Michael Hummel

List of Publications by Year
in descending order

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276	20,905	10956 71	12910 131
papers	citations	h-index	g-index

289	289	289	25229
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. Cell, 2020, 182, 1419-1440.e23.	13.5	1,162
2	A Biologic Definition of Burkitt's Lymphoma from Transcriptional and Genomic Profiling. New England Journal of Medicine, 2006, 354, 2419-2430.	13.9	915
3	Senescence-associated reprogramming promotes cancer stemness. Nature, 2018, 553, 96-100.	13.7	714
4	Molecular cloning and expression of a new member of the nerve growth factor receptor family that is characteristic for Hodgkin's disease. Cell, 1992, 68, 421-427.	13.5	626
5	Subcutaneous panniculitis-like T-cell lymphoma: definition, classification, and prognostic factors: an EORTC Cutaneous Lymphoma Group Study of 83 cases. Blood, 2008, 111, 838-845.	0.6	617
6	MYC status in concert with BCL2 and BCL6 expression predicts outcome in diffuse large B-cell lymphoma. Blood, 2013, 121, 2253-2263.	0.6	468
7	Hodgkin and Reed-Sternberg cells represent an expansion of a single clone originating from a germinal center B-cell with functional immunoglobulin gene rearrangements but defective immunoglobulin transcription. Blood, 2000, 95, 1443-1450.	0.6	437
8	Synthetic lethal metabolic targeting of cellular senescence in cancer therapy. Nature, 2013, 501, 421-425.	13.7	437
9	Epstein-Barr virus-associated Hodgkin's disease: Epidemiologic characteristics in international data. , 1997, 70, 375-382.		424
10	Lymphoproliferative lesions of the ocular adnexa. Ophthalmology, 1998, 105, 1430-1441.	2.5	410
11	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. Nature Genetics, 2012, 44, 1316-1320.	9.4	389
12	Derepression of an endogenous long terminal repeat activates the CSF1R proto-oncogene in human lymphoma. Nature Medicine, 2010, 16, 571-579.	15.2	317
13	Origin of Nodular Lymphocyte-Predominant Hodgkin's Disease from a Clonal Expansion of Highly Mutated Germinal-Center B Cells. New England Journal of Medicine, 1997, 337, 453-458.	13.9	311
14	Pharmacological and genomic profiling identifies NF-ÎºBâ€“targeted treatment strategies for mantle cell lymphoma. Nature Medicine, 2014, 20, 87-92.	15.2	303
15	Translocations activating IRF4 identify a subtype of germinal center-derived B-cell lymphoma affecting predominantly children and young adults. Blood, 2011, 118, 139-147.	0.6	281
16	Down-regulation of BOB.1/OBF.1 and Oct2 in classical Hodgkin disease but not in lymphocyte predominant Hodgkin disease correlates with immunoglobulin transcription. Blood, 2001, 97, 496-501.	0.6	264
17	Overexpression of I Kappa B Alpha Without Inhibition of NF-ÎºB Activity and Mutations in the I Kappa B Alpha Gene in Reed-Sternberg Cells. Blood, 1999, 94, 3129-3134.	0.6	249
18	PTEN loss defines a PI3K/AKT pathway-dependent germinal center subtype of diffuse large B-cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12420-12425.	3.3	233

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19	Procarbazine-Free OEPA-COPDAC Chemotherapy in Boys and Standard OPPA-COPP in Girls Have Comparable Effectiveness in Pediatric Hodgkin's Lymphoma: The GPOH-HD-2002 Study. Journal of Clinical Oncology, 2010, 28, 3680-3686.	0.8	222
20	T-cell and T/natural killer-cell lymphomas involving ocular and ocular adnexal tissues. Ophthalmology, 1999, 106, 2109-2120.	2.5	211
21	Hodgkin's Disease with Monoclonal and Polyclonal Populations of Reedâ€“Sternberg Cells. New England Journal of Medicine, 1995, 333, 901-906.	13.9	206
22	Evidence for Epithelial-Mesenchymal Transition in Cancer Stem Cells of Head and Neck Squamous Cell Carcinoma. PLoS ONE, 2011, 6, e16466.	1.1	202
23	Frequent Expression of the B-Cellâ€“Specific Activator Protein in Reed-Sternberg Cells of Classical Hodgkinâ€™s Disease Provides Further Evidence for Its B-Cell Origin. Blood, 1999, 94, 3108-3113.	0.6	197
