Claudia L Kleinman

List of Publications by Year
in descending order

70	3,198	172386 29	175177 52
papers	citations	h-index	g-index

71	71	71	5473
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	<scp>SWI</scp>/<scp>SNF</scp>â€deficient undifferentiated malignancies: where to draw the line^{â€}. Journal of Pathology, 2022, 256, 139-142.	2.1	3
2	Loss of MAT2A compromises methionine metabolism and represents a vulnerability in H3K27M mutant glioma by modulating the epigenome. Nature Cancer, 2022, 3, 629-648.	5.7	16
3	DIPG-19. FOXR2 is an oncogenic driver across pediatric and adult cancers. Neuro-Oncology, 2022, 24, i21-i22.	0.6	0
4	Structural variants shape driver combinations and outcomes in pediatric high-grade glioma. Nature Cancer, 2022, 3, 994-1011.	5.7	20
5	Dual targeting of polyamine synthesis and uptake in diffuse intrinsic pontine gliomas. Nature Communications, 2021, 12, 971.	5.8	71
6	ZFTAâ€“RELA Dictates Oncogenic Transcriptional Programs to Drive Aggressive Supratentorial Ependymoma. Cancer Discovery, 2021, 11, 2200-2215.	7.7	46
7	Glioblastoma cell populations with distinct oncogenic programs release podoplanin as procoagulant extracellular vesicles. Blood Advances, 2021, 5, 1682-1694.	2.5	46
8	Copy number and transcriptome alterations associated with metastatic lesion response to treatment in colorectal cancer. Clinical and Translational Medicine, 2021, 11, e401.	1.7	6
9	Digital Display Precision Predictor: the prototype of a global biomarker model to guide treatments with targeted therapy and predict progression-free survival. Npj Precision Oncology, 2021, 5, 33.	2.3	5
10	STAT1 potentiates oxidative stress revealing a targetable vulnerability that increases phenformin efficacy in breast cancer. Nature Communications, 2021, 12, 3299.	5.8	24
11	Mapping Angiopoietin1 Expression in the Developing and Adult Brain. Developmental Neuroscience, 2021, 43, 321-334.	1.0	2
12	Inferring Copy Number from Triple-Negative Breast Cancer Patient Derived Xenograft scRNAseq Data Using scCNA. Methods in Molecular Biology, 2021, 2381, 285-303.	0.4	2
13	Epigenetically defined therapeutic targeting in H3.3G34R/V high-grade gliomas. Science Translational Medicine, 2021, 13, eabf7860.	5.8	18
14	Histone H3.3 K27M and K36M mutations de-repress transposable elements through perturbation of antagonistic chromatin marks. Molecular Cell, 2021, 81, 4876-4890.e7.	4.5	26
15	EPCO-06. AGE- AND REGION-SPECIFIC MULTI-OMIC CHARACTERIZATION OF H3-K27M MUTANT DIFFUSE MIDLINE GLIOMA. Neuro-Oncology, 2021, 23, vi2-vi2.	0.6	0
16	Epigenomic programming in early fetal brain development. Epigenomics, 2020, 12, 1053-1070.	1.0	9
17	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. Cell, 2020, 183, 1617-1633.e22.	13.5	93
18	Alternative Splicing of a Receptor Intracellular Domain Yields Different Ectodomain Conformations, Enabling Isoform-Selective Functional Ligands. IScience, 2020, 23, 101447.	1.9	2

