Michael Hummel

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Mucosal melanomas of different anatomic sites share a common global <scp>DNA</scp> methylation profile with cutaneous melanoma but show locationâ€dependent patterns of genetic and epigenetic alterations. Journal of Pathology, 2022, 256, 61-70.	4.5	12
2	Cerebral Abnormalities in Spina Bifida: A Neuropathological Study. Pediatric and Developmental Pathology, 2022, 25, 107-123.	1.0	3
3	S100A4 Is a Strong Negative Prognostic Marker and Potential Therapeutic Target in Adenocarcinoma of the Stomach and Esophagus. Cells, 2022, 11, 1056.	4.1	4
4	Protein kinase C targeting of luminal (T-47D), luminal/HER2-positive (BT474), and triple negative (HCC1806) breast cancer cells in-vitro with AEB071 (Sotrastaurin) is efficient but mediated by subtype specific molecular effects. Archives of Gynecology and Obstetrics, 2022, 306, 1197-1210.	1.7	4
5	Inhibition of MACC1-Induced Metastasis in Esophageal and Gastric Adenocarcinomas. Cancers, 2022, 14, 1773.	3.7	4
6	Response prediction in patients with gastric and esophagogastric adenocarcinoma under neoadjuvant chemotherapy using targeted gene expression analysis and next-generation sequencing in pre-therapeutic biopsies. Journal of Cancer Research and Clinical Oncology, 2022, , 1.	2.5	2
7	Reconstitution of EBV-directed T cell immunity by adoptive transfer of peptide-stimulated T cells in a patient after allogeneic stem cell transplantation for AITL. PLoS Pathogens, 2022, 18, e1010206.	4.7	5
8	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	12.8	52
9	<scp>TFE3</scp> activation in a <scp><i>TSC1</i>â€altered</scp> malignant <scp>PEComa</scp> : challenging the dichotomy of the underlying pathogenic mechanisms. Journal of Pathology: Clinical Research, 2021, 7, 3-9.	3.0	14
10	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.	1.4	31
11	KRASG12C/TP53 co-mutations identify long-term responders to first line palliative treatment with pembrolizumab monotherapy in PD-L1 high (≥50%) lung adenocarcinoma. Translational Lung Cancer Research, 2021, 10, 737-752.	2.8	28
12	Classification of Molecular Subtypes of High-Grade Serous Ovarian Cancer by MALDI-Imaging. Cancers, 2021, 13, 1512.	3.7	14
13	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.	4.7	27
14	Stakeholder engagement to ensure the sustainability of biobanks: a survey of potential users of biobank services. European Journal of Human Genetics, 2021, , .	2.8	8
15	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34
16	Impact of dexamethasone on SARS-CoV-2 concentration kinetics and antibody response in hospitalized COVID-19 patients: results from a prospective observational study. Clinical Microbiology and Infection, 2021, 27, 1520.e7-1520.e10.	6.0	13
17	Status quo of ALK testing in lung cancer: results of an EQA scheme based on in-situ hybridization, immunohistochemistry, and RNA/DNA sequencing. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2021, 479, 247-255.	2.8	5
18	BRAF testing in metastatic colorectal carcinoma and novel, chemotherapy-free therapeutic options. Der Pathologe, 2021, 42, 98-109.	1.6	5

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19	Validation of a Targeted Next-Generation Sequencing Panel for Tumor Mutation Burden Analysis. Journal of Molecular Diagnostics, 2021, 23, 882-893.	2.8	2
20	A time-resolved proteomic and prognostic map of COVID-19. Cell Systems, 2021, 12, 780-794.e7.	6.2	125
21	Early IFN-α signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. Immunity, 2021, 54, 2650-2669.e14.	14.3	145
22	The journey to establishing an IT-infrastructure within the German Biobank Alliance. PLoS ONE, 2021, 16, e0257632.	2.5	9
23	Next-Generation Sequencing–Based Clonality Assessment of Ig Gene Rearrangements. Journal of Molecular Diagnostics, 2021, 23, 1105-1115.	2.8	25
24	Aberrant Expression of and Cell Death Induction by Engagement of the MHC-II Chaperone CD74 in Anaplastic Large Cell Lymphoma (ALCL). Cancers, 2021, 13, 5012.	3.7	1
