

Atsushi Niida

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

3,914
citations

361413
20
h-index

189892
50
g-index

57
all docs

57
docs citations

57
times ranked

8543
citing authors

#	ARTICLE	IF	CITATIONS
1	Pan-cancer methylome analysis for cancer diagnosis and classification of cancer cell of origin. <i>Cancer Gene Therapy</i> , 2022, 29, 428-436.	4.6	12
2	Impaired tumor immune response in metastatic tumors is a selective pressure for neutral evolution in CRC cases. <i>PLoS Genetics</i> , 2021, 17, e1009113.	3.5	7
3	Modeling colorectal cancer evolution. <i>Journal of Human Genetics</i> , 2021, 66, 869-878.	2.3	14
4	Single-sample enrichment analysis identified predictive biomarker candidates for nivolumab in patients with non-small cell lung cancer.. <i>Journal of Clinical Oncology</i> , 2021, 39, e21097-e21097.	1.6	0
5	Combined landscape of single-nucleotide variants and copy number alterations in clonal hematopoiesis. <i>Nature Medicine</i> , 2021, 27, 1239-1249.	30.7	78
6	The Evolving Genomic Landscape of Esophageal Squamous Cell Carcinoma Under Chemoradiotherapy. <i>Cancer Research</i> , 2021, 81, 4926-4938.	0.9	20
7	Possible Role of Cytochrome P450 1B1 in the Mechanism of Gemcitabine Resistance in Pancreatic Cancer. <i>Biomedicines</i> , 2021, 9, 1396.	3.2	9
8	Gene expression signatures as candidate biomarkers of response to PD-1 blockade in non-small cell lung cancers. <i>PLoS ONE</i> , 2021, 16, e0260500.	2.5	2
9	Ensemble smoothers for inference of hidden states and parameters in combinatorial regulatory model. <i>Journal of the Franklin Institute</i> , 2020, 357, 2916-2933.	3.4	0
10	Neoantimon: a multifunctional R package for identification of tumor-specific neoantigens. <i>Bioinformatics</i> , 2020, 36, 4813-4816.	4.1	8
11	Genetic landscape of external auditory canal squamous cell carcinoma. <i>Cancer Science</i> , 2020, 111, 3010-3019.	3.9	14
12	Depressed Colorectal Cancer: A New Paradigm in Early Colorectal Cancer. <i>Clinical and Translational Gastroenterology</i> , 2020, 11, e00269.	2.5	7
13	A unified simulation model for understanding the diversity of cancer evolution. <i>PeerJ</i> , 2020, 8, e8842.	2.0	6
14	Variant analysis of prostate cancer in Japanese patients and a new attempt to predict related biological pathways. <i>Oncology Reports</i> , 2020, 43, 943-952.	2.6	3
15	Novel oncogene 5MP1 reprograms c-Myc translation initiation to drive malignant phenotypes in colorectal cancer. <i>EBioMedicine</i> , 2019, 44, 387-402.	6.1	31
16	A clinical trial of somatic and germline analyses for healthy longevity in a postoperative cancer patient. <i>Surgery Today</i> , 2019, 49, 738-747.	1.5	0
17	Sensitivity analysis of agent-based simulation utilizing massively parallel computation and interactive data visualization. <i>PLoS ONE</i> , 2019, 14, e0210678.	2.5	12
18	Multiregion Genomic Analysis of Serially Transplanted Patient-derived Xenograft Tumors. <i>Cancer Genomics and Proteomics</i> , 2019, 16, 21-27.	2.0	13

