

Genta Nagae

List of Publications by Year in descending order

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Version: 2024-02-01

95
papers

11,051
citations

109137

35
h-index

91712

69
g-index

101
all docs

101
docs citations

101
times ranked

21030
citing authors

#	ARTICLE	IF	CITATIONS
1	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
2	Landscape of genetic lesions in 944 patients with myelodysplastic syndromes. <i>Leukemia</i> , 2014, 28, 241-247.	3.3	1,291
3	Cohesin mediates transcriptional insulation by CCCTC-binding factor. <i>Nature</i> , 2008, 451, 796-801.	13.7	1,050
4	Integrated molecular analysis of clear-cell renal cell carcinoma. <i>Nature Genetics</i> , 2013, 45, 860-867.	9.4	955
5	Integrated molecular analysis of adult T cell leukemia/lymphoma. <i>Nature Genetics</i> , 2015, 47, 1304-1315.	9.4	659
6	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. <i>Nature Genetics</i> , 2014, 46, 1267-1273.	9.4	655
7	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. <i>Nature Genetics</i> , 2016, 48, 500-509.	9.4	596
8	Methionine Metabolism Regulates Maintenance and Differentiation of Human Pluripotent Stem Cells. <i>Cell Metabolism</i> , 2014, 19, 780-794.	7.2	421
9	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. <i>Nature Genetics</i> , 2013, 45, 1232-1237.	9.4	334
10	Loss of 5-hydroxymethylcytosine is accompanied with malignant cellular transformation. <i>Cancer Science</i> , 2012, 103, 670-676.	1.7	241
11	Three DNA Methylation Epigenotypes in Human Colorectal Cancer. <i>Clinical Cancer Research</i> , 2010, 16, 21-33.	3.2	207
12	Classification of Epstein-Barr Virus-Positive Gastric Cancers by Definition of DNA Methylation Epigenotypes. <i>Cancer Research</i> , 2011, 71, 7187-7197.	0.4	200
13	Concurrent loss of <i>Ezh2</i> and <i>Tet2</i> cooperates in the pathogenesis of myelodysplastic disorders. <i>Journal of Experimental Medicine</i> , 2013, 210, 2627-2639.	4.2	162
14	H3F3A K27M mutations in thalamic gliomas from young adult patients. <i>Neuro-Oncology</i> , 2014, 16, 140-146.	0.6	151
15	Integrated genetic and epigenetic analysis defines novel molecular subgroups in rhabdomyosarcoma. <i>Nature Communications</i> , 2015, 6, 7557.	5.8	149
16	Generation of induced pluripotent stem cells from primary chronic myelogenous leukemia patient samples. <i>Blood</i> , 2012, 119, 6234-6242.	0.6	143
17	The oncogenic mutation in the pleckstrin homology domain of AKT1 in endometrial carcinomas. <i>British Journal of Cancer</i> , 2009, 101, 145-148.	2.9	141
18	Integrated Multiregional Analysis Proposing a New Model of Colorectal Cancer Evolution. <i>PLoS Genetics</i> , 2016, 12, e1005778.	1.5	134

