

Karen Dybkaer

List of Publications by Year in descending order

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Version: 2024-02-01

140
papers

4,540
citations

126907

33
h-index

118850

62
g-index

142
all docs

142
docs citations

142
times ranked

6584
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic Subtyping and Phenotypic Characterization of the Immune Microenvironment and MYC/BCL2 Double Expression Reveal Heterogeneity in Diffuse Large B-cell Lymphoma. <i>Clinical Cancer Research</i> , 2022, 28, 972-983.	7.0	22
2	Determining clinical course of diffuse large B-cell lymphoma using targeted transcriptome and machine learning algorithms. <i>Blood Cancer Journal</i> , 2022, 12, 25.	6.2	7
3	Longitudinal minimal residual disease assessment in multiple myeloma patients in complete remission – results from the NMSG flow-MRD substudy within the EMN02/HO95 MM trial. <i>BMC Cancer</i> , 2022, 22, 147.	2.6	1
4	Hsp90 inhibition sensitizes DLBCL cells to cisplatin. <i>Cancer Chemotherapy and Pharmacology</i> , 2022, 89, 431-440.	2.3	4
5	Aggressive B-cell Lymphoma with MYC/TP53 Dual Alterations Displays Distinct Clinicopathobiological Features and Response to Novel Targeted Agents. <i>Molecular Cancer Research</i> , 2021, 19, 249-260.	3.4	20
6	Dynamic Intracellular Metabolic Cell Signaling Profiles During Ag-Dependent B-Cell Differentiation. <i>Frontiers in Immunology</i> , 2021, 12, 637832.	4.8	4
7	Optimization of Preanalytical Variables for cfDNA Processing and Detection of ctDNA in Archival Plasma Samples. <i>BioMed Research International</i> , 2021, 2021, 1-9.	1.9	6
8	The mutational profile of immune surveillance genes in diagnostic and refractory/relapsed DLBCLs. <i>BMC Cancer</i> , 2021, 21, 829.	2.6	5
9	Direct costs of antineoplastic and supportive treatment for progressive multiple myeloma in a tax-based health system. <i>Future Oncology</i> , 2021, 17, 3331-3341.	2.4	0
10	Genomic complexity is associated with epigenetic regulator mutations and poor prognosis in diffuse large B-cell lymphoma. <i>Oncolmmunology</i> , 2021, 10, 1928365.	4.6	6
11	Long Non-Coding RNAs in Diffuse Large B-Cell Lymphoma. <i>Non-coding RNA</i> , 2021, 7, 1.	2.6	9
12	A bendamustine resistance gene signature in diffuse large B-cell lymphoma and multiple myeloma. , 2021, 4, 208-222.		0
13	Determining Clinical Course of Diffuse Large B-Cell Lymphoma Using Targeted Transcriptome and Machine Learning Algorithms. <i>Blood</i> , 2021, 138, 2395-2395.	1.4	1
14	Implementing the FAIR Data Principles in precision oncology: review of supporting initiatives. <i>Briefings in Bioinformatics</i> , 2020, 21, 936-945.	6.5	35
15	A refined cell-of-origin classifier with targeted NGS and artificial intelligence shows robust predictive value in DLBCL. <i>Blood Advances</i> , 2020, 4, 3391-3404.	5.2	22
16	XPO1 expression worsens the prognosis of unfavorable DLBCL that can be effectively targeted by selinexor in the absence of mutant p53. <i>Journal of Hematology and Oncology</i> , 2020, 13, 148.	17.0	27
17	MicroRNAs associated to single drug components of R-CHOP identifies diffuse large B-cell lymphoma patients with poor outcome and adds prognostic value to the international prognostic index. <i>BMC Cancer</i> , 2020, 20, 237.	2.6	9
18	Identification of BLNK and BTK as mediators of rituximab-induced programmed cell death by CRISPR screens in GCB subtype diffuse large B cell lymphoma. <i>Molecular Oncology</i> , 2020, 14, 1978-1997.	4.6	18

