

Peter Lichter

List of Publications by Year in descending order

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Version: 2024-02-01

159
papers

40,173
citations

18465

62
h-index

9579

142
g-index

164
all docs

164
docs citations

164
times ranked

48749
citing authors

#	ARTICLE	IF	CITATIONS
1	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013, 500, 415-421.	13.7	8,060
2	Genomic Aberrations and Survival in Chronic Lymphocytic Leukemia. <i>New England Journal of Medicine</i> , 2000, 343, 1910-1916.	13.9	2,967
3	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. <i>Nature</i> , 2012, 482, 226-231.	13.7	2,129
4	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	13.7	2,114
5	DNA methylation-based classification of central nervous system tumours. <i>Nature</i> , 2018, 555, 469-474.	13.7	1,872
6	Hotspot Mutations in H3F3A and IDH1 Define Distinct Epigenetic and Biological Subgroups of Glioblastoma. <i>Cancer Cell</i> , 2012, 22, 425-437.	7.7	1,551
7	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018, 555, 321-327.	13.7	1,068
8	Resistance Mechanisms for the Bruton's Tyrosine Kinase Inhibitor Ibrutinib. <i>New England Journal of Medicine</i> , 2014, 370, 2286-2294.	13.9	1,042
9	Molecular Classification of Ependymal Tumors across All CNS Compartments, Histopathological Grades, and Age Groups. <i>Cancer Cell</i> , 2015, 27, 728-743.	7.7	933
10	A Biologic Definition of Burkitt's Lymphoma from Transcriptional and Genomic Profiling. <i>New England Journal of Medicine</i> , 2006, 354, 2419-2430.	13.9	915
11	Matrix-based comparative genomic hybridization: Biochips to screen for genomic imbalances. <i>Genes Chromosomes and Cancer</i> , 1997, 20, 399-407.	1.5	879
12	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
13	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012, 488, 100-105.	13.7	765
14	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. <i>Cell</i> , 2012, 148, 59-71.	13.5	743
15	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. <i>Cell</i> , 2016, 164, 1060-1072.	13.5	702
16	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. <i>Nature Genetics</i> , 2013, 45, 927-932.	9.4	674
17	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothed Inhibition. <i>Cancer Cell</i> , 2014, 25, 393-405.	7.7	627
18	Detection of complete and partial chromosome gains and losses by comparative genomic in situ hybridization. <i>Human Genetics</i> , 1993, 90, 590-610.	1.8	544

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19	Enhancer hijacking activates GF11 family oncogenes in medulloblastoma. <i>Nature</i> , 2014, 511, 428-434.	13.7	520
20	Paediatric and adult glioblastoma: multiform (epi)genomic culprits emerge. <i>Nature Reviews Cancer</i> , 2014, 14, 92-107.	12.8	469
21	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. <i>Cancer Cell</i> , 2016, 29, 379-393.	7.7	438
22	Gene mutations and treatment outcome in chronic lymphocytic leukemia: results from the CLL8 trial. <i>Blood</i> , 2014, 123, 3247-3254.	0.6	428
23	Exosomes released by chronic lymphocytic leukemia cells induce the transition of stromal cells into cancer-associated fibroblasts. <i>Blood</i> , 2015, 126, 1106-1117.	0.6	399
24	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <i>Nature Genetics</i> , 2012, 44, 1316-1320.	9.4	389
25	BCAT1 promotes cell proliferation through amino acid catabolism in gliomas carrying wild-type IDH1. <i>Nature Medicine</i> , 2013, 19, 901-908.	15.2	388
26	Decoding the regulatory landscape of medulloblastoma using DNA methylation sequencing. <i>Nature</i> , 2014, 510, 537-541.	13.7	378
27	Longitudinal molecular trajectories of diffuse glioma in adults. <i>Nature</i> , 2019, 576, 112-120.	13.7	320
28	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. <i>Nature</i> , 2016, 530, 57-62.	13.7	318
29	Quantitative analysis of comparative genomic hybridization. <i>Cytometry</i> , 1995, 19, 27-41.	1.8	286
30	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology</i> , The, 2018, 19, 785-798.	5.1	268
31	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	5.8	266
32	Next-generation personalised medicine for high-risk paediatric cancer patients – The INFORM pilot study. <i>European Journal of Cancer</i> , 2016, 65, 91-101.	1.3	262
33	BCAT1 restricts $\hat{\pm}$ KG levels in AML stem cells leading to IDHmut-like DNA hypermethylation. <i>Nature</i> , 2017, 551, 384-388.	13.7	261
34	The landscape of viral associations in human cancers. <i>Nature Genetics</i> , 2020, 52, 320-330.	9.4	261
35	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.	9.4	254
36	Somatic CRISPR/Cas9-mediated tumour suppressor disruption enables versatile brain tumour modelling. <i>Nature Communications</i> , 2015, 6, 7391.	5.8	244

