# Seiya Imoto

List of Publications by Year
in descending order

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|---|---|---|---|
| 230 papers | 7,208 citations | 87888<br>38 h-index | 74163<br>75 g-index |
| 247 all docs | 247 docs citations | 247 times ranked | 11028 citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | Long Noncoding RNA *HOTAIR* Regulates Polycomb-Dependent Chromatin Modification and Is Associated with Poor Prognosis in Colorectal Cancers. Cancer Research, 2011, 71, 6320-6326. | 0.9 | 1,191 |
| 2 | Inferring gene networks from time series microarray data using dynamic Bayesian networks. Briefings in Bioinformatics, 2003, 4, 228-235. | 6.5 | 271 |
| 3 | Genomic Landscape of Esophageal Squamous Cell Carcinoma inÂa Japanese Population. Gastroenterology, 2016, 150, 1171-1182. | 1.3 | 265 |
| 4 | Blautia genus associated with visceral fat accumulation in adults 20â€"76 years of age. Npj Biofilms and Microbiomes, 2019, 5, 28. | 6.4 | 244 |
| 5 | Senolysis by glutaminolysis inhibition ameliorates various age-associated disorders. Science, 2021, 371, 265-270. | 12.6 | 222 |
| 6 | Plastin3 Is a Novel Marker for Circulating Tumor Cells Undergoing the Epithelialâ€"Mesenchymal Transition and Is Associated with Colorectal Cancer Prognosis. Cancer Research, 2013, 73, 2059-2069. | 0.9 | 220 |
| 7 | Dynamic Bayesian network and nonparametric regression for nonlinear modeling of gene networks from time series gene expression data. BioSystems, 2004, 75, 57-65. | 2.0 | 199 |
| 8 | A Top-r Feature Selection Algorithm for Microarray Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 754-764. | 3.0 | 152 |
| 9 | Estimating gene networks from gene expression data by combining Bayesian network model with promoter element detection. Bioinformatics, 2003, 19, ii227-ii236. | 4.1 | 146 |
| 10 | Quantitative characterization of T-cell repertoire in allogeneic hematopoietic stem cell transplant recipients. Bone Marrow Transplantation, 2015, 50, 1227-1234. | 2.4 | 109 |
| 11 | Bayesian Network and Nonparametric Heteroscedastic Regression for Nonlinear Modeling of Genetic Network. Journal of Bioinformatics and Computational Biology, 2003, 01, 231-252. | 0.8 | 104 |
| 12 | Antigen delivery targeted to tumor-associated macrophages overcomes tumor immune resistance. Journal of Clinical Investigation, 2019, 129, 1278-1294. | 8.2 | 102 |
| 13 | COMBINING MICROARRAYS AND BIOLOGICAL KNOWLEDGE FOR ESTIMATING GENE NETWORKS VIA BAYESIAN NETWORKS. Journal of Bioinformatics and Computational Biology, 2004, 02, 77-98. | 0.8 | 96 |
| 14 | Generation of a p16 Reporter Mouse and Its Use to Characterize and Target p16high Cells InÂVivo. Cell Metabolism, 2020, 32, 814-828.e6. | 16.2 | 93 |
| 15 | Statistical inference of transcriptional module-based gene networks from time course gene expression profiles by using state space models. Bioinformatics, 2008, 24, 932-942. | 4.1 | 87 |
| 16 | Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. Nature Medicine, 2021, 27, 1239-1249. | 30.7 | 78 |
| 17 | Expression and clinical significance of genes frequently mutated in small cell lung cancers defined by whole exome/RNA sequencing. Carcinogenesis, 2015, 36, 616-621. | 2.8 | 73 |
| 18 | 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. | 2.9 | 70 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor Î± and Î² chains using next-generation sequencing (NGS). OncoImmunology, 2014, 3, e968467. | 4.6 | 68 |
| 20 | INFERRING GENE REGULATORY NETWORKS FROM TIME-ORDERED GENE EXPRESSION DATA OF BACILLUS SUBTILIS USING DIFFERENTIAL EQUATIONS. , 2002, , . | | 67 |
| 21 | Principal component analysis using QR decomposition. International Journal of Machine Learning and Cybernetics, 2013, 4, 679-683. | 3.6 | 66 |
| 22 | Gene network inference and visualization tools for biologists: application to new human transcriptome datasets. Nucleic Acids Research, 2012, 40, 2377-2398. | 14.5 | 65 |
| 23 | Null space based feature selection method for gene expression data. International Journal of Machine Learning and Cybernetics, 2012, 3, 269-276. | 3.6 | 62 |