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19	Understanding intratumor heterogeneity by combining genome analysis and mathematical modeling. <i>Cancer Science</i> , 2018, 109, 884-892.	3.9	49
20	Combined Mutation of <i>Apc</i> , <i>Kras</i> , and <i>Tgfr2</i> Effectively Drives Metastasis of Intestinal Cancer. <i>Cancer Research</i> , 2018, 78, 1334-1346.	0.9	106
21	Cancer evolution and heterogeneity. <i>Annals of Gastroenterological Surgery</i> , 2018, 2, 332-338.	2.4	19
22	Serial mutational tracking in surgically resected locally advanced colorectal cancer with neoadjuvant chemotherapy. <i>British Journal of Cancer</i> , 2018, 119, 419-423.	6.4	12
23	A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. <i>Nature Communications</i> , 2018, 9, 2884.	12.8	82
24	Neutral Theory in Cancer Cell Population Genetics. <i>Molecular Biology and Evolution</i> , 2018, 35, 1316-1321.	8.9	9
25	Palindromic amplification of the <i>ERBB2</i> oncogene in primary HER2-positive breast tumors. <i>Scientific Reports</i> , 2017, 7, 41921.	3.3	28
26	Personalized Management of Pancreatic Ductal Adenocarcinoma Patients through Computational Modeling. <i>Cancer Research</i> , 2017, 77, 3325-3335.	0.9	11
27	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
28	Impediment of Replication Forks by Long Non-coding RNA Provokes Chromosomal Rearrangements by Error-Prone Restart. <i>Cell Reports</i> , 2017, 21, 2223-2235.	6.4	13
29	Interaction-Based Feature Selection for Uncovering Cancer Driver Genes Through Copy Number-Driven Expression Level. <i>Journal of Computational Biology</i> , 2017, 24, 138-152.	1.6	3
30	phyC: Clustering cancer evolutionary trees. <i>PLoS Computational Biology</i> , 2017, 13, e1005509.	3.2	12
31	8q24 Polymorphisms and Diabetes Mellitus Regulate Apolipoprotein A-IV in Colorectal Carcinogenesis. <i>Annals of Surgical Oncology</i> , 2016, 23, 546-551.	1.5	5
32	Integrated Molecular Profiling of Human Gastric Cancer Identifies <i>DDR2</i> as a Potential Regulator of Peritoneal Dissemination. <i>Scientific Reports</i> , 2016, 6, 22371.	3.3	58
33	Genomic Landscape of Esophageal Squamous Cell Carcinoma in a Japanese Population. <i>Gastroenterology</i> , 2016, 150, 1171-1182.	1.3	265
34	A likelihood-free filtering method via approximate Bayesian computation in evaluating biological simulation models. <i>Computational Statistics and Data Analysis</i> , 2016, 94, 63-74.	1.2	2
35	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. <i>PLoS Genetics</i> , 2016, 12, e1005778.	3.5	134
36	Somatic mutations in plasma cell-free DNA are diagnostic markers for esophageal squamous cell carcinoma recurrence. <i>Oncotarget</i> , 2016, 7, 62280-62291.	1.8	62

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37	Mutational landscape and clonal architecture in grade II and III gliomas. <i>Nature Genetics</i> , 2015, 47, 458-468.	21.4	729
38	An Integrative Analysis to Identify Driver Genes in Esophageal Squamous Cell Carcinoma. <i>PLoS ONE</i> , 2015, 10, e0139808.	2.5	17
39	The landscape and clonal architecture in lower grade glioma.. <i>Journal of Clinical Oncology</i> , 2015, 33, 2008-2008.	1.6	0
40	A novel cell-cycle-indicator, mVenus-p27K ^Δ , identifies quiescent cells and visualizes G0→G1 transition. <i>Scientific Reports</i> , 2014, 4, 4012.	3.3	134
41	Overexpression of Cohesion Establishment Factor DSCC1 through E2F in Colorectal Cancer. <i>PLoS ONE</i> , 2014, 9, e85750.	2.5	21
42	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.	1.5	46
43	Integrated molecular analysis of clear-cell renal cell carcinoma. <i>Nature Genetics</i> , 2013, 45, 860-867.	21.4	955
44	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
45	Multilayer Cluster Heat Map Visualizing Biological Tensor Data. <i>Lecture Notes in Computer Science</i> , 2013, , 116-125.	1.3	2
46	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
47	A Novel Network Profiling Analysis Reveals System Changes in Epithelial-Mesenchymal Transition. <i>PLoS ONE</i> , 2011, 6, e20804.	2.5	38
48	Gene Set-Based Module Discovery Decodes cis-Regulatory Codes Governing Diverse Gene Expression across Human Multiple Tissues. <i>PLoS ONE</i> , 2010, 5, e10910.	2.5	2
49	A novel meta-analysis approach of cancer transcriptomes reveals prevailing transcriptional networks in cancer cells. <i>Genome Informatics</i> , 2010, 22, 121-31.	0.4	4
50	Gene set-based module discovery in the breast cancer transcriptome. <i>BMC Bioinformatics</i> , 2009, 10, 71.	2.6	28
51	Human homolog of NOTUM, overexpressed in hepatocellular carcinoma, is regulated transcriptionally by β -catenin/TCF. <i>Cancer Science</i> , 2008, 99, 1139-1146.	3.9	47
52	DKK1, a negative regulator of Wnt signaling, is a target of the β -catenin/TCF pathway. <i>Oncogene</i> , 2004, 23, 8520-8526.	5.9	497
53	USAG-1: a bone morphogenetic protein antagonist abundantly expressed in the kidney. <i>Biochemical and Biophysical Research Communications</i> , 2004, 316, 490-500.	2.1	135
54	Agent-Based Modeling and Analysis of Cancer Evolution. , 0, , .		0