

Rui Yamaguchi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7766970/publications.pdf>

Version: 2024-02-01

129
papers

4,442
citations

201385

27
h-index

133063

59
g-index

145
all docs

145
docs citations

145
times ranked

9083
citing authors

#	ARTICLE	IF	CITATIONS
1	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
2	Senolysis by glutaminolysis inhibition ameliorates various age-associated disorders. <i>Science</i> , 2021, 371, 265-270.	6.0	222
3	Epidermal Growth Factor Receptor Tyrosine Kinase Defines Critical Prognostic Genes of Stage I Lung Adenocarcinoma. <i>PLoS ONE</i> , 2012, 7, e43923.	1.1	148
4	Circulating exosomal microRNA-203 is associated with metastasis possibly via inducing tumor-associated macrophages in colorectal cancer. <i>Oncotarget</i> , 2017, 8, 78598-78613.	0.8	132
5	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.	3.2	118
6	Quantitative characterization of T-cell repertoire in allogeneic hematopoietic stem cell transplant recipients. <i>Bone Marrow Transplantation</i> , 2015, 50, 1227-1234.	1.3	109
7	Antigen delivery targeted to tumor-associated macrophages overcomes tumor immune resistance. <i>Journal of Clinical Investigation</i> , 2019, 129, 1278-1294.	3.9	102
8	Statistical inference of transcriptional module-based gene networks from time course gene expression profiles by using state space models. <i>Bioinformatics</i> , 2008, 24, 932-942.	1.8	87
9	Expression and clinical significance of genes frequently mutated in small cell lung cancers defined by whole exome/RNA sequencing. <i>Carcinogenesis</i> , 2015, 36, 616-621.	1.3	73
10	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor α and β chains using next-generation sequencing (NGS). <i>Onc Immunology</i> , 2014, 3, e968467.	2.1	68
11	Prognostic impact of circulating tumor DNA status post-allogeneic hematopoietic stem cell transplantation in AML and MDS. <i>Blood</i> , 2019, 133, 2682-2695.	0.6	62
12	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.	5.1	51
13	A novel ASXL1-OGT axis plays roles in H3K4 methylation and tumor suppression in myeloid malignancies. <i>Leukemia</i> , 2018, 32, 1327-1337.	3.3	50
14	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. <i>EBioMedicine</i> , 2020, 53, 102659.	2.7	48
15	The Transcriptional Landscape of p53 Signalling Pathway. <i>EBioMedicine</i> , 2017, 20, 109-119.	2.7	47
16	Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. <i>Gastroenterology</i> , 2021, 160, 2089-2102.e12.	0.6	45
17	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. <i>Nature Communications</i> , 2019, 10, 5683.	5.8	41
18	Elevated β -catenin pathway as a novel target for patients with resistance to EGF receptor targeting drugs. <i>Scientific Reports</i> , 2015, 5, 13076.	1.6	40

#	ARTICLE	IF	CITATIONS
19	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, 1275-1285.	0.9	40
20	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.	2.0	40
21	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.	0.8	39
22	A Novel Network Profiling Analysis Reveals System Changes in Epithelial-Mesenchymal Transition. <i>PLoS ONE</i> , 2011, 6, e20804.	1.1	38
23	Prescription of Kampo Drugs in the Japanese Health Care Insurance Program. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-7.	0.5	38
24	Clinical significance of T cell clonality and expression levels of immune-related genes in endometrial cancer. <i>Oncology Reports</i> , 2017, 37, 2603-2610.	1.2	38
25	Detection of APC mosaicism by next-generation sequencing in an FAP patient. <i>Journal of Human Genetics</i> , 2015, 60, 227-231.	1.1	33
26	The hypusine cascade promotes cancer progression and metastasis through the regulation of RhoA in squamous cell carcinoma. <i>Oncogene</i> , 2016, 35, 5304-5316.	2.6	33
27	Metagenomic analysis of bacterial species in tongue microbiome of current and never smokers. <i>Npj Biofilms and Microbiomes</i> , 2020, 6, 11.	2.9	32
28	Statistical Analysis of <i>Hie</i> (Cold Sensation) and <i>Hiesho</i> (Cold Disorder) in Kampo Clinic. <i>Evidence-based Complementary and Alternative Medicine</i> , 2013, 2013, 1-8.	0.5	30
29	Metagenomic profiling of gut microbiome in early chronic kidney disease. <i>Nephrology Dialysis Transplantation</i> , 2021, 36, 1675-1684.	0.4	29
30	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.	2.3	28
31	Orengedokuto and berberine improve indomethacin-induced small intestinal injury via adenosine. <i>Journal of Gastroenterology</i> , 2009, 44, 380-389.	2.3	25
32	Characterization of the B-cell receptor repertoires in peanut allergic subjects undergoing oral immunotherapy. <i>Journal of Human Genetics</i> , 2018, 63, 239-248.	1.1	24
33	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.	1.2	23
34	Overexpression of Cohesion Establishment Factor DSCC1 through E2F in Colorectal Cancer. <i>PLoS ONE</i> , 2014, 9, e85750.	1.1	21
35	Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. <i>European Urology Focus</i> , 2019, 5, 416-424.	1.6	20
36	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.	1.4	19