| 24 | Prognostic impact of circulating tumor DNA status postâ€"allogeneic hematopoietic stem cell transplantation in AML and MDS. Blood, 2019, 133, 2682-2695. | 1.4 | 62 |
| 25 | Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. Bioinformatics, 2015, 31, 116-118. | 4.1 | 58 |
| 26 | Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. Genome Research, 2020, 30, 334-346. | 5.5 | 56 |
| 27 | 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. | 3.4 | 55 |
| 28 | A feature selection method using improved regularized linear discriminant analysis. Machine Vision and Applications, 2014, 25, 775-786. | 2.7 | 55 |
| 29 | 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. | 0.8 | 51 |
| 30 | Metagenome Data on Intestinal Phage-Bacteria Associations Aids the Development of Phage Therapy against Pathobionts. Cell Host and Microbe, 2020, 28, 380-389.e9. | 11.0 | 51 |
| 31 | A novel ASXL1â€"OGT axis plays roles in H3K4 methylation and tumor suppression in myeloid malignancies. Leukemia, 2018, 32, 1327-1337. | 7.2 | 50 |
| 32 | Extension and verification of the SEIR model on the 2009 influenza A (H1N1) pandemic in Japan. Mathematical Biosciences, 2013, 246, 47-54. | 1.9 | 49 |
| 33 | Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. EBioMedicine, 2020, 53, 102659. | 6.1 | 48 |
| 34 | 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 |
| 35 | The Transcriptional Landscape of p53 Signalling Pathway. EBioMedicine, 2017, 20, 109-119. | 6.1 | 47 |
| 36 | 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. | 1.5 | 46 |

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|---|---------|-----|-----------|
| 37 | Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. Gastroenterology, 2021, 160, 2089-2102.e12. | 1.3 | 45 |
| 38 | Oncogenic roles of TOPK and MELK, and effective growth suppression by small molecular inhibitors in kidney cancer cells. Oncotarget, 2016, 7, 17652-17664. | 1.8 | 44 |
| 39 | Effects of long-term intake of a yogurt fermented with *Lactobacillus delbrueckii* subsp. *bulgaricus* 2038 and *Streptococcus thermophilus* 1131 on mice. International Immunology, 2018, 30, 319-331. | 4.0 | 42 |
| 40 | Integrated exome and RNA sequencing of dedifferentiated liposarcoma. Nature Communications, 2019, 10, 5683. | 12.8 | 41 |
| 41 | A strategy to select suitable physicochemical attributes of amino acids for protein fold recognition. BMC Bioinformatics, 2013, 14, 233. | 2.6 | 40 |
| 42 | Lung adenocarcinoma subtypes definable by lung development-related miRNA expression profiles in association with clinicopathologic features. Carcinogenesis, 2014, 35, 2224-2231. | 2.8 | 40 |
| 43 | Elevated β-catenin pathway as a novel target for patients with resistance to EGF receptor targeting drugs. Scientific Reports, 2015, 5, 13076. | 3.3 | 40 |
| 44 | Characterization of T-cell Receptor Repertoire in Inflamed Tissues of Patients with CrohnÊ¼s Disease Through Deep Sequencing. Inflammatory Bowel Diseases, 2016, 22, 1275-1285. | 1.9 | 40 |
| 45 | Genome-wide association studies and heritability analysis reveal the involvement of host genetics in the Japanese gut microbiota. Communications Biology, 2020, 3, 686. | 4.4 | 40 |
| 46 | 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. | 1.8 | 39 |
| 47 | 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. | 4.0 | 38 |
| 48 | 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. | 5.6 | 38 |
| 49 | A Novel Network Profiling Analysis Reveals System Changes in Epithelial-Mesenchymal Transition. PLoS ONE, 2011, 6, e20804. | 2.5 | 38 |
| 50 | Prescription of Kampo Drugs in the Japanese Health Care Insurance Program. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-7. | 1.2 | 38 |
| 51 | Combining microarrays and biological knowledge for estimating gene networks via Bayesian networks. , 0, , . | | 36 |
| 52 | Nonlinear regression modeling via regularized radial basis function networks. Journal of Statistical Planning and Inference, 2008, 138, 3616-3633. | 0.6 | 35 |
