

Rui Yamaguchi

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.

118
papers

2,306
citations

24
h-index

46
g-index

143
ext. papers

3,556
ext. citations

5
avg, IF

7.06
L-index

#	Paper	IF	Citations
118	Repeated Lineage Switches in an Elderly Case of Refractory B-Cell Acute Lymphoblastic Leukemia With Gene Amplification: A Case Report and Literature Review.. <i>Frontiers in Oncology</i> , 2022 , 12, 799982	5.3	0
117	Perioperative Circulating Tumor DNA Enables Identification of Patients with Poor Prognosis in Upper Tract Urothelial Carcinoma.. <i>Cancer Science</i> , 2022 ,	6.9	2
116	Impact of salivary and pancreatic amylase gene copy numbers on diabetes, obesity, and functional profiles of microbiome in Northern Japanese population.. <i>Scientific Reports</i> , 2022 , 12, 7628	4.9	1
115	Enhancing breakpoint resolution with deep segmentation model: A general refinement method for read-depth based structural variant callers. <i>PLoS Computational Biology</i> , 2021 , 17, e1009186	5	
114	Halcyon: an accurate basecaller exploiting an encoder-decoder model with monotonic attention. <i>Bioinformatics</i> , 2021 , 37, 1211-1217	7.2	3
113	Automatic sparse principal component analysis. <i>Canadian Journal of Statistics</i> , 2021 , 49, 678-697	0.4	
112	Metagenomic profiling of gut microbiome in early chronic kidney disease. <i>Nephrology Dialysis Transplantation</i> , 2021 , 36, 1675-1684	4.3	6
111	Comprehensive molecular analysis of genomic profiles and PD-L1 expression in lung adenocarcinoma with a high-grade fetal adenocarcinoma component. <i>Translational Lung Cancer Research</i> , 2021 , 10, 1292-1304	4.4	3
110	Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. <i>Gastroenterology</i> , 2021 , 160, 2089-2102.e12	13.3	17
109	Application of targeted nanopore sequencing for the screening and determination of structural variants in patients with Lynch syndrome. <i>Journal of Human Genetics</i> , 2021 , 66, 1053-1060	4.3	1
108	Senolysis by glutaminolysis inhibition ameliorates various age-associated disorders. <i>Science</i> , 2021 , 371, 265-270	33.3	58
107	Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. <i>Scientific Reports</i> , 2021 , 11, 15713	4.9	1
106	Application of state-space model with skew-t measurement noise to blood test value prediction. <i>Applied Mathematical Modelling</i> , 2021 , 100, 365-378	4.5	
105	Association between Socioeconomic Status and Digestive Tract Cancers: A Case-Control Study. <i>Cancers</i> , 2020 , 12,	6.6	2
104	Successful Clinical Sequencing by Molecular Tumor Board in an Elderly Patient With Refractory Sjögren Syndrome.. <i>JCO Precision Oncology</i> , 2020 , 4, 534-560	3.6	0
103	Neoantigen load and HLA-class I expression identify a subgroup of tumors with a T-cell-inflamed phenotype and favorable prognosis in homologous recombination-proficient high-grade serous ovarian carcinoma 2020 , 8,		6
102	Prediction of blood test values under different lifestyle scenarios using time-series electronic health record. <i>PLoS ONE</i> , 2020 , 15, e0230172	3.7	3

