Yasuhito Arai

List of Publications by Year
in descending order

66	7,656	117625	106344
papers	citations	34 h-index	65 g-index

67	67	67	11566
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of novel SSX1 fusions in synovial sarcoma. Modern Pathology, 2022, 35, 228-239.	5.5	15
2	Comprehensive Genomic Profiling of Neuroendocrine Carcinomas of the Gastrointestinal System. Cancer Discovery, 2022, 12, 692-711.	9.4	58
3	Co-expression of ERG and CD31 in a subset of CIC-rearranged sarcoma: a potential diagnostic pitfall. Modern Pathology, 2022, 35, 1439-1448.	5.5	10
4	Diffusely infiltrating glioma with CREBBPâ€“BCORL1 fusion showing overexpression of not only BCORL1 but BCOR: A case report. Brain Tumor Pathology, 2022, 39, 171-178.	1.7	5
5	Ependymoma with C11orf95-MAML2 fusion: presenting with granular cell and ganglion cell features. Brain Tumor Pathology, 2021, 38, 64-70.	1.7	11
6	E74-Like Factor 3 Is a Key Regulator of Epithelial Integrity and Immune Response Genes in Biliary Tract Cancer. Cancer Research, 2021, 81, 489-500.	0.9	16
7	Molecular detection and clinicopathological characteristics of advanced/recurrent biliary tract carcinomas harboring the FGFR2 rearrangements: a prospective observational study (PRELUDE Study). Journal of Gastroenterology, 2021, 56, 250-260.	5.1	31
8	Vaginal Transmission of Cancer from Mothers with Cervical Cancer to Infants. New England Journal of Medicine, 2021, 384, 42-50.	27.0	40
9	Ependymomaâ€like tumor with mesenchymal differentiation harboring C11orf95â€NCOA1/2 or â€RELA fusion: A hitherto unclassified tumor related to ependymoma. Brain Pathology, 2021, 31, e12943.	4.1	16
10	Frequent breakpoints of focal deletion and uniparental disomy in 22q11.1 or 11.2 segmental duplication region reveal distinct tumorigenesis in rhabdoid tumor of the kidney. Genes Chromosomes and Cancer, 2021, 60, 546-558.	2.8	0
11	Single-cell DNA and RNA sequencing reveals the dynamics of intra-tumor heterogeneity in a colorectal cancer model. BMC Biology, 2021, 19, 207.	3.8	18
12	Sarcoma with MGAâ€“NUTM1 fusion in the lung: an emerging entity. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2020, 476, 317-322.	2.8	12
13	Expanding the clinicopathologic and molecular spectrum of BCORâ€associated sarcomas in adults. Histopathology, 2020, 76, 509-520.	2.9	38
14	The potential application of PD-1 blockade therapy for early-stage biliary tract cancer. International Immunology, 2020, 32, 273-281.	4.0	10
15	Primary spinal intramedullary Ewing-like sarcoma harboring CIC-DUX4 translocation: a similar cytological appearance as its soft tissue counterpart but no lobulation in association with desmoplastic stroma. Brain Tumor Pathology, 2020, 37, 111-117.	1.7	13
16	KMT2A (MLL) fusions in aggressive sarcomas in young adults. Histopathology, 2019, 75, 508-516.	2.9	22
17	Combined Genetic and Chromosomal Characterization of Wilms Tumors Identifies Chromosome 12 Gain as a Potential New Marker Predicting a Favorable Outcome. Neoplasia, 2019, 21, 117-131.	5.3	9
18	Epigenetic landscape influences the liver cancer genome architecture. Nature Communications, 2018, 9, 1643.	12.8	39

