Ralf KÃ¼ppers

List of Publications by Year
in descending order

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186	17,716	16451	14208
papers	citations	64 h-index	128 g-index

192	192	192	16545
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Human Immunoglobulin (Ig)M+IgD+ Peripheral Blood B Cells Expressing the CD27 Cell Surface Antigen Carry Somatically Mutated Variable Region Genes: CD27 as a General Marker for Somatically Mutated (Memory) B Cells. Journal of Experimental Medicine, 1998, 188, 1679-1689.	8.5	1,018
2	Hypermutation of multiple proto-oncogenes in B-cell diffuse large-cell lymphomas. Nature, 2001, 412, 341-346.	27.8	921
3	Mechanisms of B-cell lymphoma pathogenesis. Nature Reviews Cancer, 2005, 5, 251-262.	28.4	773
4	Cellular Origin of Human B-Cell Lymphomas. New England Journal of Medicine, 1999, 341, 1520-1529.	27.0	640
5	The biology of Hodgkin's lymphoma. Nature Reviews Cancer, 2009, 9, 15-27.	28.4	617
6	Mechanisms of chromosomal translocations in B cell lymphomas. Oncogene, 2001, 20, 5580-5594.	5.9	570
7	From pathogenesis to treatment of chronic lymphocytic leukaemia. Nature Reviews Cancer, 2010, 10, 37-50.	28.4	503
8	TNFAIP3 (A20) is a tumor suppressor gene in Hodgkin lymphoma and primary mediastinal B cell lymphoma. Journal of Experimental Medicine, 2009, 206, 981-989.	8.5	448
9	B cells under influence: transformation of B cells by Epsteinâ€“Barr virus. Nature Reviews Immunology, 2003, 3, 801-812.	22.7	436
10	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
11	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
12	Loss of the B-lineageâ€“specific gene expression program in Hodgkin and Reed-Sternberg cells of Hodgkin lymphoma. Blood, 2003, 101, 1505-1512.	1.4	353
13	Somatic hypermutation in normal and transformed human B cells. Immunological Reviews, 1998, 162, 261-280.	6.0	327
14	Origin and pathogenesis of nodular lymphocyteâ€“predominant Hodgkin lymphoma as revealed by global gene expression analysis. Journal of Experimental Medicine, 2008, 205, 2251-2268.	8.5	312
15	THE ORIGIN OF HODGKIN AND REED/STERNBERG CELLS IN HODGKIN'S DISEASE. Annual Review of Immunology, 1998, 16, 471-493.	21.8	291
16	Translocations activating IRF4 identify a subtype of germinal center-derived B-cell lymphoma affecting predominantly children and young adults. Blood, 2011, 118, 139-147.	1.4	281
17	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	21.4	278
18	Clonal Deleterious Mutations in the Î¹bÎ± Gene in the Malignant Cells in Hodgkin's Lymphoma. Journal of Experimental Medicine, 2000, 191, 395-402.	8.5	264

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19	Identification of Common Germinal-Center B-Cell Precursors in Two Patients with Both Hodgkin's Disease and Non-Hodgkin's Lymphoma. New England Journal of Medicine, 1999, 340, 1239-1247.	27.0	262
20	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. Nature Genetics, 2016, 48, 253-264.	21.4	254
21	Hodgkin lymphoma. Journal of Clinical Investigation, 2012, 122, 3439-3447.	8.2	248
22	Cellular origin and pathophysiology of chronic lymphocytic leukemia. Journal of Experimental Medicine, 2012, 209, 2183-2198.	8.5	227
23	Rare Occurrence of Classical Hodgkin's Disease as a T Cell Lymphoma. Journal of Experimental Medicine, 2000, 191, 387-394.	8.5	198
24	EBV-Infected B Cells in Infectious Mononucleosis. Immunity, 2000, 13, 485-495.	14.3	198
25	Identification of Hodgkin and Reed-Sternberg cell-specific genes by gene expression profiling. Journal of Clinical Investigation, 2003, 111, 529-537.	8.2	192