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19	Whole-exome sequencing of human pancreatic cancers and characterization of genomic instability caused by <i>MLH1</i> haploinsufficiency and complete deficiency. <i>Genome Research</i> , 2012, 22, 208-219.	2.4	107
20	Identification of genes preferentially methylated in hepatitis C virus-related hepatocellular carcinoma. <i>Cancer Science</i> , 2010, 101, 1501-1510.	1.7	99
21	Two distinct modes of DNMT1 recruitment ensure stable maintenance DNA methylation. <i>Nature Communications</i> , 2020, 11, 1222.	5.8	82
22	Integrated molecular profiling of juvenile myelomonocytic leukemia. <i>Blood</i> , 2018, 131, 1576-1586.	0.6	78
23	Reduced TET2 function leads to T-cell lymphoma with follicular helper T-cell-like features in mice. <i>Blood Cancer Journal</i> , 2014, 4, e264-e264.	2.8	76
24	Tissue-specific demethylation in CpG-poor promoters during cellular differentiation. <i>Human Molecular Genetics</i> , 2011, 20, 2710-2721.	1.4	66
25	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. <i>Cancer Cell</i> , 2021, 39, 793-809.e8.	7.7	65
26	Activation of Bmp2-Smad1 Signal and Its Regulation by Coordinated Alteration of H3K27 Trimethylation in Ras-Induced Senescence. <i>PLoS Genetics</i> , 2011, 7, e1002359.	1.5	59
27	High-resolution mapping of DNA methylation in human genome using oligonucleotide tiling array. <i>Human Genetics</i> , 2006, 120, 701-711.	1.8	56
28	Reduced Neoantigen Expression Revealed by Longitudinal Multiomics as a Possible Immune Evasion Mechanism in Glioma. <i>Cancer Immunology Research</i> , 2019, 7, 1148-1161.	1.6	56
29	Methylation screening of reciprocal genome-wide UPDs identifies novel human-specific imprinted genes. <i>Human Molecular Genetics</i> , 2011, 20, 3188-3197.	1.4	55
30	Fusion Kinases Identified by Genomic Analyses of Sporadic Microsatellite Instability-High Colorectal Cancers. <i>Clinical Cancer Research</i> , 2019, 25, 378-389.	3.2	49
31	Genetic and epigenetic basis of hepatoblastoma diversity. <i>Nature Communications</i> , 2021, 12, 5423.	5.8	49
32	Genetic and epigenetic stability of oligodendrogliomas at recurrence. <i>Acta Neuropathologica Communications</i> , 2017, 5, 18.	2.4	47
33	DNA Methylation Profiling of Embryonic Stem Cell Differentiation into the Three Germ Layers. <i>PLoS ONE</i> , 2011, 6, e26052.	1.1	41
34	Histone demethylase KDM4C regulates sphere formation by mediating the cross talk between Wnt and Notch pathways in colonic cancer cells. <i>Carcinogenesis</i> , 2013, 34, 2380-2388.	1.3	40
35	Distinct molecular profile of diffuse cerebellar gliomas. <i>Acta Neuropathologica</i> , 2017, 134, 941-956.	3.9	40
36	Long-term outcomes for patients with solitary hepatocellular carcinoma treated by laparoscopic microwave coagulation. <i>Cancer</i> , 2005, 103, 985-993.	2.0	35

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37	The Role of NF- κ B Signaling in the Maintenance of Pluripotency of Human Induced Pluripotent Stem Cells. PLoS ONE, 2013, 8, e56399.	1.1	34
38	Concurrent Activation of Acetylation and Tri-Methylation of H3K27 in a Subset of Hepatocellular Carcinoma with Aggressive Behavior. PLoS ONE, 2014, 9, e91330.	1.1	34
39	Comprehensive epigenome characterization reveals diverse transcriptional regulation across human vascular endothelial cells. Epigenetics and Chromatin, 2019, 12, 77.	1.8	34
40	DNA demethylation is associated with malignant progression of lower-grade gliomas. Scientific Reports, 2019, 9, 1903.	1.6	31
41	Defined lifestyle and germline factors predispose Asian populations to gastric cancer. Science Advances, 2020, 6, eaav9778.	4.7	31
42	Age-Dependent Decrease of DNA Hydroxymethylation in Human T Cells. Journal of Clinical and Experimental Hematopathology: JCEH, 2015, 55, 1-6.	0.3	25
43	Impact of AAV2 and Hepatitis B Virus Integration Into Genome on Development of Hepatocellular Carcinoma in Patients with Prior Hepatitis B Virus Infection. Clinical Cancer Research, 2019, 25, 6217-6227.	3.2	24
44	Prognostic significance of CpG island methylator phenotype in surgically resected small cell lung carcinoma. Cancer Science, 2016, 107, 320-325.	1.7	22
45	Base-Resolution Analysis of 5-Hydroxymethylcytosine by One-Pot Bisulfite-Free Chemical Conversion with Peroxotungstate. Journal of the American Chemical Society, 2016, 138, 14178-14181.	6.6	21
46	A novel sensitive detection method for DNA methylation in circulating free DNA of pancreatic cancer. PLoS ONE, 2020, 15, e0233782.	1.1	21
47	BRCC3 mutations in myeloid neoplasms. Haematologica, 2015, 100, 1051-7.	1.7	20
48	Hes1 promotes blast crisis in chronic myelogenous leukemia through MMP-9 upregulation in leukemic cells. Blood, 2014, 123, 3932-3942.	0.6	18
49	Accumulation of Molecular Aberrations Distinctive to Hepatocellular Carcinoma Progression. Cancer Research, 2020, 80, 3810-3819.	0.4	18
50	TET1 upregulation drives cancer cell growth through aberrant enhancer hydroxymethylation of HMGA2 in hepatocellular carcinoma. Cancer Science, 2021, 112, 2855-2869.	1.7	18
51	Transduced caudal-type homeobox (<sc>CDX</sc>) 2/<sc>CDX</sc>1 can induce growth inhibition on <sc>CDX</sc>-deficient gastric cancer by rapid intestinal differentiation. Cancer Science, 2018, 109, 3853-3864.	1.7	17
52	Differential regulation of CpG island methylation within divergent and unidirectional promoters in colorectal cancer. Cancer Science, 2019, 110, 1096-1104.	1.7	16
53	Landscape Of Genetic Lesions In 944 Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 521-521.	0.6	14
54	Laparoscopic radiofrequency ablation of hepatocellular carcinoma in the caudate lobe by using a new laparoscopic US probe with a forward-viewing convex-array transducer. Gastrointestinal Endoscopy, 2004, 60, 628-631.	0.5	12

