Ronald van Eijk

List of Publications by Year
in descending order

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47	5,160	236833	233338
papers	citations	25 h-index	45 g-index

49	49	49	6856
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Cell-of-origin classification using the Hans and Lymph2Cx algorithms in primary cutaneous large B-cell lymphomas. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2022, 480, 667-675.	1.4	12
2	Incidence and determinants of thrombotic and bleeding complications in patients with glioblastoma. Journal of Thrombosis and Haemostasis, 2022, 20, 1665-1673.	1.9	16
3	Frequent mutated B2M, EZH2, IRF8, and TNFRSF14 in primary bone diffuse large B-cell lymphoma reflect a GCB phenotype. Blood Advances, 2021, 5, 3760-3775.	2.5	11
4	Synchronous diffuse large B-cell lymphoma and mantle cell lymphoma: support for low-threshold biopsies and genetic testing. Leukemia and Lymphoma, 2021, , 1-5.	0.6	2
5	The complexity of screening PMS2 in DNA isolated from formalin-fixed paraffin-embedded material. European Journal of Human Genetics, 2020, 28, 333-338.	1.4	10
6	Bâ€cell lymphoblastic lymphoma with cutaneous involvement and a <scp>KMT2A</scp> gene rearrangement. American Journal of Hematology, 2020, 95, 1427-1429.	2.0	5
7	Apparent Lack of BRAFV600E Derived HLA Class I Presented Neoantigens Hampers Neoplastic Cell Targeting by CD8+ T Cells in Langerhans Cell Histiocytosis. Frontiers in Immunology, 2019, 10, 3045.	2.2	4
8	High Frequencies of Mutated EZH2 and IRF8 and Other Epigenetic Genes in Primary Bone Lymphomas Are Indicative of GCB-Phenotype. Blood, 2019, 134, 1484-1484.	0.6	0
9	High prevalence of MYD88 and CD79B mutations in intravascular large B-cell lymphoma. Blood, 2018, 131, 2086-2089.	0.6	69
10	Validation and Implementation of BRCA1/2 Variant Screening in Ovarian Tumor Tissue. Journal of Molecular Diagnostics, 2018, 20, 600-611.	1.2	18
11	Molecular Background of Colorectal Tumors From Patients With Lynch Syndrome Associated With Germline Variants in PMS2. Gastroenterology, 2018, 155, 844-851.	0.6	38
12	Statin Use After Diagnosis of Colon Cancer and Patient Survival. Gastroenterology, 2017, 153, 470-479.e4.	0.6	67
13	Evidence for genetic association between chromosome 1q loci and predisposition to colorectal neoplasia. British Journal of Cancer, 2017, 117, 1215-1223.	2.9	10
14	The Influence of BRAF and KRAS Mutation Status on the Association between Aspirin Use and Survival after Colon Cancer Diagnosis. PLoS ONE, 2017, 12, e0170775.	1.1	23
15	The clinical value of HER-2 overexpression and PIK3CA mutations in the older breast cancer population: a FOCUS study analysis. Breast Cancer Research and Treatment, 2016, 156, 361-370.	1.1	11
16	Somatic mutation profiles in primary colorectal cancers and matching ovarian metastases: Identification of driver and passenger mutations. Journal of Pathology: Clinical Research, 2016, 2, 166-174.	1.3	12
17	Target-Enriched Next-Generation Sequencing Reveals Differences between Primary and Secondary Ovarian Tumors in Formalin-Fixed, Paraffin-Embedded Tissue. Journal of Molecular Diagnostics, 2015, 17, 193-200.	1.2	8
18	Whole-Exome Sequencing Studies of Parathyroid Carcinomas Reveal NovelPRUNE2Mutations, Distinctive Mutational Spectra Related to APOBEC-Catalyzed DNA Mutagenesis and Mutational Enrichment in Kinases Associated With Cell Migration and Invasion. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E360-E364.	1.8	86

