Anke van den Berg

List of Publications by Year in descending order

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316 papers 13,489 citations

18436 62 h-index 101 g-index

327 all docs

327 docs citations

times ranked

327

17948 citing authors

#	Article	IF	CITATIONS
1	BIC and miR-155 are highly expressed in Hodgkin, primary mediastinal and diffuse large B cell lymphomas. Journal of Pathology, 2005, 207, 243-249.	2.1	640
2	MHC class II transactivator CIITA is a recurrent gene fusion partner in lymphoid cancers. Nature, 2011, 471, 377-381.	13.7	551
3	High Expression of the CC Chemokine TARC in Reed-Sternberg Cells. American Journal of Pathology, 1999, 154, 1685-1691.	1.9	349
4	Somatic mutations of the von Hippel — Lindau disease tumour suppressor gene in non-familial clear cell renal carcinoma. Human Molecular Genetics, 1994, 3, 2169-2173.	1.4	341
5	Cigarette Smoke–induced Emphysema. American Journal of Respiratory and Critical Care Medicine, 2006, 173, 751-758.	2.5	279
6	MicroRNAs, macrocontrol: Regulation of miRNA processing. Rna, 2010, 16, 1087-1095.	1.6	229
7	High expression of B-cell receptor inducible geneBIC in all subtypes of Hodgkin lymphoma. Genes Chromosomes and Cancer, 2003, 37, 20-28.	1.5	224
8	Lack of BIC and microRNA miR-155 expression in primary cases of Burkitt lymphoma. Genes Chromosomes and Cancer, 2006, 45, 147-153.	1.5	219
9	Cytoplasmic p21 expression levels determine cisplatin resistance in human testicular cancer. Journal of Clinical Investigation, 2010, 120, 3594-3605.	3.9	193
10	Circulating tumor cells in small-cell lung cancer: a predictive and prognostic factor. Annals of Oncology, 2012, 23, 2937-2942.	0.6	191
11	Expression of miR-21 and its targets (PTEN, PDCD4, TM1) in flat epithelial atypia of the breast in relation to ductal carcinoma in situ and invasive carcinoma. BMC Cancer, 2009, 9, 163.	1.1	190
12	Single-cell sequencing reveals karyotype heterogeneity in murine and human malignancies. Genome Biology, 2016, 17, 115.	3.8	178
13	A genome-wide association study of Hodgkin's lymphoma identifies new susceptibility loci at 2p16.1 (REL), 8q24.21 and 10p14 (GATA3). Nature Genetics, 2010, 42, 1126-1130.	9.4	177
14	Association with HLA class I in Epstein-Barr-virus-positive and with HLA class III in Epstein-Barr-virus-negative Hodgkin's lymphoma. Lancet, The, 2005, 365, 2216-2224.	6.3	155
15	Genome-Wide Association Study of Classical Hodgkin Lymphoma and Epstein–Barr Virus Status–Defined Subgroups. Journal of the National Cancer Institute, 2012, 104, 240-253.	3.0	141
16	Immunoâ€miRs: critical regulators of Tâ€cell development, function and ageing. Immunology, 2015, 144, 1-10.	2.0	141
17	Chemokines, cytokines and their receptors in Hodgkin's lymphoma cell lines and tissues. Annals of Oncology, 2002, 13, 52-56.	0.6	136
18	Follicular lymphoma grade 3B includes 3 cytogenetically defined subgroups with primary t(14;18), 3q27, or other translocations: t(14;18) and 3q27 are mutually exclusive. Blood, 2003, 101, 1149-1154.	0.6	136

