Hideo Matsuda

List of Publications by Citations

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	The transcriptional landscape of the mammalian genome. *Science*, **2005**, 309, 1559-63	33.3	2807
67	Diagnostic Assessment of Deep Learning Algorithms for Detection of Lymph Node Metastases in Women With Breast Cancer. *JAMA - Journal of the American Medical Association*, **2017**, 318, 2199-2210	27.4	1165
66	Biased biological functions of horizontally transferred genes in prokaryotic genomes. *Nature Genetics*, **2004**, 36, 760-6	36.3	376
65	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. *Nature Genetics*, **2009**, 41, 553-62	36.3	356
64	fastDNAmL: a tool for construction of phylogenetic trees of DNA sequences using maximum likelihood. *Bioinformatics*, **1994**, 10, 41-8	7.2	313
63	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. *PLoS Biology*, **2004**, 2, e162	9.7	255
62	Direct cell-cell contact between mature osteoblasts and osteoclasts dynamically controls their functions in vivo. *Nature Communications*, **2018**, 9, 300	17.4	89
61	Mouse proteome analysis. *Genome Research*, **2003**, 13, 1335-44	9.7	75
60	Proinflammatory cytokine interleukin-1 suppresses cold-induced thermogenesis in adipocytes. *Cytokine*, **2016**, 77, 107-14	4	66
59	Gene expression profile prospectively predicts peritoneal relapse after curative surgery of gastric cancer. *Annals of Surgical Oncology*, **2010**, 17, 1033-42	3.1	40
58	The hepatokine FGF21 is crucial for peroxisome proliferator-activated receptor- agonist-induced amelioration of metabolic disorders in obese mice. *Journal of Biological Chemistry*, **2017**, 292, 9175-9190	5.4	36
57	Correlation between genome reduction and bacterial growth. *DNA Research*, **2016**, 23, 517-525	4.5	32
56	Graph-based clustering for finding distant relationships in a large set of protein sequences. *Bioinformatics*, **2004**, 20, 243-52	7.2	31
55	Gendoo: functional profiling of gene and disease features using MeSH vocabulary. *Nucleic Acids Research*, **2009**, 37, W166-9	20.1	29
54	Development and evaluation of an automated annotation pipeline and cDNA annotation system. *Genome Research*, **2003**, 13, 1542-51	9.7	24
53	Determination of the complete nucleotide sequence and haplotypes in the D-loop region of the mitochondrial genome in the oriental white stork, Ciconia boyciana. *Genes and Genetic Systems*, **2000**, 75, 25-32	1.4	23
52	Multicolor Imaging with Fluorescent Probes Revealed the Dynamics and Function of Osteoclast Proton Pumps. *ACS Central Science*, **2019**, 5, 1059-1066	16.8	21

51	In vivo dynamic analysis of BMP-2-induced ectopic bone formation. *Scientific Reports*, **2020**, 10, 4751	4.9	20
50	Multilevel comparative analysis of the contributions of genome reduction and heat shock to the Escherichia coli transcriptome. *BMC Genomics*, **2013**, 14, 25	4.5	20
49	Exploration of novel motifs derived from mouse cDNA sequences. *Genome Research*, **2002**, 12, 367-78	9.7	16
48	Gene expression scaled by distance to the genome replication site. *Molecular BioSystems*, **2014**, 10, 375-9		14
47	Inference of S-system models of gene regulatory networks using immune algorithm. *Journal of Bioinformatics and Computational Biology*, **2011**, 9 Suppl 1, 75-86	1	14
46	BioCompass: a novel functional inference tool that utilizes MeSH hierarchy to analyze groups of genes. *In Silico Biology*, **2008**, 8, 53-61	2	14
45	Over-expression of PPARγ in obese mice adipose tissue improves insulin sensitivity. *Biochemical and Biophysical Research Communications*, **2017**, 493, 108-114	3.4	13
44	Directed evolution of cell size in Escherichia coli. *BMC Evolutionary Biology*, **2014**, 14, 257	3	12
43	SLPI is a critical mediator that controls PTH-induced bone formation. *Nature Communications*, **2021**, 12, 2136	17.4	12
42	Evolutionary Consequence of a Trade-Off between Growth and Maintenance along with Ribosomal Damages. *PLoS ONE*, **2015**, 10, e0135639	3.7	11
41	Roles of Enhancer RNAs in RANKL-induced Osteoclast Differentiation Identified by Genome-wide Cap-analysis of Gene Expression using CRISPR/Cas9. *Scientific Reports*, **2018**, 8, 7504	4.9	11
40	Anti-Inflammatory and Antioxidative Properties of Isoflavones Provide Renal Protective Effects Distinct from Those of Dietary Soy Proteins against Diabetic Nephropathy. *Molecular Nutrition and Food Research*, **2020**, 64, e2000015	5.9	8
39	An estimation method for inference of gene regulatory net-work using Bayesian network with uniting of partial problems. *BMC Genomics*, **2012**, 13 Suppl 1, S12	4.5	7
38	Sequential Prolog machine PEK. *New Generation Computing*, **1986**, 4, 51-66	0.9	7
37	An estimation method for a cellular-state-specific gene regulatory network along tree-structured gene expression profiles. *Gene*, **2013**, 518, 17-25	3.8	6
36	The dipeptidyl peptidase-4 (DPP-4) inhibitor teneligliptin enhances brown adipose tissue function, thereby preventing obesity in mice. *FEBS Open Bio*, **2018**, 8, 1782-1793	2.7	6
35	Heterogeneous Database Federation Using Grid Technology for Drug Discovery Process. *Lecture Notes in Computer Science*, **2005**, 43-52	0.9	5
34	Long non-coding RNA 2310069B03Rik functions as a suppressor of Ucp1 expression under prolonged cold exposure in murine beige adipocytes. *Bioscience, Biotechnology and Biochemistry*, **2020**, 84, 305-313	2.1	5