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37	Tumor-derived exosomes modulate PD-L1 expression in monocytes. <i>Science Immunology</i> , 2017, 2, .	5.6	236
38	Oncogenic FAM131B-BRAF fusion resulting from 7q34 deletion comprises an alternative mechanism of MAPK pathway activation in pilocytic astrocytoma. <i>Acta Neuropathologica</i> , 2011, 121, 763-774.	3.9	211
39	Clonal evolution in chronic lymphocytic leukemia: acquisition of high-risk genomic aberrations associated with unmutated VH, resistance to therapy, and short survival. <i>Haematologica</i> , 2007, 92, 1242-1245.	1.7	195
40	Minimal sizes of deletions detected by comparative genomic hybridization. <i>Genes Chromosomes and Cancer</i> , 1998, 21, 172-175.	1.5	191
41	High-resolution genomic profiling of chronic lymphocytic leukemia reveals new recurrent genomic alterations. <i>Blood</i> , 2012, 120, 4783-4794.	0.6	179
42	MAPK pathway activation in pilocytic astrocytoma. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 1799-1811.	2.4	177
43	Evolutionary Trajectories of IDHWT Glioblastomas Reveal a Common Path of Early Tumorigenesis Instigated Years ahead of Initial Diagnosis. <i>Cancer Cell</i> , 2019, 35, 692-704.e12.	7.7	172
44	Therapeutic targeting of ependymoma as informed by oncogenic enhancer profiling. <i>Nature</i> , 2018, 553, 101-105.	13.7	170
45	PD-L1 checkpoint blockade prevents immune dysfunction and leukemia development in a mouse model of chronic lymphocytic leukemia. <i>Blood</i> , 2015, 126, 203-211.	0.6	158
46	Risk-adapted therapy for young children with medulloblastoma (SJYC07): therapeutic and molecular outcomes from a multicentre, phase 2 trial. <i>Lancet Oncology</i> , 2018, 19, 768-784.	5.1	151
47	Evolution of DNA Methylation Is Linked to Genetic Aberrations in Chronic Lymphocytic Leukemia. <i>Cancer Discovery</i> , 2014, 4, 348-361.	7.7	135
48	A biobank of patient-derived pediatric brain tumor models. <i>Nature Medicine</i> , 2018, 24, 1752-1761.	15.2	124
49	Targeting Self-Renewal in High-Grade Brain Tumors Leads to Loss of Brain Tumor Stem Cells and Prolonged Survival. <i>Cell Stem Cell</i> , 2014, 15, 185-198.	5.2	123
50	A cell-based model system links chromothripsis with hyperploidy. <i>Molecular Systems Biology</i> , 2015, 11, 828.	3.2	118
51	Chd7 is indispensable for mammalian brain development through activation of a neuronal differentiation programme. <i>Nature Communications</i> , 2017, 8, 14758.	5.8	118
52	Spatial heterogeneity in medulloblastoma. <i>Nature Genetics</i> , 2017, 49, 780-788.	9.4	112
53	The Pediatric Precision Oncology INFORM Registry: Clinical Outcome and Benefit for Patients with Very High-Evidence Targets. <i>Cancer Discovery</i> , 2021, 11, 2764-2779.	7.7	110
54	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	13.7	108

