Ash A Alizadeh

List of Publications by Year
in descending order

232 papers	52,916 citations	8181 76 h-index	2385 198 g-index
238 all docs	238 docs citations	238 times ranked	54576 citing authors

#	Article	IF	Citations
1	Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. Nature, 2000, 403, 503-511.	27.8	8,977
2	Robust enumeration of cell subsets from tissue expression profiles. Nature Methods, 2015, 12, 453-457.	19.0	8,460
3	The prognostic landscape of genes and infiltrating immune cells across human cancers. Nature Medicine, 2015, 21, 938-945.	30.7	2,505
4	Determining cell type abundance and expression from bulk tissues with digital cytometry. Nature Biotechnology, 2019, 37, 773-782.	17.5	2,396
5	Profiling Tumor Infiltrating Immune Cells with CIBERSORT. Methods in Molecular Biology, 2018, 1711, 243-259.	0.9	1,936
6	An ultrasensitive method for quantitating circulating tumor DNA with broad patient coverage. Nature Medicine, 2014, 20, 548-554.	30.7	1,771
7	CD47 Is an Adverse Prognostic Factor and Therapeutic Antibody Target on Human Acute Myeloid Leukemia Stem Cells. Cell, 2009, 138, 286-299.	28.9	1,371
8	The CD47-signal regulatory protein alpha (SIRPa) interaction is a therapeutic target for human solid tumors. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6662-6667.	7.1	1,255
9	Relation of Gene Expression Phenotype to Immunoglobulin Mutation Genotype in B Cell Chronic Lymphocytic Leukemia. Journal of Experimental Medicine, 2001, 194, 1639-1648.	8.5	978
10	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. Nature Genetics, 1999, 23, 41-46.	21.4	928
11	Anti-CD47 Antibody Synergizes with Rituximab to Promote Phagocytosis and Eradicate Non-Hodgkin Lymphoma. Cell, 2010, 142, 699-713.	28.9	894
12	Prediction of Survival in Diffuse Large-B-Cell Lymphoma Based on the Expression of Six Genes. New England Journal of Medicine, 2004, 350, 1828-1837.	27.0	874
13	Integrated digital error suppression for improved detection of circulating tumor DNA. Nature Biotechnology, 2016, 34, 547-555.	17.5	837
14	Gene Expression Signature of Fibroblast Serum Response Predicts Human Cancer Progression: Similarities between Tumors and Wounds. PLoS Biology, 2004, 2, e7.	5.6	824
15	Individuality and variation in gene expression patterns in human blood. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1896-1901.	7.1	723
16	Early Detection of Molecular Residual Disease in Localized Lung Cancer by Circulating Tumor DNA Profiling. Cancer Discovery, 2017, 7, 1394-1403.	9.4	701
17	Outcomes of Observation vs Stereotactic Ablative Radiation for Oligometastatic Prostate Cancer. JAMA Oncology, 2020, 6, 650.	7.1	696
18	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604

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19	Calreticulin Is the Dominant Pro-Phagocytic Signal on Multiple Human Cancers and Is Counterbalanced by CD47. Science Translational Medicine, 2010, 2, 63ra94.	12.4	591
20	Circulating tumour DNA profiling reveals heterogeneity of EGFR inhibitor resistance mechanisms in lung cancer patients. Nature Communications, 2016, 7, 11815.	12.8	520
21	Rheumatoid arthritis is a heterogeneous disease: Evidence for differences in the activation of the STAT-1 pathway between rheumatoid tissues. Arthritis and Rheumatism, 2003, 48, 2132-2145.	6.7	418
22	'Gene shaving' as a method for identifying distinct sets of genes with similar expression patterns. Genome Biology, 2000, 1, research0003.1.	9.6	392
23	Integrating genomic features for non-invasive early lung cancer detection. Nature, 2020, 580, 245-251.	27.8	379
24	Role of interleukin 6 in myocardial dysfunction of meningococcal septic shock. Lancet, The, 2004, 363, 203-209.	13.7	378
25	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. Nucleic Acids Research, 2003, 31, 219-223.	14.5	376
26	Stereotyped and specific gene expression programs in human innate immune responses to bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 972-977.	7.1	371
27	Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA. Science Translational Medicine, 2016, 8, 364ra155.	12.4	348
28	Association of a Leukemic Stem Cell Gene Expression Signature With Clinical Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 2010, 304, 2706.	7.4	339
29	Therapeutic Antibody Targeting of CD47 Eliminates Human Acute Lymphoblastic Leukemia. Cancer Research, 2011, 71, 1374-1384.	0.9	318
30	Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2018, 36, 2845-2853.	1.6	313
31	Mutations in early follicular lymphoma progenitors are associated with suppressed antigen presentation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1116-25.	7.1	307
32	Genomic expression programs and the integration of the CD28 costimulatory signal in T cell activation. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11796-11801.	7.1	300
33	Hierarchy in somatic mutations arising during genomic evolution and progression of follicular lymphoma. Blood, 2013, 121, 1604-1611.	1.4	279
34	Cell-type specific gene expression profiles of leukocytes in human peripheral blood. BMC Genomics, 2006, 7, 115.	2.8	275
35	Noninvasive monitoring of diffuse large B-cell lymphoma by immunoglobulin high-throughput sequencing. Blood, 2015, 125, 3679-3687.	1.4	270
36	The t(14;18) defines a unique subset of diffuse large B-cell lymphoma with a germinal center B-cell gene expression profile. Blood, 2002, 99, 2285-2290.	1.4	266

