

Hideo Matsuda

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68

papers

5,994

citations

19

h-index

77

g-index

81

ext. papers

7,083

ext. citations

6.5

avg, IF

4.23

L-index

#	Paper	IF	Citations
68	Detection of Biomarkers for Epithelial-Mesenchymal Transition with Single-Cell Trajectory Inference.. <i>Frontiers in Bioscience</i> , 2022 , 27, 127		
67	Osteoclasts adapt to physioxia perturbation through DNA demethylation. <i>EMBO Reports</i> , 2021 , 22, e53085		2
66	SLPI is a critical mediator that controls PTH-induced bone formation. <i>Nature Communications</i> , 2021 , 12, 2136	17.4	12
65	Determining homologous recombination deficiency scores with whole exome sequencing and their association with responses to neoadjuvant chemotherapy in breast cancer. <i>Translational Oncology</i> , 2021 , 14, 100986	4.9	2
64	SC-JNMF: single-cell clustering integrating multiple quantification methods based on joint non-negative matrix factorization. <i>PeerJ</i> , 2021 , 9, e12087	3.1	2
63	In vivo dynamic analysis of BMP-2-induced ectopic bone formation. <i>Scientific Reports</i> , 2020 , 10, 4751	4.9	20
62	Thrombomodulin induces anti-inflammatory effects by inhibiting the rolling adhesion of leukocytes in vivo. <i>Journal of Pharmacological Sciences</i> , 2020 , 143, 17-22	3.7	1
61	URH49 exports mRNA by remodeling complex formation and mediating the NXF1-dependent pathway. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020 , 1863, 194480	6	3
60	Long non-coding RNA 2310069B03Rik functions as a suppressor of Ucp1 expression under prolonged cold exposure in murine beige adipocytes. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020 , 84, 305-313	2.1	5
59	Anti-Inflammatory and Antioxidative Properties of Isoflavones Provide Renal Protective Effects Distinct from Those of Dietary Soy Proteins against Diabetic Nephropathy. <i>Molecular Nutrition and Food Research</i> , 2020 , 64, e2000015	5.9	8
58	Glycerol kinase stimulates uncoupling protein 1 expression by regulating fatty acid metabolism in beige adipocytes. <i>Journal of Biological Chemistry</i> , 2020 , 295, 7033-7045	5.4	4
57	Multicolor Imaging with Fluorescent Probes Revealed the Dynamics and Function of Osteoclast Proton Pumps. <i>ACS Central Science</i> , 2019 , 5, 1059-1066	16.8	21
56	Improvement of detection performance of fusion genes from RNA-seq data by clustering short reads. <i>Journal of Bioinformatics and Computational Biology</i> , 2019 , 17, 1940008	1	1
55	Chromatin 3D Reconstruction from Chromosomal Contacts Using a Genetic Algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1620-1626	3	4
54	Direct cell-cell contact between mature osteoblasts and osteoclasts dynamically controls their functions in vivo. <i>Nature Communications</i> , 2018 , 9, 300	17.4	89
53	Automated transition analysis of activated gene regulation during diauxic nutrient shift in Escherichia coli and adipocyte differentiation in mouse cells. <i>BMC Bioinformatics</i> , 2018 , 19, 89	3.6	
52	The dipeptidyl peptidase-4 (DPP-4) inhibitor teneligliptin enhances brown adipose tissue function, thereby preventing obesity in mice. <i>FEBS Open Bio</i> , 2018 , 8, 1782-1793	2.7	6

