

Ash A Alizadeh

List of Publications by Year in descending order

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Version: 2024-02-01

231
papers

52,916
citations

8159

76
h-index

2375

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. <i>Nature</i> , 2000, 403, 503-511.	13.7	8,977
2	Robust enumeration of cell subsets from tissue expression profiles. <i>Nature Methods</i> , 2015, 12, 453-457.	9.0	8,460
3	The prognostic landscape of genes and infiltrating immune cells across human cancers. <i>Nature Medicine</i> , 2015, 21, 938-945.	15.2	2,505
4	Determining cell type abundance and expression from bulk tissues with digital cytometry. <i>Nature Biotechnology</i> , 2019, 37, 773-782.	9.4	2,396
5	Profiling Tumor Infiltrating Immune Cells with CIBERSORT. <i>Methods in Molecular Biology</i> , 2018, 1711, 243-259.	0.4	1,936
6	An ultrasensitive method for quantitating circulating tumor DNA with broad patient coverage. <i>Nature Medicine</i> , 2014, 20, 548-554.	15.2	1,771
7	CD47 Is an Adverse Prognostic Factor and Therapeutic Antibody Target on Human Acute Myeloid Leukemia Stem Cells. <i>Cell</i> , 2009, 138, 286-299.	13.5	1,371
8	The CD47-signal regulatory protein alpha (SIRPα) interaction is a therapeutic target for human solid tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6662-6667.	3.3	1,255
9	Relation of Gene Expression Phenotype to Immunoglobulin Mutation Genotype in B Cell Chronic Lymphocytic Leukemia. <i>Journal of Experimental Medicine</i> , 2001, 194, 1639-1648.	4.2	978
10	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. <i>Nature Genetics</i> , 1999, 23, 41-46.	9.4	928
11	Anti-CD47 Antibody Synergizes with Rituximab to Promote Phagocytosis and Eradicate Non-Hodgkin Lymphoma. <i>Cell</i> , 2010, 142, 699-713.	13.5	894
12	Prediction of Survival in Diffuse Large-B-Cell Lymphoma Based on the Expression of Six Genes. <i>New England Journal of Medicine</i> , 2004, 350, 1828-1837.	13.9	874
13	Integrated digital error suppression for improved detection of circulating tumor DNA. <i>Nature Biotechnology</i> , 2016, 34, 547-555.	9.4	837
14	Gene Expression Signature of Fibroblast Serum Response Predicts Human Cancer Progression: Similarities between Tumors and Wounds. <i>PLoS Biology</i> , 2004, 2, e7.	2.6	824
15	Individuality and variation in gene expression patterns in human blood. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1896-1901.	3.3	723
16	Early Detection of Molecular Residual Disease in Localized Lung Cancer by Circulating Tumor DNA Profiling. <i>Cancer Discovery</i> , 2017, 7, 1394-1403.	7.7	701
17	Outcomes of Observation vs Stereotactic Ablative Radiation for Oligometastatic Prostate Cancer. <i>JAMA Oncology</i> , 2020, 6, 650.	3.4	696
18	Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015, 21, 846-853.	15.2	604