#	Reference		
33	Bone marrow cavity segmentation using graph-cuts with wavelet-based texture feature. *Journal of Bioinformatics and Computational Biology*, **2017**, 15, 1740004	1	4
32	Functional specialization in regulation and quality control in thermal adaptive evolution. *Genes To Cells*, **2015**, 20, 943-55	2.3	4
31	Perfect Hamming code with a hash table for faster genome mapping. *BMC Genomics*, **2011**, 12 Suppl 3, S8	4.5	4
30	Chromatin 3D Reconstruction from Chromosomal Contacts Using a Genetic Algorithm. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2019**, 16, 1620-1626	3	4
29	Glycerol kinase stimulates uncoupling protein 1 expression by regulating fatty acid metabolism in beige adipocytes. *Journal of Biological Chemistry*, **2020**, 295, 7033-7045	5.4	4
28	URH49 exports mRNA by remodeling complex formation and mediating the NXF1-dependent pathway. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2020**, 1863, 194480	6	3
27	Exploration of potential genomic portraits associated with intrahepatic recurrence in human hepatocellular carcinoma. *Annals of Surgical Oncology*, **2010**, 17, 3145-54	3.1	3
26	Tissue-specific functions based on information content of gene ontology using cap analysis gene expression. *Medical and Biological Engineering and Computing*, **2007**, 45, 1029-36	3.1	3
25	A method for similarity search of genomic positional expression using CAGE. *PLoS Genetics*, **2006**, 2, e44	6	3
24	Detecting shifts in gene regulatory networks during time-course experiments at single-time-point temporal resolution. *Journal of Bioinformatics and Computational Biology*, **2015**, 13, 1543002	1	2
23	A Segmentation Method for Bone Marrow Cavity Imaging Using Graph Cuts **2014**,		2
22	A Graph Cuts Image Segmentation Method for Quantifying Barrier Permeation in Bone Tissue **2014**,		2
21	A challenge towards next-generation research infrastructure for advanced life science. *New Generation Computing*, **2004**, 22, 157-166	0.9	2
20	Osteoclasts adapt to physioxia perturbation through DNA demethylation. *EMBO Reports*, **2021**, 22, e53035	7.5	2
19	Metagenome fragment classification based on multiple motif-occurrence profiles. *PeerJ*, **2014**, 2, e559	3.1	2
18	Determining homologous recombination deficiency scores with whole exome sequencing and their association with responses to neoadjuvant chemotherapy in breast cancer. *Translational Oncology*, **2021**, 14, 100986	4.9	2
17	SC-JNMF: single-cell clustering integrating multiple quantification methods based on joint non-negative matrix factorization. *PeerJ*, **2021**, 9, e12087	3.1	2
16	Thrombomodulin induces anti-inflammatory effects by inhibiting the rolling adhesion of leukocytes in vivo. *Journal of Pharmacological Sciences*, **2020**, 143, 17-22	3.7	1

LIST OF PUBLICATIONS

15	Improvement of detection performance of fusion genes from RNA-seq data by clustering short reads. *Journal of Bioinformatics and Computational Biology*, **2019**, 17, 1940008	1	1
14	Improved Prediction Method for Protein Interactions Using Both Structural and Functional Characteristics of Proteins. *IPSJ Transactions on Bioinformatics*, **2010**, 3, 10-23	1.3	1
13	A Combination Method of the Tanimoto Coefficient and Proximity Measure of Random Forest for Compound Activity Prediction. *IPSJ Digital Courier*, **2008**, 4, 238-249		1
12	A priority control system for OR-parallel Prolog and its performance evaluation. *Lecture Notes in Computer Science*, **1993**, 42-53	0.9	1
11	Comparative Analysis of Transformation Methods for Gene Expression Profiles in Breast Cancer Datasets **2016**,		1
10	A simple comparison of the extrinsic noise in gene expression between native and foreign regulations in Escherichia coli. *Biochemical and Biophysical Research Communications*, **2017**, 486, 852-857	3.4	0
9	Introduction of dosim predicate to Prolog. *New Generation Computing*, **1990**, 8, 163-181	0.9	0
8	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	3.6	
7	A Method for Isoform Prediction from RNA-Seq Data by Iterative Mapping. *IPSJ Transactions on Bioinformatics*, **2012**, 5, 27-33	1.3	
6	A Distributed-Processing System for Accelerating Biological Research Using Data-Staging. *IPSJ Digital Courier*, **2008**, 4, 250-256		
5	An efficient procedure for maintaining materialized views on distributed database systems. *Systems and Computers in Japan*, **2000**, 31, 86-96		
4	An application of an OR-Parallel Prolog system to phylogenetic analysis. *Higher-Order and Symbolic Computation*, **1994**, 7, 211-229		
3	Compound-Transporter Interaction Studies using Canonical Correlation Analysis. *Chem-Bio Informatics Journal*, **2007**, 7, 24-34	0.8	
2	Inference of TFRNs (2). *Methods in Molecular Biology*, **2014**, 1164, 97-107	1.4	
1	Detection of Biomarkers for Epithelial-Mesenchymal Transition with Single-Cell Trajectory Inference.. *Frontiers in Bioscience*, **2022**, 27, 127		