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55	Recurrent copy number gain of transcription factor <i>SOX2</i> and corresponding high protein expression in oral squamous cell carcinoma. <i>Genes Chromosomes and Cancer</i> , 2010, 49, 9-16.	1.5	106
56	Experimental evidence for the influence of molecular crowding on nuclear architecture. <i>Journal of Cell Science</i> , 2007, 120, 1673-1680.	1.2	104
57	Chromothripsis in cancer cells: An update. <i>International Journal of Cancer</i> , 2016, 138, 2322-2333.	2.3	101
58	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019, 10, 1459.	5.8	99
59	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. <i>Nature</i> , 2020, 580, 396-401.	13.7	94
60	Epithelioid glioblastomas stratify into established diagnostic subsets upon integrated molecular analysis. <i>Brain Pathology</i> , 2018, 28, 656-662.	2.1	89
61	Inflammatory cytokines and signaling pathways are associated with survival of primary chronic lymphocytic leukemia cells in vitro: a dominant role of CCL2. <i>Haematologica</i> , 2011, 96, 408-416.	1.7	80
62	Molecular signatures classify astrocytic gliomas by <i>IDH1</i> mutation status. <i>International Journal of Cancer</i> , 2011, 128, 1095-1103.	2.3	75
63	The landscape of chromothripsis across adult cancer types. <i>Nature Communications</i> , 2020, 11, 2320.	5.8	75
64	Branched-chain ketoacids secreted by glioblastoma cells via MCT1 modulate macrophage phenotype. <i>EMBO Reports</i> , 2017, 18, 2172-2185.	2.0	74
65	Capture and Amplification by Tailing and Switching (CATS). <i>RNA Biology</i> , 2014, 11, 817-828.	1.5	68
66	Hypermethylation of the Inactive X Chromosome Is a Frequent Event in Cancer. <i>Cell</i> , 2013, 155, 567-581.	13.5	67
67	Defective DNA damage repair leads to frequent catastrophic genomic events in murine and human tumors. <i>Nature Communications</i> , 2018, 9, 4760.	5.8	66
68	YAP1 subgroup supratentorial ependymoma requires TEAD and nuclear factor I-mediated transcriptional programmes for tumorigenesis. <i>Nature Communications</i> , 2019, 10, 3914.	5.8	65
69	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. <i>Cancer Cell</i> , 2019, 35, 95-110.e8.	7.7	65
70	Medulloblastoma-associated DDX3 variant selectively alters the translational response to stress. <i>Oncotarget</i> , 2016, 7, 28169-28182.	0.8	62
71	Soluble CD14 is a novel monocyte-derived survival factor for chronic lymphocytic leukemia cells, which is induced by CLL cells in vitro and present at abnormally high levels in vivo. <i>Blood</i> , 2010, 116, 4223-4230.	0.6	60
72	Loss of SOX2 expression induces cell motility via vimentin upregulation and is an unfavorable risk factor for survival of head and neck squamous cell carcinoma. <i>Molecular Oncology</i> , 2015, 9, 1704-1719.	2.1	60