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19	Calreticulin Is the Dominant Pro-Phagocytic Signal on Multiple Human Cancers and Is Counterbalanced by CD47. <i>Science Translational Medicine</i> , 2010, 2, 63ra94.	5.8	591
20	Circulating tumour DNA profiling reveals heterogeneity of EGFR inhibitor resistance mechanisms in lung cancer patients. <i>Nature Communications</i> , 2016, 7, 11815.	5.8	520
21	Rheumatoid arthritis is a heterogeneous disease: Evidence for differences in the activation of the STAT-1 pathway between rheumatoid tissues. <i>Arthritis and Rheumatism</i> , 2003, 48, 2132-2145.	6.7	418
22	'Gene shaving' as a method for identifying distinct sets of genes with similar expression patterns. <i>Genome Biology</i> , 2000, 1, research0003.1.	13.9	392
23	Integrating genomic features for non-invasive early lung cancer detection. <i>Nature</i> , 2020, 580, 245-251.	13.7	379
24	Role of interleukin 6 in myocardial dysfunction of meningococcal septic shock. <i>Lancet, The</i> , 2004, 363, 203-209.	6.3	378
25	SOURCE: a unified genomic resource of functional annotations, ontologies, and gene expression data. <i>Nucleic Acids Research</i> , 2003, 31, 219-223.	6.5	376
26	Stereotyped and specific gene expression programs in human innate immune responses to bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 972-977.	3.3	371
27	Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA. <i>Science Translational Medicine</i> , 2016, 8, 364ra155.	5.8	348
28	Association of a Leukemic Stem Cell Gene Expression Signature With Clinical Outcomes in Acute Myeloid Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2010, 304, 2706.	3.8	339
29	Therapeutic Antibody Targeting of CD47 Eliminates Human Acute Lymphoblastic Leukemia. <i>Cancer Research</i> , 2011, 71, 1374-1384.	0.4	318
30	Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2018, 36, 2845-2853.	0.8	313
31	Mutations in early follicular lymphoma progenitors are associated with suppressed antigen presentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1116-25.	3.3	307
32	Genomic expression programs and the integration of the CD28 costimulatory signal in T cell activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11796-11801.	3.3	300
33	Hierarchy in somatic mutations arising during genomic evolution and progression of follicular lymphoma. <i>Blood</i> , 2013, 121, 1604-1611.	0.6	279
34	Cell-type specific gene expression profiles of leukocytes in human peripheral blood. <i>BMC Genomics</i> , 2006, 7, 115.	1.2	275
35	Noninvasive monitoring of diffuse large B-cell lymphoma by immunoglobulin high-throughput sequencing. <i>Blood</i> , 2015, 125, 3679-3687.	0.6	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. <i>Blood</i> , 2002, 99, 2285-2290.	0.6	266

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37	Towards a novel classification of human malignancies based on gene expression patterns. <i>Journal of Pathology</i> , 2001, 195, 41-52.	2.1	265
38	Profiling Cell Type Abundance and Expression in Bulk Tissues with CIBERSORTx. <i>Methods in Molecular Biology</i> , 2020, 2117, 135-157.	0.4	249
39	Prospective separation of normal and leukemic stem cells based on differential expression of TIM3, a human acute myeloid leukemia stem cell marker. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5009-5014.	3.3	248
40	Role of <i>KEAP1</i> and <i>NRF2</i> and <i>TP53</i> Mutations in Lung Squamous Cell Carcinoma Development and Radiation Resistance. <i>Cancer Discovery</i> , 2017, 7, 86-101.	7.7	239
41	Three differentiation states risk-stratify bladder cancer into distinct subtypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2078-2083.	3.3	232
42	Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens. <i>Nature</i> , 2017, 543, 723-727.	13.7	232
43	A Simple Method for Estimating Interactions Between a Treatment and a Large Number of Covariates. <i>Journal of the American Statistical Association</i> , 2014, 109, 1517-1532.	1.8	227
44	Ongoing immunoglobulin somatic mutation in germinal center B cell-like but not in activated B cell-like diffuse large cell lymphomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 10209-10213.	3.3	220
45	The Lymphochip: A Specialized cDNA Microarray for the Genomic-scale Analysis of Gene Expression in Normal and Malignant Lymphocytes. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1999, 64, 71-78.	2.0	218
46	Predicting HLA class II antigen presentation through integrated deep learning. <i>Nature Biotechnology</i> , 2019, 37, 1332-1343.	9.4	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. <i>Blood</i> , 2003, 101, 3109-3117.	0.6	212
48	FACTERA: a practical method for the discovery of genomic rearrangements at breakpoint resolution. <i>Bioinformatics</i> , 2014, 30, 3390-3393.	1.8	212
49	Noninvasive Early Identification of Therapeutic Benefit from Immune Checkpoint Inhibition. <i>Cell</i> , 2020, 183, 363-376.e13.	13.5	206
50	Transformation of follicular lymphoma to diffuse large-cell lymphoma: Alternative patterns with increased or decreased expression of <i>c-myc</i> and its regulated genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8886-8891.	3.3	204
51	Circulating tumor DNA dynamics predict benefit from consolidation immunotherapy in locally advanced non-small-cell lung cancer. <i>Nature Cancer</i> , 2020, 1, 176-183.	5.7	201
52	CD137 stimulation enhances the antilymphoma activity of anti-CD20 antibodies. <i>Blood</i> , 2011, 117, 2423-2432.	0.6	195
53	Software Tools for High-Throughput Analysis and Archiving of Immunohistochemistry Staining Data Obtained with Tissue Microarrays. <i>American Journal of Pathology</i> , 2002, 161, 1557-1565.	1.9	194
54	Prediction of survival in diffuse large B-cell lymphoma based on the expression of 2 genes reflecting tumor and microenvironment. <i>Blood</i> , 2011, 118, 1350-1358.	0.6	175