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37	Towards a novel classification of human malignancies based on gene expression patterns. Journal of Pathology, 2001, 195, 41-52.	4.5	265
38	Profiling Cell Type Abundance and Expression in Bulk Tissues with CIBERSORTx. Methods in Molecular Biology, 2020, 2117, 135-157.	0.9	249
39	Prospective separation of normal and leukemic stem cells based on differential expression of TIM3, a human acute myeloid leukemia stem cell marker. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5009-5014.	7.1	248
40	Role of *KEAP1*/*NRF2* and *TP53* Mutations in Lung Squamous Cell Carcinoma Development and Radiation Resistance. Cancer Discovery, 2017, 7, 86-101.	9.4	239
41	Three differentiation states risk-stratify bladder cancer into distinct subtypes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2078-2083.	7.1	232
42	Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens. Nature, 2017, 543, 723-727.	27.8	232
43	A Simple Method for Estimating Interactions Between a Treatment and a Large Number of Covariates. Journal of the American Statistical Association, 2014, 109, 1517-1532.	3.1	227
44	Ongoing immunoglobulin somatic mutation in germinal center B cell-like but not in activated B cell-like diffuse large cell lymphomas. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10209-10213.	7.1	220
45	The Lymphochip: A Specialized cDNA Microarray for the Genomic-scale Analysis of Gene Expression in Normal and Malignant Lymphocytes. Cold Spring Harbor Symposia on Quantitative Biology, 1999, 64, 71-78.	1.1	218
46	Predicting HLA class II antigen presentation through integrated deep learning. Nature Biotechnology, 2019, 37, 1332-1343.	17.5	218
47	Transformation of follicular lymphoma to diffuse large cell lymphoma is associated with a heterogeneous set of DNA copy number and gene expression alterations. Blood, 2003, 101, 3109-3117.	1.4	212
48	FACTERA: a practical method for the discovery of genomic rearrangements at breakpoint resolution. Bioinformatics, 2014, 30, 3390-3393.	4.1	212
49	Noninvasive Early Identification of Therapeutic Benefit from Immune Checkpoint Inhibition. Cell, 2020, 183, 363-376.e13.	28.9	206
50	Transformation of follicular lymphoma to diffuse large-cell lymphoma: Alternative patterns with increased or decreased expression of c-myc and its regulated genes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8886-8891.	7.1	204
51	Circulating tumor DNA dynamics predict benefit from consolidation immunotherapy in locally advanced non-small-cell lung cancer. Nature Cancer, 2020, 1, 176-183.	13.2	201
52	CD137 stimulation enhances the antilymphoma activity of anti-CD20 antibodies. Blood, 2011, 117, 2423-2432.	1.4	195
53	Software Tools for High-Throughput Analysis and Archiving of Immunohistochemistry Staining Data Obtained with Tissue Microarrays. American Journal of Pathology, 2002, 161, 1557-1565.	3.8	194
54	Prediction of survival in diffuse large B-cell lymphoma based on the expression of 2 genes reflecting tumor and microenvironment. Blood, 2011, 118, 1350-1358.	1.4	175

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55	Specific post-translational histone modifications of neutrophil extracellular traps as immunogens and potential targets of lupus autoantibodies. Arthritis Research and Therapy, 2012, 14, R25.	3.5	162
56	Enhanced detection of minimal residual disease by targeted sequencing of phased variants in circulating tumor DNA. Nature Biotechnology, 2021, 39, 1537-1547.	17.5	151
57	High PD-1 expression and suppressed cytokine signaling distinguish T cells infiltrating follicular lymphoma tumors from peripheral T cells. Blood, 2013, 121, 1367-1376.	1.4	147
58	Circulating Tumor DNA Analysis for Detection of Minimal Residual Disease After Chemoradiotherapy for Localized Esophageal Cancer. Gastroenterology, 2020, 158, 494-505.e6.	1.3	147
59	In Vivo Regulation of Human Skeletal Muscle Gene Expression by Thyroid Hormone. Genome Research, 2002, 12, 281-291.	5.5	143
60	B-cell signaling networks reveal a negative prognostic human lymphoma cell subset that emerges during tumor progression. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12747-12754.	7.1	143
61	Detection and Surveillance of Bladder Cancer Using Urine Tumor DNA. Cancer Discovery, 2019, 9, 500-509.	9.4	143
62	The chemoattractant chemerin suppresses melanoma by recruiting natural killer cell antitumor defenses. Journal of Experimental Medicine, 2012, 209, 1427-1435.	8.5	140
63	Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction. Cell, 2019, 178, 699-713.e19.	28.9	138
64	Fludarabine treatment of patients with chronic lymphocytic leukemia induces a p53-dependent gene expression response. Blood, 2004, 104, 1428-1434.	1.4	122
65	Treatment advances have not improved the early death rate in acute promyelocytic leukemia. Haematologica, 2012, 97, 133-136.	3.5	122
66	Therapeutic effect of CD137 immunomodulation in lymphoma and its enhancement by Treg depletion. Blood, 2009, 114, 3431-3438.	1.4	121
67	Atlas of clinically distinct cell states and ecosystems across human solid tumors. Cell, 2021, 184, 5482-5496.e28.	28.9	116
68	Detecting Liquid Remnants of Solid Tumors: Circulating Tumor DNA Minimal Residual Disease. Cancer Discovery, 2021, 11, 2968-2986.	9.4	116
69	Genomic-scale gene expression profiling of normal and malignant immune cells. Current Opinion in Immunology, 2000, 12, 219-225.	5.5	113
70	A mathematical model of ctDNA shedding predicts tumor detection size. Science Advances, 2020, 6, .	10.3	105
71	The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma. Cancer Cell, 2021, 39, 1422-1437.e10.	16.8	102
72	Predicting Radiotherapy Responses and Treatment Outcomes Through Analysis of Circulating Tumor DNA. Seminars in Radiation Oncology, 2015, 25, 305-312.	2.2	97

