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	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
2	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
3	The Biology of Ocular Adnexal Marginal Zone Lymphomas. Cancers, 2022, 14, 1264.	3.7	3
4	Loss of function mutations of BCOR in classical Hodgkin lymphoma. Leukemia and Lymphoma, 2022, 63, 1080-1090.	1.3	2
5	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	12.8	52
6	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
7	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
8	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
9	UMI or not UMI, that is the question for scRNA-seq zero-inflation. Nature Biotechnology, 2021, 39, 158-159.	17.5	24
10	Molecular biology of Hodgkin lymphoma. Leukemia, 2021, 35, 968-981.	7.2	102
11	The life of B cells according to JEM. Journal of Experimental Medicine, 2021, 218, .	8.5	3
12	OBF1 and OCT1/2 regulate the germinal center B-cell program. Blood, 2021, 137, 2862-2863.	1.4	2
13	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34
14	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
15	Context-dependent regulation of immunoglobulin mutagenesis by p53. Molecular Immunology, 2021, 138, 128-136.	2.2	1
16	PLK1â€dependent phosphorylation restrains EBNA2 activity and lymphomagenesis in EBVâ€infected mice. EMBO Reports, 2021, 22, e53007.	4.5	5
17	Sugar-modified B-cell receptors in DLBCL. Blood, 2021, 138, 1512-1514.	1.4	0
18	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

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19	Role of Specific B-Cell Receptor Antigens in Lymphomagenesis. Frontiers in Oncology, 2020, 10, 604685.	2.8	11
20	Lymphocyte predominant cells detect Moraxella catarrhalis-derived antigens in nodular lymphocyte-predominant Hodgkin lymphoma. Nature Communications, 2020, 11, 2465.	12.8	31
21	The Genomic Landscape of HIV-Associated Plasmablastic Lymphoma. Blood Cancer Discovery, 2020, 1, 23-25.	5.0	4
22	Genomic and epigenomic insights into the origin, pathogenesis, and clinical behavior of mantle cell lymphoma subtypes. Blood, 2020, 136, 1419-1432.	1.4	131
23	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
24	Î³Î´ T-cell Receptors Derived from Breast Cancerâ€“Infiltrating T Lymphocytes Mediate Antitumor Reactivity. Cancer Immunology Research, 2020, 8, 530-543.	3.4	42
25	Pathology and Molecular Pathology of Hodgkin Lymphoma. Hematologic Malignancies, 2020, , 47-68.	0.2	1
26	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
27	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
28	Migration Properties Distinguish Tumor Cells of Classical Hodgkin Lymphoma from Anaplastic Large Cell Lymphoma Cells. Cancers, 2019, 11, 1484.	3.7	7
29	CD81 as target for B cell lymphomas. Journal of Experimental Medicine, 2019, 216, 1469-1470.	8.5	4
30	MDM4 Is Targeted by 1q Gain and Drives Disease in Burkitt Lymphoma. Cancer Research, 2019, 79, 3125-3138.	0.9	19
31	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	12.8	99
32	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
33	Origin and Pathogenesis of B Cell Lymphomas. Methods in Molecular Biology, 2019, 1956, 1-33.	0.9	26
34	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
35	Critical influences on the pathogenesis of follicular lymphoma. Blood, 2018, 131, 2297-2306.	1.4	48
36	SAMHD1 is recurrently mutated in T-cell prolymphocytic leukemia. Blood Cancer Journal, 2018, 8, 11.	6.2	52

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37	CD83 in Hodgkin lymphoma. Haematologica, 2018, 103, 561-562.	3.5	2
38	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
39	IG-MYC+ neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. Blood, 2018, 132, 2280-2285.	1.4	50
40	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
41	Origin of Hodgkin Lymphoma. , 2018, , 1204-1211.		1
42	Composite Lymphomas and the Relationship of Hodgkin Lymphoma to Non-Hodgkin Lymphomas. Molecular Pathology Library, 2018, , 127-155.	0.1	1
43	Human CD30+ B cells represent a unique subset related to Hodgkin lymphoma cells. Journal of Clinical Investigation, 2018, 128, 2996-3007.	8.2	36
44	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
45	Pathogenesis and Molecular Genetics of Hodgkin Lymphoma. Molecular Pathology Library, 2018, , 35-57.	0.1	0
46	<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
47	Complex Immune Evasion Strategies in Classical Hodgkin Lymphoma. Cancer Immunology Research, 2017, 5, 1122-1132.	3.4	38
48	Structure and diversification of immunoglobulin genes in African Burkitt lymphoma. Blood Advances, 2017, 1, 1259-1260.	5.2	1
49	Quantitative Comparison of Abundance Structures of Generalized Communities: From B-Cell Receptor Repertoires to Microbiomes. PLoS Computational Biology, 2017, 13, e1005362.	3.2	17
50	Determining the Origin of Human Germinal Center B Cell-Derived Malignancies. Methods in Molecular Biology, 2017, 1623, 253-279.	0.9	1
51	Hodgkin and Reed/Sternberg Cell. , 2017, , 2093-2096.		0
52	14. Biology of Hodgkinâ€™s lymphoma. , 2016, , 257-284.		0
53	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
54	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. Blood, 2016, 128, 2666-2670.	1.4	82