26	Functional capacities of human IgM memory B cells in early inflammatory responses and secondary germinal center reactions. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E546-55.	7.1	179
27	Primary Central Nervous System Lymphomas Are Derived from Germinal-Center B Cells and Show a Preferential Usage of the V4â€“34 Gene Segment. American Journal of Pathology, 1999, 155, 2077-2086.	3.8	170
28	Pathogenesis of Classical and Lymphocyte-Predominant Hodgkin Lymphoma. Annual Review of Pathology: Mechanisms of Disease, 2009, 4, 151-174.	22.4	164
29	Molecular biology of Hodgkin's and Reed/Sternberg cells in Hodgkin's lymphoma. International Journal of Cancer, 2006, 118, 1853-1861.	5.1	161
30	Human IgM+IgD+ B cells, the major B cell subset in the peripheral blood, express VÏ° genes with no or little somatic mutation throughout life. European Journal of Immunology, 1993, 23, 3272-3277.	2.9	157
31	Somatic Mutation of the Cd95 Gene in Human B Cells as a Side-Effect of the Germinal Center Reaction. Journal of Experimental Medicine, 2000, 192, 1833-1840.	8.5	157
32	Biological characterization of adult MYC-translocation-positive mature B-cell lymphomas other than molecular Burkitt lymphoma. Haematologica, 2014, 99, 726-735.	3.5	157
33	Molecular footprints of a germinal center derivation of human IgM+(IgD+)CD27+ B cells and the dynamics of memory B cell generation. Journal of Experimental Medicine, 2009, 206, 2659-2669.	8.5	149
34	Molecular biology of Hodgkin's lymphoma. Advances in Cancer Research, 2002, 84, 277-312.	5.0	136
35	Analyzing primary Hodgkin and Reed-Sternberg cells to capture the molecular and cellular pathogenesis of classical Hodgkin lymphoma. Blood, 2012, 120, 4609-4620.	1.4	136
36	Transformation of BCR-deficient germinal-center B cells by EBV supports a major role of the virus in the pathogenesis of Hodgkin and posttransplantation lymphomas. Blood, 2005, 106, 4345-4350.	1.4	135

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37	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.	1.4	133
38	Genomic and epigenomic insights into the origin, pathogenesis, and clinical behavior of mantle cell lymphoma subtypes. Blood, 2020, 136, 1419-1432.	1.4	131
39	Diffuse large cell lymphomas are derived from mature B cells carrying V region genes with a high load of somatic mutation and evidence of selection for antibody expression. European Journal of Immunology, 1997, 27, 1398-1405.	2.9	130
40	Epsteinâ€“Barr virus-infected B cells expanding in germinal centers of infectious mononucleosis patients do not participate in the germinal center reaction. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4730-4735.	7.1	125
41	Hodgkin lymphoma: Pathology and biology. Seminars in Hematology, 2016, 53, 139-147.	3.4	121
42	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
43	Autocrine- and paracrine-activated receptor tyrosine kinases in classic Hodgkin lymphoma. Blood, 2005, 105, 4051-4059.	1.4	116
44	Inactivating SOCS1 mutations are caused by aberrant somatic hypermutation and restricted to a subset of B-cell lymphoma entities. Blood, 2009, 114, 4503-4506.	1.4	115
45	Expression of the IRTA1 receptor identifies intraepithelial and subepithelial marginal zone B cells of the mucosa-associated lymphoid tissue (MALT). Blood, 2003, 102, 3684-3692.	1.4	114
46	Survival and Clonal Expansion of Mutating â€œForbiddenâ€•(Immunoglobulin Receptorâ€“Deficient) Epstein-Barr Virusâ€“Infected B Cells in Angioimmunoblastic T Cell Lymphoma. Journal of Experimental Medicine, 2001, 194, 927-940.	8.5	106
