

Seiya Imoto

List of Publications by Year in descending order

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Version: 2024-02-01

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	Long Noncoding RNA <i>HOTAIR</i> Regulates Polycomb-Dependent Chromatin Modification and Is Associated with Poor Prognosis in Colorectal Cancers. <i>Cancer Research</i> , 2011, 71, 6320-6326.	0.4	1,191
2	Inferring gene networks from time series microarray data using dynamic Bayesian networks. <i>Briefings in Bioinformatics</i> , 2003, 4, 228-235.	3.2	271
3	Genomic Landscape of Esophageal Squamous Cell Carcinoma in a Japanese Population. <i>Gastroenterology</i> , 2016, 150, 1171-1182.	0.6	265
4	<i>Blautia</i> genus associated with visceral fat accumulation in adults 20–76 years of age. <i>Npj Biofilms and Microbiomes</i> , 2019, 5, 28.	2.9	244
5	Senolysis by glutaminolysis inhibition ameliorates various age-associated disorders. <i>Science</i> , 2021, 371, 265-270.	6.0	222
6	Plastin3 Is a Novel Marker for Circulating Tumor Cells Undergoing the Epithelial–Mesenchymal Transition and Is Associated with Colorectal Cancer Prognosis. <i>Cancer Research</i> , 2013, 73, 2059-2069.	0.4	220
7	Dynamic Bayesian network and nonparametric regression for nonlinear modeling of gene networks from time series gene expression data. <i>BioSystems</i> , 2004, 75, 57-65.	0.9	199
8	A Top- r Feature Selection Algorithm for Microarray Gene Expression Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 754-764.	1.9	152
9	Estimating gene networks from gene expression data by combining Bayesian network model with promoter element detection. <i>Bioinformatics</i> , 2003, 19, ii227-ii236.	1.8	146
10	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
11	Bayesian Network and Nonparametric Heteroscedastic Regression for Nonlinear Modeling of Genetic Network. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 231-252.	0.3	104
12	Antigen delivery targeted to tumor-associated macrophages overcomes tumor immune resistance. <i>Journal of Clinical Investigation</i> , 2019, 129, 1278-1294.	3.9	102
13	COMBINING MICROARRAYS AND BIOLOGICAL KNOWLEDGE FOR ESTIMATING GENE NETWORKS VIA BAYESIAN NETWORKS. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 02, 77-98.	0.3	96
14	Generation of a p16 Reporter Mouse and Its Use to Characterize and Target p16 ^{high} Cells In Vivo. <i>Cell Metabolism</i> , 2020, 32, 814-828.e6.	7.2	93
15	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
16	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. <i>Nature Medicine</i> , 2021, 27, 1239-1249.	15.2	78
17	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
18	Comprehensive phosphoproteome analysis unravels the core signaling network that initiates the earliest synapse pathology in preclinical Alzheimer's disease brain. <i>Human Molecular Genetics</i> , 2015, 24, 540-558.	1.4	70

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19	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor α and β chains using next-generation sequencing (NGS). <i>Oncolmmunology</i> , 2014, 3, e968467.	2.1	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. <i>International Journal of Machine Learning and Cybernetics</i> , 2013, 4, 679-683.	2.3	66
22	Gene network inference and visualization tools for biologists: application to new human transcriptome datasets. <i>Nucleic Acids Research</i> , 2012, 40, 2377-2398.	6.5	65
23	Null space based feature selection method for gene expression data. <i>International Journal of Machine Learning and Cybernetics</i> , 2012, 3, 269-276.	2.3	62
24	Prognostic impact of circulating tumor DNA status post α allogeneic hematopoietic stem cell transplantation in AML and MDS. <i>Blood</i> , 2019, 133, 2682-2695.	0.6	62
25	Genomon ITDetector: a tool for somatic internal tandem duplication detection from cancer genome sequencing data. <i>Bioinformatics</i> , 2015, 31, 116-118.	1.8	58
26	Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. <i>Genome Research</i> , 2020, 30, 334-346.	2.4	56
27	Use of Gene Networks from Full Genome Microarray Libraries to Identify Functionally Relevant Drug-affected Genes and Gene Regulation Cascades. <i>DNA Research</i> , 2003, 10, 19-25.	1.5	55
28	A feature selection method using improved regularized linear discriminant analysis. <i>Machine Vision and Applications</i> , 2014, 25, 775-786.	1.7	55
29	UTILIZING EVOLUTIONARY INFORMATION AND GENE EXPRESSION DATA FOR ESTIMATING GENE NETWORKS WITH BAYESIAN NETWORK MODELS. <i>Journal of Bioinformatics and Computational Biology</i> , 2005, 03, 1295-1313.	0.3	51
30	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
31	A novel ASXL1 α OGT axis plays roles in H3K4 methylation and tumor suppression in myeloid malignancies. <i>Leukemia</i> , 2018, 32, 1327-1337.	3.3	50
32	Extension and verification of the SEIR model on the 2009 influenza A (H1N1) pandemic in Japan. <i>Mathematical Biosciences</i> , 2013, 246, 47-54.	0.9	49
33	Classification of primary liver cancer with immunosuppression mechanisms and correlation with genomic alterations. <i>EBioMedicine</i> , 2020, 53, 102659.	2.7	48
34	Estimation of genetic networks and functional structures between genes by using Bayesian networks and nonparametric regression. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2002, , 175-86.	0.7	48
35	The Transcriptional Landscape of p53 Signalling Pathway. <i>EBioMedicine</i> , 2017, 20, 109-119.	2.7	47
36	The rs6983267 SNP Is Associated with MYC Transcription Efficiency, Which Promotes Progression and Worsens Prognosis of Colorectal Cancer. <i>Annals of Surgical Oncology</i> , 2013, 20, 1395-1402.	0.7	46