51	Roles of Enhancer RNAs in RANKL-induced Osteoclast Differentiation Identified by Genome-wide Cap-analysis of Gene Expression using CRISPR/Cas9. <i>Scientific Reports</i> , 2018 , 8, 7504	4.9	11
50	The hepatokine FGF21 is crucial for peroxisome proliferator-activated receptor- α agonist-induced amelioration of metabolic disorders in obese mice. <i>Journal of Biological Chemistry</i> , 2017 , 292, 9175-9190	5.4	36
49	A simple comparison of the extrinsic noise in gene expression between native and foreign regulations in Escherichia coli. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 486, 852-857	3.4	0
48	Bone marrow cavity segmentation using graph-cuts with wavelet-based texture feature. <i>Journal of Bioinformatics and Computational Biology</i> , 2017 , 15, 1740004	1	4
47	Over-expression of PPAR α in obese mice adipose tissue improves insulin sensitivity. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 493, 108-114	3.4	13
46	Diagnostic Assessment of Deep Learning Algorithms for Detection of Lymph Node Metastases in Women With Breast Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2017 , 318, 2199-2210	27.4	1165
45	Proinflammatory cytokine interleukin-1 β suppresses cold-induced thermogenesis in adipocytes. <i>Cytokine</i> , 2016 , 77, 107-114	4	66
44	Correlation between genome reduction and bacterial growth. <i>DNA Research</i> , 2016 , 23, 517-525	4.5	32
43	Comparative Analysis of Transformation Methods for Gene Expression Profiles in Breast Cancer Datasets 2016 ,		1
42	Functional specialization in regulation and quality control in thermal adaptive evolution. <i>Genes To Cells</i> , 2015 , 20, 943-55	2.3	4
41	Detecting shifts in gene regulatory networks during time-course experiments at single-time-point temporal resolution. <i>Journal of Bioinformatics and Computational Biology</i> , 2015 , 13, 1543002	1	2
40	Evolutionary Consequence of a Trade-Off between Growth and Maintenance along with Ribosomal Damages. <i>PLoS ONE</i> , 2015 , 10, e0135639	3.7	11
39	Gene expression scaled by distance to the genome replication site. <i>Molecular BioSystems</i> , 2014 , 10, 375-9		14
38	A Segmentation Method for Bone Marrow Cavity Imaging Using Graph Cuts 2014 ,		2
37	A Graph Cuts Image Segmentation Method for Quantifying Barrier Permeation in Bone Tissue 2014 ,		2
36	Directed evolution of cell size in Escherichia coli. <i>BMC Evolutionary Biology</i> , 2014 , 14, 257	3	12
35	Metagenome fragment classification based on multiple motif-occurrence profiles. <i>PeerJ</i> , 2014 , 2, e559	3.1	2
34	Inference of TFRNs (2). <i>Methods in Molecular Biology</i> , 2014 , 1164, 97-107	1.4	

