

Teppei Shimamura

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

6,859
citations

201674

27
h-index

91884

69
g-index

89
all docs

89
docs citations

89
times ranked

14587
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.	0.9	1,191
2	Integrated molecular analysis of clear-cell renal cell carcinoma. <i>Nature Genetics</i> , 2013, 45, 860-867.	21.4	955
3	Mutational landscape and clonal architecture in grade II and III gliomas. <i>Nature Genetics</i> , 2015, 47, 458-468.	21.4	729
4	Integrated molecular analysis of adult T cell leukemia/lymphoma. <i>Nature Genetics</i> , 2015, 47, 1304-1315.	21.4	659
5	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. <i>Nature Genetics</i> , 2013, 45, 1232-1237.	21.4	334
6	Genomic Landscape of Esophageal Squamous Cell Carcinoma in a Japanese Population. <i>Gastroenterology</i> , 2016, 150, 1171-1182.	1.3	265
7	Dynamic Change of Chromatin Conformation in Response to Hypoxia Enhances the Expression of GLUT3 (SLC2A3) by Cooperative Interaction of Hypoxia-Inducible Factor 1 and KDM3A. <i>Molecular and Cellular Biology</i> , 2012, 32, 3018-3032.	2.3	230
8	Prognostic relevance of genetic alterations in diffuse lower-grade gliomas. <i>Neuro-Oncology</i> , 2018, 20, 66-77.	1.2	225
9	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.	0.9	220
10	Comparative Analyses of Copy-Number Variation in Autism Spectrum Disorder and Schizophrenia Reveal Etiological Overlap and Biological Insights. <i>Cell Reports</i> , 2018, 24, 2838-2856.	6.4	177
11	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. <i>Nature Communications</i> , 2015, 6, 7557.	12.8	149
12	Epidermal Growth Factor Receptor Tyrosine Kinase Defines Critical Prognostic Genes of Stage I Lung Adenocarcinoma. <i>PLoS ONE</i> , 2012, 7, e43923.	2.5	148
13	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. <i>PLoS Genetics</i> , 2016, 12, e1005778.	3.5	134
14	The Tumor-Suppressive miR-497-195 Cluster Targets Multiple Cell-Cycle Regulators in Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2013, 8, e60155.	2.5	132
15	Extracellular Acidic pH Activates the Sterol Regulatory Element-Binding Protein 2 to Promote Tumor Progression. <i>Cell Reports</i> , 2017, 18, 2228-2242.	6.4	129
16	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2017, 49, 1274-1281.	21.4	100
17	Inhibition of Histone Demethylase JMJD1A Improves Anti-Angiogenic Therapy and Reduces Tumor-Associated Macrophages. <i>Cancer Research</i> , 2013, 73, 3019-3028.	0.9	82
18	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. <i>Nature Communications</i> , 2018, 9, 2884.	12.8	82