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19	Expression of HLA Class I Antigen, Aspirin Use, and Survival After a Diagnosis of Colon Cancer. JAMA Internal Medicine, 2014, 174, 732.	2.6	93
20	Nearâ€haploidization significantly associates with oncocytic adrenocortical, thyroid, and parathyroid tumors but not with mitochondrial DNA mutations. Genes Chromosomes and Cancer, 2014, 53, 833-844.	1.5	25
21	Designing a High-Throughput Somatic Mutation Profiling Panel Specifically for Gynaecological Cancers. PLoS ONE, 2014, 9, e93451.	1.1	39
22	Assessment of a fully automated high-throughput DNA extraction method from formalin-fixed, paraffin-embedded tissue for KRAS, and BRAF somatic mutation analysis. Experimental and Molecular Pathology, 2013, 94, 121-125.	0.9	64
23	Mutational analyses of epidermal growth factor receptor and downstream pathways in adrenocortical carcinoma. European Journal of Endocrinology, 2013, 169, 51-58.	1.9	16
24	Improved risk assessment of endometrial cancer by combined analysis of MSI, PI3Kâ€“AKT, Wnt/Î²-catenin and P53 pathway activation. Gynecologic Oncology, 2012, 126, 466-473.	0.6	60
25	Genome Haploidisation with Chromosome 7 Retention in Oncocytic Follicular Thyroid Carcinoma. PLoS ONE, 2012, 7, e38287.	1.1	63
26	Somatic mosaic IDH1 and IDH2 mutations are associated with enchondroma and spindle cell hemangioma in Ollier disease and Maffucci syndrome. Nature Genetics, 2011, 43, 1256-1261.	9.4	488
27	Rapid KRAS, EGFR, BRAF and PIK3CA Mutation Analysis of Fine Needle Aspirates from Non-Small-Cell Lung Cancer Using Allele-Specific qPCR. PLoS ONE, 2011, 6, e17791.	1.1	166
28	MLPAinter for MLPA interpretation: an integrated approach for the analysis, visualisation and data management of Multiplex Ligation-dependent Probe Amplification. BMC Bioinformatics, 2010, 11, 67.	1.2	12
29	A genome-wide association study of Hodgkin's lymphoma identifies new susceptibility loci at 2p16.1 (REL), 8q24.21 and 10p14 (GATA3). Nature Genetics, 2010, 42, 1126-1130.	9.4	177
30	Sensitive and Specific KRAS Somatic Mutation Analysis on Whole-Genome Amplified DNA from Archival Tissues. Journal of Molecular Diagnostics, 2010, 12, 27-34.	1.2	31
31	Enrichment of Low Penetrance Susceptibility Loci in a Dutch Familial Colorectal Cancer Cohort. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3062-3067.	1.1	64
32	Cell Cycle/Apoptosis Molecule Expression Correlates with Imatinib Response in Patients with Advanced Gastrointestinal Stromal Tumors. Clinical Cancer Research, 2009, 15, 4191-4198.	3.2	61
33	No genomic aberrations in Langerhans cell histiocytosis as assessed by diverse molecular technologies. Genes Chromosomes and Cancer, 2009, 48, 239-249.	1.5	71
34	Genome-wide copy neutral LOH is infrequent in familial and sporadic microsatellite unstable carcinomas. Familial Cancer, 2008, 7, 319-330.	0.9	23
35	Progression and Tumor Heterogeneity Analysis in Early Rectal Cancer. Clinical Cancer Research, 2008, 14, 772-781.	3.2	37
36	Genome-wide Allelic State Analysis on Flow-Sorted Tumor Fractions Provides an Accurate Measure of Chromosomal Aberrations. Cancer Research, 2008, 68, 10333-10340.	0.4	28

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37	High-resolution copy number analysis of paraffin-embedded archival tissue using SNP BeadArrays. Genome Research, 2007, 17, 368-376.	2.4	60
38	Reliable High-Throughput Genotyping and Loss-of-Heterozygosity Detection in Formalin-Fixed, Paraffin-Embedded Tumors Using Single Nucleotide Polymorphism Arrays. Cancer Research, 2005, 65, 10188-10191.	0.4	81
39	Mass Spectrometry-Based Loss of Heterozygosity Analysis of Single-Nucleotide Polymorphism Loci in Paraffin Embedded Tumors Using the MassEXTEND Assay. Journal of Molecular Diagnostics, 2005, 7, 623-630.	1.2	21
40	Multiplex Ligationâ€Dependent Probe Amplification for the Detection of 1p and 19q Chromosomal Loss in Oligodendroglial Tumors. Brain Pathology, 2005, 15, 192-197.	2.1	36
41	Visualization of regional gene expression biases by microarray data sorting. BioTechniques, 2004, 36, 592-596.	0.8	9
42	A sporadic breast tumor with a somatically acquired complex genomic rearrangement inBRCA1. , 2000, 27, 295-302.		26
43	BRCA1 Mutation Analysis in a Portuguese Population with Early-Onset Breast and/or Ovarian Cancer. Disease Markers, 1999, 15, 93-93.	0.6	2
44	BRCA1 genomic deletions are major founder mutations in Dutch breast cancer patients. Nature Genetics, 1997, 17, 341-345.	9.4	414
45	Familial Hemiplegic Migraine and Episodic Ataxia Type-2 Are Caused by Mutations in the Ca2+ Channel Gene CACNL1A4. Cell, 1996, 87, 543-552.	13.5	2,287
46	Familial hemiplegic migraine locus on 19p13 is involved in the common forms of migraine with and without aura. Human Genetics, 1995, 96, 604-608.	1.8	167
47	Genetic Heterogeneity of Familial Hemiplegic Migraine. Genomics, 1994, 22, 21-26.	1.3	136