Kentaro Shimizu

List of Publications by Year
in descending order

107 papers	1,652 citations	471509 17 h-index

107 papers	1,652 citations	471509 17 h-index	315739 38 g-index
107 all docs	107 docs citations	107 times ranked	2626 citing authors

#	Article	IF	Citations
1	TCC: an R package for comparing tag count data with robust normalization strategies. BMC Bioinformatics, 2013, 14, 219.	2.6	477
2	A weighted average difference method for detecting differentially expressed genes from microarray data. Algorithms for Molecular Biology, 2008, 3, 8.	1.2	104
3	TCC-GUI: a Shiny-based application for differential expression analysis of RNA-Seq count data. BMC Research Notes, 2019, 12, 133.	1.4	87
4	Trisaccharide containing α2,3-linked sialic acid is a receptor for mumps virus. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11579-11584.	7.1	79
5	A normalization strategy for comparing tag count data. Algorithms for Molecular Biology, 2012, 7, 5.	1.2	76
6	Evaluation of methods for differential expression analysis on multi-group RNA-seq count data. BMC Bioinformatics, 2015, 16, 361.	2.6	72
7	Roles of Hydrogen Bonding and the Hard Core of Water on Hydrophobic Hydration. Journal of Physical Chemistry B, 1998, 102, 5891-5898.	2.6	67
8	Ranking differentially expressed genes from Affymetrix gene expression data: methods with reproducibility, sensitivity, and specificity. Algorithms for Molecular Biology, 2009, 4, 7.	1.2	67
9	Preprocessing implementation for microarray (PRIM): an efficient method for processing cDNA microarray data. Physiological Genomics, 2001, 4, 183-188.	2.3	58
10	Size dependence of transfer free energies: A hard-sphere-chain- based formalism. Journal of Chemical Physics, 1999, 110, 2971-2982.	3.0	36
11	Highly accurate method for ligand–binding site prediction in unbound state (apo) protein structures. Proteins: Structure, Function and Bioinformatics, 2008, 73, 468-479.	2.6	36
12	Comparative analysis of membrane protein structure databases. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 1077-1091.	2.6	34
13	Evaluating methods for ranking differentially expressed genes applied to microArray quality control data. BMC Bioinformatics, 2011, 12, 227.	2.6	28
14	Silhouette Scores for Arbitrary Defined Groups in Gene Expression Data and Insights into Differential Expression Results. Biological Procedures Online, 2018, 20, 5.	2.9	27
15	Refinement of comparative models of protein structure by using multicanonical molecular dynamics simulations. Molecular Simulation, 2008, 34, 327-336.	2.0	26
16	Mechanism of self/nonself-discrimination in Brassica self-incompatibility. Nature Communications, 2020, 11, 4916.	12.8	26
17	Understanding the roles of amino acid residues in tertiary structure formation of chignolin by using molecular dynamics simulation. Proteins: Structure, Function and Bioinformatics, 2008, 73, 621-631.	2.6	22
18	CellFishing.jl: an ultrafast and scalable cell search method for single-cell RNA sequencing. Genome Biology, 2019, 20, 31.	8.8	22