47	Molecular biology of Hodgkin lymphoma. Leukemia, 2021, 35, 968-981.	7.2	102
48	Nodular Lymphocyte Predominant Hodgkin Lymphoma and T Cell/Histiocyte Rich Large B Cell Lymphoma - Endpoints of a Spectrum of One Disease?. PLoS ONE, 2013, 8, e78812.	2.5	99
49	Pathogenesis, diagnosis, and treatment of composite lymphomas. Lancet Oncology, The, 2014, 15, e435-e446.	10.7	99
50	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	12.8	99
51	Detection of genomic imbalances in microdissected Hodgkin and Reed-Sternberg cells of classical Hodgkin's lymphoma by array-based comparative genomic hybridization. Haematologica, 2008, 93, 1318-1326.	3.5	97
52	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.	7.1	91
53	Molecular biology of Hodgkin lymphoma. Hematology American Society of Hematology Education Program, 2009, 2009, 491-496.	2.5	89
54	Common Germinal-Center B-Cell Origin of the Malignant Cells in Two Composite Lymphomas, Involving Classical Hodgkinâ€™s Disease and Either Follicular Lymphoma or B-CLL. Molecular Medicine, 2001, 7, 285-292.	4.4	86

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55	Mutations of CARD11 but not TNFAIP3 may activate the NF-Î²B pathway in primary CNS lymphoma. Acta Neuropathologica, 2010, 120, 529-535.	7.7	86
56	Chromosomal Breakpoints Affecting Immunoglobulin Loci Are Recurrent in Hodgkin and Reed-Sternberg Cells of Classical Hodgkin Lymphoma. Cancer Research, 2006, 66, 10332-10338.	0.9	85
57	Genetic lesions of the <scp>TRAF</scp>3 and <scp>MAP</scp>3K14 genes in classical <scp>H</scp>odgkin lymphoma. British Journal of Haematology, 2012, 157, 702-708.	2.5	84
58	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. Blood, 2016, 128, 2666-2670.	1.4	82
59	Identification of Hodgkin and Reed-Sternberg cell-specific genes by gene expression profiling. Journal of Clinical Investigation, 2003, 111, 529-537.	8.2	82
60	The Hodgkin and Reed/Sternberg cell. International Journal of Biochemistry and Cell Biology, 2005, 37, 511-517.	2.8	79
61	Regulation of immunoglobulin light chain gene rearrangements during early B cell development in the human. European Journal of Immunology, 2001, 31, 3631-3637.	2.9	78
62	NF-Î²B deregulation in Hodgkin lymphoma. Seminars in Cancer Biology, 2016, 39, 32-39.	9.6	74
63	Aberrant Expression of ID2, a Suppressor of B-Cell-Specific Gene Expression, in Hodgkin's Lymphoma. American Journal of Pathology, 2006, 169, 655-664.	3.8	72
64	Detection of genomic aberrations in molecularly defined Burkitt's lymphoma by array-based, high resolution, single nucleotide polymorphism analysis. Haematologica, 2010, 95, 2047-2055.	3.5	70
65	Incomplete cytokinesis and re-fusion of small mononucleated Hodgkin cells lead to giant multinucleated Reedâ€“Sternberg cells. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20729-20734.	7.1	69
66	Molecular Ig gene analysis reveals that monocytoid B cell lymphoma is a malignancy of mature B cells carrying somatically mutated V region genes and suggests that rearrangement of the kappa-deleting element (resulting in deletion of the Ig kappa enhancers) abolishes somatic hypermutation in the human. European Journal of Immunology, 1996, 26, 1794-1800.	2.9	61
67	Mutations in the genes coding for the NF-ÂB regulating factors IÂBÂ and A20 are uncommon in nodular lymphocyte-predominant Hodgkin's lymphoma. Haematologica, 2010, 95, 153-157.	3.5	60
68	New insights in the biology of Hodgkin lymphoma. Hematology American Society of Hematology Education Program, 2012, 2012, 328-334.	2.5	60