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73	Probing lymphocyte biology by genomic-scale gene expression analysis. Journal of Clinical Immunology, 1998, 18, 373-379.	3.8	96
74	<i>KEAP1/NFE2L2</i> Mutations Predict Lung Cancer Radiation Resistance That Can Be Targeted by Glutaminase Inhibition. Cancer Discovery, 2020, 10, 1826-1841.	9.4	93
75	Large-Scale and Comprehensive Immune Profiling and Functional Analysis of Normal Human Aging. PLoS ONE, 2015, 10, e0133627.	2.5	90
76	T Cell Receptor-Independent Basal Signaling via Erk and Abl Kinases Suppresses RAG Gene Expression. PLoS Biology, 2003, 1, e53.	5.6	88
77	HGAL is a novel interleukin-4â€"inducible gene that strongly predicts survival in diffuse large B-cell lymphoma. Blood, 2003, 101, 433-440.	1.4	84
78	Crebbp loss cooperates with Bcl2 overexpression to promote lymphoma in mice. Blood, 2017, 129, 2645-2656.	1.4	84
79	Self-antigen recognition by follicular lymphoma B-cell receptors. Blood, 2012, 120, 4182-4190.	1.4	81
80	Active Idiotypic Vaccination Versus Control Immunotherapy for Follicular Lymphoma. Journal of Clinical Oncology, 2014, 32, 1797-1803.	1.6	75
81	Potential clinical utility of ultrasensitive circulating tumor DNA detection with CAPP-Seq. Expert Review of Molecular Diagnostics, 2015, 15, 715-719.	3.1	75
82	Circulating Tumor DNA Analysis to Assess Risk of Progression after Long-term Response to PD-(L)1 Blockade in NSCLC. Clinical Cancer Research, 2020, 26, 2849-2858.	7.0	74
83	Transient expression of Bcl6 is sufficient for oncogenic function and induction of mature B-cell lymphoma. Nature Communications, 2014, 5, 3904.	12.8	73
84	AID is expressed in germinal center B-cell-like and activated B-cell-like diffuse large-cell lymphomas and is not correlated with intraclonal heterogeneity. Leukemia, 2004, 18, 1775-1779.	7.2	70
85	Distinct patterns of B-cell receptor signaling in non-Hodgkin lymphomas identified by single-cell profiling. Blood, 2017, 129, 759-770.	1.4	69
86	Diagnosis of a Critical Respiratory Illness Caused by Human Metapneumovirus by Use of a Pan-Virus Microarray. Journal of Clinical Microbiology, 2007, 45, 2340-2343.	3.9	67
87	High-throughput sequencing for noninvasive disease detection in hematologic malignancies. Blood, 2017, 130, 440-452.	1.4	66
88	Single cell analysis reveals distinct immune landscapes in transplant and primary sarcomas that determine response or resistance to immunotherapy. Nature Communications, 2020, 11, 6410.	12.8	66
89	Integrating Tumor and Stromal Gene Expression Signatures With Clinical Indices for Survival Stratification of Early-Stage Nonâ€"Small Cell Lung Cancer. Journal of the National Cancer Institute, 2015, 107, djv211.	6.3	64
90	Distinct IL-4-induced gene expression, proliferation, and intracellular signaling in germinal center B-cell-like and activated B-cell-like diffuse large-cell lymphomas. Blood, 2005, 105, 2924-2932.	1.4	63

