Seiya Imoto

List of Publications by Year
in descending order

230 papers	7,208 citations	87723 38 h-index	74018 75 g-index
247 all docs	247 docs citations	247 times ranked	11028 citing authors

#	Article	IF	Citations
1	Uncovering Molecular Mechanisms of Drug Resistance via Network-Constrained Common Structure Identification. Journal of Computational Biology, 2022, , .	0.8	1
2	COVID-19 wastewater surveillance implemented in the Tokyo 2020 Olympic and Paralympic Village. Journal of Travel Medicine, 2022, 29, .	1.4	15
3	Early dynamics of circulating tumor DNA predict clinical response to immune checkpoint inhibitors in metastatic renal cell carcinoma. International Journal of Urology, 2022, 29, 462-469.	0.5	6
4	Two Blautia Species Associated with Visceral Fat Accumulation: A One-Year Longitudinal Study. Biology, 2022, 11, 318.	1.3	16
5	COVID-19 testing systems and their effectiveness in small, semi-isolated groups for sports events. PLoS ONE, 2022, 17, e0266197.	1.1	7
6	Repeated Lineage Switches in an Elderly Case of Refractory B-Cell Acute Lymphoblastic Leukemia With MLL Gene Amplification: A Case Report and Literature Review. Frontiers in Oncology, 2022, 12, 799982.	1.3	2
7	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
8	Assessment of COVID-19 risk and prevention effectiveness among spectators of mass gathering events. Microbial Risk Analysis, 2022, 21, 100215.	1.3	10
9	Bronchoalveolar lavage fluid reveals factors contributing to the efficacy of PD-1 blockade in lung cancer. JCI Insight, 2022, 7, .	2.3	10
10	Effects of test timing and isolation length to reduce the risk of COVID-19 infection associated with airplane travel, as determined by infectious disease dynamics modeling. Microbial Risk Analysis, 2022, 20, 100199.	1.3	4
11	Improvement of the Japanese healthcare data system for the effective management of patients with COVID-19: A national survey. International Journal of Medical Informatics, 2022, 162, 104752.	1.6	3
12	Role of the Orphan Transporter SLC35E1 in the Nuclear Egress of Herpes Simplex Virus 1. Journal of Virology, 2022, , e0030622.	1.5	1
13	Impact of salivary and pancreatic amylase gene copy numbers on diabetes, obesity, and functional profiles of microbiome in Northern Japanese population. Scientific Reports, 2022, 12, 7628.	1.6	3
14	Xprediction: Explainable EGFR-TKIs response prediction based on drug sensitivity specific gene networks. PLoS ONE, 2022, 17, e0261630.	1.1	1
15	Trop-2 in Upper Tract Urothelial Carcinoma. Current Oncology, 2022, 29, 3911-3921.	0.9	13
16	Genome-wide causal mediation analysis identifies genetic loci associated with uterine fibroids mediated by age at menarche. Human Reproduction, 2022, 37, 2197-2212.	0.4	1
17	Metagenomic profiling of gut microbiome in early chronic kidney disease. Nephrology Dialysis Transplantation, 2021, 36, 1675-1684.	0.4	29
18	Fecal Microbiome Composition in Healthy Adults in Ghana. Japanese Journal of Infectious Diseases, 2021, 74, 42-47.	0.5	9