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55	Specific post-translational histone modifications of neutrophil extracellular traps as immunogens and potential targets of lupus autoantibodies. <i>Arthritis Research and Therapy</i> , 2012, 14, R25.	1.6	162
56	Enhanced detection of minimal residual disease by targeted sequencing of phased variants in circulating tumor DNA. <i>Nature Biotechnology</i> , 2021, 39, 1537-1547.	9.4	151
57	High PD-1 expression and suppressed cytokine signaling distinguish T cells infiltrating follicular lymphoma tumors from peripheral T cells. <i>Blood</i> , 2013, 121, 1367-1376.	0.6	147
58	Circulating Tumor DNA Analysis for Detection of Minimal Residual Disease After Chemoradiotherapy for Localized Esophageal Cancer. <i>Gastroenterology</i> , 2020, 158, 494-505.e6.	0.6	147
59	In Vivo Regulation of Human Skeletal Muscle Gene Expression by Thyroid Hormone. <i>Genome Research</i> , 2002, 12, 281-291.	2.4	143
60	B-cell signaling networks reveal a negative prognostic human lymphoma cell subset that emerges during tumor progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12747-12754.	3.3	143
61	Detection and Surveillance of Bladder Cancer Using Urine Tumor DNA. <i>Cancer Discovery</i> , 2019, 9, 500-509.	7.7	143
62	The chemoattractant chemerin suppresses melanoma by recruiting natural killer cell antitumor defenses. <i>Journal of Experimental Medicine</i> , 2012, 209, 1427-1435.	4.2	140
63	Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction. <i>Cell</i> , 2019, 178, 699-713.e19.	13.5	138
64	Fludarabine treatment of patients with chronic lymphocytic leukemia induces a p53-dependent gene expression response. <i>Blood</i> , 2004, 104, 1428-1434.	0.6	122
65	Treatment advances have not improved the early death rate in acute promyelocytic leukemia. <i>Haematologica</i> , 2012, 97, 133-136.	1.7	122
66	Therapeutic effect of CD137 immunomodulation in lymphoma and its enhancement by Treg depletion. <i>Blood</i> , 2009, 114, 3431-3438.	0.6	121
67	Atlas of clinically distinct cell states and ecosystems across human solid tumors. <i>Cell</i> , 2021, 184, 5482-5496.e28.	13.5	116
68	Detecting Liquid Remnants of Solid Tumors: Circulating Tumor DNA Minimal Residual Disease. <i>Cancer Discovery</i> , 2021, 11, 2968-2986.	7.7	116
69	Genomic-scale gene expression profiling of normal and malignant immune cells. <i>Current Opinion in Immunology</i> , 2000, 12, 219-225.	2.4	113
70	A mathematical model of ctDNA shedding predicts tumor detection size. <i>Science Advances</i> , 2020, 6, .	4.7	105
71	The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma. <i>Cancer Cell</i> , 2021, 39, 1422-1437.e10.	7.7	102
72	Predicting Radiotherapy Responses and Treatment Outcomes Through Analysis of Circulating Tumor DNA. <i>Seminars in Radiation Oncology</i> , 2015, 25, 305-312.	1.0	97