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91	Inferring gene expression from cell-free DNA fragmentation profiles. Nature Biotechnology, 2022, 40, 585-597.	17.5	63
92	Mixed Phenotype Acute Leukemia. American Journal of Clinical Pathology, 2014, 142, 803-808.	0.7	62
93	Pembrolizumab for Treatment of Relapsed/Refractory Mycosis Fungoides and Sezary Syndrome: Clinical Efficacy in a Citn Multicenter Phase 2 Study. Blood, 2016, 128, 181-181.	1.4	56
94	A proteomic approach for the identification of novel lysine methyltransferase substrates. Epigenetics and Chromatin, 2011, 4, 19.	3.9	55
95	Utility of positron emission tomography scans in mantle cell lymphoma. American Journal of Hematology, 2011, 86, 841-845.	4.1	55
96	A pluripotency signature predicts histologic transformation and influences survival in follicular lymphoma patients. Blood, 2009, 114, 3158-3166.	1.4	52
97	CD137 Is Expressed in Follicular Dendritic Cell Tumors and in Classical Hodgkin and T-Cell Lymphomas. American Journal of Pathology, 2012, 181, 795-803.	3.8	52
98	Targetable genetic alterations of <i>TCF4</i> (<i>E2-2</i>) drive immunoglobulin expression in diffuse large B cell lymphoma. Science Translational Medicine, 2019, 11, .	12.4	51
99	Combination Approach for Detecting Different Types of Alterations in Circulating Tumor DNA in Leiomyosarcoma. Clinical Cancer Research, 2018, 24, 2688-2699.	7.0	45
100	High-throughput genomic profiling of tumor-infiltrating leukocytes. Current Opinion in Immunology, 2016, 41, 77-84.	5.5	43
101	Organocatalytic removal of formaldehyde adducts from RNA and DNA bases. Nature Chemistry, 2015, 7, 752-758.	13.6	41
102	Second‐line mitoxantrone, etoposide, and cytarabine for acute myeloid leukemia: A single‐center experience. American Journal of Hematology, 2010, 85, 877-881.	4.1	37
103	Germinal centre protein HGAL promotes lymphoid hyperplasia and amyloidosis via BCR-mediated Syk activation. Nature Communications, 2013, 4, 1338.	12.8	37
104	Short Diagnosis-to-Treatment Interval Is Associated With Higher Circulating Tumor DNA Levels in Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2021, 39, 2605-2616.	1.6	37
105	B-cell lymphomas present immunoglobulin neoantigens. Blood, 2019, 133, 878-881.	1.4	36
106	CD20-Targeted Therapy Ablates <i>De Novo</i> Antibody Response to Vaccination but Spares Preestablished Immunity. Blood Cancer Discovery, 2022, 3, 95-102.	5.0	36
107	Immunophenotypic features of acute myeloid leukemia with inv(3)(q21q26.2)/t(3;3)(q21;q26.2). Leukemia Research, 2010, 34, 594-597.	0.8	29
108	Functional significance of U2AF1 S34F mutations in lung adenocarcinomas. Nature Communications, 2019, 10, 5712.	12.8	27

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109	Early prediction of clinical outcomes in resected stage II and III colorectal cancer (CRC) through deep sequencing of circulating tumor DNA (ctDNA).. Journal of Clinical Oncology, 2017, 35, 3591-3591.	1.6	27
110	Autologous tumor cell vaccine induces antitumor T cell immune responses in patients with mantle cell lymphoma: A phase I/II trial. Journal of Experimental Medicine, 2020, 217, .	8.5	26
111	Impact of TET2 mutations on mRNA expression and clinical outcomes in MDS patients treated with DNA methyltransferase inhibitors. Hematological Oncology, 2011, 29, 157-160.	1.7	25
112	Data normalization considerations for digital tumor dissection. Genome Biology, 2017, 18, 128.	8.8	25
113	Circulating Tumor DNA in Lymphoma: Principles and Future Directions. Blood Cancer Discovery, 2022, 3, 5-15.	5.0	25
114	Evaluation and management of angioimmunoblastic T-cell lymphoma: a review of current approaches and future strategies. Clinical Advances in Hematology and Oncology, 2008, 6, 899-909.	0.3	25
115	Genomic analysis of renal allograft dysfunction using cDNA microarrays. Transplantation Proceedings, 2001, 33, 297-298.	0.6	23
116	Expression profiles of adult T-cell leukemiaâ€"lymphoma and associations with clinical responses to zidovudine and interferon Î±. Leukemia and Lymphoma, 2010, 51, 1200-1216.	1.3	23
117	Absolute lymphocyte count at day 28 independently predicts eventâ€free and overall survival in adults with newly diagnosed acute lymphoblastic leukemia. American Journal of Hematology, 2012, 87, 957-960.	4.1	22
118	Molecular Outcome Prediction in Diffuse Large-B-Cell Lymphoma. New England Journal of Medicine, 2009, 360, 2794-2795.	27.0	19
119	Role of Smad Proteins in Resistance to BMP-Induced Growth Inhibition in B-Cell Lymphoma. PLoS ONE, 2012, 7, e46117.	2.5	18
120	Examining the Living Genome in Health and Disease With DNA Microarrays. JAMA - Journal of the American Medical Association, 2000, 283, 2298.	7.4	17
121	Common progenitor cells in mature B-cell malignancies. Current Opinion in Hematology, 2014, 21, 333-340.	2.5	17
122	Surprise! HSC Are Aberrant in Chronic Lymphocytic Leukemia. Cancer Cell, 2011, 20, 135-136.	16.8	15
123	First Isolation of Cryptococcus uzbekistanensis from an Immunocompromised Patient with Lymphoma. Journal of Clinical Microbiology, 2012, 50, 1125-1127.	3.9	15
124	A Comprehensive Circulating Tumor DNA Assay for Detection of Translocation and Copy-Number Changes in Pediatric Sarcomas. Molecular Cancer Therapeutics, 2021, 20, 2016-2025.	4.1	15
125	Profiling of Circulating Tumor DNA for Noninvasive Disease Detection, Risk Stratification, and MRD Monitoring in Patients with CNS Lymphoma. Blood, 2021, 138, 6-6.	1.4	15
126	A Subpopulation of Follicular Lymphoma Tumor Infiltrating T Cells Shows Suppressed Common Gamma Chain Cytokine Signaling.. Blood, 2009, 114, 759-759.	1.4	14