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19	SETD2: an epigenetic modifier with tumor suppressor functionality. Oncotarget, 2016, 7, 50719-50734.	0.8	136
20	Isolation of the Human Semaphorin III/F Gene (SEMA3F) at Chromosome 3p21, a Region Deleted in Lung Cancer. Genomics, 1996, 32, 39-48.	1.3	134
21	Hodgkin Lymphoma Cell Lines Are Characterized by a Specific miRNA Expression Profile. Neoplasia, 2009, 11, 167-IN9.	2.3	133
22	HLA-A*02 is associated with a reduced risk and HLA-A*01 with an increased risk of developing EBV+ Hodgkin lymphoma. Blood, 2007, 110, 3310-3315.	0.6	131
23	Regulation of pri-microRNA BIC transcription and processing in Burkitt lymphoma. Oncogene, 2007, 26, 3769-3776.	2.6	131
24	Rapid Generation of MicroRNA Sponges for MicroRNA Inhibition. PLoS ONE, 2012, 7, e29275.	1.1	125
25	Gene expression profiling of microdissected Hodgkin Reed-Sternberg cells correlates with treatment outcome in classical Hodgkin lymphoma. Blood, 2012, 120, 3530-3540.	0.6	122
26	Plasma vesicle miRNAs for therapy response monitoring in Hodgkin lymphoma patients. JCI Insight, 2016, 1, e89631.	2.3	121
27	HLA Class II Expression by Hodgkin Reed-Sternberg Cells Is an Independent Prognostic Factor in Classical Hodgkin's Lymphoma. Journal of Clinical Oncology, 2007, 25, 3101-3108.	0.8	118
28	Aging disturbs the balance between effector and regulatory CD4+ T cells. Experimental Gerontology, 2014, 60, 190-196.	1.2	115
29	Proteomics analysis of Hodgkin lymphoma: identification of new players involved in the cross-talk between HRS cells and infiltrating lymphocytes. Blood, 2008, 111, 2339-2346.	0.6	114
30	Comprehensive analysis of miRNA expression in T-cell subsets of rheumatoid arthritis patients reveals defined signatures of naive and memory Tregs. Genes and Immunity, 2014, 15, 115-125.	2.2	111
31	Serum chemokine levels in Hodgkin lymphoma patients: highly increased levels of CCL17 and CCL22. British Journal of Haematology, 2008, 140, 527-536.	1.2	110
32	miRNA analysis in Bâ€cell chronic lymphocytic leukaemia: proliferation centres characterized by low miRâ€150 and high <i>BIC</i> /miRâ€155 expression. Journal of Pathology, 2008, 215, 13-20.	2.1	109
33	A high throughput experimental approach to identify miRNA targets in human cells. Nucleic Acids Research, 2009, 37, e137-e137.	6.5	105
34	Randomized, Placebo-Controlled Phase III Study of Docetaxel Plus Carboplatin With Celecoxib and Cyclooxygenase-2 Expression As a Biomarker for Patients With Advanced Non–Small-Cell Lung Cancer: The NVALT-4 Study. Journal of Clinical Oncology, 2011, 29, 4320-4326.	0.8	105
35	miRNA profiling of B-cell subsets: specific miRNA profile for germinal center B cells with variation between centroblasts and centrocytes. Laboratory Investigation, 2009, 89, 708-716.	1.7	103
36	The microenvironment in classical Hodgkin lymphoma: An actively shaped and essential tumor component. Seminars in Cancer Biology, 2014, 24, 15-22.	4.3	102

