Hiromichi Suzuki

List of Publications by Year
in descending order

63	7,911	136740	155451
papers	citations	32 h-index	55 g-index

67	67	67	14334
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrated molecular analysis of clear-cell renal cell carcinoma. Nature Genetics, 2013, 45, 860-867.	9.4	955
2	Mutational landscape and clonal architecture in grade II and III gliomas. Nature Genetics, 2015, 47, 458-468.	9.4	729
3	Integrated molecular analysis of adult T cell leukemia/lymphoma. Nature Genetics, 2015, 47, 1304-1315.	9.4	659
4	Aberrant PD-L1 expression through 3â€²-UTR disruption in multiple cancers. Nature, 2016, 534, 402-406.	13.7	536
5	Somatic Mutations and Clonal Hematopoiesis in Aplastic Anemia. New England Journal of Medicine, 2015, 373, 35-47.	13.9	508
6	Age-related remodelling of oesophageal epithelia by mutated cancer drivers. Nature, 2019, 565, 312-317.	13.7	476
7	Dynamics of clonal evolution in myelodysplastic syndromes. Nature Genetics, 2017, 49, 204-212.	9.4	348
8	The landscape of somatic mutations in Down syndromeâ€“related myeloid disorders. Nature Genetics, 2013, 45, 1293-1299.	9.4	324
9	Longitudinal molecular trajectories of diffuse glioma in adults. Nature, 2019, 576, 112-120.	13.7	320
10	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. Nature, 2019, 572, 67-73.	13.7	293
11	Genetic abnormalities in myelodysplasia and secondary acute myeloid leukemia: impact on outcome of stem cell transplantation. Blood, 2017, 129, 2347-2358.	0.6	268
12	Genomic Landscape of Esophageal Squamous Cell Carcinoma inÂa Japanese Population. Gastroenterology, 2016, 150, 1171-1182.	0.6	265
13	Prognostic relevance of genetic alterations in diffuse lower-grade gliomas. Neuro-Oncology, 2018, 20, 66-77.	0.6	225
14	Recurrent somatic mutations underlie corticotropin-independent Cushingâ€™s syndrome. Science, 2014, 344, 917-920.	6.0	177
15	Glioma progression is shaped by genetic evolution and microenvironment interactions. Cell, 2022, 185, 2184-2199.e16.	13.5	163
16	Aberrant splicing and defective mRNA production induced by somatic spliceosome mutations in myelodysplasia. Nature Communications, 2018, 9, 3649.	5.8	140
17	Recurrent noncoding U1ÂsnRNA mutations drive cryptic splicing in SHH medulloblastoma. Nature, 2019, 574, 707-711.	13.7	129
18	The U1 spliceosomal RNA is recurrently mutated in multiple cancers. Nature, 2019, 574, 712-716.	13.7	128

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19	Prognostic relevance of integrated genetic profiling in adult T-cell leukemia/lymphoma. Blood, 2018, 131, 215-225.	0.6	124
20	Î±4Î²1- and Î±6Î²1-integrins are functional receptors for midkine, a heparin-binding growth factor. Journal of Cell Science, 2004, 117, 5405-5415.	1.2	110
21	Recurrent SPI1 (PU.1) fusions in high-risk pediatric T cell acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1274-1281.	9.4	100
22	Variegated RHOA mutations in adult T-cell leukemia/lymphoma. Blood, 2016, 127, 596-604.	0.6	98
23	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. Cell, 2020, 183, 1617-1633.e22.	13.5	93
24	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. Cell, 2020, 181, 1329-1345.e24.	13.5	79
25	Frequent germline mutations of HAVCR2 in sporadic subcutaneous panniculitis-like T-cell lymphoma. Blood Advances, 2019, 3, 588-595.	2.5	73
26	Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer Cell, 2021, 39, 793-809.e8.	7.7	65
27	Gene expression and risk of leukemic transformation in myelodysplasia. Blood, 2017, 130, 2642-2653.	0.6	64
28	Invariant patterns of clonal succession determine specific clinical features of myelodysplastic syndromes. Nature Communications, 2019, 10, 5386.	5.8	53
29	DDX3X Suppresses the Susceptibility of Hindbrain Lineages to Medulloblastoma. Developmental Cell, 2020, 54, 455-470.e5.	3.1	47
30	The transcriptional landscape of Shh medulloblastoma. Nature Communications, 2021, 12, 1749.	5.8	47
31	Significance of perivascular tumour cells defined by CD109 expression in progression of glioma. Journal of Pathology, 2017, 243, 468-480.	2.1	36
32	Integrated multiomics analysis of hepatoblastoma unravels its heterogeneity and provides novel druggable targets. Npj Precision Oncology, 2020, 4, 20.	2.3	30
33	Integrated Molecular Characterization of the Lethal Pediatric Cancer Pancreatoblastoma. Cancer Research, 2018, 78, 865-876.	0.4	25
34	Identification of the genetic and clinical characteristics of neuroblastomas using genome-wide analysis. Oncotarget, 2017, 8, 107513-107529.	0.8	23
35	A novel all-in-one intraoperative genotyping system for IDH1-mutant glioma. Brain Tumor Pathology, 2017, 34, 91-97.	1.1	16
36	Immunohistochemical ATRX expression is not a surrogate for 1p19q codeletion. Brain Tumor Pathology, 2018, 35, 106-113.	1.1	16

