

Christopher C Oakes

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1437522/publications.pdf>

Version: 2024-02-01

85
papers

4,050
citations

147801

31
h-index

123424

61
g-index

89
all docs

89
docs citations

89
times ranked

7998
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and Targeting of the Developmental Blockade in Extranodal Natural Killer/T-cell Lymphoma. <i>Blood Cancer Discovery</i> , 2022, 3, 154-169.	5.0	8
2	Uncontrolled CD21 ^{low} age-associated and B1 B cell accumulation caused by failure of an EGR2/3 tolerance checkpoint. <i>Cell Reports</i> , 2022, 38, 110259.	6.4	15
3	Recurrent XPO1 mutations alter pathogenesis of chronic lymphocytic leukemia. <i>Journal of Hematology and Oncology</i> , 2021, 14, 17.	17.0	31
4	DNA methylation epitypes highlight underlying developmental and disease pathways in acute myeloid leukemia. <i>Genome Research</i> , 2021, 31, 747-761.	5.5	20
5	STK11/LKB1 Loss of Function Is Associated with Global DNA Hypomethylation and Adenosyl-Methionine Depletion in Human Lung Adenocarcinoma. <i>Cancer Research</i> , 2021, 81, 4194-4204.	0.9	4
6	Human Cord Blood B Cells Differ from the Adult Counterpart by Conserved Ig Repertoires and Accelerated Response Dynamics. <i>Journal of Immunology</i> , 2021, 206, 2839-2851.	0.8	18
7	Multi-omics reveals clinically relevant proliferative drive associated with mTOR-MYC-OXPHOS activity in chronic lymphocytic leukemia. <i>Nature Cancer</i> , 2021, 2, 853-864.	13.2	32
8	Selinexor in combination with decitabine in patients with acute myeloid leukemia: results from a phase 1 study. <i>Leukemia and Lymphoma</i> , 2020, 61, 387-396.	1.3	29
9	Single-cell analysis based dissection of clonality in myelofibrosis. <i>Nature Communications</i> , 2020, 11, 73.	12.8	46
10	The proliferative history shapes the DNA methylome of B-cell tumors and predicts clinical outcome. <i>Nature Cancer</i> , 2020, 1, 1066-1081.	13.2	51
11	Epigenetic reprogramming sensitizes immunologically silent EBV+ lymphomas to virus-directed immunotherapy. <i>Blood</i> , 2020, 135, 1870-1881.	1.4	39
12	Identification of two DNA methylation subtypes of Waldenström's macroglobulinemia with plasma and memory B cell features. <i>Blood</i> , 2020, 136, 585-595.	1.4	10
13	Methylome-based cell-of-origin modeling (Methyl-COOM) identifies aberrant expression of immune regulatory molecules in CLL. <i>Genome Medicine</i> , 2020, 12, 29.	8.2	15
14	Genetic Characterization and Prognostic Relevance of Acquired Uniparental Disomies in Cytogenetically Normal Acute Myeloid Leukemia. <i>Clinical Cancer Research</i> , 2019, 25, 6524-6531.	7.0	12
15	Developmental subtypes assessed by DNA methylation-iPLEX forecast the natural history of chronic lymphocytic leukemia. <i>Blood</i> , 2019, 134, 688-698.	1.4	26
16	Time-to-progression after front-line fludarabine, cyclophosphamide, and rituximab chemoimmunotherapy for chronic lymphocytic leukaemia: a retrospective, multicohort study. <i>Lancet Oncology</i> , 2019, 20, 1576-1586.	10.7	26
17	DNA methylation at an enhancer of the three prime repair exonuclease 2 gene (TREX2) is linked to gene expression and survival in laryngeal cancer. <i>Clinical Epigenetics</i> , 2019, 11, 67.	4.1	19
18	Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials. <i>Blood Advances</i> , 2019, 3, 2474-2481.	5.2	25