#	Article	IF	Citations
19	Senolysis by glutaminolysis inhibition ameliorates various age-associated disorders. Science, 2021, 371, 265-270.	6.0	222
20	Comprehensive molecular analysis of genomic profiles and PD-L1 expression in lung adenocarcinoma with a high-grade fetal adenocarcinoma component. Translational Lung Cancer Research, 2021, 10, 1292-1304.	1.3	7
21	COVID-19 risk assessment at the opening ceremony of the Tokyo 2020 Olympic Games. Microbial Risk Analysis, 2021, 19, 100162.	1.3	20
22	Role of Circulating Tumor DNA in Hematological Malignancy. Cancers, 2021, 13, 2078.	1.7	11
23	Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. Gastroenterology, 2021, 160, 2089-2102.e12.	0.6	45
24	Dysbiotic Fecal Microbiome in HIV-1 Infected Individuals in Ghana. Frontiers in Cellular and Infection Microbiology, 2021, 11, 646467.	1.8	24
25	HEAL: an automated deep learning framework for cancer histopathology image analysis. Bioinformatics, 2021, 37, 4291-4295.	1.8	18
26	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
27	Living with COVID-19: mass gatherings and minimizing risk. QJM - Monthly Journal of the Association of Physicians, 2021, 114, 437-439.	0.2	13
28	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. Nature Medicine, 2021, 27, 1239-1249.	15.2	78
29	Circulating cell-free DNA in the peripheral blood plasma of patients is an informative biomarker for multiple myeloma relapse. International Journal of Clinical Oncology, 2021, 26, 2142-2150.	1.0	9
30	Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. Scientific Reports, 2021, 11, 15713.	1.6	10
31	Oral MucoRice-CTB vaccine for safety and microbiota-dependent immunogenicity in humans: a phase 1 randomised trial. Lancet Microbe, The, 2021, 2, e429-e440.	3.4	27
32	Clinical Characteristics of Patients with Coronavirus Disease (COVID-19): Preliminary Baseline Report of Japan COVID-19 Task Force, a Nationwide Consortium to Investigate Host Genetics of COVID-19. International Journal of Infectious Diseases, 2021, 113, 74-81.	1.5	24
33	Application of state-space model with skew-t measurement noise to blood test value prediction. Applied Mathematical Modelling, 2021, 100, 365-378.	2.2	0
34	Enhancing breakpoint resolution with deep segmentation model: A general refinement method for read-depth based structural variant callers. PLoS Computational Biology, 2021, 17, e1009186.	1.5	0
35	The effect of age on the association between daily gait speed and abdominal obesity in Japanese adults. Scientific Reports, 2021, 11, 19975.	1.6	2
36	Possible Role of Cytochrome P450 1B1 in the Mechanism of Gemcitabine Resistance in Pancreatic Cancer. Biomedicines, 2021, 9, 1396.	1.4	9

#	Article	IF	Citations
37	Halcyon: an accurate basecaller exploiting an encoder–decoder model with monotonic attention. Bioinformatics, 2021, 37, 1211-1217.	1.8	17
38	Automatic sparse principal component analysis. Canadian Journal of Statistics, 2021, 49, 678-697.	0.6	0
39	7. Applications of Artificial Intelligence (AI) to Clinical and Genomic Medicine. The Journal of the Japanese Society of Internal Medicine, 2021, 110, 492-498.	0.0	0
40	Ovariectomy-Induced Dysbiosis May Have a Minor Effect on Bone in Mice. Microorganisms, 2021, 9, 2563.	1.6	4
41	Discovering microbe functionality in human disease with a gene-ontology-aware model. , 2021, , .		0
42	3081 – SINGLE-CELL RNA-SEQ REVEALS ALTERATIONS IN HETEROGENEITY OF HEMATOPOIETIC STEM CELLS WITH AGING. Experimental Hematology, 2021, 100, S81.	0.2	0
43	Ensemble smoothers for inference of hidden states and parameters in combinatorial regulatory model. Journal of the Franklin Institute, 2020, 357, 2916-2933.	1.9	0
44	Neoantimon: a multifunctional R package for identification of tumor-specific neoantigens. Bioinformatics, 2020, 36, 4813-4816.	1.8	8
45	Genome-wide association studies and heritability analysis reveal the involvement of host genetics in the Japanese gut microbiota. Communications Biology, 2020, 3, 686.	2.0	40
46	Data science and precision health care. Nutrition Reviews, 2020, 78, 53-57.	2.6	3
47	Association of single nucleotide polymorphisms in the NRF2 promoter with vascular stiffness with aging. PLoS ONE, 2020, 15, e0236834.	1.1	9
48	Generation of a p16 Reporter Mouse and Its Use to Characterize and Target p16high Cells In Vivo. Cell Metabolism, 2020, 32, 814-828.e6.	7.2	93
49	The relationship between cigarette smoking and the tongue microbiome in an East Asian population. Journal of Oral Microbiology, 2020, 12, 1742527.	1.2	18
50	Successful Clinical Sequencing by Molecular Tumor Board in an Elderly Patient With Refractory Sézary Syndrome. JCO Precision Oncology, 2020, 4, 534-560.	1.5	1
51	Prediction of blood test values under different lifestyle scenarios using time-series electronic health record. PLoS ONE, 2020, 15, e0230172.	1.1	5
52	Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. Genome Research, 2020, 30, 334-346.	2.4	56
53	Metagenomic analysis of bacterial species in tongue microbiome of current and never smokers. Npj Biofilms and Microbiomes, 2020, 6, 11.	2.9	32
54	Metagenome Data on Intestinal Phage-Bacteria Associations Aids the Development of Phage Therapy against Pathobionts. Cell Host and Microbe, 2020, 28, 380-389.e9.	5.1	51