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19	Prediction of protein structure classes and secondary structures by means of hidden Markov models. Systems and Computers in Japan, 1999, 30, 13-22.	0.2	21
20	NRBP1-Containing CRL2/CRL4A Regulates Amyloid β Production by Targeting BRI2 and BRI3 for Degradation. Cell Reports, 2020, 30, 3478-3491.e6.	6.4	20
21	Prediction of Antifungal Peptides by Deep Learning with Character Embedding. IPSJ Transactions on Bioinformatics, 2019, 12, 21-29.	0.2	18
22	High-Throughput Sequencing of the Expressed Torafugu (Takifugu rubripes) Antibody Sequences Distinguishes IgM and IgT Repertoires and Reveals Evidence of Convergent Evolution. Frontiers in Immunology, 2018, 9, 251.	4.8	17
23	Development of a protein–ligand-binding site prediction method based on interaction energy and sequence conservation. Journal of Structural and Functional Genomics, 2016, 17, 39-49.	1.2	15
24	Understanding the Molecular Mechanism Underlying the High Catalytic Activity of <i>p</i>-Hydroxybenzoate Hydroxylase Mutants for Producing Gallic Acid. Biochemistry, 2019, 58, 4543-4558.	2.5	14
25	Identifying short disorder-to-order binding regions in disordered proteins with a deep convolutional neural network method. Journal of Bioinformatics and Computational Biology, 2019, 17, 1950004.	0.8	14
26	Quercetin 3,5,7,3′,4′-pentamethyl ether from Kaempferia parviflora directly and effectively activates human SIRT1. Communications Biology, 2021, 4, 209.	4.4	13
27	Identification of difructose dianhydride I synthase/hydrolase from an oral bacterium establishes a novel glycoside hydrolase family. Journal of Biological Chemistry, 2021, 297, 101324.	3.4	13
28	Automatic generation of bioinformatics tools for predicting protein–ligand binding sites. Bioinformatics, 2016, 32, 901-907.	4.1	12
29	Accurate Classification of Differential Expression Patterns in a Bayesian Framework With Robust Normalization for Multi-Group RNA-Seq Count Data. Bioinformatics and Biology Insights, 2019, 13, 117793221986081.	2.0	12
30	Molecular Dynamics Simulations in Aqueous Solution: Application to Free Energy Calculation of Oligopeptides. Journal of Physical Chemistry B, 1998, 102, 6419-6424.	2.6	11
31	Development of a sugar-binding residue prediction system from protein sequences using support vector machine. Computational Biology and Chemistry, 2017, 66, 36-43.	2.3	11
32	A Recently Formed Triploid Cardamine insueta Inherits Leaf Vivipary and Submergence Tolerance Traits of Parents. Frontiers in Genetics, 2020, 11, 567262.	2.3	11
33	Rapid Heme Transfer Reactions between NEAr Transporter Domains of Staphylococcus aureus: A Theoretical Study Using QM/MM and MD Simulations. PLoS ONE, 2015, 10, e0145125.	2.5	10
34	Differential expression analysis using a model-based gene clustering algorithm for RNA-seq data. BMC Bioinformatics, 2021, 22, 511.	2.6	9
35	MoRFPred_en: Sequence-based prediction of MoRFs using an ensemble learning strategy. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940015.	0.8	8
36	Prediction and analysis of antifreeze proteins. Heliyon, 2021, 7, e07953.	3.2	8