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19	Biallelic <i>DICER1</i> Mutations in Sporadic Pleuropulmonary Blastoma. <i>Cancer Research</i> , 2014, 74, 2742-2749.	0.9	67
20	Recursive regularization for inferring gene networks from time-course gene expression profiles. <i>BMC Systems Biology</i> , 2009, 3, 41.	3.0	61
21	ATR inhibition controls aggressive prostate tumors deficient in Y-linked histone demethylase KDM5D. <i>Journal of Clinical Investigation</i> , 2018, 128, 2979-2995.	8.2	53
22	Dynamically and epigenetically coordinated GATA/ETS/SOX transcription factor expression is indispensable for endothelial cell differentiation. <i>Nucleic Acids Research</i> , 2017, 45, 4344-4358.	14.5	52
23	A mixture-of-experts deep generative model for integrated analysis of single-cell multiomics data. <i>Cell Reports Methods</i> , 2021, 1, 100071.	2.9	47
24	Elevated β -catenin pathway as a novel target for patients with resistance to EGF receptor targeting drugs. <i>Scientific Reports</i> , 2015, 5, 13076.	3.3	40
25	A Novel Network Profiling Analysis Reveals System Changes in Epithelial-Mesenchymal Transition. <i>PLoS ONE</i> , 2011, 6, e20804.	2.5	38
26	Long Noncoding RNA JHDM1D-AS1 Promotes Tumor Growth by Regulating Angiogenesis in Response to Nutrient Starvation. <i>Molecular and Cellular Biology</i> , 2017, 37, .	2.3	37
27	Coordinated demethylation of H3K9 and H3K27 is required for rapid inflammatory responses of endothelial cells. <i>EMBO Journal</i> , 2020, 39, e103949.	7.8	37
28	Replication stress triggers microsatellite destabilization and hypermutation leading to clonal expansion in vitro. <i>Nature Communications</i> , 2019, 10, 3925.	12.8	36
29	NECAB3 Promotes Activation of Hypoxia-inducible factor-1 during Normoxia and Enhances Tumorigenicity of Cancer Cells. <i>Scientific Reports</i> , 2016, 6, 22784.	3.3	30
30	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. <i>Npj Precision Oncology</i> , 2020, 4, 20.	5.4	30
31	Phosphoethanolamine Accumulation Protects Cancer Cells under Glutamine Starvation through Downregulation of PCYT2. <i>Cell Reports</i> , 2019, 29, 89-103.e7.	6.4	29
32	PRC2-Mediated Transcriptomic Alterations at the Embryonic Stage Govern Tumorigenesis and Clinical Outcome in MYCN-Driven Neuroblastoma. <i>Cancer Research</i> , 2017, 77, 5259-5271.	0.9	28
33	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.	2.9	22
34	Regnase-1-mediated post-transcriptional regulation is essential for hematopoietic stem and progenitor cell homeostasis. <i>Nature Communications</i> , 2019, 10, 1072.	12.8	19
35	N-cadherin expression is a potential survival mechanism of gefitinib-resistant lung cancer cells. <i>American Journal of Cancer Research</i> , 2011, 1, 823-33.	1.4	19
36	An Integrative Analysis to Identify Driver Genes in Esophageal Squamous Cell Carcinoma. <i>PLoS ONE</i> , 2015, 10, e0139808.	2.5	17

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37	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
38	WEIGHTED LASSO IN GRAPHICAL GAUSSIAN MODELING FOR LARGE GENE NETWORK ESTIMATION BASED ON MICROARRAY DATA. , 2007, , .		14
39	Estimating exogenous variables in data with more variables than observations. <i>Neural Networks</i> , 2011, 24, 875-880.	5.9	14
40	Uncertainty in treatment of head-and-neck tumors by use of intraoral mouthpiece and embedded fiducials. <i>International Journal of Radiation Oncology Biology Physics</i> , 2006, 64, 1581-1588.	0.8	13
41	Inferring dynamic gene networks under varying conditions for transcriptomic network comparison. <i>Bioinformatics</i> , 2010, 26, 1064-1072.	4.1	12
42	Statistical model-based testing to evaluate the recurrence of genomic aberrations. <i>Bioinformatics</i> , 2012, 28, i115-i120.	4.1	12
43	Aberrant Methylation of FOXE1 Contributes to a Poor Prognosis for Patients with Colorectal Cancer. <i>Annals of Surgical Oncology</i> , 2016, 23, 3948-3955.	1.5	12
44	phyC: Clustering cancer evolutionary trees. <i>PLoS Computational Biology</i> , 2017, 13, e1005509.	3.2	12
45	Allelic Imbalance at an 8q24 Oncogenic SNP is Involved in Activating MYC in Human Colorectal Cancer. <i>Annals of Surgical Oncology</i> , 2014, 21, 515-521.	1.5	11
46	Loss of CDCP1 Expression Promotes Invasiveness and Poor Prognosis in Esophageal Squamous Cell Carcinoma. <i>Annals of Surgical Oncology</i> , 2014, 21, 640-647.	1.5	11
47	Depletion of central memory CD8+ T cells might impede the antitumor therapeutic effect of Mogamulizumab. <i>Nature Communications</i> , 2021, 12, 7280.	12.8	11
48	Japanese genome-wide association study identifies a significant colorectal cancer susceptibility locus at chromosome 10p14. <i>Cancer Science</i> , 2017, 108, 2239-2247.	3.9	10
49	Model-based cell clustering and population tracking for time-series flow cytometry data. <i>BMC Bioinformatics</i> , 2019, 20, 633.	2.6	10
50	Robust Prediction of Anti-Cancer Drug Sensitivity and Sensitivity-Specific Biomarker. <i>PLoS ONE</i> , 2014, 9, e108990.	2.5	9
51	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.	3.0	7
52	A restricted level of PQBP1 is needed for the best longevity of <i>Drosophila</i> . <i>Neurobiology of Aging</i> , 2013, 34, 356.e11-356.e20.	3.1	7
53	Predicting differences in gene regulatory systems by state space models. <i>Genome Informatics</i> , 2008, 21, 101-13.	0.4	7
54	Pathogenic Epigenetic Consequences of Genetic Alterations in IDH-Wild-Type Diffuse Astrocytic Gliomas. <i>Cancer Research</i> , 2019, 79, 4814-4827.	0.9	6