25	Unification of Treatments and Interventions for Tinnitus Patients (UNITI): a study protocol for a multi-center randomized clinical trial. Trials, 2021, 22, 875.	1.6	12
26	Testing <i>NTRK</i> testing: Wetâ€lab and in silico comparison of RNAâ€based targeted sequencing assays. Genes Chromosomes and Cancer, 2020, 59, 178-188.	2.8	52
27	Evaluating the German Biobank Node as Coordinating Institution of the German Biobank Alliance: Engaging with Stakeholders via Survey Research. Biopreservation and Biobanking, 2020, 18, 64-72.	1.0	11
28	H3K9me3-mediated epigenetic regulation of senescence in mice predicts outcome of lymphoma patients. Nature Communications, 2020, 11, 3651.	12.8	15
29	Immunoprofiling in Neuroendocrine Neoplasms Unveil Immunosuppressive Microenvironment. Cancers, 2020, 12, 3448.	3.7	12
30	Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. Cell, 2020, 182, 1419-1440.e23.	28.9	1,162
31	Synthetic Notch-Receptor-Mediated Transmission of a Transient Signal into Permanent Information via CRISPR/Cas9-Based Genome Editing. Cells, 2020, 9, 1929.	4.1	3
32	Acquired resistance to DZNep-mediated apoptosis is associated with copy number gains of AHCY in a B-cell lymphoma model. BMC Cancer, 2020, 20, 427.	2.6	3
33	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.	4.7	79
34	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.	1.1	81
35	<scp>NTRK</scp> testing: First results of the <scp>QuiPâ€EQA</scp> scheme and a comprehensive map of <scp><i>NTRK</i></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.	2.8	27
36	Sample Quality as Basic Prerequisite for Data Quality: A Quality Management System for Biobanks. Lecture Notes in Computer Science, 2020, , 89-94.	1.3	0

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37	Integrative genomic analysis focused on cell cycle genes for MYC-driven aggressive mature B-cell lymphoma. Journal of Clinical and Experimental Hematopathology: JCEH, 2020, 60, 87-96.	0.8	1
38	DZNep-mediated apoptosis in B-cell lymphoma is independent of the lymphoma type, EZH2 mutation status and MYC, BCL2 or BCL6 translocations. PLoS ONE, 2019, 14, e0220681.	2.5	10
39	Position Statement from the German Biobank Alliance on the Cooperation Between Academic Biobanks and Industry Partners. Biopreservation and Biobanking, 2019, 17, 372-374.	1.0	6
40	Discovery and Validation of Novel Biomarkers for Detection of Epithelial Ovarian Cancer. Cells, 2019, 8, 713.	4.1	32
41	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.	7.2	177
42	Next generation sequencing of lung adenocarcinoma subtypes with intestinal differentiation reveals distinct molecular signatures associated with histomorphology and therapeutic options. Lung Cancer, 2019, 138, 43-51.	2.0	24
43	Pan-European Data Harmonization for Biobanks in ADOPT BBMRI-ERIC. Applied Clinical Informatics, 2019, 10, 679-692.	1.7	12
44	DNA methylation profiling reliably distinguishes pulmonary enteric adenocarcinoma from metastatic colorectal cancer. Modern Pathology, 2019, 32, 855-865.	5.5	36
45	Quality control and quantification in IG/TR next-generation sequencing marker identification: protocols and bioinformatic functionalities by EuroClonality-NGS. Leukemia, 2019, 33, 2254-2265.	7.2	70
46	Characterization of the tumor immune micromilieu and its interference with outcome after concurrent chemoradiation in patients with oropharyngeal carcinomas. Oncolmmunology, 2019, 8, 1614858.	4.6	24
47	Next-generation sequencing of immunoglobulin gene rearrangements for clonality assessment: a technical feasibility study by EuroClonality-NGS. Leukemia, 2019, 33, 2227-2240.	7.2	92
48	Clinical Impact of Rare and Compound Mutations of Epidermal Growth Factor Receptor in Patients With Non–Small-Cell Lung Cancer. Clinical Lung Cancer, 2019, 20, 350-362.e4.	2.6	10
49	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. Cancer Research, 2019, 79, 3125-3138.	0.9	19