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37	Structural and Molecular Basis of the Catalytic Mechanism of Geranyl Pyrophosphate C6–Methyltransferase: Creation of an Unprecedented Farnesyl Pyrophosphate C6–Methyltransferase. Angewandte Chemie - International Edition, 2022, 61, .	13.8	8
38	Structural analysis of Î²â€Lâ€arabinobioseâ€binding protein in the metabolic pathway of hydroxyprolineâ€rich glycoproteins inBifidobacterium longum. FEBS Journal, 2020, 287, 5114-5129.	4.7	7
39	Development of a prediction system for tail-anchored proteins. BMC Bioinformatics, 2016, 17, 378.	2.6	6
40	Electron Transport in a Dioxygenase-Ferredoxin Complex: Long Range Charge Coupling between the Rieske and Non-Heme Iron Center. PLoS ONE, 2016, 11, e0162031.	2.5	6
41	EXPRORER: Rational Cosolvent Set Construction Method for Cosolvent Molecular Dynamics Using Large-Scale Computation. Journal of Chemical Information and Modeling, 2021, 61, 2744-2753.	5.4	6
42	Functional characterisation of two ferric-ion coordination modes of TtFbpA, the periplasmic subunit of an ABC-type iron transporter from <i>Thermus thermophilus</i> HB8. Metallomics, 2019, 11, 2078-2088.	2.4	5
43	Commentary: A Systematic Evaluation of Single Cell RNA-Seq Analysis Pipelines. Frontiers in Genetics, 2020, 11, 941.	2.3	5
44	Parallel algorithm for efficient calculation of second derivatives of conformational energy function in internal coordinates. Journal of Computational Chemistry, 1998, 19, 1716-1723.	3.3	4
45	Tyrosine Kinase Ligand-Receptor Pair Prediction by Using Support Vector Machine. Advances in Bioinformatics, 2015, 2015, 1-5.	5.7	4
46	Virtual screening identification of novel chemical inhibitors for aberrant interactions between pathogenic mutant SOD1 and tubulin. Neurochemistry International, 2019, 126, 19-26.	3.8	4
47	High-Density Scanning Combined with Digital Image of Real Objects for Complete Reproduction of Cultural Artifacts. , 2006, , .		3
48	High-Precision Geometric Modeling of 3D Artifacts for Virtual Restoration. , 2006, , .		3
49	Engineering the allosteric properties of archaeal non-phosphorylating glyceraldehyde-3-phosphate dehydrogenases. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 759-766.	2.3	3
50	Prediction of Protein-Protein Interaction Sites Using Only Sequence Information and Using Both Sequence and Structural Information. IPSJ Digital Courier, 2008, 4, 217-227.	0.3	2
51	Overdominance Effect of the Bovine Ghrelin Receptor (GHSR1a)-DelR242 Locus on Growth in Japanese Shorthorn Weaner Bulls: Heterozygote Advantage in Bull Selection and Molecular Mechanisms. G3: Genes, Genomes, Genetics, 2015, 5, 271-279.	1.8	2
52	High-Precision Modeling of Cultural Heritage Artifacts and Reproduction. , 2006, , .		1
53	Methods for analyzing next-generation sequencing data III. From setting a Linux environment to manipulating <i>Lactobacillus</i> RNA-seq data. Japanese Journal of Lactic Acid Bacteria, 2015, 26, 32-41.	0.1	1
54	Mutagenesis Analysis of GMN Motif in <i>Arabidopsis thaliana</i> Mg2+ Transporter MRS2-1. Bioscience, Biotechnology and Biochemistry, 2022, , .	1.3	1

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55	Distributed Shared Arrays: Portable Shared-Memory Programming Interface for Multiple Computer Systems. Cluster Computing, 2004, 7, 65-72.	5.0	0
56	Identification of GPI-(like)-Anchored Proteins by Using SVM. , 2006, , .		0
57	1P573 Folding simulation of the B-domain of staphylococcal protein A(27. Molecular dynamics) Tj ETQq1 1 0.784314 rgBT /Overlock S290.	0.1	0
58	1P060 Development of a protein tertiary structure prediction server(1. Protein structure and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 S161.	0.1	0
59	1P486 Prediction of Protein-Protein Interaction Sites Using Evolutionary and Structural Information(23. Bioinformatics, genomics and proteomics (I),Poster Session,Abstract,Meeting Program) Tj ETQq1 1 0.784314 rgBT /	0.1	0
60	1P581 Improving efficiency of conformation sampling in multicanonical molecular dynamics simulation(27. Molecular dynamics simulation,Poster Session,Abstract,Meeting Program of EABS & BSJ) Tj ETQq0 0 0 rgBT /Overlock 10	0.1	0
61	2P171 Dependency of thermostability on loop sequence in DNA minihairpin molecule revealed by locally enhanced sampling method(36. DNA to chromatin,Poster Session,Abstract,Meeting Program of EABS) Tj ETQq1 1 0.784314 rgBT /Ove	0.1	0
62	2P398 A multicanonical ab initio molecular dynamics method : application to conformation sampling of alanine tripeptide(45. Electronic structure,Poster Session,Abstract,Meeting Program of EABS &) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.1	0
63	2P448 Improvement to a Protein-Protein Docking Algorithm by Introducing Layers in Molecular Expression Space(48. Bioinformatics, genomics and proteomics (II),Poster Session,Abstract,Meeting) Tj ETQq1 1 0.784314 rgBT /Ove	0.1	0
64	2P505 Protein tertiary structure prediction based on contact number prediction(51. New methods and) Tj ETQq0 0 0 rgBT /Overlock 10 S422.	0.1	0
65	1P587 Folding free-energy landscapes of 10-residue proteins(27. Molecular dynamics simulation,Poster) Tj ETQq1 1 0.784314 rgBT /Ove	0.1	0
66	1P059 Predicting ligand binding sites of uncharacterized protein structure(1. Protein structure and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 S161.	0.1	0
67	S2e1-3 Structural propensity of protein fragments and tertiary structure prediction of proteins(S2-e1:) Tj ETQq1 1 0.784314 rgBT /Ov	0.1	0
68	2P105 Folding simulation of the B-domain of staphylococcal protein A(Proteins-stability, folding, and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.1	0
69	3P113 Solvent effect on biomolecule : a multicanonical QM/MM molecular dynamics study(Electronic) Tj ETQq1 1 0.784314 rgBT /Ov	0.1	0
70	1P132 Dynamical analysis of protein-DNA duplex structures using principal component analysis method(Nucleic acid,Poster Presentations). Seibutsu Butsuri, 2007, 47, S56.	0.1	0
71	2P-027 Protein-protein docking system with refinement stage(The 46th Annual Meeting of the) Tj ETQq1 1 0.784314 rgBT /Overlock	0.1	0
72	3P-012 Folding simulation of the B-domain of staphylococcal protein A(The 46th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10	0.1	0

