Research, 2007, 35, D145-D148.	14.5	134
14	The Functional RNA Database 3.0: databases to support mining and annotation of functional RNAs. Nucleic Acids Research, 2009, 37, D89-D92.	14.5	119
15	Marginalized kernels for biological sequences. Bioinformatics, 2002, 18, S268-S275.	4.1	112
16	MIDDAS-M: Motif-Independent De Novo Detection of Secondary Metabolite Gene Clusters through the Integration of Genome Sequencing and Transcriptome Data. PLoS ONE, 2013, 8, e84028.	2.5	106
17	RactIP: fast and accurate prediction of RNA-RNA interaction using integer programming. Bioinformatics, 2010, 26, i460-i466.	4.1	99
18	Lnc <scp>RNA</scp> â€dependent nuclear stress bodies promote intron retention through <scp>SR</scp> protein phosphorylation. EMBO Journal, 2020, 39, e102729.	7.8	99

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19	A fast structural multiple alignment method for long RNA sequences. BMC Bioinformatics, 2008, 9, 33.	2.6	95
20	Prediction of protein secondary structure by the hidden Markov model. Bioinformatics, 1993, 9, 141-146.	4.1	86
21	Class of cyclic ribosomal peptide synthetic genes in filamentous fungi. Fungal Genetics and Biology, 2016, 86, 58-70.	2.1	84
22	PBSIM2: a simulator for long-read sequencers with a novel generative model of quality scores. Bioinformatics, 2021, 37, 589-595.	4.1	81
23	CapR: revealing structural specificities of RNA-binding protein target recognition using CLIP-seq data. Genome Biology, 2014, 15, R16.	9.6	80
24	Training alignment parameters for arbitrary sequencers with LAST-TRAIN. Bioinformatics, 2017, 33, 926-928.	4.1	70
25	Murlet: a practical multiple alignment tool for structural RNA sequences. Bioinformatics, 2007, 23, 1588-1598.	4.1	69
26	A detailed investigation of accessibilities around target sites of siRNAs and miRNAs. Bioinformatics, 2011, 27, 1788-1797.	4.1	62
27	Ustiloxins, fungal cyclic peptides, are ribosomally synthesized in <i>Ustilaginoidea virens</i>. Bioinformatics, 2015, 31, 981-985.	4.1	62
28	Improving the accuracy of predicting secondary structure for aligned RNA sequences. Nucleic Acids Research, 2011, 39, 393-402.	14.5	59
29	Selective integration of multiple biological data for supervised network inference. Bioinformatics, 2005, 21, 2488-2495.	4.1	58
30	A mostly traditional approach improves alignment of bisulfite-converted DNA. Nucleic Acids Research, 2012, 40, e100-e100.	14.5	55
31	Comprehensive prediction of lncRNA–RNA interactions in human transcriptome. BMC Genomics, 2016, 17, 12.	2.8	54
32	Rfold: an exact algorithm for computing local base pairing probabilities. Bioinformatics, 2008, 24, 367-373.	4.1	53
33	miRRim: A novel system to find conserved miRNAs with high sensitivity and specificity. Rna, 2007, 13, 2081-2090.	3.5	51
34	Robust prediction of consensus secondary structures using averaged base pairing probability matrices. Bioinformatics, 2007, 23, 434-441.	4.1	51
35	Predictions of RNA secondary structure by combining homologous sequence information. Bioinformatics, 2009, 25, i330-i338.	4.1	51
36	Transcripts of unknown function in multiple-signaling pathways involved in human stem cell differentiation. Nucleic Acids Research, 2009, 37, 4987-5000.	14.5	51

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37	Conic Programming for Multitask Learning. IEEE Transactions on Knowledge and Data Engineering, 2010, 22, 957-968.	5.7	49
38	Genome sequence of *Aspergillus luchuensis* NBRC 4314. DNA Research, 2016, 23, 507-515.	3.4	48
39	SCARNA: fast and accurate structural alignment of RNA sequences by matching fixed-length stem fragments. Bioinformatics, 2006, 22, 1723-1729.	4.1	45
40	CentroidAlign: fast and accurate aligner for structured RNAs by maximizing expected sum-of-pairs score. Bioinformatics, 2009, 25, 3236-3243.	4.1	45