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73	Interleukin-10 receptor signaling promotes the maintenance of a PD-1int TCF-1+ CD8+ TÂcell population that sustains anti-tumor immunity. <i>Immunity</i> , 2021, 54, 2825-2841.e10.	6.6	57
74	TelomereHunter â€“ in silico estimation of telomere content and composition from cancer genomes. <i>BMC Bioinformatics</i> , 2019, 20, 272.	1.2	56
75	Control of chronic lymphocytic leukemia development by clonally-expanded CD8+ T-cells that undergo functional exhaustion in secondary lymphoid tissues. <i>Leukemia</i> , 2019, 33, 625-637.	3.3	55
76	The genomic and transcriptional landscape of primary central nervous system lymphoma. <i>Nature Communications</i> , 2022, 13, 2558.	5.8	52
77	Brainstem biopsy in pediatric diffuse intrinsic pontine glioma in the era of precision medicine: the INFORM study experience. <i>European Journal of Cancer</i> , 2019, 114, 27-35.	1.3	51
78	PI3KÎ inhibition modulates regulatory and effector T-cell differentiation and function in chronic lymphocytic leukemia. <i>Leukemia</i> , 2019, 33, 1427-1438.	3.3	51
79	Molecular subgrouping of primary pineal parenchymal tumors reveals distinct subtypes correlated with clinical parameters and genetic alterations. <i>Acta Neuropathologica</i> , 2020, 139, 243-257.	3.9	50
80	Glioblastoma epigenome profiling identifies SOX10 as a master regulator of molecular tumour subtype. <i>Nature Communications</i> , 2020, 11, 6434.	5.8	48
81	Kinome-wide shRNA Screen Identifies the Receptor Tyrosine Kinase AXL as a Key Regulator for Mesenchymal Glioblastoma Stem-like Cells. <i>Stem Cell Reports</i> , 2015, 4, 899-913.	2.3	47
82	Telomere dysfunction and chromothripsis. <i>International Journal of Cancer</i> , 2016, 138, 2905-2914.	2.3	42
83	Evidence for multi-copy Mega-NUMT<i>s</i> in the human genome. <i>Nucleic Acids Research</i> , 2021, 49, 1517-1531.	6.5	42
84	The need for a worldwide consensus for cell line authentication: Experience implementing a mandatory requirement at the <i>International Journal of Cancer</i> . <i>PLoS Biology</i> , 2017, 15, e2001438.	2.6	41
85	17p Deletion Predicts for Inferior Overall Survival after Fludarabine - Based First Line Therapy in Chronic Lymphocytic Leukemia: First Analysis of Genetics in the CLL4 Trial of the GCLLSG.. <i>Blood</i> , 2005, 106, 715-715.	0.6	41
86	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019, 15, e8339.	3.2	39
87	Reprogramming of the ERRÎ± and ERÎ± Target Gene Landscape Triggers Tamoxifen Resistance in Breast Cancer. <i>Cancer Research</i> , 2015, 75, 720-731.	0.4	36
88	Rapid analysis of mouse-hamster hybrid cell lines by in situ hybridization. <i>Genomics</i> , 1990, 7, 127-130.	1.3	34
89	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	3.3	34
90	<i>NFATC1</i> activation by <sc>DNA</sc> hypomethylation in chronic lymphocytic leukemia correlates with clinical staging and can be inhibited by ibrutinib. <i>International Journal of Cancer</i> , 2018, 142, 322-333.	2.3	33

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91	No correlation between NF1 mutation position and risk of optic pathway glioma in 77 unrelated NF1 patients. <i>Human Genetics</i> , 2016, 135, 469-475.	1.8	29
92	EOMES and IL-10 regulate antitumor activity of T regulatory type 1 CD4+ T cells in chronic lymphocytic leukemia. <i>Leukemia</i> , 2021, 35, 2311-2324.	3.3	27
93	Low-dose Actinomycin-D treatment re-establishes the tumoursuppressive function of P53 in RELA-positive ependymoma. <i>Oncotarget</i> , 2016, 7, 61860-61873.	0.8	27
94	Kruppel-like factor 4 (KLF4) inactivation in chronic lymphocytic leukemia correlates with promoter DNA-methylation and can be reversed by inhibition of NOTCH signaling. <i>Haematologica</i> , 2016, 101, e249-e253.	1.7	26
95	Tumor necrosis factor receptor signaling is a driver of chronic lymphocytic leukemia that can be therapeutically targeted by the flavonoid wogonin. <i>Haematologica</i> , 2018, 103, 688-697.	1.7	26
96	Combining ibrutinib and checkpoint blockade improves CD8+ T-cell function and control of chronic lymphocytic leukemia in Em-TCL1 mice. <i>Haematologica</i> , 2021, 106, 968-977.	1.7	26
97	A novel cloning strategy for one-step assembly of multiplex CRISPR vectors. <i>Scientific Reports</i> , 2018, 8, 17499.	1.6	25
98	Altered nuclear envelope structure and proteasome function of micronuclei. <i>Experimental Cell Research</i> , 2018, 371, 353-363.	1.2	25
99	DECIPHER pooled shRNA library screen identifies PP2A and FGFR signaling as potential therapeutic targets for diffuse intrinsic pontine gliomas. <i>Neuro-Oncology</i> , 2019, 21, 867-877.	0.6	24
100	Cytogenetic characterization of head and neck squamous cell carcinoma cell lines as model systems for the functional analyses of tumor-associated genes. <i>Journal of Oral Pathology and Medicine</i> , 2010, 39, 382-389.	1.4	23
101	Oxidative stress as candidate therapeutic target to overcome microenvironmental protection of CLL. <i>Leukemia</i> , 2020, 34, 115-127.	3.3	23
102	Recollections of a scientific journey published in human genetics: from chromosome territories to interphase cytogenetics and comparative genome hybridization. <i>Human Genetics</i> , 2014, 133, 403-416.	1.8	22
103	Antagonizing inactivated tumor suppressor genes and activated oncogenes by a versatile transgenesis system: application in mantle cell lymphoma. <i>FASEB Journal</i> , 2006, 20, 1188-1190.	0.2	21
104	CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. <i>JCO Precision Oncology</i> , 2021, 5, 676-686.	1.5	20
105	Biologic and Clinical Markers for Outcome after Fludarabine (F) or F Plus Cyclophosphamide (FC) - Comprehensive Analysis of the CLL4 Trial of the GCLLSG.. <i>Blood</i> , 2008, 112, 2089-2089.	0.6	18
106	CD8 ⁺ T-cells of CLL-bearing mice acquire a transcriptional program of T-cell activation and exhaustion. <i>Leukemia and Lymphoma</i> , 2020, 61, 351-356.	0.6	17
107	Extracellular vesicles in chronic lymphocytic leukemia. <i>Leukemia and Lymphoma</i> , 2013, 54, 1826-1830.	0.6	15
108	CITED4 gene silencing in colorectal cancer cells modulates adherens/tight junction gene expression and reduces cell proliferation. <i>Journal of Cancer Research and Clinical Oncology</i> , 2016, 142, 225-237.	1.2	15