69	Complexity of the human memory B-cell compartment is determined by the versatility of clonal diversification in germinal centers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5281-9.	7.1	58
70	Human IgA- and IgM-secreting intestinal plasma cells carry heavily mutated VH region genes. European Journal of Immunology, 1998, 28, 2971-2977.	2.9	57
71	Profiling of Hodgkinâ€™s Lymphoma Cell Line L1236 and Germinal Center B Cells: Identification of Hodgkinâ€™s Lymphoma-specific Genes. Molecular Medicine, 2003, 9, 85-95.	4.4	54
72	Origin and Pathogenesis of B Cell Lymphomas. Methods in Molecular Biology, 2013, 971, 1-25.	0.9	54

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73	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
74	Human splenic marginal zone Bâ€„cells lack expression of activation-induced cytidine deaminase. European Journal of Immunology, 2005, 35, 3002-3007.	2.9	52
75	<scp>TET2</scp> mutations in B cells of patients affected by angioimmunoblastic Tâ€cell lymphoma. Journal of Pathology, 2017, 242, 129-133.	4.5	52
76	SAMHD1 is recurrently mutated in T-cell prolymphocytic leukemia. Blood Cancer Journal, 2018, 8, 11.	6.2	52
77	Recurrent mutations in NF-ÎºB pathway components, KMT2D, and NOTCH1/2 in ocular adnexal MALT-type marginal zone lymphomas. Oncotarget, 2016, 7, 62627-62639.	1.8	52
78	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	12.8	52
79	Recurrent Inactivation of the PRDM1 Gene in Primary Central Nervous System Lymphoma. Journal of Neuropathology and Experimental Neurology, 2008, 67, 720-727.	1.7	51
80	IG-MYC+ neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. Blood, 2018, 132, 2280-2285.	1.4	50
81	Critical influences on the pathogenesis of follicular lymphoma. Blood, 2018, 131, 2297-2306.	1.4	48
82	Common features and differences in the transcriptome of large cell anaplastic lymphoma and classical Hodgkin's lymphoma. Haematologica, 2006, 91, 596-604.	3.5	48
83	Analysis of a Clonally Related Mantle Cell and Hodgkin Lymphoma Indicates Epstein-Barr Virus Infection of a Hodgkin/Reed-Sternberg Cell Precursor in a Germinal Center. American Journal of Surgical Pathology, 2003, 27, 1483-1488.	3.7	47
84	Absence of Immunoglobulin Class Switch in Primary Lymphomas of the Central Nervous System. American Journal of Pathology, 2005, 166, 1773-1779.	3.8	47
85	Mechanisms of aberrant GATA3 expression in classical Hodgkin lymphoma and its consequences for the cytokine profile of Hodgkin and Reed/Sternberg cells. Blood, 2010, 116, 4202-4211.	1.4	45
86	JUNB, DUSP2, SGK1, SOCS1 and CREBBP are frequently mutated in T-cell/histiocyte-rich large B-cell lymphoma. Haematologica, 2019, 104, 330-337.	3.5	45
87	Transcriptional Profiling of the Nuclear Factor-ÎºB Pathway Identifies a Subgroup of Primary Lymphoma of the Central Nervous System With Low BCL10 Expression. Journal of Neuropathology and Experimental Neurology, 2007, 66, 230-237.	1.7	44
88	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
89	CEACAM1 induces B-cell survival and is essential for protective antiviral antibody production. Nature Communications, 2015, 6, 6217.	12.8	42
90	The role of T cells in the microenvironment of Hodgkin lymphoma. Journal of Leukocyte Biology, 2016, 99, 45-50.	3.3	42

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91	Î³Î´ T-cell Receptors Derived from Breast Cancerâ€“Infiltrating T Lymphocytes Mediate Antitumor Reactivity. Cancer Immunology Research, 2020, 8, 530-543.	3.4	42
92	Complex Immune Evasion Strategies in Classical Hodgkin Lymphoma. Cancer Immunology Research, 2017, 5, 1122-1132.	3.4	38