#	ARTICLE	IF	CITATIONS
37	The Difference between the Two Representative Kampo Formulas for Treating Dysmenorrhea: An Observational Study. Evidence-based Complementary and Alternative Medicine, 2016, 2016, 1-10.	0.5	17
38	Reduced expression of APC-1B but not APC-1A by the deletion of promoter 1B is responsible for familial adenomatous polyposis. Scientific Reports, 2016, 6, 26011.	1.6	17
39	Circulating tumor DNA dynamically predicts response and/or relapse in patients with hematological malignancies. International Journal of Hematology, 2018, 108, 402-410.	0.7	17
40	Nanopore basecalling from a perspective of instance segmentation. BMC Bioinformatics, 2020, 21, 136.	1.2	17
41	Halcyon: an accurate basecaller exploiting an encoder-decoder model with monotonic attention. Bioinformatics, 2021, 37, 1211-1217.	1.8	17
42	ALPHLARD: a Bayesian method for analyzing HLA genes from whole genome sequence data. BMC Genomics, 2018, 19, 790.	1.2	16
43	Weighted lasso in graphical Gaussian modeling for large gene network estimation based on microarray data. Genome Informatics, 2007, 19, 142-53.	0.4	16
44	Inference of Gene Regulatory Networks Incorporating Multi-Source Biological Knowledge via a State Space Model with L1 Regularization. PLoS ONE, 2014, 9, e105942.	1.1	15
45	WEIGHTED LASSO IN GRAPHICAL GAUSSIAN MODELING FOR LARGE GENE NETWORK ESTIMATION BASED ON MICROARRAY DATA. , 2007, , .		14
46	Sequence-specific bias correction for RNA-seq data using recurrent neural networks. BMC Genomics, 2017, 18, 1044.	1.2	14
47	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, e000375.		14
48	Analysis of Questionnaire for Traditional Medicine and Development of Decision Support System. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-8.	0.5	12
49	Application of targeted nanopore sequencing for the screening and determination of structural variants in patients with Lynch syndrome. Journal of Human Genetics, 2021, 66, 1053-1060.	1.1	12
50	State-space approach with the maximum likelihood principle to identify the system generating time-course gene expression data of yeast. International Journal of Data Mining and Bioinformatics, 2006, 1, 77.	0.1	11
51	Gene set differential analysis of time course expression profiles via sparse estimation in functional logistic model with application to time-dependent biomarker detection. Biostatistics, 2016, 17, 235-248.	0.9	11
52	Perioperative circulating tumor DNA enables the identification of patients with poor prognosis in upper tract urothelial carcinoma. Cancer Science, 2022, 113, 1830-1842.	1.7	11
53	Phenotype-based gene analysis allowed successful diagnosis of X-linked neutropenia associated with a novel WASp mutation. Annals of Hematology, 2018, 97, 367-369.	0.8	10
54	Cell-lineage level-targeted sequencing to identify acute myeloid leukemia with myelodysplasia-related changes. Blood Advances, 2018, 2, 2513-2521.	2.5	10

#	ARTICLE	IF	CITATIONS
55	Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. <i>Scientific Reports</i> , 2021, 11, 15713.	1.6	10
56	Requirement of glycosylation machinery in TLR responses revealed by CRISPR/Cas9 screening. <i>International Immunology</i> , 2017, 29, 347-355.	1.8	9
57	Association between Socioeconomic Status and Digestive Tract Cancers: A Case-Control Study. <i>Cancers</i> , 2020, 12, 3258.	1.7	9
58	Prediction of deficiency-excess pattern in Japanese Kampo medicine: Multi-centre data collection. <i>Complementary Therapies in Medicine</i> , 2019, 45, 228-233.	1.3	8
59	Neoantimon: a multifunctional R package for identification of tumor-specific neoantigens. <i>Bioinformatics</i> , 2020, 36, 4813-4816.	1.8	8
60	Discrimination of prediction models between cold-heat and deficiency-excess patterns. <i>Complementary Therapies in Medicine</i> , 2020, 49, 102353.	1.3	8
61	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.	1.1	7
62	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.	1.3	7
63	Predicting differences in gene regulatory systems by state space models. <i>Genome Informatics</i> , 2008, 21, 101-113.	0.4	7
64	Statistical Absolute Evaluation of Gene Ontology Terms with Gene Expression Data. , 2007, , 146-157.		6
65	SiGN-SSM: open source parallel software for estimating gene networks with state space models. <i>Bioinformatics</i> , 2011, 27, 1172-1173.	1.8	6
66	Attenuated familial adenomatous polyposis with desmoids caused by an APC mutation. <i>Human Genome Variation</i> , 2015, 2, 15011.	0.4	6
67	The first case of elderly <i><i>TCF3-HLF</i></i> -positive B-cell acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2019, 60, 2821-2824.	0.6	6
68	A Bayesian model integration for mutation calling through data partitioning. <i>Bioinformatics</i> , 2019, 35, 4247-4254.	1.8	6
69	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.	0.8	6
70	Global gene network exploration based on explainable artificial intelligence approach. <i>PLoS ONE</i> , 2020, 15, e0241508.	1.1	6
71	Identification of a p53-repressed gene module in breast cancer cells. <i>Oncotarget</i> , 2017, 8, 55821-55836.	0.8	6
72	Early dynamics of circulating tumor DNA predict clinical response to immune checkpoint inhibitors in metastatic renal cell carcinoma. <i>International Journal of Urology</i> , 2022, 29, 462-469.	0.5	6