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19	Development of a Precision Medicine Workflow in Hematological Cancers, Aalborg University Hospital, Denmark. <i>Cancers</i> , 2020, 12, 312.	3.7	8
20	Normal myeloid progenitor cell subset-associated gene signatures for acute myeloid leukaemia subtyping with prognostic impact. <i>PLoS ONE</i> , 2020, 15, e0229593.	2.5	3
21	Mutational landscape of immune surveillance genes in diffuse large B-cell lymphoma. <i>Expert Review of Hematology</i> , 2020, 13, 655-668.	2.2	3
22	DNA methylation biomarkers in peripheral blood of patients with head and neck squamous cell carcinomas. A systematic review. <i>PLoS ONE</i> , 2020, 15, e0244101.	2.5	8
23	High-Throughput Sequencing-Based Investigation of Viruses in Human Cancers by Multi-enrichment Approach. <i>Journal of Infectious Diseases</i> , 2019, 220, 1312-1324.	4.0	13
24	Immunoglobulin somatic hypermutation has clinical impact in DLBCL and potential implications for immune checkpoint blockade and neoantigen-based immunotherapies. <i>Journal of Clinical Oncology</i> , 2019, 37, 2722.		22
25	PD-1/PD-L1 expression and interaction by automated quantitative immunofluorescent analysis show adverse prognostic impact in patients with diffuse large B-cell lymphoma having T-cell infiltration: a study from the International DLBCL Consortium Program. <i>Modern Pathology</i> , 2019, 32, 741-754.	5.5	39
26	Expression of NOTCH3 exon 16 differentiates Diffuse Large B-cell Lymphoma into molecular subtypes and is associated with prognosis. <i>Scientific Reports</i> , 2019, 9, 335.	3.3	7
27	Aspects of vincristine-induced neuropathy in hematologic malignancies: a systematic review. <i>Cancer Chemotherapy and Pharmacology</i> , 2019, 84, 471-485.	2.3	71
28	Immune Profiling and Quantitative Analysis Decipher the Clinical Role of Immune-Checkpoint Expression in the Tumor Immune Microenvironment of DLBCL. <i>Cancer Immunology Research</i> , 2019, 7, 644-657.	3.4	106
29	MicroRNA-155 controls vincristine sensitivity and predicts superior clinical outcome in diffuse large B-cell lymphoma. <i>Blood Advances</i> , 2019, 3, 1185-1196.	5.2	19
30	Addition of Drug-Response Specific Micro-RNAs to the International Prognostic Index Improves Prognostic Stratification of GCB-DLBCL Patients Treated with R-CHOP. <i>Blood</i> , 2019, 134, 1623-1623.	1.4	1
31	MYC and BCL2 mRNA Expression As Determined By NGS Predicts Survival in DLBCL in GCB but Not in ABC Subgroup. <i>Blood</i> , 2019, 134, 5092-5092.	1.4	1
32	High CXCR4 expression impairs rituximab response and the prognosis of R-CHOP-treated diffuse large B-cell lymphoma patients. <i>Oncotarget</i> , 2019, 10, 717-731.	1.8	19
33	Cell of Origin Classification of DLBCL Using Targeted NGS Expression Profiling and Deep Learning. <i>Blood</i> , 2019, 134, 2891-2891.	1.4	1
34	Higher Stability of Mutant mRNA As Compared to Wild-Type mRNA in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2019, 134, 1499-1499.	1.4	1
35	Real world data on rituximab maintenance therapy after frontline immunochemotherapy in grade 1-3a follicular lymphoma. <i>British Journal of Haematology</i> , 2018, 182, 297-301.	2.5	7
36	Stringent or nonstringent complete remission and prognosis in acute myeloid leukemia: a Danish population-based study. <i>Blood Advances</i> , 2018, 2, 559-564.	5.2	8