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127	Genomic Profiling of Bronchoalveolar Lavage Fluid in Lung Cancer. Cancer Research, 2022, 82, 2838-2847.	0.9	14
128	Identification of gene microarray expression profiles in patients with chronic graft-versus-host disease following allogeneic hematopoietic cell transplantation. Clinical Immunology, 2013, 148, 124-135.	3.2	13
129	Tumor antigen discovery through translation of the cancer genome. Immunologic Research, 2014, 58, 292-299.	2.9	13
130	Molecular and Immunologic Signatures are Related to Clinical Benefit from Treatment with Vocimagene Amiretrorepvec (Toca 511) and 5-Fluorocytosine (Toca FC) in Patients with Glioma. Clinical Cancer Research, 2020, 26, 6176-6186.	7.0	13
131	Circulating DNA for Molecular Response Prediction, Characterization of Resistance Mechanisms and Quantification of CAR T-Cells during Axicabtagene Ciloleucel Therapy. Blood, 2019, 134, 550-550.	1.4	13
132	A retrospective study evaluating the efficacy and safety of bendamustine in the treatment of mantle cell lymphoma. Leukemia and Lymphoma, 2012, 53, 1299-1305.	1.3	12
133	Correction: Specific post-translational histone modifications of neutrophil extracellular traps as immunogens and potential targets of lupus autoantibodies. Arthritis Research and Therapy, 2012, 14, 403.	3.5	12
134	Rituximab use and survival after diffuse large B-cell or follicular lymphoma: a population-based study. Leukemia and Lymphoma, 2013, 54, 743-751.	1.3	12
135	Surgical and molecular characterization of primary and metastatic disease in a neuroendocrine tumor arising in a tailgut cyst. Journal of Physical Education and Sports Management, 2018, 4, a003004.	1.2	10
136	Noninvasive Genotyping and Assessment of Treatment Response in Diffuse Large B Cell Lymphoma. Blood, 2015, 126, 114-114.	1.4	10
137	Examining the Living Genome in Health and Disease With DNA Microarrays. JAMA - Journal of the American Medical Association, 2000, 283, 2298-2299.	7.4	9
138	Towards Non-Invasive Classification of DLBCL Genetic Subtypes By Ctdna Profiling. Blood, 2019, 134, 551-551.	1.4	9
139	Dynamic Noninvasive Genomic Monitoring for Outcome Prediction in Diffuse Large B-Cell Lymphoma. Blood, 2015, 126, 130-130.	1.4	9
140	SWOG 1918: A phase II/III randomized study of R-miniCHOP with or without oral azacitidine (CC-486) in participants age 75Âyears or older with newly diagnosed aggressive non-Hodgkin lymphomas â€" Aiming to improve therapy, outcomes, and validate a prospective frailty tool. Journal of Geriatric Oncology, 2022, 13, 258-264.	1.0	9
141	Evaluating upfront high-dose consolidation after R-CHOP for follicular lymphoma by clinical and genetic risk models. Blood Advances, 2020, 4, 4451-4462.	5.2	8
142	Development and Validation of Biopsy-Free Genotyping for Molecular Subtyping of Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 1089-1089.	1.4	8
143	Noninvasive Detection of Ibrutinib Resistance in Non-Hodgkin Lymphoma Using Cell-Free DNA. Blood, 2016, 128, 1752-1752.	1.4	8
144	Noninvasive Detection of BCL2, BCL6, and MYC Translocations in Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 2930-2930.	1.4	8