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19	Molecular genomic landscapes of hepatobiliary cancer. Cancer Science, 2018, 109, 1282-1291.	3.9	43
20	A computational tool to detect DNA alterations tailored to formalin-fixed paraffin-embedded samples in cancer clinical sequencing. Genome Medicine, 2018, 10, 44.	8.2	37
21	Integrated genetic and epigenetic analysis of myxofibrosarcoma. Nature Communications, 2018, 9, 2765.	12.8	54
22	NUTM2A-CIC fusion small round cell sarcoma: a genetically distinct variant of CIC-rearranged sarcoma. Human Pathology, 2017, 65, 225-230.	2.0	56
23	<scp>CIC</scp> breakâ€apart fluorescence inâ€situ hybridization misses a subset of <scp>CIC</scp>â€“<scp>DUX</scp>4 sarcomas: a clinicopathological and molecular study. Histopathology, 2017, 71, 461-469.	2.9	56
24	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. Cancer Discovery, 2017, 7, 1116-1135.	9.4	637
25	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. Nature Genetics, 2016, 48, 500-509.	21.4	596
26	Genomic Sequencing Identifies ELF3 as a Driver of Ampullary Carcinoma. Cancer Cell, 2016, 29, 229-240.	16.8	147
27	Heat Shock Protein 90 Is a Potential Therapeutic Target in Cholangiocarcinoma. Molecular Cancer Therapeutics, 2015, 14, 1985-1993.	4.1	24
28	Genomic spectra of biliary tract cancer. Nature Genetics, 2015, 47, 1003-1010.	21.4	907
29	A Novel CIC-FOXO4 Gene Fusion in Undifferentiated Small Round Cell Sarcoma. American Journal of Surgical Pathology, 2014, 38, 1571-1576.	3.7	147
30	Fibroblast growth factor receptor 2 tyrosine kinase fusions define a unique molecular subtype of cholangiocarcinoma. Hepatology, 2014, 59, 1427-1434.	7.3	420
31	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. Nature Genetics, 2014, 46, 1267-1273.	21.4	655
32	Unique mutation portraits and frequent COL2A1 gene alteration in chondrosarcoma. Genome Research, 2014, 24, 1411-1420.	5.5	85
33	Immunohistochemical detection of ROS1 is useful for identifying ROS1 rearrangements in lung cancers. Modern Pathology, 2014, 27, 711-720.	5.5	137
34	Meiosis error and subsequent genetic and epigenetic alterations invoke the malignant transformation of germ cell tumor. Genes Chromosomes and Cancer, 2013, 52, 274-286.	2.8	8
35	ROS1-Rearranged Lung Cancer. American Journal of Surgical Pathology, 2013, 37, 554-562.	3.7	155
36	Mouse Model for ROS1-Rearranged Lung Cancer. PLoS ONE, 2013, 8, e56010.	2.5	54

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37	Whole-genome sequencing of liver cancers identifies etiological influences on mutation patterns and recurrent mutations in chromatin regulators. Nature Genetics, 2012, 44, 760-764.	21.4	781
38	KIF5B-RET fusions in lung adenocarcinoma. Nature Medicine, 2012, 18, 375-377.	30.7	753
39	Methylation of the RASSF1A promoter is predictive of poor outcome among patients with Wilms tumor. Pediatric Blood and Cancer, 2012, 59, 499-505.	1.5	19
40	Different incidences of epigenetic but not genetic abnormalities between <scp>W</scp>ilms tumors in <scp>J</scp>apanese and <scp>C</scp>aucasian children. Cancer Science, 2012, 103, 1129-1135.	3.9	23
41	High-resolution characterization of a hepatocellular carcinoma genome. Nature Genetics, 2011, 43, 464-469.	21.4	265
42	Association of germline or somatic TP53 missense mutation with oncogene amplification in tumors developed in patients with Liâ€Fraumeni or Liâ€Fraumeniâ€like syndrome. Genes Chromosomes and Cancer, 2011, 50, 535-545.	2.8	15
43	Genomeâ€wide analysis of allelic imbalances reveals 4q deletions as a poor prognostic factor and MDM4 amplification at 1q32.1 in hepatoblastoma. Genes Chromosomes and Cancer, 2010, 49, 596-609.	2.8	42
44	Resequencing and copy number analysis of the human tyrosine kinase gene family in poorly differentiated gastric cancer. Carcinogenesis, 2009, 30, 1857-1864.	2.8	38
45	KrÃ¼ppelâ€like factor 12 plays a significant role in poorly differentiated gastric cancer progression. International Journal of Cancer, 2009, 125, 1859-1867.	5.1	64
46	Alteration of enhancer of polycomb 1 at 10p11.2 is one of the genetic events leading to development of adult Tâ€cell leukemia/lymphoma. Genes Chromosomes and Cancer, 2009, 48, 768-776.	2.8	25
47	Two candidate tumor suppressor genes, MEOX2 and SOSTDC1, identified in a 7p21 homozygous deletion region in a Wilms tumor. Genes Chromosomes and Cancer, 2009, 48, 1037-1050.	2.8	31
48	Yolk sac tumor but not seminoma or teratoma is associated with abnormal epigenetic reprogramming pathway and shows frequent hypermethylation of various tumor suppressor genes. Cancer Science, 2009, 100, 698-708.	3.9	30
49	Resequencing Analysis of the Human Tyrosine Kinase Gene Family in Pancreatic Cancer. Pancreas, 2009, 38, e200-e206.	1.1	18
50	Duplication of paternal IGF2 or loss of maternal IGF2 imprinting occurs in half of Wilms tumors with various structural WT1 abnormalities. Genes Chromosomes and Cancer, 2008, 47, 712-727.	2.8	45
51	Loss of imprinting of IGF2 correlates with hypermethylation of the H19 differentially methylated region in hepatoblastoma. British Journal of Cancer, 2008, 99, 1891-1899.	6.4	92
52	Clonal and Parallel Evolution of Primary Lung Cancers and Their Metastases Revealed by Molecular Dissection of Cancer Cells. Clinical Cancer Research, 2007, 13, 111-120.	7.0	34
53	Clonality and heterogeneity of pulmonary blastoma from the viewpoint of genetic alterations: A case report. Lung Cancer, 2007, 57, 103-108.	2.0	24
54	Homozygous deletion scanning of the lung cancer genome at a 100â€kb resolution. Genes Chromosomes and Cancer, 2007, 46, 1000-1010.	2.8	63