24	Detection of clonal T-cell receptor gamma-chain gene rearrangements in Reed-Sternberg cells of classic Hodgkin disease. Blood, 2000, 95, 3020-3024.	0.6	196
25	A recurrent 11q aberration pattern characterizes a subset of MYC-negative high-grade B-cell lymphomas resembling Burkitt lymphoma. Blood, 2014, 123, 1187-1198.	0.6	185
26	Clinical Impact of the Cell-of-Origin Classification and the MYC/BCL2 Dual Expresser Status in Diffuse Large B-Cell Lymphoma Treated Within Prospective Clinical Trials of the German High-Grade Non-Hodgkin's Lymphoma Study Group. Journal of Clinical Oncology, 2017, 35, 2515-2526.	0.8	179
27	Standardized next-generation sequencing of immunoglobulin and T-cell receptor gene recombinations for MRD marker identification in acute lymphoblastic leukaemia; a EuroClonality-NGS validation study. Leukemia, 2019, 33, 2241-2253.	3.3	177
28	Immunoblastic morphology but not the immunohistochemical GCB/nonGCB classifier predicts outcome in diffuse large B-cell lymphoma in the RICOVER-60 trial of the DSHNHL. Blood, 2010, 116, 4916-4925.	0.6	176
29	High-accuracy determination of internal circadian time from a single blood sample. Journal of Clinical Investigation, 2018, 128, 3826-3839.	3.9	174
30	Intrinsic inhibition of transcription factor E2A by HLH proteins ABF-1 and Id2 mediates reprogramming of neoplastic B cells in Hodgkin lymphoma. Nature Immunology, 2006, 7, 207-215.	7.0	168
31	The prognostic impact of variant histology in nodular lymphocyte-predominant Hodgkin lymphoma: a report from the German Hodgkin Study Group (GHSG). Blood, 2013, 122, 4246-4252.	0.6	168
32	Patient age at diagnosis is associated with the molecular characteristics of diffuse large B-cell lymphoma. Blood, 2012, 119, 1882-1887.	0.6	163
33	Biological characterization of adult MYC-translocation-positive mature B-cell lymphomas other than molecular Burkitt lymphoma. Haematologica, 2014, 99, 726-735.	1.7	157
34	Immunoglobulin gene analysis reveals 2 distinct cells of origin for EBV-positive and EBV-negative Burkitt lymphomas. Blood, 2005, 106, 1031-1036.	0.6	153
35	Evaluation of vitrectomy specimens and chorioretinal biopsies in the diagnosis of primary intraocular lymphoma in patients with Masquerade syndrome. Graefe's Archive for Clinical and Experimental Ophthalmology, 2003, 241, 860-870.	1.0	152
36	Expression of vascular endothelial growth factor in lymphomas and castleman's disease. , 1997, 183, 44-50.		151

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37	Early IFN-Î± signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. Immunity, 2021, 54, 2650-2669.e14.	6.6	145
38	Ocular Adnexal Lymphomas. Survey of Ophthalmology, 2002, 47, 470-490.	1.7	139
39	Inactivating I kappa B epsilon mutations in Hodgkin/Reed-Sternberg cells. Journal of Pathology, 2003, 201, 413-420.	2.1	134
40	New insights into the biology and origin of mature aggressive B-cell lymphomas by combined epigenomic, genomic, and transcriptional profiling. Blood, 2009, 113, 2488-2497.	0.6	133
41	The human OX40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen. European Journal of Immunology, 1994, 24, 677-683.	1.6	128
42	Classical Hodgkin's Disease and Follicular Lymphoma Originating From the Same Germinal Center B Cell. Journal of Clinical Oncology, 1999, 17, 3804-3809.	0.8	127
43	A time-resolved proteomic and prognostic map of COVID-19. Cell Systems, 2021, 12, 780-794.e7.	2.9	125
44	Epstein-Barr virus in B-cell non-Hodgkin's lymphomas: Unexpected infection patterns and different infection incidence in low- and high-grade types. Journal of Pathology, 1995, 175, 263-271.	2.1	123
45	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. Nature Genetics, 2015, 47, 1316-1325.	9.4	119
46	EBV infection patterns in Hodgkin's disease and normal lymphoid tissue: expression and cellular localization of EBV gene products. British Journal of Haematology, 1992, 82, 689-694.	1.2	113
