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	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. Nature Genetics, 2016, 48, 253-264.	21.4	254
2	Long Noncoding RNA TARID Directs Demethylation and Activation of the Tumor Suppressor TCF21 via GADD45A. Molecular Cell, 2014, 55, 604-614.	9.7	242
3	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. Nature Genetics, 2017, 49, 1052-1060.	21.4	235
4	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. Cell Reports, 2014, 8, 798-806.	6.4	219
5	Developmental acquisition of genome-wide DNA methylation occurs prior to meiosis in male germ cells. Developmental Biology, 2007, 307, 368-379.	2.0	210
6	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
7	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
8	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. Nature Genetics, 2015, 47, 22-30.	21.4	141
9	Evolution of DNA Methylation Is Linked to Genetic Aberrations in Chronic Lymphocytic Leukemia. Cancer Discovery, 2014, 4, 348-361.	9.4	135
10	Epigenetic Upregulation of lncRNAs at 13q14.3 in Leukemia Is Linked to the In Cis Downregulation of a Gene Cluster That Targets NF-kB. PLoS Genetics, 2013, 9, e1003373.	3.5	134
11	Drug-perturbation-based stratification of blood cancer. Journal of Clinical Investigation, 2017, 128, 427-445.	8.2	124
12	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
13	High-content screening identifies kinase inhibitors that overcome venetoclax resistance in activated CLL cells. Blood, 2016, 128, 934-947.	1.4	104
14	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
15	Epigenetics in Acute Myeloid Leukemia. Seminars in Oncology, 2008, 35, 378-387.	2.2	82
16	Genomic analysis of hairy cell leukemia identifies novel recurrent genetic alterations. Blood, 2017, 130, 1644-1648.	1.4	82
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Adverse Effects of 5-Aza-2â€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
20	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
21	Down-regulation of tumor suppressor a kinase anchor protein 12 in human hepatocarcinogenesis by epigenetic mechanisms. Hepatology, 2010, 52, 2023-2033.	7.3	61
22	Loss of DNMT1o Disrupts Imprinted X Chromosome Inactivation and Accentuates Placental Defects in Females. PLoS Genetics, 2013, 9, e1003873.	3.5	61
23	Validation of ZAP-70 methylation and its relative significance in predicting outcome in chronic lymphocytic leukemia. Blood, 2014, 124, 42-48.	1.4	60
24	Surface IgM expression and function are associated with clinical behavior, genetic abnormalities, and DNA methylation in CLL. Blood, 2016, 128, 816-826.	1.4	54
25	Epigenetic silencing of miR-708 enhances NF-ÎºB signaling in chronic lymphocytic leukemia. International Journal of Cancer, 2015, 137, 1352-1361.	5.1	52
26	The proliferative history shapes the DNA methylome of B-cell tumors and predicts clinical outcome. Nature Cancer, 2020, 1, 1066-1081.	13.2	51
27	Epigenetic regulation of diacylglycerol kinase alpha promotes radiation-induced fibrosis. Nature Communications, 2016, 7, 10893.	12.8	46
28	Single-cell analysis based dissection of clonality in myelofibrosis. Nature Communications, 2020, 11, 73.	12.8	46
29	Epigenetic reprogramming sensitizes immunologically silent EBV+ lymphomas to virus-directed immunotherapy. Blood, 2020, 135, 1870-1881.	1.4	39
30	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
31	Prognostic and biological significance of the proangiogenic factor EGFL7 in acute myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4641-E4647.	7.1	36
32	Transient DNMT1 suppression reveals hidden heritable marks in the genome. Nucleic Acids Research, 2015, 43, 1485-1497.	14.5	35
33	Early aberrant DNA methylation events in a mouse model of acute myeloid leukemia. Genome Medicine, 2014, 6, 34.	8.2	34