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145	KLHL6 Is Preferentially Expressed in Germinal Center–Derived B-Cell Lymphomas. American Journal of Clinical Pathology, 2017, 148, 465-476.	0.7	7
146	Hit-and-run lymphomagenesis by theBcl6oncogene. Cell Cycle, 2014, 13, 1831-1832.	2.6	6
147	Early Mortality in Acute Promyelocytic Leukemia May Be Higher Than Previously Reported.. Blood, 2009, 114, 1015-1015.	1.4	6
148	Concurrent Pembrolizumab with AVD for Untreated Classical Hodgkin Lymphoma. Blood, 2021, 138, 233-233.	1.4	6
149	Phased Variant Enrichment for Enhanced Minimal Residual Disease Detection from Cell-Free DNA. Blood, 2019, 134, 552-552.	1.4	5
150	A phase 2 study of glembatumumab vedotin (GV), an antibody-drug conjugate (ADC) targeting gpNMB, in advanced melanoma. Annals of Oncology, 2016, 27, vi393.	1.2	4
151	Leveraging phased variants for personalized minimal residual disease detection in localized non-small cell lung cancer.. Journal of Clinical Oncology, 2021, 39, 8518-8518.	1.6	4
152	Distinct Chromatin Accessibility Profiles of Lymphoma Subtypes Revealed By Targeted Cell Free DNA Profiling. Blood, 2018, 132, 672-672.	1.4	4
153	An Atlas of Clinically-Distinct Tumor Cellular Ecosystems in Diffuse Large B Cell Lymphoma. Blood, 2019, 134, 655-655.	1.4	4
154	Noninvasive detection of clinically relevant copy number alterations in diffuse large B-cell lymphoma.. Journal of Clinical Oncology, 2017, 35, 7507-7507.	1.6	4
155	Development of a Dynamic Model for Personalized Risk Assessment in Large B-Cell Lymphoma. Blood, 2017, 130, 826-826.	1.4	4
156	A few good genes. Cell Cycle, 2011, 10, 3615-3616.	2.6	3
157	CAPP-Seq Circulating Tumor DNA Analysis for Early Detection of Tumor Progression After Definitive Radiation Therapy for Lung Cancer. International Journal of Radiation Oncology Biology Physics, 2016, 96, S41-S42.	0.8	3
158	Abstract P5-04-03: Deconvoluting immune cell populations using 'in silico flow cytometry' with CIBERSORT: Association with neoadjuvant therapy response and genomic instability in TNBC. , 2015, , .		3
159	Interim Circulating Tumor DNA As a Prognostic Biomarker in the Setting of Interim PET-Based Adaptive Therapy for DLBCL. Blood, 2019, 134, 1600-1600.	1.4	3
160	Profiling T-Cell Receptor Diversity and Dynamics during Lymphoma Immunotherapy Using Cell-Free DNA (cfDNA). Blood, 2020, 136, 49-50.	1.4	3
161	The Impact of Distance to Treatment Center on the Outcome of AML. Blood, 2010, 116, 4742-4742.	1.4	3
162	Prediction of therapeutic outcomes in DLBCL from circulating tumor DNA dynamics.. Journal of Clinical Oncology, 2016, 34, 7511-7511.	1.6	3

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163	Circulating tumor DNA analysis for outcome prediction in localized esophageal cancer.. Journal of Clinical Oncology, 2017, 35, 4055-4055.	1.6	3
164	Analysis of circulating tumor DNA in localized lung cancer for detection of molecular residual disease and personalization of adjuvant strategies.. Journal of Clinical Oncology, 2017, 35, 8519-8519.	1.6	3
165	Systematic Deconvolution of Hematolymphoid Tumor Transcriptomes Reveals Infiltrating Immune Cell Signatures Related to Survival.. Blood, 2012, 120, 2390-2390.	1.4	3
166	Abstract PR09: The prognostic landscape of genes and infiltrating immune cells across human cancers. Cancer Research, 2015, 75, PR09-PR09.	0.9	3
167	Early Assessment of Chemotherapy Response in Advanced Non-Small Cell Lung Cancer with Circulating Tumor DNA. Cancers, 2022, 14, 2479.	3.7	3
168	Utility in prognostic value added by molecular profiles for diffuse large B-cell lymphoma. Blood, 2013, 121, 3052-3054.	1.4	2
169	Reply to J. Wang et al. Journal of Clinical Oncology, 2019, 37, 755-757.	1.6	2
170	Recurrent Crebbp Mutations in Follicular Lymphoma Appear Localized to the Committed B-Cell Lineage. Blood, 2020, 136, 30-31.	1.4	2
171	NF-κB Signaling In Response to CpG Stratifies Mantle Cell Lymphoma Patient Outcome. Blood, 2010, 116, 144-144.	1.4	2
172	Potentiated B-Cell Antigen Receptor Signaling In Mantle Cell Lymphoma Is Associated With Overexpression Of Surface CD79B and IgM. Blood, 2013, 122, 1768-1768.	1.4	2
173	Inter- and intra-patient heterogeneity of resistance mechanisms to the mutant EGFR selective inhibitor rociletinib.. Journal of Clinical Oncology, 2016, 34, 9000-9000.	1.6	2
174	Prediction of Survival in Diffuse Large B-Cell Lymphoma Based On the Expression of Two Genes: Integration of Tumor and Microenvironment Contributions.. Blood, 2009, 114, 622-622.	1.4	2
175	Abstract CN07-03: CD47 is an adverse prognostic factor and therapeutic antibody target on human AML stem cells. , 2009, , .		2
176	Noninvasive molecular subtyping and risk stratification of DLBCL.. Journal of Clinical Oncology, 2016, 34, 7554-7554.	1.6	2
177	Double trouble in follicular lymphoma: A rare and unusual synergy of oncogenes in the germinal center. Leukemia and Lymphoma, 2008, 49, 377-380.	1.3	1
178	Ultrasensitive Detection of Circulating Tumor DNA in Non-Small Cell Lung Cancer by Deep Sequencing. International Journal of Radiation Oncology Biology Physics, 2014, 90, S75.	0.8	1
179	Analysis of Circulating Tumor DNA in Esophageal Carcinoma Patients Treated With Chemoradiation Therapy. International Journal of Radiation Oncology Biology Physics, 2015, 93, S104-S105.	0.8	1
180	PHASE I/II CLINICAL TRIAL OF AN ACTIVATED WHOLE TUMOR CELL VACCINE FOLLOWED BY TRANSFER OF IMMUNE T CELLS IN PATIENTS WITH MANTLE CELL LYMPHOMA. Hematological Oncology, 2017, 35, 207-208.	1.7	1