47	Macrophage development from HSCs requires PU.1-coordinated microRNA expression. Blood, 2011, 118, 2275-2284.	0.6	113
48	Molecular profiling of pediatric mature B-cell lymphoma treated in population-based prospective clinical trials. Blood, 2008, 112, 1374-1381.	0.6	112
49	A 2015 update on predictive molecular pathology and its role in targeted cancer therapy: a review focussing on clinical relevance. Cancer Gene Therapy, 2015, 22, 417-430.	2.2	112
50	CD56-positive haematological neoplasms of the skin: a multicentre study of the Cutaneous Lymphoma Project Group of the European Organisation for Research and Treatment of Cancer. Journal of Clinical Pathology, 2006, 60, 981-989.	1.0	110
51	High detection rate of T-cell receptor beta chain rearrangements in T-cell lymphoproliferations by family specific polymerase chain reaction in combination with the GeneScan technique and DNA sequencing. Blood, 2000, 96, 640-646.	0.6	109
52	Extranodal marginal zone B cell lymphomas of the uvea: an analysis of 13 cases. Journal of Pathology, 2002, 197, 333-340.	2.1	105
53	Clonal T-cell receptor ?-chain gene rearrangement by PCR-based GeneScan analysis in advanced cutaneous T-cell lymphoma: a critical evaluation. , 1999, 188, 146-154.		100
54	Epigenetic silencing of the immunoglobulin heavy-chain gene in classical Hodgkin lymphoma-derived cell lines contributes to the loss of immunoglobulin expression. Blood, 2004, 104, 3326-3334.	0.6	100

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55	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	5.8	99
56	Gene deregulation and spatial genome reorganization near breakpoints prior to formation of translocations in anaplastic large cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5831-5836.	3.3	94
57	Next-generation sequencing of immunoglobulin gene rearrangements for clonality assessment: a technical feasibility study by EuroClonality-NGS. Leukemia, 2019, 33, 2227-2240.	3.3	92
58	MINCR is a MYC-induced lncRNA able to modulate MYCâ€™s transcriptional network in Burkitt lymphoma cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5261-70.	3.3	91
59	Early TCR-Î² and TCR-Î³ PCR detection of T-cell clonality indicates minimal tumor disease in lymph nodes of cutaneous T-cell lymphoma: diagnostic and prognostic implications. Blood, 2005, 105, 503-510.	0.6	90
60	Opposing roles of NF-ÎºB in anti-cancer treatment outcome unveiled by cross-species investigations. Genes and Development, 2011, 25, 2137-2146.	2.7	90
61	Deep Sequencing of MYC DNA-Binding Sites in Burkitt Lymphoma. PLoS ONE, 2011, 6, e26837.	1.1	90
62	Primary intraocular lymphoma of T-cell type: report of a case and review of the literature. Graefe's Archive for Clinical and Experimental Ophthalmology, 2005, 243, 189-197.	1.0	88
63	Classical Hodgkin lymphoma is characterized by high constitutive expression of activating transcription factor 3 (ATF3), which promotes viability of Hodgkin/Reed-Sternberg cells. Blood, 2006, 107, 2536-2539.	0.6	87
64	Metastatic canine mammary carcinomas can be identified by a gene expression profile that partly overlaps with human breast cancer profiles. BMC Cancer, 2010, 10, 618.	1.1	87
65	Molecular Analysis of Immunoglobulin Genes in Primary Intraocular Lymphoma. , 2005, 46, 3507.		82
66	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. Blood, 2016, 128, 2666-2670.	0.6	82
67	Integration of next-generation sequencing in clinical diagnostic molecular pathology laboratories for analysis of solid tumours; an expert opinion on behalf of IQN Path ASBL. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2017, 470, 5-20.	1.4	82
68	Differential EÂµ enhancer activity and expression of BOB.1/OBF.1, Oct2, PU.1, and immunoglobulin in reactive B-cell populations, B-cell non-Hodgkin lymphomas, and Hodgkin lymphomas. Journal of Pathology, 2004, 202, 60-69.	2.1	81