33	An estimation method for a cellular-state-specific gene regulatory network along tree-structured gene expression profiles. <i>Gene</i> , 2013 , 518, 17-25	3.8	6
32	Multilevel comparative analysis of the contributions of genome reduction and heat shock to the <i>Escherichia coli</i> transcriptome. <i>BMC Genomics</i> , 2013 , 14, 25	4.5	20
31	An estimation method for inference of gene regulatory network using Bayesian network with uniting of partial problems. <i>BMC Genomics</i> , 2012 , 13 Suppl 1, S12	4.5	7
30	A Method for Isoform Prediction from RNA-Seq Data by Iterative Mapping. <i>IPSJ Transactions on Bioinformatics</i> , 2012 , 5, 27-33	1.3	
29	Perfect Hamming code with a hash table for faster genome mapping. <i>BMC Genomics</i> , 2011 , 12 Suppl 3, S8	4.5	4
28	Inference of S-system models of gene regulatory networks using immune algorithm. <i>Journal of Bioinformatics and Computational Biology</i> , 2011 , 9 Suppl 1, 75-86	1	14
27	Exploration of potential genomic portraits associated with intrahepatic recurrence in human hepatocellular carcinoma. <i>Annals of Surgical Oncology</i> , 2010 , 17, 3145-54	3.1	3
26	Improved Prediction Method for Protein Interactions Using Both Structural and Functional Characteristics of Proteins. <i>IPSJ Transactions on Bioinformatics</i> , 2010 , 3, 10-23	1.3	1
25	Gene expression profile prospectively predicts peritoneal relapse after curative surgery of gastric cancer. <i>Annals of Surgical Oncology</i> , 2010 , 17, 1033-42	3.1	40
24	Gendoo: functional profiling of gene and disease features using MeSH vocabulary. <i>Nucleic Acids Research</i> , 2009 , 37, W166-9	20.1	29
23	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009 , 41, 553-62	36.3	356
22	A Combination Method of the Tanimoto Coefficient and Proximity Measure of Random Forest for Compound Activity Prediction. <i>IPSJ Digital Courier</i> , 2008 , 4, 238-249		1
21	A Distributed-Processing System for Accelerating Biological Research Using Data-Staging. <i>IPSJ Digital Courier</i> , 2008 , 4, 250-256		
20	BioCompass: a novel functional inference tool that utilizes MeSH hierarchy to analyze groups of genes. <i>In Silico Biology</i> , 2008 , 8, 53-61	2	14
19	Tissue-specific functions based on information content of gene ontology using cap analysis gene expression. <i>Medical and Biological Engineering and Computing</i> , 2007 , 45, 1029-36	3.1	3
18	Compound-Transporter Interaction Studies using Canonical Correlation Analysis. <i>Chem-Bio Informatics Journal</i> , 2007 , 7, 24-34	0.8	
17	A method for similarity search of genomic positional expression using CAGE. <i>PLoS Genetics</i> , 2006 , 2, e446		3
16	The transcriptional landscape of the mammalian genome. <i>Science</i> , 2005 , 309, 1559-63	33.3	2807

15	Heterogeneous Database Federation Using Grid Technology for Drug Discovery Process. <i>Lecture Notes in Computer Science</i> , 2005 , 43-52	0.9	5
14	Graph-based clustering for finding distant relationships in a large set of protein sequences. <i>Bioinformatics</i> , 2004 , 20, 243-52	7.2	31
13	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
12	Biased biological functions of horizontally transferred genes in prokaryotic genomes. <i>Nature Genetics</i> , 2004 , 36, 760-6	36.3	376
11	A challenge towards next-generation research infrastructure for advanced life science. <i>New Generation Computing</i> , 2004 , 22, 157-166	0.9	2
10	Development and evaluation of an automated annotation pipeline and cDNA annotation system. <i>Genome Research</i> , 2003 , 13, 1542-51	9.7	24
9	Mouse proteome analysis. <i>Genome Research</i> , 2003 , 13, 1335-44	9.7	75
8	Exploration of novel motifs derived from mouse cDNA sequences. <i>Genome Research</i> , 2002 , 12, 367-78	9.7	16
7	An efficient procedure for maintaining materialized views on distributed database systems. <i>Systems and Computers in Japan</i> , 2000 , 31, 86-96		
6	Determination of the complete nucleotide sequence and haplotypes in the D-loop region of the mitochondrial genome in the oriental white stork, <i>Ciconia boyciana</i> . <i>Genes and Genetic Systems</i> , 2000 , 75, 25-32	1.4	23
5	An application of an OR-Parallel Prolog system to phylogenetic analysis. <i>Higher-Order and Symbolic Computation</i> , 1994 , 7, 211-229		
4	fastDNAmL: a tool for construction of phylogenetic trees of DNA sequences using maximum likelihood. <i>Bioinformatics</i> , 1994 , 10, 41-8	7.2	313
3	A priority control system for OR-parallel Prolog and its performance evaluation. <i>Lecture Notes in Computer Science</i> , 1993 , 42-53	0.9	1
2	Introduction of dosim predicate to Prolog. <i>New Generation Computing</i> , 1990 , 8, 163-181	0.9	0
1	Sequential Prolog machine PEK. <i>New Generation Computing</i> , 1986 , 4, 51-66	0.9	7