#	ARTICLE	IF	CITATIONS
19	Genome-wide promoter methylation of hairy cell leukemia. <i>Blood Advances</i> , 2019, 3, 384-396.	5.2	16
20	Genome-wide association study identifies an acute myeloid leukemia susceptibility locus near BICRA. <i>Leukemia</i> , 2019, 33, 771-775.	7.2	15
21	Charting the dynamic epigenome during B-cell development. <i>Seminars in Cancer Biology</i> , 2018, 51, 139-148.	9.6	22
22	Trametinib for the treatment of IGHV4-34, MAP2K1-mutant variant hairy cell leukemia. <i>Leukemia and Lymphoma</i> , 2018, 59, 1008-1011.	1.3	29
23	Epigenetic and Posttranscriptional Regulation of CD16 Expression during Human NK Cell Development. <i>Journal of Immunology</i> , 2018, 200, 565-572.	0.8	33
24	Insight into origins, mechanisms, and utility of DNA methylation in B-cell malignancies. <i>Blood</i> , 2018, 132, 999-1006.	1.4	24
25	Trisomy 12 chronic lymphocytic leukemia expresses a unique set of activated and targetable pathways. <i>Haematologica</i> , 2018, 103, 2069-2078.	3.5	25
26	Telomere Length Is Associated with Epigenetic Programming in CLL and Is a Superior Predictor of Clinical Outcome with the Ability to Bifurcate Patients with the Same CLL-IPI Score. <i>Blood</i> , 2018, 132, 1833-1833.	1.4	0
27	Uniparental Disomies (UPD) of Chromosome 13q Is Associated with Shorter Disease-Free Survival in Adult Patients (Pts) with De Novo Cytogenetically Normal Acute Myeloid Leukemia (CN-AML). <i>Blood</i> , 2018, 132, 2777-2777.	1.4	0
28	Infection at the Time of Initial Therapy for Hairy Cell Leukemia Is Associated with Inferior Time to Next Treatment. <i>Blood</i> , 2018, 132, 2305-2305.	1.4	11
29	The ETS1 Transcription Factor Is Implicated in Human and Murine Intermediate NK Cell Development Stages. <i>Blood</i> , 2018, 132, 2567-2567.	1.4	0
30	Genome-Wide Association Study (GWAS) Identifies a Significant Acute Myeloid Leukemia (AML) Susceptibility Locus Near BICRA. <i>Blood</i> , 2018, 132, 85-85.	1.4	0
31	Down-Regulation of CD25 Antigen in Hairy Cell Leukemia Patients after Treatment. <i>Blood</i> , 2018, 132, 4143-4143.	1.4	1
32	Prognostic and biological significance of the proangiogenic factor EGFL7 in acute myeloid leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4641-E4647.	7.1	36
33	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. <i>Nature Genetics</i> , 2017, 49, 1052-1060.	21.4	235
34	BET-bromodomain inhibitors modulate epigenetic patterns at the diacylglycerol kinase alpha enhancer associated with radiation-induced fibrosis. <i>Radiotherapy and Oncology</i> , 2017, 125, 168-174.	0.6	9
35	Genomic analysis of hairy cell leukemia identifies novel recurrent genetic alterations. <i>Blood</i> , 2017, 130, 1644-1648.	1.4	82
36	Mutational Landscape and Gene Expression Patterns in Adult Acute Myeloid Leukemias with Monosomy 7 as a Sole Abnormality. <i>Cancer Research</i> , 2017, 77, 207-218.	0.9	23