93	Single-Cell PCR Analysis of T Helper Cells in Human Lymph Node Germinal Centers. American Journal of Pathology, 2000, 156, 1067-1071.	3.8	37
94	Rare occurrence of biallelic CYLD gene mutations in classical Hodgkin lymphoma. Genes Chromosomes and Cancer, 2010, 49, 803-809.	2.8	37
95	Alterations of the CD58 gene in classical Hodgkin lymphoma. Genes Chromosomes and Cancer, 2015, 54, 638-645.	2.8	36
96	Recurrent alterations ofTNFAIP3(A20) in T-cell large granular lymphocytic leukemia. International Journal of Cancer, 2016, 138, 121-124.	5.1	36
97	Human CD30+ B cells represent a unique subset related to Hodgkin lymphoma cells. Journal of Clinical Investigation, 2018, 128, 2996-3007.	8.2	36
98	New insights in the biology of Hodgkin lymphoma. Hematology American Society of Hematology Education Program, 2012, 2012, 328-34.	2.5	36
99	Typing the histogenetic origin of the tumor cells of lymphocyte-rich classical Hodgkin's lymphoma in relation to tumor cells of classical and lymphocyte-predominance Hodgkin's lymphoma. Cancer Research, 2003, 63, 1644-51.	0.9	35
100	Genetic Evidence for Latent Septata intestinalis Infection in Human Immunodeficiency Virus-Infected Patients with Intestinal Microsporidiosis. Journal of Infectious Diseases, 1996, 173, 1038-1040.	4.0	34
101	Receptor revision plays no major role in shaping the receptor repertoire of human memory B cells after the onset of somatic hypermutation. European Journal of Immunology, 2001, 31, 3638-3648.	2.9	34
102	Identification of candidate tumour suppressor gene loci for Hodgkin and Reedâ€Sternberg cells by characterisation of homozygous deletions in classical Hodgkin lymphoma cell lines. British Journal of Haematology, 2008, 142, 916-924.	2.5	34
103	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34
104	Whole exome sequencing of microdissected splenic marginal zone lymphoma: a study to discover novel tumor-specific mutations. BMC Cancer, 2015, 15, 773.	2.6	33
105	Lymphocyte predominant cells detect Moraxella catarrhalis-derived antigens in nodular lymphocyte-predominant Hodgkin lymphoma. Nature Communications, 2020, 11, 2465.	12.8	31
106	A model for the development of human IgD-only B cells: Genotypic analyses suggest their generation in superantigen driven immune responses. Molecular Immunology, 2009, 46, 630-639.	2.2	30
107	Advances in Biology, Diagnostics, and Treatment of Hodgkinâ€™s Disease. Biology of Blood and Marrow Transplantation, 2006, 12, 66-76.	2.0	29
108	The aberrant coexpression of several receptor tyrosine kinases is largely restricted to EBV-negative cases of classical Hodgkin's lymphoma. International Journal of Cancer, 2007, 120, 2504-2509.	5.1	29

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109	Molecular Single-Cell Analysis of Hodgkin- and Reed-Sternberg Cells Harboring Unmutated Immunoglobulin Variable Region Genes. Laboratory Investigation, 2001, 81, 289-295.	3.7	28
110	Autocrine NGFÎ²/TRKA signalling is an important survival factor for Hodgkin lymphoma derived cell lines. Leukemia Research, 2008, 32, 163-167.	0.8	28
111	Recurrent deletions of the TNFSF7 and TNFSF9 genes in 19p13.3 in diffuse large Bâ€cell and Burkitt lymphomas. International Journal of Cancer, 2012, 131, E830-5.	5.1	28
112	A novel immunohistochemical classifier to distinguish Hodgkin lymphoma from ALK anaplastic large cell lymphoma. Modern Pathology, 2014, 27, 1345-1354.	5.5	28
113	Biased IGH VDJ gene repertoire and clonal expansions in B cells of chronically hepatitis C virusâ€“infected individuals. Blood, 2018, 131, 546-557.	1.4	28