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19	Differential expression of tissue-restricted antigens among mTEC is associated with distinct autoreactive T cell fates. Nature Communications, 2020, 11, 3734.	5.8	12
20	H3.3 G34W Promotes Growth and Impedes Differentiation of Osteoblast-Like Mesenchymal Progenitors in Giant Cell Tumor of Bone. Cancer Discovery, 2020, 10, 1968-1987.	7.7	40
21	Satellite cell expansion is mediated by P-eIF2Î± dependent Tacc3 translation. Development (Cambridge), 2020, 148, .	1.2	8
22	A non-canonical role for the EDC4 decapping factor in regulating MARF1-mediated mRNA decay. ELife, 2020, 9, .	2.8	11
23	Single-Cell Transcriptomic Profiling of De Novo and Relapsed Acute Myeloid Leukemia Identifies a Leukemic Stemness Program Shared across Diverse Phenotypes. Blood, 2020, 136, 1-1.	0.6	0
24	A C19MC-LIN28A-MYCN Oncogenic Circuit Driven by Hijacked Super-enhancers Is a Distinct Therapeutic Vulnerability in ETMRs: A Lethal Brain Tumor. Cancer Cell, 2019, 36, 51-67.e7.	7.7	69
25	Mutant H3 histones drive human pre-leukemic hematopoietic stem cell expansion and promote leukemic aggressiveness. Nature Communications, 2019, 10, 2891.	5.8	36
26	Identification of genes functionally involved in the detrimental effects of mutant histone H3.3-K27M in Drosophila melanogaster. Neuro-Oncology, 2019, 21, 628-639.	0.6	5
27	The leukodystrophy mutation Polr3b R103H causes homozygote mouse embryonic lethality and impairs RNA polymerase III biogenesis. Molecular Brain, 2019, 12, 59.	1.3	24
28	Pervasive H3K27 Acetylation Leads to ERV Expression and a Therapeutic Vulnerability in H3K27M Gliomas. Cancer Cell, 2019, 35, 782-797.e8.	7.7	143
29	Childhood cerebellar tumours mirror conserved fetal transcriptional programs. Nature, 2019, 572, 67-73.	13.7	293
30	Leukodystrophy-associated POLR3A mutations down-regulate the RNA polymerase III transcript and important regulatory RNA BC200. Journal of Biological Chemistry, 2019, 294, 7445-7459.	1.6	39
31	SWI/SNF-Compromised Cancers Are Susceptible to Bromodomain Inhibitors. Cancer Research, 2019, 79, 2761-2774.	0.4	54
32	H3K27M induces defective chromatin spread of PRC2-mediated repressive H3K27me2/me3 and is essential for glioma tumorigenesis. Nature Communications, 2019, 10, 1262.	5.8	215
33	Tungsten Blocks Murine B Lymphocyte Differentiation and Proliferation Through Downregulation of IL-7 Receptor/Pax5 Signaling. Toxicological Sciences, 2019, 170, 45-56.	1.4	10
34	Stalled developmental programs at the root of pediatric brain tumors. Nature Genetics, 2019, 51, 1702-1713.	9.4	136
35	PRMT5 is essential for B cell development and germinal center dynamics. Nature Communications, 2019, 10, 22.	5.8	61
36	Single Cell Transcriptomic Analysis of the Histone H3 K27M Mutation in Pre-Leukemic Hematopoietic Stem Cells. Blood, 2019, 134, 3773-3773.	0.6	0

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37	Integration of Distinct ShcA Signaling Complexes Promotes Breast Tumor Growth and Tyrosine Kinase Inhibitor Resistance. Molecular Cancer Research, 2018, 16, 894-908.	1.5	6
38	GENE-21. A COMMON FETAL DEVELOPMENTAL ORIGIN FOR PFA EPENDYMOMA, PFB EPENDYMOMA, AND CEREBELLAR PILOCYTIC ASTROCYTOMAS?. Neuro-Oncology, 2018, 20, vi107-vi107.	0.6	0
39	PDTM-21. MATCHING OF SINGLE CELL TRANSCRIPTOMICS FROM CEREBELLAR DEVELOPMENT IDENTIFIES PUTATIVE SUBGROUP SPECIFIC CELLS OF ORIGIN FOR MEDULLOBLASTOMA. Neuro-Oncology, 2018, 20, vi208-vi208.	0.6	1
40	TRPV4 and KRAS and FGFR1 gain-of-function mutations drive giant cell lesions of the jaw. Nature Communications, 2018, 9, 4572.	5.8	58
41	DIPG-06. IDENTIFICATION OF GENES FUNCTIONALLY INVOLVED IN THE DETRIMENTAL EFFECTS OF MUTANT HISTONE K27M-H3.3 USING DROSOPHILA MELANOGASTER. Neuro-Oncology, 2018, 20, i50-i50.	0.6	0
42	Loss of PRMT5 Promotes PDGFRÎ± Degradation during Oligodendrocyte Differentiation and Myelination. Developmental Cell, 2018, 46, 426-440.e5.	3.1	40
43	Mutations in Human Histone H3 are Pre-Leukemic Events and Promote Hematopoietic Stem Cell Expansion and Leukemic Aggressiveness. Experimental Hematology, 2018, 64, S55-S56.	0.2	0
44	chromswitch: a flexible method to detect chromatin state switches. Bioinformatics, 2018, 34, 2286-2288.	1.8	10
45	The Shc1 adaptor simultaneously balances Stat1 and Stat3 activity to promote breast cancer immune suppression. Nature Communications, 2017, 8, 14638.	5.8	52
46	ChIP-seq analysis of the LuxR-type regulator VjbR reveals novel insights into the Brucella virulence gene expression network. Nucleic Acids Research, 2017, 45, 5757-5769.	6.5	30
47	Cell Line Phenotypic Enrichement based on Migration and Morphology. Biophysical Journal, 2017, 112, 134a.	0.2	0
48	Gene networks show associations with seed region connectivity. Human Brain Mapping, 2017, 38, 3126-3140.	1.9	32
49	A pseudouridine synthase module is essential for mitochondrial protein synthesis and cell viability. EMBO Reports, 2017, 18, 28-38.	2.0	120
50	H3.3K27M Cooperates with Trp53 Loss and PDGFRA Gain in Mouse Embryonic Neural Progenitor Cells to Induce Invasive High-Grade Gliomas. Cancer Cell, 2017, 32, 684-700.e9.	7.7	192
51	A Targetable EGFR-Dependent Tumor-Initiating Program in Breast Cancer. Cell Reports, 2017, 21, 1140-1149.	2.9	70
52	Transcriptome profiling of mouse brains with qkI-deficient oligodendrocytes reveals major alternative splicing defects including self-splicing. Scientific Reports, 2017, 7, 7554.	1.6	26
53	Absence of neurological abnormalities in mice homozygous for the Polr3a G672E hypomyelinating leukodystrophy mutation. Molecular Brain, 2017, 10, 13.	1.3	33
54	Characterizing temporal genomic heterogeneity in pediatric high-grade gliomas. Acta Neuropathologica Communications, 2017, 5, 78.	2.4	48