#	Article	IF	Citations
55	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. EBioMedicine, 2020, 53, 102659.	2.7	48
56	Discrimination of prediction models between cold-heat and deficiency-excess patterns. Complementary Therapies in Medicine, 2020, 49, 102353.	1.3	8
57	Nanopore basecalling from a perspective of instance segmentation. BMC Bioinformatics, 2020, 21, 136.	1.2	17
58	Proton pump inhibitors enhance intestinal permeability via dysbiosis of gut microbiota under stressed conditions in mice. Neurogastroenterology and Motility, 2020, 32, e13841.	1.6	33
59	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	9.4	11
60	Global gene network exploration based on explainable artificial intelligence approach. PLoS ONE, 2020, 15, e0241508.	1.1	6
61	Variant analysis of prostate cancer in Japanese patients and a new attempt to predict related biological pathways. Oncology Reports, 2020, 43, 943-952.	1.2	3
62	Prediction Model for Deficiency-Excess Patterns, Including Medium Pattern. Kampo Medicine, 2020, 71, 315-325.	0.1	0
63	Title is missing!. , 2020, 15, e0236834.		0
64	Title is missing!. , 2020, 15, e0236834.		0
65	Title is missing!. , 2020, 15, e0236834.		0
66	Title is missing!. , 2020, 15, e0236834.		0
67	Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. European Urology Focus, 2019, 5, 416-424.	1.6	20
68	Prediction of deficiency-excess pattern in Japanese Kampo medicine: Multi-centre data collection. Complementary Therapies in Medicine, 2019, 45, 228-233.	1.3	8
69	Quantifying immune-based counterselection of somatic mutations. PLoS Genetics, 2019, 15, e1008227.	1.5	14
70	Blautia genus associated with visceral fat accumulation in adults 20â€"76 years of age. Npj Biofilms and Microbiomes, 2019, 5, 28.	2.9	244
71	Association between Nutrients and Visceral Fat in Healthy Japanese Adults: A 2-Year Longitudinal Study Brief Title: Micronutrients Associated with Visceral Fat Accumulation. Nutrients, 2019, 11, 2698.	1.7	17
72	An Unusually Short Latent Period of Therapy-Related Myeloid Neoplasm Harboring a Rare MLL-EP300 Rearrangement: Case Report and Literature Review. Case Reports in Hematology, 2019, 2019, 1-6.	0.3	3

#	Article	IF	Citations
73	Robust Sample-Specific Stability Selection with Effective Error Control. Journal of Computational Biology, 2019, 26, 202-217.	0.8	3
74	Capturing the differences between humoral immunity in the normal and tumor environments from repertoire-seq of B-cell receptors using supervised machine learning. BMC Bioinformatics, 2019, 20, 267.	1.2	23
75	Classification of patients with cold sensation by a review of systems database: A single-centre observational study. Complementary Therapies in Medicine, 2019, 45, 7-13.	1.3	3
76	Massively parallel sequencing of tenosynovial giant cell tumors reveals novel CSF1 fusion transcripts and novel somatic CBL mutations. International Journal of Cancer, 2019, 145, 3276-3284.	2.3	28
77	The first case of elderly <i>TCF3-HLF</i>-positive B-cell acute lymphoblastic leukemia. Leukemia and Lymphoma, 2019, 60, 2821-2824.	0.6	6
78	Development of an MSI-positive colon tumor with aberrant DNA methylation in a PPAP patient. Journal of Human Genetics, 2019, 64, 729-740.	1.1	7
79	A Bayesian model integration for mutation calling through data partitioning. Bioinformatics, 2019, 35, 4247-4254.	1.8	6
80	Prognostic impact of circulating tumor DNA status post–allogeneic hematopoietic stem cell transplantation in AML and MDS. Blood, 2019, 133, 2682-2695.	0.6	62
81	ALPHLARD-NT: Bayesian Method for Human Leukocyte Antigen Genotyping and Mutation Calling through Simultaneous Analysis of Normal and Tumor Whole-Genome Sequence Data. Journal of Computational Biology, 2019, 26, 923-937.	0.8	6
82	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. Nature Communications, 2019, 10, 5683.	5.8	41
83	Antigen delivery targeted to tumor-associated macrophages overcomes tumor immune resistance. Journal of Clinical Investigation, 2019, 129, 1278-1294.	3.9	102
84	Genomic Analysis of Therapy-Related Myeloid Neoplasms and Tracking of the Founder Clone By Circulating Tumor DNA. Blood, 2019, 134, 5393-5393.	0.6	0
85	A novel ASXL1–OGT axis plays roles in H3K4 methylation and tumor suppression in myeloid malignancies. Leukemia, 2018, 32, 1327-1337.	3.3	50
86	Azacitidine effectively reduces TP53-mutant leukemic cell burden in secondary acute myeloid leukemia after cord blood transplantation. Leukemia and Lymphoma, 2018, 59, 2755-2756.	0.6	0
87	Targeting Tyro3 ameliorates a model of PGRN-mutant FTLD-TDP via tau-mediated synaptic pathology. Nature Communications, 2018, 9, 433.	5.8	23
88	Different clonal dynamics of chronic myeloid leukaemia between bone marrow and the central nervous system. British Journal of Haematology, 2018, 183, 842-845.	1.2	0
89	Characterization of the B-cell receptor repertoires in peanut allergic subjects undergoing oral immunotherapy. Journal of Human Genetics, 2018, 63, 239-248.	1.1	24
90	Adaptive NetworkProfiler for Identifying Cancer Characteristic-Specific Gene Regulatory Networks. Journal of Computational Biology, 2018, 25, 130-145.	0.8	5