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55	Identification of chromosome arm 9p as the most frequent target of homozygous deletions in lung cancer. Genes Chromosomes and Cancer, 2005, 44, 405-414.	2.8	81
56	Automated Steering Control Design by Visual Feedback Approach-System Identification and Control Experiments with a Radio-Controlled Car-. IEEJ Transactions on Industry Applications, 2003, 123, 628-633.	0.2	4
57	A BAC-Based STS-Content Map Spanning a 35-Mb Region of Human Chromosome 1p35â€“p36. Genomics, 2001, 74, 55-70.	2.9	153
58	Involvement of the NUP98 Gene in a Chromosomal Translocation t(11;20)(p15;q11.2) in a Patient With Acute Monocytic Leukemia (FAB-M5b). International Journal of Hematology, 2001, 74, 53-57.	1.6	4
59	Fusion of the Nucleoporin Gene, NUP98, and the Putative RNA Helicase Gene, DDX10, by Inversion 11 (p15q22) Chromosome Translocation in a Patient with Etoposide-related Myelodysplastic Syndrome.. Internal Medicine, 2000, 39, 412-415.	0.7	22
60	Generation of the NUP98-HOXD13 fusion transcript by a rare translocation, t(2;11)(q31;p15), in a case of infant leukaemia. British Journal of Haematology, 2000, 110, 210-213.	2.5	23
61	A 2-Mb Sequence-Ready Contig Map and a Novel Immunoglobulin Superfamily Gene IGSF4 in the LOH Region of Chromosome 11q23.2. Genomics, 1999, 62, 139-146.	2.9	108
62	The inv(11)(p15q22) Chromosome Translocation of De Novo and Therapy-Related Myeloid Malignancies Results in Fusion of the Nucleoporin Gene, NUP98, With the Putative RNA Helicase Gene, DDX10. Blood, 1997, 89, 3936-3944.	1.4	152
63	A complete Not I restriction map covering the entire long arm of human chromosome 11. Genes To Cells, 1997, 2, 345-357.	1.2	12
64	Inversion of chromosome 11, inv(11)(p15q22), as a recurring chromosomal aberration associated with de novo and secondary myeloid malignancies: Identification of a P1 clone spanning the 11q22 breakpoint. Genes Chromosomes and Cancer, 1997, 19, 150-155.	2.8	19
65	A Yeast Artificial Chromosome Contig andNotI Restriction Map That Spans the Tumor Suppressor Gene(s) Locus, 11q22.2â€“q23.3. Genomics, 1996, 35, 196-206.	2.9	43
66	A NotI restriction map of the entire long arm of human chromosome 21. Nature Genetics, 1993, 4, 361-366.	21.4	90