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37	Generation of miRNA sponge constructs. Methods, 2012, 58, 113-117.	1.9	95
38	Strongly enhanced IL-10 production using stable galectin-1 homodimers. Molecular Immunology, 2007, 44, 506-513.	1.0	93
39	The role of microRNAs in normal hematopoiesis and hematopoietic malignancies. Leukemia, 2006, 20, 1931-1936.	3.3	92
40	Resistance mechanisms after tyrosine kinase inhibitors afatinib and crizotinib in non-small cell lung cancer, a review of the literature. Critical Reviews in Oncology/Hematology, 2016, 100, 107-116.	2.0	92
41	A gene in the chromosomal region 3p21 with greatly reduced expression in lung cancer is similar to the gene for ubiquitin-activating enzyme Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 6071-6075.	3.3	91
42	Dimeric galectin-1 induces IL-10 production in T-lymphocytes: an important tool in the regulation of the immune response. Journal of Pathology, 2004, 204, 511-518.	2.1	87
43	Interaction between host T cells and Reed–Sternberg cells in Hodgkin lymphomas. Seminars in Cancer Biology, 2000, 10, 345-350.	4.3	84
44	HLA dependent immune escape mechanisms in B-cell lymphomas: Implications for immune checkpoint inhibitor therapy?. Oncolmmunology, 2017, 6, e1295202.	2.1	84
45	Latent Epstein-Barr Virus Infection of Tumor Cells in Classical Hodgkin's Lymphoma Predicts Adverse Outcome in Older Adult Patients. Journal of Clinical Oncology, 2009, 27, 3815-3821.	0.8	83
46	Clonal relation in a case of CLL, ALCL, and Hodgkin composite lymphoma. Blood, 2002, 100, 1425-1429.	0.6	79
47	Specific expression of miR-17-5p and miR-127 in testicular and central nervous system diffuse large B-cell lymphoma. Modern Pathology, 2009, 22, 547-555.	2.9	78
48	A meta-analysis of Hodgkin lymphoma reveals 19p13.3 TCF3 as a novel susceptibility locus. Nature Communications, 2014, 5, 3856.	5.8	78
49	HLAâ€G protein expression as a potential immune escape mechanism in classical Hodgkin's lymphoma. Tissue Antigens, 2008, 71, 219-226.	1.0	76
50	Rheumatoid Arthritis, Immunosenescence and the Hallmarks of Aging. Current Aging Science, 2015, 8, 131-146.	0.4	76
51	The mutational landscape of Hodgkin lymphoma cell lines determined by whole-exome sequencing. Leukemia, 2014, 28, 2248-2251.	3.3	74
52	An Alternative Route for Multistep Tumorigenesis in a Novel Case of Hereditary Renal Cell Cancer and a t(2;3)(q35;q21) Chromosome Translocation. American Journal of Human Genetics, 1998, 62, 1475-1483.	2.6	73
53	MiRNA profiling in B nonâ€Hodgkin lymphoma: a <i>MYC</i> å€related miRNA profile characterizes Burkitt lymphoma. British Journal of Haematology, 2010, 149, 896-899.	1.2	71
54	Involvement of multiple loci on chromosome 3 in renal cell cancer development., 1997, 19, 59-76.		69