| 53 | Selection of smoothing parameters inB-spline nonparametric regression models using information criteria. Annals of the Institute of Statistical Mathematics, 2003, 55, 671-687. | 0.8 | 33 |
| 54 | Detection of APC mosaicism by next-generation sequencing in an FAP patient. Journal of Human Genetics, 2015, 60, 227-231. | 2.3 | 33 |

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|---|---------|-----|-----------|
| 55 | The hypusine cascade promotes cancer progression and metastasis through the regulation of RhoA in squamous cell carcinoma. Oncogene, 2016, 35, 5304-5316. | 5.9 | 33 |
| 56 | Proton pump inhibitors enhance intestinal permeability via dysbiosis of gut microbiota under stressed conditions in mice. Neurogastroenterology and Motility, 2020, 32, e13841. | 3.0 | 33 |
| 57 | Analysis of PPARÎ±-dependent and PPARÎ±-independent transcript regulation following fenofibrate treatment of human endothelial cells. Angiogenesis, 2009, 12, 221-229. | 7.2 | 32 |
| 58 | Cell Cycle Gene Networks Are Associated with Melanoma Prognosis. PLoS ONE, 2012, 7, e34247. | 2.5 | 32 |
| 59 | Metagenomic analysis of bacterial species in tongue microbiome of current and never smokers. Npj Biofilms and Microbiomes, 2020, 6, 11. | 6.4 | 32 |
| 60 | In utero gene therapy rescues microcephaly caused by Pqbp1-hypofunction in neural stem progenitor cells. Molecular Psychiatry, 2015, 20, 459-471. | 7.9 | 31 |
| 61 | Statistical Analysis of *Hie* (Cold Sensation) and *Hiesho* (Cold Disorder) in Kampo Clinic. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-8. | 1.2 | 30 |
| 62 | Metagenomic profiling of gut microbiome in early chronic kidney disease. Nephrology Dialysis Transplantation, 2021, 36, 1675-1684. | 0.7 | 29 |
| 63 | Forecasting Japan's Physician Shortage in 2035 as the First Full-Fledged Aged Society. PLoS ONE, 2012, 7, e50410. | 2.5 | 28 |
| 64 | 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. | 5.1 | 28 |
| 65 | Genome-wide screening of DNA methylation associated with lymph node metastasis in esophageal squamous cell carcinoma. Oncotarget, 2017, 8, 37740-37750. | 1.8 | 27 |
| 66 | Oral MucoRice-CTB vaccine for safety and microbiota-dependent immunogenicity in humans: a phase 1 randomised trial. Lancet Microbe, The, 2021, 2, e429-e440. | 7.3 | 27 |
| 67 | Use of Gene Networks for Identifying and Validating Drug Targets. Journal of Bioinformatics and Computational Biology, 2003, 01, 459-474. | 0.8 | 25 |
| 68 | Predicting gene regulation by sigma factors in Bacillus subtilis from genome-wide data. Bioinformatics, 2004, 20, i101-i108. | 4.1 | 25 |
| 69 | Orengedokuto and berberine improve indomethacin-induced small intestinal injury via adenosine. Journal of Gastroenterology, 2009, 44, 380-389. | 5.1 | 25 |
| 70 | A Filter Based Feature Selection Algorithm Using Null Space of Covariance Matrix for DNA Microarray Gene Expression Data. Current Bioinformatics, 2012, 7, 289-294. | 1.5 | 24 |
| 71 | Characterization of the B-cell receptor repertoires in peanut allergic subjects undergoing oral immunotherapy. Journal of Human Genetics, 2018, 63, 239-248. | 2.3 | 24 |
| 72 | Dysbiotic Fecal Microbiome in HIV-1 Infected Individuals in Ghana. Frontiers in Cellular and Infection Microbiology, 2021, 11, 646467. | 3.9 | 24 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 73 | 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. | 3.3 | 24 |
| 74 | HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. Bioinformatics, 2014, 30, 3302-3309. | 4.1 | 23 |
| 75 | Targeting Tyro3 ameliorates a model of PGRN-mutant FTLD-TDP via tau-mediated synaptic pathology. Nature Communications, 2018, 9, 433. | 12.8 | 23 |
| 76 | 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. | 2.6 | 23 |
| 77 | Combining microarrays and biological knowledge for estimating gene networks via Bayesian networks. Proceedings, 2003, 2, 104-13. | 0.1 | 23 |
| 78 | A BETWEEN-CLASS OVERLAPPING FILTER-BASED METHOD FOR TRANSCRIPTOME DATA ANALYSIS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1250010. | 0.8 | 22 |
| 79 | 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. | 2.9 | 22 |
| 80 | 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. | 1.7 | 22 |