41	Transformations for the compression of FASTQ quality scores of next-generation sequencing data. Bioinformatics, 2012, 28, 628-635.	4.1	45
42	Bioinformatics tools for lncRNA research. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 23-30.	1.9	45
43	Motif-Independent Prediction of a Secondary Metabolism Gene Cluster Using Comparative Genomics: Application to Sequenced Genomes of Aspergillus and Ten Other Filamentous Fungal Species. DNA Research, 2014, 21, 447-457.	3.4	44
44	Mining frequent stem patterns from unaligned RNA sequences. Bioinformatics, 2006, 22, 2480-2487.	4.1	40
45	DAFS: simultaneous aligning and folding of RNA sequences via dual decomposition. Bioinformatics, 2012, 28, 3218-3224.	4.1	40
46	Exchange of endogenous and heterogeneous yeast terminators in *Pichia pastoris* to tune mRNA stability and gene expression. Nucleic Acids Research, 2020, 48, 13000-13012.	14.5	37
47	m^{6}A modification of HSATIII lncRNAs regulates temperature€dependent splicing. EMBO Journal, 2021, 40, e107976.	7.8	36
48	Identification and characterization of human non-coding RNAs with tissue-specific expression. Biochemical and Biophysical Research Communications, 2007, 357, 991-996.	2.1	33
49	Coordinated expression of ncRNAs and HOX mRNAs in the human HOXA locus. Biochemical and Biophysical Research Communications, 2007, 357, 724-730.	2.1	32
50	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	1.6	31
51	Extracting relations between promoter sequences and their strengths from microarray data. Bioinformatics, 2005, 21, 1062-1068.	4.1	27
52	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	1.6	26
53	Prediction of RNA secondary structure by maximizing pseudo-expected accuracy. BMC Bioinformatics, 2010, 11, 586.	2.6	24
54	Modeling splicing sites with pairwise correlations. Bioinformatics, 2002, 18, S27-S34.	4.1	23

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55	Improved Accuracy in RNA–Protein Rigid Body Docking by Incorporating Force Field for Molecular Dynamics Simulation into the Scoring Function. Journal of Chemical Theory and Computation, 2016, 12, 4688-4697.	5.3	23
56	CentroidHomfold-LAST: accurate prediction of RNA secondary structure using automatically collected homologous sequences. Nucleic Acids Research, 2011, 39, W100-W106.	14.5	22
57	Genome Sequence of *Ustilaginoidea virens* IPU010, a Rice Pathogenic Fungus Causing False Smut. Genome Announcements, 2016, 4, .	0.8	22
58	Rtools: a web server for various secondary structural analyses on single RNA sequences. Nucleic Acids Research, 2016, 44, W302-W307.	14.5	21
59	Improving the prediction accuracy of protein abundance in Escherichia coli using mRNA accessibility. Nucleic Acids Research, 2020, 48, e81-e81.	14.5	20
60	Predicting RNA Duplex Dimerization Free-Energy Changes upon Mutations Using Molecular Dynamics Simulations. Journal of Physical Chemistry Letters, 2015, 6, 4348-4351.	4.6	19
61	STEM KERNELS FOR RNA SEQUENCE ANALYSES. Journal of Bioinformatics and Computational Biology, 2007, 05, 1103-1122.	0.8	18
62	Antagonistic RNA aptamer specific to a heterodimeric form of human interleukin-17A/F. Biochimie, 2011, 93, 1081-1088.	2.6	18
63	Accurate extraction of functional associations between proteins based on common interaction partners and common domains. Bioinformatics, 2005, 21, 2043-2048.	4.1	17
64	Rtips: fast and accurate tools for RNA 2D structure prediction using integer programming. Nucleic Acids Research, 2012, 40, W29-W34.	14.5	17
65	Rchange: algorithms for computing energy changes of RNA secondary structures in response to base mutations. Bioinformatics, 2012, 28, 1093-1101.	4.1	17
66	A local multiple alignment method for detection of non-coding RNA sequences. Bioinformatics, 2009, 25, 1498-1505.	4.1	16
67	Probabilistic alignments with quality scores: an application to short-read mapping toward accurate SNP/indel detection. Bioinformatics, 2011, 27, 3085-3092.	4.1	16