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55	Mitoxantrone resistance in a small cell lung cancer cell line is associated with ABCA2 upregulation. British Journal of Cancer, 2004, 90, 2411-2417.	2.9	69
56	Treatment of the bronchial tree from beginning to end: targeting small airway inflammation in asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2013, 68, 16-26.	2.7	69
57	Long noncoding RNAs as a novel component of the Myc transcriptional network. FASEB Journal, 2015, 29, 2338-2346.	0.2	67
58	The European Hematology Association Roadmap for European Hematology Research: a consensus document. Haematologica, 2016, 101, 115-208.	1.7	67
59	Common and differential chemokine expression patterns in rs cells of NLP, EBV positive and negative classical hodgkin lymphomas. International Journal of Cancer, 2002, 99, 665-672.	2.3	66
60	Development of Lymphoma in Autoimmune Lymphoproliferative Syndrome (ALPS) and its Relationship to Fas Gene Mutations. Leukemia and Lymphoma, 2004, 45, 423-431.	0.6	66
61	A homozygous deletion in a small cell lung cancer cell line involving a 3p21 region with a marked instability in yeast artificial chromosomes. Cancer Research, 1994, 54, 4183-7.	0.4	66
62	Molecular, cytogenetic, and immunophenotypic characterization of follicular lymphoma grade 3B; a separate entity or part of the spectrum of diffuse large B-cell lymphoma or follicular lymphoma?. Human Pathology, 2006, 37, 528-533.	1.1	65
63	Protease activity of plasma hemopexin. Kidney International, 2005, 68, 603-610.	2.6	63
64	Differential expression and distribution of epithelial adhesion molecules in non-small cell lung cancer and normal bronchus. Journal of Clinical Pathology, 2007, 60, 608-614.	1.0	63
65	Current smokingâ€specific gene expression signature in normal bronchial epithelium is enhanced in squamous cell lung cancer. Journal of Pathology, 2009, 218, 182-191.	2.1	63
66	The CD4+CD26â^ T-cell population in classical Hodgkin's lymphoma displays a distinctive regulatory T-cell profile. Laboratory Investigation, 2008, 88, 482-490.	1.7	62
67	Dichotomous ALK-IHC Is a Better Predictor for ALK Inhibition Outcome than Traditional ALK-FISH in Advanced Non–Small Cell Lung Cancer. Clinical Cancer Research, 2017, 23, 4251-4258.	3.2	62
68	Dual Role of miR-21 in CD4+ T-Cells: Activation-Induced miR-21 Supports Survival of Memory T-Cells and Regulates CCR7 Expression in Naive T-Cells. PLoS ONE, 2013, 8, e76217.	1.1	61
69	A cosmid and cDNA fine physical map of a human chromosome 13q14 region frequently lost in B-cell chronic lymphocytic leukemia and identification of a new putative tumor suppressor gene, Leu5. FEBS Letters, 1998, 426, 266-270.	1.3	59
70	Genomic aberrations in squamous cell lung carcinoma related to lymph node or distant metastasis. Lung Cancer, 2009, 66, 372-378.	0.9	57
71	Expression of the T-Cell Transcription Factors, GATA-3 and T-bet, in the Neoplastic Cells of Hodgkin Lymphomas. American Journal of Pathology, 2005, 166, 127-134.	1.9	56
72	Plasma thymus and activation-regulated chemokine as an early response marker in classical Hodgkin's lymphoma. Haematologica, 2012, 97, 410-415.	1.7	56

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73	TP53 gene mutations in Hodgkin lymphoma are infrequent and not associated with absence of Epstein-Barr virus. International Journal of Cancer, 2001, 94, 60-66.	2.3	54
74	Low Frequency of FAS Mutations in Reed-Sternberg Cells of Hodgkin's Lymphoma. American Journal of Pathology, 2003, 162, 29-35.	1.9	54
75	Toll-like receptors in the pathogenesis of human B cell malignancies. Journal of Hematology and Oncology, 2014, 7, 57.	6.9	54
76	Major role for a 3p21 region and lack of involvement of the t(3;8) breakpoint region in the development of renal cell carcinoma suggested by loss of heterozygosity analysis., 1996, 15, 64-72.		52
77	HLA Associations in Classical Hodgkin Lymphoma: EBV Status Matters. PLoS ONE, 2012, 7, e39986.	1.1	52
78	Genetic Associations in Classical Hodgkin Lymphoma: A Systematic Review and Insights into Susceptibility Mechanisms. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2737-2747.	1.1	52
79	Extensive mutation scanning of RET in sporadic medullary thyroid carcinoma and of RET and VHL in sporadic pheochromocytoma reveals involvement of these genes in only a minority of cases. Journal of Clinical Endocrinology and Metabolism, 1996, 81, 2881-2884.	1.8	49
80	The role of female sex hormones in the development and severity of allergic and nonâ€allergic asthma. Clinical and Experimental Allergy, 2009, 39, 1477-1481.	1.4	48
81	Prognostic Model to Predict Post-Autologous Stem-Cell Transplantation Outcomes in Classical Hodgkin Lymphoma. Journal of Clinical Oncology, 2017, 35, 3722-3733.	0.8	48
82	Combining genomewide association study and lung <scp>eQTL</scp> analysis provides evidence for novel genes associated with asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2016, 71, 1712-1720.	2.7	47
83	Building bridges for innovation in ageing: Synergies between action groups of the EIP on AHA. Journal of Nutrition, Health and Aging, 2017, 21, 92-104.	1.5	47
84	miR-24-3p Is Overexpressed in Hodgkin Lymphoma and Protects Hodgkin and Reed-Sternberg Cells from Apoptosis. American Journal of Pathology, 2017, 187, 1343-1355.	1.9	46
85	A comparison of genomic structures and expression patterns of two closely related flanking genes in a critical lung cancer region at 3p21.3. European Journal of Human Genetics, 1999, 7, 478-486.	1.4	45
86	Intricate crosstalk between <scp>MYC</scp> and nonâ€coding <scp>RNA</scp> s regulates hallmarks of cancer. Molecular Oncology, 2019, 13, 26-45.	2.1	45
87	Immune reactions in classical Hodgkin's lymphoma. Seminars in Hematology, 1999, 36, 253-9.	1.8	45
88	Genetic susceptibility to Hodgkin's lymphoma associated with the human leukocyte antigen region. European Journal of Haematology, 2005, 75, 34-41.	1.1	44
89	Analysis of serum immune markers in seropositive and seronegative rheumatoid arthritis and in high-risk seropositive arthralgia patients. Scientific Reports, 2016, 6, 26021.	1.6	44
90	Biomarkers for evaluation of treatment response in classical Hodgkin lymphoma: comparison of <scp>sG</scp> alectinâ€1, <scp>sCD</scp> 163 and <scp>sCD</scp> 30 with TARC. British Journal of Haematology, 2016, 175, 868-875.	1.2	44