69	Harmonization and Standardization of Panel-Based Tumor Mutational Burden Measurement: Real-World Results and Recommendations ofÂtheÂQuality in Pathology Study. Journal of Thoracic Oncology, 2020, 15, 1177-1189.	0.5	81
70	Single-cell analysis of CD30+ cells in lymphomatoid papulosis demonstrates a common clonal T-cell origin. Blood, 2002, 100, 578-584.	0.6	80
71	Detection of Subclinical Systemic Disease in Primary CNS Lymphoma by Polymerase Chain Reaction of the Rearranged Immunoglobulin Heavy-Chain Genes. Journal of Clinical Oncology, 2006, 24, 4754-4757.	0.8	80
72	Differential micro-RNA expression in primary CNS and nodal diffuse large B-cell lymphomas. Neuro-Oncology, 2011, 13, 1090-1098.	0.6	79

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73	Essential role of IRF4 and MYC signaling for survival of anaplastic large cell lymphoma. Blood, 2015, 125, 124-132.	0.6	79
74	Studying the pathophysiology of coronavirus disease 2019: a protocol for the Berlin prospective COVID-19 patient cohort (Pa-COVID-19). Infection, 2020, 48, 619-626.	2.3	79
75	Clonal T cell receptor Î³-chain gene rearrangement by PCR-based GeneScan analysis in the skin and blood of patients with parapsoriasis and early-stage mycosis fungoides. Journal of Pathology, 2002, 197, 348-354.	2.1	78
76	Alterations in myocardial tissue factor expression and cellular localization in dilated cardiomyopathy. Journal of the American College of Cardiology, 2005, 45, 1081-1089.	1.2	78
77	New Approaches to Lymphoma Diagnosis. Hematology American Society of Hematology Education Program, 2001, 2001, 194-220.	0.9	75
78	Expression of functional T-cell markers and T-cell receptor Vbeta repertoire in endomyocardial biopsies from patients presenting with acute myocarditis and dilated cardiomyopathy. European Journal of Heart Failure, 2011, 13, 611-618.	2.9	75
79	Micro<scp>RNA</scp>â€142 is mutated in about 20% of diffuse large <scp>B</scp>â€cell lymphoma. Cancer Medicine, 2012, 1, 141-155.	1.3	74
80	Machine Learning-based Classification of Diffuse Large B-cell Lymphoma Patients by Their Protein Expression Profiles. Molecular and Cellular Proteomics, 2015, 14, 2947-2960.	2.5	73
81	Aberrant expression of Notch1 interferes with the B-lymphoid phenotype of neoplastic B cells in classical Hodgkin lymphoma. Leukemia, 2008, 22, 1587-1594.	3.3	72
82	DCLRE1C(ARTEMIS) mutations causing phenotypes ranging from atypical severe combined immunodeficiency to mere antibody deficiency. Human Molecular Genetics, 2015, 24, 7361-7372.	1.4	72
83	Defective octamer-dependent transcription is responsible for silenced immunoglobulin transcription in Reed-Sternberg cells. Blood, 2001, 97, 3191-3196.	0.6	71
84	Cloning and expression of an inhibitor of microbial metalloproteinases from insects contributing to innate immunity. Biochemical Journal, 2004, 382, 315-322.	1.7	70
85	Microarrayâ€based genomic profiling reveals novel genomic aberrations in follicular lymphoma which associate with patient survival and gene expression status. Genes Chromosomes and Cancer, 2009, 48, 39-54.	1.5	70
86	Detection of genomic aberrations in molecularly defined Burkitt's lymphoma by array-based, high resolution, single nucleotide polymorphism analysis. Haematologica, 2010, 95, 2047-2055.	1.7	70
87	IÎºB-Î¶ controls the constitutive NF-ÎºB target gene network and survival of ABC DLBCL. Blood, 2013, 122, 2242-2250.	0.6	70
88	The AP-1-BATF and -BATF3 module is essential for growth, survival and TH17/ILC3 skewing of anaplastic large cell lymphoma. Leukemia, 2018, 32, 1994-2007.	3.3	70
89	Quality control and quantification in IG/TR next-generation sequencing marker identification: protocols and bioinformatic functionalities by EuroClonality-NGS. Leukemia, 2019, 33, 2254-2265.	3.3	70