34	Epigenetic and Posttranscriptional Regulation of CD16 Expression during Human NK Cell Development. Journal of Immunology, 2018, 200, 565-572.	0.8	33
35	Multi-omics reveals clinically relevant proliferative drive associated with mTOR-MYC-OXPHOS activity in chronic lymphocytic leukemia. Nature Cancer, 2021, 2, 853-864.	13.2	32
36	Recurrent XPO1 mutations alter pathogenesis of chronic lymphocytic leukemia. Journal of Hematology and Oncology, 2021, 14, 17.	17.0	31

#	ARTICLE	IF	CITATIONS
37	Trametinib for the treatment of IGHV4-34, MAP2K1-mutant variant hairy cell leukemia. Leukemia and Lymphoma, 2018, 59, 1008-1011.	1.3	29
38	Selinexor in combination with decitabine in patients with acute myeloid leukemia: results from a phase 1 study. Leukemia and Lymphoma, 2020, 61, 387-396.	1.3	29
39	Critical Period of Nonpromoter DNA Methylation Acquisition during Prenatal Male Germ Cell Development. PLoS ONE, 2011, 6, e24156.	2.5	26
40	Developmental subtypes assessed by DNA methylation-iPLEX forecast the natural history of chronic lymphocytic leukemia. Blood, 2019, 134, 688-698.	1.4	26
41	Time-to-progression after front-line fludarabine, cyclophosphamide, and rituximab chemoimmunotherapy for chronic lymphocytic leukaemia: a retrospective, multicohort study. Lancet Oncology, The, 2019, 20, 1576-1586.	10.7	26
42	Trisomy 12 chronic lymphocytic leukemia expresses a unique set of activated and targetable pathways. Haematologica, 2018, 103, 2069-2078.	3.5	25
43	Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials. Blood Advances, 2019, 3, 2474-2481.	5.2	25
44	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
45	Germline Allele-Specific Expression of DAPK1 in Chronic Lymphocytic Leukemia. PLoS ONE, 2013, 8, e55261.	2.5	24
46	Insight into origins, mechanisms, and utility of DNA methylation in B-cell malignancies. Blood, 2018, 132, 999-1006.	1.4	24
47	Mutational Landscape and Gene Expression Patterns in Adult Acute Myeloid Leukemias with Monosomy 7 as a Sole Abnormality. Cancer Research, 2017, 77, 207-218.	0.9	23
48	Restriction Digestion and Real-Time PCR (qAMP). Methods in Molecular Biology, 2009, 507, 271-280.	0.9	23
49	Charting the dynamic epigenome during B-cell development. Seminars in Cancer Biology, 2018, 51, 139-148.	9.6	22
50	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
51	DNA methylation epitypes highlight underlying developmental and disease pathways in acute myeloid leukemia. Genome Research, 2021, 31, 747-761.	5.5	20
52	DNA methylation at an enhancer of the three prime repair exonuclease 2 gene (TREX2) is linked to gene expression and survival in laryngeal cancer. Clinical Epigenetics, 2019, 11, 67.	4.1	19
53	Human Cord Blood B Cells Differ from the Adult Counterpart by Conserved Ig Repertoires and Accelerated Response Dynamics. Journal of Immunology, 2021, 206, 2839-2851.	0.8	18
54	Genome-wide promoter methylation of hairy cell leukemia. Blood Advances, 2019, 3, 384-396.	5.2	16

#	ARTICLE	IF	CITATIONS
55	Genome-wide association study identifies an acute myeloid leukemia susceptibility locus near BICRA. Leukemia, 2019, 33, 771-775.	7.2	15
56	Methylome-based cell-of-origin modeling (Methyl-COOM) identifies aberrant expression of immune regulatory molecules in CLL. Genome Medicine, 2020, 12, 29.	8.2	15
57	Uncontrolled CD21low age-associated and B1 B cell accumulation caused by failure of an EGR2/3 tolerance checkpoint. Cell Reports, 2022, 38, 110259.	6.4	15
58	Emerging insights on the pathogenesis and treatment of extranodal NK/T cell lymphomas (ENKTL). Discovery Medicine, 2017, 23, 189-199.	0.5	14
59	Genetic Characterization and Prognostic Relevance of Acquired Uniparental Disomies in Cytogenetically Normal Acute Myeloid Leukemia. Clinical Cancer Research, 2019, 25, 6524-6531.	7.0	12