| 81 | Estimating time-dependent gene networks from time series microarray data by dynamic linear models with Markov switching. , 2005, , 289-98. | | 21 |
| 82 | Strategy of finding optimal number of features on gene expression data. Electronics Letters, 2011, 47, 480. | 1.0 | 21 |
| 83 | Overexpression of Cohesion Establishment Factor DSCC1 through E2F in Colorectal Cancer. PLoS ONE, 2014, 9, e85750. | 2.5 | 21 |
| 84 | Error tolerant model for incorporating biological knowledge with expression data in estimating geneÂnetworks. Statistical Methodology, 2006, 3, 1-16. | 0.5 | 20 |
| 85 | Vasohibin-1 is identified as a master-regulator of endothelial cell apoptosis using gene network analysis. BMC Genomics, 2013, 14, 23. | 2.8 | 20 |
| 86 | Genomic Heterogeneity Within Individual Prostate Cancer Foci Impacts Predictive Biomarkers of Targeted Therapy. European Urology Focus, 2019, 5, 416-424. | 3.1 | 20 |
| 87 | COVID-19 risk assessment at the opening ceremony of the Tokyo 2020 Olympic Games. Microbial Risk Analysis, 2021, 19, 100162. | 2.3 | 20 |
| 88 | Evaluation of Sequence Features from Intrinsically Disordered Regions for the Estimation of Protein Function. PLoS ONE, 2014, 9, e89890. | 2.5 | 19 |
| 89 | Sparse Overlapping Group Lasso for Integrative Multi-Omics Analysis. Journal of Computational Biology, 2015, 22, 73-84. | 1.6 | 18 |
| 90 | The relationship between cigarette smoking and the tongue microbiome in an East Asian population. Journal of Oral Microbiology, 2020, 12, 1742527. | 2.7 | 18 |

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|---|---------|----|-----------| 
| 91 | HEAL: an automated deep learning framework for cancer histopathology image analysis. Bioinformatics, 2021, 37, 4291-4295. | 4.1 | 18 |
| 92 | The Difference between the Two Representative Kampo Formulas for Treating Dysmenorrhea: An Observational Study. Evidence-based Complementary and Alternative Medicine, 2016, 2016, 1-10. | 1.2 | 17 |
| 93 | 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. | 3.3 | 17 |
| 94 | Circulating tumor DNA dynamically predicts response and/or relapse in patients with hematological malignances. International Journal of Hematology, 2018, 108, 402-410. | 1.6 | 17 |
| 95 | 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. | 4.1 | 17 |
| 96 | Nanopore basecalling from a perspective of instance segmentation. BMC Bioinformatics, 2020, 21, 136. | 2.6 | 17 |
| 97 | Halcyon: an accurate basecaller exploiting an encoderâ€"decoder model with monotonic attention. Bioinformatics, 2021, 37, 1211-1217. | 4.1 | 17 |
| 98 | Bayesian network and nonparametric heteroscedastic regression for nonlinear modeling of genetic network. , 0, , . | | 16 |
| 99 | ALPHLARD: a Bayesian method for analyzing HLA genes from whole genome sequence data. BMC Genomics, 2018, 19, 790. | 2.8 | 16 |
| 100 | Weighted lasso in graphical Gaussian modeling for large gene network estimation based on microarray data. Genome Informatics, 2007, 19, 142-53. | 0.4 | 16 |
| 101 | Two Blautia Species Associated with Visceral Fat Accumulation: A One-Year Longitudinal Study. Biology, 2022, 11, 318. | 2.8 | 16 |
| 102 | Identification of AFAP1L1 as a prognostic marker for spindle cell sarcomas. Oncogene, 2011, 30, 4015-4025. | 5.9 | 15 |
| 103 | Recursive Random Lasso (RRLasso) for Identifying Anti-Cancer Drug Targets. PLoS ONE, 2015, 10, e0141869. | 2.5 | 15 |
| 104 | Inference of Gene Regulatory Networks Incorporating Multi-Source Biological Knowledge via a State Space Model with L1 Regularization. PLoS ONE, 2014, 9, e105942. | 2.5 | 15 |
| 105 | COVID-19 wastewater surveillance implemented in the Tokyo 2020 Olympic and Paralympic Village. Journal of Travel Medicine, 2022, 29, . | 3.0 | 15 |
| 106 | WEIGHTED LASSO IN GRAPHICAL GAUSSIAN MODELING FOR LARGE GENE NETWORK ESTIMATION BASED ON MICROARRAY DATA. , 2007, , . | | 14 |
| 107 | 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. | 1.2 | 14 |
