Yoji Kukita

List of Publications by Year
in descending order

59	1,244	430874 18	395702 33
papers	citations	h-index	g-index

60	60	60	1764
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Sweat-gland carcinoma with neuroendocrine differentiation (SCAND): a clinicopathologic study of 13 cases with genetic analysis. Modern Pathology, 2022, 35, 33-43.	5.5	10
2	Fragmentation Coefficient of RNA in Formalin-Fixed Paraffin-Embedded Samples Stored for Long-Term at Room Temperature. journal of applied laboratory medicine, The, 2022, 7, 619-622.	1.3	0
3	Coâ€existence of <scp>BRAF V600E</scp>â€mutated malignant melanoma and <scp>BRAF V600Eâ€mutated Langerhans</scp> cell histiocytosis: A case report. Journal of Cutaneous Pathology, 2022, 49, 393-398.	1.3	1
4	Atezolizumab with bevacizumab, paclitaxelÂand carboplatin was effective for patients with SMARCA4-deficient thoracic sarcoma. Immunotherapy, 2021, 13, 799-806.	2.0	29
5	Late recurrence of lung adenocarcinoma harboring EGFR exon 20 insertion (A763_Y764insFQEA) mutation successfully treated with osimertinib. Cancer Genetics, 2021, 256-257, 57-61.	0.4	8
6	EML4-ALK fusion variant.3 and co-occurrent PIK3CA E542K mutation exhibiting primary resistance to three generations of ALK inhibitors. Cancer Genetics, 2021, 256-257, 131-135.	0.4	8
7	Bclâ€2â€negative IGHâ€BCL2 translocationâ€negative follicular lymphoma of the thyroid differs genetically and epigenetically from Bclâ€2â€positive IGHâ€BCL2 translocationâ€positive follicular lymphoma. Histopathology, 2021, 79, 521-532.	2.9	3
8	Signetâ€ring cell/histiocytoid carcinoma of the axilla: a clinicopathological and genetic analysis of 11 cases, review of the literature, and comparison with potentially related tumours. Histopathology, 2021, 79, 926-939.	2.9	4
9	Î±-Methylacyl-CoA racemase: a useful immunohistochemical marker of breast carcinoma with apocrine differentiation. Human Pathology, 2021, 116, 39-48.	2.0	7
10	Conversion Surgery for Advanced Thoracic SMARCA4-Deficient Undifferentiated Tumor With Atezolizumab in Combination With Bevacizumab, Paclitaxel, and Carboplatin Treatment: A Case Report. JTO Clinical and Research Reports, 2021, 2, 100235.	1.1	6
11	Clinical Utility of Pancreatic Cancer Circulating Tumor DNA in Predicting Disease Progression, Prognosis, and Response to Chemotherapy. Pancreas, 2020, 49, e93-e95.	1.1	3
12	Quantitative detection of ALK fusion breakpoints in plasma cell-free DNA from patients with non-small cell lung cancer using PCR-based target sequencing with a tiling primer set and two-step mapping/alignment. PLoS ONE, 2019, 14, e0222233.	2.5	8
13	Highâ€throughput screening in colorectal cancer tissueâ€originated spheroids. Cancer Science, 2019, 110, 345-355.	3.9	96
14	Detection of circulating tumor DNA from pancreatic cancer using next-generation sequencing and possible clinical applications. Suizo, 2018, 33, 937-943.	0.1	0
15	Selective identification of somatic mutations in pancreatic cancer cells through a combination of next-generation sequencing of plasma DNA using molecular barcodes and a bioinformatic variant filter. PLoS ONE, 2018, 13, e0192611.	2.5	15
16	Rectal Cancer in a Patient with Bartter Syndrome: A Case Report. Genes, 2017, 8, 139.	2.4	1
17	HLA genotyping by next-generation sequencing of complementary DNA. BMC Genomics, 2017, 18, 914.	2.8	19
18	Early responses of EGFR circulating tumor DNA to EGFR tyrosine kinase inhibitors in lung cancer treatment. Oncotarget, 2016, 7, 71782-71789.	1.8	16