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37	A B-cell-associated gene signature classification of diffuse large B-cell lymphoma by NanoString technology. <i>Blood Advances</i> , 2018, 2, 1542-1546.	5.2	13
38	A multiple myeloma classification system that associates normal B-cell subset phenotypes with prognosis. <i>Blood Advances</i> , 2018, 2, 2400-2411.	5.2	5
39	Clinical Significance of PTEN Deletion, Mutation, and Loss of PTEN Expression in De Novo Diffuse Large B-Cell Lymphoma. <i>Neoplasia</i> , 2018, 20, 574-593.	5.3	64
40	Oral mucosa tissue gene expression profiling before, during, and after radiation therapy for tonsil squamous cell carcinoma. <i>PLoS ONE</i> , 2018, 13, e0190709.	2.5	13
41	Subtype assignment of CLL based on B-cell subset associated gene signatures from normal bone marrow – A proof of concept study. <i>PLoS ONE</i> , 2018, 13, e0193249.	2.5	8
42	Estimating a common covariance matrix for network meta-analysis of gene expression datasets in diffuse large B-cell lymphoma. <i>Annals of Applied Statistics</i> , 2018, 12, .	1.1	1
43	Molecular classification of tissue from a transformed non-Hodgkin's lymphoma case with unexpected long-time remission. <i>Experimental Hematology and Oncology</i> , 2017, 6, 3.	5.0	2
44	Interactions between SNPs affecting inflammatory response genes are associated with multiple myeloma disease risk and survival. <i>Leukemia and Lymphoma</i> , 2017, 58, 2695-2704.	1.3	11
45	Anthropometrics and prognosis in diffuse large B-cell lymphoma: a multicentre study of 653 patients. <i>European Journal of Haematology</i> , 2017, 98, 355-362.	2.2	2
46	AKT Hyperactivation and the Potential of AKT-Targeted Therapy in Diffuse Large B-Cell Lymphoma. <i>American Journal of Pathology</i> , 2017, 187, 1700-1716.	3.8	39
47	Hepatitis C virus positive diffuse large B-cell lymphomas have distinct molecular features and lack BCL2 translocations. <i>British Journal of Cancer</i> , 2017, 117, 1685-1688.	6.4	13
48	A systematic review of molecular responses to cancer therapy in normal human mucosa. <i>Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology</i> , 2017, 124, 355-366.	0.4	3
49	Human papillomavirus infects placental trophoblast and Hofbauer cells, but appears not to play a causal role in miscarriage and preterm labor. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2017, 96, 1188-1196.	2.8	28
50	HPV16 E6 and E7 Upregulate Interferon-Induced Antiviral Response Genes ISG15 and IFIT1 in Human Trophoblast Cells. <i>Pathogens</i> , 2017, 6, 40.	2.8	17
51	Molecular Characteristics of High-Dose Melphalan Associated Oral Mucositis in Patients with Multiple Myeloma: A Gene Expression Study on Human Mucosa. <i>PLoS ONE</i> , 2017, 12, e0169286.	2.5	10
52	Prognostic impact of concurrent <i>MYC</i> and <i>BCL6</i> rearrangements and expression in <i>de novo</i> diffuse large B-cell lymphoma. <i>Oncotarget</i> , 2016, 7, 2401-2416.	1.8	93
53	Human Papillomavirus Infection as a Possible Cause of Spontaneous Abortion and Spontaneous Preterm Delivery. <i>Infectious Diseases in Obstetrics and Gynecology</i> , 2016, 2016, 1-19.	1.5	66
54	miR-155 as a Biomarker in B-Cell Malignancies. <i>BioMed Research International</i> , 2016, 2016, 1-14.	1.9	56