| 108 | Sequence-specific bias correction for RNA-seq data using recurrent neural networks. BMC Genomics, 2017, 18, 1044. | 2.8 | 14 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 109 | Quantifying immune-based counterselection of somatic mutations. PLoS Genetics, 2019, 15, e1008227. | 3.5 | 14 |
| 110 | Increased Risk for CRC in Diabetic Patients with the Nonrisk Allele of SNPs at 8q24. Annals of Surgical Oncology, 2012, 19, 2853-2858. | 1.5 | 13 |
| 111 | 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. | 2.8 | 13 |
| 112 | Living with COVID-19: mass gatherings and minimizing risk. QJM - Monthly Journal of the Association of Physicians, 2021, 114, 437-439. | 0.5 | 13 |
| 113 | Trop-2 in Upper Tract Urothelial Carcinoma. Current Oncology, 2022, 29, 3911-3921. | 2.2 | 13 |
| 114 | Analysis of Questionnaire for Traditional Medicine and Development of Decision Support System. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-8. | 1.2 | 12 |
| 115 | The miR-199a/Brm/EGR1 axis is a determinant of anchorage-independent growth in epithelial tumor cell lines. Scientific Reports, 2015, 5, 8428. | 3.3 | 12 |
| 116 | The hnRNP-Htt axis regulates necrotic cell death induced by transcriptional repression through impaired RNA splicing. Cell Death and Disease, 2016, 7, e2207-e2207. | 6.3 | 12 |
| 117 | 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. | 2.3 | 12 |
| 118 | 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. | 1.5 | 11 |
| 119 | Role of Circulating Tumor DNA in Hematological Malignancy. Cancers, 2021, 13, 2078. | 3.7 | 11 |
| 120 | Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292. | 17.5 | 11 |
| 121 | Perioperative circulating tumor DNA enables the identification of patients with poor prognosis in upper tract urothelial carcinoma. Cancer Science, 2022, 113, 1830-1842. | 3.9 | 11 |
| 122 | A Structure Learning Algorithm for Inference of Gene Networks from Microarray Gene Expression Data Using Bayesian Networks. , 2007, , . | | 10 |
| 123 | Multi-omics Approach for Estimating Metabolic Networks Using Low-Order Partial Correlations. Journal of Computational Biology, 2013, 20, 571-582. | 1.6 | 10 |
| 124 | Phenotype-based gene analysis allowed successful diagnosis of X-linked neutropenia associated with a novel WASp mutation. Annals of Hematology, 2018, 97, 367-369. | 1.8 | 10 |
| 125 | Cell-lineage level–targeted sequencing to identify acute myeloid leukemia with myelodysplasia-related changes. Blood Advances, 2018, 2, 2513-2521. | 5.2 | 10 |
| 126 | Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. Scientific Reports, 2021, 11, 15713. | 3.3 | 10 |

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|---|---------|-----|-----------|
| 127 | Assessment of COVID-19 risk and prevention effectiveness among spectators of mass gathering events. Microbial Risk Analysis, 2022, 21, 100215. | 2.3 | 10 |
| 128 | Bronchoalveolar lavage fluid reveals factors contributing to the efficacy of PD-1 blockade in lung cancer. JCI Insight, 2022, 7, . | 5.0 | 10 |
| 129 | Requirement of glycosylation machinery in TLR responses revealed by CRISPR/Cas9 screening. International Immunology, 2017, 29, 347-355. | 4.0 | 9 |
| 130 | Association of single nucleotide polymorphisms in the NRF2 promoter with vascular stiffness with aging. PLoS ONE, 2020, 15, e0236834. | 2.5 | 9 |
| 131 | Fecal Microbiome Composition in Healthy Adults in Ghana. Japanese Journal of Infectious Diseases, 2021, 74, 42-47. | 1.2 | 9 |
| 132 | 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. | 2.2 | 9 |
| 133 | Robust Prediction of Anti-Cancer Drug Sensitivity and Sensitivity-Specific Biomarker. PLoS ONE, 2014, 9, e108990. | 2.5 | 9 |
| 134 | Possible Role of Cytochrome P450 1B1 in the Mechanism of Gemcitabine Resistance in Pancreatic Cancer. Biomedicines, 2021, 9, 1396. | 3.2 | 9 |
| 135 | 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 |
| 136 | Sign: large-scale gene network estimation environment for high performance computing. Genome Informatics, 2011, 25, 40-52. | 0.4 | 9 |
| 137 | Analysis of Gene Networks for Drug Target Discovery and Validation. , 2007, 360, 33-56. | | 8 |