50	A modular transcriptome map of mature B cell lymphomas. Genome Medicine, 2019, 11, 27.	8.2	51
51	Mutational Diversity and Therapy Response in Breast Cancer: A Sequencing Analysis in the Neoadjuvant GeparSepto Trial. Clinical Cancer Research, 2019, 25, 3986-3995.	7.0	32
52	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	12.8	99
53	Localization-associated immune phenotypes of clonally expanded tumor-infiltrating T cells and distribution of their target antigens in rectal cancer. Oncolmmunology, 2019, 8, e1586409.	4.6	20
54	Identification of ADGRE5 as discriminating MYC target between Burkitt lymphoma and diffuse large B-cell lymphoma. BMC Cancer, 2019, 19, 322.	2.6	8

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55	Precise detection of genomic imbalances at single-cell resolution reveals intra-patient heterogeneity in Hodgkin's lymphoma. Blood Cancer Journal, 2019, 9, 92.	6.2	8
56	A New and Simple TRG Multiplex PCR Assay for Assessment of T ell Clonality: A Comparative Study from the EuroClonality Consortium. HemaSphere, 2019, 3, e255.	2.7	9
57	Biobanks for future medicine. Journal of Laboratory Medicine, 2019, 43, 383-388.	1.1	8
58	A Phase I/II first-line study of R-CHOP plus B-cell receptor/NF-κB-double-targeting to molecularly assess therapy response. International Journal of Hematologic Oncology, 2019, 8, IJH20.	1.6	7
59	Comparison of Gold Standard Genescan with NGS-Based TCR-Beta Clonality Analysis Using Oncomine TCR Beta-Short Read Assay. Blood, 2019, 134, 4664-4664.	1.4	0
60	T-cell repertoires in refractory coeliac disease. Gut, 2018, 67, gutjnl-2016-311816.	12.1	21
61	Big data and precision medicine: challenges and strategies with healthcare data. International Journal of Data Science and Analytics, 2018, 6, 241-249.	4.1	24
62	Intratumoral morphological heterogeneity can be an indicator of genetic heterogeneity in colorectal cancer. Experimental and Molecular Pathology, 2018, 104, 76-81.	2.1	6
63	Senescence-associated reprogramming promotes cancer stemness. Nature, 2018, 553, 96-100.	27.8	714
64	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.	3.5	34
65	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.	7.2	70
66	Advanced patient age at diagnosis of diffuse large B-cell lymphoma is associated with molecular characteristics including ABC-subtype and high expression of MYC. Leukemia and Lymphoma, 2018, 59, 1213-1221.	1.3	18
67	Mechanisms of Targeting the MDM2-p53-FOXM1 Axis in Well-Differentiated Intestinal Neuroendocrine Tumors. Neuroendocrinology, 2018, 107, 1-23.	2.5	5
68	RNA-based analysis of ALK fusions in non-small cell lung cancer cases showing IHC/FISH discordance. BMC Cancer, 2018, 18, 1158.	2.6	17
69	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.	1.8	32
70	Immunohistochemical Study of Mitosis-regulatory Proteins in Gastroenteropancreatic Neuroendocrine Neoplasms. Anticancer Research, 2018, 38, 3863-3870.	1.1	7
71	Mutational frequencies of <i>CD79B</i> and <i>MYD88</i> vary greatly between primary testicular DLBCL and gastrointestinal DLBCL. Leukemia and Lymphoma, 2018, 59, 1260-1263.	1.3	14
72	High-accuracy determination of internal circadian time from a single blood sample. Journal of Clinical Investigation, 2018, 128, 3826-3839.	8.2	174

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73	Comparative assessment of differential network analysis methods. Briefings in Bioinformatics, 2017, 18, bbw061.	6.5	65
74	Comprehensive Metaboproteomics of Burkitt's and Diffuse Large B-Cell Lymphoma Cell Lines and Primary Tumor Tissues Reveals Distinct Differences in Pyruvate Content and Metabolism. Journal of Proteome Research, 2017, 16, 1105-1120.	3.7	22
75	High-Throughput Immunogenetics for Clinical and Research Applications in Immunohematology: Potential and Challenges. Journal of Immunology, 2017, 198, 3765-3774.	0.8	61
76	Influence of mucinous and necrotic tissue in colorectal cancer samples on KRAS mutation analysis. Pathology Research and Practice, 2017, 213, 606-611.	2.3	3