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55	hemaClass.org: Online One-By-One Microarray Normalization and Classification of Hematological Cancers for Precision Medicine. PLoS ONE, 2016, 11, e0163711.	2.5	7
56	Assessment of CD37 B-cell antigen and cell of origin significantly improves risk prediction in diffuse large B-cell lymphoma. Blood, 2016, 128, 3083-3100.	1.4	59
57	The myeloma stem cell concept, revisited: from phenomenology to operational terms. Haematologica, 2016, 101, 1451-1459.	3.5	55
58	Clinical and Biologic Significance of <i>MYC</i> Genetic Mutations in <i>De Novo</i> Diffuse Large B-cell Lymphoma. Clinical Cancer Research, 2016, 22, 3593-3605.	7.0	48
59	The CXCR4 antagonist plerixafor enhances the effect of rituximab in diffuse large B-cell lymphoma cell lines. Biomarker Research, 2016, 4, 12.	6.8	29
60	Unaccounted uncertainty from qPCR efficiency estimates entails uncontrolled false positive rates. BMC Bioinformatics, 2016, 17, 159.	2.6	6
61	Characterization of memory B cells from thymus and its impact for DLBCL classification. Experimental Hematology, 2016, 44, 982-990.e11.	0.4	3
62	Blood on the tracks " toward precision medicine. Leukemia and Lymphoma, 2016, 57, 1753-1754.	1.3	0
63	High miR-34a expression improves response to doxorubicin in diffuse large B-cell lymphoma. Experimental Hematology, 2016, 44, 238-246.e2.	0.4	46
64	The application of human phase 0 microdosing trials: A systematic review and perspectives. Leukemia and Lymphoma, 2016, 57, 1281-1290.	1.3	9
65	Anti-Apoptotic Effects of Lentiviral Vector Transduction Promote Increased Rituximab Tolerance in Cancerous B-Cells. PLoS ONE, 2016, 11, e0153069.	2.5	2
66	p63 expression confers significantly better survival outcomes in high-risk diffuse large B-cell lymphoma and demonstrates p53-like and p53-independent tumor suppressor function. Aging, 2016, 8, 345-365.	3.1	19
67	RelA NF- κ B subunit activation as a therapeutic target in diffuse large B-cell lymphoma. Aging, 2016, 8, 3321-3340.	3.1	29
68	GMCM : Unsupervised Clustering and Meta-Analysis Using Gaussian Mixture Copula Models. Journal of Statistical Software, 2016, 70, .	3.7	15
69	Alternative pre-mRNA splicing leads to potential biomarkers in diffuse large B-cell lymphoma - a systematic review. Danish Medical Journal, 2016, 63, .	0.5	1
70	Global microRNA expression profiling uncovers molecular markers for classification and prognosis in aggressive B-cell lymphoma. Blood, 2015, 125, 1137-1145.	1.4	110
71	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. Scientific Reports, 2015, 5, 13201.	3.3	34
72	Long Noncoding RNA Expression during Human B-Cell Development. PLoS ONE, 2015, 10, e0138236.	2.5	80

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73	Dysregulated CXCR4 expression promotes lymphoma cell survival and independently predicts disease progression in germinal center B-cell-like diffuse large B-cell lymphoma. <i>Oncotarget</i> , 2015, 6, 5597-5614.	1.8	61
74	Stable phenotype of B-cell subsets following cryopreservation and thawing of normal human lymphocytes stored in a tissue biobank. , 2015, 88, 40-49.		22
75	Predicting response to multidrug regimens in cancer patients using cell line experiments and regularised regression models. <i>BMC Cancer</i> , 2015, 15, 235.	2.6	44
76	Diffuse Large B-Cell Lymphoma Classification System That Associates Normal B-Cell Subset Phenotypes With Prognosis. <i>Journal of Clinical Oncology</i> , 2015, 33, 1379-1388.	1.6	94
77	Inherited variation in immune response genes in follicular lymphoma and diffuse large B-cell lymphoma. <i>Leukemia and Lymphoma</i> , 2015, 56, 3257-3266.	1.3	7
78	Clinical features, tumor biology, and prognosis associated with MYC rearrangement and Myc overexpression in diffuse large B-cell lymphoma patients treated with rituximab-CHOP. <i>Modern Pathology</i> , 2015, 28, 1555-1573.	5.5	48
79	Circulating tumor necrosis factor- α and YKL-40 level is associated with remission status following salvage therapy in relapsed non-Hodgkin lymphoma. <i>Leukemia and Lymphoma</i> , 2015, 56, 2476-2478.	1.3	7
80	A population-based study of prognosis in advanced stage follicular lymphoma managed by watch and wait. <i>British Journal of Haematology</i> , 2015, 169, 435-444.	2.5	27
81	Prognostic and biological significance of survivin expression in patients with diffuse large B-cell lymphoma treated with rituximab-CHOP therapy. <i>Modern Pathology</i> , 2015, 28, 1297-1314.	5.5	21
82	Evaluation of NF- κ B subunit expression and signaling pathway activation demonstrates that p52 expression confers better outcome in germinal center B-cell-like diffuse large B-cell lymphoma in association with CD30 and BCL2 functions. <i>Modern Pathology</i> , 2015, 28, 1202-1213.	5.5	17
83	Global Myeloma Research Clusters, Output, and Citations: A Bibliometric Mapping and Clustering Analysis. <i>PLoS ONE</i> , 2015, 10, e0116966.	2.5	10
84	MicroRNAs in B-cells: from normal differentiation to treatment of malignancies. <i>Oncotarget</i> , 2015, 6, 7-25.	1.8	24
85	Clinical and biological significance of <i>de novo</i> CD5+ diffuse large B-cell lymphoma in Western countries. <i>Oncotarget</i> , 2015, 6, 5615-5633.	1.8	72
86	Prognostic impact of c-Rel nuclear expression and <i>REL</i> amplification and crosstalk between c-Rel and the p53 pathway in diffuse large B-cell lymphoma. <i>Oncotarget</i> , 2015, 6, 23157-23180.	1.8	35
87	Age cutoff for Epstein-Barr virus-positive diffuse large B-cell lymphoma-is it necessary?. <i>Oncotarget</i> , 2015, 6, 13933-13945.	1.8	33
88	Subtyping of B-Cell Malignancies By B-Cell Subset Associated Gene Signatures (BAGS), Generated from Human Primary and Secondary Lymphoid Organs.. <i>Blood</i> , 2015, 126, 5347-5347.	1.4	0
89	Cell of origin associated classification of B-cell malignancies by gene signatures of the normal B-cell hierarchy. <i>Leukemia and Lymphoma</i> , 2014, 55, 1251-1260.	1.3	15
90	Reproducible probe-level analysis of the Affymetrix Exon 1.0 ST array with R/Bioconductor. <i>Briefings in Bioinformatics</i> , 2014, 15, 519-533.	6.5	10