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37	Functional Restoration of Bacteriomes and Viromes by Fecal Microbiota Transplantation. <i>Gastroenterology</i> , 2021, 160, 2089-2102.e12.	0.6	45
38	Oncogenic roles of TOPK and MELK, and effective growth suppression by small molecular inhibitors in kidney cancer cells. <i>Oncotarget</i> , 2016, 7, 17652-17664.	0.8	44
39	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. <i>International Immunology</i> , 2018, 30, 319-331.	1.8	42
40	Integrated exome and RNA sequencing of dedifferentiated liposarcoma. <i>Nature Communications</i> , 2019, 10, 5683.	5.8	41
41	A strategy to select suitable physicochemical attributes of amino acids for protein fold recognition. <i>BMC Bioinformatics</i> , 2013, 14, 233.	1.2	40
42	Lung adenocarcinoma subtypes definable by lung development-related miRNA expression profiles in association with clinicopathologic features. <i>Carcinogenesis</i> , 2014, 35, 2224-2231.	1.3	40
43	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
44	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
45	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
46	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
47	Understanding endothelial cell apoptosis: what can the transcriptome, glycome and proteome reveal?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1469-1487.	1.8	38
48	Finding module-based gene networks with state-space models - Mining high-dimensional and short time-course gene expression data. <i>IEEE Signal Processing Magazine</i> , 2007, 24, 37-46.	4.6	38
49	A Novel Network Profiling Analysis Reveals System Changes in Epithelial-Mesenchymal Transition. <i>PLoS ONE</i> , 2011, 6, e20804.	1.1	38
50	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
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. <i>Journal of Statistical Planning and Inference</i> , 2008, 138, 3616-3633.	0.4	35
53	Selection of smoothing parameters in B-spline nonparametric regression models using information criteria. <i>Annals of the Institute of Statistical Mathematics</i> , 2003, 55, 671-687.	0.5	33
54	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