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91	Non-Coding RNAs in Cancer Radiosensitivity: MicroRNAs and IncRNAs as Regulators of Radiation-Induced Signaling Pathways. Cancers, 2020, 12, 1662.	1.7	44
92	Involvement of multiple loci on chromosome 3 in renal cell cancer development. Genes Chromosomes and Cancer, 1997, 19, 59-76.	1.5	44
93	MicroRNA profiling of human primary macrophages exposed to dengue virus identifies miRNA-3614-5p as antiviral and regulator of ADAR1 expression. PLoS Neglected Tropical Diseases, 2017, 11, e0005981.	1.3	43
94	Inhibition of the miR-155 target NIAM phenocopies the growth promoting effect of miR-155 in B-cell lymphoma. Oncotarget, 2016, 7, 2391-2400.	0.8	43
95	A High Throughput Experimental Approach to Identify miRNA Target Genes in Hodgkin Lymphoma Blood, 2008, 112, 1461-1461.	0.6	42
96	Analysis of multiple renal cell adenomas and carcinomas suggests allelic loss at 3p21 to be a prerequisite for malignant development., 1997, 19, 228-232.		41
97	Splenic Marginal Zone Lymphomas Presenting with Splenomegaly and Typical Immunophenotype Are Characterized by Allelic Loss in 7q31-32. Modern Pathology, 2003, 16, 1210-1217.	2.9	41
98	Cytokine gene expression profile distinguishes CD4+/CD57+ T cells of the nodular lymphocyte predominance type of Hodgkin's lymphoma from their tonsillar counterparts. Journal of Pathology, 2006, 208, 423-430.	2.1	41
99	Rapid BRAF mutation tests in patients with advanced melanoma: comparison of immunohistochemistry, Droplet Digital PCR, and the Idylla Mutation Platform. Melanoma Research, 2018, 28, 96-104.	0.6	41
100	The Microenvironment in Epstein–Barr Virus-Associated Malignancies. Pathogens, 2018, 7, 40.	1.2	40
101	CD58 mutations are common in Hodgkin lymphoma cell lines and loss of CD58 expression in tumor cells occurs in Hodgkin lymphoma patients who relapse. Genes and Immunity, 2016, 17, 363-366.	2.2	39
102	ZDHHC11 and ZDHHC11B are critical novel components of the oncogenic MYC-miR-150-MYB network in Burkitt lymphoma. Leukemia, 2017, 31, 1470-1473.	3.3	39
103	Mutations in EMT-Related Genes in ALK Positive Crizotinib Resistant Non-Small Cell Lung Cancers. Cancers, 2018, 10, 10.	1.7	39
104	Partial 3q duplication syndrome and assignment of D3S5 to 3q25–3q28. Human Genetics, 1991, 87, 151-154.	1.8	38
105	NormalFHIT transcripts in renal cell cancer- and lung cancer-derived cell lines, including a cell line with a homozygous deletion in the FRA3B region. , 1997, 19, 220-227.		38
106	An 80 Kb P1 clone from chromosome 3p21.3 suppresses tumor growth in vivo. Oncogene, 1996, 13, 2387-96.	2.6	38
107	Induction of glomerular alkaline phosphatase after challenge with lipopolysaccharide. International Journal of Experimental Pathology, 2003, 84, 135-144.	0.6	37
108	Emerging roles for long noncoding RNAs in B-cell development and malignancy. Critical Reviews in Oncology/Hematology, 2017, 120, 77-85.	2.0	37