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91	Human B-cell cancer cell lines as a preclinical model for studies of drug effect in diffuse large B-cell lymphoma and multiple myeloma. <i>Experimental Hematology</i> , 2014, 42, 927-938.	0.4	15
92	Rearrangements of MYC gene facilitate risk stratification in diffuse large B-cell lymphoma patients treated with rituximab-CHOP. <i>Modern Pathology</i> , 2014, 27, 958-971.	5.5	112
93	Exposure time independent summary statistics for assessment of drug dependent cell line growth inhibition. <i>BMC Bioinformatics</i> , 2014, 15, 168.	2.6	16
94	Validation and implementation of a method for microarray gene expression profiling of minor B-cell subpopulations in man. <i>BMC Immunology</i> , 2014, 15, 3.	2.2	10
95	Clinical Implications of Phosphorylated STAT3 Expression in <i>De Novo</i> Diffuse Large B-cell Lymphoma. <i>Clinical Cancer Research</i> , 2014, 20, 5113-5123.	7.0	60
96	Prevalence and clinical implications of cyclin D1 expression in diffuse large B-cell lymphoma (DLBCL) treated with immunochemotherapy: A report from the International DLBCL Rituximab-CHOP Consortium Program. <i>Cancer</i> , 2014, 120, 1818-1829.	4.1	32
97	IDH2 R172 Mutations Define a Unique Subgroup of Patients in Angioimmunoblastic T-Cell Lymphoma. <i>Blood</i> , 2014, 124, 3580-3580.	1.4	3
98	NF- κ B Subunit c-Rel Cooperates with Myc and Mutated p53 to Confer Significantly Worse Survival in Patients with Diffuse Large B-Cell Lymphoma: A Report from the International DLBCL Rituximab-CHOP Consortium Program. <i>Blood</i> , 2014, 124, 1620-1620.	1.4	0
99	Akt Activation Confers an Inferior Survival in Patients with Activated B-Cell Subtype of Diffuse Large B-Cell Lymphoma: A Report from the International DLBCL Rituximab-CHOP Consortium Program. <i>Blood</i> , 2014, 124, 143-143.	1.4	1
100	MYC/BCL2 protein coexpression contributes to the inferior survival of activated B-cell subtype of diffuse large B-cell lymphoma and demonstrates high-risk gene expression signatures: a report from The International DLBCL Rituximab-CHOP Consortium Program. <i>Blood</i> , 2013, 121, 4021-4031.	1.4	596
101	Gene expression profiling of murine T-cell lymphoblastic lymphoma identifies deregulation of S-phase initiating genes. <i>Leukemia Research</i> , 2013, 37, 1383-1390.	0.8	3
102	CD30 expression defines a novel subgroup of diffuse large B-cell lymphoma with favorable prognosis and distinct gene expression signature: a report from the International DLBCL Rituximab-CHOP Consortium Program Study. <i>Blood</i> , 2013, 121, 2715-2724.	1.4	206
103	Patients with diffuse large B-cell lymphoma of germinal center origin with BCL2 translocations have poor outcome, irrespective of MYC status: a report from an International DLBCL rituximab-CHOP Consortium Program Study. <i>Haematologica</i> , 2013, 98, 255-263.	3.5	142
104	microRNA expression profiling identifies molecular signatures associated with anaplastic large cell lymphoma. <i>Blood</i> , 2013, 122, 2083-2092.	1.4	84
105	MDM2 phenotypic and genotypic profiling, respective to TP53 genetic status, in diffuse large B-cell lymphoma patients treated with rituximab-CHOP immunochemotherapy: a report from the International DLBCL Rituximab-CHOP Consortium Program. <i>Blood</i> , 2013, 122, 2630-2640.	1.4	46
106	Single nucleotide variation in the TP53 3' untranslated region in diffuse large B-cell lymphoma treated with rituximab-CHOP: a report from the International DLBCL Rituximab-CHOP Consortium Program. <i>Blood</i> , 2013, 121, 4529-4540.	1.4	41
107	Proof of the Concept to Use a Malignant B Cell Line Drug Screen Strategy for Identification and Weight of Melphalan Resistance Genes in Multiple Myeloma. <i>PLoS ONE</i> , 2013, 8, e83252.	2.5	13
108	Cell Cycle Gene Sets Coordination In Multiple Myeloma and Plasma Cell Leukemia. <i>Blood</i> , 2013, 122, 1901-1901.	1.4	1

