Teppei Shimamura

List of Publications by Year in descending order

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	Hierarchical non-negative matrix factorization using clinical information for microbial communities. BMC Genomics, 2021, 22, 104.	2.8	2
2	A mixture-of-experts deep generative model for integrated analysis of single-cell multiomics data. Cell Reports Methods, 2021, 1, 100071.	2.9	47
3	CYBERTRACK2.0: zero-inflated model-based cell clustering and population tracking method for longitudinal mass cytometry data. Bioinformatics, 2021, 37, 1632-1634.	4.1	1
4	Depletion of central memory CD8+ T cells might impede the antitumor therapeutic effect of Mogamulizumab. Nature Communications, 2021, 12, 7280.	12.8	11
5	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. Npj Precision Oncology, 2020, 4, 20.	5.4	30
6	Model-based clustering for flow and mass cytometry data with clinical information. BMC Bioinformatics, 2020, 21, 393.	2.6	5
7	Coordinated demethylation of H3K9 and H3K27 is required for rapid inflammatory responses of endothelial cells. EMBO Journal, 2020, 39, e103949.	7.8	37
8	Replication stress triggers microsatellite destabilization and hypermutation leading to clonal expansion in vitro. Nature Communications, 2019, 10, 3925.	12.8	36
9	Phosphoethanolamine Accumulation Protects Cancer Cells under Glutamine Starvation through Downregulation of PCYT2. Cell Reports, 2019, 29, 89-103.e7.	6.4	29
10	Pathogenic Epigenetic Consequences of Genetic Alterations in IDH-Wild-Type Diffuse Astrocytic Gliomas. Cancer Research, 2019, 79, 4814-4827.	0.9	6
11	ENIGMA: an enterotype-like unigram mixture model for microbial association analysis. BMC Genomics, 2019, 20, 191.	2.8	3
12	Regnase-1-mediated post-transcriptional regulation is essential for hematopoietic stem and progenitor cell homeostasis. Nature Communications, 2019, 10, 1072.	12.8	19
13	Model-based cell clustering and population tracking for time-series flow cytometry data. BMC Bioinformatics, 2019, 20, 633.	2.6	10
14	A network of networks approach for modeling interconnected brain tissue-specific networks. Bioinformatics, 2019, 35, 3092-3101.	4.1	5
15	GIMLET: Identifying Biological Modulators in Context-Specific Gene Regulation Using Local Energy Statistics. Lecture Notes in Computer Science, 2019, , 124-137.	1.3	1
16	Tumor Subclonal Progression Model for Cancer Hallmark Acquisition. Lecture Notes in Computer Science, 2019, , 115-123.	1.3	0
17	Prognostic relevance of genetic alterations in diffuse lower-grade gliomas. Neuro-Oncology, 2018, 20, 66-77.	1.2	225
18	Adaptive NetworkProfiler for Identifying Cancer Characteristic-Specific Gene Regulatory Networks. Journal of Computational Biology, 2018, 25, 130-145.	1.6	5