114	Systematic memory B cell archiving and random display shape the human splenic marginal zone throughout life. Journal of Experimental Medicine, 2021, 218, .	8.5	27
115	Macrophages in T cell/histiocyte rich large B cell lymphoma strongly express metal-binding proteins and show a bi-activated phenotype. International Journal of Cancer, 2013, 133, n/a-n/a.	5.1	26
116	Origin and Pathogenesis of B Cell Lymphomas. Methods in Molecular Biology, 2019, 1956, 1-33.	0.9	26
117	Somatic Hypermutation and B Cell Receptor Selection in Normal and Transformed Human B Cells. Annals of the New York Academy of Sciences, 2003, 987, 173-179.	3.8	25
118	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
119	BCL2 and BCL3 are recurrent translocation partners of the IGH locus. Cancer Genetics and Cytogenetics, 2008, 186, 110-114.	1.0	24
120	UMI or not UMI, that is the question for scRNA-seq zero-inflation. Nature Biotechnology, 2021, 39, 158-159.	17.5	24
121	CD5-positive B cells in healthy elderly humans are a polyclonal B cell population. European Journal of Immunology, 2000, 30, 2918-2923.	2.9	23
122	Indications for peripheral light-chain revision and somatic hypermutation without a functional B-cell receptor in precursors of a composite diffuse large B-cell and Hodgkin's lymphoma. Laboratory Investigation, 2004, 84, 253-262.	3.7	23
123	Immunoglobulin Repertoire of Primary Lymphomas of the Central Nervous System. Journal of Neuropathology and Experimental Neurology, 2014, 73, 1116-1125.	1.7	23
124	Clonotypic B cells in classic Hodgkin lymphoma. Blood, 2009, 114, 3970-3971.	1.4	22
125	B Cells in Chronically Hepatitis C Virus-Infected Individuals Lack a Virus-Induced Mutation Signature in theTP53,CTNNB1, andBCL6Genes. Journal of Virology, 2013, 87, 2956-2962.	3.4	22
126	Absence of measles virus genome and transcripts in Hodgkin-Reed/Sternberg cells of a cohort of Hodgkin lymphoma patients. International Journal of Cancer, 2007, 121, 448-453.	5.1	20

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127	Subclonal evolution of a classical Hodgkin lymphoma from a germinal center Bâ€cellâ€derived mantle cell lymphoma. International Journal of Cancer, 2014, 134, 832-843.	5.1	20
128	CD30 expression in neoplastic T cells of follicular T cell lymphoma is a helpful diagnostic tool in the differential diagnosis of Hodgkin lymphoma. Modern Pathology, 2019, 32, 37-47.	5.5	19
129	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. Cancer Research, 2019, 79, 3125-3138.	0.9	19
130	Clonally related splenic marginal zone lymphoma and Hodgkin lymphoma with unmutated V gene rearrangements and a 15-yr time gap between diagnoses. European Journal of Haematology, 2004, 73, 210-214.	2.2	18
131	Pathogenesis of Hodgkin's lymphoma. European Journal of Haematology, 2005, 75, 26-33.	2.2	18
132	Human Cord Blood B Cells Differ from the Adult Counterpart by Conserved Ig Repertoires and Accelerated Response Dynamics. Journal of Immunology, 2021, 206, 2839-2851.	0.8	18
133	Quantitative Comparison of Abundance Structures of Generalized Communities: From B-Cell Receptor Repertoires to Microbiomes. PLoS Computational Biology, 2017, 13, e1005362.	3.2	17
134	Identifying Genetic Lesions in Ocular Adnexal Extranodal Marginal Zone Lymphomas of the MALT Subtype by Whole Genome, Whole Exome and Targeted Sequencing. Cancers, 2020, 12, 986.	3.7	17
135	Mutation analysis of the TNFAIP3 (A20) tumor suppressor gene in CLL. International Journal of Cancer, 2011, 128, 1747-1750.	5.1	16