101	Metagenomic analysis of bacterial species in tongue microbiome of current and never smokers. <i>Npj Biofilms and Microbiomes</i> , 2020 , 6, 11	8.2	16
100	Metagenome Data on Intestinal Phage-Bacteria Associations Aids the Development of Phage Therapy against Pathobionts. <i>Cell Host and Microbe</i> , 2020 , 28, 380-389.e9	23.4	19
99	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. <i>EBioMedicine</i> , 2020 , 53, 102659	8.8	26
98	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
97	Discrimination of prediction models between cold-heat and deficiency-excess patterns. <i>Complementary Therapies in Medicine</i> , 2020 , 49, 102353	3.5	6
96	Nanopore basecalling from a perspective of instance segmentation. <i>BMC Bioinformatics</i> , 2020 , 21, 136	3.6	4
95	Global gene network exploration based on explainable artificial intelligence approach. <i>PLoS ONE</i> , 2020 , 15, e0241508	3.7	2
94	Variant analysis of prostate cancer in Japanese patients and a new attempt to predict related biological pathways. <i>Oncology Reports</i> , 2020 , 43, 943-952	3.5	0
93	Theoretical Foundation of the Performance of Phylogeny-Based Somatic Variant Detection. <i>Lecture Notes in Computer Science</i> , 2020 , 87-101	0.9	
92	Ensemble smoothers for inference of hidden states and parameters in combinatorial regulatory model. <i>Journal of the Franklin Institute</i> , 2020 , 357, 2916-2933	4	
91	Neoantimon: a multifunctional R package for identification of tumor-specific neoantigens. <i>Bioinformatics</i> , 2020 , 36, 4813-4816	7.2	2
90	Genome-wide association studies and heritability analysis reveal the involvement of host genetics in the Japanese gut microbiota. <i>Communications Biology</i> , 2020 , 3, 686	6.7	5
89	Data science and precision health care. <i>Nutrition Reviews</i> , 2020 , 78, 53-57	6.4	1
88	Epithelial-to-Mesenchymal Transition is a Cause of Both Intrinsic and Acquired Resistance to KRAS G12C Inhibitor in KRAS G12C-Mutant Non-Small Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 5962-5973	12.9	40
87	Prediction Model for Deficiency-Excess Patterns, Including Medium Pattern. <i>Kampo Medicine</i> , 2020 , 71, 315-325	0.1	
86	Capturing the differences between humoral immunity in the normal and tumor environments from repertoire-seq of B-cell receptors using supervised machine learning. <i>BMC Bioinformatics</i> , 2019 , 20, 267	3.6	12
85	Classification of patients with cold sensation by a review of systems database: A single-centre observational study. <i>Complementary Therapies in Medicine</i> , 2019 , 45, 7-13	3.5	1
84	Massively parallel sequencing of tenosynovial giant cell tumors reveals novel CSF1 fusion transcripts and novel somatic CBL mutations. <i>International Journal of Cancer</i> , 2019 , 145, 3276-3284	7.5	9

83	The first case of elderly -positive B-cell acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2019 , 60, 2821-2824	1.9	2
82	Development of an MSI-positive colon tumor with aberrant DNA methylation in a PPAP patient. <i>Journal of Human Genetics</i> , 2019 , 64, 729-740	4.3	5
81	A Bayesian model integration for mutation calling through data partitioning. <i>Bioinformatics</i> , 2019 , 35, 4247-4254	7.2	4
80	Prognostic impact of circulating tumor DNA status post-allogeneic hematopoietic stem cell transplantation in AML and MDS. <i>Blood</i> , 2019 , 133, 2682-2695	2.2	34
79	ALPHLARD-NT: Bayesian Method for Human Leukocyte Antigen Genotyping and Mutation Calling through Simultaneous Analysis of Normal and Tumor Whole-Genome Sequence Data. <i>Journal of Computational Biology</i> , 2019 , 26, 923-937	1.7	3
78	Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. <i>European Urology Focus</i> , 2019 , 5, 416-424	5.1	12
77	Prediction of deficiency-excess pattern in Japanese Kampo medicine: Multi-centre data collection. <i>Complementary Therapies in Medicine</i> , 2019 , 45, 228-233	3.5	7
76	An Unusually Short Latent Period of Therapy-Related Myeloid Neoplasm Harboring a Rare MLL-EP300 Rearrangement: Case Report and Literature Review. <i>Case Reports in Hematology</i> , 2019 , 2019, 4532434	0.7	1
75	Antigen delivery targeted to tumor-associated macrophages overcomes tumor immune resistance. <i>Journal of Clinical Investigation</i> , 2019 , 129, 1278-1294	15.9	62
74	Accurate and Flexible Bayesian Mutation Call from Multi-regional Tumor Samples. <i>Lecture Notes in Computer Science</i> , 2019 , 47-61	0.9	1
73	Genomic Analysis of Therapy-Related Myeloid Neoplasms and Tracking of the Founder Clone By Circulating Tumor DNA. <i>Blood</i> , 2019 , 134, 5393-5393	2.2	
72	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. <i>Nature Communications</i> , 2019 , 10, 5683	17.4	26
71	Virtual Grid Engine: a simulated grid engine environment for large-scale supercomputers. <i>BMC Bioinformatics</i> , 2019 , 20, 591	3.6	
70	Evaluation of ALK Fusion Newly Identified in Colon Cancer by a Comprehensive Genomic Analysis.. <i>JCO Precision Oncology</i> , 2019 , 3, 1-5	3.6	1
69	A novel ASXL1-OGT axis plays roles in H3K4 methylation and tumor suppression in myeloid malignancies. <i>Leukemia</i> , 2018 , 32, 1327-1337	10.7	33
68	Azacitidine effectively reduces -mutant leukemic cell burden in secondary acute myeloid leukemia after cord blood transplantation. <i>Leukemia and Lymphoma</i> , 2018 , 59, 2755-2756	1.9	
67	Different clonal dynamics of chronic myeloid leukaemia between bone marrow and the central nervous system. <i>British Journal of Haematology</i> , 2018 , 183, 842-845	4.5	
66	Characterization of the B-cell receptor repertoires in peanut allergic subjects undergoing oral immunotherapy. <i>Journal of Human Genetics</i> , 2018 , 63, 239-248	4.3	16