#	Article	IF	Citations
181	Genomic feature selection by coverage design optimization. Journal of Applied Statistics, 2018, 45, 2658-2676.	1.3	1
182	Early Detection of Post-Transplant Lymphoproliferative Disorder Using Circulating Tumor DNA. Journal of Heart and Lung Transplantation, 2019, 38, S12-S13.	0.6	1
183	Phased variants improve DLBCL minimal residual disease detection at the end of therapy.. Journal of Clinical Oncology, 2021, 39, 7565-7565.	1.6	1
184	CD47 Is An Independent Prognostic Factor and Therapeutic Antibody Target on Human Acute Myeloid Leukemia Stem Cells. Blood, 2008, 112, 766-766.	1.4	1
185	Therapeutic Antibody Targeting of CD47 Synergizes with Rituximab to Completely Eradicate Human B-Cell Lymphoma Xenografts.. Blood, 2009, 114, 2716-2716.	1.4	1
186	HGAL-a Germinal Center Specific Protein, Enhances B-Cell Receptor Signaling by Activation of Syk, Leading to Follicular Lymphoproliferation. Blood, 2011, 118, 584-584.	1.4	1
187	DNA Copy Number Gains of TCF4 (E2-2) Are Associated with Poor Outcome in Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 2686-2686.	1.4	1
188	Integrated digital error suppression for noninvasive detection of circulating tumor DNA in NSCLC.. Journal of Clinical Oncology, 2016, 34, e20500-e20500.	1.6	1
189	Early detection of post-transplant lymphoproliferative disorder using circulating tumor DNA.. Journal of Clinical Oncology, 2018, 36, 7572-7572.	1.6	1
190	ctDNA analysis for personalization of consolidation immunotherapy in localized non-small cell lung cancer.. Journal of Clinical Oncology, 2019, 37, 2547-2547.	1.6	1
191	Therapeutic Potential of Anti-CD137 Antibody in Lymphoma.. Blood, 2009, 114, 722-722.	1.4	1
192	Is Time of the Essence in Adult Acute Myeloid Leukemia (AML)? Time to Blast Clearance and Time to Induction Therapy Fail to Predict Overall Survival (OS).. Blood, 2009, 114, 1617-1617.	1.4	1
193	The Diffuse Large B-Cell Lymphoma Infiltrating Macrophage Transcriptome Signature Is Enriched for Both M1 and M2 Genes and Provides an Excellent Platform for Functional Validation of Macrophage Biology in DLBCL. Blood, 2012, 120, 790-790.	1.4	1
194	Absence of Evidence Implicating Hematopoietic Stem Cells As Common Progenitors for DLBCL Mutations. Blood, 2016, 128, 4107-4107.	1.4	1
195	Kohrt HE, Houot R, Goldstein MJ, Weiskopf K, Alizadeh AA, Brody J, Müller A, Pachynski R, Czerwinski D, Coutre S, Chao MP, Chen L, Tedder TF, Levy R. CD137 stimulation enhances the antilymphoma activity of anti-CD20 antibodies. Blood. 2011;117(8):2423-2432.. Blood, 2019, 134, 658-658.	1.4	1
196	Follicular Lymphoma Organoids for Investigating the Tumor Microenvironment. Blood, 2019, 134, 2799-2799.	1.4	1
197	Tumor-Confirmed Follicular Lymphoma Mutations Are Detectable in Peripheral Blood Years Prior to Clinical Diagnosis. Blood, 2021, 138, 709-709.	1.4	1
198	Heterogeneity of Regulatory T Cells in B-Cell Non-Hodgkin Lymphoma. Blood, 2020, 136, 27-28.	1.4	1