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73	3P-109 Solvent effects on biomolecule : Multicanonical QM/MM molecular dynamics study(The 46th) Tj ETQq1 1 0.784314 rgBT /Overlock	0.1	0
74	2P-068 Dynamics of amino acids in the electron transfer pathways between Oxygenase and Ferredoxin components in Rieske oxygenase system(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S85.	0.1	0
75	2P-095 Folding simulation of an all-β protein by molecular dynamics simulation with secondary structure restraints(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S89-S90.	0.1	0
76	2P-125 A new DNA-deformation energy function taking account of the anharmonicity of the conformational distribution(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S94.	0.1	0
77	1P-015 Development of protein-ligand complex's database considering biological units(Protein:Structure, The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2009, 49, S65-S66.	0.1	0
78	2P-088 Role of indirect readout in protein-DNA recognition assessed by a Bayesian approach(Nucleic) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.1	0
79	3P-041 Multicanonical molecular dynamics simulation of an all-β protein with secondary structure restraints(Protein:Property,The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2009, 49, S157-S158.	0.1	0
80	2SP6-05 The role of H-doping in the electronic structure, spin localization and electron transfer of iron-sulfur [2Fe-2S] proteins(2SP6 Towards Supercomputing for Electronic Structures of Biological) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 49, S15.	0.1	0
81	2P295 Development of a method for predicting carbohydrate-binding proteins(The 48th Annual) Tj ETQq1 1 0.784314 rgBT /Overlock	0.1	0
82	3P297 Development of structure prediction server and model quality assessment platform for proteins(Bioinformatics: Structural genomics,The 48th Annual Meeting of the Biophysical Society of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.1	0
83	1P071 Protein tertiary structure prediction by folding simulation with secondary structure restraints(Protein:Property,The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S31.	0.1	0
84	2P071 Generality of the protein structure prediction method based on molecular dynamics simulation with secondary structure information(The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S94.	0.1	0
85	1P132 Evaluation of force field parameters for nucleic acid : A case of Z-DNA(Nucleic acid:Structure) Tj ETQq1 1 0.784314 rgBT /Over S42.	0.1	0
86	3B0936 Identification of Tail-anchored Proteins by Using Support Vector Machine(3B Membrane) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2 S108-S109.	0.1	0
87	1E1512 Protein tertiary structure prediction by multicanonical MD simulation with restraints based on secondary structure prediction(Genome biology, Bioinformatics,The 49th Annual Meeting of the) Tj ETQq1 1 0.784314 rgBT /Overlock	0.1	0
88	3D1012 Protein-ligand binding simulation with a coarse-graind force field, MARTINI(3D Protein:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 14 Butsuri, 2011, 51, S117-S118.	0.1	0
89	1C1448 Molecular dynamics simulations of B-Z DNA junction structure(Nucleic acid,The 49th Annual) Tj ETQq1 1 0.784314 rgBT /Over	0.1	0
90	2PT010 Prediction of the types of carbohydrate-binding proteins(The 50th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.1	0