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19	Transient appearance of circulating tumor DNA associated with de novo treatment. Scientific Reports, 2016, 6, 38639.	3.3	11
20	Monitoring of treatment responses and clonal evolution of tumor cells by circulating tumor DNA of heterogeneous mutant EGFR genes in lung cancer. Lung Cancer, 2016, 94, 68-73.	2.0	67
21	Characterization of the Tâ€cell receptor beta chain repertoire in tumorâ€infiltrating lymphocytes. Cancer Medicine, 2016, 5, 2513-2521.	2.8	17
22	Homozygous inactivation of CHEK2 is linked to a familial case of multiple primary lung cancer with accompanying cancers in other organs. Journal of Physical Education and Sports Management, 2016, 2, a001032.	1.2	16
23	Numerical indices based on circulating tumor DNA for the evaluation of therapeutic response and disease progression in lung cancer patients. Scientific Reports, 2016, 6, 29093.	3.3	16
24	Dynamics of circulating tumor <scp>DNA</scp> represented by the activating and resistant mutations in epidermal growth factor receptor tyrosine kinase inhibitor treatment. Cancer Science, 2016, 107, 353-358.	3.9	28
25	Analysis of ERBB Ligand-Induced Resistance Mechanism to Crizotinib by Primary Culture of Lung Adenocarcinoma with EML4-ALK Fusion Gene. Journal of Thoracic Oncology, 2015, 10, 527-530.	1.1	32
26	Diagnostic Accuracy of Noninvasive Genotyping of EGFR in Lung Cancer Patients by Deep Sequencing of Plasma Cell-Free DNA. Clinical Chemistry, 2015, 61, 1191-1196.	3.2	99
27	High-fidelity target sequencing of individual molecules identified using barcode sequences:de novodetection and absolute quantitation of mutations in plasma cell-free DNA from cancer patients. DNA Research, 2015, 22, 269-277.	3.4	72
28	Prognostic prediction of glioblastoma by quantitative assessment of the methylation status of the entire MGMT promoter region. BMC Cancer, 2014, 14, 641.	2.6	20
29	A definitive haplotype map of structural variations determined by microarray analysis of duplicated haploid genomes. Genomics Data, 2014, 2, 55-59.	1.3	1
30	Quantitative Identification of Mutant Alleles Derived from Lung Cancer in Plasma Cell-Free DNA via Anomaly Detection Using Deep Sequencing Data. PLoS ONE, 2013, 8, e81468.	2.5	61
31	A Definitive Haplotype Map as Determined by Genotyping Duplicated Haploid Genomes Finds a Predominant Haplotype Preference at Copy-Number Variation Events. American Journal of Human Genetics, 2010, 86, 918-928.	6.2	8
32	Impact of group IVA cytosolic phospholipase A 2 gene polymorphisms on phenotypic features of patients with familial adenomatous polyposis. International Journal of Colorectal Disease, 2010, 25, 293-301.	2.2	10
33	Conversion of a molecular classifier obtained by gene expression profiling into a classifier based on real-time PCR: a prognosis predictor for gliomas. BMC Medical Genomics, 2010, 3, 52.	1.5	1
34	Estimation of SNP Allele Frequencies by SSCP Analysis of Pooled DNA. Methods in Molecular Biology, 2009, 578, 193-207.	0.9	8
35	Evaluation of Haplotype Inference Using Definitive Haplotype Data Obtained from Complete Hydatidiform Moles, and Its Significance for the Analyses of Positively Selected Regions. PLoS Genetics, 2009, 5, e1000468.	3.5	18
36	Narrowing of the regions of allelic losses of chromosome 1p36 in meningioma tissues by an improved SSCP analysis. International Journal of Cancer, 2008, 122, 1820-1826.	5.1	13