#	Article	IF	Citations
19	Comprehensive genetic analysis of donor cell derived leukemia with *KMT2A* rearrangement. Pediatric Blood and Cancer, 2018, 65, e26823.	1.5	4
20	A latent allocation model for the analysis of microbial composition and disease. BMC Bioinformatics, 2018, 19, 519.	2.6	5
21	Comparative Analyses of Copy-Number Variation in Autism Spectrum Disorder and Schizophrenia Reveal Etiological Overlap and Biological Insights. Cell Reports, 2018, 24, 2838-2856.	6.4	177
22	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. Nature Communications, 2018, 9, 2884.	12.8	82
23	ATR inhibition controls aggressive prostate tumors deficient in Y-linked histone demethylase KDM5D. Journal of Clinical Investigation, 2018, 128, 2979-2995.	8.2	53
24	Extracellular Acidic pH Activates the Sterol Regulatory Element-Binding Protein 2 to Promote Tumor Progression. Cell Reports, 2017, 18, 2228-2242.	6.4	129
25	Dynamically and epigenetically coordinated GATA/ETS/SOX transcription factor expression is indispensable for endothelial cell differentiation. Nucleic Acids Research, 2017, 45, 4344-4358.	14.5	52
26	Japanese genome‑wide association study identifies a significant colorectal cancer susceptibility locus at chromosome 10p14. Cancer Science, 2017, 108, 2239-2247.	3.9	10
27	PRC2-Mediated Transcriptomic Alterations at the Embryonic Stage Govern Tumorigenesis and Clinical Outcome in MYCN-Driven Neuroblastoma. Cancer Research, 2017, 77, 5259-5271.	0.9	28
28	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1274-1281.	21.4	100
29	Long Noncoding RNA JHDM1D-AS1 Promotes Tumor Growth by Regulating Angiogenesis in Response to Nutrient Starvation. Molecular and Cellular Biology, 2017, 37, .	2.3	37
30	phyC: Clustering cancer evolutionary trees. PLoS Computational Biology, 2017, 13, e1005509.	3.2	12
31	NECAB3 Promotes Activation of Hypoxia-inducible factor-1 during Normoxia and Enhances Tumourigenicity of Cancer Cells. Scientific Reports, 2016, 6, 22784.	3.3	30
32	Aberrant Methylation of FOXE1 Contributes to a Poor Prognosis for Patients with Colorectal Cancer. Annals of Surgical Oncology, 2016, 23, 3948-3955.	1.5	12
33	Genomic Landscape of Esophageal Squamous Cell Carcinoma inÂa Japanese Population. Gastroenterology, 2016, 150, 1171-1182.	1.3	265
34	D3M: detection of differential distributions of methylation levels. Bioinformatics, 2016, 32, 2248-2255.	4.1	4
35	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
36	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. PLoS Genetics, 2016, 12, e1005778.	3.5	134

#	Article	IF	Citations
37	High performance computing of a fusion gene detection pipeline on the K computer. , 2015, , .		3
38	Elevated Î²-catenin pathway as a novel target for patients with resistance to EGF receptor targeting drugs. Scientific Reports, 2015, 5, 13076.	3.3	40
39	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. Nature Communications, 2015, 6, 7557.	12.8	149
40	Genomic data assimilation using a higher moment filtering technique for restoration of gene regulatory networks. BMC Systems Biology, 2015, 9, 14.	3.0	2
41	Mutational landscape and clonal architecture in grade II and III gliomas. Nature Genetics, 2015, 47, 458-468.	21.4	729
42	Integrated molecular analysis of adult T cell leukemia/lymphoma. Nature Genetics, 2015, 47, 1304-1315.	21.4	659
43	An Integrative Analysis to Identify Driver Genes in Esophageal Squamous Cell Carcinoma. PLoS ONE, 2015, 10, e0139808.	2.5	17
44	Allelic Imbalance at an 8q24 Oncogenic SNP is Involved in Activating MYC in Human Colorectal Cancer. Annals of Surgical Oncology, 2014, 21, 515-521.	1.5	11
45	Biallelic <i>DICER1</i> Mutations in Sporadic Pleuropulmonary Blastoma. Cancer Research, 2014, 74, 2742-2749.	0.9	67
46	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
47	Loss of CDCP1 Expression Promotes Invasiveness and Poor Prognosis in Esophageal Squamous Cell Carcinoma. Annals of Surgical Oncology, 2014, 21, 640-647.	1.5	11
48	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. Blood, 2014, 124, 75-75.	1.4	1
49	Robust Prediction of Anti-Cancer Drug Sensitivity and Sensitivity-Specific Biomarker. PLoS ONE, 2014, 9, e108990.	2.5	9
50	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. Nature Genetics, 2013, 45, 1232-1237.	21.4	334
51	A restricted level of PQBP1 is needed for the best longevity of Drosophila. Neurobiology of Aging, 2013, 34, 356.e11-356.e20.	3.1	7
52	Integrated molecular analysis of clear-cell renal cell carcinoma. Nature Genetics, 2013, 45, 860-867.	21.4	955
53	Inhibition of Histone Demethylase JMJD1A Improves Anti-Angiogenic Therapy and Reduces Tumor-Associated Macrophages. Cancer Research, 2013, 73, 3019-3028.	0.9	82
54	The Tumor-Suppressive miR-497-195 Cluster Targets Multiple Cell-Cycle Regulators in Hepatocellular Carcinoma. PLoS ONE, 2013, 8, e60155.	2.5	132