136	Potential role of hypoxia in early stages of Hodgkin lymphoma pathogenesis. Haematologica, 2015, 100, 1320-1326.	3.5	16
137	Reprogramming of the tumour B-cell phenotype in Hodgkin lymphoma. Trends in Immunology, 2006, 27, 203-205.	6.8	15
138	Laser-Based Microdissection of Single Cells from Tissue Sections and PCR Analysis of Rearranged Immunoglobulin Genes from Isolated Normal and Malignant Human B Cells. Methods in Molecular Biology, 2013, 971, 49-63.	0.9	15
139	Hodgkin-Reed-Sternberg Cells in Classical Hodgkin Lymphoma Show Alterations of Genes Encoding the NADPH Oxidase Complex and Impaired Reactive Oxygen Species Synthesis Capacity. PLoS ONE, 2013, 8, e84928.	2.5	15
140	A strong host response and lack of MYC expression are characteristic for diffuse large B cell lymphoma transformed from nodular lymphocyte predominant Hodgkin lymphoma. Oncotarget, 2016, 7, 72197-72210.	1.8	14
141	The process of somatic hypermutation increases polyreactivity for central nervous system antigens in primary central nervous system lymphoma. Haematologica, 2021, 106, 708-717.	3.5	14
142	Fibroblasts in Nodular Sclerosing Classical Hodgkin Lymphoma Are Defined by a Specific Phenotype and Protect Tumor Cells from Brentuximab-Vedotin Induced Injury. Cancers, 2019, 11, 1687.	3.7	12
143	Role of Specific B-Cell Receptor Antigens in Lymphomagenesis. Frontiers in Oncology, 2020, 10, 604685.	2.8	11
144	Molecular Single-Cell PCR Analysis of Rearranged Immunoglobulin Genes As a Tool to Determine the Clonal Composition of Normal and Malignant Human B Cells. , 2004, 271, 225-238.		10

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145	Novel IGH and MYC Translocation Partners in Diffuse Large Bâ€Cell Lymphomas. Genes Chromosomes and Cancer, 2016, 55, 932-943.	2.8	10
146	Tumor-infiltrating HLA-matched CD4⁺T cells retargeted against Hodgkin and Reedâ€“Sternberg cells. OncoImmunology, 2016, 5, e1160186.	4.6	9
147	Human memory B cells: Memory B cells of a special kind. Immunology and Cell Biology, 2008, 86, 635-636.	2.3	8
148	Ectopic expression of transcription factor BATF3 induces B-cell lymphomas in a murine B-cell transplantation model. Oncotarget, 2018, 9, 15942-15951.	1.8	8
149	Impact of a Faulty Germinal Center Reaction on the Pathogenesis of Primary Diffuse Large B Cell Lymphoma of the Central Nervous System. Cancers, 2021, 13, 6334.	3.7	8
150	Role of hepatitis C virus in B cell lymphoproliferations. Virologica Sinica, 2014, 29, 3-6.	3.0	7
151	Migration Properties Distinguish Tumor Cells of Classical Hodgkin Lymphoma from Anaplastic Large Cell Lymphoma Cells. Cancers, 2019, 11, 1484.	3.7	7
152	Laser-Based Microdissection of Single Cells from Tissue Sections and PCR Analysis of Rearranged Immunoglobulin Genes from Isolated Normal and Malignant Human B Cells. Methods in Molecular Biology, 2019, 1956, 61-75.	0.9	7
153	Intrahepatic <scp>B</scp>â€cell follicles of chronically hepatitis <scp>C</scp> virusâ€infected individuals lack signs of an ectopic germinal center reaction. European Journal of Immunology, 2014, 44, 1842-1850.	2.9	6
154	A large fraction of human tonsillar B cells expressing CD27 are germinal center B cells. Immunology and Cell Biology, 2015, 93, 429-430.	2.3	6
155	Regulation of immunoglobulin light chain gene rearrangements during early Bâ€‰cell development in the human. European Journal of Immunology, 2001, 31, 3631.	2.9	6
156	PLK1â€dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBVâ€infected mice. EMBO Reports, 2021, 22, e53007.	4.5	5