#	ARTICLE	IF	CITATIONS
73	Clustering for Visual Analogue Scale Data in Symbolic Data Analysis. <i>Procedia Computer Science</i> , 2011, 6, 370-374.	1.2	5
74	8q24 Polymorphisms and Diabetes Mellitus Regulate Apolipoprotein A-IV in Colorectal Carcinogenesis. <i>Annals of Surgical Oncology</i> , 2016, 23, 546-551.	0.7	5
75	Identification of an immunogenic neo-epitope encoded by mouse sarcoma using CXCR3 ligand mRNAs as sensors. <i>OncImmunology</i> , 2017, 6, e1306617.	2.1	5
76	Prediction of blood test values under different lifestyle scenarios using time-series electronic health record. <i>PLoS ONE</i> , 2020, 15, e0230172.	1.1	5
77	Comprehensive Pharmacogenomic Pathway Screening by Data Assimilation. <i>Lecture Notes in Computer Science</i> , 2011, , 160-171.	1.0	5
78	Identifying regulational alterations in gene regulatory networks by state space representation of vector autoregressive models and variational annealing. <i>BMC Genomics</i> , 2012, 13, S6.	1.2	4
79	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.	1.5	4
80	Does Twitter Trigger Bursts in Signature Collections?. <i>PLoS ONE</i> , 2013, 8, e58252.	1.1	4
81	Identification of activated transcription factors from microarray gene expression data of Kampo medicine-treated mice. <i>Genome Informatics</i> , 2007, 18, 119-29.	0.4	4
82	COMPARISON OF GENE EXPRESSION PROFILES PRODUCED BY CAGE, ILLUMINA MICROARRAY AND REAL TIME RT-PCR. , 2010, , .		3
83	Identifying Hidden Confounders in Gene Networks by Bayesian Networks. , 2010, , .		3
84	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, 785-798.	0.8	3
85	An efficient method of exploring simulation models by assimilating literature and biological observational data. <i>BioSystems</i> , 2014, 121, 54-66.	0.9	3
86	Identification of a p53 target, CD137L, that mediates growth suppression and immune response of osteosarcoma cells. <i>Scientific Reports</i> , 2017, 7, 10739.	1.6	3
87	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, 1-6.	0.3	3
88	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.	1.3	3
89	Data science and precision health care. <i>Nutrition Reviews</i> , 2020, 78, 53-57.	2.6	3
90	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.	1.2	3