#	ARTICLE	IF	CITATIONS
55	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.	0.9	220
56	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. Molecular and Cellular Biology, 2012, 32, 3018-3032.	2.3	230
57	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
58	Statistical model-based testing to evaluate the recurrence of genomic aberrations. Bioinformatics, 2012, 28, i115-i120.	4.1	12
59	Epidermal Growth Factor Receptor Tyrosine Kinase Defines Critical Prognostic Genes of Stage I Lung Adenocarcinoma. PLoS ONE, 2012, 7, e43923.	2.5	148
60	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
61	Inferring Contagion in Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 570-576.	3.0	1
62	A Novel Network Profiling Analysis Reveals System Changes in Epithelial-Mesenchymal Transition. PLoS ONE, 2011, 6, e20804.	2.5	38
63	Estimating exogenous variables in data with more variables than observations. Neural Networks, 2011, 24, 875-880.	5.9	14
64	N-cadherin expression is a potential survival mechanism of gefitinib-resistant lung cancer cells. American Journal of Cancer Research, 2011, 1, 823-33.	1.4	19
65	COLLOCATION-BASED SPARSE ESTIMATION FOR CONSTRUCTING DYNAMIC GENE NETWORKS. , 2010, , .		0
66	COMPARISON OF GENE EXPRESSION PROFILES PRODUCED BY CAGE, ILLUMINA MICROARRAY AND REAL TIME RT-PCR. , 2010, , .		3
67	Inferring dynamic gene networks under varying conditions for transcriptomic network comparison. Bioinformatics, 2010, 26, 1064-1072.	4.1	12
68	Model-free unsupervised gene set screening based on information enrichment in expression profiles. Bioinformatics, 2010, 26, 3090-3097.	4.1	1
69	Discovering functional gene pathways associated with cancer heterogeneity via sparse supervised learning. , 2010, , .		0
70	Discovery of Exogenous Variables in Data with More Variables Than Observations. Lecture Notes in Computer Science, 2010, , 67-76.	1.3	1
71	Collocation-based sparse estimation for constructing dynamic gene networks. Genome Informatics, 2010, 24, 164-78.	0.4	0
72	Recursive regularization for inferring gene networks from time-course gene expression profiles. BMC Systems Biology, 2009, 3, 41.	3.0	61

#	Article	IF	Citations
73	A NOVEL STRATEGY TO SEARCH CONSERVED TRANSCRIPTION FACTOR BINDING SITES AMONG COEXPRESSING GENES IN HUMAN. , 2008, , .		0
74	PREDICTING DIFFERENCES IN GENE REGULATORY SYSTEMS BY STATE SPACE MODELS. , 2008, , .		1
75	Predicting differences in gene regulatory systems by state space models. Genome Informatics, 2008, 21, 101-13.	0.4	7
76	WEIGHTED LASSO IN GRAPHICAL GAUSSIAN MODELING FOR LARGE GENE NETWORK ESTIMATION BASED ON MICROARRAY DATA. , 2007, , .		14
77	Weighted lasso in graphical Gaussian modeling for large gene network estimation based on microarray data. Genome Informatics, 2007, 19, 142-53.	0.4	16
78	Uncertainty in treatment of head-and-neck tumors by use of intraoral mouthpiece and embedded fiducials. International Journal of Radiation Oncology Biology Physics, 2006, 64, 1581-1588.	0.8	13