77	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.	2.8	51
78	Pharmacological restoration and therapeutic targeting of the B-cell phenotype in classical Hodgkin lymphoma. Blood, 2017, 129, 71-81.	1.4	11
79	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.	2.8	29
80	Synergy of interleukin 10 and tollâ€like receptor 9 signalling in B cell proliferation: Implications for lymphoma pathogenesis. International Journal of Cancer, 2017, 140, 1147-1158.	5.1	5
81	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.	2.8	82
82	In Vitro Evaluation of Glycoengineered RSV-F in the Human Artificial Lymph Node Reactor. Bioengineering, 2017, 4, 70.	3.5	4
83	Clinical Impact of the Cell-of-Origin Classification and the <i>MYC</i> / <i>BCL2</i> 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.	1.6	179
84	Proteasome inhibitor bortezomib enhances the effect of standard chemotherapy in small cell lung cancer. Oncotarget, 2017, 8, 97061-97078.	1.8	22
85	A Decentralized IT Architecture for Locating and Negotiating Access to Biobank Samples. Studies in Health Technology and Informatics, 2017, 243, 75-79.	0.3	7
86	Proof-of-Concept Integration of Heterogeneous Biobank IT Infrastructures into a Hybrid Biobanking Network. Studies in Health Technology and Informatics, 2017, 243, 100-104.	0.3	11
87	Poorly Differentiated Medullary Phenotype Predicts Poor Survival in Early Lymph Node-Negative Gastro-Esophageal Adenocarcinomas. PLoS ONE, 2016, 11, e0168237.	2.5	2
88	Inactivation of RUNX3/p46 Promotes Cutaneous T-Cell Lymphoma. Journal of Investigative Dermatology, 2016, 136, 2287-2296.	0.7	12
89	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. Blood, 2016, 128, 2666-2670.	1.4	82
90	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.	3.5	43

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91	Multicenter Evaluation of a Novel Automated Rapid Detection System of BRAF Status in Formalin-Fixed, Paraffin-Embedded Tissues. Journal of Molecular Diagnostics, 2016, 18, 370-377.	2.8	25
92	Age and cellular composition influence overall survival in a collective of non-immunocompromised patients with EBV-positive diffuse large B-cell lymphoma from a German lymphoma center. Leukemia and Lymphoma, 2016, 57, 2791-2803.	1.3	2
93	Prevalence and associated survival of high-risk HPV-related adenoid cystic carcinoma of the salivary glands. International Journal of Oncology, 2016, 49, 803-811.	3.3	15
94	Novel <i>IGH</i> and <i>MYC</i> Translocation Partners in Diffuse Large B ell Lymphomas. Genes Chromosomes and Cancer, 2016, 55, 932-943.	2.8	10
95	A roadmap of constitutive NF-κB activity in Hodgkin lymphoma: Dominant roles of p50 and p52 revealed by genome-wide analyses. Genome Medicine, 2016, 8, 28.	8.2	47
96	A novel approach to detect resistance mechanisms reveals FGR as a factor mediating HDAC inhibitor SAHA resistance in Bâ€cell lymphoma. Molecular Oncology, 2016, 10, 1232-1244.	4.6	13
97	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.	0.7	35
98	NGS-based BRCA1/2 mutation testing of high-grade serous ovarian cancer tissue: results and conclusions of the first international round robin trial. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2016, 468, 697-705.	2.8	24
99	The Clinical Impact of the Cell-of-Origin Classification and the MYC+/BCL2+ Double Expresser Status in DLBCL Treated within Prospective Clinical Trials of the Dshnhl. Blood, 2016, 128, 151-151.	1.4	2
100	Adoptive Transfer of CMV- and EBV- Specific Peptide-Stimulated T Cells after Allogeneic Stem Cell Transplantation: First Results of a Phase I/IIa Clinical Trial [Multivir-01]. Blood, 2016, 128, 2179-2179.	1.4	1
101	ÎFΌΒΙΕ Deletions: A Novel Marker of Clinical Aggressiveness in Primary Mediastinal B-Cell Lymphoma. Blood, 2016, 128, 609-609.	1.4	Ο
102	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
103	Essential role of IRF4 and MYC signaling for survival of anaplastic large cell lymphoma. Blood, 2015, 125, 124-132.	1.4	79