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109	Combined osimertinib, dabrafenib and trametinib treatment for advanced non-small-cell lung cancer patients with an osimertinib-induced BRAF V600E mutation. Lung Cancer, 2020, 146, 358-361.	0.9	37
110	T-cell Activation Induces Dynamic Changes in miRNA Expression Patterns in CD4 and CD8 T-cell Subsets. MicroRNA (Shariqah, United Arab Emirates), 2015, 4, 117-122.	0.6	37
111	The Human Leukocyte Antigen Class I Region Is Associated with EBV-Positive Hodgkin's Lymphoma: HLA-A and HLA Complex Group 9 Are Putative Candidate Genes. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2280-2284.	1.1	36
112	Long Noncoding RNA Expression Profiling in Normal B-Cell Subsets and Hodgkin Lymphoma Reveals Hodgkin and Reed-Sternberg Cell–Specific Long Noncoding RNAs. American Journal of Pathology, 2016, 186, 2462-2472.	1.9	36
113	High expression of calcium-binding proteins, S100A10, S100A11 and CALM2 in anaplastic large cell lymphoma. British Journal of Haematology, 2005, 131, 596-608.	1.2	35
114	Brain Death Induces Inflammation in the Donor Intestine. Transplantation, 2008, 86, 148-154.	0.5	35
115	MiRâ€17/106b seed family regulates p21 in Hodgkin's lymphoma. Journal of Pathology, 2011, 225, 609-617.	2.1	35
116	A gene from human chromosome region 3p21 with reduced expression in small cell lung cancer. Cancer Research, 1992, 52, 1536-41.	0.4	35
117	Germline FAS gene mutation in a case of ALPS and NLP Hodgkin lymphoma. Blood, 2002, 99, 1492-1494.	0.6	34
118	P53 Mutation Analysis of Colorectal Liver Metastases: Relation to Actual Survival, Angiogenic Status, and p53 Overexpression. Clinical Cancer Research, 2005, 11, 4067-4073.	3.2	34
119	Age-related gene and miRNA expression changes in airways of healthy individuals. Scientific Reports, 2019, 9, 3765.	1.6	34
120	Identification of transforming growth factor-beta-regulated microRNAs and the microRNA-targetomes in primary lung fibroblasts. PLoS ONE, 2017, 12, e0183815.	1.1	34
121	Direct molecular analysis of a deletion of 3p in tumors from patients with sporadic renal cell carcinoma. Cancer Genetics and Cytogenetics, 1988, 32, 281-285.	1.0	33
122	Maternal smoking during pregnancy decreases Wnt signalling in neonatal mice. Thorax, 2010, 65, 553-554.	2.7	33
123	Primary and acquired resistance mechanisms to immune checkpoint inhibition in Hodgkin lymphoma. Cancer Treatment Reviews, 2020, 82, 101931.	3.4	33
124	Analysis of Released Circulating Tumor Cells During Surgery for Non-Small Cell Lung Cancer. Clinical Cancer Research, 2020, 26, 1656-1666.	3.2	33
125	Analysis of chromosomal copy number changes and oncoprotein expression in primary central nervous system lymphomas: frequent loss of chromosome arm 6q. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2003, 443, 164-169.	1.4	32
126	Relevance and Effectiveness of Molecular Tumor Board Recommendations for Patients With Non–Small-Cell Lung Cancer With Rare or Complex Mutational Profiles. JCO Precision Oncology, 2020, 4, 393-410.	1.5	32