#	ARTICLE	IF	CITATIONS
91	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.	1.6	3
92	Genomic data assimilation using a higher moment filtering technique for restoration of gene regulatory networks. <i>BMC Systems Biology</i> , 2015, 9, 14.	3.0	2
93	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.	0.7	2
94	Evaluation of ALK Fusion Newly Identified in Colon Cancer by a Comprehensive Genomic Analysis. <i>JCO Precision Oncology</i> , 2019, 3, 1-5.	1.5	2
95	IDENTIFICATION OF ACTIVATED TRANSCRIPTION FACTORS FROM MICROARRAY GENE EXPRESSION DATA OF KAMPO MEDICINE-TREATED MICE. , 2007, , .		2
96	Repeated Lineage Switches in an Elderly Case of Refractory B-Cell Acute Lymphoblastic Leukemia With MLL Gene Amplification: A Case Report and Literature Review. <i>Frontiers in Oncology</i> , 2022, 12, 799982.	1.3	2
97	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.	0.9	1
98	Kampo Traditional Pattern Diagnosis and the Clustering Analysis of Patients with Cold Sensation. <i>Journal of Alternative and Complementary Medicine</i> , 2014, 20, A47-A47.	2.1	1
99	OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 116-122.	2.2	1
100	Reconstruction of high read-depth signals from low-depth whole genome sequencing data using deep learning. , 2017, , .		1
101	Successful Clinical Sequencing by Molecular Tumor Board in an Elderly Patient With Refractory SÅ©zary Syndrome. <i>JCO Precision Oncology</i> , 2020, 4, 534-560.	1.5	1
102	Clinical Guideline-Guided Outcome Consistency for Surgically Resected Stage III Non-Small Cell Lung Cancer: A Retrospective Study. <i>Cancers</i> , 2021, 13, 2531.	1.7	1
103	PREDICTING DIFFERENCES IN GENE REGULATORY SYSTEMS BY STATE SPACE MODELS. , 2008, , .		1
104	Abstract 502: Circulating exosomal miR-203 is associated with metastasis via inducing tumor-associated macrophages in colorectal cancer. , 2018, , .		1
105	Accurate and Flexible Bayesian Mutation Call from Multi-regional Tumor Samples. <i>Lecture Notes in Computer Science</i> , 2019, , 47-61.	1.0	1
106	Clustering samples characterized by time course gene expression profiles using the mixture of state space models. <i>Genome Informatics</i> , 2007, 18, 258-66.	0.4	1
107	Analyzing Time Course Gene Expression Data with Biological and Technical Replicates to Estimate Gene Networks by State Space Models. , 2008, , .		0
108	Discovering functional gene pathways associated with cancer heterogeneity via sparse supervised learning. , 2010, , .		0

#	ARTICLE	IF	CITATIONS
109	Azacitidine effectively reduces TP53-mutant leukemic cell burden in secondary acute myeloid leukemia after cord blood transplantation. <i>Leukemia and Lymphoma</i> , 2018, 59, 2755-2756.	0.6	0
110	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.	1.2	0
111	Virtual Grid Engine: Accelerating thousands of omics sample analyses using large-scale supercomputers. , 2018, , .		0
112	Virtual Grid Engine: a simulated grid engine environment for large-scale supercomputers. <i>BMC Bioinformatics</i> , 2019, 20, 591.	1.2	0
113	Ensemble smoothers for inference of hidden states and parameters in combinatorial regulatory model. <i>Journal of the Franklin Institute</i> , 2020, 357, 2916-2933.	1.9	0
114	MO18-1 EMT is a cause of both intrinsic and acquired resistance to KRAS G12C inhibitor in KRAS G12C mutant NSCLC. <i>Annals of Oncology</i> , 2021, 32, S307.	0.6	0
115	Application of state-space model with skew-t measurement noise to blood test value prediction. <i>Applied Mathematical Modelling</i> , 2021, 100, 365-378.	2.2	0
116	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.	1.5	0
117	A NOVEL STRATEGY TO SEARCH CONSERVED TRANSCRIPTION FACTOR BINDING SITES AMONG COEXPRESSING GENES IN HUMAN. , 2008, , .		0
118	Gene Networks Viewed through Two Models. <i>Lecture Notes in Computer Science</i> , 2009, , 54-66.	1.0	0
119	Abstract 4921: Next-generation sequencing as a potential tool in the diagnostics of APC mosaicism in FAP patient. , 2015, , .		0
120	Abstract 2278: The hypusine cascade promotes cancer progression and metastasis through the regulation of RhoA in squamous cell carcinoma. , 2015, , .		0
121	Exploratory Introduction of Cognitive Computing to Clinical Sequencing in Hematological Malignancies. <i>Blood</i> , 2016, 128, 5262-5262.	0.6	0
122	Abstract PR02: Antigen delivery targeting tumor-infiltrating macrophages leads to eradication of tumor highly resistant to immune checkpoint inhibitors. , 2017, , .		0
123	Revealing phenotype-associated functional differences by genome-wide scan of ancient haplotype blocks. <i>PLoS ONE</i> , 2017, 12, e0176530.	1.1	0
124	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.	0.6	0
125	Artificial Intelligence Guided Precision Medicine Approach to Hematological Disease. <i>Blood</i> , 2018, 132, 2254-2254.	0.6	0
126	Genomic Analysis of Therapy-Related Myeloid Neoplasms and Tracking of the Founder Clone By Circulating Tumor DNA. <i>Blood</i> , 2019, 134, 5393-5393.	0.6	0

#	ARTICLE	IF	CITATIONS
127	Automatic sparse principal component analysis. Canadian Journal of Statistics, 2021, 49, 678-697.	0.6	0
128	Theoretical Foundation of the Performance of Phylogeny-Based Somatic Variant Detection. Lecture Notes in Computer Science, 2020, , 87-101.	1.0	0
129	Prediction Model for Deficiency-Excess Patterns, Including Medium Pattern. Kampo Medicine, 2020, 71, 315-325.	0.1	0