104	The glucosinolate metabolite 1â€methoxyâ€3â€indolylmethyl alcohol induces a gene expression profile in mouse liver similar to the expression signature caused by known genotoxic hepatocarcinogens. Molecular Nutrition and Food Research, 2015, 59, 685-697.	3.3	12
105	Proximal weakness in a patient with <scp>MALT</scp> lymphoma: a case report and discussion of possible pathogenesis. Neuropathology and Applied Neurobiology, 2015, 41, 686-689.	3.2	0
106	The <i>PCBP1</i> gene encoding poly(rc) binding protein i is recurrently mutated in <scp>B</scp> urkitt lymphoma. Genes Chromosomes and Cancer, 2015, 54, 555-564.	2.8	29
107	A new method to prevent carry-over contaminations in two-step PCR NGS library preparations. Nucleic Acids Research, 2015, 43, gkv694.	14.5	40
108	Activity-Based Probes for Detection of Active MALT1 Paracaspase in Immune Cells and Lymphomas. Chemistry and Biology, 2015, 22, 129-138.	6.0	36

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109	Bone Marrow Work-up: Report of a Pilot Study. Recent Results in Cancer Research, 2015, 199, 95-105.	1.8	1
110	Automation of ALK gene rearrangement testing with fluorescence in situ hybridization (FISH): A feasibility study. Experimental and Molecular Pathology, 2015, 98, 113-118.	2.1	9
111	Algorithms for differential splicing detection using exon arrays: a comparative assessment. BMC Genomics, 2015, 16, 136.	2.8	3
112	Aurora Kinase A Is Upregulated in Cutaneous T-Cell Lymphoma and Represents a Potential Therapeutic Target. Journal of Investigative Dermatology, 2015, 135, 2292-2300.	0.7	21
113	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.	21.4	119
114	Machine Learning-based Classification of Diffuse Large B-cell Lymphoma Patients by Their Protein Expression Profiles. Molecular and Cellular Proteomics, 2015, 14, 2947-2960.	3.8	73
115	<i>DCLRE1C</i> (ARTEMIS) mutations causing phenotypes ranging from atypical severe combined immunodeficiency to mere antibody deficiency. Human Molecular Genetics, 2015, 24, 7361-7372.	2.9	72
116	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.	4.6	112
117	MINCR is a MYC-induced IncRNA able to modulate MYC's transcriptional network in Burkitt lymphoma cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5261-70.	7.1	91
118	ALK-FISH borderline cases in non-small cell lung cancer: Implications for diagnostics and clinical decision making. Lung Cancer, 2015, 90, 465-471.	2.0	36
119	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.	2.0	54
120	Characterization of genomic imbalances in diffuse large Bâ€cell lymphoma by detailed SNPâ€chip analysis. International Journal of Cancer, 2015, 136, 1033-1042.	5.1	25
121	Unusual relapse of an angioimmunoblastic T cell lymphoma 11Âyears after initial manifestation. Annals of Hematology, 2015, 94, 347-349.	1.8	0
122	FOXM1: A novel drug target in gastroenteropancreatic neuroendocrine tumors. Oncotarget, 2015, 6, 8185-8199.	1.8	26
123	Histopathological features and their prognostic impact in nodular lymphocyteâ€predominant Hodgkin lymphoma – a matched pair analysis from the German Hodgkin Study Group (GHSG). British Journal of Haematology, 2014, 167, 238-242.	2.5	35
124	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.	2.4	42
125	Multicenter Immunohistochemical ALK-Testing of Non–Small-Cell Lung Cancer Shows High Concordance after Harmonization of Techniques and Interpretation Criteria. Journal of Thoracic Oncology, 2014, 9, 1685-1692.	1.1	66
126	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.	1.4	54

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127	Multicenter ALK Testing in Non–Small-Cell Lung Cancer: Results of a Round Robin Test. Journal of Thoracic Oncology, 2014, 9, 1464-1469.	1.1	17
128	Pharmacological and genomic profiling identifies NF-κB–targeted treatment strategies for mantle cell lymphoma. Nature Medicine, 2014, 20, 87-92.	30.7	303