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55	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
56	Recurrent alterations ofTNFAIP3(A20) in T-cell large granular lymphocytic leukemia. International Journal of Cancer, 2016, 138, 121-124.	5.1	36
57	Novel IGH and MYC Translocation Partners in Diffuse Large Bâ€Cell Lymphomas. Genes Chromosomes and Cancer, 2016, 55, 932-943.	2.8	10
58	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
59	NF-Î°B deregulation in Hodgkin lymphoma. Seminars in Cancer Biology, 2016, 39, 32-39.	9.6	74
60	Hodgkin lymphoma: Pathology and biology. Seminars in Hematology, 2016, 53, 139-147.	3.4	121
61	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
62	Tumor-infiltrating HLA-matched CD4⁺T cells retargeted against Hodgkin and Reedâ€“Sternberg cells. OncoImmunology, 2016, 5, e1160186.	4.6	9
63	The role of T cells in the microenvironment of Hodgkin lymphoma. Journal of Leukocyte Biology, 2016, 99, 45-50.	3.3	42
64	Recurrent mutations in NF-Î°B pathway components, KMT2D, and NOTCH1/2 in ocular adnexal MALT-type marginal zone lymphomas. Oncotarget, 2016, 7, 62627-62639.	1.8	52
65	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
66	Potential role of hypoxia in early stages of Hodgkin lymphoma pathogenesis. Haematologica, 2015, 100, 1320-1326.	3.5	16
67	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
68	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	21.4	278
69	Pathology and Molecular Pathology of Hodgkin Lymphoma. Hematologic Malignancies, 2015, , 45-64.	0.2	0
70	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
71	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
72	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

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73	CEACAM1 induces B-cell survival and is essential for protective antiviral antibody production. Nature Communications, 2015, 6, 6217.	12.8	42
74	Alterations of the CD58 gene in classical Hodgkin lymphoma. Genes Chromosomes and Cancer, 2015, 54, 638-645.	2.8	36
75	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
76	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
77	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
78	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
79	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
80	Immunoglobulin Repertoire of Primary Lymphomas of the Central Nervous System. Journal of Neuropathology and Experimental Neurology, 2014, 73, 1116-1125.	1.7	23
81	Role of hepatitis C virus in B cell lymphoproliferations. Virologica Sinica, 2014, 29, 3-6.	3.0	7
82	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
83	Pathogenesis, diagnosis, and treatment of composite lymphomas. Lancet Oncology, The, 2014, 15, e435-e446.	10.7	99
84	A novel immunohistochemical classifier to distinguish Hodgkin lymphoma from ALK anaplastic large cell lymphoma. Modern Pathology, 2014, 27, 1345-1354.	5.5	28
85	Biological characterization of adult MYC-translocation-positive mature B-cell lymphomas other than molecular Burkitt lymphoma. Haematologica, 2014, 99, 726-735.	3.5	157
86	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
87	Origin and Pathogenesis of B Cell Lymphomas. Methods in Molecular Biology, 2013, 971, 1-25.	0.9	54
88	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
89	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
90	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

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91	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
92	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
93	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
94	Cellular origin and pathophysiology of chronic lymphocytic leukemia. Journal of Experimental Medicine, 2012, 209, 2183-2198.	8.5	227
95	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
96	New insights in the biology of Hodgkin lymphoma. Hematology American Society of Hematology Education Program, 2012, 2012, 328-334.	2.5	60
97	Hodgkin lymphoma. Journal of Clinical Investigation, 2012, 122, 3439-3447.	8.2	248
98	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
99	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
100	New insights in the biology of Hodgkin lymphoma. Hematology American Society of Hematology Education Program, 2012, 2012, 328-34.	2.5	36
101	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
102	CCR7 & lymphotoxin in lymphoma niche. Blood, 2011, 118, 831-832.	1.4	1
103	Mutation analysis of the TNFAIP3 (A20) tumor suppressor gene in CLL. International Journal of Cancer, 2011, 128, 1747-1750.	5.1	16
104	Hodgkin and Reed/Sternberg Cell. , 2011, , 1712-1715.		0
105	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
106	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
107	Genomic imbalances in Hodgkin lymphoma. Blood, 2010, 116, 309-311.	1.4	2
108	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