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109	A PRDX1 α heterodimer amplifies MET-driven invasion of <i>IDH</i> wildtype and <i>IDH</i> mutant gliomas. <i>International Journal of Cancer</i> , 2018, 143, 1176-1187.	2.3	14
110	Mismatch Repair Deficiency Drives Durable Complete Remission by Targeting Programmed Death Receptor 1 in a Metastatic Luminal Breast Cancer Patient. <i>Breast Care</i> , 2019, 14, 53-59.	0.8	13
111	Rejection of adoptively transferred E μ -TCL1 chronic lymphocytic leukemia cells in C57BL/6 substrains or knockout mouse lines. <i>Leukemia</i> , 2019, 33, 1514-1539.	3.3	12
112	Association of mutation signature effectuating processes with mutation hotspots in driver genes and non-coding regions. <i>Nature Communications</i> , 2022, 13, 178.	5.8	12
113	TBET-expressing Th1 CD4 ⁺ T cells accumulate in chronic lymphocytic leukaemia without affecting disease progression in E μ -TCL1 mice. <i>British Journal of Haematology</i> , 2020, 189, 133-145.	1.2	11
114	Chromothripsis in Human Breast Cancer. <i>Cancer Research</i> , 2020, 80, 4918-4931.	0.4	11
115	Clonal evolution in chronic lymphocytic leukemia is scant in relapsed but accelerated in refractory cases after chemo(immune) therapy. <i>Haematologica</i> , 2022, 107, 604-614.	1.7	11
116	Genetics of Patients with F-Refractory CLL or Early Relapse After FC or FCR: Results From the CLL8 Trial of the GCLLSC. <i>Blood</i> , 2010, 116, 2427-2427.	0.6	11
117	All You Need Is a Mir-acle: The Role of Nontranslated RNAs in the Suppression of B Cell Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2010, 17, 3-4.	7.7	10
118	Pilocytic astrocytoma demethylation and transcriptional landscapes link bZIP transcription factors to immune response. <i>Neuro-Oncology</i> , 2020, 22, 1327-1338.	0.6	10
119	In Acute Myeloid Leukemia with Complex Karyotype TP53 Alterations Are Associated with Specific Genomic Aberrations and Predict Inferior Survival.. <i>Blood</i> , 2009, 114, 2632-2632.	0.6	10
120	IGF2 knockdown in two colorectal cancer cell lines decreases survival, adhesion and modulates survival-associated genes. <i>Tumor Biology</i> , 2016, 37, 12485-12495.	0.8	9
121	confFuse: High-Confidence Fusion Gene Detection across Tumor Entities. <i>Frontiers in Genetics</i> , 2017, 8, 137.	1.1	9
122	TALLEN/CRISPR-mediated engineering of a promoterless anti-viral RNAi hairpin into an endogenous miRNA locus. <i>Nucleic Acids Research</i> , 2017, 45, e3-e3.	6.5	8
123	Selective BTK inhibition improves bendamustine therapy response and normalizes immune effector functions in chronic lymphocytic leukemia. <i>International Journal of Cancer</i> , 2019, 144, 2762-2773.	2.3	8
124	Cited4 is a sex-biased mediator of the antidiabetic glitazone response in adipocyte progenitors. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	7
125	Gene Mutations and Treatment Outcome in Chronic Lymphocytic Leukemia: Results From the CLL8 Trial. <i>Blood</i> , 2012, 120, 433-433.	0.6	7
126	Cortactin expression: Association with disease progression and survival in oral squamous cell carcinoma. <i>Head and Neck</i> , 2018, 40, 2685-2694.	0.9	6