#	Article	IF	Citations
199	Leukemic Stem Cell Gene Expression Signature and Clinical Outcomes in Acute Myeloid Leukemiaâ€"Reply. JAMA - Journal of the American Medical Association, 2011, 305, 1094.	7.4	0
200	Cell-free DNA as a Biomarker of Residual Disease Following Radiation Therapy for Non-small Cell Lung Cancer. International Journal of Radiation Oncology Biology Physics, 2012, 84, S713.	0.8	0
201	Noninvasive Cancer Classification Using Diverse Genomic Features in Circulating Tumor DNA. , 2016, , .		0
202	(S012) Circulating Tumor DNA Detects Residual Disease and Anticipates Tumor Progression Earlier Than CT Imaging. International Journal of Radiation Oncology Biology Physics, 2017, 98, E4.	0.8	0
203	MA 13.01 Clinical and Pathological Variables Influencing Noninvasive Detection of Early Stage Lung Cancer Using Circulating Tumor DNA. Journal of Thoracic Oncology, 2017, 12, S1851.	1.1	0
204	(OA02) Circulating Tumor DNA Quantitation for Early Response Assessment of Immune Checkpoint Inhibitors for Metastatic Non-Small Cell Lung Cancer. International Journal of Radiation Oncology Biology Physics, 2018, 101, e1-e2.	0.8	0
205	P2.05-01 Broad Genomic Profiling of Bronchoalveolar Lavage Fluid in Lung Cancer. Journal of Thoracic Oncology, 2019, 14, S747-S748.	1.1	0
206	LMO2 Protein Expression Predicts Survival in Patients with Diffuse Large B-Cell Lymphoma Treated with Immunochemotherapy (RCHOP): A Multicenter Validation Study. Blood, 2008, 112, 3769-3769.	1.4	0
207	Gene Expression Signature of Host Immune Response Is Predictive of Follicular Lymphoma Patient Survival in Independent Cohorts, and Correlates with Transformation to Diffuse Large B-Cell Lymphoma.. Blood, 2009, 114, 2951-2951.	1.4	0
208	Abstract PR5: Prediction of survival in diffuse large B-cell lymphoma based on the expression of two genes integrating tumor and microenvironment. , 2010, , .		0
209	Self-Antigen Recognition by the B Cell Receptors of Follicular Lymphoma. Blood, 2010, 116, 4124-4124.	1.4	0
210	A Novel Missense Mutation In An MDS Patient and Effects on TET2 mRNA Expression and Clinical Outcomes. Blood, 2010, 116, 1889-1889.	1.4	0
211	Clinical and Pathological Features of Non-Hodgkin Lymphomas Harboring Concurrent t(14;18) and 8q24 Anomalies. Blood, 2010, 116, 3134-3134.	1.4	0
212	Prediction of Survival In Diffuse Large B-Cell Lymphoma Based On the Expression of Two Genes Reflecting Tumor and Microenvironment. Blood, 2010, 116, 2006-2006.	1.4	0
213	A Multicenter Study Evaluating the Efficacy and Safety of Bendamustine in the Treatment of Mantle Cell Lymphoma. Blood, 2011, 118, 4940-4940.	1.4	0
214	Absolute Lymphocyte Count At Day 28 Independently Predicts Event-Free and Overall Survival in Adults with Newly Diagnosed Acute Lymphocytic Leukemia. Blood, 2011, 118, 2552-2552.	1.4	0
215	Genome-Wide Characterization of Human Hematopoietic Progenitor Cell Heterogeneity by Expression Profiling of Single Cells: A Pilot Study. Blood, 2012, 120, 1231-1231.	1.4	0
216	Targeting B-Cell Lymphoma with Idiotype-Specific Peptibodies: Toward a Personalized and Tumor-Specific Therapy. Blood, 2012, 120, 3713-3713.	1.4	0

#	Article	IF	Citations
217	Hierarchy in Somatic Mutations Arising During Genomic Evolution and Progression of Follicular Lymphoma. Blood, 2012, 120, 148-148.	1.4	0
218	Identification of Candidate Transcriptional Biomarkers Associated with Chronic Graft-Versus-Host Disease Following Allogeneic Hematopoietic Cell Transplantation. Blood, 2012, 120, 4190-4190.	1.4	0
219	Abstract A74: The chemoattractant chemerin suppresses melanoma by recruiting natural killer cell antitumor defenses.. , 2013, , .		0
220	Noninvasive monitoring of cellular versus acellular tumor DNA from immunoglobulin genes for DLBCL.. Journal of Clinical Oncology, 2014, 32, 8504-8504.	1.6	0
221	Noninvasive and ultrasensitive quantitation of circulating tumor DNA by hybrid capture and deep sequencing.. Journal of Clinical Oncology, 2014, 32, 11016-11016.	1.6	0
222	Pre-treatment circulating tumor DNA as a biomarker for disease burden in diffuse large B cell lymphoma (DLBCL).. Journal of Clinical Oncology, 2015, 33, 8539-8539.	1.6	0
223	Antigen Presentation Profiling Reveals T-Cell Recognition of Lymphoma Immunoglobulin Neoantigens. Blood, 2016, 128, 915-915.	1.4	0
224	Elucidation of distinct mutational patterns between diffuse large B cell lymphoma subtypes utilizing circulating tumor DNA.. Journal of Clinical Oncology, 2017, 35, 7538-7538.	1.6	0
225	Post-transplant head and neck cancers: A prospective analysis of clinical factors for risk stratification.. Journal of Clinical Oncology, 2018, 36, e18051-e18051.	1.6	0
226	Abstract B49: Quantitating circulating tumor DNA in translocation-positive sarcoma patients using CAPP-Seq. , 2018, , .		0
227	Lymphoma Virome Dynamics Revealed By Cell-Free DNA Sequencing. Blood, 2018, 132, 2861-2861.	1.4	0
228	Short Diagnosis-to-Treatment Interval Is Associated with Higher Levels of Circulating Tumor DNA in Aggressive B-Cell Non-Hodgkin Lymphoma. Blood, 2019, 134, 491-491.	1.4	0
229	Circulating tumor DNA in Genetic Profiling and Monitoring of Pediatric Hodgkin Lymphoma. , 2020, 232, .		0
230	Noninvasive Cell-of-Origin Classification of Diffuse Large B-Cell Lymphoma Using Inferred Gene Expression from Cell-Free DNA Sequencing. Blood, 2021, 138, 37-37.	1.4	0
231	Diversity of Intratumoral Regulatory T Cells in Non-Hodgkin Lymphoma. Blood, 2021, 138, 3519-3519.	1.4	0
232	Time Since Last Anti-CD20 Treatment Is a Major Determinant of Sars-Cov-2 Vaccine Response in a Large Cohort of Patients with B-Cell Lymphoma. Blood, 2021, 138, 2064-2064.	1.4	0