68	Discovery of short pseudogenes derived from messenger RNAs. Nucleic Acids Research, 2010, 38, 1163-1171.	14.5	15
69	Generalized Centroid Estimators in Bioinformatics. PLoS ONE, 2011, 6, e16450.	2.5	15
70	Directed acyclic graph kernels for structural RNA analysis. BMC Bioinformatics, 2008, 9, 318.	2.6	14
71	Learning chromatin states with factorized information criteria. Bioinformatics, 2015, 31, 2426-2433.	4.1	14
72	RNA Structural Alignments, Part II: Non-Sankoff Approaches for Structural Alignments. Methods in Molecular Biology, 2014, 1097, 291-301.	0.9	14

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73	Network-based de-noising improves prediction from microarray data. BMC Bioinformatics, 2006, 7, S4.	2.6	13
74	A Classification of Bioinformatics Algorithms from the Viewpoint of Maximizing Expected Accuracy (MEA). Journal of Computational Biology, 2012, 19, 532-549.	1.6	13
75	Prediction of Conserved Precursors of miRNAs and Their Mature Forms by Integrating Position-Specific Structural Features. PLoS ONE, 2012, 7, e44314.	2.5	12
76	A semi-supervised learning approach for RNA secondary structure prediction. Computational Biology and Chemistry, 2015, 57, 72-79.	2.3	12
77	A NON-PARAMETRIC BAYESIAN APPROACH FOR PREDICTING RNA SECONDARY STRUCTURES. Journal of Bioinformatics and Computational Biology, 2010, 08, 727-742.	0.8	11
78	Efficient calculation of exact probability distributions of integer features on RNA secondary structures. BMC Genomics, 2014, 15, S6.	2.8	11
79	Analysis of base-pairing probabilities of RNA molecules involved in protein–RNA interactions. Bioinformatics, 2013, 29, 2524-2528.	4.1	10
80	Privacy-preserving search for chemical compound databases. BMC Bioinformatics, 2015, 16, S6.	2.6	10
81	CDSfold: an algorithm for designing a protein-coding sequence with the most stable secondary structure. Bioinformatics, 2016, 32, 828-834.	4.1	10
82	Evolutionary design of multiple genes encoding the same protein. Bioinformatics, 2017, 33, 1613-1620.	4.1	10
83	Marginalized kernels for RNA sequence data analysis. Genome Informatics, 2002, 13, 112-22.	0.4	10
84	Expansion of signaling genes for adaptive immune system evolution in early vertebrates. BMC Genomics, 2008, 9, 218.	2.8	9
85	Secure Division Protocol and Applications to Privacy-preserving Chi-squared Tests. , 2018, , .		8
86	Capturing alternative secondary structures of RNA by decomposition of base-pairing probabilities. BMC Bioinformatics, 2018, 19, 38.	2.6	8
87	Shape-based alignment of genomic landscapes in multi-scale resolution. Nucleic Acids Research, 2012, 40, 6435-6448.	14.5	7
88	Processing sequence annotation data using the Lua programming language. Genome Informatics, 2003, 14, 154-63.	0.4	7
89	Minimizing the Cross Validation Error to Mix Kernel Matrices of Heterogeneous Biological Data. Neural Processing Letters, 2004, 19, 63-72.	3.2	6
90	Tertiary Structure Prediction of RNA–RNA Complexes Using a Secondary Structure and Fragment-Based Method. Journal of Chemical Information and Modeling, 2014, 54, 672-682.	5.4	6

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91	COSMO: A dynamic programming algorithm for multicriteria codon optimization. Computational and Structural Biotechnology Journal, 2020, 18, 1811-1818.	4.1	6
92	Hybrid De Novo Genome Assembly Using MiSeq and SOLiD Short Read Data. PLoS ONE, 2015, 10, e0126289.	2.5	6
93	ConsAlifold: considering RNA structural alignments improves prediction accuracy of RNA consensus secondary structures. Bioinformatics, 2022, 38, 710-719.	4.1	6
94	A streamlined strain engineering workflow with genome-wide screening detects enhanced protein secretion in Komagataella phaffii. Communications Biology, 2022, 5, .	4.4	6
95	Software.ncrna.org: web servers for analyses of RNA sequences. Nucleic Acids Research, 2008, 36, W75-W78.	14.5	5