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73	Probing lymphocyte biology by genomic-scale gene expression analysis. <i>Journal of Clinical Immunology</i> , 1998, 18, 373-379.	2.0	96
74	<i>KEAP1/NFE2L2</i> Mutations Predict Lung Cancer Radiation Resistance That Can Be Targeted by Glutaminase Inhibition. <i>Cancer Discovery</i> , 2020, 10, 1826-1841.	7.7	93
75	Large-Scale and Comprehensive Immune Profiling and Functional Analysis of Normal Human Aging. <i>PLoS ONE</i> , 2015, 10, e0133627.	1.1	90
76	T Cell Receptor-Independent Basal Signaling via Erk and Abl Kinases Suppresses RAG Gene Expression. <i>PLoS Biology</i> , 2003, 1, e53.	2.6	88
77	HGAL is a novel interleukin-4-inducible gene that strongly predicts survival in diffuse large B-cell lymphoma. <i>Blood</i> , 2003, 101, 433-440.	0.6	84
78	Crebbp loss cooperates with Bcl2 overexpression to promote lymphoma in mice. <i>Blood</i> , 2017, 129, 2645-2656.	0.6	84
79	Self-antigen recognition by follicular lymphoma B-cell receptors. <i>Blood</i> , 2012, 120, 4182-4190.	0.6	81
80	Active Idiotypic Vaccination Versus Control Immunotherapy for Follicular Lymphoma. <i>Journal of Clinical Oncology</i> , 2014, 32, 1797-1803.	0.8	75
81	Potential clinical utility of ultrasensitive circulating tumor DNA detection with CAPP-Seq. <i>Expert Review of Molecular Diagnostics</i> , 2015, 15, 715-719.	1.5	75
82	Circulating Tumor DNA Analysis to Assess Risk of Progression after Long-term Response to PD-(L)1 Blockade in NSCLC. <i>Clinical Cancer Research</i> , 2020, 26, 2849-2858.	3.2	74
83	Transient expression of Bcl6 is sufficient for oncogenic function and induction of mature B-cell lymphoma. <i>Nature Communications</i> , 2014, 5, 3904.	5.8	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. <i>Leukemia</i> , 2004, 18, 1775-1779.	3.3	70
85	Distinct patterns of B-cell receptor signaling in non-Hodgkin lymphomas identified by single-cell profiling. <i>Blood</i> , 2017, 129, 759-770.	0.6	69
86	Diagnosis of a Critical Respiratory Illness Caused by Human Metapneumovirus by Use of a Pan-Virus Microarray. <i>Journal of Clinical Microbiology</i> , 2007, 45, 2340-2343.	1.8	67
87	High-throughput sequencing for noninvasive disease detection in hematologic malignancies. <i>Blood</i> , 2017, 130, 440-452.	0.6	66
88	Single cell analysis reveals distinct immune landscapes in transplant and primary sarcomas that determine response or resistance to immunotherapy. <i>Nature Communications</i> , 2020, 11, 6410.	5.8	66
89	Integrating Tumor and Stromal Gene Expression Signatures With Clinical Indices for Survival Stratification of Early-Stage Non-Small Cell Lung Cancer. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv211.	3.0	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. <i>Blood</i> , 2005, 105, 2924-2932.	0.6	63