#	Article	IF	Citations
91	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
92	ALPHLARD: a Bayesian method for analyzing HLA genes from whole genome sequence data. BMC Genomics, 2018, 19, 790.	1.2	16
93	Cell-lineage level–targeted sequencing to identify acute myeloid leukemia with myelodysplasia-related changes. Blood Advances, 2018, 2, 2513-2521.	2.5	10
94	Effects of long-term intake of a yogurt fermented with <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> 2038 and <i>Streptococcus thermophilus</i> 1131 on mice. International Immunology, 2018, 30, 319-331.	1.8	42
95	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
96	Prognostic Impact of Circulating Tumor DNA Status Post-Allogeneic Hematopoietic Stem Cell Transplantation in Acute Myeloid Leukemia and Myelodysplastic Syndrome. Blood, 2018, 132, 247-247.	0.6	0
97	Artificial Intelligence Guided Precision Medicine Approach to Hematological Disease. Blood, 2018, 132, 2254-2254.	0.6	0
98	OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads. IEEE Transactions on Nanobioscience, 2017, 16, 116-122.	2.2	1
99	The Transcriptional Landscape of p53 Signalling Pathway. EBioMedicine, 2017, 20, 109-119.	2.7	47
100	Identification of an immunogenic neo-epitope encoded by mouse sarcoma using CXCR3 ligand mRNAs as sensors. OncoImmunology, 2017, 6, e1306617.	2.1	5
101	Identification of a p53 target, CD137L, that mediates growth suppression and immune response of osteosarcoma cells. Scientific Reports, 2017, 7, 10739.	1.6	3
102	Requirement of glycosylation machinery in TLR responses revealed by CRISPR/Cas9 screening. International Immunology, 2017, 29, 347-355.	1.8	9
103	Sequence-specific bias correction for RNA-seq data using recurrent neural networks. BMC Genomics, 2017, 18, 1044.	1.2	14
104	Interaction-Based Feature Selection for Uncovering Cancer Driver Genes Through Copy Number-Driven Expression Level. Journal of Computational Biology, 2017, 24, 138-152.	0.8	3
105	Reconstruction of high read-depth signals from low-depth whole genome sequencing data using deep learning. , 2017, , .		1
106	Genome-wide screening of DNA methylation associated with lymph node metastasis in esophageal squamous cell carcinoma. Oncotarget, 2017, 8, 37740-37750.	0.8	27
107	Identification of a p53-repressed gene module in breast cancer cells. Oncotarget, 2017, 8, 55821-55836.	0.8	6
108	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