65	Prognostic Impact of Circulating Tumor DNA Status Post-Allogeneic Hematopoietic Stem Cell Transplantation in Acute Myeloid Leukemia and Myelodysplastic Syndrome. <i>Blood</i> , 2018 , 132, 247-247	2.2	
64	Artificial Intelligence Guided Precision Medicine Approach to Hematological Disease. <i>Blood</i> , 2018 , 132, 2254-2254	2.2	
63	Phenotype-based gene analysis allowed successful diagnosis of X-linked neutropenia associated with a novel WASp mutation. <i>Annals of Hematology</i> , 2018 , 97, 367-369	3	5
62	ALPHLARD: a Bayesian method for analyzing HLA genes from whole genome sequence data. <i>BMC Genomics</i> , 2018 , 19, 790	4.5	11
61	Cell-lineage level-targeted sequencing to identify acute myeloid leukemia with myelodysplasia-related changes. <i>Blood Advances</i> , 2018 , 2, 2513-2521	7.8	7
60	Circulating tumor DNA dynamically predicts response and/or relapse in patients with hematological malignancies. <i>International Journal of Hematology</i> , 2018 , 108, 402-410	2.3	13
59	OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads. <i>IEEE Transactions on Nanobioscience</i> , 2017 , 16, 116-122	3.4	1
58	Clinical significance of T cell clonality and expression levels of immune-related genes in endometrial cancer. <i>Oncology Reports</i> , 2017 , 37, 2603-2610	3.5	29
57	The Transcriptional Landscape of p53 Signalling Pathway. <i>EBioMedicine</i> , 2017 , 20, 109-119	8.8	30
56	Identification of an immunogenic neo-epitope encoded by mouse sarcoma using CXCR3 ligand mRNAs as sensors. <i>Oncolimmunology</i> , 2017 , 6, e1306617	7.2	3
55	Circulating exosomal microRNA-203 is associated with metastasis possibly via inducing tumor-associated macrophages in colorectal cancer. <i>Oncotarget</i> , 2017 , 8, 78598-78613	3.3	92
54	Identification of a p53 target, CD137L, that mediates growth suppression and immune response of osteosarcoma cells. <i>Scientific Reports</i> , 2017 , 7, 10739	4.9	3
53	Requirement of glycosylation machinery in TLR responses revealed by CRISPR/Cas9 screening. <i>International Immunology</i> , 2017 , 29, 347-355	4.9	4
52	Sequence-specific bias correction for RNA-seq data using recurrent neural networks. <i>BMC Genomics</i> , 2017 , 18, 1044	4.5	10
51	Reconstruction of high read-depth signals from low-depth whole genome sequencing data using deep learning 2017 ,		1
50	Identification of a p53-repressed gene module in breast cancer cells. <i>Oncotarget</i> , 2017 , 8, 55821-55836	3.3	5
49	Revealing phenotype-associated functional differences by genome-wide scan of ancient haplotype blocks. <i>PLoS ONE</i> , 2017 , 12, e0176530	3.7	
48	Predicting Japanese Kampo formulas by analyzing database of medical records: a preliminary observational study. <i>BMC Medical Informatics and Decision Making</i> , 2016 , 16, 118	3.6	4