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55	Aberrant DNA methylation of pregnane X receptor underlies metabolic gene alterations in the diabetic kidney. <i>American Journal of Physiology - Renal Physiology</i> , 2018, 314, F551-F560.	1.3	12
56	Reply: Somatic mutations are present in all members of the AKT family in endometrial carcinoma. <i>British Journal of Cancer</i> , 2009, 101, 1220-1221.	2.9	11
57	Spatial and temporal expansion of intrahepatic metastasis by molecularly defined clonality in multiple liver cancers. <i>Cancer Science</i> , 2020, 111, 601-609.	1.7	11
58	DNA-friendly Cu(II)/TEMPO-catalyzed 5-hydroxymethylcytosine-specific oxidation. <i>Chemical Communications</i> , 2017, 53, 5756-5759.	2.2	10
59	Genome-wide analysis of DNA methylation identifies the apoptosis-related gene <i>UQCRH</i> as a tumor suppressor in renal cancer. <i>Molecular Oncology</i> , 2022, 16, 732-749.	2.1	9
60	An Excess of CYP24A1, Lack of CaSR, and a Novel lncRNA Near the PTH Gene Characterize an Ectopic PTH-Producing Tumor. <i>Journal of the Endocrine Society</i> , 2017, 1, 691-711.	0.1	5
61	LAPAROSCOPIC ABLATION THERAPY FOR HEPATOCELLULAR CARCINOMA. <i>Digestive Endoscopy</i> , 2005, 17, 1-8.	1.3	3
62	FREQUENT H3F3A K27M MUTATIONS IN THALAMIC GLIOMAS FROM YOUNG ADULT PATIENTS. <i>Neuro-Oncology</i> , 2014, 16, iii9-iii10.	0.6	2
63	Base-resolution analysis of 5-hydroxymethylcytosine by selective oxidation and reverse transcription arrest. <i>Organic and Biomolecular Chemistry</i> , 2021, 19, 6478-6486.	1.5	1
64	Hypermethylation of Bcl6 Is a Potential Cause of Development of Lymphoma with Tfh Features in Tet2 Knockdown Mice. <i>Blood</i> , 2013, 122, 2490-2490.	0.6	1
65	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. <i>Blood</i> , 2014, 124, 75-75.	0.6	1
66	Two Novel Distinct Subtypes of Myeloid Neoplasms Molecularly Associated with Histone H3K36 Methylations. <i>Blood</i> , 2015, 126, 2841-2841.	0.6	1
67	Recurrent Mutations of Multiple Components of Cohesin Complex in Myeloid Neoplasms. <i>Blood</i> , 2012, 120, 782-782.	0.6	1
68	EG-13 * GENOME-WIDE METHYLATION ANALYSIS IDENTIFIES GENOMIC DNA DEMETHYLATION DURING MALIGNANT PROGRESSION OF GLIOMAS. <i>Neuro-Oncology</i> , 2014, 16, v77-v77.	0.6	0
69	GENT-23. MOLECULAR PATHOLOGICAL ANALYSIS ON IDH-WILDTYPE ADULT LOW-GRADE GLIOMAS. <i>Neuro-Oncology</i> , 2016, 18, vi78-vi79.	0.6	0
70	GENE-10. CHARACTERISTIC MOLECULAR PROFILE CHANGES IN PRIMARY AND RECURRENT GLIOMAS DEPENDING ON THEIR HISTOPATHOLOGY. <i>Neuro-Oncology</i> , 2017, 19, vi94-vi94.	0.6	0
71	IMMU-58. REDUCED NEOANTIGEN EXPRESSION AS A POSSIBLE IMMUNE EVASION MECHANISM DURING GLIOMA PROGRESSION. <i>Neuro-Oncology</i> , 2018, 20, vi134-vi134.	0.6	0
72	Successful treatment with hemodiafiltration for a chronic renal failure patient with hyperchloremic metabolic acidosis associated with hepatic coma. <i>Nihon Toseki Igakkai Zasshi</i> , 2004, 37, 1809-1813.	0.2	0