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55	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
56	Proton pump inhibitors enhance intestinal permeability via dysbiosis of gut microbiota under stressed conditions in mice. <i>Neurogastroenterology and Motility</i> , 2020, 32, e13841.	1.6	33
57	Analysis of PPAR α -dependent and PPAR α -independent transcript regulation following fenofibrate treatment of human endothelial cells. <i>Angiogenesis</i> , 2009, 12, 221-229.	3.7	32
58	Cell Cycle Gene Networks Are Associated with Melanoma Prognosis. <i>PLoS ONE</i> , 2012, 7, e34247.	1.1	32
59	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
60	In utero gene therapy rescues microcephaly caused by Pqbp1-hypofunction in neural stem progenitor cells. <i>Molecular Psychiatry</i> , 2015, 20, 459-471.	4.1	31
61	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
62	Metagenomic profiling of gut microbiome in early chronic kidney disease. <i>Nephrology Dialysis Transplantation</i> , 2021, 36, 1675-1684.	0.4	29
63	Forecasting Japan's Physician Shortage in 2035 as the First Full-Fledged Aged Society. <i>PLoS ONE</i> , 2012, 7, e50410.	1.1	28
64	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
65	Genome-wide screening of DNA methylation associated with lymph node metastasis in esophageal squamous cell carcinoma. <i>Oncotarget</i> , 2017, 8, 37740-37750.	0.8	27
66	Oral MucoRice-CTB vaccine for safety and microbiota-dependent immunogenicity in humans: a phase 1 randomised trial. <i>Lancet Microbe</i> , The, 2021, 2, e429-e440.	3.4	27
67	Use of Gene Networks for Identifying and Validating Drug Targets. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 459-474.	0.3	25
68	Predicting gene regulation by sigma factors in <i>Bacillus subtilis</i> from genome-wide data. <i>Bioinformatics</i> , 2004, 20, i101-i108.	1.8	25
69	Orengedokuto and berberine improve indomethacin-induced small intestinal injury via adenosine. <i>Journal of Gastroenterology</i> , 2009, 44, 380-389.	2.3	25
70	A Filter Based Feature Selection Algorithm Using Null Space of Covariance Matrix for DNA Microarray Gene Expression Data. <i>Current Bioinformatics</i> , 2012, 7, 289-294.	0.7	24
71	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
72	Dysbiotic Fecal Microbiome in HIV-1 Infected Individuals in Ghana. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 646467.	1.8	24

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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. <i>International Journal of Infectious Diseases</i> , 2021, 113, 74-81.	1.5	24
74	HapMuC: somatic mutation calling using heterozygous germ line variants near candidate mutations. <i>Bioinformatics</i> , 2014, 30, 3302-3309.	1.8	23
75	Targeting Tyro3 ameliorates a model of PGRN-mutant FTLTDP via tau-mediated synaptic pathology. <i>Nature Communications</i> , 2018, 9, 433.	5.8	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. <i>BMC Bioinformatics</i> , 2019, 20, 267.	1.2	23
77	Combining microarrays and biological knowledge for estimating gene networks via Bayesian networks. <i>Proceedings</i> , 2003, 2, 104-13.	0.1	23
78	A BETWEEN-CLASS OVERLAPPING FILTER-BASED METHOD FOR TRANSCRIPTOME DATA ANALYSIS. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1250010.	0.3	22
79	Systems biology analysis of <i>Drosophila</i> in vivo screen data elucidates core networks for DNA damage repair in SCA1. <i>Human Molecular Genetics</i> , 2014, 23, 1345-1364.	1.4	22
80	Probabilistic expression of spatially varied amino acid dimers into general form of Chou \times 3s pseudo amino acid composition for protein fold recognition. <i>Journal of Theoretical Biology</i> , 2015, 380, 291-298.	0.8	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. <i>Electronics Letters</i> , 2011, 47, 480.	0.5	21
83	Overexpression of Cohesion Establishment Factor DSCC1 through E2F in Colorectal Cancer. <i>PLoS ONE</i> , 2014, 9, e85750.	1.1	21
84	Error tolerant model for incorporating biological knowledge with expression data in estimating gene networks. <i>Statistical Methodology</i> , 2006, 3, 1-16.	0.5	20
85	Vasohibin-1 is identified as a master-regulator of endothelial cell apoptosis using gene network analysis. <i>BMC Genomics</i> , 2013, 14, 23.	1.2	20
86	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
87	COVID-19 risk assessment at the opening ceremony of the Tokyo 2020 Olympic Games. <i>Microbial Risk Analysis</i> , 2021, 19, 100162.	1.3	20
88	Evaluation of Sequence Features from Intrinsically Disordered Regions for the Estimation of Protein Function. <i>PLoS ONE</i> , 2014, 9, e89890.	1.1	19
89	Sparse Overlapping Group Lasso for Integrative Multi-Omics Analysis. <i>Journal of Computational Biology</i> , 2015, 22, 73-84.	0.8	18
90	The relationship between cigarette smoking and the tongue microbiome in an East Asian population. <i>Journal of Oral Microbiology</i> , 2020, 12, 1742527.	1.2	18