| 138 | Enhancement of Collective Immunity in Tokyo Metropolitan Area by Selective Vaccination against an Emerging Influenza Pandemic. PLoS ONE, 2013, 8, e72866. | 2.5 | 8 |
| 139 | Prediction of deficiency-excess pattern in Japanese Kampo medicine: Multi-centre data collection. Complementary Therapies in Medicine, 2019, 45, 228-233. | 2.7 | 8 |
| 140 | Neoantimon: a multifunctional R package for identification of tumor-specific neoantigens. Bioinformatics, 2020, 36, 4813-4816. | 4.1 | 8 |
| 141 | Discrimination of prediction models between cold-heat and deficiency-excess patterns. Complementary Therapies in Medicine, 2020, 49, 102353. | 2.7 | 8 |
| 142 | Identifying Gene Pathways Associated with Cancer Characteristics via Sparse Statistical Methods. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 966-972. | 3.0 | 7 |
| 143 | Development of an MSI-positive colon tumor with aberrant DNA methylation in a PPAP patient. Journal of Human Genetics, 2019, 64, 729-740. | 2.3 | 7 |
| 144 | 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. | 2.8 | 7 |

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|---|---------|----|-----------| 
| 145 | Identifying drug active pathways from gene networks estimated by gene expression data. Genome Informatics, 2005, 16, 182-91. | 0.4 | 7 |
| 146 | Predicting differences in gene regulatory systems by state space models. Genome Informatics, 2008, 21, 101-13. | 0.4 | 7 |
| 147 | COVID-19 testing systems and their effectiveness in small, semi-isolated groups for sports events. PLoS ONE, 2022, 17, e0266197. | 2.5 | 7 |
| 148 | Statistical Absolute Evaluation of Gene Ontology Terms with Gene Expression Data. , 2007, , 146-157. | | 6 |
| 149 | Attenuated familial adenomatous polyposis with desmoids caused by an APC mutation. Human Genome Variation, 2015, 2, 15011. | 0.7 | 6 |
| 150 | The first case of elderly *TCF3-HLF*-positive B-cell acute lymphoblastic leukemia. Leukemia and Lymphoma, 2019, 60, 2821-2824. | 1.3 | 6 |
| 151 | A Bayesian model integration for mutation calling through data partitioning. Bioinformatics, 2019, 35, 4247-4254. | 4.1 | 6 |
| 152 | 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. | 1.6 | 6 |
| 153 | Global gene network exploration based on explainable artificial intelligence approach. PLoS ONE, 2020, 15, e0241508. | 2.5 | 6 |
| 154 | Identification of a p53-repressed gene module in breast cancer cells. Oncotarget, 2017, 8, 55821-55836. | 1.8 | 6 |
| 155 | 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 |
| 156 | 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. | 1.0 | 6 |
| 157 | Case-control study of binary disease trait considering interactions between SNPs and environmental effects using logistic regression. , 0, , . | | 5 |
| 158 | Clustering for Visual Analogue Scale Data in Symbolic Data Analysis. Procedia Computer Science, 2011, 6, 370-374. | 2.0 | 5 |
| 159 | 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. | 1.0 | 5 |
| 160 | Identification of an immunogenic neo-epitope encoded by mouse sarcoma using CXCR3 ligand mRNAs as sensors. OncoImmunology, 2017, 6, e1306617. | 4.6 | 5 |
| 161 | Adaptive NetworkProfiler for Identifying Cancer Characteristic-Specific Gene Regulatory Networks. Journal of Computational Biology, 2018, 25, 130-145. | 1.6 | 5 |
| 162 | Prediction of blood test values under different lifestyle scenarios using time-series electronic health record. PLoS ONE, 2020, 15, e0230172. | 2.5 | 5 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 163 | Genetic algorithm for an optimized weighted voting scheme incorporating k-separated bigram transition probabilities to improve protein fold recognition. , 2014, , . | | 4 |
| 164 | Predicting Japanese Kampo formulas by analyzing database of medical records: a preliminary observational study. BMC Medical Informatics and Decision Making, 2016, 16, 118. | 3.0 | 4 |
| 165 | Does Twitter Trigger Bursts in Signature Collections?. PLoS ONE, 2013, 8, e58252. | 2.5 | 4 |
| 166 | Estimating Nonlinear Regression Models based on Radial Basis Function Networks. Oyo Tokeigaku, 2001, 30, 19-35. | 0.1 | 4 |