157	The Splenic Marginal Zone in Children Is Characterized by a Subpopulation of CD27-Negative, Lowly IGHV-Mutated B Cells. Frontiers in Immunology, 2022, 13, 825619.	4.8	5
158	Expression profile of translation initiation factor eIF2B5 in diffuse large B-cell lymphoma and its correlation to clinical outcome. Blood Cancer Journal, 2018, 8, 79.	6.2	4
159	CD81 as target for B cell lymphomas. Journal of Experimental Medicine, 2019, 216, 1469-1470.	8.5	4
160	The Genomic Landscape of HIV-Associated Plasmablastic Lymphoma. Blood Cancer Discovery, 2020, 1, 23-25.	5.0	4
161	Molecular analysis of IgD-positive human germinal centres. International Immunology, 2010, 22, 289-298.	4.0	3
162	Side population cells in Hodgkin lymphoma. Leukemia and Lymphoma, 2010, 51, 741-742.	1.3	3

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163	The life of B cells according to JEM. Journal of Experimental Medicine, 2021, 218, .	8.5	3
164	The Biology of Ocular Adnexal Marginal Zone Lymphomas. Cancers, 2022, 14, 1264.	3.7	3
165	Genomic imbalances in Hodgkin lymphoma. Blood, 2010, 116, 309-311.	1.4	2
166	CD83 in Hodgkin lymphoma. Haematologica, 2018, 103, 561-562.	3.5	2
167	OBF1 and OCT1/2 regulate the germinal center B-cell program. Blood, 2021, 137, 2862-2863.	1.4	2
168	Human IgA- and IgM-secreting intestinal plasma cells carry heavily mutated VH region genes. , 1998, 28, 2971.		2
169	Loss of function mutations of BCOR in classical Hodgkin lymphoma. Leukemia and Lymphoma, 2022, 63, 1080-1090.	1.3	2
170	Focal structural variants revealed by whole genome sequencing disrupt the histone demethylase KDM4C in B-cell lymphomas. Haematologica, 2023, 108, 543-554.	3.5	2
171	Distinct Chemokine Receptor Expression Profiles in De Novo DLBCL, Transformed Follicular Lymphoma, Richterâ€™s Trans-Formed DLBCL and Germinal Center B-Cells. International Journal of Molecular Sciences, 2022, 23, 7874.	4.1	2
172	CCR7 & lymphotoxin in lymphoma niche. Blood, 2011, 118, 831-832.	1.4	1
173	Structure and diversification of immunoglobulin genes in African Burkitt lymphoma. Blood Advances, 2017, 1, 1259-1260.	5.2	1
174	Origin of Hodgkin Lymphoma. , 2018, , 1204-1211.		1
175	Context-dependent regulation of immunoglobulin mutagenesis by p53. Molecular Immunology, 2021, 138, 128-136.	2.2	1
176	Determining the Origin of Human Germinal Center B Cell-Derived Malignancies. Methods in Molecular Biology, 2017, 1623, 253-279.	0.9	1
177	Composite Lymphomas and the Relationship of Hodgkin Lymphoma to Non-Hodgkin Lymphomas. Molecular Pathology Library, 2018, , 127-155.	0.1	1
178	Pathology and Molecular Pathology of Hodgkin Lymphoma. Hematologic Malignancies, 2020, , 47-68.	0.2	1
179	Pathology and Molecular Pathology of Hodgkin Lymphoma. Hematologic Malignancies, 2015, , 45-64.	0.2	0
180	14. Biology of Hodgkinâ€™s lymphoma. , 2016, , 257-284.		0

#	Article	IF	Citations
181	Hodgkin and Reed/Sternberg Cell. , 2011, , 1712-1715.		0
182	Dynamical Modeling of Clonal Evolution in Paired Primary and Relapsed Follicular Lymphoma Predicts a Link Between Cell Migration and Evolutionary Heterogeneity. Blood, 2016, 128, 2929-2929.	1.4	0
183	Hodgkin and Reed/Sternberg Cell. , 2017, , 2093-2096.		0
184	Pathogenesis and Molecular Genetics of Hodgkin Lymphoma. Molecular Pathology Library, 2018, , 35-57.	0.1	0
185	Sugar-modified B-cell receptors in DLBCL. Blood, 2021, 138, 1512-1514.	1.4	0
186	Prognostic significance of Epstein-Barr virus-infected cells in the bone marrow of patients with nasal natural killer/T cell lymphoma. Haematologica, 2005, 90, 1011A.	3.5	0