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37	Integrated genetic and epigenetic analysis revealed heterogeneity of acute lymphoblastic leukemia in Down syndrome. Cancer Science, 2019, 110, 3358-3367.	1.7	15
38	DNA methylation-based classification reveals difference between pediatric T-cell acute lymphoblastic leukemia and normal thymocytes. Leukemia, 2020, 34, 1163-1168.	3.3	14
39	The landscape of genetic aberrations in myxofibrosarcoma. International Journal of Cancer, 2022, 151, 565-577.	2.3	13
40	An immuno-wall microdevice exhibits rapid and sensitive detection of IDH1-R132H mutation specific to grade II and III gliomas. Science and Technology of Advanced Materials, 2016, 17, 618-625.	2.8	12
41	Identification of a novel fusion gene HMGA2â€EGFR in glioblastoma. International Journal of Cancer, 2018, 142, 1627-1639.	2.3	12
42	Association of high-risk neuroblastoma classification based on expression profiles with differentiation and metabolism. PLoS ONE, 2021, 16, e0245526.	1.1	11
43	Comprehensive genetic analysis of pediatric germ cell tumors identifies potential drug targets. Communications Biology, 2020, 3, 544.	2.0	9
44	Olig2 labeling index is correlated with histological and molecular classifications in low-grade diffuse gliomas. Journal of Neuro-Oncology, 2014, 120, 283-291.	1.4	7
45	Mathematical Modeling and Mutational Analysis Reveal Optimal Therapy to Prevent Malignant Transformation in Grade II IDH-Mutant Gliomas. Cancer Research, 2021, 81, 4861-4873.	0.4	7
46	Rapid sensitive analysis ofIDH1mutation in lower-grade gliomas by automated genetic typing involving a quenching probe. Cancer Investigation, 2016, 34, 12-15.	0.6	6
47	Pathogenic Epigenetic Consequences of Genetic Alterations in IDH-Wild-Type Diffuse Astrocytic Gliomas. Cancer Research, 2019, 79, 4814-4827.	0.4	6
48	Chronological Analysis of Clonal Evolution in Acquired Aplastic Anemia. Blood, 2014, 124, 253-253.	0.6	4
49	Clinical Application of Comprehensive Genomic Profiling Tests for Diffuse Gliomas. Cancers, 2022, 14, 2454.	1.7	3
50	Transposase-driven rearrangements in human tumors. Nature Genetics, 2017, 49, 975-977.	9.4	1
51	IMMU-03. TUMOR NECROSIS FACTOR OVERCOMES IMMUNE EVASION IN P53-MUTANT MEDULLOBLASTOMA. Neuro-Oncology, 2019, 21, ii93-ii93.	0.6	1
52	Landscape of Genetic Alterations in Adult T-Cell Leukemia/Lymphoma. Blood, 2014, 124, 75-75.	0.6	1
53	MBRS-14. REGULATION OF MEDULLOBLASTOMA IMMUNOGENICITY BY TP53 AND TNF ALPHA. Neuro-Oncology, 2018, 20, i131-i131.	0.6	0
54	MEDU-39. HIGHLY RECURRENT U1 SMALL NUCLEAR RNA HOTSPOT MUTATIONS DRIVE ALTERNATIVE SPLICING IN SONIC HEDGEHOG MEDULLOBLASTOMA. Neuro-Oncology, 2019, 21, ii111-ii111.	0.6	0

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55	Invariant Patterns of Clonal Succession Determines Specific Phenotypic and Clinical Features of Myelodysplastic Syndromes (MDS). Blood, 2018, 132, 104-104.	0.6	0
56	Novel and Significant Impact of Germline Variants Predisposed to Pathogenic Somatic Mutations and Loss of Heterozygosity (LOH) in Myelodysplastic Syndromes (MDS) and Clonal Hematopoiesis of Indeterminate Potential (CHIP). Blood, 2018, 132, 108-108.	0.6	0
57	Abstract 3403: Genetic analysis of pheochromocytoma. , 2019, , .		0
58	Abstract 3405: Integrated analysis of urothelial carcinoma. , 2019, , .		0
59	Abstract 3322: Chronology and risk-dependence of age-related remodelling of oesophageal epithelia. , 2019, , .		0
60	Abstract 738: Myxofibrosarcoma is characterized by frequent abnormalities in TP53 and increased genetic instability. , 2019, , .		0
61	The U1 Spliceosomal RNA: A Novel Non-Coding Hotspot Driver Mutation Independently Associated with Clinical Outcome in Chronic Lymphocytic Leukemia. Blood, 2019, 134, 847-847.	0.6	0
62	Abstract 1309: Distinct molecular subtypes and a high diagnostic urinary biomarker of upper urinary tract urothelial carcinoma. , 2020, , .		0
63	Abstract 225: Frequent abnormalities in TP53 and increased genetic instability in myxofibrosarcoma. , 2020, , .		0