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127	Production of hemopexin by TNF-α stimulated human mesangial cells. Kidney International, 2003, 63, 1681-1686.	2.6	31
128	BCL6 alternative translocation breakpoint cluster region associated with follicular lymphoma grade 3B. Genes Chromosomes and Cancer, 2005, 44, 301-304.	1.5	31
129	Prolonged protection of the new inhaled corticosteroid fluticasone furoate against AMP hyperresponsiveness in patients with asthma. Allergy: European Journal of Allergy and Clinical Immunology, 2010, 65, 1531-1535.	2.7	31
130	Budesonide and fluticasone propionate differentially affect the airway epithelial barrier. Respiratory Research, 2016, 17, 2.	1.4	30
131	Treatment of patients with MYC rearrangement positive large B-cell lymphoma with R-CHOP plus lenalidomide: results of a multicenter HOVON phase II trial. Haematologica, 2020, 105, 2805-2812.	1.7	30
132	BCL6 alternative breakpoint region break and homozygous deletion of 17q24 in the nodular lymphocyte predominance type of Hodgkin's lymphoma–derived cell line DEV. Human Pathology, 2006, 37, 675-683.	1.1	29
133	Expression of the c-Met oncogene by tumor cells predicts a favorable outcome in classical Hodgkin's lymphoma. Haematologica, 2012, 97, 572-578.	1.7	29
134	SF Treg cells transcribing high levels of Bcl-2 and microRNA-21 demonstrate limited apoptosis in RA. Rheumatology, 2015, 54, 950-958.	0.9	29
135	Mutation patterns in small cell and non-small cell lung cancer patients suggest a different level of heterogeneity between primary and metastatic tumors. Carcinogenesis, 2017, 38, bgw128.	1.3	29
136	The microenvironment of classical Hodgkin lymphoma: heterogeneity by Epstein–Barr virus presence and location within the tumor. Blood Cancer Journal, 2016, 6, e417-e417.	2.8	29
137	Identification of chromosomal copy number changes associated with transformation of follicular lymphoma to diffuse large B-cell lymphoma. Human Pathology, 2003, 34, 915-923.	1.1	28
138	KRAS Mutation as a Resistance Mechanism to BRAF/MEK Inhibition in NSCLC. Journal of Thoracic Oncology, 2018, 13, e249-e251.	0.5	28
139	Rosetting T cells in Hodgkin lymphoma are activated by immunological synapse components HLA class II and CD58. Blood, 2020, 136, 2437-2441.	0.6	28
140	Epidemiology of Classical Hodgkin Lymphoma and Its Association with Epstein Barr Virus in Northern China. PLoS ONE, 2011, 6, e21152.	1.1	28
141	Gene expression analysis of dendritic/Langerhans cells and Langerhans cell histiocytosis. Journal of Pathology, 2006, 209, 474-483.	2.1	27
142	A chronic obstructive pulmonary disease related signature in squamous cell lung cancer. Lung Cancer, 2011, 72, 177-183.	0.9	26
143	The entire miRâ€200 seed family is strongly deregulated in clear cell renal cell cancer compared to the proximal tubular epithelial cells of the kidney. Genes Chromosomes and Cancer, 2013, 52, 165-173.	1.5	26
144	HLA-A*02:07 Is a Protective Allele for EBV Negative and a Susceptibility Allele for EBV Positive Classical Hodgkin Lymphoma in China. PLoS ONE, 2012, 7, e31865.	1.1	25