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37	Prevalence of copy-number neutral LOH in glioblastomas revealed by genomewide analysis of laser-microdissected tissues. Neuro-Oncology, 2008, 10, 995-1003.	1.2	34
38	1P-318 The establishment of the building method for designable self-assembled DNA nanostructures(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S71.	0.1	0
39	D-HaploDB: a database of definitive haplotypes determined by genotyping complete hydatidiform mole samples. Nucleic Acids Research, 2007, 35, D685-D689.	14.5	7
40	Impact of Phospholipase A2 Group IIa Gene Polymorphism on Phenotypic Features of Patients with Familial Adenomatous Polyposis. Diseases of the Colon and Rectum, 2007, 50, 223-231.	1.3	10
41	Optimization of capillary array electrophoresis single-strand conformation polymorphism analysis for routine molecular diagnostics. Electrophoresis, 2006, 27, 3816-3822.	2.4	21
42	QSNPlite, a software system for quantitative analysis of SNPs based on capillary array SSCP analysis. Electrophoresis, 2006, 27, 3869-3878.	2.4	8
43	Allelic Losses of Chromosome 10 in Glioma Tissues Detected by Quantitative Single-Strand Conformation Polymorphism Analysis. Clinical Chemistry, 2006, 52, 370-378.	3.2	31
44	dbQSNP: A database of SNPs in human promoter regions with allele frequency information determined by single-strand conformation polymorphism-based methods. Human Mutation, 2005, 26, 69-77.	2.5	11
45	Gastric juvenile polyposis associated with germline SMAD4 mutation. American Journal of Medical Genetics, Part A, 2005, 134A, 326-329.	1.2	16
46	Genome-wide definitive haplotypes determined using a collection of complete hydatidiform moles. Genome Research, 2005, 15, 1511-1518.	5.5	16
47	SNP Detection and Allele Frequency Determination by SSCP. , 2003, 212, 037-046.		3
48	Single-Stranded Conformational Polymorphism Analysis Using Automated Capillary Array Electrophoresis Apparatuses. BioTechniques, 2003, 34, 746-750.	1.8	27
49	Software for Machine-Independent Quantitative Interpretation of SSCP in Capillary Array Electrophoresis (QUISCA). BioTechniques, 2002, 33, 1342-1348.	1.8	19
50	Hemi-Stranded SSCP Analysis of SNPs in Short Sequence-Tagged Sites. BioTechniques, 2002, 33, 1118-1121.	1.8	2
51	Multicolor Post-PCR Labeling of DNA Fragments with Fluorescent ddNTPs. BioTechniques, 2002, 33, 502-506.	1.8	22
52	A single-strand conformation polymorphism method for the large-scale analysis of mutations/polymorphisms using capillary array electrophoresis. Electrophoresis, 2002, 23, 2259.	2.4	39
53	Multicolor Post-PCR Labeling of DNA Fragments with Fluorescent ddNTPs. BioTechniques, 2002, 33, 502-506.	1.8	5
54	Precise Estimation of Allele Frequencies of Single-Nucleotide Polymorphisms by a Quantitative SSCP Analysis of Pooled DNA. American Journal of Human Genetics, 2001, 68, 214-218.	6.2	93

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55	Distinct pattern of PCRâ€“SSCP analysis of p53 mutations in human astrocytomas. Cancer Letters, 1999, 141, 195-201.	7.2	6
56	ATM mutations in patients with ataxia telangiectasia screened by a hierarchical strategy. Human Mutation, 1998, 12, 186-195.	2.5	19
57	Characterization of the GALC Gene in Three Japanese Patients with Adult-Onset Krabbe Disease. Genetic Testing and Molecular Biomarkers, 1997, 1, 217-223.	1.7	10
58	SSCP analysis of long DNA fragments in low pH gel. Human Mutation, 1997, 10, 400-407.	2.5	98
59	SSCP analysis of long DNA fragments in low pH gel. Human Mutation, 1997, 10, 400-407.	2.5	8