

# Hideo Matsuda

## List of Publications by Year in descending order

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Version: 2024-02-01

78  
papers

8,096  
citations

361045

20  
h-index

143772

57  
g-index

82  
all docs

82  
docs citations

82  
times ranked

12847  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	6.0	3,227
2	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.	3.8	2,003
3	fastDNAMl: a tool for construction of phylogenetic trees of DNA sequences using maximum likelihood. <i>Bioinformatics</i> , 1994, 10, 41-48.	1.8	582
4	Biased biological functions of horizontally transferred genes in prokaryotic genomes. <i>Nature Genetics</i> , 2004, 36, 760-766.	9.4	459
5	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	9.4	408
6	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
7	Direct cell-cell contact between mature osteoblasts and osteoclasts dynamically controls their functions in vivo. <i>Nature Communications</i> , 2018, 9, 300.	5.8	128
8	Mouse Proteome Analysis. <i>Genome Research</i> , 2003, 13, 1335-1344.	2.4	91
9	Proinflammatory cytokine interleukin-1 $\beta$ suppresses cold-induced thermogenesis in adipocytes. <i>Cytokine</i> , 2016, 77, 107-114.	1.4	88
10	Correlation between genome reduction and bacterial growth. <i>DNA Research</i> , 2016, 23, 517-525.	1.5	72
11	Gene Expression Profile Prospectively Predicts Peritoneal Relapse After Curative Surgery of Gastric Cancer. <i>Annals of Surgical Oncology</i> , 2010, 17, 1033-1042.	0.7	69
12	The hepatokine FGF21 is crucial for peroxisome proliferator-activated receptor- $\alpha$ agonist-induced amelioration of metabolic disorders in obese mice. <i>Journal of Biological Chemistry</i> , 2017, 292, 9175-9190.	1.6	48
13	<i>In Vivo</i> Multicolor Imaging with Fluorescent Probes Revealed the Dynamics and Function of Osteoclast Proton Pumps. <i>ACS Central Science</i> , 2019, 5, 1059-1066.	5.3	41
14	In vivo dynamic analysis of BMP-2-induced ectopic bone formation. <i>Scientific Reports</i> , 2020, 10, 4751.	1.6	41
15	Graph-based clustering for finding distant relationships in a large set of protein sequences. <i>Bioinformatics</i> , 2004, 20, 243-252.	1.8	39
16	Gendoo: Functional profiling of gene and disease features using MeSH vocabulary. <i>Nucleic Acids Research</i> , 2009, 37, W166-W169.	6.5	35
17	Development and Evaluation of an Automated Annotation Pipeline and cDNA Annotation System. <i>Genome Research</i> , 2003, 13, 1542-1551.	2.4	34
18	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.	1.2	31

#	ARTICLE	IF	CITATIONS
19	SLPI is a critical mediator that controls PTH-induced bone formation. <i>Nature Communications</i> , 2021, 12, 2136.	5.8	28
20	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.	0.2	26
21	Exploration of Novel Motifs Derived from Mouse cDNA Sequences. <i>Genome Research</i> , 2002, 12, 367-378.	2.4	21
22	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.	1.5	21
23	INFERENCE OF S-SYSTEM MODELS OF GENE REGULATORY NETWORKS USING IMMUNE ALGORITHM. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 75-86.	0.3	20
24	Directed evolution of cell size in <i>Escherichia coli</i> . <i>BMC Evolutionary Biology</i> , 2014, 14, 257.	3.2	19
25	Gene expression scaled by distance to the genome replication site. <i>Molecular BioSystems</i> , 2014, 10, 375-379.	2.9	18
26	Over-expression of PPAR $\alpha$ in obese mice adipose tissue improves insulin sensitivity. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 108-114.	1.0	18
27	Evolutionary Consequence of a Trade-Off between Growth and Maintenance along with Ribosomal Damages. <i>PLoS ONE</i> , 2015, 10, e0135639.	1.1	17
28	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.	1.6	15
29	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.	1.6	15
30	BioCompass: a novel functional inference tool that utilizes MeSH hierarchy to analyze groups of genes. <i>In Silico Biology</i> , 2008, 8, 53-61.	0.4	15
31	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.	1.0	13
32	Osteoclasts adapt to physioxia perturbation through DNA demethylation. <i>EMBO Reports</i> , 2021, 22, e53035.	2.0	13
33	Chromatin 3D Reconstruction from Chromosomal Contacts Using a Genetic Algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1620-1626.	1.9	12
34	Heterogeneous Database Federation Using Grid Technology for Drug Discovery Process. <i>Lecture Notes in Computer Science</i> , 2005, , 43-52.	1.0	11
35	An estimation method for inference of gene regulatory network using Bayesian network with uniting of partial problems. <i>BMC Genomics</i> , 2012, 13, S12.	1.2	11
36	Functional specialization in regulation and quality control in thermal adaptive evolution. <i>Genes To Cells</i> , 2015, 20, 943-955.	0.5	9