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91	Inferring gene expression from cell-free DNA fragmentation profiles. <i>Nature Biotechnology</i> , 2022, 40, 585-597.	9.4	63
92	Mixed Phenotype Acute Leukemia. <i>American Journal of Clinical Pathology</i> , 2014, 142, 803-808.	0.4	62
93	Pembrolizumab for Treatment of Relapsed/Refractory Mycosis Fungoides and Sezary Syndrome: Clinical Efficacy in a CItn Multicenter Phase 2 Study. <i>Blood</i> , 2016, 128, 181-181.	0.6	56
94	A proteomic approach for the identification of novel lysine methyltransferase substrates. <i>Epigenetics and Chromatin</i> , 2011, 4, 19.	1.8	55
95	Utility of positron emission tomography scans in mantle cell lymphoma. <i>American Journal of Hematology</i> , 2011, 86, 841-845.	2.0	55
96	A pluripotency signature predicts histologic transformation and influences survival in follicular lymphoma patients. <i>Blood</i> , 2009, 114, 3158-3166.	0.6	52
97	CD137 Is Expressed in Follicular Dendritic Cell Tumors and in Classical Hodgkin and T-Cell Lymphomas. <i>American Journal of Pathology</i> , 2012, 181, 795-803.	1.9	52
98	Targetable genetic alterations of <i>TCF4</i> (<i>E2-2</i>) drive immunoglobulin expression in diffuse large B cell lymphoma. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	51
99	Combination Approach for Detecting Different Types of Alterations in Circulating Tumor DNA in Leiomyosarcoma. <i>Clinical Cancer Research</i> , 2018, 24, 2688-2699.	3.2	45
100	High-throughput genomic profiling of tumor-infiltrating leukocytes. <i>Current Opinion in Immunology</i> , 2016, 41, 77-84.	2.4	43
101	Organocatalytic removal of formaldehyde adducts from RNA and DNA bases. <i>Nature Chemistry</i> , 2015, 7, 752-758.	6.6	41
102	Second-line mitoxantrone, etoposide, and cytarabine for acute myeloid leukemia: A single-center experience. <i>American Journal of Hematology</i> , 2010, 85, 877-881.	2.0	37
103	Germinal centre protein HGAL promotes lymphoid hyperplasia and amyloidosis via BCR-mediated Syk activation. <i>Nature Communications</i> , 2013, 4, 1338.	5.8	37
104	Short Diagnosis-to-Treatment Interval Is Associated With Higher Circulating Tumor DNA Levels in Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2021, 39, 2605-2616.	0.8	37
105	B-cell lymphomas present immunoglobulin neoantigens. <i>Blood</i> , 2019, 133, 878-881.	0.6	36
106	CD20-Targeted Therapy Ablates <i>De Novo</i> Antibody Response to Vaccination but Spares Preestablished Immunity. <i>Blood Cancer Discovery</i> , 2022, 3, 95-102.	2.6	36
107	Immunophenotypic features of acute myeloid leukemia with <i>inv(3)(q21q26.2)/t(3;3)(q21;q26.2)</i> . <i>Leukemia Research</i> , 2010, 34, 594-597.	0.4	29
108	Functional significance of U2AF1 S34F mutations in lung adenocarcinomas. <i>Nature Communications</i> , 2019, 10, 5712.	5.8	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.	0.8	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, .	4.2	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.	0.8	25
112	Data normalization considerations for digital tumor dissection. Genome Biology, 2017, 18, 128.	3.8	25
113	Circulating Tumor DNA in Lymphoma: Principles and Future Directions. Blood Cancer Discovery, 2022, 3, 5-15.	2.6	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.	0.3	23
116	Expression profiles of adult T-cell leukemia lymphoma and associations with clinical responses to zidovudine and interferon β . Leukemia and Lymphoma, 2010, 51, 1200-1216.	0.6	23
117	Absolute lymphocyte count at day 28 independently predicts event-free and overall survival in adults with newly diagnosed acute lymphoblastic leukemia. American Journal of Hematology, 2012, 87, 957-960.	2.0	22
118	Molecular Outcome Prediction in Diffuse Large-B-Cell Lymphoma. New England Journal of Medicine, 2009, 360, 2794-2795.	13.9	19
119	Role of Smad Proteins in Resistance to BMP-Induced Growth Inhibition in B-Cell Lymphoma. PLoS ONE, 2012, 7, e46117.	1.1	18
120	Examining the Living Genome in Health and Disease With DNA Microarrays. JAMA - Journal of the American Medical Association, 2000, 283, 2298.	3.8	17
121	Common progenitor cells in mature B-cell malignancies. Current Opinion in Hematology, 2014, 21, 333-340.	1.2	17
122	Surprise! HSC Are Aberrant in Chronic Lymphocytic Leukemia. Cancer Cell, 2011, 20, 135-136.	7.7	15
123	First Isolation of <i>Cryptococcus uzbekistanensis</i> from an Immunocompromised Patient with Lymphoma. Journal of Clinical Microbiology, 2012, 50, 1125-1127.	1.8	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.	1.9	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.	0.6	15
126	A Subpopulation of Follicular Lymphoma Tumor Infiltrating T Cells Shows Suppressed Common Gamma Chain Cytokine Signaling.. Blood, 2009, 114, 759-759.	0.6	14