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109	Radiation Therapy Significantly Improves Survival Of Patients With Diffuse Large B-Cell Lymphoma Associated With MYC Translocation: A Report From The International DLBCL Rituximab-CHOP Consortium Program. <i>Blood</i> , 2013, 122, 641-641.	1.4	3
110	STAT3 Expression and Clinical Implications In De Novo Diffuse Large B-Cell Lymphoma: A Report From The International DLBCL Rituximab-CHOP Consortium Program. <i>Blood</i> , 2013, 122, 365-365.	1.4	1
111	MYC Mutation Profiling In 708 De Novo Diffuse Large B-Cell Lymphoma Demonstrates That Genetic Abnormalities In The Coding Sequence and Untranslated Regions Have Different Prognostic and Clinical Significance: A Report From The International DLBCL Rituximab-CHOP Consortium Program. <i>Blood</i> , 2013, 122, 363-363.	1.4	0
112	Radiation Therapy Significantly Improves Survival Of Patients With Diffuse Large B-Cell Lymphoma Associated With MYC Translocation: A Report From The International DLBCL Rituximab-CHOP Consortium Program. <i>Blood</i> , 2013, 122, 213-213.	1.4	0
113	Mutational profile and prognostic significance of TP53 in diffuse large B-cell lymphoma patients treated with R-CHOP: report from an International DLBCL Rituximab-CHOP Consortium Program Study. <i>Blood</i> , 2012, 120, 3986-3996.	1.4	301
114	A model system for assessing and comparing the ability of exon microarray and tag sequencing to detect genes specific for malignant B-cells. <i>BMC Genomics</i> , 2012, 13, 596.	2.8	1
115	Clinical impact of leukemic blast heterogeneity at diagnosis in cytogenetic intermediate-risk acute myeloid leukemia. <i>Cytometry Part B - Clinical Cytometry</i> , 2012, 82B, 123-131.	1.5	11
116	Prognostic Significance and Phenotypic Manifestations of MYC/BCL2 Protein Expression in Diffuse Large B-Cell Lymphoma (DLBCL) with Extranodal Organ Involvement: A Report of the International DLBCL Rituximab-CHOP Consortium Program Study. <i>Blood</i> , 2012, 120, 544-544.	1.4	1
117	Gene Expression Profiling of Murine T-Cell Lymphoblastic Lymphoma Identifies Deregulation of S-Phase Initiating Genes.. <i>Blood</i> , 2012, 120, 2395-2395.	1.4	4
118	Generation of a Predictive Melphalan Resistance Index by Drug Screen of B-Cell Cancer Cell Lines. <i>PLoS ONE</i> , 2011, 6, e19322.	2.5	18
119	Multiparametric Flow Cytometry for Identification and Fluorescence Activated Cell Sorting of Five Distinct B-Cell Subpopulations in Normal Tonsil Tissue. <i>American Journal of Clinical Pathology</i> , 2011, 136, 960-969.	0.7	35
120	The t(14;18)(q32;q21) Characterizes a Subset of Patients with Diffuse Large-B Cell Lymphoma of Germinal Center Origin with Poor Outcome: Report From the International DLBCL Rituximab-CHOP Consortium Program Study. <i>Blood</i> , 2011, 118, 949-949.	1.4	3
121	Molecular signatures to improve diagnosis in peripheral T-cell lymphoma and prognostication in angioimmunoblastic T-cell lymphoma. <i>Blood</i> , 2010, 115, 1026-1036.	1.4	353
122	Multiparametric flow cytometry profiling of neoplastic plasma cells in multiple myeloma. <i>Cytometry Part B - Clinical Cytometry</i> , 2010, 78B, 338-347.	1.5	28
123	The in Vivo Toxicity of Hydroxyurea Depends on Its Direct Target Catalase. <i>Journal of Biological Chemistry</i> , 2010, 285, 21411-21415.	3.4	49
124	Loss of MicroRNA Targets in the 3' Untranslated Region as a Mechanism of Retroviral Insertional Activation of Growth Factor Independence 1. <i>Journal of Virology</i> , 2009, 83, 8051-8061.	3.4	25
125	Cancer stem cells and the cellular hierarchy in haematological malignancies. <i>European Journal of Cancer</i> , 2009, 45, 194-201.	2.8	20
126	Clinical Impact of TP53 Gene Mutations in Diffuse Large B-Cell Lymphoma (DLBCL): An International DLBCL Rituxan-CHOP Consortium Program Study.. <i>Blood</i> , 2009, 114, 967-967.	1.4	1