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91	HEAL: an automated deep learning framework for cancer histopathology image analysis. <i>Bioinformatics</i> , 2021, 37, 4291-4295.	1.8	18
92	The Difference between the Two Representative Kampo Formulas for Treating Dysmenorrhea: An Observational Study. <i>Evidence-based Complementary and Alternative Medicine</i> , 2016, 2016, 1-10.	0.5	17
93	Reduced expression of APC-1B but not APC-1A by the deletion of promoter 1B is responsible for familial adenomatous polyposis. <i>Scientific Reports</i> , 2016, 6, 26011.	1.6	17
94	Circulating tumor DNA dynamically predicts response and/or relapse in patients with hematological malignancies. <i>International Journal of Hematology</i> , 2018, 108, 402-410.	0.7	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. <i>Nutrients</i> , 2019, 11, 2698.	1.7	17
96	Nanopore basecalling from a perspective of instance segmentation. <i>BMC Bioinformatics</i> , 2020, 21, 136.	1.2	17
97	Halcyon: an accurate basecaller exploiting an encoder-decoder model with monotonic attention. <i>Bioinformatics</i> , 2021, 37, 1211-1217.	1.8	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. <i>BMC Genomics</i> , 2018, 19, 790.	1.2	16
100	Weighted lasso in graphical Gaussian modeling for large gene network estimation based on microarray data. <i>Genome Informatics</i> , 2007, 19, 142-53.	0.4	16
101	Two <i>Blautia</i> Species Associated with Visceral Fat Accumulation: A One-Year Longitudinal Study. <i>Biology</i> , 2022, 11, 318.	1.3	16
102	Identification of AFAP1L1 as a prognostic marker for spindle cell sarcomas. <i>Oncogene</i> , 2011, 30, 4015-4025.	2.6	15
103	Recursive Random Lasso (RRLasso) for Identifying Anti-Cancer Drug Targets. <i>PLoS ONE</i> , 2015, 10, e0141869.	1.1	15
104	Inference of Gene Regulatory Networks Incorporating Multi-Source Biological Knowledge via a State Space Model with L1 Regularization. <i>PLoS ONE</i> , 2014, 9, e105942.	1.1	15
105	COVID-19 wastewater surveillance implemented in the Tokyo 2020 Olympic and Paralympic Village. <i>Journal of Travel Medicine</i> , 2022, 29, .	1.4	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 <i>“Hie”</i> (Oversensitivity to Coldness) in Men and Pre- and Postmenopausal Women. <i>Evidence-based Complementary and Alternative Medicine</i> , 2014, 2014, 1-9.	0.5	14
108	Sequence-specific bias correction for RNA-seq data using recurrent neural networks. <i>BMC Genomics</i> , 2017, 18, 1044.	1.2	14

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109	Quantifying immune-based counterselection of somatic mutations. <i>PLoS Genetics</i> , 2019, 15, e1008227.	1.5	14
110	Increased Risk for CRC in Diabetic Patients with the Nonrisk Allele of SNPs at 8q24. <i>Annals of Surgical Oncology</i> , 2012, 19, 2853-2858.	0.7	13
111	AFAP 1L1, a novel associating partner with vinculin, modulates cellular morphology and motility, and promotes the progression of colorectal cancers. <i>Cancer Medicine</i> , 2014, 3, 759-774.	1.3	13
112	Living with COVID-19: mass gatherings and minimizing risk. <i>QJM - Monthly Journal of the Association of Physicians</i> , 2021, 114, 437-439.	0.2	13
113	Trop-2 in Upper Tract Urothelial Carcinoma. <i>Current Oncology</i> , 2022, 29, 3911-3921.	0.9	13
114	Analysis of Questionnaire for Traditional Medicine and Development of Decision Support System. <i>Evidence-based Complementary and Alternative Medicine</i> , 2014, 2014, 1-8.	0.5	12
115	The miR-199a/Brm/EGR1 axis is a determinant of anchorage-independent growth in epithelial tumor cell lines. <i>Scientific Reports</i> , 2015, 5, 8428.	1.6	12
116	The hnRNP-Htt axis regulates necrotic cell death induced by transcriptional repression through impaired RNA splicing. <i>Cell Death and Disease</i> , 2016, 7, e2207-e2207.	2.7	12
117	Application of targeted nanopore sequencing for the screening and determination of structural variants in patients with Lynch syndrome. <i>Journal of Human Genetics</i> , 2021, 66, 1053-1060.	1.1	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. <i>Biostatistics</i> , 2016, 17, 235-248.	0.9	11
119	Role of Circulating Tumor DNA in Hematological Malignancy. <i>Cancers</i> , 2021, 13, 2078.	1.7	11
120	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , 2020, 38, 288-292.	9.4	11
121	Perioperative circulating tumor DNA enables the identification of patients with poor prognosis in upper tract urothelial carcinoma. <i>Cancer Science</i> , 2022, 113, 1830-1842.	1.7	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. <i>Journal of Computational Biology</i> , 2013, 20, 571-582.	0.8	10
124	Phenotype-based gene analysis allowed successful diagnosis of X-linked neutropenia associated with a novel WASp mutation. <i>Annals of Hematology</i> , 2018, 97, 367-369.	0.8	10
125	Cell-lineage level targeted sequencing to identify acute myeloid leukemia with myelodysplasia-related changes. <i>Blood Advances</i> , 2018, 2, 2513-2521.	2.5	10
126	Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. <i>Scientific Reports</i> , 2021, 11, 15713.	1.6	10