#	Article	IF	Citations
109	Characterization of T-cell Receptor Repertoire in Inflamed Tissues of Patients with CrohnÊ¼s Disease Through Deep Sequencing. Inflammatory Bowel Diseases, 2016, 22, 1275-1285.	0.9	40
110	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
111	The hypusine cascade promotes cancer progression and metastasis through the regulation of RhoA in squamous cell carcinoma. Oncogene, 2016, 35, 5304-5316.	2.6	33
112	The hnRNP-Htt axis regulates necrotic cell death induced by transcriptional repression through impaired RNA splicing. Cell Death and Disease, 2016, 7, e2207-e2207.	2.7	12
113	Predicting Japanese Kampo formulas by analyzing database of medical records: a preliminary observational study. BMC Medical Informatics and Decision Making, 2016, 16, 118.	1.5	4
114	Characterization of the T cell repertoire by deep T cell receptor sequencing in tissues and blood from patients with advanced colorectal cancer. Oncology Letters, 2016, 11, 3643-3649.	0.8	39
115	Genomic Landscape of Esophageal Squamous Cell Carcinoma inÂa Japanese Population. Gastroenterology, 2016, 150, 1171-1182.	0.6	265
116	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
117	A likelihood-free filtering method via approximate Bayesian computation in evaluating biological simulation models. Computational Statistics and Data Analysis, 2016, 94, 63-74.	0.7	2
118	Oncogenic roles of TOPK and MELK, and effective growth suppression by small molecular inhibitors in kidney cancer cells. Oncotarget, 2016, 7, 17652-17664.	0.8	44
119	Exploratory Introduction of Cognitive Computing to Clinical Sequencing in Hematological Malignancies. Blood, 2016, 128, 5262-5262.	0.6	0
120	Elevated Î²-catenin pathway as a novel target for patients with resistance to EGF receptor targeting drugs. Scientific Reports, 2015, 5, 13076.	1.6	40
121	Attenuated familial adenomatous polyposis with desmoids caused by an APC mutation. Human Genome Variation, 2015, 2, 15011.	0.4	6
122	Recursive Random Lasso (RRLasso) for Identifying Anti-Cancer Drug Targets. PLoS ONE, 2015, 10, e0141869.	1.1	15
123	The miR-199a/Brm/EGR1 axis is a determinant of anchorage-independent growth in epithelial tumor cell lines. Scientific Reports, 2015, 5, 8428.	1.6	12
124	Sparse Overlapping Group Lasso for Integrative Multi-Omics Analysis. Journal of Computational Biology, 2015, 22, 73-84.	0.8	18
125	Comprehensive phosphoproteome analysis unravels the core signaling network that initiates the earliest synapse pathology in preclinical Alzheimer's disease brain. Human Molecular Genetics, 2015, 24, 540-558.	1.4	70
126	Detection of APC mosaicism by next-generation sequencing in an FAP patient. Journal of Human Genetics, 2015, 60, 227-231.	1.1	33

#	Article	IF	Citations
127	Probabilistic expression of spatially varied amino acid dimers into general form of Chou×³s pseudo amino acid composition for protein fold recognition. Journal of Theoretical Biology, 2015, 380, 291-298.	0.8	22
128	Quantitative characterization of T-cell repertoire in allogeneic hematopoietic stem cell transplant recipients. Bone Marrow Transplantation, 2015, 50, 1227-1234.	1.3	109
129	Genomic data assimilation using a higher moment filtering technique for restoration of gene regulatory networks. BMC Systems Biology, 2015, 9, 14.	3.0	2
130	Expression and clinical significance of genes frequently mutated in small cell lung cancers defined by whole exome/RNA sequencing. Carcinogenesis, 2015, 36, 616-621.	1.3	73
131	In utero gene therapy rescues microcephaly caused by Pqbp1-hypofunction in neural stem progenitor cells. Molecular Psychiatry, 2015, 20, 459-471.	4.1	31
132	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. Bioinformatics, 2015, 31, 116-118.	1.8	58
133	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
134	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor α and β chains using next-generation sequencing (NGS). OncoImmunology, 2014, 3, e968467.	2.1	68
135	Clinical Data Mining Related to the Japanese Kampo Concept â€œ<i>Hie</i>â€•(Oversensitivity to Coldness) in Men and Pre- and Postmenopausal Women. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-9.	0.5	14
136	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. Bioinformatics, 2014, 30, 3302-3309.	1.8	23
137	AFAP 1L1, a novel associating partner with vinculin, modulates cellular morphology and motility, and promotes the progression of colorectal cancers. Cancer Medicine, 2014, 3, 759-774.	1.3	13
138	Genetic algorithm for an optimized weighted voting scheme incorporating k-separated bigram transition probabilities to improve protein fold recognition. , 2014, , .		4
139	A feature selection method using fixed-point algorithm for DNA microarray gene expression data. International Journal of Knowledge-Based and Intelligent Engineering Systems, 2014, 18, 55-59.	0.7	5
140	Gene Networks: Estimation, Modeling, and Simulation. , 2014, , 89-112.		1
141	Systems biology analysis of Drosophila in vivo screen data elucidates core networks for DNA damage repair in SCA1. Human Molecular Genetics, 2014, 23, 1345-1364.	1.4	22
142	Kampo Traditional Pattern Diagnosis and the Clustering Analysis of Patients with Cold Sensation. Journal of Alternative and Complementary Medicine, 2014, 20, A47-A47.	2.1	1
143	An Efficient Data Assimilation Schema for Restoration and Extension of Gene Regulatory Networks Using Time-Course Observation Data. Journal of Computational Biology, 2014, 21, 785-798.	0.8	3
144	A feature selection method using improved regularized linear discriminant analysis. Machine Vision and Applications, 2014, 25, 775-786.	1.7	55