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37	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.	0.6	9
38	Sequential Prolog machine PEK. <i>New Generation Computing</i> , 1986, 4, 51-66.	2.5	8
39	A challenge towards next-generation research infrastructure for advanced life science. <i>New Generation Computing</i> , 2004, 22, 157-166.	2.5	8
40	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.	0.9	7
41	An estimation method for a cellular-state-specific gene regulatory network along tree-structured gene expression profiles. <i>Gene</i> , 2013, 518, 17-25.	1.0	6
42	SC-JNMF: single-cell clustering integrating multiple quantification methods based on joint non-negative matrix factorization. <i>PeerJ</i> , 2021, 9, e12087.	0.9	6
43	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, 1029-1036.	1.6	5
44	Perfect Hamming code with a hash table for faster genome mapping. <i>BMC Genomics</i> , 2011, 12, S8.	1.2	5
45	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.	1.7	5
46	A Method for Similarity Search of Genomic Positional Expression Using CAGE. <i>PLoS Genetics</i> , 2006, 2, e44.	1.5	4
47	A simple comparison of the extrinsic noise in gene expression between native and foreign regulations in <i>Escherichia coli</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017, 486, 852-857.	1.0	4
48	Bone marrow cavity segmentation using graph-cuts with wavelet-based texture feature. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1740004.	0.3	4
49	Exploration of Potential Genomic Portraits Associated with Intrahepatic Recurrence in Human Hepatocellular Carcinoma. <i>Annals of Surgical Oncology</i> , 2010, 17, 3145-3154.	0.7	3
50	A Segmentation Method for Bone Marrow Cavity Imaging Using Graph Cuts. , 2014, , .		3
51	A Graph Cuts Image Segmentation Method for Quantifying Barrier Permeation in Bone Tissue. , 2014, , .		3
52	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.	0.3	3
53	Analyzing Leukocyte Migration Trajectories by Deformable Image Matching. , 2019, , .		3
54	Thrombomodulin induces anti-inflammatory effects by inhibiting the rolling adhesion of leukocytes in vivo. <i>Journal of Pharmacological Sciences</i> , 2020, 143, 17-22.	1.1	3

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55	Comparative Analysis of Transformation Methods for Gene Expression Profiles in Breast Cancer Datasets. , 2016, , .		2
56	Single-cell Transcriptome Analysis of Mouse Leukocytes in Inflammatory Stimulation. , 2019, , .		2
57	Metagenome fragment classification based on multiple motif-occurrence profiles. PeerJ, 2014, 2, e559.	0.9	2
58	Introduction of dosim predicate to Prolog. New Generation Computing, 1990, 8, 163-181.	2.5	1
59	Fast phylogenetic analysis on a massively parallel machine. , 1994, , .		1
60	An application of an OR-Parallel Prolog system to phylogenetic analysis. Higher-Order and Symbolic Computation, 1994, 7, 211-229.	1.2	1
61	A Combination Method of the Tanimoto Coefficient and Proximity Measure of Random Forest for Compound Activity Prediction. IPSJ Digital Courier, 2008, 4, 238-249.	0.3	1
62	Improved Prediction Method for Protein Interactions Using Both Structural and Functional Characteristics of Proteins. IPSJ Transactions on Bioinformatics, 2010, 3, 10-23.	0.2	1
63	Asymmetric Integration of Single-Cell Transcriptomic Data using Latent Dirichlet Allocation and Procrustes Analysis. , 2018, , .		1
64	Improvement of detection performance of fusion genes from RNA-seq data by clustering short reads. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940008.	0.3	1
65	A CNN-based cell tracking method for multi-slice intravital imaging data. , 2021, , .		1
66	Detection of Biomarkers for Epithelial-Mesenchymal Transition with Single-Cell Trajectory Inference. Frontiers in Bioscience, 2022, 27, 127.	0.8	1
67	An efficient procedure for maintaining materialized views on distributed database systems. Systems and Computers in Japan, 2000, 31, 86-96.	0.2	0
68	GO based Tissue Specific Functions of Mouse using Countable Gene Expression Profiles. , 2007, , .		0
69	A Distributed-Processing System for Accelerating Biological Research Using Data-Staging. IPSJ Digital Courier, 2008, 4, 250-256.	0.3	0
70	A Method for Isoform Prediction from RNA-Seq Data by Iterative Mapping. IPSJ Transactions on Bioinformatics, 2012, 5, 27-33.	0.2	0
71	A bone marrow cavity segmentation method using wavelet-based texture feature. , 2016, , .		0
72	Detection of Fusion Genes from Human Breast Cancer Cell-Line RNA-Seq Data Using Shifted Short Read Clustering. , 2018, , .		0

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73	Automated transition analysis of activated gene regulation during diauxic nutrient shift in Escherichia coli and adipocyte differentiation in mouse cells. BMC Bioinformatics, 2018, 19, 89.	1.2	0
74	DO GRID TECHNOLOGIES HELP LIFE SCIENCES? LESSONS LEARNT FROM BIOGRID PROJECT IN JAPAN. , 2006, , .		0
75	A FRAMEWORK FOR BIOLOGICAL ANALYSIS ON THE GRID. , 2006, , .		0
76	Compound-Transporter Interaction Studies using Canonical Correlation Analysis. Chem-Bio Informatics Journal, 2007, 7, 24-34.	0.1	0
77	Inference of TFRNs (2). Methods in Molecular Biology, 2014, 1164, 97-107.	0.4	0
78	A Method for Detection of Markers for Epithelial-Mesenchymal Transition based on Single Cell Transcriptomic Data. , 2022, , .		0