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109	Rare occurrence of biallelic CYLD gene mutations in classical Hodgkin lymphoma. Genes Chromosomes and Cancer, 2010, 49, 803-809.	2.8	37
110	From pathogenesis to treatment of chronic lymphocytic leukaemia. Nature Reviews Cancer, 2010, 10, 37-50.	28.4	503
111	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
112	Molecular analysis of IgD-positive human germinal centres. International Immunology, 2010, 22, 289-298.	4.0	3
113	Side population cells in Hodgkin lymphoma. Leukemia and Lymphoma, 2010, 51, 741-742.	1.3	3
114	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
115	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
116	The biology of Hodgkin's lymphoma. Nature Reviews Cancer, 2009, 9, 15-27.	28.4	617
117	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
118	Pathogenesis of Classical and Lymphocyte-Predominant Hodgkin Lymphoma. Annual Review of Pathology: Mechanisms of Disease, 2009, 4, 151-174.	22.4	164
119	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
120	Molecular biology of Hodgkin lymphoma. Hematology American Society of Hematology Education Program, 2009, 2009, 491-496.	2.5	89
121	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
122	Clonotypic B cells in classic Hodgkin lymphoma. Blood, 2009, 114, 3970-3971.	1.4	22
123	Autocrine NGFÎ²/TRKA signalling is an important survival factor for Hodgkin lymphoma derived cell lines. Leukemia Research, 2008, 32, 163-167.	0.8	28
124	Human memory B cells: Memory B cells of a special kind. Immunology and Cell Biology, 2008, 86, 635-636.	2.3	8
125	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
126	BCL2 and BCL3 are recurrent translocation partners of the IGH locus. Cancer Genetics and Cytogenetics, 2008, 186, 110-114.	1.0	24

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127	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
128	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
129	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
130	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
131	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
132	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
133	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
134	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
135	Advances in Biology, Diagnostics, and Treatment of Hodgkinâ€™s Disease. Biology of Blood and Marrow Transplantation, 2006, 12, 66-76.	2.0	29
136	Reprogramming of the tumour B-cell phenotype in Hodgkin lymphoma. Trends in Immunology, 2006, 27, 203-205.	6.8	15
137	Molecular biology of Hodgkin's and Reed/Sternberg cells in Hodgkin's lymphoma. International Journal of Cancer, 2006, 118, 1853-1861.	5.1	161
138	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
139	Autocrine- and paracrine-activated receptor tyrosine kinases in classic Hodgkin lymphoma. Blood, 2005, 105, 4051-4059.	1.4	116
140	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
141	Mechanisms of B-cell lymphoma pathogenesis. Nature Reviews Cancer, 2005, 5, 251-262.	28.4	773
142	Pathogenesis of Hodgkin's lymphoma. European Journal of Haematology, 2005, 75, 26-33.	2.2	18
143	Human splenic marginal zone Bâ€„cells lack expression of activation-induced cytidine deaminase. European Journal of Immunology, 2005, 35, 3002-3007.	2.9	52
144	The Hodgkin and Reed/Sternberg cell. International Journal of Biochemistry and Cell Biology, 2005, 37, 511-517.	2.8	79

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145	Absence of Immunoglobulin Class Switch in Primary Lymphomas of the Central Nervous System. American Journal of Pathology, 2005, 166, 1773-1779.	3.8	47
146	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
147	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
148	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
149	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
150	B cells under influence: transformation of B cells by Epsteinâ€“Barr virus. Nature Reviews Immunology, 2003, 3, 801-812.	22.7	436
151	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
152	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
153	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
154	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
155	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
156	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
157	Identification of Hodgkin and Reed-Sternberg cell-specific genes by gene expression profiling. Journal of Clinical Investigation, 2003, 111, 529-537.	8.2	82
158	Identification of Hodgkin and Reed-Sternberg cell-specific genes by gene expression profiling. Journal of Clinical Investigation, 2003, 111, 529-537.	8.2	192
159	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
160	Molecular biology of Hodgkin's lymphoma. Advances in Cancer Research, 2002, 84, 277-312.	5.0	136
161	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
162	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

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163	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
164	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
165	Mechanisms of chromosomal translocations in B cell lymphomas. Oncogene, 2001, 20, 5580-5594.	5.9	570
166	Hypermutation of multiple proto-oncogenes in B-cell diffuse large-cell lymphomas. Nature, 2001, 412, 341-346.	27.8	921
167	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
168	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
169	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
170	Rare Occurrence of Classical Hodgkin's Disease as a T Cell Lymphoma. Journal of Experimental Medicine, 2000, 191, 387-394.	8.5	198
171	Clonal Deleterious Mutations in the Ĩ³bĴ± Gene in the Malignant Cells in Hodgkin's Lymphoma. Journal of Experimental Medicine, 2000, 191, 395-402.	8.5	264
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