#	Article	IF	Citations
145	Lung adenocarcinoma subtypes definable by lung development-related miRNA expression profiles in association with clinicopathologic features. Carcinogenesis, 2014, 35, 2224-2231.	1.3	40
146	An efficient method of exploring simulation models by assimilating literature and biological observational data. BioSystems, 2014, 121, 54-66.	0.9	3
147	Overexpression of Cohesion Establishment Factor DSCC1 through E2F in Colorectal Cancer. PLoS ONE, 2014, 9, e85750.	1.1	21
148	Evaluation of Sequence Features from Intrinsically Disordered Regions for the Estimation of Protein Function. PLoS ONE, 2014, 9, e89890.	1.1	19
149	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
150	Robust Prediction of Anti-Cancer Drug Sensitivity and Sensitivity-Specific Biomarker. PLoS ONE, 2014, 9, e108990.	1.1	9
151	Principal component analysis using QR decomposition. International Journal of Machine Learning and Cybernetics, 2013, 4, 679-683.	2.3	66
152	Multi-omics Approach for Estimating Metabolic Networks Using Low-Order Partial Correlations. Journal of Computational Biology, 2013, 20, 571-582.	0.8	10
153	The rs6983267 SNP Is Associated with MYC Transcription Efficiency, Which Promotes Progression and Worsens Prognosis of Colorectal Cancer. Annals of Surgical Oncology, 2013, 20, 1395-1402.	0.7	46
154	A strategy to select suitable physicochemical attributes of amino acids for protein fold recognition. BMC Bioinformatics, 2013, 14, 233.	1.2	40
155	Vasohibin-1 is identified as a master-regulator of endothelial cell apoptosis using gene network analysis. BMC Genomics, 2013, 14, 23.	1.2	20
156	Extension and verification of the SEIR model on the 2009 influenza A (H1N1) pandemic in Japan. Mathematical Biosciences, 2013, 246, 47-54.	0.9	49
157	Plastin3 Is a Novel Marker for Circulating Tumor Cells Undergoing the Epithelial–Mesenchymal Transition and Is Associated with Colorectal Cancer Prognosis. Cancer Research, 2013, 73, 2059-2069.	0.4	220
158	Enhancement of Collective Immunity in Tokyo Metropolitan Area by Selective Vaccination against an Emerging Influenza Pandemic. PLoS ONE, 2013, 8, e72866.	1.1	8
159	Statistical Analysis of *Hie* (Cold Sensation) and *Hiesho* (Cold Disorder) in Kampo Clinic. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-8.	0.5	30
160	Prescription of Kampo Drugs in the Japanese Health Care Insurance Program. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-7.	0.5	38
161	Does Twitter Trigger Bursts in Signature Collections?. PLoS ONE, 2013, 8, e58252.	1.1	4
162	A BETWEEN-CLASS OVERLAPPING FILTER-BASED METHOD FOR TRANSCRIPTOME DATA ANALYSIS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1250010.	0.3	22

#	Article	IF	Citations
163	A Filter Based Feature Selection Algorithm Using Null Space of Covariance Matrix for DNA Microarray Gene Expression Data. Current Bioinformatics, 2012, 7, 289-294.	0.7	24
164	Gene network inference and visualization tools for biologists: application to new human transcriptome datasets. Nucleic Acids Research, 2012, 40, 2377-2398.	6.5	65
165	Identifying Gene Pathways Associated with Cancer Characteristics via Sparse Statistical Methods. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 966-972.	1.9	7
166	Analysis of questionnaire for traditional medical and develop decision support system. , 2012, , .		0
167	Null space based feature selection method for gene expression data. International Journal of Machine Learning and Cybernetics, 2012, 3, 269-276.	2.3	62
168	Increased Risk for CRC in Diabetic Patients with the Nonrisk Allele of SNPs at 8q24. Annals of Surgical Oncology, 2012, 19, 2853-2858.	0.7	13
169	A Top-r Feature Selection Algorithm for Microarray Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 754-764.	1.9	152
170	Cell Cycle Gene Networks Are Associated with Melanoma Prognosis. PLoS ONE, 2012, 7, e34247.	1.1	32
171	Forecasting Japan's Physician Shortage in 2035 as the First Full-Fledged Aged Society. PLoS ONE, 2012, 7, e50410.	1.1	28
172	Long Noncoding RNA *HOTAIR* Regulates Polycomb-Dependent Chromatin Modification and Is Associated with Poor Prognosis in Colorectal Cancers. Cancer Research, 2011, 71, 6320-6326.	0.4	1,191
173	A Novel Network Profiling Analysis Reveals System Changes in Epithelial-Mesenchymal Transition. PLoS ONE, 2011, 6, e20804.	1.1	38
174	Identification of AFAP1L1 as a prognostic marker for spindle cell sarcomas. Oncogene, 2011, 30, 4015-4025.	2.6	15
175	Clustering for Visual Analogue Scale Data in Symbolic Data Analysis. Procedia Computer Science, 2011, 6, 370-374.	1.2	5
176	Strategy of finding optimal number of features on gene expression data. Electronics Letters, 2011, 47, 480.	0.5	21
177	Computational Drug Target Pathway Discovery: A Bayesian Network Approach. , 2011, , 501-532.		0
178	Sign: large-scale gene network estimation environment for high performance computing. Genome Informatics, 2011, 25, 40-52.	0.4	9
179	COMPARISON OF GENE EXPRESSION PROFILES PRODUCED BY CAGE, ILLUMINA MICROARRAY AND REAL TIME RT-PCR. , 2010, , .		3
180	Network-Based Predictions and Simulations by Biological State Space Models: Search for Drug Mode of Action. Journal of Computer Science and Technology, 2010, 25, 131-153.	0.9	1