| 167 | Bayesian network and nonparametric heteroscedastic regression for nonlinear modeling of genetic network. Proceedings, 2002, 1, 219-27. | 0.1 | 4 |
| 168 | Identification of activated transcription factors from microarray gene expression data of Kampo medicine-treated mice. Genome Informatics, 2007, 18, 119-29. | 0.4 | 4 |
| 169 | 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. | 2.3 | 4 |
| 170 | Ovariectomy-Induced Dysbiosis May Have a Minor Effect on Bone in Mice. Microorganisms, 2021, 9, 2563. | 3.6 | 4 |
| 171 | Partial Order-Based Bayesian Network Learning Algorithm for Estimating Gene Networks. , 2008, , . | | 3 |
| 172 | COMPARISON OF GENE EXPRESSION PROFILES PRODUCED BY CAGE, ILLUMINA MICROARRAY AND REAL TIME RT-PCR. , 2010, , . | | 3 |
| 173 | Identifying Hidden Confounders in Gene Networks by Bayesian Networks. , 2010, , . | | 3 |
| 174 | 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. | 1.6 | 3 |
| 175 | An efficient method of exploring simulation models by assimilating literature and biological observational data. BioSystems, 2014, 121, 54-66. | 2.0 | 3 |
| 176 | Identification of a p53 target, CD137L, that mediates growth suppression and immune response of osteosarcoma cells. Scientific Reports, 2017, 7, 10739. | 3.3 | 3 |
| 177 | Interaction-Based Feature Selection for Uncovering Cancer Driver Genes Through Copy Number-Driven Expression Level. Journal of Computational Biology, 2017, 24, 138-152. | 1.6 | 3 |
| 178 | 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. | 0.4 | 3 |
| 179 | Robust Sample-Specific Stability Selection with Effective Error Control. Journal of Computational Biology, 2019, 26, 202-217. | 1.6 | 3 |
| 180 | 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. | 2.7 | 3 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 181 | Data science and precision health care. Nutrition Reviews, 2020, 78, 53-57. | 5.8 | 3 |
| 182 | Variant analysis of prostate cancer in Japanese patients and a new attempt to predict related biological pathways. Oncology Reports, 2020, 43, 943-952. | 2.6 | 3 |
| 183 | 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. | 3.3 | 3 |
| 184 | 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. | 3.3 | 3 |
| 185 | Gene Set-Based Module Discovery Decodes cis-Regulatory Codes Governing Diverse Gene Expression across Human Multiple Tissues. PLoS ONE, 2010, 5, e10910. | 2.5 | 2 |
| 186 | Genomic data assimilation using a higher moment filtering technique for restoration of gene regulatory networks. BMC Systems Biology, 2015, 9, 14. | 3.0 | 2 |
| 187 | A likelihood-free filtering method via approximate Bayesian computation in evaluating biological simulation models. Computational Statistics and Data Analysis, 2016, 94, 63-74. | 1.2 | 2 |
| 188 | Estimation of B-spline Nonlinear Regression Models Using Information Criteria. Oyo Tokeigaku, 1999, 28, 137-150. | 0.1 | 2 |
| 189 | The effect of age on the association between daily gait speed and abdominal obesity in Japanese adults. Scientific Reports, 2021, 11, 19975. | 3.3 | 2 |
| 190 | IDENTIFICATION OF ACTIVATED TRANSCRIPTION FACTORS FROM MICROARRAY GENE EXPRESSION DATA OF KAMPO MEDICINE-TREATED MICE. , 2007, , . | | 2 |
| 191 | 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 |
| 192 | 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. | 2.8 | 2 |
| 193 | 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. | 1.0 | 1 |
| 194 | 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. | 1.5 | 1 |
| 195 | Gene Networks: Estimation, Modeling, and Simulation. , 2014, , 89-112. | | 1 |
| 196 | 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 |
| 197 | OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads. IEEE Transactions on Nanobioscience, 2017, 16, 116-122. | 3.3 | 1 |
| 198 | Reconstruction of high read-depth signals from low-depth whole genome sequencing data using deep learning. , 2017, , . | | 1 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 199 | Successful Clinical Sequencing by Molecular Tumor Board in an Elderly Patient With Refractory Sézary Syndrome. JCO Precision Oncology, 2020, 4, 534-560. | 3.0 | 1 |