90	Monocytoid B Cells Are Distinct From Splenic Marginal Zone Cells and Commonly Derive From Unmutated Naive B Cells and Less Frequently From Postgerminal Center B Cells by Polyclonal Transformation. Blood, 1999, 94, 2800-2808.	0.6	69

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91	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. Cell, 2013, 155, 567-581.	13.5	67
92	Multicenter Immunohistochemical ALK-Testing of Nonâ€“Small-Cell Lung Cancer Shows High Concordance after Harmonization of Techniques and Interpretation Criteria. Journal of Thoracic Oncology, 2014, 9, 1685-1692.	0.5	66
93	CD30-Induced Signaling Is Absent in Hodgkin's Cells but Present in Anaplastic Large Cell Lymphoma Cells. American Journal of Pathology, 2008, 172, 510-520.	1.9	65
94	Comparative assessment of differential network analysis methods. Briefings in Bioinformatics, 2017, 18, bbw061.	3.2	65
95	Prognostic significance of ALDH1A1-positive cancer stem cells in patients with locally advanced, metastasized head and neck squamous cell carcinoma. Journal of Cancer Research and Clinical Oncology, 2014, 140, 1151-1158.	1.2	64
96	Common clonal origin of an acute B-lymphoblastic leukemia and a Langerhans' cell sarcoma: evidence for hematopoietic plasticity. Haematologica, 2010, 95, 1461-1466.	1.7	62
97	Comparison of targeted next-generation sequencing and Sanger sequencing for the detection of PIK3CA mutations in breast cancer. BMC Clinical Pathology, 2015, 15, 20.	1.8	61
98	High-Throughput Immunogenetics for Clinical and Research Applications in Immunohematology: Potential and Challenges. Journal of Immunology, 2017, 198, 3765-3774.	0.4	61
99	Preamplification techniques for real-time RT-PCR analyses of endomyocardial biopsies. BMC Molecular Biology, 2008, 9, 3.	3.0	60
100	Predictive molecular pathology and its role in targeted cancer therapy: a review focussing on clinical relevance. Cancer Gene Therapy, 2013, 20, 211-221.	2.2	58
101	CDK9/CYCLIN T1 expression during normal lymphoid differentiation and malignant transformation. Journal of Pathology, 2004, 203, 946-952.	2.1	54
102	Abnormally differentiated CD4+ or CD8+ T cells with phenotypic and genetic features of double negative T cells in human Fas deficiency. Blood, 2014, 124, 851-860.	0.6	54
103	Parallel screening for ALK, MET and ROS1 alterations in non-small cell lung cancer with implications for daily routine testing. Lung Cancer, 2015, 87, 122-129.	0.9	54
104	Mapping of transcription factor motifs in active chromatin identifies IRF5 as key regulator in classical Hodgkin lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4513-22.	3.3	53
105	Diversification of Ig Heavy Chain Genes in Human Preterm Neonates Prematurely Exposed to Environmental Antigens. Journal of Immunology, 2002, 169, 1349-1356.	0.4	52
106	Testing NTRK testing: Wetâ€lab and in silico comparison of RNAâ€based targeted sequencing assays. Genes Chromosomes and Cancer, 2020, 59, 178-188.	1.5	52
107	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	5.8	52
108	MONOKINE EXPRESSION IN LANGERHANS' CELL HISTIOCYTOSIS AND SINUS HISTIOCYTOSIS WITH MASSIVE LYMPHADENOPATHY (ROSAI-DORFMAN DISEASE). , 1996, 179, 60-65.		51

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109	MiR-200b and miR-155 as predictive biomarkers for the efficacy of chemoradiation in locally advanced head and neck squamous cell carcinoma. European Journal of Cancer, 2017, 77, 3-12.	1.3	51
110	A modular transcriptome map of mature B cell lymphomas. Genome Medicine, 2019, 11, 27.	3.6	51
111	Frequent expansion of Epstein-Barr virus (EBV) infected cells in germinal centres of tonsils from an area with a high incidence of EBV-associated lymphoma. , 1999, 187, 326-330.		49
112	The diversity of rearranged immunoglobulin heavy chain variable region genes in peripheral blood B cells of preterm infants is restricted by short third complementarity-determining regions but not by limited gene segment usage. Blood, 2001, 97, 1511-1513.	0.6	49