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127	Impact of Growth Factor Independence 1 in Human T-Cell Lymphomas; Pathogenic Potential Identified by Insertional Mutagenesis in a Murine T-Cell Lymphoma Model.. Blood, 2009, 114, 5047-5047.	1.4	0
128	Genomic Analyses Reveal Global Functional Alterations That Promote Tumor Growth and Novel Tumor Suppressor Genes in Natural Killer-Cell Malignancies. Blood, 2008, 112, 3792-3792.	1.4	0
129	Genome wide transcriptional analysis of resting and IL2 activated human natural killer cells: gene expression signatures indicative of novel molecular signaling pathways. BMC Genomics, 2007, 8, 230.	2.8	82
130	A Novel Chemo Sensitivity Index for Melphalan Based on Gene Expression Profiling (GEP).. Blood, 2007, 110, 4191-4191.	1.4	0
131	Analysis of Gene Expression Patterns and Gene Copy Number Changes in Human NK Cell Malignancies.. Blood, 2006, 108, 2228-2228.	1.4	0
132	Suitability of Stratagene reference RNA for analysis of lymphoid tissues. BioTechniques, 2004, 37, 470-474.	1.8	4
133	Application and Evaluation of RT-PCR and ELISA for the Nucleoprotein and RT-PCR for Detection of Low-Pathogenic H5 and H7 Subtypes of Avian Influenza Virus. Journal of Veterinary Diagnostic Investigation, 2004, 16, 51-56.	1.1	16
134	Distinct gene expression profiles in different B-cell compartments in human peripheral lymphoid organs. BMC Immunology, 2004, 5, 20.	2.2	59
135	Molecular Diagnosis and Outcome Prediction in Diffuse Large B-Cell Lymphoma and Other Subtypes of Lymphoma. Clinical Lymphoma and Myeloma, 2004, 5, 19-28.	2.1	21
136	RT-PCR-ELISA as a Tool for Diagnosis of Low-Pathogenicity Avian Influenza. Avian Diseases, 2003, 47, 1075-1078.	1.0	9
137	Single site polymorphisms and alternative splicing of the human CD13 gene - different splicing frequencies among patients with acute myeloid leukaemia and healthy individuals. British Journal of Haematology, 2001, 112, 691-696.	2.5	9
138	Stromal-mediated down-regulation of CD13 in bone marrow cells originating from acute myeloid leukemia patients. European Journal of Haematology, 2001, 66, 168-177.	2.2	4
139	Identification of acute myeloid leukemia patients with diminished expression of CD13 myeloid transcripts by competitive reverse transcription polymerase chain reaction (RT-PCR). Leukemia Research, 2000, 24, 497-506.	0.8	6
140	Extended Minus-Strand DNA as Template for R-U5-Mediated Second-Strand Transfer in Recombinational Rescue of Primer Binding Site-Modified Retroviral Vectors. Journal of Virology, 1998, 72, 2519-2525.	3.4	16