96	Reference-free prediction of rearrangement breakpoint reads. Bioinformatics, 2014, 30, 2559-2567.	4.1	5
97	Free-Energy Calculation of Ribonucleic Inosines and Its Application to Nearest-Neighbor Parameters. Journal of Chemical Theory and Computation, 2020, 16, 5923-5935.	5.3	5
98	MOSBY: a molecular structure viewer program with portability and extensibility. Journal of Molecular Graphics and Modelling, 2002, 20, 411-413.	2.4	4
99	Sorting next generation sequencing data improves compression effectiveness. , 2010, , .		4
100	CentroidAlign-Web: A Fast and Accurate Multiple Aligner for Long Non-Coding RNAs. International Journal of Molecular Sciences, 2013, 14, 6144-6156.	4.1	4
101	Estimating Energy Parameters for RNA Secondary Structure Predictions Using Both Experimental and Computational Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1645-1655.	3.0	4
102	Finding Protein-Coding Genes through Human Polymorphisms. PLoS ONE, 2013, 8, e54210.	2.5	3
103	Jointly aligning a group of DNA reads improves accuracy of identifying large deletions. Nucleic Acids Research, 2018, 46, e18-e18.	14.5	3
104	A New Variational Framework for Rigid-Body Alignment. Lecture Notes in Computer Science, 2004, , 171-179.	1.3	3
105	Identification of Glycosyltransferases Focusing on Golgi Transmembrane Region. Trends in Glycoscience and Glycotechnology, 2007, 19, 41-47.	0.1	3
106	Finding the direct optimal RNA barrier energy and improving pathways with an arbitrary energy model. Bioinformatics, 2020, 36, i227-i235.	4.1	2
107	Statistical evaluation of a bottom-up clustering for single particle molecular images. Genome Informatics, 2005, 16, 125-35.	0.4	2
108	Inference of Euler angles for single-particle analysis by means of evolutionary algorithms. BioSystems, 2003, 72, 43-55.	2.0	1

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109	Retention of genes involved in the adenohypophysis-mediated endocrine system in early vertebrates. Gene, 2008, 412, 71-83.	2.2	1
110	Large Scale Similarity Search for Locally Stable Secondary Structures among RNA Sequences. IPSJ Transactions on Bioinformatics, 2009, 2, 36-46.	0.2	1
111	Guest Editorial for the 25th International Conference on Genome Informatics (GIW/ISCB-Asia 2014). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 761-762.	3.0	1
112	RNA Structure Prediction. , 2019, , 575-584.		1
113	A robust model for quantitative prediction of the silencing efficacy of wild-type and A-to-I edited miRNAs. RNA Biology, 2020, 17, 264-280.	3.1	1
114	A Non-parametric Bayesian Approach for Predicting RNA Secondary Structures. Lecture Notes in Computer Science, 2009, , 286-297.	1.3	1
115	FLOW MODEL OF THE PROTEIN-PROTEIN INTERACTION NETWORK FOR FINDING CREDIBLE INTERACTIONS. , 2007, , .		1
116	Learning Kernels from Distance Constraints. IPSJ Digital Courier, 2006, 2, 441-451.	0.3	0
117	A New Direction for the Computational Biology Research Center. Asia Pacific Biotech News, 2007, 11, 1027-1029.	0.0	0
118	In search of true reads: A classification approach to next generation sequencing data selection. , 2010, , .		0
119	RecountDB: a database of mapped and count corrected transcribed sequences. Nucleic Acids Research, 2012, 40, D1089-D1092.	14.5	0
120	Combining probabilistic alignments with read pair information improves accuracy of split-alignments. Bioinformatics, 2018, 34, 3631-3637.	4.1	0
121	RintC: fast and accuracy-aware decomposition of distributions of RNA secondary structures with extended logsumexp. BMC Bioinformatics, 2020, 21, 210.	2.6	0
122	Inference of Euler angles for single particle analysis by using Genetic Algorithms. Genome Informatics, 2002, 13, 133-42.	0.4	0
123	QRNAstruct: a method for extracting secondary structural features of RNA via regression with biological activity. Nucleic Acids Research, 2022, , .	14.5	0