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127	DNA methylation of chronic lymphocytic leukemia with differential response to chemotherapy. <i>Scientific Data</i> , 2020, 7, 133.	2.4	6
128	Dissecting the Prognostic Significance and Functional Role of Progranulin in Chronic Lymphocytic Leukemia. <i>Cancers</i> , 2019, 11, 822.	1.7	5
129	A synergistic interaction between HDAC and PARP inhibitors in childhood tumors with chromothripsis. <i>International Journal of Cancer</i> , 2022, 151, 590-606.	2.3	5
130	TP53 Alterations in Acute Myeloid Leukemia with Complex Karyotype Correlate with Specific Copy Number Alterations, Monosomal Karyotype, and Dismal Outcome. <i>Blood</i> , 2011, 118, 3558-3558.	0.6	4
131	Correlation of Quantitative Gene Expression by RQ-PCR with Clinical and Biologic Factors in Mantle Cell Lymphoma. <i>Blood</i> , 2004, 104, 696-696.	0.6	4
132	A versatile system to introduce clusters of genomic double-strand breaks in large cell populations. <i>Genes Chromosomes and Cancer</i> , 2021, 60, 303-313.	1.5	3
133	Longitudinal analyses of CLL in mice identify leukemia-related clonal changes including a Myc gain predicting poor outcome in patients. <i>Leukemia</i> , 2021, , .	3.3	3
134	Quantitative Gene Expression Analysis of Surrogate Markers for Genetic Risk Groups and Survival in CLL. <i>Blood</i> , 2008, 112, 4170-4170.	0.6	2
135	Focal structural variants revealed by whole genome sequencing disrupt the histone demethylase KDM4C in B-cell lymphomas. <i>Haematologica</i> , 2023, 108, 543-554.	1.7	2
136	CRISPR-mediated Loss of Function Analysis in Cerebellar Granule Cells Using <i>In Utero</i> Electroporation-based Gene Transfer. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	1
137	Clonal Evolution in Chronic Lymphocytic Leukemia: Acquisition of High-Risk Genomic Aberrations Associated with Unmutated VH, Resistance to Therapy, and Short Survival. <i>Blood</i> , 2006, 108, 296-296.	0.6	1
138	MicroRNA-130a Targets ATG2B, AGO4 and DICER1, Inhibits Autophagy and Induces Cell Death in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2011, 118, 1768-1768.	0.6	1
139	CLL Exosome-Derived Y RNA hY4 Induces TLR7/8-Mediated Inflammation and PD-L1 Expression in Monocytes. <i>Blood</i> , 2016, 128, 3217-3217.	0.6	1
140	Disclosure of Copy Number Alterations in AML with Normal Karyotype Using Matrix-Based Comparative Genomic Hybridization. <i>Blood</i> , 2005, 106, 759-759.	0.6	1
141	NF1 Alterations Are Common In AML with Complex Karyotype and Correlate with Specific Genomic Imbalances. <i>Blood</i> , 2010, 116, 4179-4179.	0.6	1
142	GENE-06. DISTINCT MOLECULAR SUBGROUPS OF TUMORS OF THE PINEAL REGION CORRELATE WITH CLINICAL PARAMETERS AND GENETIC ALTERATIONS. <i>Neuro-Oncology</i> , 2019, 21, ii81-ii82.	0.6	0
143	High Resolution Screening of Genomic Aberrations in Follicular Lymphoma Using Microarray Based Comparative Genomic Hybridization (MATRIX-CGH). <i>Blood</i> , 2004, 104, 2271-2271.	0.6	0
144	Identification of Genomic Imbalances in AML with Complex Karyotype Using Matrix-Based Comparative Genomic Hybridization. <i>Blood</i> , 2004, 104, 3382-3382.	0.6	0