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55	Adaptive NetworkProfiler for Identifying Cancer Characteristic-Specific Gene Regulatory Networks. Journal of Computational Biology, 2018, 25, 130-145.	1.6	5
56	A latent allocation model for the analysis of microbial composition and disease. BMC Bioinformatics, 2018, 19, 519.	2.6	5
57	A network of networks approach for modeling interconnected brain tissue-specific networks. Bioinformatics, 2019, 35, 3092-3101.	4.1	5
58	Model-based clustering for flow and mass cytometry data with clinical information. BMC Bioinformatics, 2020, 21, 393.	2.6	5
59	D3M: detection of differential distributions of methylation levels. Bioinformatics, 2016, 32, 2248-2255.	4.1	4
60	Comprehensive genetic analysis of donor cell derived leukemia with <i>KMT2A</i> rearrangement. Pediatric Blood and Cancer, 2018, 65, e26823.	1.5	4
61	COMPARISON OF GENE EXPRESSION PROFILES PRODUCED BY CAGE, ILLUMINA MICROARRAY AND REAL TIME RT-PCR. , 2010, , .		3
62	High performance computing of a fusion gene detection pipeline on the K computer. , 2015, , .		3
63	ENIGMA: an enterotype-like unigram mixture model for microbial association analysis. BMC Genomics, 2019, 20, 191.	2.8	3
64	Genomic data assimilation using a higher moment filtering technique for restoration of gene regulatory networks. BMC Systems Biology, 2015, 9, 14.	3.0	2
65	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
66	Hierarchical non-negative matrix factorization using clinical information for microbial communities. BMC Genomics, 2021, 22, 104.	2.8	2
67	Model-free unsupervised gene set screening based on information enrichment in expression profiles. Bioinformatics, 2010, 26, 3090-3097.	4.1	1
68	Inferring Contagion in Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 570-576.	3.0	1
69	GIMLET: Identifying Biological Modulators in Context-Specific Gene Regulation Using Local Energy Statistics. Lecture Notes in Computer Science, 2019, , 124-137.	1.3	1
70	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. Blood, 2014, 124, 75-75.	1.4	1
71	PREDICTING DIFFERENCES IN GENE REGULATORY SYSTEMS BY STATE SPACE MODELS. , 2008, , .		1
72	Discovery of Exogenous Variables in Data with More Variables Than Observations. Lecture Notes in Computer Science, 2010, , 67-76.	1.3	1

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73	CYBERTRACK2.0: zero-inflated model-based cell clustering and population tracking method for longitudinal mass cytometry data. <i>Bioinformatics</i> , 2021, 37, 1632-1634.	4.1	1
74	COLLOCATION-BASED SPARSE ESTIMATION FOR CONSTRUCTING DYNAMIC GENE NETWORKS. , 2010, , .		0
75	Discovering functional gene pathways associated with cancer heterogeneity via sparse supervised learning. , 2010, , .		0
76	A NOVEL STRATEGY TO SEARCH CONSERVED TRANSCRIPTION FACTOR BINDING SITES AMONG COEXPRESSING GENES IN HUMAN. , 2008, , .		0
77	Tumor Subclonal Progression Model for Cancer Hallmark Acquisition. <i>Lecture Notes in Computer Science</i> , 2019, , 115-123.	1.3	0
78	Collocation-based sparse estimation for constructing dynamic gene networks. <i>Genome Informatics</i> , 2010, 24, 164-78.	0.4	0