| 200 | Gene Networks: Estimation, Modeling, and Simulation. , 2006, , 205-228. | | 1 |
| 201 | PREDICTING DIFFERENCES IN GENE REGULATORY SYSTEMS BY STATE SPACE MODELS. , 2008, , . | | 1 |
| 202 | Uncovering Molecular Mechanisms of Drug Resistance via Network-Constrained Common Structure Identification. Journal of Computational Biology, 2022, , . | 1.6 | 1 |
| 203 | Role of the Orphan Transporter SLC35E1 in the Nuclear Egress of Herpes Simplex Virus 1. Journal of Virology, 2022, , e0030622. | 3.4 | 1 |
| 204 | Xprediction: Explainable EGFR-TKIs response prediction based on drug sensitivity specific gene networks. PLoS ONE, 2022, 17, e0261630. | 2.5 | 1 |
| 205 | Genome-wide causal mediation analysis identifies genetic loci associated with uterine fibroids mediated by age at menarche. Human Reproduction, 2022, 37, 2197-2212. | 0.9 | 1 |
| 206 | Analyzing Time Course Gene Expression Data with Biological and Technical Replicates to Estimate Gene Networks by State Space Models. , 2008, , . | | 0 |
| 207 | Discovering functional gene pathways associated with cancer heterogeneity via sparse supervised learning. , 2010, , . | | 0 |
| 208 | Analysis of questionnaire for traditional medical and develop decision support system. , 2012, , . | | 0 |
| 209 | Azacitidine effectively reduces TP53-mutant leukemic cell burden in secondary acute myeloid leukemia after cord blood transplantation. Leukemia and Lymphoma, 2018, 59, 2755-2756. | 1.3 | 0 |
| 210 | Different clonal dynamics of chronic myeloid leukaemia between bone marrow and the central nervous system. British Journal of Haematology, 2018, 183, 842-845. | 2.5 | 0 |
| 211 | Ensemble smoothers for inference of hidden states and parameters in combinatorial regulatory model. Journal of the Franklin Institute, 2020, 357, 2916-2933. | 3.4 | 0 |
| 212 | Application of state-space model with skew-t measurement noise to blood test value prediction. Applied Mathematical Modelling, 2021, 100, 365-378. | 4.2 | 0 |
| 213 | Enhancing breakpoint resolution with deep segmentation model: A general refinement method for read-depth based structural variant callers. PLoS Computational Biology, 2021, 17, e1009186. | 3.2 | 0 |
| 214 | A NOVEL STRATEGY TO SEARCH CONSERVED TRANSCRIPTION FACTOR BINDING SITES AMONG COEXPRESSING GENES IN HUMAN. , 2008, , . | | 0 |
| 215 | Gene Networks Viewed through Two Models. Lecture Notes in Computer Science, 2009, , 54-66. | 1.3 | 0 |
| 216 | GENE REGULATORY NETWORK CLUSTERING FOR GRAPH LAYOUT BASED ON MICROARRAY GENE EXPRESSION DATA. , 2010, , . | | 0 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 217 | Computational Drug Target Pathway Discovery: A Bayesian Network Approach. , 2011, , 501-532. | | 0 |
| 218 | Exploratory Introduction of Cognitive Computing to Clinical Sequencing in Hematological Malignancies. Blood, 2016, 128, 5262-5262. | 1.4 | 0 |
| 219 | 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. | 1.4 | 0 |
| 220 | Artificial Intelligence Guided Precision Medicine Approach to Hematological Disease. Blood, 2018, 132, 2254-2254. | 1.4 | 0 |
| 221 | Genomic Analysis of Therapy-Related Myeloid Neoplasms and Tracking of the Founder Clone By Circulating Tumor DNA. Blood, 2019, 134, 5393-5393. | 1.4 | 0 |
| 222 | Automatic sparse principal component analysis. Canadian Journal of Statistics, 2021, 49, 678-697. | 0.9 | 0 |
| 223 | 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 |
| 224 | Discovering microbe functionality in human disease with a gene-ontology-aware model. , 2021, , . | | 0 |
| 225 | Prediction Model for Deficiency-Excess Patterns, Including Medium Pattern. Kampo Medicine, 2020, 71, 315-325. | 0.1 | 0 |
| 226 | Title is missing!. , 2020, 15, e0236834. | | 0 |
| 227 | Title is missing!. , 2020, 15, e0236834. | | 0 |
| 228 | Title is missing!. , 2020, 15, e0236834. | | 0 |
| 229 | Title is missing!. , 2020, 15, e0236834. | | 0 |
| 230 | 3081 â€" SINGLE-CELL RNA-SEQ REVEALS ALTERATIONS IN HETEROGENEITY OF HEMATOPOIETIC STEM CELLS WITH AGING. Experimental Hematology, 2021, 100, S81. | 0.4 | 0 |