60	Lag Times between Lymphoproliferative Disorder and Clinical Diagnosis of Chronic Lymphocytic Leukemia: A Prospective Analysis Using Plasma Soluble CD23. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 538-545.	2.5	11
61	Infection at the Time of Initial Therapy for Hairy Cell Leukemia Is Associated with Inferior Time to Next Treatment. Blood, 2018, 132, 2305-2305.	1.4	11
62	Identification of two DNA methylation subtypes of WaldenstrÃ¶m's macroglobulinemia with plasma and memory B cell features. Blood, 2020, 136, 585-595.	1.4	10
63	BET-bromodomain inhibitors modulate epigenetic patterns at the diacylglycerol kinase alpha enhancer associated with radiation-induced fibrosis. Radiotherapy and Oncology, 2017, 125, 168-174.	0.6	9
64	Hsp90 inhibition increases SOCS3 transcript and regulates migration and cell death in chronic lymphocytic leukemia. Oncotarget, 2016, 7, 28684-28696.	1.8	9
65	Identification and Targeting of the Developmental Blockade in Extranodal Natural Killer/T-cell Lymphoma. Blood Cancer Discovery, 2022, 3, 154-169.	5.0	8
66	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
67	STK11/LKB1 Loss of Function Is Associated with Global DNA Hypomethylation and <i>S</i>-Adenosyl-Methionine Depletion in Human Lung Adenocarcinoma. Cancer Research, 2021, 81, 4194-4204.	0.9	4
68	Comparative Evaluation of Prognostic Factors That Assess the Natural History of Chronic Lymphocytic Leukemia. Blood, 2016, 128, 968-968.	1.4	4
69	Progressive Epigenetic Programming during B Cell Maturation Is Reflected in a Continuum of Epigenetic Disease Phenotypes in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 2436-2436.	1.4	1
70	Role of Histone Deacetylase-Mediated Gene Silencing in Chronic Lymphocytic Leukemia Progression. Blood, 2016, 128, 2705-2705.	1.4	1
71	Down-Regulation of CD25 Antigen in Hairy Cell Leukemia Patients after Treatment. Blood, 2018, 132, 4143-4143.	1.4	1
72	Reduced c-FOS Is Associated with Poor Prognosis and Clinical Course in Chronic Lymphocytic Leukemia. Blood, 2011, 118, 2433-2433.	1.4	0

#	Article	IF	Citations
73	Abstract 2180: Identification of nuclear transcription factor Y (NF-Y) as a novel key transcriptional regulator of the tumor-suppressor geneDAPK1. , 2012, , .		0
74	Heterogeneity and Evolution Of DNA Methylation In Chronic Lymphocytic Leukemia. Blood, 2013, 122, 1626-1626.	1.4	0
75	Abstract 5557: Systematic mapping of drug sensitivity in hematological malignancies identifies vulnerability of chronic lymphocytic leukemia with mutant p53. , 2014, , .		0
76	Abstract 3445: Diacylglycerol kinase alpha as a novel epigenetically regulated risk marker for radiotherapy-induced fibrosis. , 2015, , .		0
77	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
78	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
79	Epigenetic Drug Treatment Globally Induces Cryptic Transcription Start Sites Encoded in Long Terminal Repeats. Blood, 2016, 128, 3931-3931.	1.4	0
80	Aberrant Methylation and Decreased Expression of NRIP1 in IGHV-Unmutated CLL. Blood, 2016, 128, 1527-1527.	1.4	0
81	Abstract 3364: DNA methylation loss at an enhancer site of the DNA repair geneTREX2is an epigenetic feature in multiple cancers. , 2017, , .		0
82	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. Blood, 2018, 132, 1833-1833.	1.4	0
83	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). Blood, 2018, 132, 2777-2777.	1.4	0
84	The ETS1 Transcription Factor Is Implicated in Human and Murine Intermediate NK Cell Development Stages. Blood, 2018, 132, 2567-2567.	1.4	0
85	Genome-Wide Association Study (GWAS) Identifies a Significant Acute Myeloid Leukemia (AML) Susceptibility Locus Near BICRA. Blood, 2018, 132, 85-85.	1.4	0