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145	High ZAP-70 and Differential Expression of B-Cell Receptor Related Genes in Chronic Lymphocytic Leukemia with V3-21 Gene Usage.. Blood, 2004, 104, 773-773.	0.6	0
146	Protein Expression Analysis of Chromosome 12 Candidate Genes in Chronic Lymphocytic Leukemia (B-CLL).. Blood, 2004, 104, 4797-4797.	0.6	0
147	A Lymphoid Progenitor Propagates AML in a Mouse Model of CALM/AF10 Positive Leukemia.. Blood, 2005, 106, 101-101.	0.6	0
148	Parallel Analyses Disclose Novel Genomic Imbalances in Acute Myeloid Leukemia with Complex Karyotypes.. Blood, 2005, 106, 2357-2357.	0.6	0
149	Identification of High-Level DNA Amplifications in AML with Complex Karyotype Using Array-CGH.. Blood, 2006, 108, 1914-1914.	0.6	0
150	Uncovering the Epigenetic Pathomechanism in 13q14.. Blood, 2007, 110, 487-487.	0.6	0
151	Epimutation of the Tumor Suppressor Mechanism in 13q14.3 Involves Monoallelic Expression, Non-Coding RNA Genes and Deregulation of NFkB Signalling. Blood, 2008, 112, 783-783.	0.6	0
152	High-Resolution Genomic Profiling (array-CGH) of Childhood T-ALL Identifies Deletions at 6q15-16.1 as a Predictive Marker for Early Treatment Response.. Blood, 2008, 112, 1484-1484.	0.6	0
153	The Toll-Like Receptor-Like Molecule CD180 and Soluble CD14 Transmit Survival Signals in B-Cell Chronic Lymphocytic Leukemia Cells Presumably by Acting As Co-Receptors., Blood, 2011, 118, 3883-3883.	0.6	0
154	Neoadjuvant epirubicin, gemcitabine, and docetaxel for primary breast cancer: Survival and prognostic factors in two consecutive neoadjuvant phase I/II trials.. Journal of Clinical Oncology, 2012, 30, 1096-1096.	0.8	0
155	Lenalidomide Reduces Survival of Chronic Lymphocytic Leukemia Cells in Primary Co-Cultures by Altering the Myeloid Microenvironment. Blood, 2012, 120, 3894-3894.	0.6	0
156	Microenvironmental Factors and The Role Of Tumor Necrosis Factor Receptor Type 1 (TNFR-1) In Chronic Lymphocytic Leukemia. Blood, 2013, 122, 4149-4149.	0.6	0
157	Heterogeneity and Evolution Of DNA Methylation In Chronic Lymphocytic Leukemia. Blood, 2013, 122, 1626-1626.	0.6	0
158	Modelling Single Cell B-Cell Receptor Signaling Reveals Enhanced Activity in Primary CLL Cells Compared to Non-Malignant Cells While Fundamental Network Circuit Topology Remains Stable Even with Novel Therapeutic Inhibitors. Blood, 2019, 134, 4275-4275.	0.6	0
159	Modeling the Bâ€cell receptor signaling on single cell level reveals a stable network circuit topology between nonâ€malignant B cells and chronic lymphocytic leukemia cells and between untreated cells and cells treated with kinase inhibitors. International Journal of Cancer, 2022, , .	2.3	0