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55	Transcriptome profiling in preadipocytes identifies long noncoding RNAs as Sam68 targets. Oncotarget, 2017, 8, 81994-82005.	0.8	13
56	Live single-cell laser tag. Nature Communications, 2016, 7, 11636.	5.8	22
57	NPM and BRG1 Mediate Transcriptional Resistance to Retinoic Acid in Acute Promyelocytic Leukemia. Cell Reports, 2016, 14, 2938-2949.	2.9	13
58	Painting cells with light. Biochemist, 2016, 38, 8-11.	0.2	3
59	Macrocyclic lactone resistance in Dirofilaria immitis: Failure of heartworm preventives and investigation of genetic markers for resistance. Veterinary Parasitology, 2015, 210, 167-178.	0.7	122
60	HIV-1 Infection Causes a Down-Regulation of Genes Involved in Ribosome Biogenesis. PLoS ONE, 2014, 9, e113908.	1.1	29
61	Fusion of TTYH1 with the C19MC microRNA cluster drives expression of a brain-specific DNMT3B isoform in the embryonal brain tumor ETMR. Nature Genetics, 2014, 46, 39-44.	9.4	167
62	Polyadenylation-Dependent Control of Long Noncoding RNA Expression by the Poly(A)-Binding Protein Nuclear 1. PLoS Genetics, 2012, 8, e1003078.	1.5	140
63	Comment on â€œWidespread RNA and DNA Sequence Differences in the Human Transcriptomeâ€• Science, 2012, 335, 1302-1302.	6.0	139
64	RNA editing of protein sequences: A rare event in human transcriptomes. Rna, 2012, 18, 1586-1596.	1.6	42
65	RNA sequencing reveals the role of splicing polymorphisms in regulating human gene expression. Genome Research, 2011, 21, 545-554.	2.4	107
66	Statistical Potentials for Improved Structurally Constrained Evolutionary Models. Molecular Biology and Evolution, 2010, 27, 1546-1560.	3.5	49
67	Computational Methods for Evaluating Phylogenetic Models of Coding Sequence Evolution with Dependence between Codons. Molecular Biology and Evolution, 2009, 26, 1663-1676.	3.5	45
68	Fast optimization of statistical potentials for structurally constrained phylogenetic models. BMC Evolutionary Biology, 2009, 9, 227.	3.2	2
69	Consolidation of the Thioredoxin Fold by Peptide Recognition:â€‰ Interaction between E. coli Thioredoxin Fragments 1â^'93 and 94â^'108. Biochemistry, 2007, 46, 5148-5159.	1.2	13
70	A maximum likelihood framework for protein design. BMC Bioinformatics, 2006, 7, 326.	1.2	28