#	Article	IF	Citations
181	Gene Set-Based Module Discovery Decodes cis-Regulatory Codes Governing Diverse Gene Expression across Human Multiple Tissues. PLoS ONE, 2010, 5, e10910.	1.1	2
182	Discovering functional gene pathways associated with cancer heterogeneity via sparse supervised learning. , 2010, , .		0
183	Identifying Hidden Confounders in Gene Networks by Bayesian Networks. , 2010, , .		3
184	GENE REGULATORY NETWORK CLUSTERING FOR GRAPH LAYOUT BASED ON MICROARRAY GENE EXPRESSION DATA. , 2010, , .		0
185	Orengedokuto and berberine improve indomethacin-induced small intestinal injury via adenosine. Journal of Gastroenterology, 2009, 44, 380-389.	2.3	25
186	Analysis of PPARÎ±-dependent and PPARÎ±-independent transcript regulation following fenofibrate treatment of human endothelial cells. Angiogenesis, 2009, 12, 221-229.	3.7	32
187	Gene Networks Viewed through Two Models. Lecture Notes in Computer Science, 2009, , 54-66.	1.0	0
188	Nonlinear regression modeling via regularized radial basis function networks. Journal of Statistical Planning and Inference, 2008, 138, 3616-3633.	0.4	35
189	Partial Order-Based Bayesian Network Learning Algorithm for Estimating Gene Networks. , 2008, , .		3
190	Statistical inference of transcriptional module-based gene networks from time course gene expression profiles by using state space models. Bioinformatics, 2008, 24, 932-942.	1.8	87
191	Analyzing Time Course Gene Expression Data with Biological and Technical Replicates to Estimate Gene Networks by State Space Models. , 2008, , .		0
192	A NOVEL STRATEGY TO SEARCH CONSERVED TRANSCRIPTION FACTOR BINDING SITES AMONG COEXPRESSING GENES IN HUMAN. , 2008, , .		0
193	PREDICTING DIFFERENCES IN GENE REGULATORY SYSTEMS BY STATE SPACE MODELS. , 2008, , .		1
194	Predicting differences in gene regulatory systems by state space models. Genome Informatics, 2008, 21, 101-13.	0.4	7
195	Analysis of Gene Networks for Drug Target Discovery and Validation. , 2007, 360, 33-56.		8
196	Understanding endothelial cell apoptosis: what can the transcriptome, glycome and proteome reveal?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2007, 362, 1469-1487.	1.8	38
197	Statistical Absolute Evaluation of Gene Ontology Terms with Gene Expression Data. , 2007, , 146-157.		6
198	WEIGHTED LASSO IN GRAPHICAL GAUSSIAN MODELING FOR LARGE GENE NETWORK ESTIMATION BASED ON MICROARRAY DATA. , 2007, , .		14