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127	Genomic Profiling of Bronchoalveolar Lavage Fluid in Lung Cancer. <i>Cancer Research</i> , 2022, 82, 2838-2847.	0.4	14
128	Identification of gene microarray expression profiles in patients with chronic graft-versus-host disease following allogeneic hematopoietic cell transplantation. <i>Clinical Immunology</i> , 2013, 148, 124-135.	1.4	13
129	Tumor antigen discovery through translation of the cancer genome. <i>Immunologic Research</i> , 2014, 58, 292-299.	1.3	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. <i>Clinical Cancer Research</i> , 2020, 26, 6176-6186.	3.2	13
131	Circulating DNA for Molecular Response Prediction, Characterization of Resistance Mechanisms and Quantification of CAR T-Cells during Axicabtagene CiloleuceL Therapy. <i>Blood</i> , 2019, 134, 550-550.	0.6	13
132	A retrospective study evaluating the efficacy and safety of bendamustine in the treatment of mantle cell lymphoma. <i>Leukemia and Lymphoma</i> , 2012, 53, 1299-1305.	0.6	12
133	Correction: Specific post-translational histone modifications of neutrophil extracellular traps as immunogens and potential targets of lupus autoantibodies. <i>Arthritis Research and Therapy</i> , 2012, 14, 403.	1.6	12
134	Rituximab use and survival after diffuse large B-cell or follicular lymphoma: a population-based study. <i>Leukemia and Lymphoma</i> , 2013, 54, 743-751.	0.6	12
135	Surgical and molecular characterization of primary and metastatic disease in a neuroendocrine tumor arising in a tailgut cyst. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a003004.	0.5	10
136	Noninvasive Genotyping and Assessment of Treatment Response in Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2015, 126, 114-114.	0.6	10
137	Towards Non-Invasive Classification of DLBCL Genetic Subtypes By Ctdna Profiling. <i>Blood</i> , 2019, 134, 551-551.	0.6	9
138	Dynamic Noninvasive Genomic Monitoring for Outcome Prediction in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2015, 126, 130-130.	0.6	9
139	SWOG 1918: A phase II/III randomized study of R-miniCHOP with or without oral azacitidine (CC-486) in participants age 75 years or older with newly diagnosed aggressive non-Hodgkin lymphomas â€“ Aiming to improve therapy, outcomes, and validate a prospective frailty tool. <i>Journal of Geriatric Oncology</i> , 2022, 13, 258-264.	0.5	9
140	Evaluating upfront high-dose consolidation after R-CHOP for follicular lymphoma by clinical and genetic risk models. <i>Blood Advances</i> , 2020, 4, 4451-4462.	2.5	8
141	Development and Validation of Biopsy-Free Genotyping for Molecular Subtyping of Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2016, 128, 1089-1089.	0.6	8
142	Noninvasive Detection of Ibrutinib Resistance in Non-Hodgkin Lymphoma Using Cell-Free DNA. <i>Blood</i> , 2016, 128, 1752-1752.	0.6	8
143	Noninvasive Detection of BCL2, BCL6, and MYC Translocations in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2016, 128, 2930-2930.	0.6	8
144	KLHL6 Is Preferentially Expressed in Germinal Centerâ€“Derived B-Cell Lymphomas. <i>American Journal of Clinical Pathology</i> , 2017, 148, 465-476.	0.4	7

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145	Hit-and-run lymphomagenesis by the Bcl6 oncogene. <i>Cell Cycle</i> , 2014, 13, 1831-1832.	1.3	6
146	Early Mortality in Acute Promyelocytic Leukemia May Be Higher Than Previously Reported. <i>Blood</i> , 2009, 114, 1015-1015.	0.6	6
147	Concurrent Pembrolizumab with AVD for Untreated Classical Hodgkin Lymphoma. <i>Blood</i> , 2021, 138, 233-233.	0.6	6
148	Phased Variant Enrichment for Enhanced Minimal Residual Disease Detection from Cell-Free DNA. <i>Blood</i> , 2019, 134, 552-552.	0.6	5
149	A phase 2 study of glembatumumab vedotin (GV), an antibody-drug conjugate (ADC) targeting gpNMB, in advanced melanoma. <i>Annals of Oncology</i> , 2016, 27, vi393.	0.6	4
150	Leveraging phased variants for personalized minimal residual disease detection in localized non-small cell lung cancer. <i>Journal of Clinical Oncology</i> , 2021, 39, 8518-8518.	0.8	4
151	Distinct Chromatin Accessibility Profiles of Lymphoma Subtypes Revealed By Targeted Cell Free DNA Profiling. <i>Blood</i> , 2018, 132, 672-672.	0.6	4
152	An Atlas of Clinically-Distinct Tumor Cellular Ecosystems in Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2019, 134, 655-655.	0.6	4
153	Noninvasive detection of clinically relevant copy number alterations in diffuse large B-cell lymphoma. <i>Journal of Clinical Oncology</i> , 2017, 35, 7507-7507.	0.8	4
154	Development of a Dynamic Model for Personalized Risk Assessment in Large B-Cell Lymphoma. <i>Blood</i> , 2017, 130, 826-826.	0.6	4
155	A few good genes. <i>Cell Cycle</i> , 2011, 10, 3615-3616.	1.3	3
156	CAPP-Seq Circulating Tumor DNA Analysis for Early Detection of Tumor Progression After Definitive Radiation Therapy for Lung Cancer. <i>International Journal of Radiation Oncology Biology Physics</i> , 2016, 96, S41-S42.	0.4	3
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