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145	Brain death causes structural and inflammatory changes in donor intestine. Transplantation Proceedings, 2005, 37, 448-449.	0.3	24
146	Global correlation of genome and transcriptome changes in classical Hodgkin lymphoma. Hematological Oncology, 2007, 25, 21-29.	0.8	24
147	Expression of CD1d and presence of invariant NKT cells in classical Hodgkin lymphoma. American Journal of Hematology, 2010, 85, 539-541.	2.0	24
148	Shifted T-cell polarisation after agricultural dust exposure in mice and men. Thorax, 2014, 69, 630-637.	2.7	24
149	Impact of acute exposure to cigarette smoke on airway gene expression. Physiological Genomics, 2018, 50, 705-713.	1.0	24
150	Recommendations for the clinical interpretation and reporting of copy number gains using gene panel NGS analysis in routine diagnostics. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2019, 474, 673-680.	1.4	24
151	Cellular Localization and Processing of Primary Transcripts of Exonic MicroRNAs. PLoS ONE, 2013, 8, e76647.	1.1	24
152	Characterization of the Microenvironment of Nodular Lymphocyte Predominant Hodgkin Lymphoma. International Journal of Molecular Sciences, 2016, 17, 2127.	1.8	23
153	Functional Studies on Primary Tubular Epithelial Cells Indicate a Tumor Suppressor Role of SETD2 in Clear Cell Renal Cell Carcinoma. Neoplasia, 2016, 18, 339-346.	2.3	23
154	Differential miRNA Expression Profiles in Cumulus and Mural Granulosa Cells from Human Pre-ovulatory Follicles. MicroRNA (Shariqah, United Arab Emirates), 2018, 8, 61-67.	0.6	23
155	Age-Associated Differences in MiRNA Signatures Are Restricted to CD45RO Negative T Cells and Are Associated with Changes in the Cellular Composition, Activation and Cellular Ageing. PLoS ONE, 2015, 10, e0137556.	1.1	23
156	Clonal relation in a case of CLL, ALCL, and Hodgkin composite lymphoma. Blood, 2002, 100, 1425-9.	0.6	23
157	Insulin-Like Growth Factor 1 Receptor Is a Prognostic Factor in Classical Hodgkin Lymphoma. PLoS ONE, 2014, 9, e87474.	1.1	22
158	Array comparative genomic hybridization reveals a very high frequency of deletions of the long arm of chromosome 6 in testicular lymphoma. Genes Chromosomes and Cancer, 2006, 45, 976-981.	1.5	21
159	Overall survival in EGFR mutated non-small-cell lung cancer patients treated with afatinib after EGFR TKI and resistant mechanisms upon disease progression. PLoS ONE, 2017, 12, e0182885.	1.1	21
160	Alpine altitude climate treatment for severe and uncontrolled asthma: An EAACI position paper. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 1991-2024.	2.7	21
161	An Evolutionary Rearrangement of the Xp11.3–11.23 Region in 3p21.3, a Region Frequently Deleted in a Variety of Cancers. Genomics, 1999, 60, 238-240.	1.3	20
162	High expression of Mcl-1 in ALK positive and negative anaplastic large cell lymphoma. Journal of Clinical Pathology, 2005, 58, 520-524.	1.0	20

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163	A Novel Risk Locus at 6p21.3 for Epstein–Barr Virus-Positive Hodgkin Lymphoma. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1838-1843.	1.1	20
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