129	Participation in and support of clinical studies and other scientific investigations – Statement of the German Society for Pathology. Pathology Research and Practice, 2014, 210, 705-712.	2.3	3
130	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.	7.1	53
131	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.	2.5	64
132	Reference gene stability in peripheral blood mononuclear cells determined by qPCR and NanoString. Mikrochimica Acta, 2014, 181, 1733-1742.	5.0	9
133	A recurrent 11q aberration pattern characterizes a subset of MYC-negative high-grade B-cell lymphomas resembling Burkitt lymphoma. Blood, 2014, 123, 1187-1198.	1.4	185
134	Biological characterization of adult MYC-translocation-positive mature B-cell lymphomas other than molecular Burkitt lymphoma. Haematologica, 2014, 99, 726-735.	3.5	157
135	RIP1 expression is necessary for CD30-mediated cell death induction in anaplastic large-cell lymphoma cells. Laboratory Investigation, 2013, 93, 677-689.	3.7	5
136	Synthetic lethal metabolic targeting of cellular senescence in cancer therapy. Nature, 2013, 501, 421-425.	27.8	437
137	Hypermutation of the Inactive X Chromosome Is a Frequent Event in Cancer. Cell, 2013, 155, 567-581.	28.9	67
138	Predictive molecular pathology and its role in targeted cancer therapy: a review focussing on clinical relevance. Cancer Gene Therapy, 2013, 20, 211-221.	4.6	58
139	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.	2.0	48
140	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.	7.1	233
141	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.	2.6	34
142	Histone acetylation and DNA demethylation of T cells result in an anaplastic large cell lymphoma-like phenotype. Haematologica, 2013, 98, 247-254.	3.5	15
143	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.	1.4	168
144	MYC status in concert with BCL2 and BCL6 expression predicts outcome in diffuse large B-cell lymphoma. Blood, 2013, 121, 2253-2263.	1.4	468

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145	lκB-ζ controls the constitutive NF-κB target gene network and survival of ABC DLBCL. Blood, 2013, 122, 2242-2250.	1.4	70
146	Molecular diagnostics in cutaneous lymphomas. JDDG - Journal of the German Society of Dermatology, 2013, 11, 25-35.	0.8	13
147	Molekulare Diagnostik kutaner Lymphome. JDDG - Journal of the German Society of Dermatology, 2013, 11, 26-36.	0.8	3
148	Massive Transcriptional Perturbation in Subgroups of Diffuse Large B-Cell Lymphomas. PLoS ONE, 2013, 8, e76287.	2.5	4
149	Acquired Stem Cell Properties In Therapy-Induced Senescence Of Lymphomas and Acute Leukemias In Vitro and In Vivo. Blood, 2013, 122, 4193-4193.	1.4	1
150	The Prognostic Impact Of Gene Rearrangements and Protein Expression Of MYC, BCL2 and BCL6 In Young High-Risk Patients With DLBCL. Blood, 2013, 122, 4262-4262.	1.4	1
151	Detection of clonal T-cell-receptor (TCR) Vbeta rearrangements in explanted dilated cardiomyopathy hearts by semi-nested PCR, GeneScan, and direct sequencing. Medical Science Monitor Basic Research, 2013, 19, 111-117.	2.6	5
152	In-Depth miRNA Profiling Of Germinal Center Derived B-Cell Lymphomas By Next Generation Sequencing: A Report From The German Icgc-Mmml-Seq Project. Blood, 2013, 122, 2500-2500.	1.4	4
153	Prognostic Biomarkers and EBV Infection Research in Diffuse Large B-Cell Lymphoma of the Palatine Tonsils. ISRN Oncology, 2012, 2012, 1-7.	2.1	3
154	Patient age at diagnosis is associated with the molecular characteristics of diffuse large B-cell lymphoma. Blood, 2012, 119, 1882-1887.	1.4	163
155	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.	2.8	74
156	Transcriptome and proteome analysis of tyrosine kinase inhibitor treated canine mast cell tumour cells identifies potentially kit signaling-dependent genes. BMC Veterinary Research, 2012, 8, 96.	1.9	12
157	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. Nature Genetics, 2012, 44, 1316-1320.	21.4	389
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