#	ARTICLE	IF	CITATIONS
37	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 427-445.	8.2	124
38	Abstract 3364: DNA methylation loss at an enhancer site of the DNA repair gene <i>TREX2</i> is an epigenetic feature in multiple cancers. , 2017, , .		0
39	Emerging insights on the pathogenesis and treatment of extranodal NK/T cell lymphomas (ENKTL). <i>Discovery Medicine</i> , 2017, 23, 189-199.	0.5	14
40	High-content screening identifies kinase inhibitors that overcome venetoclax resistance in activated CLL cells. <i>Blood</i> , 2016, 128, 934-947.	1.4	104
41	Surface IgM expression and function are associated with clinical behavior, genetic abnormalities, and DNA methylation in CLL. <i>Blood</i> , 2016, 128, 816-826.	1.4	54
42	Epigenetic regulation of diacylglycerol kinase alpha promotes radiation-induced fibrosis. <i>Nature Communications</i> , 2016, 7, 10893.	12.8	46
43	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2016, 48, 253-264.	21.4	254
44	Role of Histone Deacetylase-Mediated Gene Silencing in Chronic Lymphocytic Leukemia Progression. <i>Blood</i> , 2016, 128, 2705-2705.	1.4	1
45	Comparative Evaluation of Prognostic Factors That Assess the Natural History of Chronic Lymphocytic Leukemia. <i>Blood</i> , 2016, 128, 968-968.	1.4	4
46	Hsp90 inhibition increases SOCS3 transcript and regulates migration and cell death in chronic lymphocytic leukemia. <i>Oncotarget</i> , 2016, 7, 28684-28696.	1.8	9
47	Epigenetic Drug Treatment Globally Induces Cryptic Transcription Start Sites Encoded in Long Terminal Repeats. <i>Blood</i> , 2016, 128, 3931-3931.	1.4	0
48	Aberrant Methylation and Decreased Expression of NRIP1 in IGHV-Unmutated CLL. <i>Blood</i> , 2016, 128, 1527-1527.	1.4	0
49	Epigenetic silencing of miR-708 enhances NF- κ B signaling in chronic lymphocytic leukemia. <i>International Journal of Cancer</i> , 2015, 137, 1352-1361.	5.1	52
50	Lag Times between Lymphoproliferative Disorder and Clinical Diagnosis of Chronic Lymphocytic Leukemia: A Prospective Analysis Using Plasma Soluble CD23. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 538-545.	2.5	11
51	Transient DNMT1 suppression reveals hidden heritable marks in the genome. <i>Nucleic Acids Research</i> , 2015, 43, 1485-1497.	14.5	35
52	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. <i>Nature Genetics</i> , 2015, 47, 22-30.	21.4	141
53	Progressive Epigenetic Programming during B Cell Maturation Is Reflected in a Continuum of Epigenetic Disease Phenotypes in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 2436-2436.	1.4	1
54	Abstract 3445: Diacylglycerol kinase alpha as a novel epigenetically regulated risk marker for radiotherapy-induced fibrosis. , 2015, , .		0

#	ARTICLE	IF	CITATIONS
55	Abstract B25: Progressive epigenetic programming during B cell maturation yields a continuum of clonal disease phenotypes with distinct etiologies in chronic lymphocytic leukemia.. , 2015, , .		0
56	IL-10 Production By CLL Cells Is Enhanced in the Anergic IGHV Mutated Subset and Associates with Reduced DNA Methylation of the IL-10 Locus. Blood, 2015, 126, 2917-2917.	1.4	0
57	Long Noncoding RNA TARID Directs Demethylation and Activation of the Tumor Suppressor TCF21 via GADD45A. Molecular Cell, 2014, 55, 604-614.	9.7	242
58	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. Cell Reports, 2014, 8, 798-806.	6.4	219
59	p19-INK4d inhibits neuroblastoma cell growth, induces differentiation and is hypermethylated and downregulated in MYCN-amplified neuroblastomas. Human Molecular Genetics, 2014, 23, 6826-6837.	2.9	21
60	Early aberrant DNA methylation events in a mouse model of acute myeloid leukemia. Genome Medicine, 2014, 6, 34.	8.2	34
61	Evolution of DNA Methylation Is Linked to Genetic Aberrations in Chronic Lymphocytic Leukemia. Cancer Discovery, 2014, 4, 348-361.	9.4	135
62	Unbiased RNAi screen for hepcidin regulators links hepcidin suppression to proliferative Ras/RAF and nutrient-dependent mTOR signaling. Blood, 2014, 123, 1574-1585.	1.4	62
63	Validation of ZAP-70 methylation and its relative significance in predicting outcome in chronic lymphocytic leukemia. Blood, 2014, 124, 42-48.	1.4	60
64	Abstract 5557: Systematic mapping of drug sensitivity in hematological malignancies identifies vulnerability of chronic lymphocytic leukemia with mutant p53. , 2014, , .		0
65	NFATc1 Is Transcriptionally Activated in Chronic Lymphocytic Leukemia (CLL) By Promotor DNA-Hypomethylation Which Correlates with in-Vitro Vulnerability to Calcineurin Inhibitors. Blood, 2014, 124, 1941-1941.	1.4	6
66	Germline variants of base excision repair genes and breast cancer: A polymorphism in DNA polymerase gamma modifies gene expression and breast cancer risk. International Journal of Cancer, 2013, 132, 55-62.	5.1	24
67	Epigenetic Upregulation of lncRNAs at 13q14.3 in Leukemia Is Linked to the In Cis Downregulation of a Gene Cluster That Targets NF- κ B. PLoS Genetics, 2013, 9, e1003373.	3.5	134
68	Loss of DNMT1o Disrupts Imprinted X Chromosome Inactivation and Accentuates Placental Defects in Females. PLoS Genetics, 2013, 9, e1003873.	3.5	61
69	Germline Allele-Specific Expression of DAPK1 in Chronic Lymphocytic Leukemia. PLoS ONE, 2013, 8, e55261.	2.5	24
70	Heterogeneity and Evolution Of DNA Methylation In Chronic Lymphocytic Leukemia. Blood, 2013, 122, 1626-1626.	1.4	0
71	Quantitative DNA Methylation Analysis Identifies a Single CpG Dinucleotide Important for ZAP-70 Expression and Predictive of Prognosis in Chronic Lymphocytic Leukemia. Journal of Clinical Oncology, 2012, 30, 2483-2491.	1.6	120
72	Abstract 2180: Identification of nuclear transcription factor Y (NF-Y) as a novel key transcriptional regulator of the tumor-suppressor gene DAPK1. , 2012, , .		0