113	Frequency and diagnostic patterns of lymphomas in liver biopsies with respect to the WHO classification. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2007, 450, 493-502.	1.4	48
114	Exon Array Analysis using re-defined probe sets results in reliable identification of alternatively spliced genes in non-small cell lung cancer. BMC Genomics, 2010, 11, 676.	1.2	48
115	Anaplastic lymphoma kinase (ALK) gene rearrangement in non-small cell lung cancer (NSCLC): Results of a multi-centre ALK-testing. Lung Cancer, 2013, 81, 200-206.	0.9	48
116	A roadmap of constitutive NF-ÎºB activity in Hodgkin lymphoma: Dominant roles of p50 and p52 revealed by genome-wide analyses. Genome Medicine, 2016, 8, 28.	3.6	47
117	Defective tight junctions in refractory celiac disease. Annals of the New York Academy of Sciences, 2012, 1258, 43-51.	1.8	45
118	Loss of HLA-DR expression and immunoblastic morphology predict adverse outcome in diffuse large B-cell lymphoma - analyses of cases from two prospective randomized clinical trials. Haematologica, 2009, 94, 1569-1580.	1.7	44
119	The Postnatal Maturation of the Immunoglobulin Heavy Chain IgG Repertoire in Human Preterm Neonates Is Slower than in Term Neonates. Journal of Immunology, 2007, 178, 1180-1188.	0.4	43
120	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. Haematologica, 2016, 101, 1380-1389.	1.7	43
121	T-cell clonality of undetermined significance. Blood, 2001, 98, 247-248.	0.6	42
122	First-in-Man Clinical Results With Good Manufacturing Practice (GMP)-compliant Polypeptide-expanded Adenovirus-specific T Cells After Haploidentical Hematopoietic Stem Cell Transplantation. Journal of Immunotherapy, 2014, 37, 245-249.	1.2	42
123	Gain of chromosome region 18q21 including the MALT1 gene is associated with the activated B-cell-like gene expression subtype and increased BCL2 gene dosage and protein expression in diffuse large B-cell lymphoma. Haematologica, 2008, 93, 688-696.	1.7	41
124	Genomic loss of the putative tumor suppressor gene E2A in human lymphoma. Journal of Experimental Medicine, 2011, 208, 1585-1593.	4.2	41
125	A new method to prevent carry-over contaminations in two-step PCR NGS library preparations. Nucleic Acids Research, 2015, 43, gkv694.	6.5	40
126	Molecular profiles and clinical outcome of stage UICC II colon cancer patients. International Journal of Colorectal Disease, 2011, 26, 847-858.	1.0	38

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127	Assessment of HOPE fixation in vitrectomy specimens in patients with chronic bilateral uveitis (masquerade syndrome). Graefe's Archive for Clinical and Experimental Ophthalmology, 2005, 243, 847-852.	1.0	37
128	Gene-expression analysis identifies novel RBL2/p130 target genes in endemic Burkitt lymphoma cell lines and primary tumors. Blood, 2007, 110, 1301-1307.	0.6	37
129	Demonstration of constant upregulation of the telomerase RNA component in human gastric carcinomas usingin situ hybridization. , 1998, 185, 139-144.		36
130	Activity-Based Probes for Detection of Active MALT1 Paracaspase in Immune Cells and Lymphomas. Chemistry and Biology, 2015, 22, 129-138.	6.2	36
131	ALK-FISH borderline cases in non-small cell lung cancer: Implications for diagnostics and clinical decision making. Lung Cancer, 2015, 90, 465-471.	0.9	36
132	DNA methylation profiling reliably distinguishes pulmonary enteric adenocarcinoma from metastatic colorectal cancer. Modern Pathology, 2019, 32, 855-865.	2.9	36
133	Skewed expression of natural-killer (NK)-associated antigens on lymphoproliferations of large granular lymphocytes (LGL). Hematological Oncology, 2006, 24, 78-85.	0.8	35
134	Histopathological features and their prognostic impact in nodular lymphocyteâ€predominant Hodgkin lymphoma â€“ a matched pair analysis from the German Hodgkin Study Group (GHSG). British Journal of Haematology, 2014, 167, 238-242.	1.2	35