47	Characterization of the T cell repertoire by deep T cell receptor sequencing in tissues and blood from patients with advanced colorectal cancer. <i>Oncology Letters</i> , 2016 , 11, 3643-3649	2.6	30
46	Gene set differential analysis of time course expression profiles via sparse estimation in functional logistic model with application to time-dependent biomarker detection. <i>Biostatistics</i> , 2016 , 17, 235-48	3.7	8
45	A likelihood-free filtering method via approximate Bayesian computation in evaluating biological simulation models. <i>Computational Statistics and Data Analysis</i> , 2016 , 94, 63-74	1.6	1
44	OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads. <i>Lecture Notes in Computer Science</i> , 2016 , 40-51	0.9	
43	Exploratory Introduction of Cognitive Computing to Clinical Sequencing in Hematological Malignancies. <i>Blood</i> , 2016 , 128, 5262-5262	2.2	
42	The Difference between the Two Representative Kampo Formulas for Treating Dysmenorrhea: An Observational Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2016 , 2016, 3159617	2.3	13
41	Characterization of T-cell Receptor Repertoire in Inflamed Tissues of Patients with Crohn's Disease Through Deep Sequencing. <i>Inflammatory Bowel Diseases</i> , 2016 , 22, 1275-85	4.5	28
40	8q24 Polymorphisms and Diabetes Mellitus Regulate Apolipoprotein A-IV in Colorectal Carcinogenesis. <i>Annals of Surgical Oncology</i> , 2016 , 23, 546-551	3.1	3
39	Reduced expression of APC-1B but not APC-1A by the deletion of promoter 1B is responsible for familial adenomatous polyposis. <i>Scientific Reports</i> , 2016 , 6, 26011	4.9	10
38	The hypusine cascade promotes cancer progression and metastasis through the regulation of RhoA in squamous cell carcinoma. <i>Oncogene</i> , 2016 , 35, 5304-5316	9.2	29
37	Detection of APC mosaicism by next-generation sequencing in an FAP patient. <i>Journal of Human Genetics</i> , 2015 , 60, 227-31	4.3	28
36	Quantitative characterization of T-cell repertoire in allogeneic hematopoietic stem cell transplant recipients. <i>Bone Marrow Transplantation</i> , 2015 , 50, 1227-34	4.4	81
35	Genomic data assimilation using a higher moment filtering technique for restoration of gene regulatory networks. <i>BMC Systems Biology</i> , 2015 , 9, 14	3.5	2
34	Expression and clinical significance of genes frequently mutated in small cell lung cancers defined by whole exome/RNA sequencing. <i>Carcinogenesis</i> , 2015 , 36, 616-21	4.6	57
33	Elevated Ectenin pathway as a novel target for patients with resistance to EGF receptor targeting drugs. <i>Scientific Reports</i> , 2015 , 5, 13076	4.9	32
32	Attenuated familial adenomatous polyposis with desmoids caused by an APC mutation. <i>Human Genome Variation</i> , 2015 , 2, 15011	1.8	3
31	An efficient data assimilation schema for restoration and extension of gene regulatory networks using time-course observation data. <i>Journal of Computational Biology</i> , 2014 , 21, 785-98	1.7	2
30	An efficient method of exploring simulation models by assimilating literature and biological observational data. <i>BioSystems</i> , 2014 , 121, 54-66	1.9	3