#	Article	IF	Citations
199	A Structure Learning Algorithm for Inference of Gene Networks from Microarray Gene Expression Data Using Bayesian Networks. , 2007, , .		10
200	Finding module-based gene networks with state-space models - Mining high-dimensional and short time-course gene expression data. IEEE Signal Processing Magazine, 2007, 24, 37-46.	4.6	38
201	IDENTIFICATION OF ACTIVATED TRANSCRIPTION FACTORS FROM MICROARRAY GENE EXPRESSION DATA OF KAMPO MEDICINE-TREATED MICE. , 2007, , .		2
202	Identification of activated transcription factors from microarray gene expression data of Kampo medicine-treated mice. Genome Informatics, 2007, 18, 119-29.	0.4	4
203	Weighted lasso in graphical Gaussian modeling for large gene network estimation based on microarray data. Genome Informatics, 2007, 19, 142-53.	0.4	16
204	Error tolerant model for incorporating biological knowledge with expression data in estimating geneÂnetworks. Statistical Methodology, 2006, 3, 1-16.	0.5	20
205	STATISTICAL MODEL SELECTION METHOD TO ANALYZE COMBINATORIAL EFFECTS OF SNPS AND ENVIRONMENTAL FACTORS FOR BINARY DISEASE. International Journal on Artificial Intelligence Tools, 2006, 15, 711-724.	0.7	1
206	Gene Networks: Estimation, Modeling, and Simulation. , 2006, , 205-228.		1
207	Computational strategy for discovering druggable gene networks from genome-wide RNA expression profiles. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 559-71.	0.7	9
208	A statistical framework for genome-wide discovery of biomarker splice variations with GeneChip Human Exon 1.0 ST Arrays. Genome Informatics, 2006, 17, 88-99.	0.4	6
209	UTILIZING EVOLUTIONARY INFORMATION AND GENE EXPRESSION DATA FOR ESTIMATING GENE NETWORKS WITH BAYESIAN NETWORK MODELS. Journal of Bioinformatics and Computational Biology, 2005, 03, 1295-1313.	0.3	51
210	Estimating time-dependent gene networks from time series microarray data by dynamic linear models with Markov switching. , 2005, , 289-98.		21
211	Identifying drug active pathways from gene networks estimated by gene expression data. Genome Informatics, 2005, 16, 182-91.	0.4	7
212	Predicting gene regulation by sigma factors in Bacillus subtilis from genome-wide data. Bioinformatics, 2004, 20, i101-i108.	1.8	25
213	COMBINING MICROARRAYS AND BIOLOGICAL KNOWLEDGE FOR ESTIMATING GENE NETWORKS VIA BAYESIAN NETWORKS. Journal of Bioinformatics and Computational Biology, 2004, 02, 77-98.	0.3	96
214	Dynamic Bayesian network and nonparametric regression for nonlinear modeling of gene networks from time series gene expression data. BioSystems, 2004, 75, 57-65.	0.9	199
215	Kernel mixture survival models for identifying cancer subtypes, predicting patient's cancer types and survival probabilities. Genome Informatics, 2004, 15, 201-10.	0.4	2
216	Selection of smoothing parameters inB-spline nonparametric regression models using information criteria. Annals of the Institute of Statistical Mathematics, 2003, 55, 671-687.	0.5	33

#	Article	IF	Citations
217	Bayesian Network and Nonparametric Heteroscedastic Regression for Nonlinear Modeling of Genetic Network. Journal of Bioinformatics and Computational Biology, 2003, 01, 231-252.	0.3	104
218	Estimating gene networks from gene expression data by combining Bayesian network model with promoter element detection. Bioinformatics, 2003, 19, ii227-ii236.	1.8	146
219	Use of Gene Networks for Identifying and Validating Drug Targets. Journal of Bioinformatics and Computational Biology, 2003, 01, 459-474.	0.3	25
220	Inferring gene networks from time series microarray data using dynamic Bayesian networks. Briefings in Bioinformatics, 2003, 4, 228-235.	3.2	271
221	Use of Gene Networks from Full Genome Microarray Libraries to Identify Functionally Relevant Drug-affected Genes and Gene Regulation Cascades. DNA Research, 2003, 10, 19-25.	1.5	55
222	Combining microarrays and biological knowledge for estimating gene networks via Bayesian networks. Proceedings, 2003, 2, 104-13.	0.1	23
223	INFERRING GENE REGULATORY NETWORKS FROM TIME-ORDERED GENE EXPRESSION DATA OF BACILLUS SUBTILIS USING DIFFERENTIAL EQUATIONS. , 2002, , .		67
224	Estimation of genetic networks and functional structures between genes by using Bayesian networks and nonparametric regression. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2002, , 175-86.	0.7	48
225	Bayesian network and nonparametric heteroscedastic regression for nonlinear modeling of genetic network. Proceedings, 2002, 1, 219-27.	0.1	4
226	Estimating Nonlinear Regression Models based on Radial Basis Function Networks. Oyo Tokeigaku, 2001, 30, 19-35.	0.2	4
227	Estimation of B-spline Nonlinear Regression Models Using Information Criteria. Oyo Tokeigaku, 1999, 28, 137-150.	0.2	2
228	Bayesian network and nonparametric heteroscedastic regression for nonlinear modeling of genetic network. , 0, , .		16
229	Combining microarrays and biological knowledge for estimating gene networks via Bayesian networks. , 0, , .		36
230	Case-control study of binary disease trait considering interactions between SNPs and environmental effects using logistic regression. , 0, , .		5