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91	2PT133 Coarse-grained MD simulations of ligand binding to proteins : Effect of the conformational changes of the proteins(The 50th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2012, 52, S127.	0.1	0
92	Methods for analyzing next-generation sequencing data II. From graphical user interface to command line interface. Japanese Journal of Lactic Acid Bacteria, 2014, 25, 166-174.	0.1	0
93	Methods for analyzing next-generation sequencing data IV. FASTQ quality control and program installation. Japanese Journal of Lactic Acid Bacteria, 2015, 26, 124-132.	0.1	0
94	<i>Methods for analyzing next-generation sequencing data </i><i>VII. long-read assembly </i>. Japanese Journal of Lactic Acid Bacteria, 2016, 27, 101-110.	0.1	0
95	Methods for analyzing next-generation sequencing data VIII. Post-assembly analysis. Japanese Journal of Lactic Acid Bacteria, 2016, 27, 187-195.	0.1	0
96	Methods for analyzing next-generation sequencing dataVI. genome assembly . Japanese Journal of Lactic Acid Bacteria, 2016, 27, 41-52.	0.1	0
97	Methods for analyzing next-generation sequencing data IX.Genome annotation, visualization, and registration to DDBJ . Japanese Journal of Lactic Acid Bacteria, 2017, 28, 3-11.	0.1	0
98	Functional effect of nobiletin as a food-derived allosteric modulator of mouse CRFR2β in skeletal muscle. Biochemical and Biophysical Research Communications, 2020, 529, 328-334.	2.1	0
99	Structural and Molecular Basis of the Catalytic Mechanism of Geranyl Pyrophosphate Câ€6 Methyltransferase: Creation of an Unprecedented Farnesyl Pyrophosphate Câ€6 Methyltransferase. Angewandte Chemie, 0, , .	2.0	0
100	COMPREHENSIVE ANALYSIS OF SEQUENCE-STRUCTURE RELATIONSHIPS IN THE LOOP REGIONS OF PROTEINS. , 2009, , .		0
101	1E1412 Development of a method for predicting carbohtdrate-binding proteins(Genome biology,) Tj ETQq1 1 0.784314 rgBT /Overlock S40.	0.1	0
102	Linked Open Data Construction of Purpose Oriented Interactomics by Integration of Life Sciences LOD. Transactions of the Japanese Society for Artificial Intelligence, 2014, 29, 356-363.	0.1	0
103	Methods for analyzing next-generation sequencing data X. Registration to DDBJ through Mass Submission System . Japanese Journal of Lactic Acid Bacteria, 2017, 28, 94-100.	0.1	0
104	Methods for analyzing next-generation sequencing data XI.Galaxy -an integrated data analysis environment . Japanese Journal of Lactic Acid Bacteria, 2017, 28, 167-175.	0.1	0
105	Methods for analyzing next-generation sequencing data XII.Galaxy - Sharing histories and workflows. Japanese Journal of Lactic Acid Bacteria, 2018, 29, 79-88.	0.1	0
106	Methods for analyzing next-generation sequencing data XIII.RNA-seq analysis (Part 1). Japanese Journal of Lactic Acid Bacteria, 2019, 30, 38-45.	0.1	0
107	Methods for analyzing next-generation sequencing data XV. RNA-seq analysis (Part 3). Japanese Journal of Lactic Acid Bacteria, 2020, 31, 25-34.	0.1	0