29	Analysis of questionnaire for traditional medicine and development of decision support system. <i>Evidence-based Complementary and Alternative Medicine</i> , 2014 , 2014, 974139	2.3	10
28	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor α and β chains using next-generation sequencing (NGS). <i>Oncology</i> , 2014 , 3, e968467	7.2	56
27	Overexpression of cohesion establishment factor DSCC1 through E2F in colorectal cancer. <i>PLoS ONE</i> , 2014 , 9, e85750	3.7	14
26	Inference of gene regulatory networks incorporating multi-source biological knowledge via a state space model with L1 regularization. <i>PLoS ONE</i> , 2014 , 9, e105942	3.7	13
25	Statistical analysis of hie (cold sensation) and hiesho (cold disorder) in kampo clinic. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013 , 2013, 398458	2.3	26
24	Prescription of kampo drugs in the Japanese health care insurance program. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013 , 2013, 576973	2.3	25
23	Does Twitter trigger bursts in signature collections?. <i>PLoS ONE</i> , 2013 , 8, e58252	3.7	4
22	Identifying regulational alterations in gene regulatory networks by state space representation of vector autoregressive models and variational annealing. <i>BMC Genomics</i> , 2012 , 13 Suppl 1, S6	4.5	3
21	Epidermal growth factor receptor tyrosine kinase defines critical prognostic genes of stage I lung adenocarcinoma. <i>PLoS ONE</i> , 2012 , 7, e43923	3.7	94
20	A novel network profiling analysis reveals system changes in epithelial-mesenchymal transition. <i>PLoS ONE</i> , 2011 , 6, e20804	3.7	28
19	Clustering for Visual Analogue Scale Data in Symbolic Data Analysis. <i>Procedia Computer Science</i> , 2011 , 6, 370-374	1.6	5
18	SiGN-SSM: open source parallel software for estimating gene networks with state space models. <i>Bioinformatics</i> , 2011 , 27, 1172-3	7.2	6
17	N-cadherin expression is a potential survival mechanism of gefitinib-resistant lung cancer cells. <i>American Journal of Cancer Research</i> , 2011 , 1, 823-33	4.4	19
16	Comprehensive Pharmacogenomic Pathway Screening by Data Assimilation. <i>Lecture Notes in Computer Science</i> , 2011 , 160-171	0.9	3
15	Identifying Hidden Confounders in Gene Networks by Bayesian Networks 2010 ,		1
14	Network-Based Predictions and Simulations by Biological State Space Models: Search for Drug Mode of Action. <i>Journal of Computer Science and Technology</i> , 2010 , 25, 131-153	1.7	1
13	Orengedokuto and berberine improve indomethacin-induced small intestinal injury via adenosine. <i>Journal of Gastroenterology</i> , 2009 , 44, 380-9	6.9	22
12	Gene Networks Viewed through Two Models. <i>Lecture Notes in Computer Science</i> , 2009 , 54-66	0.9	

11	Statistical inference of transcriptional module-based gene networks from time course gene expression profiles by using state space models. <i>Bioinformatics</i> , 2008 , 24, 932-42	7.2	75
10	Predicting differences in gene regulatory systems by state space models. <i>Genome Informatics</i> , 2008 , 21, 101-13		7
9	Statistical Absolute Evaluation of Gene Ontology Terms with Gene Expression Data 2007 , 146-157		5
8	WEIGHTED LASSO IN GRAPHICAL GAUSSIAN MODELING FOR LARGE GENE NETWORK ESTIMATION BASED ON MICROARRAY DATA 2007 ,		12
7	IDENTIFICATION OF ACTIVATED TRANSCRIPTION FACTORS FROM MICROARRAY GENE EXPRESSION DATA OF KAMPO MEDICINE-TREATED MICE 2007 ,		2
6	Identification of activated transcription factors from microarray gene expression data of Kampo medicine-treated mice. <i>Genome Informatics</i> , 2007 , 18, 119-29		3
5	Clustering samples characterized by time course gene expression profiles using the mixture of state space models. <i>Genome Informatics</i> , 2007 , 18, 258-66		1
4	Weighted lasso in graphical Gaussian modeling for large gene network estimation based on microarray data. <i>Genome Informatics</i> , 2007 , 19, 142-53		15
3	State-space approach with the maximum likelihood principle to identify the system generating time-course gene expression data of yeast. <i>International Journal of Data Mining and Bioinformatics</i> , 2006 , 1, 77-87	0.5	8
2	Capturing the Differences between Humoral Immunity in the Normal and Tumor Environments from Repertoire-Seq of B-Cell Receptors Using Supervised Machine Learning		1
1	On the application of BERT models for nanopore methylation detection		2