#	ARTICLE	IF	CITATIONS
73	Critical Period of Nonpromoter DNA Methylation Acquisition during Prenatal Male Germ Cell Development. PLoS ONE, 2011, 6, e24156.	2.5	26
74	Reduced c-FOS Is Associated with Poor Prognosis and Clinical Course in Chronic Lymphocytic Leukemia. Blood, 2011, 118, 2433-2433.	1.4	0
75	Down-regulation of tumor suppressor a kinase anchor protein 12 in human hepatocarcinogenesis by epigenetic mechanisms. Hepatology, 2010, 52, 2023-2033.	7.3	61
76	Restriction Digestion and Real-Time PCR (qAMP). Methods in Molecular Biology, 2009, 507, 271-280.	0.9	23
77	Epigenetics in Acute Myeloid Leukemia. Seminars in Oncology, 2008, 35, 378-387.	2.2	82
78	A unique configuration of genome-wide DNA methylation patterns in the testis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 228-233.	7.1	149
79	Adverse Effects of 5-Aza-2-Deoxycytidine on Spermatogenesis Include Reduced Sperm Function and Selective Inhibition of de Novo DNA Methylation. Journal of Pharmacology and Experimental Therapeutics, 2007, 322, 1171-1180.	2.5	65
80	Developmental acquisition of genome-wide DNA methylation occurs prior to meiosis in male germ cells. Developmental Biology, 2007, 307, 368-379.	2.0	210
81	Loss of spermatogonia and wide-spread DNA methylation defects in newborn male mice deficient in DNMT3L. BMC Developmental Biology, 2007, 7, 104.	2.1	81
82	Restriction Landmark Genomic Scanning (RLGS) spot identification by second generation virtual RLGS in multiple genomes with multiple enzyme combinations. BMC Genomics, 2007, 8, 446.	2.8	37
83	Evaluation of a Quantitative DNA Methylation Analysis Technique using Methylation-Sensitive/Dependent Restriction Enzymes and Real-Time PCR. Epigenetics, 2006, 1, 146-152.	2.7	85
84	Aging results in hypermethylation of ribosomal DNA in sperm and liver of male rats. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1775-1780.	7.1	177
85	Impact of Dnmt1 deficiency, with and without low folate diets, on tumor numbers and DNA methylation in Min mice. Carcinogenesis, 2003, 24, 39-45.	2.8	65