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127	Assessment of COVID-19 risk and prevention effectiveness among spectators of mass gathering events. <i>Microbial Risk Analysis</i> , 2022, 21, 100215.	1.3	10
128	Bronchoalveolar lavage fluid reveals factors contributing to the efficacy of PD-1 blockade in lung cancer. <i>JCI Insight</i> , 2022, 7, .	2.3	10
129	Requirement of glycosylation machinery in TLR responses revealed by CRISPR/Cas9 screening. <i>International Immunology</i> , 2017, 29, 347-355.	1.8	9
130	Association of single nucleotide polymorphisms in the NRF2 promoter with vascular stiffness with aging. <i>PLoS ONE</i> , 2020, 15, e0236834.	1.1	9
131	Fecal Microbiome Composition in Healthy Adults in Ghana. <i>Japanese Journal of Infectious Diseases</i> , 2021, 74, 42-47.	0.5	9
132	Circulating cell-free DNA in the peripheral blood plasma of patients is an informative biomarker for multiple myeloma relapse. <i>International Journal of Clinical Oncology</i> , 2021, 26, 2142-2150.	1.0	9
133	Robust Prediction of Anti-Cancer Drug Sensitivity and Sensitivity-Specific Biomarker. <i>PLoS ONE</i> , 2014, 9, e108990.	1.1	9
134	Possible Role of Cytochrome P450 1B1 in the Mechanism of Gemcitabine Resistance in Pancreatic Cancer. <i>Biomedicines</i> , 2021, 9, 1396.	1.4	9
135	Computational strategy for discovering druggable gene networks from genome-wide RNA expression profiles. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2006, , 559-71.	0.7	9
136	Sign: large-scale gene network estimation environment for high performance computing. <i>Genome Informatics</i> , 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. <i>PLoS ONE</i> , 2013, 8, e72866.	1.1	8
139	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
140	Neoantimon: a multifunctional R package for identification of tumor-specific neoantigens. <i>Bioinformatics</i> , 2020, 36, 4813-4816.	1.8	8
141	Discrimination of prediction models between cold-heat and deficiency-excess patterns. <i>Complementary Therapies in Medicine</i> , 2020, 49, 102353.	1.3	8
142	Identifying Gene Pathways Associated with Cancer Characteristics via Sparse Statistical Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 966-972.	1.9	7
143	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
144	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

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145	Identifying drug active pathways from gene networks estimated by gene expression data. <i>Genome Informatics</i> , 2005, 16, 182-91.	0.4	7
146	Predicting differences in gene regulatory systems by state space models. <i>Genome Informatics</i> , 2008, 21, 101-13.	0.4	7
147	COVID-19 testing systems and their effectiveness in small, semi-isolated groups for sports events. <i>PLoS ONE</i> , 2022, 17, e0266197.	1.1	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. <i>Human Genome Variation</i> , 2015, 2, 15011.	0.4	6
150	The first case of elderly <i>TCF3-HLF</i> -positive B-cell acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2019, 60, 2821-2824.	0.6	6
151	A Bayesian model integration for mutation calling through data partitioning. <i>Bioinformatics</i> , 2019, 35, 4247-4254.	1.8	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. <i>Journal of Computational Biology</i> , 2019, 26, 923-937.	0.8	6
153	Global gene network exploration based on explainable artificial intelligence approach. <i>PLoS ONE</i> , 2020, 15, e0241508.	1.1	6
154	Identification of a p53-repressed gene module in breast cancer cells. <i>Oncotarget</i> , 2017, 8, 55821-55836.	0.8	6
155	A statistical framework for genome-wide discovery of biomarker splice variations with GeneChip Human Exon 1.0 ST Arrays. <i>Genome Informatics</i> , 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. <i>International Journal of Urology</i> , 2022, 29, 462-469.	0.5	6
157	Case-control study of binary disease trait considering interactions between SNPs and environmental effects using logistic regression. , 0, , .		5
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