135	Clonality Analysis of Immunoglobulin Gene Rearrangement by Next-Generation Sequencing in Endemic Burkitt Lymphoma Suggests Antigen Drive Activation of BCR as Opposed to Sporadic Burkitt Lymphoma. American Journal of Clinical Pathology, 2016, 145, 116-127.	0.4	35
136	Disappearance of the Epstein-Barr virus in a relapse of Hodgkin's disease. , 1997, 182, 475-479.		34
137	Influence of antigen on the development of MALT lymphoma. Blood, 2006, 107, 1141-1148.	0.6	34
138	ALDH1-positive cancer stem-like cells are enriched in nodal metastases of oropharyngeal squamous cell carcinoma independent of HPV status. Oncology Reports, 2013, 29, 1777-1784.	1.2	34
139	Gene expression profiling reveals a close relationship between follicular lymphoma grade 3A and 3B, but distinct profiles of follicular lymphoma grade 1 and 2. Haematologica, 2018, 103, 1182-1190.	1.7	34
140	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	3.3	34
141	The high frequency of EBV infection in pediatric Hodgkin lymphoma is related to the classical type in Bahia, Brazil. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2006, 449, 315-319.	1.4	32
142	Validation and comparison of two NGS assays for the detection of EGFR T790M resistance mutation in liquid biopsies of NSCLC patients. Oncotarget, 2018, 9, 18529-18539.	0.8	32
143	Discovery and Validation of Novel Biomarkers for Detection of Epithelial Ovarian Cancer. Cells, 2019, 8, 713.	1.8	32
144	Mutational Diversity and Therapy Response in Breast Cancer: A Sequencing Analysis in the Neoadjuvant GeparSepto Trial. Clinical Cancer Research, 2019, 25, 3986-3995.	3.2	32

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145	Evaluation of T-cell Clonality in Archival Skin Biopsy Samples of Cutaneous T-cell Lymphomas Using the Biomed-2 PCR Protocol. Diagnostic Molecular Pathology, 2010, 19, 70-77.	2.1	31
146	Towards a unification of treatments and interventions for tinnitus patients: The EU research and innovation action UNITI. Progress in Brain Research, 2021, 260, 441-451.	0.9	31
147	Secondary ocular involvement in systemic â€œmemoryâ€•B-cell lymphocytic leukemia. Ophthalmology, 2001, 108, 1289-1295.	2.5	29
148	The PCBP1 gene encoding poly(rc) binding protein i is recurrently mutated in <scp>B</scp>urkitt lymphoma. Genes Chromosomes and Cancer, 2015, 54, 555-564.	1.5	29
149	EGFR T790M mutation testing of non-small cell lung cancer tissue and blood samples artificially spiked with circulating cell-free tumor DNA: results of a round robin trial. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2017, 471, 509-520.	1.4	29
150	KRASG12C/TP53 co-mutations identify long-term responders to first line palliative treatment with pembrolizumab monotherapy in PD-L1 high (â‰¥50%) lung adenocarcinoma. Translational Lung Cancer Research, 2021, 10, 737-752.	1.3	28
151	<scp>NTRK</scp> testing: First results of the <scp>QuiPâ€EQA</scp> scheme and a comprehensive map of <scp>NTRK</scp> fusion variants and their diagnostic coverage by targeted <scp>RNA</scp>â€based <scp>NGS</scp> assays. Genes Chromosomes and Cancer, 2020, 59, 445-453.	1.5	27
152	Clinical and virological characteristics of hospitalised COVID-19 patients in a German tertiary care centre during the first wave of the SARS-CoV-2 pandemic: a prospective observational study. Infection, 2021, 49, 703-714.	2.3	27
153	FOXM1: A novel drug target in gastroenteropancreatic neuroendocrine tumors. Oncotarget, 2015, 6, 8185-8199.	0.8	26
154	NS1 Specific CD8+ T-Cells with Effector Function and TRBV11 Dominance in a Patient with Parvovirus B19 Associated Inflammatory Cardiomyopathy. PLoS ONE, 2008, 3, e2361.	1.1	25
155	Characterization of genomic imbalances in diffuse large Bâ€cell lymphoma by detailed SNPâ€chip analysis. International Journal of Cancer, 2015, 136, 1033-1042.	2.3	25
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