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73	Abstract 4930: Integrative analysis of genome-wide methylation and expression profiles for metastatic colorectal cancer. , 2012, , .		0
74	Abstract 4602: Recurrent pathway mutations of multiple components of cohesin complex in myeloid neoplasms.. , 2013, , .		0
75	Abstract 3184: Integrative analysis of clear cell renal cell carcinoma.. , 2013, , .		0
76	Abstract 4020: Genome-wide analysis of stepwise hepatocarcinogenesis using next generation sequencer.. , 2013, , .		0
77	Modeling Chronic Myelomonocytic Leukemia Through Patient-Derived Induced Pluripotent Stem Cells. Blood, 2013, 122, 864-864.	0.6	0
78	Abstract 1356: FrequentH3F3AK27M mutations in thalamic gliomas from young adult patients. , 2014, , .		0
79	Abstract 482: Integrated genetic and epigenetic analysis defines novel molecular clusters in rhabdomyosarcoma. , 2015, , .		0
80	Abstract 958: Early hepatocellular carcinoma as another entity from classical hepatocellular carcinoma by integrated genomic analysis. , 2015, , .		0
81	Abstract 1072: DNA methylation profile analysis of gliomas revealed a change in methylation status during malignant progression. , 2015, , .		0
82	Abstract A1-30: Integrated genomic analysis identified sequential molecular aberrations in stepwise progression from early to classical hepatocellular carcinomas. , 2015, , .		0
83	Landscape of DNA Methylation and Genetic Profiles in 291 Patients with Myelodysplastic Syndromes. Blood, 2015, 126, 5205-5205.	0.6	0
84	Myelodysplastic Syndrome Patients Show Mutation-Specific DNA Methylation Patterns. Blood, 2015, 126, 1646-1646.	0.6	0
85	Abstract 163: Genetic difference between multicentric carcinogenesis and intrahepatic metastasis of hepatocellular carcinoma. , 2016, , .		0
86	Abstract 4448: Development of DNA methylation biomarkers for pancreatic cancer diagnosis. , 2016, , .		0
87	Genetic difference between multicentric carcinogenesis and intrahepatic metastasis of multiple hepatocellular carcinoma.. Journal of Clinical Oncology, 2017, 35, 307-307.	0.8	0
88	Abstract 4392: Genetic diagnosis of multiple hepatocellular carcinoma. , 2017, , .		0
89	Abstract 4879: Genomic and epigenomic profiling of high-stage neuroblastoma. , 2017, , .		0
90	Abstract 3394: Actionable fusion kinases in microsatellite instability-high colorectal cancers. , 2018, , .		0

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91	Abstract 3429: Genome and epigenome profiling of high stage neuroblastoma. , 2018, , .		0
92	Abstract 3331: Development of a sensitive method to detect aberrant DNA methylation in cfDNA for pancreas cancer diagnosis. , 2018, , .		0
93	Abstract 416: Impact of virus integration into the genomes of hepatocellular carcinoma patients with prior hepatitis B virus infection. , 2018, , .		0
94	DNA Methylation and Genetic Profiles in 320 Patients with Myelodysplastic Syndromes. Blood, 2018, 132, 1799-1799.	0.6	0
95	EPEN-27. Epigenetic dissection of spinal ependymomas (SP-EPN) separates tumors with and without <i>NF2</i> mutation. Neuro-Oncology, 2022, 24, i44-i45.	0.6	0